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(71) Applicant *(for all designated States except US)*: RIBOZYME PHARMACEUTICALS, INC. [US/US]; 2950 Wilderness Place, Boulder, CO 80301-5411 (US).

(72) Inventors; and
(75) Inventors/Applicants *(for US only)*: PAVCO, Pamela, A. [US/US]; 705 Barberry Circle, Lafayette, CO 80026 (US). ROBERTS, Elisabeth [US/US]; 10025 Eliot Circle, Federal Heights, CO 80221 (US). JARVIS, Thale [US/US]; 3720 Smuggler Place, Boulder, CO 80303 (US). COESHOTT, Claire [GB/US]; 875 S. Josephine Street, Denver, CO 80209 (US). MCSWIGGEN, James, A. [US/US]; 4866 Franklin Drive, Boulder, CO 80301 (US).

(74) Agent: WARBURG, Richard, J.; Lyon & Lyon LLP, Suite 4700, 633 West Fifth Street, Los Angeles, CA 90071-2066 (US).

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(57) Abstract

Nucleic acid molecule which modulates the synthesis, expression and/or stability of an mRNA encoding for angiogenic factors selected from aryl hydrocarbon nuclear transport (ARNT), intergrin subunit beta 3 (β3), integrin subunit alpha 6 (α6) and tie – 2RNA. This invention further provides a treatment for indications related to angiogenesis using the nucleic acid molecules.

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DESCRIPTION

Method And Reagents For The Treatment Of Diseases Or Conditions Related To Molecules Involved In Angiogenic Responses

Background Of The Invention

This invention relates to methods and reagents for the treatment of diseases or conditions relating to the levels of expression of angiogenic factors and receptors involved in the regulation of angiogenesis.

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

The formation of blood vessels in vertebrates can be described in two embyronic stages. During the first stage, known as vasculogenesis, yolk sac splanchnopleuric mesenchyme differentiates into vascular progenitor cells and then to blood island aggregates which are primitive blood cells surrounded by fused endothelial progenitors (angioblasts). These blood islands then fuse and go on to form a vascular plexus which supplies nutrients to the embryo (Merenmies *et al.*, 1997, *Gell Growth & Development* 8, 3-10). The next vascular developmental step is known as angiogenesis. From the vessels formed during vasculogenesis, new blood vessels sprout, elongate and develop into capillary loop formations of endothelial cells. It is a highly complex event involving local basement membrane disruption, endothelial cell proliferation, migration and microvessel morphogenesis (Rak *et al.*, 1995, *Anti-Cancer Drugs* 6, 3-18). Organs such as the brain and kidney are vascularized through the angiogenic process (Dumont *et al.*, 1995, *Developmental Dynamics* 203, 80-92).

Angiogenesis has been described to occur through two mechanisms, vascular sprouting and intussusception. Intussusception of pre-existing vessels occur after proliferation of endothelial cells producing a wide lumen. Through the utilization of transcapillary pillars or posts of extracellular matrix, the lumen is split to form two vessels (Risau, 1997, *Nature* 386, 671-674). Sprouting angiogenesis also originates from pre-existing blood vessels and consists of new blood vessels sprouting, elongating and developing into capillary loop formations of endothelial cells. It is a highly complex event involving disruption of extracellular matrix, endothelial cell proliferation, chemotaxic migration and microvessel morphogenesis (Rak, *supra*). Many factors regulating positive and negative control of angiogenesis have been reported demonstrating the sophistication of this process. An example of an angiogenic factor is Vascular Endothelial Growth Factor receptor (VEGFr) which has been shown to be specific to endothelial cells and is discussed in Pavco *et al.*, Int. PCT Pub. No. WO 97/15662.

Unlike vasculogenesis, angiogenesis not only occurs in embyronic development, but can also occur throughout the lifespan of the organism during such events as wound healing, bone repair, inflammation, and female menstral cycles. Local delivery of oxygen and nutrients and the removal of waste requires a complex system of blood vessels which has the ability to adapt as the tissue requirements changes. Involvement of a large number of positive and negative factors in angiogenic regulation demonstrates the complexity of this process. When the balance between upregulating factors and downregulating factors is disrupted in favor of increased angiogenesis, disease states have been known to occur.

Many factors have been identified which contribute to increased angiogenesis including:

1) ryl Hydrocarbon Nuclear Transporter (ARNT): ARNT (also known as HIF-1β) forms heterodimers with several factors including HIF-α(Maxwell *et al.*, 1997, *Proc. Natl. Acad. Sci. USA* 94, 8104-8109). When HIF-α and ARNT complex together, they form a complex called HIF-1. HIF -1 is believed to be regulate genes involved in the response to oxygen deprivation. ARNT -/- embryonic stem cells fail to induce VEGF expression in response to hypoxia. ARNT -/- mice are not viable beyond embryonic day 10.5. Like VEGF knockout mice, these embryos show defective angiogenesis of the yolk sac (Maltepe *et al.*, 1997, *Nature* 386, 403-407).

Hepatoma cells containing an ARNT mutation that is functionally deficient in dimerizing with HIF-1α shows greatly reduced VEGF expression in response to hypoxia compared to normal cells (Wood *et al.*, 1996, *J. Biol. Chem.* 271, 15117-15123). Tumor xenografts derived from these cells show reduced vascularity and approximately 2-fold reduced tumor growth rates (Maxwell *et al.*, 1997, *supra*).

2) Tie-2: Tie-2 (also known as Tek), is a tyrosine kinase protein receptor which consists of 1122 amino acids and is produced in endothelial (Merenmies *et al.*, 1997, *Cell Growth & Differentiation* 8, 3-10) as well as early hematopoeitic cells (Maisonpierree *et al.*, 1993, *Oncogene* 8, 1631-1637). Tie-2 expression has been demonstrated in mice, rats and humans. The human gene is thought to be located on chromosome 9p21 (Dumont *et al.*, 1994, *Genes & Development* 8, 1897-1909). Tie-2 homozygous mutant endothelial cells were examined using anti-PECAM monoclonal antibody (Sato *et al.*, 1997, *Nature* 376, 70-74). All of the homozygous mutants were dead within 10.5 days with obvious deformities in the head and heart present by day 9.5. In addition, large vessels were indistinguishable from small vessels and no capillary

sprouts were seen in the brain. These observations suggested that Tie-2 plays an important role in angiogenesis rather than vasculogenesis. The earlier effects of Tie-2 mutant compared to the Tie-1 mutant indicates separate roles for the two RTK's in angiogenesis.

Ligands to Tie-2 have been discovered and named angiopoietin 1 and 2 (ang1 and 2) (Davis, S. *et al.*, 1993, *Cell* **87**, 1161; Maisonpierre, P.C. *et al.*,1997, *Science*, **277**, 55-60). Both factors consist of an NH_2-terminal coiled-coil domain as well as a COOH-terminal fibrinogen-like domain. Ang1 binds to Tie-2/Tek but not Tie-1 and stimulates angiogenesis through autophosphorylation. Ang2 is a 496 amino acid polypeptide whose human and mouse homologs are 85% identical. Autophosphorylation caused by Ang1 binding to the Tie-2 receptor can be blocked with the addition of Ang2. The Tie-2 receptor is unusual in that it utilizes both positive and negative control mechanisms.

3) Integrins: Integrins are a family of cell adhesion and migration mediating proteins that are comprised of at least 15 alpha and 8 beta subunits that are expressed as a number of different αβ non-covalently bound heterodimers on cell surfaces (Varner, 1997, *Regulation of Angiogenesis*, ed I.D Goldberg & E.M. Rosen, 361-390; Brooks, 1996, *Eur J Cancer* 14, 2423-2429). Each combination of integrin subunits is thought to have angiogenic capabilities, for example $\alpha_6\beta_1$ has been implicated in capillary tube formation Additionally, distinct integrins allow for the attachment to many different extracellular matrix (ECM) components including fibronectin, vitronectin, laminin and collagen (Stromblad & Cheresh, 1996, Chemistry & Biochemistry 3, 881-885). Integrin production has been shown to be induced by a number a stimuli including intracellular pH increases, calcium concentration, inositol lipid synthesis, tyrosine

phosphorylation of a focal contact associated tyrosine kinase, and activation of p34/cdc2 and cyclin A (Varner & Cheresh, 1996, *Curr Op in Cell Biol* 8,724-730).

$\alpha_v\beta_3$ a 160kDa protein is the most well characterized molecule of the integrin family and is believed to play a large role in angiogenesis (Varner, 1997, *supra*). $\alpha_v\beta_3$ binds the largest number of ECM components of all known heterodimers indicating any cell with these molecules on the cell surface could adhere to or migrate on almost any of the ECM components (Varner, 1997, *supra*). When vascular endothelial cells are in their quiescent state very little $\alpha_v\beta_3$ is expressed, but is highly upregulated in several pathological conditions including neoplasms. Antagonists to $\alpha_v\beta_3$ can inhibit angiogenesis in the chick chorioallentoic membrane (CAM) model and in SCID mice and even reduce the tumor volume. When antibodies are administered for $A_v\beta_3$, apoptosis is observed in the proliferating vascular vessels. This has led to suggestions that $\alpha_v\beta_3$ provides a survival signal for vascular cells allowing for continued proliferation (Stromblad & Cheresh, 1996, *supra*; Varner, 1997 *supra*).

Other angiogenic targets are included and their characteristics are defined in the following references, all of which are incorporated herein by reference in their entirety: Methionine Aminopeptidase: (Arfin *et al*., 1995, *PNAS* 92, 7714-7718 (Genbank Accession No. U29607) ; Sin, N. *et.al*., 1997, *PNAS* 94, 6099-6103; Griffith *et al*., 1997, *Chem Biol*. 4(6), 461-471); Transcription factor Ets-1: (Iwasaka, C. *et al*. 1996.*J. Cell Physiol*. 169, 522-531; Chen, Z. *et al*. ,1997, *Cancer Res*. 57, 2013-2019; Hultgardh-Nilsson A, *et al*., 1996, *Circ Res*. 78(4), 589-595; Reddy *et al*., 1988, *Oncogene Res*. 3 (3), 239-246 (Genbank accession No. X14798)); Platelet-derived endothelial cell growth factor and its receptor (PD-ECGF & PD-ECGFr): (Furukawa, T. *et al*., 1992, *Nature* 356, 668;

Moghaddam, A. *et al.*, 1995, *Proc. Natl. Acad. Sci.*; Clark, R.A.F. *et al.* ,1996, *Am J. Pathol.* 148, 1407; Hoshina, T.M., *et al.*, 1995, *Int. J. Cancer* 64, 79-82; Nakanishi, A.K., *et al.*, 1992, *J. Biol. Chem* 267, 20311-20316; Finnis *et al.*, unpublished (Genbank accession No. M63193); Transforming Growth factors (TGFs): (Schreiber *et al.*, 1986, *Science* 232, 1250; Maione, T.E. and Sharpe, R.J.,1990, *Trends Pharm. Sci.*, 11, 457-461; Noma *et al.*, 1991,*Growth Factors* 4 (4), 247-255; Sukurai (unpublished) (Genbank accession No. AB009356);Transforming growth factor receptor: (Miyazono, K.,1996, *Nippon Yakurigaku Zasshu* 107, 133-140; Mahooti-Brooks. *et al.*,1996, *J. Clin. Invest.* 97, 1436-1446; Lopez-Casillas *et al.*, 1991, Cell 67 (4), 797-805; Lopez-Casillas *et al.*, 1991, *Cell* 67 (4), 785-795 (Genbank Accession No. L07594); Angiogenin: (Fett *et al.*, 1985, *Biochemistry* 24, 5480-5486; Bicknell & Vallee, 1988, *PNAS* 85, 5961-5965; Vallee & Riordan,1988, *Adv. Exp. Med. Biol* 234, 41-53; Shapiro & Vallee,1987, *PNAS* 84, 2238-2241; Shapiro *et al.*,1986, *Biochemistry* 25, 3527-3532; Olson *et al.*, 1994, *Cancer Res.* 54, 4576-4579; Kurachi *et al.*, 1985, *Biochemistry* 24, 5494-5499; Kurachi *et al.*, 1985, Biochemistry 24 (20), 5494-5499(Genbank Accession No. M11567)); Tumor necrosis factor receptor: (Naismith *et al.*,1995,. *J. Inflamm* 47, 1-7; Loetscher *et al.*, 1990, *Cell* 61, 351-359; Himmler *et al.*, 1990, *DNA Cell Biol.* 9, 705-715 (Genbank Accession No. M63121 M75861); Endothelial cell stimulating angiogenesis factor (ESAF): (Brown & Weiss,1988,. *Ann. Rheum. Dis.*, 47, 881-885); Interleukin-8 (IL-8): (Elner *et al.*, 1991, , *Am J. Pathol.* 139, 977-988; *Strieter et al.*,1992, *Am. J. Pathol.* 141, 1279-1284; Mukaida *et al.*, 1989, *J. Immunol.* 143 (4), 1366-1371(Genbank Accession No. M28130)); Angiopoietin 1: (Davis, S. *et al.*,1996, *Cell* 87, 1161; Iwama, A. *et al.*,1993, *Biochem Biophys. Res. Commun.* 195, 301; Dumont, D.J. *et al.*,1995, *Genes Dev* 8, 1897; Sato, T.N. *et al.*,1995, *Nature* 376, 70; Suri, C. *et al.*, 1996) *Cell* 87, 1171(Genbank Accession No. U83508)); Angiopoietin 2: (Maisonpierre, *et al.*,1997, *Science*, 277, 55-60; Hanahan, 1997, *Science* 277, 48-50; Genbank Accession No. AF004327 (unpublished));Insulin-like growth factor (IGF-1): (Warren, R.S. *et al.*,1996, *J. Biol. Chem.* 271, 29483-29488; Grant *et.al.*, 1993,*Diabetologia* 36, 282-291; Nicosia *et al.*, 1994,*Am. J. Pathol.* 145, 1023-1029; Steenbergh *et al.*, *Biochem. Biophys. Res. Commun.* 175, 507-514 (Genbank Accession: X57025); Insulin-like growth factor receptor (IGF-1r): (Ullrich *et al.*, 1986, *EMBO* J. 5, 2503-2512 (Genbank Accession No. X04434 M24599); B61: (Pandey, A. *et al.*, 1995, *Science* 268, 567-569; Holzman *et al.*, 1990, *Mol. Cell. Biol.* 10, 5830-5838 (Genbank Accession No. M57730 M37476); B61 receptor (Eck): (Pandey, A. *et al.*, 1995, *Science* 268, 567-569; Lindberg & Hunter, 1990, Mol. Cell. Biol. 10 (12), 6316-6324 (Genbank Accession No. M59371 M36395); Protein kinase C: (Morris *et al.*, 1988, *Cell Physiol.* 23, C318-C322; Oikawa, T. *et al.*, 1992, *J. Antibiot.* 45, 1155-1160; Finkenzeller. *et al.*, 1992, *Cancer Res.* 52, 4821-4823; Kubo *et al.*, 1987, FEBS Lett. 223 (1), 138-142 (Genbank Accession No. X06318 M27545);); SH2 domain (Guo, D. *et al.*, 1995, *J. Biol. Chem* 270, 6729-6733)

a. Phospholipase c-g:(Guo, D. at al., 1995, *J. Biol. Chem* 270, 6729-6733; Rhee, S.G. et al. (1992) *J. Biol. Chem* 267, 12393-12396; Burgess et al., 1990, Mol. Cell. Biol. 10, 4770-4777 (Genbank Accession No. M34667))

b. Phosphatidylinositol 3 kinase (PI-3): (Downs, C.P. *et al.*,1991, *Cell Signalling* **3**, 501-513; Genbank accession No. Z29090; Genbank accession No. Z46973)

c. Ras GTPase activating protein (GAP): (Trahey, M. *et al.*,1987, *Science* **238**, 542-545; Guo, D. *et al.*, 1995, *J. Biol. Chem* **270**, 6729-6733; Trahey *et al.*, 1988, Science 242, 1697-1700 (Genbank accession No. M23612))

d. Oncogene adaptor protein Nck:(Park & Rhee, 1992, *Mol. Cell. Biol.* **12**, 5816-5823; Johnson, 1990, *Nucleic Acids Res.* 18 (4), 1048 (Genbank accession No. X17576)); Granulocyte Colony-Stimulating Factor: (Devlin *et al.*, 1987, *J. Leukoc. Biol.* 41, 302-306 (Genbank accession No. M17706)); Hepatocyte growth factor: (Miyazawa *et al.*, 1991, *Eur. J. Biochem.* 197 (1), 15-22 (Genbank accession No. X57574); Proliferin: (Groskopf *et al.*, 1997, *Endocrinology* 138(7), 2835-2840; Jackson D, *et al.*, 1994, *Science.* 266(5190), 1581-1584; Volpert *et al.*, 1996 , *Endocrinology* 137(9): 3871-3876); Placental growth factor: (Kodama et al., 1997, *Eur J Gynaecol Oncol.*; 18(6), 508-510; Ziche *et al.*, 1997, *Lab Invest.* 76(4), 517-531; Relf *et al.*, 1997, *Cancer Res.* 57(5), 963-969; Genbank accession No. Y09268)

Summary Of The Invention

The invention features the use of enzymatic nucleic acid molecules and methods for their use to down regulate or inhibit the expression of angiogenic factors. Specifically, the enzymatic nucleic acids of the present invention are used as a treatment for indications relating to angiogenesis including but not limited to cancer, age related macular degeneration (ARMD), diabetic retinopathy, inflammation, arthritis, psoriasis and the like.

In a preferred embodiment, the invention features enzymatic nucleic acid molecules that cleave RNAs encoding angiogenic selected from a group comprising: Tie-2, integrin subunit β3, integrin subunit α6, and aryl hydrocarbon nuclear transporter (ARNT).

By "inhibit" it is meant that the activity of the cleaved RNA 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 inactive RNA molecule that is able to bind to the same site on the mRNA, but is unable to cleave that RNA.

By "angiogenic factors" is meant a peptide molecule which is involved in a process or pathway necessary for the formation of novel blood vessels.

In another preferred embodiment, the invention features the use of enzymatic nucleic acids that cleave the RNAs encoded by angiogenic factors selected from a group comprising: Methionine Aminopeptidase; Ets-1 Transcription factor; integrins; platelet derived endothelial cell growth factor (PD-ECGF); PD-ECGF receptor; Transforming Growth factors (TGFs); Transforming growth factor receptor; Angiogenin; Endothelial cell stimulating angiogenesis factor (ESAF); Interleukin-8 (IL-8); Angiopoietin 1 and 2; TIE-1; insulin-like growth factor (IGF-1); insulin-like growth factor receptor (IGF-1r); B61; B61 receptor (Eck); Protein kinase C; an SH2 domain (*e.g.* Phospholipase c-g, Phosphatidylinositol 3 kinase (PI-3), Ras GTPase activating protein (GAP); Oncogene adaptor protein Nck; Granulocyte Colony-Stimulating Factor; Hepatocyte growth factor; Proliferin; and Placental growth factor.

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 meant to be limiting 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 have 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. 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 12-100 nucleotides; more specifically 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).

By DNAzyme is meant, an enzymatic nucleic acid molecule lacking a 2′-OH group.

In one of the preferred embodiments, 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 or DNAzymes. 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; of the hepatitis d virus motif is described by Perrotta and Been, 1992 *Biochemistry* 31, 16; of the RNaseP 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. 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).

By "equivalent" RNA to Tie-2, integrin subunit β3, integrin subunit α6, or ARNT is meant to include those naturally occurring RNA molecules having homology (partial or complete) to Tie-2, integrin subunit β3, integrin subunit α6, or ARNT or encoding for proteins with similar function as Tie-2, integrin subunit β3, integrin subunit α6, or ARNT 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 "homology" is meant the nucleotide sequence of two or more nucleic acid molecules is partially or completely identical.

By "complementarity" is meant a nucleic acid molecules that can form hydrogen bond(s) with another nucleic acid sequence by either traditional Watson-Crick or other non-traditional types (for example, Hoogsteen type) of base-paired interactions.

In a preferred embodiment the invention provides a method for producing a class of enzymatic cleaving agents which exhibit a high degree of specificity for the RNA of a desired target. The enzymatic nucleic acid molecule is preferably targeted to a highly conserved sequence region of a target RNAs encoding Tie-2, integrin subunit β3, integrin subunit α6, or ARNT proteins such that specific treatment of a disease or condition can be provided with either one or several enzymatic nucleic acids. Such enzymatic nucleic acid molecules can be delivered exogenously to specific cells as required. Alternatively, the ribozymes can be expressed from DNA/RNA vectors that are delivered to specific cells.

By "highly conserved sequence region" is meant a nucleotide sequence of one or more regions in a nucleic acid molecule does not vary significantly from one generation to the other or from one biological system to the other.

Such ribozymes are useful for the prevention of the diseases and conditions including cancer, diabetic retinopathy, macular degeneration, neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca vulgaris, angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome and any other diseases or conditions that are related to the levels of Tie-2, integrin subunit β3, integrin subunit α6, or ARNT activity in a cell or tissue.

By "related" is meant that the inhibition of Tie-2, integrin subunit β3, integrin subunit α6, and/or ARNT RNAs and thus reduction in the level respective protein activity will relieve to some extent the symptoms of the disease or condition.

In preferred embodiments, the ribozymes have binding arms which are complementary to the target sequences in **Tables III-X.** Examples of such ribozymes are also shown in **Tables III-X.** Tables III and IV display target sequences and ribozymes for ARNT, Tables V and VI display target sequences and ribozymes for Tie-2, tables VII and VIII display target sequences and ribozymes for integrin subunit alpha 6, and tables IX and X display target sequences and ribozymes for integrin subunit beta 3. Examples of such ribozymes consist essentially of sequences defined in these Tables.

By "consists essentially of" is meant that the active ribozyme contains an enzymatic center or core equivalent to those in the examples, and binding arms able to bind mRNA such that cleavage at the target site occurs. Other sequences may be present which do not interfere with such cleavage.

Thus, in a first aspect, the invention features ribozymes that inhibit gene expression and/or cell proliferation. These chemically or enzymatically synthesized RNA molecules contain substrate binding domains that bind to accessible regions of their target mRNAs. The RNA molecules also contain domains that catalyze the cleavage of RNA. The RNA molecules are preferably ribozymes of the hammerhead or hairpin motif. Alternatively, the ribozymes are DNAzymes. Upon binding, the ribozymes cleave the target mRNAs, preventing translation and protein accumulation. In the absence of the expression of the target gene, cell proliferation is inhibited. Chemically synthesized RNA molecules also include RNA molecules assembled together from various fragments of RNA using a chemical or an enzymatic ligation method.

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 Tie-2, integrin subunit β3, integrin subunit α6, or ARNT expression (e.g. tumor cells, endothelial cells) in an appropriate liposomal vehicle.

In another aspect of the invention, ribozymes that cleave target molecules and inhibit Tie-2, integrin subunit β3, integrin subunit α6, or ARNT 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.

These ribozymes, individually, or in combination or in conjunction with other drugs, can be used to treat diseases or conditions discussed above. For example, to treat a disease or condition associated with Tie-2, integrin subunit β3, integrin subunit α6, or ARNT, the patient may be treated, or other appropriate cells may be treated, as is evident to those skilled in the art.

In a further embodiment, the described ribozymes can be used in combination with other known treatments to treat conditions or diseases discussed above. For example, the described ribozymes could be used in combination with one or more known therapeutic agents to treat cancer.

In preferred embodiments, the ribozymes have binding arms which are complementary to the sequences in the tables, shown as **Seq. I.D. Nos. 394-786, 849-910, 1612-2312, 2381-2448, 3588-4726, 4821-4914, 5702-6488, and 6569-6648.** Examples of such ribozymes are shown as **Seq. I.D. Nos.1-393, 787-848, 911-1611, 2313-2380, 2449-3587,**

4727-4820. 4915-5701, and 6489-6568. Other sequences may be present which do not interfere with such cleavage.

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 a diagrammatic representation of a hammerhead ribozyme targeted against Tie-2 at position 1037.

Enzymatic Nucleic Acid Molecules

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 is advantageous over other technologies, since 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.

Ribozymes that cleave the specified sites in Tie-2, integrin subunit β3, integrin subunit α6, and aryl hydrocarbon nuclear transporter (ARNT) mRNAs represent a novel therapeutic approach to treat cancer, macular degeneration, diabetic retinopathy, inflammation, psoriasis and other diseases. Applicant indicates that ribozymes are able to inhibit the activity of Tie-2; integrin subunit β3; integrin subunit α6; and aryl hydrocarbon nuclear transporter (ARNT) and that the catalytic activity of the ribozymes is required for their inhibitory effect. Those of ordinary skill in the art will find that it is clear from the examples described that other ribozymes that cleave Tie-2, integrin subunit β3, integrin subunit α6, and aryl hydrocarbon nuclear transporter (ARNT) mRNAs may be readily designed and are within the scope of the invention.

Target sites

Targets for useful ribozymes can be determined as disclosed in Draper *et al.,* WO 93/23569; Sullivan *et al.,* WO 93/23057; Thompson *et al.,* WO 94/02595; Draper *et al.,* WO 95/04818; McSwiggen *et al.,* US Patent No. 5,525,468 and hereby incorporated by reference herein in totality. Rather than repeat the guidance provided in those documents here, below are provided specific examples of such methods, not limiting to those in the art. Ribozymes to such targets are designed as described in those applications and synthesized to be tested *in vitro* and *in vivo,* as also described. Such ribozymes can also be optimized and delivered as described therein.

The sequence of human Tie-2, integrin subunit β3, integrin subunit α6, and aryl hydrocarbon nuclear transporter (ARNT) mRNAs were screened for optimal ribozyme target sites using a computer folding algorithm. Hammerhead or hairpin ribozyme cleavage sites were identified. These sites are shown in Tables III-X (All sequences are 5′ to 3′ in the tables) The nucleotide base position is noted in the Tables as that site to be cleaved by the designated type of ribozyme. The nucleotide base position is noted in the tables as that site to be cleaved by the designated type of ribozyme.

Hammerhead or hairpin ribozymes were designed that could bind and were individually analyzed by computer folding (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 are eliminated from consideration. 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. Ribozymes of the hammerhead or hairpin motif were designed to anneal to various sites in the mRNA message. The binding arms are complementary to the target site sequences described above.

Ribozyme Synthesis

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 (*e.g.*, antisense oligonucleotides, hammerhead or the hairpin ribozymes) are used for exogenous delivery. The simple structure of these molecules increases the ability of the nucleic acid to invade targeted regions of the mRNA structure. However, these nucleic acid molecules can also 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; Sullenger 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). 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 WO93/23569, and Sullivan *et al.*, PCT WO94/02595, both hereby incorporated in their totality by reference herein; 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).

The ribozymes were chemically synthesized. The method of synthesis used follows 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.*, 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 synthesis were conducted on a 394 Applied Biosystems, Inc. synthesizer using a modified 2.5 µmol scale protocol with a 5 min coupling step for alkylsilyl protected nucleotides and 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. A 6.5-fold excess (163 µL of 0.1 M = 16.3 µmol) of phosphoramidite and a 24-fold excess of *S*-ethyl tetrazole (238 µL of 0.25 M = 59.5 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 2% 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 (Millipore). B & J Synthesis Grade acetonitrile was used directly from the reagent bottle. *S*-Ethyl tetrazole solution (0.25 M in acetonitrile) was made up from the solid obtained from American International Chemical, Inc.

Deprotection of the RNA was performed as follows. The polymer-bound oligoribonucleotide, trityl-off, was transferred from the synthesis column to a 4mL glass screw top vial and suspended in a solution of methylamine (MA) 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:H_2O/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 (250 µL of a solution of 1.5mL *N*-methylpyrrolidinone, 750 µL TEA and 1.0 mL TEA•3HF to provide a 1.4M HF concentration) and heated to 65°C for 1.5 h. The resulting, fully deprotected, oligomer was quenched with 50 mM TEAB (9 mL) prior to anion exchange desalting.

For anion exchange desalting of the deprotected oligomer, the TEAB solution was loaded onto a Qiagen 500® anion exchange cartridge (Qiagen Inc.) that was prewashed with 50 mM TEAB (10 mL). After washing the loaded cartridge with 50 mM TEAB (10 mL), the RNA was eluted with 2 M TEAB (10 mL) and dried down to a white powder.

Inactive hammerhead ribozymes 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).

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 are modified to enhance stability and/or enhance catalytic activity by modification with nuclease resistant groups, for example, 2'-amino, 2'-*C*-allyl, 2'-flouro, 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* 6, 14090).

Ribozymes were purified by gel electrophoresis using general methods or are purified by high pressure liquid chromatography (HPLC; See Stinchcomb *et al.*, International PCT Publication No. WO 95/23225, the totality of which is hereby incorporated herein by reference) and are resuspended in water.

The sequences of the ribozymes that are chemically synthesized, useful in this study, are shown in Tables III-X. Those in the art will recognize that these sequences are representative only of many more such sequences where the enzymatic portion of the ribozyme (all but the binding arms) is altered to affect activity. For example, stem-loop II sequence of hammerhead ribozymes can be altered (substitution, deletion, and/or insertion) to contain any sequences provided a minimum of two base-paired stem structure can form. Similarly, stem-loop IV sequence of hairpin ribozymes, can be altered (substitution, deletion, and/or insertion) to contain any sequence, provided a minimum of two base-paired stem structure can form. Preferably, no more than 200 bases are inserted at these locations. The sequences listed in Tables III-X may be formed of ribonucleotides or other nucleotides or non-nucleotides. Such ribozymes (which have enzymatic activity) are equivalent to the ribozymes described specifically in the Tables.

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'-flouro, 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 "nucleotide" as used herein is as recognized in the art to include natural bases (standard), and modified bases well known in the art. Such bases are generally located at the 1' position of a sugar moiety. Nucleotide generally comprise a base, sugar and a phosphate group. The nucleotides can be unmodified or modified at the sugar, phosphate and/or base moiety, (also referred to interchangeably as nucleotide analogs, modified nucleotides, non-natural nucleotides, non-standard nucleotides and other; see for example, Usman and McSwiggen, *supra;* Eckstein *et al.,* International PCT Publication No. WO 92/07065; Usman *et al.,* International PCT Publication No. WO 93/15187; all hereby incorporated by reference herein). There are several examples of modified nucleic acid bases known in the art and has recently been summarized by Limbach *et al.,* 1994, *Nucleic Acids Res.* 22, 2183. Some of the non-limiting examples of base modifications that can be introduced into enzymatic nucleic acids without significantly effecting their catalytic activity include, inosine, purine, pyridin-4-one, pyridin-2-one, phenyl, pseudouracil, 2, 4, 6-trimethoxy benzene, 3-methyl uracil, dihydrouridine, naphthyl, aminophenyl, 5-alkylcytidines (*e.g.*, 5-methylcytidine), 5-alkyluridines (*e.g.*, ribothymidine), 5-halouridine (*e.g.*, 5-bromouridine) or 6-azapyrimidines or 6-alkylpyrimidines (*e.g.* 6-methyluridine) and others (Burgin *et al.,* 1996, *Biochemistry,* 35, 14090). By "modified bases" in this aspect is meant nucleotide bases other than adenine, guanine, cytosine and uracil at 1' position or their equivalents; such bases may be used within the catalytic core of the enzyme and/or in the substrate-binding regions.

By "unmodified nucleoside" is meant one of the bases adenine, cytosine, guanine, uracil joined to the 1' carbon of b-D-ribo-furanose.

By "modified nucleoside" is meant any nucleotide base which contains a modification in the chemical structure of an unmodified nucleotide base, sugar and/or phosphate.

Various modifications to ribozyme structure can be made to enhance the utility of ribozymes. Such modifications will enhance shelf-life, half-life *in vitro,* stability, and ease of introduction of such ribozymes to the target site, *e.g.,* to enhance penetration of cellular membranes, and confer the ability to recognize and bind to targeted cells.

Administration of Ribozymes

Sullivan *et al.,* PCT WO 94/02595, describes the general methods for delivery of enzymatic RNA molecules . Ribozymes 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, ribozymes may be directly delivered *ex vivo* to cells or tissues with or without the aforementioned vehicles. Alternatively, the RNA/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 ribozyme 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 the 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.

Alternatively, the enzymatic nucleic acid molecules of the instant invention 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 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 *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 catalyst of the instant invention is disclosed. The nucleic acid sequence encoding the nucleic acid catalyst of the instant invention is operable 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 catalyst 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 catalyst of the invention; and/or an intron (intervening sequences).

Transcription of the ribozyme 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 ribozyme 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 catalytic 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.

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 Tie-2, integrin subunit b3, integrin subunit $\alpha 6$, and aryl hydrocarbon nuclear transporter (ARNT). The methods described herein represent a scheme by which ribozymes may be derived that cleave other RNA targets required for angiogenesis. Also provided is a description of how such ribozymes may be delivered to cells. The examples demonstrate that upon delivery, the ribozymes inhibit cell proliferation in culture and modulate gene expression *in vivo*. Moreover, significantly reduced inhibition is observed if mutated ribozymes that are catalytically inactive are applied to the cells. Thus, inhibition requires the catalytic activity of the ribozymes.

Example 1: Identification of Potential Ribozyme Cleavage Sites in TIE-2

The sequence of human Tie-2 was screened for accessible sites using a computer folding algorithm. Regions of the mRNA that did not form secondary folding structures and contained potential hammerhead and/or hairpin ribozyme cleavage sites were identified. The sequences of these cleavage sites are shown in **tables V-VI**.

Example 2: Selection of Ribozyme Cleavage Sites in Human TIE-2 RNA

To test whether the sites predicted by the computer-based RNA folding algorithm corresponded to accessible sites in Tie-2 RNA, 20 hammerhead sites were selected for analysis. Ribozyme target sites were chosen by analyzing genomic sequences of Tie-2 (Ziegler et al., 1993, Oncogene 8 (3), 663-670 (Genbank sequence **HUMTEKRPTK** accession number: M69238) 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 Tie-2 is shown in figure 2.

Example 3: Chemical Synthesis and Purification of Ribozymes for Efficient Cleavage of TIE-2 RNA

Ribozymes of the hammerhead or hairpin motif 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 were synthesized in two parts and annealed to reconstruct the active ribozyme (Chowrira and Burke, 1992 Nucleic Acids Res., 20, 2835-2840). Ribozymes were 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'-flouro, 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 V-VI**.

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

Ribozymes targeted to the human Tie-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 Tie-2 mRNA are given in Table V.

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 [a-^{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.

Use of Ribozymes Targeting TIE-2

The rate of tumor growth is believed to be a function of blood supplied and therefore a function of angiogenesis (Rak, *Supra;* Blood & Zetter, 1990, *Biochimica et Biophysica Acta 1032,* 89-118). Elevated levels of a number of these angiogenic factors including Tie-2; integrin subunit β3; integrin subunit α6; and aryl hydrocarbon nuclear transporter have been reported in a number of cancers. Thus, inhibition of expression of these angiogenic factors (for example using ribozymes) would potentially reduce that rate of growth of these tumors. The use of ribozymes would be desirable over such therapies as chemotherapeutics since, chemotherapeutic compounds such as doxorubicin because of its highly specific inhibition and reduction of the likelihood for side effects. Ribozymes, with their catalytic activity and increased site specificity (see above), are likely to represent a potent and safe therapeutic molecule for the treatment of cancer. Tumor angiogenesis and other indications are discussed below.

Indications

1) Tumor angiogenesis: Angiogenesis has been shown to be necessary for tumors to grow into pathological size (Folkman, 1971, *PNAS* 76, 5217-5221; Wellstein & Czubayko, 1996, *Breast Cancer Res and Treatment* 38, 109-119). In addition, it allows tumor cells to travel through the circulatory system during metastasis. Increased levels of gene expression of a number of angiogenic factors such as vascular endothelial growth factor (VEGF) have been reported in vascularized and edema-associated brain tumors (Berkman *et al.,* 1993 *J. Clini. Invest.* 91, 153). A more direct demostration of the role of VEGF in tumor angiogenesis was demonstrated by Jim Kim *et al.,* 1993 *Nature* 362,841 wherein, monoclonal antibodies against VEGF were successfully used to inhibit the growth of rhabdomyosarcoma, glioblastoma multiforme cells in nude mice. Similarly, expression of a dominant negative mutated form of the flt-1 VEGF receptor inhibits vascularization induced by human glioblastoma cells in nude mice (Millauer *et al.,* 1994, *Nature* 367, 576).

2) Ocular diseases: Neovascularization has been shown to cause or exacerbate ocular diseases including but not limited to, macular degeneration, neovascular glaucoma, diabetic retinopathy, myopic degeneration, and trachoma (Norrby, 1997, *APMIS* 105, 417-437). Aiello *et al.,* 1994 *New Engl. J. Med.* 331, 1480, showed that the ocular fluid, of a majority of patients suffering from diabetic retinopathy and other retinal disorders, contains

a high concentration of VEGF. Miller *et al.*, 1994 *Am. J. Pathol.* 145, 574, reported elevated levels of VEGF mRNA in patients suffering from retinal ischemia. These observations support a direct role for VEGF in ocular diseases. Other factors including those that stimulate VEGF synthesis may also contribute to these indications.

3) Dermatological Disorders: Many indications have been identified which may by angiogenesis dependent including but not limited to psoriasis, verruca vulgaris, angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, and Osler-Weber-Rendu syndrome (Norrby, *supra*). Intradermal injection of the angiogenic factor b-FGF demonstrated angiogenesis in nude mice (Weckbecker et al., 1992, *Angiogenesis: Key principles-Science-Technology-Medicine*, ed R. Steiner) Detmar *et al.*, 1994 *J. Exp. Med.* 180, 1141 reported that VEGF and its receptors were over-expressed in psoriatic skin and psoriatic dermal microvessels, suggesting that VEGF plays a significant role in psoriasis.

4) Rheumatoid arthritis: Immunohistochemistry and *in situ* hybridization studies on tissues from the joints of patients suffering from rheumatoid arthritis show an increased level of VEGF and its receptors (Fava *et al.*, 1994 *J. Exp. Med.* 180, 341). Additionally, Koch *et al.*, 1994 *J. Immunol.* 152, 4149, found that VEGF-specific antibodies were able to significantly reduce the mitogenic activity of synovial tissues from patients suffering from rheumatoid arthritis. These observations support a direct role for VEGF in rheumatoid arthritis. Other angiogenic factors including those of the present invention may also be involved in arthritis.

Animal Models

There are several animal models in which the anti-angiogenesis effect of nucleic acids of the present invention, such as ribozymes, directed against ARNT RNAs can be tested. Typically a corneal model has been used to study angiogenesis in rat and rabbit since recruitment of vessels can easily be followed in this normally avascular tissue (Pandey *et al.,* 1995 *Science* 268: 567-569). In these models, a small Teflon or Hydron disk pretreated with an angiogenic compound is inserted into a pocket surgically created in the cornea. Angiogenesis is monitored 3 to 5 days later. Ribozymes directed against ARNT, Tie-2 or integrin subunit RNAs would be delivered in the disk as well, or dropwise to the eye over the time course of the experiment. In another eye model, hypoxia has been shown to cause both increased expression of VEGF and neovascularization in the retina (Pierce *et al.,* 1995 *Proc. Natl. Acad. Sci.* USA. 92: 905-909; Shweiki *et al.,* 1992 *J. Clin. Invest.* 91: 2235-2243).

Another animal model that addresses neovascularization involves Matrigel, an extract of basement membrane that becomes a solid gel when injected subcutaneously (Passaniti *et al.,* 1992 *Lab. Invest.* 67: 519-528). When the Matrigel is supplemented with angiogenesis factors, vessels grow into the Matrigel over a period of 3 to 5 days and angiogenesis can be assessed. Again, ribozymes directed against ARNT, Tie-2 or integrin subunit RNAs would be delivered in the Matrigel.

Several animal models exist for screening of anti-angiogenic agents. These include corneal vessel formation following corneal injury (Burger *et al.,* 1985 *Cornea* 4: 35-41; Lepri, *et al.,* 1994 *J. Ocular Pharmacol.* 10: 273-280; Ormerod *et al.,* 1990 *Am. J. Pathol.* 137: 1243-1252) or intracorneal growth factor implant (Grant *et al.,* 1993 *Diabetologia* 36: 282-291; Pandey *et al.* 1995 *supra;*

Zieche *et al.,* 1992 *Lab. Invest.* 67: 711-715), vessel growth into Matrigel matrix containing growth factors (Passaniti *et al.,* 1992 *supra*), female reproductive organ neovascularization following hormonal manipulation (Shweiki *et al.,* 1993 *Clin. Invest.* 91: 2235-2243), several models involving inhibition of tumor growth in highly vascularized solid tumors (O'Reilly *et al.,* 1994 *Cell* 79: 315-328; Senger *et al.,* 1993 *Cancer and Metas. Rev.* 12: 303-324; Takahasi *et al.,* 1994 *Cancer Res.* 54: 4233-4237; Kim *et al.,* 1993 *supra*), and transient hypoxia-induced neovascularization in the mouse retina (Pierce *et al.,* 1995 *Proc. Natl. Acad. Sci.* USA. 92: 905-909).

The cornea model, described in Pandey et al. *supra*, is the most common and well characterized anti-angiogenic agent efficacy screening model. This model involves an avascular tissue into which vessels are recruited by a stimulating agent (growth factor, thermal or alkalai burn, endotoxin). The corneal model would utilize the intrastromal corneal implantation of a Teflon pellet soaked in a angiogenic compound-Hydron solution to recruit blood vessels toward the pellet which can be quantitated using standard microscopic and image analysis techniques. To evaluate their anti-angiogenic efficacy, ribozymes are applied topically to the eye or bound within Hydron on the Teflon pellet itself. This avascular cornea as well as the Matrigel (see below) provide for low background assays. While the corneal model has been performed extensively in the rabbit, studies in the rat have also been conducted.

The mouse model (Passaniti et al., *supra*) is a non-tissue model which utilizes Matrigel, an extract of basement membrane (Kleinman et al., 1986) or Millipore® filter disk, which can be impregnated with growth factors and anti-angiogenic agents in a liquid form prior to injection. Upon subcutaneous administration at body temperature, the Matrigel or Millipore® filter disk forms a solid implant. An angiogenic compound would be embedded in the Matrigel or Millipore® filter disk which would be used to recruit vessels within the matrix of the Matrigel or Millipore® filter disk that can be processed histologically for endothelial cell specific vWF (factor VIII antigen) immunohistochemistry, Trichrome-Masson stain, or hemoglobin content. Like the cornea, the Matrigel or Millipore® filter disk are avascular; however, it is not tissue. In the Matrigel or Millipore® filter disk model, ribozymes are administered within the matrix of the Matrigel or Millipore® filter disk to test their anti-angiogenic efficacy. Thus, delivery issues in this model, as with delivery of ribozymes by Hydron- coated Teflon pellets in the rat cornea model, may be less problematic due to the homogeneous presence of the ribozyme within the respective matrix.

These models offer a distinct advantage over several other angiogenic models listed previously. The ability to use VEGF as a pro-angiogenic stimulus in both models is highly desirable since ribozymes will target only VEGFr RNA. In other words, the involvement of other non-specific types of stimuli in the cornea and Matrigel models is not advantageous from the standpoint of understanding the pharmacologic mechanism by which the anti-VEGFr RNA ribozymes produce their effects. In addition, the models will allow for testing the specificity of the anti-VEGFr RNA ribozymes by using either a- or bFGF as a pro-angiogenic factor. Vessel recruitment using FGF should not be affected in either model by anti-VEGFr RNA ribozymes. Other models of angiogenesis including vessel formation in the female reproductive system using hormonal manipulation (Shweiki *et al.*, 1993 *supra*); a variety of vascular solid tumor models which involve indirect correltations with angiogenesis (O'Reilly *et al.*, 1994 *supra*; Senger *et al.*, 1993 *supra*; Takahasi *et al.*, 1994 *supra*; Kim *et al.*, 1993 *supra*); and retinal neovascularization following transient hypoxia (Pierce *et al.*, 1995 *supra*) were not selected for efficacy screening due to their non-specific nature, although there is a correlation between VEGF and angiogenesis in these models.

Other model systems to study tumor angiogenesis is reviewed by Folkman, 1985 *Adv. Cancer. Res.*. 43, 175.

Use of murine models

For a typical systemic study involving 10 mice (20 g each) per dose group, 5 doses (1, 3, 10, 30 and 100 mg/kg daily over 14 days continuous administration), approximately 400 mg of ribozyme, formulated in saline would be used. A similar study in young adult rats (200 g) would require over 4 g. Parallel pharmacokinetic studies may involve the use of similar quantities of ribozymes further justifying the use of murine models.

Ribozymes and Lewis lung carcinoma and B-16 melanoma murine models

Identifying a common animal model for systemic efficacy testing of ribozymes is an efficient way of screening ribozymes for systemic efficacy.

The Lewis lung carcinoma and B-16 murine melanoma models are well accepted models of primary and metastatic cancer and are used for initial screening of anti-cancer. These murine models are not dependent upon the use of immunodeficient mice, are relatively inexpensive, and minimize housing concerns. Both the Lewis lung and B-16 melanoma models involve subcutaneous implantation of approximately 10^6 tumor cells from metastatically aggressive tumor cell lines (Lewis lung lines 3LL or D122, LLc-LN7; B-16-BL6 melanoma) in C57BL/6J mice.

Alternatively, the Lewis lung model can be produced by the surgical implantation of tumor spheres (approximately 0.8 mm in diameter). Metastasis also may be modeled by injecting the tumor cells directly *i.v.*. In the Lewis lung model, microscopic metastases can be observed approximately 14 days following implantation with quantifiable macroscopic metastatic tumors developing within 21-25 days. The B-16 melanoma exhibits a similar time course with tumor neovascularization beginning 4 days following implantation. Since both primary and metastatic tumors exist in these models after 21-25 days in the same animal, multiple measurements can be taken as indices of efficacy. Primary tumor volume and growth latency as well as the number of micro- and macroscopic metastatic lung foci or number of animals exhibiting metastases can be quantitated. The percent increase in lifespan can also be measured. Thus, these models would provide suitable primary efficacy assays for screening systemically administered ribozymes/ribozyme formulations.

In the Lewis lung and B-16 melanoma models, systemic pharmacotherapy with a wide variety of agents usually begins 1-7 days following tumor implantation/inoculation with either continuous or multiple administration regimens. Concurrent pharmacokinetic studies can be performed to determine whether sufficient tissue levels of ribozymes can be achieved for pharmacodynamic effect to be expected. Furthermore, primary tumors and secondary lung metastases can be removed and subjected to a variety of *in vitro* studies (*i.e.* target RNA reduction).

Delivery of ribozymes and ribozyme formulations in the Lewis lung model

Several ribozyme formulations, including cationic lipid complexes which may be useful for inflammatory diseases (*e.g.* DIMRIE/DOPE, *etc.*) and RES evading liposomes which may be used to enhance vascular exposure of the ribozymes, are of interest in cancer models due to their presumed biodistribution to the lung. Thus, liposome formulations can be used for delivering ribozymes to sites of pathology linked to an angiogenic response.

Diagnostic uses

Ribozymes of this invention may be used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of Tie-2; integrin subunit $\beta3$; integrin subunit $\alpha6$; and/or aryl hydrocarbon nuclear transporter RNA in a cell. 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. These experiments will lead to better treatment of the disease progression by affording the possibility of combinational therapies (e.g., multiple ribozymes targeted to different genes, ribozymes coupled with known small molecule inhibitors, or intermittent treatment with combinations of ribozymes and/or other chemical or biological molecules). Other in vitro uses of ribozymes of this invention are well known in the art, and include detection of the presence of RNAs associated with Tie-2; integrin subunit $\beta3$; integrin subunit $\alpha6$; and/or aryl hydrocarbon nuclear transporter related condition. 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 (*i.e.*, Tie-2; integrin subunit β3; integrin subunit α6; ARNT) 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.

Other embodiments are 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 [1,2].
- Complete kinetic framework established for one ribozyme [3,4,5,6].

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[1] Michel, Francois; Westhof, Eric. Slippery substrates. Nat. Struct. Biol. (1994), 1(1), 5-7.

[2] Lisacek, Frederique; Diaz, Yolande; Michel, Francois. Automatic identification of group I intron cores in genomic DNA sequences. J. Mol. Biol. (1994), 235(4), 1206-17.

[3] Herschlag, Daniel; Cech, Thomas R.. Catalysis of RNA cleavage by the Tetrahymena thermophila ribozyme. 1. Kinetic description of the

- Studies of ribozyme folding and substrate docking underway [7,8,9].

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reaction of an RNA substrate complementary to the active site. Biochemistry (1990), 29(44), 10159-71.

[4] Herschlag, Daniel; Cech, Thomas R.. Catalysis of RNA cleavage by the Tetrahymena thermophila ribozyme. 2. Kinetic description of the reaction of an RNA substrate that forms a mismatch at the active site. Biochemistry (1990), 29(44), 10172-80.

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[6] Bevilacqua, Philip C.; Sugimoto, Naoki; Turner, Douglas H.. A mechanistic framework for the second step of splicing catalyzed by the Tetrahymena ribozyme. Biochemistry (1996), 35(2), 648-58.

[7] Li, Yi; Bevilacqua, Philip C.; Mathews, David; Turner, Douglas H.. Thermodynamic and activation parameters for binding of a pyrene-labeled substrate by the Tetrahymena ribozyme: docking is not diffusion-controlled and is driven by a favorable entropy change. Biochemistry (1995), 34(44), 14394-9.

[8] Banerjee, Aloke Raj; Turner, Douglas H.. The time dependence of chemical modification reveals slow steps in the folding of a group I ribozyme. Biochemistry (1995), 34(19), 6504-12.

[9] Zarrinkar, Patrick P.; Williamson, James R.. The P9.1-P9.2 peripheral extension helps guide folding of the Tetrahymena ribozyme. Nucleic Acids Res. (1996), 24(5), 854-8.

- Chemical modification investigation of important residues well established [10,11].
- 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 [12].

RNAse P RNA (M1 RNA)

- Size: ~290 to 400 nucleotides.
- RNA portion of a ubiquitous ribonucleoprotein enzyme.
- Cleaves tRNA precursors to form mature tRNA [13].
- Reaction mechanism: possible attack by M^{2+}-OH to generate cleavage products with 3'-OH and 5'-phosphate.

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[10] Strobel, Scott A.; Cech, Thomas R.. Minor groove recognition of the conserved G.cntdot.U pair at the Tetrahymena ribozyme reaction site. Science (Washington, D. C.) (1995), 267(5198), 675-9.

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[12] Sullenger, Bruce A.; Cech, Thomas R.. Ribozyme-mediated repair of defective mRNA by targeted trans-splicing. Nature (London) (1994), 371(6498), 619-22.

[13] Robertson, H.D.; Altman, S.; Smith, J.D. J. Biol. Chem., 247, 5243-5251 (1972).

- 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 [14,15]
- Important phosphate and 2′ OH contacts recently identified [16,17]

Group II Introns

- Size: >1000 nucleotides.
- Trans cleavage of target RNAs recently demonstrated [18,19].

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[14] Forster, Anthony C.; Altman, Sidney. External guide sequences for an RNA enzyme. Science (Washington, D. C., 1883-) (1990), 249(4970), 783-6.

[15] Yuan, Y.; Hwang, E. S.; Altman, S. Targeted cleavage of mRNA by human RNase P. Proc. Natl. Acad. Sci. USA (1992) 89, 8006-10.

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[18] Pyle, Anna Marie; Green, Justin B.. Building a Kinetic Framework for Group II Intron Ribozyme Activity: Quantitation of Interdomain Binding and Reaction Rate. Biochemistry (1994), 33(9), 2716-25.

- 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 [20,21] in addition to RNA cleavage and ligation.
- Major structural features largely established through phylogenetic comparisons [22].
- Important 2′ OH contacts beginning to be identified [23]

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[19] Michels, William J. Jr.; Pyle, Anna Marie. Conversion of a Group II Intron into a New Multiple-Turnover Ribozyme that Selectively Cleaves Oligonucleotides: Elucidation of Reaction Mechanism and Structure/Function Relationships. Biochemistry (1995), 34(9), 2965-77.

[20] Zimmerly, Steven; Guo, Huatao; Eskes, Robert; Yang, Jian; Perlman, Philip S.; Lambowitz, Alan M.. A group II intron RNA is a catalytic component of a DNA endonuclease involved in intron mobility. Cell (Cambridge, Mass.) (1995), 83(4), 529-38.

[21] Griffin, Edmund A., Jr.; Qin, Zhifeng; Michels, Williams J., Jr.; Pyle, Anna Marie. Group II intron ribozymes that cleave DNA and RNA linkages with similar efficiency, and lack contacts with substrate 2'-hydroxyl groups. Chem. Biol. (1995), 2(11), 761-70.

[22] Michel, Francois; Ferat, Jean Luc. Structure and activities of group II introns. Annu. Rev. Biochem. (1995), 64, 435-61.

[23] Abramovitz, Dana L.; Friedman, Richard A.; Pyle, Anna Marie. Catalytic role of 2'-hydroxyl groups within a group II intron active site. Science (Washington, D. C.) (1996), 271(5254), 1410-13.

- Kinetic framework under development [24]

Neurospora VS RNA

- Size: ~144 nucleotides.
- Trans cleavage of hairpin target RNAs recently demonstrated [25].
- 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.

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[24] Daniels, Danette L.; Michels, William J., Jr.; Pyle, Anna Marie. Two competing pathways for self-splicing by group II introns: a quantitative analysis of in vitro reaction rates and products. J. Mol. Biol. (1996), 256(1), 31-49.

[25] Guo, Hans C. T.; Collins, Richard A.. Efficient trans-cleavage of a stem-loop RNA substrate by a ribozyme derived from Neurospora VS RNA. EMBO J. (1995), 14(2), 368-76.

- 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 [26,27]
- Minimal ligation activity demonstrated (for engineering through *in vitro* selection) [28]
- Complete kinetic framework established for two or more ribozymes [29].
- Chemical modification investigation of important residues well established [30].

Hairpin Ribozyme

- Size: ~50 nucleotides.

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[26] Scott, W.G., Finch, J.T., Aaron,K. The crystal structure of an all RNA hammerhead ribozyme:Aproposed mechanism for RNA catalytic cleavage. Cell, (1995), 81, 991-1002.

[27] McKay, Structure and function of the hammerhead ribozyme: an unfinished story. RNA, (1996), 2, 395-403.

[28] Long, D., Uhlenbeck, O., Hertel, K. Ligation with hammerhead ribozymes. US Patent No. 5,633,133.

[29] Hertel, K.J., Herschlag, D., Uhlenbeck, O. A kinetic and thermodynamic framework for the hammerhead ribozyme reaction. Biochemistry, (1994) 33, 3374-3385.Beigelman, L., *et al.,* Chemical modifications of hammerhead ribozymes. J. Biol. Chem., (1995) 270, 25702-25708.

[30] Beigelman, L., *et al.,* Chemical modifications of hammerhead ribozymes. J. Biol. Chem., (1995) 270, 25702-25708.

- 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 [[31],[32],[33],[34]]

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[31] Hampel, Arnold; Tritz, Richard; Hicks, Margaret; Cruz, Phillip. 'Hairpin' catalytic RNA model: evidence for helixes and sequence requirement for substrate RNA. Nucleic Acids Res. (1990), 18(2), 299-304.

[32] Chowrira, Bharat M.; Berzal-Herranz, Alfredo; Burke, John M.. Novel guanosine requirement for catalysis by the hairpin ribozyme. Nature (London) (1991), 354(6351), 320-2.

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[34] Joseph, Simpson; Berzal-Herranz, Alfredo; Chowrira, Bharat M.; Butcher, Samuel E.. Substrate selection rules for the hairpin ribozyme determined by in vitro selection, mutation, and analysis of mismatched substrates. Genes Dev. (1993), 7(1), 130-8.

- Ligation activity (in addition to cleavage activity) makes ribozyme amenable to engineering through *in vitro* selection [35]
- Complete kinetic framework established for one ribozyme [36].
- Chemical modification investigation of important residues begun [37,38].

Hepatitis Delta Virus (HDV) Ribozyme

- Size: ~60 nucleotides.
- Trans cleavage of target RNAs demonstrated [39].

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[35] Berzal-Herranz, Alfredo; Joseph, Simpson; Burke, John M.. In vitro selection of active hairpin ribozymes by sequential RNA-catalyzed cleavage and ligation reactions. Genes Dev. (1992), 6(1), 129-34.

[36] Hegg, Lisa A.; Fedor, Martha J.. Kinetics and Thermodynamics of Intermolecular Catalysis by Hairpin Ribozymes. Biochemistry (1995), 34(48), 15813-28.

[37] Grasby, Jane A.; Mersmann, Karin; Singh, Mohinder; Gait, Michael J.. Purine Functional Groups in Essential Residues of the Hairpin Ribozyme Required for Catalytic Cleavage of RNA. Biochemistry (1995), 34(12), 4068-76.

[38] Schmidt, Sabine; Beigelman, Leonid; Karpeisky, Alexander; Usman, Nassim; Sorensen, Ulrik S.; Gait, Michael J.. Base and sugar requirements for RNA cleavage of essential nucleoside residues in internal loop B of the hairpin ribozyme: implications for secondary structure. Nucleic Acids Res. (1996), 24(4), 573-81.

[39] Perrotta, Anne T.; Been, Michael D.. Cleavage of oligoribonucleotides by a ribozyme derived from the hepatitis .delta. virus RNA sequence. Biochemistry (1992), 31(1), 16-21.

- Binding sites and structural requirements not fully determined, although no sequences 5' of cleavage site are required. Folded ribozyme contains a pseudoknot structure [[40]].
- 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 [[41]]

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[40] Perrotta, Anne T.; Been, Michael D.. A pseudoknot-like structure required for efficient self-cleavage of hepatitis delta virus RNA. Nature (London) (1991), 350(6317), 434-6.

[41] Puttaraju, M.; Perrotta, Anne T.; Been, Michael D.. A circular trans-acting hepatitis delta virus ribozyme. Nucleic Acids Res. (1993), 21(18), 4253-8.

Table II: 2.5 µmol RNA Synthesis Cycle

Reagent	Equivalents	Amount	Time*
Phosphoramidites	6.5	163 µL	2.5
S-Ethyl Tetrazole	23.8	238 µL	2.5
Acetic Anhydride	100	233 µL	5 sec
N-Methyl Imidazole	186	233 µL	5 sec
TCA	83.2	1.73 mL	21 sec
Iodine	8.0	1.18 mL	45 sec
Acetonitrile	NA	6.67 mL	NA

* Wait time does not include contact time during delivery.

TABLE III: HAMMERHEAD RIBOZYME AND SITE SEQUENCES FOR ARNT

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
10	AGUGGGAG CUGAUGAG X CGAA AGCCGCCA	1	UGGCGGCUC CUCCCACU	394
13	CCCAGUGG CUGAUGAG X CGAA AGGAGCCG	2	CGGCUCCUC CCACUGGG	395
49	UGGCCGCA CUGAUGAG X CGAA AUGCCACC	3	GGUGGCAUC UGCGGCCA	396
69	GUUGGCAG CUGAUGAG X CGAA AGUCGCCG	4	CGGCGACUA CUGCCAAC	397
91	GUACAUCU CUGAUGAG X CGAA AUGUCAUU	5	AAUGACAUC AGAUGUAC	398
98	AGUGAUGG CUGAUGAG X CGAA ACAUCUGA	6	UCAGAUGUA CCAUCACU	399
103	GACCCAGU CUGAUGAG X CGAA AUGGUACA	7	UGUACCAUC ACUGGGUC	400
111	AAUGGCUG CUGAUGAG X CGAA ACCCAGUG	8	CACUGGGUC CAGCCAUU	401
119	CCAGAGGC CUGAUGAG X CGAA AUGGCUGG	9	CCAGCCAUU GCCUCUGG	402
124	AGUUUCCA CUGAUGAG X CGAA AGGCAAUG	10	CAUUGCCUC UGGAAACU	403
133	CAGGUCCA CUGAUGAG X CGAA AGUUUCCA	11	UGGAAACUC UGGACCUG	404
146	CCACCUUG CUGAUGAG X CGAA AUUCCAGG	12	CCUGGAAUU CAAGGUGG	405
147	UCCACCUU CUGAUGAG X CGAA AAUUCCAG	13	CUGGAAUUC AAGGUGGA	406
164	CUCUGGAC CUGAUGAG X CGAA AUGGCUCC	14	GGAGCCAUU GUCCAGAG	407
167	GCCCUCUG CUGAUGAG X CGAA ACAAUGGC	15	GCCAUUGUC CAGAGGGC	408

Posi-tion	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
177	CCGCUUAA CUGAUGAG X CGAA AGCCCUCU	16	AGAGGGCUA UUAAGCGG	409
179	CGCCGCUU CUGAUGAG X CGAA AUAGCCCU	17	AGGGCUAUU AAGCGGCG	410
180	UCGCCGCU CUGAUGAG X CGAA AAUAGCCC	18	GGGCUAUUA AGCGGCGA	411
201	AUCAUCAA CUGAUGAG X CGAA AUCCAGCC	19	GGCUGGAUU UUGAUGAU	412
202	CAUCAUCA CUGAUGAG X CGAA AAUCCAGC	20	GCUGGAUUU UGAUGAUG	413
203	UCAUCAUC CUGAUGAG X CGAA AAAUCCAG	21	CUGGAUUUU GAUGAUGA	414
228	CAAAAAUU CUGAUGAG X CGAA ACUGUUCC	22	GGAACAGUA AAUUUUUG	415
232	ACCUCAAA CUGAUGAG X CGAA AUUUACUG	23	CAGUAAAUU UUUGAGGU	416
233	CACCUCAA CUGAUGAG X CGAA AAUUUACU	24	AGUAAAUUU UUGAGGUG	417
234	ACACCUCA CUGAUGAG X CGAA AAAUUUAC	25	GUAAAUUUU UGAGGUGU	418
235	CACACCUC CUGAUGAG X CGAA AAAAUUUA	26	UAAAUUUUU GAGGUGUG	419
252	AGACAUCU CUGAUGAG X CGAA AUCAUCAU	27	AUGAUGAUC AGAUGUCU	420
259	UAUCGUUA CUGAUGAG X CGAA ACAUCUGA	28	UCAGAUGUC UAACGAUA	421
261	CUUAUCGU CUGAUGAG X CGAA AGACAUCU	29	AGAUGUCUA ACGAUAAG	422
267	CCGCUCCU CUGAUGAG X CGAA AUCGUUAG	30	CUAACGAUA AGGAGCGG	423
277	ACCUGGCA CUGAUGAG X CGAA ACCGCUCC	31	GGAGCGGUU UGCCAGGU	424

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
278	GACCUGGC CUGAUGAG X CGAA AACCGCUC	32	GAGCGGUUU GCCAGGUC	425
286	CAUCAUCC CUGAUGAG X CGAA ACCUGGCA	33	UGCCAGGUC GGAUGAUG	426
304	UAUCCGCA CUGAUGAG X CGAA AGCUCUGC	34	GCAGAGCUC UGCGGAUA	427
312	UCUCUCUU CUGAUGAG X CGAA AUCCGCAG	35	CUGCGGAUA AAGAGAGA	428
323	UCCCUGGC CUGAUGAG X CGAA AGUCUCUC	36	GAGAGACUU GCCAGGGA	429
336	UUCACUGU CUGAUGAG X CGAA AUUUUCCC	37	GGGAAAAUC ACAGUGAA	430
347	CGCCGUUC CUGAUGAG X CGAA AUUUCACU	38	AGUGAAAUU GAACGGCG	431
379	CUGUGAUG CUGAUGAG X CGAA AGGCUGUC	39	GACAGCCUA CAUCACAG	432
383	AGUUCUGU CUGAUGAG X CGAA AUGUAGGC	40	GCCUACAUC ACAGAACU	433
394	CCAUAUCU CUGAUGAG X CGAA ACAGUUCU	41	AGAACUGUC AGAUAUGG	434
399	GGGUACCA CUGAUGAG X CGAA AUCUGACA	42	UGUCAGAUA UGGUACCC	435
404	CAGGUGGG CUGAUGAG X CGAA ACCAUAUC	43	GAUAUGGUA CCCACCUG	436
414	CAGGGCAC CUGAUGAG X CGAA ACAGGUGG	44	CCACCUGUA GUGCCCUG	437
426	UGGUUUUC CUGAUGAG X CGAA AGCCAGGG	45	CCCUGGCUC GAAAACCA	438
443	AAGAUGGU CUGAUGAG X CGAA AGCUUGUC	46	GACAAGCUA ACCAUCUU	439
449	AUGCGUAA CUGAUGAG X CGAA AUGGUUAG	47	CUAACCAUC UUACGCAU	440

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
451	CCAUGCGU CUGAUGAG X CGAA AGAUGGUU	48	AACCAUCUU ACGCAUGG	441
452	GCCAUGCG CUGAUGAG X CGAA AAGAUGGU	49	ACCAUCUUA CGCAUGGC	442
464	AUGUGAGA CUGAUGAG X CGAA ACUGCCAU	50	AUGGCAGUU UCUCACAU	443
465	CAUGUGAG CUGAUGAG X CGAA AACUGCCA	51	UGGCAGUUU CUCACAUG	444
466	UCAUGUGA CUGAUGAG X CGAA AAACUGCC	52	GGCAGUUUC UCACAUGA	445
468	CUUCAUGU CUGAUGAG X CGAA AGAAACUG	53	CAGUUUCUC ACAUGAAG	446
478	CCCGCAAG CUGAUGAG X CGAA ACUUCAUG	54	CAUGAAGUC CUUGCGGG	447
481	UUCCCCGC CUGAUGAG X CGAA AGGACUUC	55	GAAGUCCUU GCGGGGAA	448
502	CAUCAGUG CUGAUGAG X CGAA AUGUGUUG	56	CAACACAUC CACUGAUG	449
514	GCUUAUAG CUGAUGAG X CGAA AGCCAUCA	57	UGAUGGCUC CUAUAAGC	450
517	ACGGCUUA CUGAUGAG X CGAA AGGAGCCA	58	UGGCUCCUA UAAGCCGU	451
519	AGACGGCU CUGAUGAG X CGAA AUAGGAGC	59	GCUCCUAUA AGCCGUCU	452
526	UGAGGAAA CUGAUGAG X CGAA ACGGCUUA	60	UAAGCCGUC UUUCCUCA	453
528	AGUGAGGA CUGAUGAG X CGAA AGACGGCU	61	AGCCGUCUU UCCUCACU	454
529	CAGUGAGG CUGAUGAG X CGAA AAGACGGC	62	GCCGUCUUU CCUCACUG	455
530	UCAGUGAG CUGAUGAG X CGAA AAAGACGG	63	CCGUCUUUC CUCACUGA	456

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
533	UGAUCAGU CUGAUGAG X CGAA AGGAAAGA	64	UCUUUCCUC ACUGAUCA	457
540	CAGUUCCU CUGAUGAG X CGAA AUCAGUGA	65	UCACUGAUC AGGAACUG	458
555	CAAGAUCA CUGAUGAG X CGAA AUGUUUCA	66	UGAAACAUU UGAUCUUG	459
556	CCAAGAUC CUGAUGAG X CGAA AAUGUUUC	67	GAAACAUUU GAUCUUGG	460
560	GCCUCCAA CUGAUGAG X CGAA AUCAAAUG	68	CAUUUGAUC UUGGAGGC	461
562	CUGCCUCC CUGAUGAG X CGAA AGAUCAAA	69	UUUGAUCUU GGAGGCAG	462
580	UAAACAGA CUGAUGAG X CGAA AGCCAUCU	70	AGAUGGCUU UCUGUUUA	463
581	AUAAACAG CUGAUGAG X CGAA AAGCCAUC	71	GAUGGCUUU CUGUUUAU	464
582	AAUAAACA CUGAUGAG X CGAA AAAGCCAU	72	AUGGCUUUC UGUUUAUU	465
586	AGACAAUA CUGAUGAG X CGAA ACAGAAAG	73	CUUUCUGUU UAUUGUCU	466
587	GAGACAAU CUGAUGAG X CGAA AACAGAAA	74	UUUCUGUUU AUUGUCUC	467
588	UGAGACAA CUGAUGAG X CGAA AAACAGAA	75	UUCUGUUUA UUGUCUCA	468
590	CAUGAGAC CUGAUGAG X CGAA AUAAACAG	76	CUGUUUAUU GUCUCAUG	469
593	UCACAUGA CUGAUGAG X CGAA ACAAUAAA	77	UUUAUUGUC UCAUGUGA	470
595	UCUCACAU CUGAUGAG X CGAA AGACAAUA	78	UAUUGUCUC AUGUGAGA	471
619	CAGACACA CUGAUGAG X CGAA ACACCACC	79	GGUGGUGUA UGUGUCUG	472

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
625	CGGAGUCA CUGAUGAG X CGAA ACACAUAC	80	GUAUGUGUC UGACUCCG	473
631	GAGUCACG CUGAUGAG X CGAA AGUCAGAC	81	GUCUGACUC CGUGACUC	474
639	CAAAACAG CUGAUGAG X CGAA AGUCACGG	82	CCGUGACUC CUGUUUUG	475
644	UGGUUCAA CUGAUGAG X CGAA ACAGGAGU	83	ACUCCUGUU UUGAACCA	476
645	CUGGUUCA CUGAUGAG X CGAA AACAGGAG	84	CUCCUGUUU UGAACCAG	477
646	GCUGGUUC CUGAUGAG X CGAA AAACAGGA	85	UCCUGUUUU GAACCAGC	478
661	ACCAUUCA CUGAUGAG X CGAA ACUGUGGC	86	GCCACAGUC UGAAUGGU	479
670	UGCUGCCA CUGAUGAG X CGAA ACCAUUCA	87	UGAAUGGUU UGGCAGCA	480
671	GUGCUGCC CUGAUGAG X CGAA AACCAUUC	88	GAAUGGUUU GGCAGCAC	481
683	UGAUCAUA CUGAUGAG X CGAA AGUGUGCU	89	AGCACACUC UAUGAUCA	482
685	CCUGAUCA CUGAUGAG X CGAA AGAGUGUG	90	CACACUCUA UGAUCAGG	483
690	GUGCACCU CUGAUGAG X CGAA AUCAUAGA	91	UCUAUGAUC AGGUGCAC	484
714	ACGAAGUU CUGAUGAG X CGAA AUCCACAU	92	AUGUGGAUA AACUUCGU	485
719	UGCUCACG CUGAUGAG X CGAA AGUUUAUC	93	GAUAAACUU CGUGAGCA	486
720	CUGCUCAC CUGAUGAG X CGAA AAGUUUAU	94	AUAAACUUC GUGAGCAG	487
731	GAAGUGGA CUGAUGAG X CGAA AGCUGCUC	95	GAGCAGCUU UCCACUUC	488

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
732	UGAAGUGG CUGAUGAG X CGAA AAGCUGCU	96	AGCAGCUUU CCACUUCA	489
733	CUGAAGUG CUGAUGAG X CGAA AAAGCUGC	97	GCAGCUUUC CACUUCAG	490
738	AUUUUCUG CUGAUGAG X CGAA AGUGGAAA	98	UUUCCACUU CAGAAAAU	491
739	CAUUUUCU CUGAUGAG X CGAA AAGUGGAA	99	UUCCACUUC AGAAAAUG	492
762	AUCCAGGA CUGAUGAG X CGAA ACGCCCUG	100	CAGGGCGUA UCCUGGAU	493
764	AGAUCCAG CUGAUGAG X CGAA AUACGCCC	101	GGGCGUAUC CUGGAUCU	494
771	AGUCUUUA CUGAUGAG X CGAA AUCCAGGA	102	UCCUGGAUC UAAAGACU	495
773	CCAGUCUU CUGAUGAG X CGAA AGAUCCAG	103	CUGGAUCUA AAGACUGG	496
801	AGACUGCU CUGAUGAG X CGAA ACCUUCCU	104	AGGAAGGUC AGCAGUCU	497
808	UCAUGGAA CUGAUGAG X CGAA ACUGCUGA	105	UCAGCAGUC UUCCAUGA	498
810	UCUCAUGG CUGAUGAG X CGAA AGACUGCU	106	AGCAGUCUU CCAUGAGA	499
811	UUCUCAUG CUGAUGAG X CGAA AAGACUGC	107	GCAGUCUUC CAUGAGAA	500
825	UGAGCCCA CUGAUGAG X CGAA ACACAUUC	108	GAAUGUGUA UGGGCUCA	501
832	AUCUCCUU CUGAUGAG X CGAA AGCCCAUA	109	UAUGGGCUC AAGGAGAU	502
841	AAAUAAAC CUGAUGAG X CGAA AUCUCCUU	110	AAGGAGAUC GUUUAUUU	503
844	GGCAAAUA CUGAUGAG X CGAA ACGAUCUC	111	GAGAUCGUU UAUUUGCC	504

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
845	CGGCAAAU CUGAUGAG X CGAA AACGAUCU	112	AGAUCGUUU AUUUGCCG	505
846	UCGGCAAA CUGAUGAG X CGAA AAACGAUC	113	GAUCGUUUA UUUGCCGA	506
848	AUUCGGCA CUGAUGAG X CGAA AUAAACGA	114	UCGUUUAUU UGCCGAAU	507
849	CAUUCGGC CUGAUGAG X CGAA AAUAAACG	115	CGUUUAUUU GCCGAAUG	508
870	CACAGAGC CUGAUGAG X CGAA ACUGCCAC	116	GUGGCAGUA GCUCUGUG	509
874	GGUCCACA CUGAUGAG X CGAA AGCUACUG	117	CAGUAGCUC UGUGGACC	510
887	UUCACAGA CUGAUGAG X CGAA ACUGGGUC	118	GACCCAGUU UCUGUGAA	511
888	AUUCACAG CUGAUGAG X CGAA AACUGGGU	119	ACCCAGUUU CUGUGAAU	512
889	UAUUCACA CUGAUGAG X CGAA AAACUGGG	120	CCCAGUUUC UGUGAAUA	513
897	GCUCAGCC CUGAUGAG X CGAA AUUCACAG	121	CUGUGAAUA GGCUGAGC	514
907	UCCUCACA CUGAUGAG X CGAA AGCUCAGC	122	GCUGAGCUU UGUGAGGA	515
908	UUCCUCAC CUGAUGAG X CGAA AAGCUCAG	123	CUGAGCUUU GUGAGGAA	516
935	ACAGAGCC CUGAUGAG X CGAA AGUCCAUU	124	AAUGGACUU GGCUCUGU	517
940	CCUUUACA CUGAUGAG X CGAA AGCCAAGU	125	ACUUGGCUC UGUAAAGG	518
944	CCAUCCUU CUGAUGAG X CGAA ACAGAGCC	126	GGCUCUGUA AAGGAUGG	519
960	CACGAAGU CUGAUGAG X CGAA AGGUUCCC	127	GGGAACCUC ACUUCGUG	520

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
964	CCACCACG CUGAUGAG X CGAA AGUGAGGU	128	ACCUCACUU CGUGGUGG	521
965	ACCACCAC CUGAUGAG X CGAA AAGUGAGG	129	CCUCACUUC GUGGUGGU	522
974	GUGCAGUG CUGAUGAG X CGAA ACCACCAC	130	GUGGUGGUC CACUGCAC	523
988	CCUUGAUG CUGAUGAG X CGAA AGCCUGUG	131	CACAGGCUA CAUCAAGG	524
992	CAGGCCUU CUGAUGAG X CGAA AUGUAGCC	132	GGCUACAUC AAGGCCUG	525
1016	GGGAGGGA CUGAUGAG X CGAA ACACCUGC	133	GCAGGUGUU UCCCUCCC	526
1017	UGGGAGGG CUGAUGAG X CGAA AACACCUG	134	CAGGUGUUU CCCUCCCA	527
1018	CUGGGAGG CUGAUGAG X CGAA AAACACCU	135	AGGUGUUUC CCUCCCAG	528
1022	UCAUCUGG CUGAUGAG X CGAA AGGGAAAC	136	GUUUCCCUC CCAGAUGA	529
1060	CUAGGCAA CUGAUGAG X CGAA ACUUGCUU	137	AAGCAAGUU UUGCCUAG	530
1061	ACUAGGCA CUGAUGAG X CGAA AACUUGCU	138	AGCAAGUUU UGCCUAGU	531
1062	CACUAGGC CUGAUGAG X CGAA AAACUUGC	139	GCAAGUUUU GCCUAGUG	532
1067	AUGGCCAC CUGAUGAG X CGAA AGGCAAAA	140	UUUUGCCUA GUGGCCAU	533
1076	AAUCUGCC CUGAUGAG X CGAA AUGGCCAC	141	GUGGCCAUU GGCAGAUU	534
1084	UUACCUGC CUGAUGAG X CGAA AUCUGCCA	142	UGGCAGAUU GCAGGUAA	535
1091	GAACUAGU CUGAUGAG X CGAA ACCUGCAA	143	UUGCAGGUA ACUAGUUC	536

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1095	GGGAGAAC CUGAUGAG X CGAA AGUUACCU	144	AGGUAACUA GUUCUCCC	537
1098	GUUGGGAG CUGAUGAG X CGAA ACUAGUUA	145	UAACUAGUU CUCCCAAC	538
1099	AGUUGGGA CUGAUGAG X CGAA AACUAGUU	146	AACUAGUUC UCCCAACU	539
1101	ACAGUUGG CUGAUGAG X CGAA AGAACUAG	147	CUAGUUCUC CCAACUGU	540
1110	CAUGUCUG CUGAUGAG X CGAA ACAGUUGG	148	CCAACUGUA CAGACAUG	541
1122	ACAAACAU CUGAUGAG X CGAA ACUCAUGU	149	ACAUGAGUA AUGUUUGU	542
1127	GGUUGACA CUGAUGAG X CGAA ACAUUACU	150	AGUAAUGUU UGUCAACC	543
1128	UGGUUGAC CUGAUGAG X CGAA AACAUUAC	151	GUAAUGUUU GUCAACCA	544
1131	UGUUGGUU CUGAUGAG X CGAA ACAAACAU	152	AUGUUUGUC AACCAACA	545
1144	GGGAGAUG CUGAUGAG X CGAA ACUCUGUU	153	AACAGAGUU CAUCUCCC	546
1145	CGGGAGAU CUGAUGAG X CGAA AACUCUGU	154	ACAGAGUUC AUCUCCCG	547
1148	UGUCGGGA CUGAUGAG X CGAA AUGAACUC	155	GAGUUCAUC UCCCGACA	548
1150	UGUGUCGG CUGAUGAG X CGAA AGAUGAAC	156	GUUCAUCUC CCGACACA	549
1163	AUACCCUC CUGAUGAG X CGAA AUGUUGUG	157	CACAACAUU GAGGGUAU	550
1170	AGUGAAGA CUGAUGAG X CGAA ACCCUCAA	158	UUGAGGGUA UCUUCACU	551
1172	AAAGUGAA CUGAUGAG X CGAA AUACCCUC	159	GAGGGUAUC UUCACUUU	552

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1174	CAAAAGUG CUGAUGAG X CGAA AGAUACCC	160	GGGUAUCUUCACUUUUG	553
1175	ACAAAAGU CUGAUGAG X CGAA AAGAUACC	161	GGUAUCUUCACUUUUGU	554
1179	AUCCACAA CUGAUGAG X CGAA AGUGAAGA	162	UCUUCACUUUUGUGGAU	555
1180	GAUCCACA CUGAUGAG X CGAA AAGUGAAG	163	CUUCACUUUUGUGGAUC	556
1181	UGAUCCAC CUGAUGAG X CGAA AAAGUGAA	164	UUCACUUUUGUGGAUCA	557
1188	ACAGCGGU CUGAUGAG X CGAA AUCCACAA	165	UUGUGGAUCACCGCUGU	558
1203	GCCAACAG CUGAUGAG X CGAA AGCCACAC	166	GUGUGGCUACUGUUGGC	559
1208	UGGUAGCC CUGAUGAG X CGAA ACAGUAGC	167	GCUACUGUUGGCUACCA	560
1213	GUGGCUGG CUGAUGAG X CGAA AGCCAACA	168	UGUUGGCUACCAGCCAC	561
1229	UUUCCUAA CUGAUGAG X CGAA AGUUCCUG	169	CAGGAACUCUUAGGAAA	562
1231	UCUUUCCU CUGAUGAG X CGAA AGAGUUCC	170	GGAACUCUUAGGAAAGA	563
1232	UUCUUUCC CUGAUGAG X CGAA AAGAGUUC	171	GAACUCUUAGGAAAGAA	564
1242	UUCUACAA CUGAUGAG X CGAA AUUCUUUC	172	GAAAGAAUAUUGUAGAA	565
1244	AAUUCUAC CUGAUGAG X CGAA AUAUUCUU	173	AAGAAUAUUGUAGAAUU	566
1247	CAGAAUUC CUGAUGAG X CGAA ACAAUAUU	174	AAUAUUGUAGAAUUCUG	567
1252	GAUGACAG CUGAUGAG X CGAA AUUCUACA	175	UGUAGAAUUCUGUCAUC	568

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1253	GGAUGACA CUGAUGAG X CGAA AAUUCUAC	176	GUAGAAUUC UGUCAUCC	569
1257	UUCAGGAU CUGAUGAG X CGAA ACAGAAUU	177	AAUUCUGUC AUCCUGAA	570
1260	GUCUUCAG CUGAUGAG X CGAA AUGACAGA	178	UCUGUCAUC CUGAAGAC	571
1277	UCUCUUAG CUGAUGAG X CGAA AGCUGCUG	179	CAGCAGCUU CUAAGAGA	572
1278	GUCUCUUA CUGAUGAG X CGAA AAGCUGCU	180	AGCAGCUUC UAAGAGAC	573
1280	CUGUCUCU CUGAUGAG X CGAA AGAAGCUG	181	CAGCUUCUA AGAGACAG	574
1291	CCUGUUGG CUGAUGAG X CGAA AGCUGUCU	182	AGACAGCUU CCAACAGG	575
1292	ACCUGUUG CUGAUGAG X CGAA AAGCUGUC	183	GACAGCUUC CAACAGGU	576
1301	AAUUUCAC CUGAUGAG X CGAA ACCUGUUG	184	CAACAGGUA GUGAAAUU	577
1309	GGCCUUUU CUGAUGAG X CGAA AUUUCACU	185	AGUGAAAUU AAAAGGCC	578
1310	UGGCCUUU CUGAUGAG X CGAA AAUUUCAC	186	GUGAAAUUA AAAGGCCA	579
1327	ACAUGACA CUGAUGAG X CGAA ACAGCACU	187	AGUGCUGUC UGUCAUGU	580
1331	CGGAACAU CUGAUGAG X CGAA ACAGACAG	188	CUGUCUGUC AUGUUCCG	581
1336	GGAACCGG CUGAUGAG X CGAA ACAUGACA	189	UGUCAUGUU CCGGUUCC	582
1337	CGGAACCG CUGAUGAG X CGAA AACAUGAC	190	GUCAUGUUC CGGUUCCG	583
1342	UAGACCGG CUGAUGAG X CGAA ACCGGAAC	191	GUUCCGGUU CCGGUCUA	584

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1343	UUAGACCG CUGAUGAG X CGAA AACCGGAA	192	UUCCGGUUC CGGUCUAA	585
1348	GGUUCUUA CUGAUGAG X CGAA ACCGGAAC	193	GUUCCGGUC UAAGAACC	586
1350	UUGGUUCU CUGAUGAG X CGAA AGACCGGA	194	UCCGGUCUA AGAACCAA	587
1367	CUCAUCCA CUGAUGAG X CGAA AGCCAUUC	195	GAAUGGCUC UGGAUGAG	588
1384	AAGUAAAG CUGAUGAG X CGAA AGCUGGUU	196	AACCAGCUC CUUUACUU	589
1387	GGAAAGUA CUGAUGAG X CGAA AGGAGCUG	197	CAGCUCCUU UACUUUCC	590
1388	UGGAAAGU CUGAUGAG X CGAA AAGGAGCU	198	AGCUCCUUU ACUUUCCA	591
1389	CUGGAAAG CUGAUGAG X CGAA AAAGGAGC	199	GCUCCUUUA CUUUCCAG	592
1392	GUUCUGGA CUGAUGAG X CGAA AGUAAAGG	200	CCUUUACUU UCCAGAAC	593
1393	GGUUCUGG CUGAUGAG X CGAA AAGUAAAG	201	CUUUACUUU CCAGAACC	594
1394	GGGUUCUG CUGAUGAG X CGAA AAAGUAAA	202	UUUACUUUC CAGAACCC	595
1404	AUCUGAGU CUGAUGAG X CGAA AGGGUUCU	203	AGAACCCUU ACUCAGAU	596
1405	CAUCUGAG CUGAUGAG X CGAA AAGGGUUC	204	GAACCCUUA CUCAGAUG	597
1408	UUUCAUCU CUGAUGAG X CGAA AGUAAGGG	205	CCCUUACUC AGAUGAAA	598
1418	AUGUACUC CUGAUGAG X CGAA AUUUCAUC	206	GAUGAAAUU GAGUACAU	599
1423	AGAUGAUG CUGAUGAG X CGAA ACUCAAUU	207	AAUUGAGUA CAUCAUCU	600

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1427	GUACAGAU CUGAUGAG X CGAA AUGUACUC	208	GAGUACAUC AUCUGUAC	601
1430	UUGGUACA CUGAUGAG X CGAA AUGAUGUA	209	UACAUCAUC UGUACCAA	602
1434	GGUGUUGG CUGAUGAG X CGAA ACAGAUGA	210	UCAUCUGUA CCAACACC	603
1456	CUUGGCUA CUGAUGAG X CGAA AGUUCUUC	211	GAAGAACUC UAGCCAAG	604
1458	UUCUUGGC CUGAUGAG X CGAA AGAGUUCU	212	AGAACUCUA GCCAAGAA	605
1476	GGAGAGUG CUGAUGAG X CGAA AGGCCGUG	213	CACGGCCUA CACUCUCC	606
1481	GUGUUGGA CUGAUGAG X CGAA AGUGUAGG	214	CCUACACUC UCCAACAC	607
1483	UUGUGUUG CUGAUGAG X CGAA AGAGUGUA	215	UACACUCUC CAACACAA	608
1493	GGCCUCUG CUGAUGAG X CGAA AUUGUGUU	216	AACACAAUC CAGAGGCC	609
1508	GUGGGACC CUGAUGAG X CGAA AGUUGUGG	217	CCACAACUA GGUCCCAC	610
1512	AGCUGUGG CUGAUGAG X CGAA ACCUAGUU	218	AACUAGGUC CCACAGCU	611
1521	GGGUAAAU CUGAUGAG X CGAA AGCUGUGG	219	CCACAGCUA AUUUACCC	612
1524	CAGGGGUA CUGAUGAG X CGAA AUUAGCUG	220	CAGCUAAUU UACCCCUG	613
1525	CCAGGGGU CUGAUGAG X CGAA AAUUAGCU	221	AGCUAAUUU ACCCCUGG	614
1526	UCCAGGGG CUGAUGAG X CGAA AAAUUAGC	222	GCUAAUUUA CCCCUGGA	615
1543	GCUGUCCU CUGAUGAG X CGAA AGCCCAUC	223	GAUGGGCUC AGGACAGC	616

Posi-tion	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1585	CCAUGUCC CUGAUGAG X CGAA AUUCUGUU	224	AACAGAAUU GGACAUGG	617
1595	CUUCCUGG CUGAUGAG X CGAA ACCAUGUC	225	GACAUGGUA CCAGGAAG	618
1621	AAUGAUUG CUGAUGAG X CGAA AGCUGGCC	226	GGCCAGCUA CAAUCAUU	619
1626	CUGGGAAU CUGAUGAG X CGAA AUUGUAGC	227	GCUACAAUC AUUCCCAG	620
1629	CACCUGGG CUGAUGAG X CGAA AUGAUUGU	228	ACAAUCAUU CCCAGGUG	621
1630	CCACCUGG CUGAUGAG X CGAA AAUGAUUG	229	CAAUCAUUC CCAGGUGG	622
1640	ACAGGCUG CUGAUGAG X CGAA ACCACCUG	230	CAGGUGGUU CAGCCUGU	623
1641	CACAGGCU CUGAUGAG X CGAA AACCACCU	231	AGGUGGUUC AGCCUGUG	624
1682	GACUUCUC CUGAUGAG X CGAA AGGGGCUU	232	AAGCCCCUU GAGAAGUC	625
1690	AACCAUCU CUGAUGAG X CGAA ACUUCUCA	233	UGAGAAGUC AGAUGGUU	626
1698	GGCAAAUA CUGAUGAG X CGAA ACCAUCUG	234	CAGAUGGUU UAUUUGCC	627
1699	GGGCAAAU CUGAUGAG X CGAA AACCAUCU	235	AGAUGGUUU AUUUGCCC	628
1700	UGGGCAAA CUGAUGAG X CGAA AAACCAUC	236	GAUGGUUUA UUUGCCCA	629
1702	CCUGGGCA CUGAUGAG X CGAA AUAAACCA	237	UGGUUUAUU UGCCCAGG	630
1703	UCCUGGGC CUGAUGAG X CGAA AAUAAACC	238	GGUUUAUUU GCCCAGGA	631
1713	UGGAUCUC CUGAUGAG X CGAA AUCCUGGG	239	CCCAGGAUA GAGAUCCA	632

Posi-tion	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1719	AAAUCUUG CUGAUGAG X CGAA AUCUCUAU	240	AUAGAGAUC CAAGAUUU	633
1726	UUUCUGAA CUGAUGAG X CGAA AUCUUGGA	241	UCCAAGAUU UUCAGAAA	634
1727	AUUUCUGA CUGAUGAG X CGAA AAUCUUGG	242	CCAAGAUUU UCAGAAAU	635
1728	GAUUUCUG CUGAUGAG X CGAA AAAUCUUG	243	CAAGAUUUU CAGAAAUC	636
1729	AGAUUUCU CUGAUGAG X CGAA AAAAUCUU	244	AAGAUUUUC AGAAAUCU	637
1736	UUGUGAUA CUGAUGAG X CGAA AUUUCUGA	245	UCAGAAAUC UAUCACAA	638
1738	UGUUGUGA CUGAUGAG X CGAA AGAUUUCU	246	AGAAAUCUA UCACAACA	639
1740	GAUGUUGU CUGAUGAG X CGAA AUAGAUUU	247	AAAUCUAUC ACAACAUC	640
1748	UCCGCAUU CUGAUGAG X CGAA AUGUUGUG	248	CACAACAUC AAUGCGGA	641
1758	UUUACUCU CUGAUGAG X CGAA AUCCGCAU	249	AUGCGGAUC AGAGUAAA	642
1764	GAUGCCUU CUGAUGAG X CGAA ACUCUGAU	250	AUCAGAGUA AAGGCAUC	643
1772	CUGGAGGA CUGAUGAG X CGAA AUGCCUUU	251	AAAGGCAUC UCCUCCAG	644
1774	UGCUGGAG CUGAUGAG X CGAA AGAUGCCU	252	AGGCAUCUC CUCCAGCA	645
1777	CAGUGCUG CUGAUGAG X CGAA AGGAGAUG	253	CAUCUCCUC CAGCACUG	646
1787	GUGGCAGG CUGAUGAG X CGAA ACAGUGCU	254	AGCACUGUC CCUGCCAC	647
1805	UGGGAGAA CUGAUGAG X CGAA AGCUGUUG	255	CAACAGCUA UUCUCCCA	648

Posi-tion	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1807	CCUGGGAG CUGAUGAG X CGAA AUAGCUGU	256	ACAGCUAUU CUCCCAGG	649
1808	CCCUGGGA CUGAUGAG X CGAA AAUAGCUG	257	CAGCUAUUC UCCCAGGG	650
1810	UGCCCUGG CUGAUGAG X CGAA AGAAUAGC	258	GCUAUUCUC CCAGGGCA	651
1825	UAGGAGGG CUGAUGAG X CGAA AUGUGUUG	259	CAACACAUU CCCUCCUA	652
1826	GUAGGAGG CUGAUGAG X CGAA AAUGUGUU	260	AACACAUUC CCUCCUAC	653
1830	GGGGGUAG CUGAUGAG X CGAA AGGGAAUG	261	CAUUCCCUC CUACCCCC	654
1833	CCGGGGGG CUGAUGAG X CGAA AGGAGGGA	262	UCCCUCCUA CCCCCCGG	655
1854	AUUCCUGA CUGAUGAG X CGAA AUUCUCUG	263	CAGAGAAUU UCAGGAAU	656
1855	UAUUCCUG CUGAUGAG X CGAA AAUUCUCU	264	AGAGAAUUU CAGGAAUA	657
1856	CUAUUCCU CUGAUGAG X CGAA AAAUUCUC	265	GAGAAUUUC AGGAAUAG	658
1863	UAGGCCAC CUGAUGAG X CGAA AUUCCUGA	266	UCAGGAAUA GUGGCCUA	659
1871	GGAGGGGC CUGAUGAG X CGAA AGGCCACU	267	AGUGGCCUA GCCCCUCC	660
1878	GGUUACAG CUGAUGAG X CGAA AGGGGCUA	268	UAGCCCCUC CUGUAACC	661
1883	ACAAUGGU CUGAUGAG X CGAA ACAGGAGG	269	CCUCCUGUA ACCAUUGU	662
1889	GGCUGGAC CUGAUGAG X CGAA AUGGUUAC	270	GUAACCAUU GUCCAGCC	663
1892	GAUGGCUG CUGAUGAG X CGAA ACAAUGGU	271	ACCAUUGUC CAGCCAUC	664

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1900	CAGAAGCU CUGAUGAG X CGAA AUGGCUGG	272	CCAGCCAUC AGCUUCUG	665
1905	UCCUGCAG CUGAUGAG X CGAA AGCUGAUG	273	CAUCAGCUU CUGCAGGA	666
1906	GUCCUGCA CUGAUGAG X CGAA AAGCUGAU	274	AUCAGCUUC UGCAGGAC	667
1921	UCUGGGCC CUGAUGAG X CGAA ACAUCUGU	275	ACAGAUGUU GGCCCAGA	668
1931	UGGCGGGA CUGAUGAG X CGAA AUCUGGGC	276	GCCCAGAUU UCCCGCCA	669
1932	GUGGCGGG CUGAUGAG X CGAA AAUCUGGG	277	CCCAGAUUU CCCGCCAC	670
1933	AGUGGCGG CUGAUGAG X CGAA AAAUCUGG	278	CCAGAUUUC CCGCCACU	671
1942	UGGGGUUG CUGAUGAG X CGAA AGUGGCGG	279	CCGCCACUC CAACCCCA	672
1971	AGGGGUCC CUGAUGAG X CGAA AGUUGGGG	280	CCCCAACUU GGACCCCU	673
1980	GCGGGUAG CUGAUGAG X CGAA AGGGGUCC	281	GGACCCCUA CUACCCGC	674
1983	UGAGCGGG CUGAUGAG X CGAA AGUAGGGG	282	CCCCUACUA CCCGCUCA	675
1990	AAAAGCCU CUGAUGAG X CGAA AGCGGGUA	283	UACCCGCUC AGGCUUUU	676
1996	GGGCAGAA CUGAUGAG X CGAA AGCCUGAG	284	CUCAGGCUU UUCUGCCC	677
1997	UGGGCAGA CUGAUGAG X CGAA AAGCCUGA	285	UCAGGCUUU UCUGCCCA	678
1998	CUGGGCAG CUGAUGAG X CGAA AAAGCCUG	286	CAGGCUUUU CUGCCCAG	679
1999	GCUGGGCA CUGAUGAG X CGAA AAAAGCCU	287	AGGCUUUUC UGCCCAGC	680

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2016	AGCCUGGG CUGAUGAG X CGAA AGCCACCU	288	AGGUGGCUA CCCAGGCU	681
2025	CUUAGCAG CUGAUGAG X CGAA AGCCUGGG	289	CCCAGGCUA CUGCUAAG	682
2031	ACGAGUCU CUGAUGAG X CGAA AGCAGUAG	290	CUACUGCUA AGACUCGU	683
2037	GGAAGUAC CUGAUGAG X CGAA AGUCUUAG	291	CUAAGACUC GUACUUCC	684
2040	CUGGGAAG CUGAUGAG X CGAA ACGAGUCU	292	AGACUCGUA CUUCCCAG	685
2043	AAACUGGG CUGAUGAG X CGAA AGUACGAG	293	CUCGUACUU CCCAGUUU	686
2044	CAAACUGG CUGAUGAG X CGAA AAGUACGA	294	UCGUACUUC CCAGUUUG	687
2050	CCACACCA CUGAUGAG X CGAA ACUGGGAA	295	UUCCCAGUU UGGUGUGG	688
2051	CCCACACC CUGAUGAG X CGAA AACUGGGA	296	UCCCAGUUU GGUGUGGG	689
2065	GAGUCUGA CUGAUGAG X CGAA AGCUGCCC	297	GGGCAGCUU UCAGACUC	690
2066	GGAGUCUG CUGAUGAG X CGAA AAGCUGCC	298	GGCAGCUUU CAGACUCC	691
2067	UGGAGUCU CUGAUGAG X CGAA AAAGCUGC	299	GCAGCUUUC AGACUCCA	692
2073	GGAGGAUG CUGAUGAG X CGAA AGUCUGAA	300	UUCAGACUC CAUCCUCC	693
2077	UGAAGGAG CUGAUGAG X CGAA AUGGAGUC	301	GACUCCAUC CUCCUUCA	694
2080	AGCUGAAG CUGAUGAG X CGAA AGGAUGGA	302	UCCAUCCUC CUUCAGCU	695
2083	UGGAGCUG CUGAUGAG X CGAA AGGAGGAU	303	AUCCUCCUU CAGCUCCA	696

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2084	AUGGAGCU CUGAUGAG X CGAA AAGGAGGA	304	UCCUCCUUC AGCUCCAU	697
2089	GGGACAUG CUGAUGAG X CGAA AGCUGAAG	305	CUUCAGCUC CAUGUCCC	698
2095	CAGGGAGG CUGAUGAG X CGAA ACAUGGAG	306	CUCCAUGUC CCUCCCUG	699
2099	GCACCAGG CUGAUGAG X CGAA AGGGACAU	307	AUGUCCCUC CCUGGUGC	700
2119	CACCAGGC CUGAUGAG X CGAA AUGCAGUU	308	AACUGCAUC GCCUGGUG	701
2137	GACUAGGG CUGAUGAG X CGAA AGGCAGCA	309	UGCUGCCUA CCCUAGUC	702
2142	GGUGAGAC CUGAUGAG X CGAA AGGGUAGG	310	CCUACCCUA GUCUCACC	703
2145	AUUGGUGA CUGAUGAG X CGAA ACUAGGGU	311	ACCCUAGUC UCACCAAU	704
2147	CGAUUGGU CUGAUGAG X CGAA AGACUAGG	312	CCUAGUCUC ACCAAUCG	705
2154	AGAUCCAC CUGAUGAG X CGAA AUUGGUGA	313	UCACCAAUC GUGGAUCU	706
2161	CAAAGUUA CUGAUGAG X CGAA AUCCACGA	314	UCGUGGAUC UAACUUUG	707
2163	AGCAAAGU CUGAUGAG X CGAA AGAUCCAC	315	GUGGAUCUA ACUUUGCU	708
2167	CAGGAGCA CUGAUGAG X CGAA AGUUAGAU	316	AUCUAACUU UGCUCCUG	709
2168	UCAGGAGC CUGAUGAG X CGAA AAGUUAGA	317	UCUAACUUU GCUCCUGA	710
2172	AGUCUCAG CUGAUGAG X CGAA AGCAAAGU	318	ACUUUGCUC CUGAGACU	711
2200	GUGUCUGG CUGAUGAG X CGAA AUUGUCCU	319	AGGACAAUU CCAGACAC	712

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2201	CGUGUCUG CUGAUGAG X CGAA AAUUGUCC	320	GGACAAUUC CAGACACG	713
2231	UGUGGCCA CUGAUGAG X CGAA ACACCCAC	321	GUGGGUGUC UGGCCACA	714
2259	ACGAUGAU CUGAUGAG X CGAA AGGCUGCU	322	AGCAGCCUC AUCAUCGU	715
2262	UGAACGAU CUGAUGAG X CGAA AUGAGGCU	323	AGCCUCAUC AUCGUUCA	716
2265	ACUUGAAC CUGAUGAG X CGAA AUGAUGAG	324	CUCAUCAUC GUUCAAGU	717
2268	AGAACUUG CUGAUGAG X CGAA ACGAUGAU	325	AUCAUCGUU CAAGUUCU	718
2269	UAGAACUU CUGAUGAG X CGAA AACGAUGA	326	UCAUCGUUC AAGUUCUA	719
2274	CUCACUAG CUGAUGAG X CGAA ACUUGAAC	327	GUUCAAGUU CUAGUGAG	720
2275	GCUCACUA CUGAUGAG X CGAA AACUUGAA	328	UUCAAGUUC UAGUGAGC	721
2277	UUGCUCAC CUGAUGAG X CGAA AGAACUUG	329	CAAGUUCUA GUGAGCAA	722
2291	GGUUGUUG CUGAUGAG X CGAA ACAUGUUG	330	CAACAUGUU CAACAACC	723
2292	CGGUUGUU CUGAUGAG X CGAA AACAUGUU	331	AACAUGUUC AACAACCG	724
2330	UCCUGGAA CUGAUGAG X CGAA ACCUCAGG	332	CCUGAGGUC UUCCAGGA	725
2332	UCUCCUGG CUGAUGAG X CGAA AGACCUCA	333	UGAGGUCUU CCAGGAGA	726
2333	AUCUCCUG CUGAUGAG X CGAA AAGACCUC	334	GAGGUCUUC CAGGAGAU	727
2347	CCAGCAUG CUGAUGAG X CGAA ACAGCAUC	335	GAUGCUGUC CAUGCUGG	728

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2361	GUUGCUCU CUGAUGAG X CGAA AUCUCCCA	336	UGGGAGAUC AGAGCAAC	729
2374	CAUUGUUG CUGAUGAG X CGAA AGCUGUUG	337	CAACAGCUA CAACAAUG	730
2389	GAUCAGGG CUGAUGAG X CGAA AUUCUUCA	338	UGAAGAAUU CCCUGAUC	731
2390	AGAUCAGG CUGAUGAG X CGAA AAUUCUUC	339	GAAGAAUUC CCUGAUCU	732
2397	CAUAGUUA CUGAUGAG X CGAA AUCAGGGA	340	UCCCUGAUC UAACUAUG	733
2399	AACAUAGU CUGAUGAG X CGAA AGAUCAGG	341	CCUGAUCUA ACUAUGUU	734
2403	GGGAAACA CUGAUGAG X CGAA AGUUAGAU	342	AUCUAACUA UGUUUCCC	735
2407	AGGGGGGA CUGAUGAG X CGAA ACAUAGUU	343	AACUAUGUU UCCCCCCU	736
2408	AAGGGGGG CUGAUGAG X CGAA AACAUAGU	344	ACUAUGUUU CCCCCCUU	737
2409	AAAGGGGG CUGAUGAG X CGAA AAACAUAG	345	CUAUGUUUC CCCCCUUU	738
2416	AUUCUGAA CUGAUGAG X CGAA AGGGGGGA	346	UCCCCCCUU UUCAGAAU	739
2417	UAUUCUGA CUGAUGAG X CGAA AAGGGGGG	347	CCCCCCUUU UCAGAAUA	740
2418	CUAUUCUG CUGAUGAG X CGAA AAAGGGGG	348	CCCCCUUUU CAGAAUAG	741
2419	UCUAUUCU CUGAUGAG X CGAA AAAAGGGG	349	CCCCUUUUC AGAAUAGA	742
2425	AAUAGUUC CUGAUGAG X CGAA AUUCUGAA	350	UUCAGAAUA GAACUAUU	743
2431	CACCCCAA CUGAUGAG X CGAA AGUUCUAU	351	AUAGAACUA UUGGGGUG	744

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2433	CUCACCCC CUGAUGAG X CGAA AUAGUUCU	352	AGAACUAUU GGGGUGAG	745
2445	CCACCCCU CUGAUGAG X CGAA AUCCUCAC	353	GUGAGGAUA AGGGGUGG	746
2466	CAAACAGU CUGAUGAG X CGAA AUUUUUUC	354	GAAAAAAUC ACUGUUUG	747
2472	UAAAAACA CUGAUGAG X CGAA ACAGUGAU	355	AUCACUGUU UGUUUUUA	748
2473	UUAAAAAC CUGAUGAG X CGAA AACAGUGA	356	UCACUGUUU GUUUUUAA	749
2476	UUUUUAAA CUGAUGAG X CGAA ACAAACAG	357	CUGUUUGUU UUUAAAAA	750
2477	CUUUUUAA CUGAUGAG X CGAA AACAAACA	358	UGUUUGUUU UUAAAAAG	751
2478	GCUUUUUA CUGAUGAG X CGAA AAACAAAC	359	GUUUGUUUU UAAAAAGC	752
2479	UGCUUUUU CUGAUGAG X CGAA AAAACAAA	360	UUUGUUUUU AAAAAGCA	753
2480	UUGCUUUU CUGAUGAG X CGAA AAAAACAA	361	UUGUUUUUA AAAAGCAA	754
2491	UACAGAAA CUGAUGAG X CGAA AUUUGCUU	362	AAGCAAAUC UUUCUGUA	755
2493	UUUACAGA CUGAUGAG X CGAA AGAUUUGC	363	GCAAAUCUU UCUGUAAA	756
2494	GUUUACAG CUGAUGAG X CGAA AAGAUUUG	364	CAAAUCUUU CUGUAAAC	757
2495	UGUUUACA CUGAUGAG X CGAA AAAGAUUU	365	AAAUCUUUC UGUAAACA	758
2499	AUUCUGUU CUGAUGAG X CGAA ACAGAAAG	366	CUUUCUGUA AACAGAAU	759
2508	GGAACUUU CUGAUGAG X CGAA AUUCUGUU	367	AACAGAAUA AAAGUUCC	760

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2514	GGGAGAGG CUGAUGAG X CGAA ACUUUUAU	368	AUAAAAGUU CCUCUCCC	761
2515	AGGGAGAG CUGAUGAG X CGAA AACUUUUA	369	UAAAAGUUC CUCUCCCU	762
2518	GGAAGGGA CUGAUGAG X CGAA AGGAACUU	370	AAGUUCCUC UCCCUUCC	763
2520	AGGGAAGG CUGAUGAG X CGAA AGAGGAAC	371	GUUCCUCUC CCUUCCCU	764
2524	GGGAAGGG CUGAUGAG X CGAA AGGGAGAG	372	CUCUCCCUU CCCUUCCC	765
2525	AGGGAAGG CUGAUGAG X CGAA AAGGGAGA	373	UCUCCCUUC CCUUCCCU	766
2529	GGUGAGGG CUGAUGAG X CGAA AGGGAAGG	374	CCUUCCCUU CCCUCACC	767
2530	GGGUGAGG CUGAUGAG X CGAA AAGGGAAG	375	CUUCCCUUC CCUCACCC	768
2534	UCAGGGGU CUGAUGAG X CGAA AGGGAAGG	376	CCUUCCCUC ACCCCUGA	769
2548	AAAGGGGG CUGAUGAG X CGAA ACAUGUCA	377	UGACAUGUA CCCCCUUU	770
2555	AGAAGGGA CUGAUGAG X CGAA AGGGGGUA	378	UACCCCCUU UCCCUUCU	771
2556	CAGAAGGG CUGAUGAG X CGAA AAGGGGGU	379	ACCCCCUUU CCCUUCUG	772
2557	CCAGAAGG CUGAUGAG X CGAA AAAGGGGG	380	CCCCCUUUC CCUUCUGG	773
2561	ACAGCCAG CUGAUGAG X CGAA AGGGAAAG	381	CUUUCCCUU CUGGCUGU	774
2562	AACAGCCA CUGAUGAG X CGAA AAGGGAAA	382	UUUCCCUUC UGGCUGUU	775
2570	AGCAGGGG CUGAUGAG X CGAA ACAGCCAG	383	CUGGCUGUU CCCCUGCU	776

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2571	GAGCAGGG CUGAUGAG X CGAA AACAGCCA	384	UGGCUGUUC CCCUGCUC	777
2579	AGGCAACA CUGAUGAG X CGAA AGCAGGGG	385	CCCCUGCUC UGUUGCCU	778
2583	UAGGAGGC CUGAUGAG X CGAA ACAGAGCA	386	UGCUCUGUU GCCUCCUA	779
2588	UACCUUAG CUGAUGAG X CGAA AGGCAACA	387	UGUUGCCUC CUAAGGUA	780
2591	UGUUACCU CUGAUGAG X CGAA AGGAGGCA	388	UGCCUCCUA AGGUAACA	781
2596	AUAAAUGU CUGAUGAG X CGAA ACCUUAGG	389	CCUAAGGUA ACAUUUAU	782
2601	UUUUUAUA CUGAUGAG X CGAA AUGUUACC	390	GGUAACAUU UAUAAAAA	783
2602	UUUUUUAU CUGAUGAG X CGAA AAUGUUAC	391	GUAACAUUU AUAAAAAA	784
2603	UUUUUUUA CUGAUGAG X CGAA AAAUGUUA	392	UAACAUUUA UAAAAAAA	785
2605	UUUUUUUU CUGAUGAG X CGAA AUAAAUGU	393	ACAUUUAUA AAAAAAAA	786

Table IV: Hairpin Ribozyme Sequences and Target Sites for ARNT

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
6	GGGAGG AGAA GCCA ACCAGAGAAACA X GUACAUUACCUGGUA	787	UGGCG GCU CCUCCC	849
92	UGGUAC AGAA GAUG ACCAGAGAAACA X GUACAUUACCUGGUA	788	CAUCA GAU GUACCA	850
253	UUAGAC AGAA GAUC ACCAGAGAAACA X GUACAUUACCUGGUA	789	GAUCA GAU GUCUAA	851
274	CUGGCA AGAA GCUC ACCAGAGAAACA X GUACAUUACCUGGUA	790	GAGCG GUU UGCCAG	852
287	CUCAUC AGAA GACC ACCAGAGAAACA X GUACAUUACCUGGUA	791	GGUCG GAU GAUGAG	853
374	GAUGUA AGAA GUCA ACCAGAGAAACA X GUACAUUACCUGGUA	792	UGACA GCC UACAUC	854
411	GGGCAC AGAA GGUG ACCAGAGAAACA X GUACAUUACCUGGUA	793	CACCU GUA GUGCCC	855
461	GUGAGA AGAA GCCA ACCAGAGAAACA X GUACAUUACCUGGUA	794	UGGCA GUU UCUCAC	856
506	GGAGCC AGAA GUGG ACCAGAGAAACA X GUACAUUACCUGGUA	795	CCACU GAU GGCUCC	857
523	AGGAAA AGAA GCUU ACCAGAGAAACA X GUACAUUACCUGGUA	796	AAGCC GUC UUUCCU	858
536	UUCCUG AGAA GUGA ACCAGAGAAACA X GUACAUUACCUGGUA	797	UCACU GAU CAGGAA	859
572	AAAGCC AGAA GCUG ACCAGAGAAACA X GUACAUUACCUGGUA	798	CAGCA GAU GGCUUU	860
583	ACAAUA AGAA GAAA ACCAGAGAAACA X GUACAUUACCUGGUA	799	UUUCU GUU UAUUGU	861
626	CACGGA AGAA GACA ACCAGAGAAACA X GUACAUUACCUGGUA	800	UGUCU GAC UCCGUG	862
641	GUUCAA AGAA GGAG ACCAGAGAAACA X GUACAUUACCUGGUA	801	CUCCU GUU UUGAAC	863

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
658	CAUUCA AGAA GUGG ACCAGAGAAACA X GUACAUUACCUGGUA	802	CCACA GUC UGAAUG	864
701	CACAUC AGAA GGGU ACCAGAGAAACA X GUACAUUACCUGGUA	803	ACCCA GAU GAUGUG	865
727	GUGGAA AGAA GCUC ACCAGAGAAACA X GUACAUUACCUGGUA	804	GAGCA GCU UUCCAC	866
805	AUGGAA AGAA GCUG ACCAGAGAAACA X GUACAUUACCUGGUA	805	CAGCA GUC UUCCAU	867
867	CAGAGC AGAA GCCA ACCAGAGAAACA X GUACAUUACCUGGUA	806	UGGCA GUA GCUCUG	868
884	CACAGA AGAA GGGU ACCAGAGAAACA X GUACAUUACCUGGUA	807	ACCCA GUU UCUGUG	869
918	UCCUGC AGAA GUUC ACCAGAGAAACA X GUACAUUACCUGGUA	808	GAACA GAU GCAGGA	870
1025	GUCAUC AGAA GGGA ACCAGAGAAACA X GUACAUUACCUGGUA	809	UCCCA GAU GAUGAC	871
1080	CCUGCA AGAA GCCA ACCAGAGAAACA X GUACAUUACCUGGUA	810	UGGCA GAU UGCAGG	872
1107	UGUCUG AGAA GUUG ACCAGAGAAACA X GUACAUUACCUGGUA	811	CAACU GUA CAGACA	873
1191	CCACAC AGAA GUGA ACCAGAGAAACA X GUACAUUACCUGGUA	812	UCACC GCU GUGUGG	874
1205	GUAGCC AGAA GUAG ACCAGAGAAACA X GUACAUUACCUGGUA	813	CUACU GUU GGCUAC	875
1273	CUUAGA AGAA GCUG ACCAGAGAAACA X GUACAUUACCUGGUA	814	CAGCA GCU UCUAAG	876
1287	GUUGGA AGAA GUCU ACCAGAGAAACA X GUACAUUACCUGGUA	815	AGACA GCU UCCAAC	877
1324	AUGACA AGAA GCAC ACCAGAGAAACA X GUACAUUACCUGGUA	816	GUGCU GUC UGUCAU	878
1339	GACCGG AGAA GGAA ACCAGAGAAACA X GUACAUUACCUGGUA	817	UUCCG GUU CCGGUC	879

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1345	UUCUUA AGAA GGAA ACCAGAGAAACA X GUACAUUACCUGGUA	818	UUCCG GUC UAAGAA	880
1380	UAAAGG AGAA GGUU ACCAGAGAAACA X GUACAUUACCUGGUA	819	AACCA GCU CCUUUA	881
1409	AAUUUC AGAA GAGU ACCAGAGAAACA X GUACAUUACCUGGUA	820	ACUCA GAU GAAAUU	882
1431	UGUUGG AGAA GAUG ACCAGAGAAACA X GUACAUUACCUGGUA	821	CAUCU GUA CCAACA	883
1471	AGUGUA AGAA GUGG ACCAGAGAAACA X GUACAUUACCUGGUA	822	CCACG GCC UACACU	884
1549	GGUGCC AGAA GUCC ACCAGAGAAACA X GUACAUUACCUGGUA	823	GGACA GCU GGCACC	885
1642	GUCACA AGAA GAAC ACCAGAGAAACA X GUACAUUACCUGGUA	824	GUUCA GCC UGUGAC	886
1691	UAAACC AGAA GACU ACCAGAGAAACA X GUACAUUACCUGGUA	825	AGUCA GAU GGUUUA	887
1754	ACUCUG AGAA GCAU ACCAGAGAAACA X GUACAUUACCUGGUA	826	AUGCG GAU CAGAGU	888
1784	GGCAGG AGAA GUGC ACCAGAGAAACA X GUACAUUACCUGGUA	827	GCACU GUC CCUGCC	889
1840	UCUGCC AGAA GGGG ACCAGAGAAACA X GUACAUUACCUGGUA	828	CCCCG GCC GGCAGA	890
1901	UGCAGA AGAA GAUG ACCAGAGAAACA X GUACAUUACCUGGUA	829	CAUCA GCU UCUGCA	891
1915	GCCAAC AGAA GUCC ACCAGAGAAACA X GUACAUUACCUGGUA	830	GGACA GAU GUUGGC	892
1927	CGGGAA AGAA GGGC ACCAGAGAAACA X GUACAUUACCUGGUA	831	GCCCA GAU UUCCCG	893
1986	AGCCUG AGAA GGUA ACCAGAGAAACA X GUACAUUACCUGGUA	832	UACCC GCU CAGGCU	894
2000	CUGCUG AGAA GAAA ACCAGAGAAACA X GUACAUUACCUGGUA	833	UUUCU GCC CAGCAG	895

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2047	ACACCA AGAA GGGA ACCAGAGAAACA X GUACAUUACCUGGUA	834	UCCCA GUU UGGUGU	896
2061	UCUGAA AGAA GCCC ACCAGAGAAACA X GUACAUUACCUGGUA	835	GGGCA GCU UUCAGA	897
2068	GAUGGA AGAA GAAA ACCAGAGAAACA X GUACAUUACCUGGUA	836	UUUCA GAC UCCAUC	898
2085	ACAUGG AGAA GAAG ACCAGAGAAACA X GUACAUUACCUGGUA	837	CUUCA GCU CCAUGU	899
2129	GUAGGC AGAA GCAC ACCAGAGAAACA X GUACAUUACCUGGUA	838	GUGCU GCU GCCUAC	900
2132	AGGGUA AGAA GCAG ACCAGAGAAACA X GUACAUUACCUGGUA	839	CUGCU GCC UACCCU	901
2185	CCUGCA AGAA GUCC ACCAGAGAAACA X GUACAUUACCUGGUA	840	GGACA GAC UGCAGG	902
2254	UGAUGA AGAA GCUG ACCAGAGAAACA X GUACAUUACCUGGUA	841	CAGCA GCC UCAUCA	903
2320	ACCUCA AGAA GGCC ACCAGAGAAACA X GUACAUUACCUGGUA	842	GGCCA GCC UGAGGU	904
2344	AGCAUG AGAA GCAU ACCAGAGAAACA X GUACAUUACCUGGUA	843	AUGCU GUC CAUGCU	905
2393	AGUUAG AGAA GGGA ACCAGAGAAACA X GUACAUUACCUGGUA	844	UCCCU GAU CUAACU	906
2469	AAAACA AGAA GUGA ACCAGAGAAACA X GUACAUUACCUGGUA	845	UCACU GUU UGUUUU	907
2567	CAGGGG AGAA GCCA ACCAGAGAAACA X GUACAUUACCUGGUA	846	UGGCU GUU CCCCUG	908
2575	CAACAG AGAA GGGG ACCAGAGAAACA X GUACAUUACCUGGUA	847	CCCCU GCU CUGUUG	909
2580	GGAGGC AGAA GAGC ACCAGAGAAACA X GUACAUUACCUGGUA	848	GCUCU GUU GCCUCC	910

TABLE V: HAMMERHEAD RIBOZYMES AND TARGET SITES FOR TIE

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
13	CAAGAAGG CUGAUGAG X CGAA ACAGCACA	911	UGUGCUGUU CCUUCUUG	1612
14	GCAAGAAG CUGAUGAG X CGAA AACAGCAC	912	GUGCUGUUC CUUCUUGC	1613
17	GAGGCAAG CUGAUGAG X CGAA AGGAACAG	913	CUGUUCCUU CUUGCCUC	1614
18	AGAGGCAA CUGAUGAG X CGAA AAGGAACA	914	UGUUCCUUC UUGCCUCU	1615
20	UUAGAGGC CUGAUGAG X CGAA AGAAGGAA	915	UUCCUUCUU GCCUCUAA	1616
25	ACAAGUUA CUGAUGAG X CGAA AGGCAAGA	916	UCUUGCCUC UAACUUGU	1617
27	UUACAAGU CUGAUGAG X CGAA AGAGGCAA	917	UUGCCUCUA ACUUGUAA	1618
31	UUGUUUAC CUGAUGAG X CGAA AGUUAGAG	918	CUCUAACUU GUAAACAA	1619
34	GUCUUGUU CUGAUGAG X CGAA ACAAGUUA	919	UAACUUGUA AACAAGAC	1620
45	CGUCCUAG CUGAUGAG X CGAA ACGUCUUG	920	CAAGACGUA CUAGGACG	1621
48	CAUCGUCC CUGAUGAG X CGAA AGUACGUC	921	GACGUACUA GGACGAUG	1622
59	CUUUCCAU CUGAUGAG X CGAA AGCAUCGU	922	ACGAUGCUA AUGGAAAG	1623
69	CGGUUUGU CUGAUGAG X CGAA ACUUUCCA	923	UGGAAAGUC ACAAACCG	1624
84	CUUUCAAA CUGAUGAG X CGAA ACCCAGCG	924	CGCUGGGUU UUUGAAAG	1625
85	CCUUUCAA CUGAUGAG X CGAA AACCCAGC	925	GCUGGGUUU UUGAAAGG	1626

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
86	UCCUUUCA CUGAUGAG X CGAA AAACCCAG	926	CUGGGUUUU UGAAAGGA	1627
87	AUCCUUUC CUGAUGAG X CGAA AAAACCCA	927	UGGGUUUUU GAAAGGAU	1628
96	GUCCCAAG CUGAUGAG X CGAA AUCCUUUC	928	GAAAGGAUC CUUGGGAC	1629
99	GAGGUCCC CUGAUGAG X CGAA AGGAUCCU	929	AGGAUCCUU GGGACCUC	1630
107	AUGUGCAU CUGAUGAG X CGAA AGGUCCCA	930	UGGGACCUC AUGCACAU	1631
116	UUUCCACA CUGAUGAG X CGAA AUGUGCAU	931	AUGCACAUU UGUGGAAA	1632
117	GUUUCCAC CUGAUGAG X CGAA AAUGUGCA	932	UGCACAUUU GUGGAAAC	1633
139	CUUCCCCA CUGAUGAG X CGAA AUCUCUCC	933	GGAGAGAUU UGGGGAAG	1634
140	GCUUCCCC CUGAUGAG X CGAA AAUCUCUC	934	GAGAGAUUU GGGGAAGC	1635
156	UGGCUAAA CUGAUGAG X CGAA AGUCCAUG	935	CAUGGACUC UUUAGCCA	1636
158	GCUGGCUA CUGAUGAG X CGAA AGAGUCCA	936	UGGACUCUU UAGCCAGC	1637
159	AGCUGGCU CUGAUGAG X CGAA AAGAGUCC	937	GGACUCUUU AGCCAGCU	1638
160	AAGCUGGC CUGAUGAG X CGAA AAAGAGUC	938	GACUCUUUA GCCAGCUU	1639
168	AGAGAACU CUGAUGAG X CGAA AGCUGGCU	939	AGCCAGCUU AGUUCUCU	1640
169	CAGAGAAC CUGAUGAG X CGAA AAGCUGGC	940	GCCAGCUUA GUUCUCUG	1641
172	CCACAGAG CUGAUGAG X CGAA ACUAAGCU	941	AGCUUAGUU CUCUGUGG	1642

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
173	UCCACAGA CUGAUGAG X CGAA AACUAAGC	942	GCUUAGUUC UCUGUGGA	1643
175	ACUCCACA CUGAUGAG X CGAA AGAACUAA	943	UUAGUUCUC UGUGGAGU	1644
184	AGCAAGCU CUGAUGAG X CGAA ACUCCACA	944	UGUGGAGUC AGCUUGCU	1645
189	AAAGGAGC CUGAUGAG X CGAA AGCUGACU	945	AGUCAGCUU GCUCCUUU	1646
193	CCAGAAAG CUGAUGAG X CGAA AGCAAGCU	946	AGCUUGCUC CUUUCUGG	1647
196	GUUCCAGA CUGAUGAG X CGAA AGGAGCAA	947	UUGCUCCUU UCUGGAAC	1648
197	AGUUCCAG CUGAUGAG X CGAA AAGGAGCA	948	UGCUCCUUU CUGGAACU	1649
198	CAGUUCCA CUGAUGAG X CGAA AAAGGAGC	949	GCUCCUUUC UGGAACUG	1650
225	UCAAGAUC CUGAUGAG X CGAA AGUCCAUG	950	CAUGGACUU GAUCUUGA	1651
229	UUGAUCAA CUGAUGAG X CGAA AUCAAGUC	951	GACUUGAUC UUGAUCAA	1652
231	AAUUGAUC CUGAUGAG X CGAA AGAUCAAG	952	CUUGAUCUU GAUCAAUU	1653
235	AGGGAAUU CUGAUGAG X CGAA AUCAAGAU	953	AUCUUGAUC AAUUCCCU	1654
239	AGGUAGGG CUGAUGAG X CGAA AUUGAUCA	954	UGAUCAAUU CCCUACCU	1655
240	GAGGUAGG CUGAUGAG X CGAA AAUUGAUC	955	GAUCAAUUC CCUACCUC	1656
244	ACAAGAGG CUGAUGAG X CGAA AGGGAAUU	956	AAUUCCCUA CCUCUUGU	1657
248	AGAUACAA CUGAUGAG X CGAA AGGUAGGG	957	CCCUACCUC UUGUAUCU	1658

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
250	UCAGAUAC CUGAUGAG X CGAA AGAGGUAG	958	CUACCUCUU GUAUCUGA	1659
253	GCAUCAGA CUGAUGAG X CGAA ACAAGAGG	959	CCUCUUGUA UCUGAUGC	1660
255	CAGCAUCA CUGAUGAG X CGAA AUACAAGA	960	UCUUGUAUC UGAUGCUG	1661
270	AGGUGAGA CUGAUGAG X CGAA AUGUUUCA	961	UGAAACAUC UCUCACCU	1662
272	GCAGGUGA CUGAUGAG X CGAA AGAUGUUU	962	AAACAUCUC UCACCUGC	1663
274	AUGCAGGU CUGAUGAG X CGAA AGAGAUGU	963	ACAUCUCUC ACCUGCAU	1664
283	CCAGAGGC CUGAUGAG X CGAA AUGCAGGU	964	ACCUGCAUU GCCUCUGG	1665
288	GCCACCCA CUGAUGAG X CGAA AGGCAAUG	965	CAUUGCCUC UGGGUGGC	1666
313	CCUAUGGU CUGAUGAG X CGAA AUGGGCUC	966	GAGCCCAUC ACCAUAGG	1667
319	UCCCUUCC CUGAUGAG X CGAA AUGGUGAU	967	AUCACCAUA GGAAGGGA	1668
330	AGGCUUCA CUGAUGAG X CGAA AGUCCCUU	968	AAGGGACUU UGAAGCCU	1669
331	AAGGCUUC CUGAUGAG X CGAA AAGUCCCU	969	AGGGACUUU GAAGCCUU	1670
339	GGUUCAUU CUGAUGAG X CGAA AGGCUUCA	970	UGAAGCCUU AAUGAACC	1671
340	UGGUUCAU CUGAUGAG X CGAA AAGGCUUC	971	GAAGCCUUA AUGAACCA	1672
359	UUCCAGCG CUGAUGAG X CGAA AUCCUGGU	972	ACCAGGAUC CGCUGGAA	1673
370	UCUUGAGU CUGAUGAG X CGAA ACUUCCAG	973	CUGGAAGUU ACUCAAGA	1674

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
371	AUCUUGAG CUGAUGAG X CGAA AACUUCCA	974	UGGAAGUUA CUCAAGAU	1675
374	CACAUCUU CUGAUGAG X CGAA AGUAACUU	975	AAGUUACUC AAGAUGUG	1676
398	AACUUUUU CUGAUGAG X CGAA AGCCCAUU	976	AAUGGGCUA AAAAAGUU	1677
406	UUCCAAAC CUGAUGAG X CGAA ACUUUUUU	977	AAAAAAGUU GUUUGGAA	1678
409	CUCUUCCA CUGAUGAG X CGAA ACAACUUU	978	AAAGUUGUU UGGAAGAG	1679
410	UCUCUUCC CUGAUGAG X CGAA AACAACUU	979	AAGUUGUUU GGAAGAGA	1680
428	GAUCUUAC CUGAUGAG X CGAA AGCCUUUU	980	AAAAGGCUA GUAAGAUC	1681
431	AUUGAUCU CUGAUGAG X CGAA ACUAGCCU	981	AGGCUAGUA AGAUCAAU	1682
436	GCACCAUU CUGAUGAG X CGAA AUCUUACU	982	AGUAAGAUC AAUGGUGC	1683
446	ACAGAAAU CUGAUGAG X CGAA AGCACCAU	983	AUGGUGCUU AUUUCUGU	1684
447	CACAGAAA CUGAUGAG X CGAA AAGCACCA	984	UGGUGCUUA UUUCUGUG	1685
449	UUCACAGA CUGAUGAG X CGAA AUAAGCAC	985	GUGCUUAUU UCUGUGAA	1686
450	CUUCACAG CUGAUGAG X CGAA AAUAAGCA	986	UGCUUAUUU CUGUGAAG	1687
451	CCUUCACA CUGAUGAG X CGAA AAAUAAGC	987	GCUUAUUUC UGUGAAGG	1688
466	UCUCCUCG CUGAUGAG X CGAA ACUCGCCC	988	GGGCGAGUU CGAGGAGA	1689
467	CUCUCCUC CUGAUGAG X CGAA AACUCGCC	989	GGCGAGUUC GAGGAGAG	1690

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
481	CGUAUCCU CUGAUGAG X CGAA AUUGCCUC	990	GAGGCAAUC AGGAUACG	1691
487	AUGGUUCG CUGAUGAG X CGAA AUCCUGAU	991	AUCAGGAUA CGAACCAU	1692
506	AGCUUGUU CUGAUGAG X CGAA ACGCAUCU	992	AGAUGCGUC AACAAGCU	1693
515	UAGGAAGG CUGAUGAG X CGAA AGCUUGUU	993	AACAAGCUU CCUUCCUA	1694
516	GUAGGAAG CUGAUGAG X CGAA AAGCUUGU	994	ACAAGCUUC CUUCCUAC	1695
519	CUGGUAGG CUGAUGAG X CGAA AGGAAGCU	995	AGCUUCCUU CCUACCAG	1696
520	GCUGGUAG CUGAUGAG X CGAA AAGGAAGC	996	GCUUCCUUC CUACCAGC	1697
523	GUAGCUGG CUGAUGAG X CGAA AGGAAGGA	997	UCCUUCCUA CCAGCUAC	1698
530	AGUUAAAG CUGAUGAG X CGAA AGCUGGUA	998	UACCAGCUA CUUUAACU	1699
533	CAUAGUUA CUGAUGAG X CGAA AGUAGCUG	999	CAGCUACUU UAACUAUG	1700
534	UCAUAGUU CUGAUGAG X CGAA AAGUAGCU	1000	AGCUACUUU AACUAUGA	1701
535	GUCAUAGU CUGAUGAG X CGAA AAAGUAGC	1001	GCUACUUUA ACUAUGAC	1702
539	CACAGUCA CUGAUGAG X CGAA AGUUAAAG	1002	CUUUAACUA UGACUGUG	1703
560	GUUCACGU CUGAUGAG X CGAA AUCUCCCU	1003	AGGGAGAUA ACGUGAAC	1704
571	UUGAAAGA CUGAUGAG X CGAA AUGUUCAC	1004	GUGAACAUA UCUUUCAA	1705
573	UUUUGAAA CUGAUGAG X CGAA AUAUGUUC	1005	GAACAUAUC UUUCAAAA	1706

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
575	CUUUUUGA CUGAUGAG X CGAA AGAUAUGU	1006	ACAUAUCUU UCAAAAAG	1707
576	CCUUUUUG CUGAUGAG X CGAA AAGAUAUG	1007	CAUAUCUUU CAAAAAGG	1708
577	ACCUUUUU CUGAUGAG X CGAA AAAGAUAU	1008	AUAUCUUUC AAAAAGGU	1709
586	UUAAUCAA CUGAUGAG X CGAA ACCUUUUU	1009	AAAAAGGUA UUGAUUAA	1710
588	CUUUAAUC CUGAUGAG X CGAA AUACCUUU	1010	AAAGGUAUU GAUUAAAG	1711
592	UCUUCUUU CUGAUGAG X CGAA AUCAAUAC	1011	GUAUUGAUU AAAGAAGA	1712
593	UUCUUCUU CUGAUGAG X CGAA AAUCAAUA	1012	UAUUGAUUA AAGAAGAA	1713
613	UUUUUGUA CUGAUGAG X CGAA AUCACUGC	1013	GCAGUGAUU UACAAAAA	1714
614	AUUUUUGU CUGAUGAG X CGAA AAUCACUG	1014	CAGUGAUUU ACAAAAAU	1715
615	CAUUUUUG CUGAUGAG X CGAA AAAUCACU	1015	AGUGAUUUA CAAAAAUG	1716
626	GAUGAAGG CUGAUGAG X CGAA ACCAUUUU	1016	AAAAUGGUU CCUUCAUC	1717
627	GGAUGAAG CUGAUGAG X CGAA AACCAUUU	1017	AAAUGGUUC CUUCAUCC	1718
630	AAUGGAUG CUGAUGAG X CGAA AGGAACCA	1018	UGGUUCCUU CAUCCAUU	1719
631	GAAUGGAU CUGAUGAG X CGAA AAGGAACC	1019	GGUUCCUUC AUCCAUUC	1720
634	ACUGAAUG CUGAUGAG X CGAA AUGAAGGA	1020	UCCUUCAUC CAUUCAGU	1721
638	GGGCACUG CUGAUGAG X CGAA AUGGAUGA	1021	UCAUCCAUU CAGUGCCC	1722

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
639	GGGGCACU CUGAUGAG X CGAA AAUGGAUG	1022	CAUCCAUUC AGUGCCCC	1723
658	AUAUCAGG CUGAUGAG X CGAA ACUUCAUG	1023	CAUGAAGUA CCUGAUAU	1724
665	UUCUAGAA CUGAUGAG X CGAA AUCAGGUA	1024	UACCUGAUA UUCUAGAA	1725
667	ACUUCUAG CUGAUGAG X CGAA AUAUCAGG	1025	CCUGAUAUU CUAGAAGU	1726
668	UACUUCUA CUGAUGAG X CGAA AAUAUCAG	1026	CUGAUAUUC UAGAAGUA	1727
670	UGUACUUC CUGAUGAG X CGAA AGAAUAUC	1027	GAUAUUCUA GAAGUACA	1728
676	GGCAGGUG CUGAUGAG X CGAA ACUUCUAG	1028	CUAGAAGUA CACCUGCC	1729
686	CUGAGCAU CUGAUGAG X CGAA AGGCAGGU	1029	ACCUGCCUC AUGCUCAG	1730
692	CUGGGGCU CUGAUGAG X CGAA AGCAUGAG	1030	CUCAUGCUC AGCCCCAG	1731
714	UGGCCGAG CUGAUGAG X CGAA ACACUCCA	1031	UGGAGUGUA CUCGGCCA	1732
717	ACCUGGCC CUGAUGAG X CGAA AGUACACU	1032	AGUGUACUC GGCCAGGU	1733
726	CUCCUAUA CUGAUGAG X CGAA ACCUGGCC	1033	GGCCAGGUA UAUAGGAG	1734
728	UCCUCCUA CUGAUGAG X CGAA AUACCUGG	1034	CCAGGUAUA UAGGAGGA	1735
730	UUUCCUCC CUGAUGAG X CGAA AUAUACCU	1035	AGGUAUAUA GGAGGAAA	1736
742	GAGGUGAA CUGAUGAG X CGAA AGGUUUCC	1036	GGAAACCUC UUCACCUC	1737
744	CCGAGGUG CUGAUGAG X CGAA AGAGGUUU	1037	AAACCUCUU CACCUCGG	1738

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
745	GCCGAGGU CUGAUGAG X CGAA AAGAGGUU	1038	AACCUCUUC ACCUCGGC	1739
750	UGAAGGCC CUGAUGAG X CGAA AGGUGAAG	1039	CUUCACCUC GGCCUUCA	1740
756	GCCUGGUG CUGAUGAG X CGAA AGGCCGAG	1040	CUCGGCCUU CACCAGGC	1741
757	AGCCUGGU CUGAUGAG X CGAA AAGGCCGA	1041	UCGGCCUUC ACCAGGCU	1742
769	CUCCGGAC CUGAUGAG X CGAA AUCAGCCU	1042	AGGCUGAUA GUCCGGAG	1743
772	CAUCUCCG CUGAUGAG X CGAA ACUAUCAG	1043	CUGAUAGUC CGGAGAUG	1744
815	AGUACAGA CUGAUGAG X CGAA AUGGUUGC	1044	GCAACCAUC UCUGUACU	1745
817	GCAGUACA CUGAUGAG X CGAA AGAUGGUU	1045	AACCAUCUC UGUACUGC	1746
821	ACAAGCAG CUGAUGAG X CGAA ACAGAGAU	1046	AUCUCUGUA CUGCUUGU	1747
827	GUUCAUAC CUGAUGAG X CGAA AGCAGUAC	1047	GUACUGCUU GUAUGAAC	1748
830	AUUGUUCA CUGAUGAG X CGAA ACAAGCAG	1048	CUGCUUGUA UGAACAAU	1749
844	UCAUGGCA CUGAUGAG X CGAA ACACCAUU	1049	AAUGGUGUC UGCCAUGA	1750
857	UUCUCCAG CUGAUGAG X CGAA AUCUUCAU	1050	AUGAAGAUA CUGGAGAA	1751
871	GGAGGGCA CUGAUGAG X CGAA AUGCAUUC	1051	GAAUGCAUU UGCCCUCC	1752
872	AGGAGGGC CUGAUGAG X CGAA AAUGCAUU	1052	AAUGCAUUU GCCCUCCU	1753
878	AAACCCAG CUGAUGAG X CGAA AGGGCAAA	1053	UUUGCCCUC CUGGGUUU	1754

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
885	UUCCCAUA CUGAUGAG X CGAA ACCCAGGA	1054	UCCUGGGUU UAUGGGAA	1755
886	CUUCCCAU CUGAUGAG X CGAA AACCCAGG	1055	CCUGGGUUU AUGGGAAG	1756
887	CCUUCCCA CUGAUGAG X CGAA AAACCCAG	1056	CUGGGUUUA UGGGAAGG	1757
911	CAGUUCAC CUGAUGAG X CGAA AGCCUUCU	1057	AGAAGGCUU GUGAACUG	1758
927	UUCUGCCA CUGAUGAG X CGAA ACGUGUGC	1058	GCACACGUU UGGCAGAA	1759
928	GUUCUGCC CUGAUGAG X CGAA AACGUGUG	1059	CACACGUUU GGCAGAAC	1760
938	UUCUUUAC CUGAUGAG X CGAA AGUUCUGC	1060	GCAGAACUU GUAAAGAA	1761
941	CCUUUCUU CUGAUGAG X CGAA ACAAGUUC	1061	GAACUUGUA AAGAAAGG	1762
975	ACACAUAA CUGAUGAG X CGAA ACUUGCAU	1062	AUGCAAGUC UUAUGUGU	1763
977	GAACACAU CUGAUGAG X CGAA AGACUUGC	1063	GCAAGUCUU AUGUGUUC	1764
978	AGAACACA CUGAUGAG X CGAA AAGACUUG	1064	CAAGUCUUA UGUGUUCU	1765
984	GGAGACAG CUGAUGAG X CGAA ACACAUAA	1065	UUAUGUGUU CUGUCUCC	1766
985	GGGAGACA CUGAUGAG X CGAA AACACAUA	1066	UAUGUGUUC UGUCUCCC	1767
989	GUCAGGGA CUGAUGAG X CGAA ACAGAACA	1067	UGUUCUGUC UCCCUGAC	1768
991	GGGUCAGG CUGAUGAG X CGAA AGACAGAA	1068	UUCUGUCUC CCUGACCC	1769
1002	AACACCCA CUGAUGAG X CGAA AGGGGUCA	1069	UGACCCCUA UGGGUGUU	1770

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1010	GGCACAGG CUGAUGAG X CGAA ACACCCAU	1070	AUGGGUGUU CCUGUGCC	1771
1011	UGGCACAG CUGAUGAG X CGAA AACACCCA	1071	UGGGUGUUC CUGUGCCA	1772
1034	GCACUGCA CUGAUGAG X CGAA ACCCUUCC	1072	GGAAGGGUC UGCAGUGC	1773
1064	CCCGUAAA CUGAUGAG X CGAA ACCAGGGU	1073	ACCCUGGUU UUUACGGG	1774
1065	GCCCGUAA CUGAUGAG X CGAA AACCAGGG	1074	CCCUGGUUU UUACGGGC	1775
1066	GGCCCGUA CUGAUGAG X CGAA AAACCAGG	1075	CCUGGUUUU UACGGGCC	1776
1067	UGGCCCGU CUGAUGAG X CGAA AAAACCAG	1076	CUGGUUUUU ACGGGCCA	1777
1068	CUGGCCCG CUGAUGAG X CGAA AAAAACCA	1077	UGGUUUUUA CGGGCCAG	1778
1079	AAGCUUAC CUGAUGAG X CGAA AUCUGGCC	1078	GGCCAGAUU GUAAGCUU	1779
1082	CCUAAGCU CUGAUGAG X CGAA ACAAUCUG	1079	CAGAUUGUA AGCUUAGG	1780
1087	CUGCACCU CUGAUGAG X CGAA AGCUUACA	1080	UGUAAGCUU AGGUGCAG	1781
1088	GCUGCACC CUGAUGAG X CGAA AAGCUUAC	1081	GUAAGCUUA GGUGCAGC	1782
1121	UUGGAAGC CUGAUGAG X CGAA AUCACACA	1082	UGUGUGAUC GCUUCCAA	1783
1125	AUCCUUGG CUGAUGAG X CGAA AGCGAUCA	1083	UGAUCGCUU CCAAGGAU	1784
1126	CAUCCUUG CUGAUGAG X CGAA AAGCGAUC	1084	GAUCGCUUC CAAGGAUG	1785
1136	AGAGCAGA CUGAUGAG X CGAA ACAUCCUU	1085	AAGGAUGUC UCUGCUCU	1786

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1138	GGAGAGCA CUGAUGAG X CGAA AGACAUCC	1086	GGAUGUCUC UGCUCUCC	1787
1143	AUCCUGGA CUGAUGAG X CGAA AGCAGAGA	1087	UCUCUGCUC UCCAGGAU	1788
1145	CCAUCCUG CUGAUGAG X CGAA AGAGCAGA	1088	UCUGCUCUC CAGGAUGG	1789
1162	UCACACUG CUGAUGAG X CGAA AGCCCCUG	1089	CAGGGGCUC CAGUGUGA	1790
1183	AUCCUCGG CUGAUGAG X CGAA AUGCCUUC	1090	GAAGGCAUA CCGAGGAU	1791
1204	AAAUCCAC CUGAUGAG X CGAA AUCUUUGG	1091	CCAAAGAUA GUGGAUUU	1792
1211	AUCUGGCA CUGAUGAG X CGAA AUCCACUA	1092	UAGUGGAUU UGCCAGAU	1793
1212	GAUCUGGC CUGAUGAG X CGAA AAUCCACU	1093	AGUGGAUUU GCCAGAUC	1794
1220	UUCUAUAU CUGAUGAG X CGAA AUCUGGCA	1094	UGCCAGAUC AUAUAGAA	1795
1223	UACUUCUA CUGAUGAG X CGAA AUGAUCUG	1095	CAGAUCAUA UAGAAGUA	1796
1225	UUUACUUC CUGAUGAG X CGAA AUAUGAUC	1096	GAUCAUAUA GAAGUAAA	1797
1231	CCACUGUU CUGAUGAG X CGAA ACUUCUAU	1097	AUAGAAGUA AACAGUGG	1798
1241	AUUAAAUU CUGAUGAG X CGAA ACCACUGU	1098	ACAGUGGUA AAUUUAAU	1799
1245	UGGGAUUA CUGAUGAG X CGAA AUUUACCA	1099	UGGUAAAUU UAAUCCCA	1800
1246	AUGGGAUU CUGAUGAG X CGAA AAUUUACC	1100	GGUAAAUUU AAUCCCAU	1801
1247	AAUGGGAU CUGAUGAG X CGAA AAAUUUAC	1101	GUAAAUUUA AUCCCAUU	1802

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1250	GCAAAUGG CUGAUGAG X CGAA AUUAAAUU	1102	AAUUUAAUC CCAUUUGC	1803
1255	GCUUUGCA CUGAUGAG X CGAA AUGGGAUU	1103	AAUCCCAUU UGCAAAGC	1804
1256	AGCUUUGC CUGAUGAG X CGAA AAUGGGAU	1104	AUCCCAUUU GCAAAGCU	1805
1265	CCAGCCAG CUGAUGAG X CGAA AGCUUUGC	1105	GCAAAGCUU CUGGCUGG	1806
1266	GCCAGCCA CUGAUGAG X CGAA AAGCUUUG	1106	CAAAGCUUC UGGCUGGC	1807
1279	UUAGUAGG CUGAUGAG X CGAA AGCGGCCA	1107	UGGCCGCUA CCUACUAA	1808
1283	UUCAUUAG CUGAUGAG X CGAA AGGUAGCG	1108	CGCUACCUA CUAAUGAA	1809
1286	UUCUUCAU CUGAUGAG X CGAA AGUAGGUA	1109	UACCUACUA AUGAAGAA	1810
1327	UUUGGAUG CUGAUGAG X CGAA AGCACUGU	1110	ACAGUGCUC CAUCCAAA	1811
1331	GUCUUUUG CUGAUGAG X CGAA AUGGAGCA	1111	UGCUCCAUC CAAAAGAC	1812
1341	UAUGGUUA CUGAUGAG X CGAA AGUCUUUU	1112	AAAAGACUU UAACCAUA	1813
1342	GUAUGGUU CUGAUGAG X CGAA AAGUCUUU	1113	AAAGACUUU AACCAUAC	1814
1343	CGUAUGGU CUGAUGAG X CGAA AAAGUCUU	1114	AAGACUUUA ACCAUACG	1815
1349	AUGAUCCG CUGAUGAG X CGAA AUGGUUAA	1115	UUAACCAUA CGGAUCAU	1816
1355	UGAGAAAU CUGAUGAG X CGAA AUCCGUAU	1116	AUACGGAUC AUUUCUCA	1817
1358	UACUGAGA CUGAUGAG X CGAA AUGAUCCG	1117	CGGAUCAUU UCUCAGUA	1818

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1359	CUACUGAG CUGAUGAG X CGAA AAUGAUCC	1118	GGAUCAUUU CUCAGUAG	1819
1360	GCUACUGA CUGAUGAG X CGAA AAAUGAUC	1119	GAUCAUUUC UCAGUAGC	1820
1362	UGGCUACU CUGAUGAG X CGAA AGAAAUGA	1120	UCAUUUCUC AGUAGCCA	1821
1366	AAUAUGGC CUGAUGAG X CGAA ACUGAGAA	1121	UUCUCAGUA GCCAUAUU	1822
1372	AUGGUGAA CUGAUGAG X CGAA AUGGCUAC	1122	GUAGCCAUA UUCACCAU	1823
1374	GGAUGGUG CUGAUGAG X CGAA AUAUGGCU	1123	AGCCAUAUU CACCAUCC	1824
1375	UGGAUGGU CUGAUGAG X CGAA AAUAUGGC	1124	GCCAUAUUC ACCAUCCA	1825
1381	AUCCGGUG CUGAUGAG X CGAA AUGGUGAA	1125	UUCACCAUC CACCGGAU	1826
1390	GGGGGGAG CUGAUGAG X CGAA AUCCGGUG	1126	CACCGGAUC CUCCCCCC	1827
1393	UCAGGGGG CUGAUGAG X CGAA AGGAUCCG	1127	CGGAUCCUC CCCCCUGA	1828
1404	AAACUCCU CUGAUGAG X CGAA AGUCAGGG	1128	CCCUGACUC AGGAGUUU	1829
1411	CAGACCCA CUGAUGAG X CGAA ACUCCUGA	1129	UCAGGAGUU UGGGUCUG	1830
1412	GCAGACCC CUGAUGAG X CGAA AACUCCUG	1130	CAGGAGUUU GGGUCUGC	1831
1417	ACACUGCA CUGAUGAG X CGAA ACCCAAAC	1131	GUUUGGGUC UGCAGUGU	1832
1458	AAAUGUUG CUGAUGAG X CGAA AGGGCUUU	1132	AAAGCCCUU CAACAUUU	1833
1459	GAAAUGUU CUGAUGAG X CGAA AAGGGCUU	1133	AAGCCCUUC AACAUUUC	1834

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1465	UUAACAGA CUGAUGAG X CGAA AUGUUGAA	1134	UUCAACAUU UCUGUUAA	1835
1466	UUUAACAG CUGAUGAG X CGAA AAUGUUGA	1135	UCAACAUUU CUGUUAAA	1836
1467	CUUUAACA CUGAUGAG X CGAA AAAUGUUG	1136	CAACAUUUC UGUUAAAG	1837
1471	AGAACUUU CUGAUGAG X CGAA ACAGAAAU	1137	AUUUCUGUU AAAGUUCU	1838
1472	AAGAACUU CUGAUGAG X CGAA AACAGAAA	1138	UUUCUGUUA AAGUUCUU	1839
1477	UUUGGAAG CUGAUGAG X CGAA ACUUUAAC	1139	GUUAAAGUU CUUCCAAA	1840
1478	CUUUGGAA CUGAUGAG X CGAA AACUUUAA	1140	UUAAAGUUC UUCCAAAG	1841
1480	GGCUUUGG CUGAUGAG X CGAA AGAACUUU	1141	AAAGUUCUU CCAAAGCC	1842
1481	GGGCUUUG CUGAUGAG X CGAA AAGAACUU	1142	AAGUUCUUC CAAAGCCC	1843
1510	CCAGUGUC CUGAUGAG X CGAA AUCACGUU	1143	AACGUGAUU GACACUGG	1844
1523	AGCAAAGU CUGAUGAG X CGAA AUGUCCAG	1144	CUGGACAUA ACUUUGCU	1845
1527	UGACAGCA CUGAUGAG X CGAA AGUUAUGU	1145	ACAUAACUU UGCUGUCA	1846
1528	AUGACAGC CUGAUGAG X CGAA AAGUUAUG	1146	CAUAACUUU GCUGUCAU	1847
1534	AUGUUGAU CUGAUGAG X CGAA ACAGCAAA	1147	UUUGCUGUC AUCAACAU	1848
1537	CUGAUGUU CUGAUGAG X CGAA AUGACAGC	1148	GCUGUCAUC AACAUCAG	1849
1543	UCAGAGCU CUGAUGAG X CGAA AUGUUGAU	1149	AUCAACAUC AGCUCUGA	1850

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1548	AAGGCUCA CUGAUGAG X CGAA AGCUGAUG	1150	CAUCAGCUC UGAGCCUU	1851
1556	CCCAAAGU CUGAUGAG X CGAA AGGCUCAG	1151	CUGAGCCUU ACUUUGGG	1852
1557	CCCCAAAG CUGAUGAG X CGAA AAGGCUCA	1152	UGAGCCUUA CUUUGGGG	1853
1560	CAUCCCCA CUGAUGAG X CGAA AGUAAGGC	1153	GCCUUACUU UGGGGAUG	1854
1561	CCAUCCCC CUGAUGAG X CGAA AAGUAAGG	1154	CCUUACUUU GGGGAUGG	1855
1576	UUGGAUUU CUGAUGAG X CGAA AUUGGUCC	1155	GGACCAAUC AAAUCCAA	1856
1581	GCUUCUUG CUGAUGAG X CGAA AUUUGAUU	1156	AAUCAAAUC CAAGAAGC	1857
1591	UUGUAUAG CUGAUGAG X CGAA AGCUUCUU	1157	AAGAAGCUU CUAUACAA	1858
1592	UUUGUAUA CUGAUGAG X CGAA AAGCUUCU	1158	AGAAGCUUC UAUACAAA	1859
1594	GGUUUGUA CUGAUGAG X CGAA AGAAGCUU	1159	AAGCUUCUA UACAAACC	1860
1596	CGGGUUUG CUGAUGAG X CGAA AUAGAAGC	1160	GCUUCUAUA CAAACCCG	1861
1606	UAGUGAUU CUGAUGAG X CGAA ACGGGUUU	1161	AAACCCGUU AAUCACUA	1862
1607	AUAGUGAU CUGAUGAG X CGAA AACGGGUU	1162	AACCCGUUA AUCACUAU	1863
1610	CUCAUAGU CUGAUGAG X CGAA AUUAACGG	1163	CCGUUAAUC ACUAUGAG	1864
1614	AAGCCUCA CUGAUGAG X CGAA AGUGAUUA	1164	UAAUCACUA UGAGGCUU	1865
1622	AUGUUGCC CUGAUGAG X CGAA AGCCUCAU	1165	AUGAGGCUU GGCAACAU	1866

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1631	CACUUGAA CUGAUGAG X CGAA AUGUUGCC	1166	GGCAACAUA UUCAAGUG	1867
1633	GUCACUUG CUGAUGAG X CGAA AUAUGUUG	1167	CAACAUAUU CAAGUGAC	1868
1634	UGUCACUU CUGAUGAG X CGAA AAUAUGUU	1168	AACAUAUUC AAGUGACA	1869
1651	AGUGUAAC CUGAUGAG X CGAA AUCUCAUU	1169	AAUGAGAUU GUUACACU	1870
1654	UUGAGUGU CUGAUGAG X CGAA ACAAUCUC	1170	GAGAUUGUU ACACUCAA	1871
1655	GUUGAGUG CUGAUGAG X CGAA AACAAUCU	1171	AGAUUGUUA CACUCAAC	1872
1660	AAAUAGUU CUGAUGAG X CGAA AGUGUAAC	1172	GUUACACUC AACUAUUU	1873
1665	GUUCCAAA CUGAUGAG X CGAA AGUUGAGU	1173	ACUCAACUA UUUGGAAC	1874
1667	AGGUUCCA CUGAUGAG X CGAA AUAGUUGA	1174	UCAACUAUU UGGAACCU	1875
1668	GAGGUUCC CUGAUGAG X CGAA AAUAGUUG	1175	CAACUAUUU GGAACCUC	1876
1676	UUCUGUCC CUGAUGAG X CGAA AGGUUCCA	1176	UGGAACCUC GGACAGAA	1877
1686	AGAGUUCA CUGAUGAG X CGAA AUUCUGUC	1177	GACAGAAUA UGAACUCU	1878
1693	UGCACACA CUGAUGAG X CGAA AGUUCAUA	1178	UAUGAACUC UGUGUGCA	1879
1708	CCACGACG CUGAUGAG X CGAA ACCAGUUG	1179	CAACUGGUC CGUCGUGG	1880
1712	CUCUCCAC CUGAUGAG X CGAA ACGGACCA	1180	UGGUCCGUC GUGGAGAG	1881
1736	AGGUCCAG CUGAUGAG X CGAA AUGCCCUU	1181	AAGGGCAUC CUGGACCU	1882

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1755	CUGUUGUG CUGAUGAG X CGAA AGCGUCUC	1182	GAGACGCUU CACAACAG	1883
1756	GCUGUUGU CUGAUGAG X CGAA AAGCGUCU	1183	AGACGCUUC ACAACAGC	1884
1766	UCCGAUAG CUGAUGAG X CGAA AGCUGUUG	1184	CAACAGCUU CUAUCGGA	1885
1767	GUCCGAUA CUGAUGAG X CGAA AAGCUGUU	1185	AACAGCUUC UAUCGGAC	1886
1769	GAGUCCGA CUGAUGAG X CGAA AGAAGCUG	1186	CAGCUUCUA UCGGACUC	1887
1771	GGGAGUCC CUGAUGAG X CGAA AUAGAAGC	1187	GCUUCUAUC GGACUCCC	1888
1777	GGAGGAGG CUGAUGAG X CGAA AGUCCGAU	1188	AUCGGACUC CCUCCUCC	1889
1781	UCUUGGAG CUGAUGAG X CGAA AGGGAGUC	1189	GACUCCCUC CUCCAAGA	1890
1784	ACCUCUUG CUGAUGAG X CGAA AGGAGGGA	1190	UCCCUCCUC CAAGAGGU	1891
1793	GAGAUUUA CUGAUGAG X CGAA ACCUCUUG	1191	CAAGAGGUC UAAAUCUC	1892
1795	AGGAGAUU CUGAUGAG X CGAA AGACCUCU	1192	AGAGGUCUA AAUCUCCU	1893
1799	AGGCAGGA CUGAUGAG X CGAA AUUUAGAC	1193	GUCUAAAUC UCCUGCCU	1894
1801	UUAGGCAG CUGAUGAG X CGAA AGAUUUAG	1194	CUAAAUCUC CUGCCUAA	1895
1808	CUGACUUU CUGAUGAG X CGAA AGGCAGGA	1195	UCCUGCCUA AAAGUCAG	1896
1814	AGUGGUCU CUGAUGAG X CGAA ACUUUUAG	1196	CUAAAAGUC AGACCACU	1897
1823	CAAAUUUA CUGAUGAG X CGAA AGUGGUCU	1197	AGACCACUC UAAAUUUG	1898

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1825	GUCAAAUU CUGAUGAG X CGAA AGAGUGGU	1198	ACCACUCUA AAUUUGAC	1899
1829	CCAGGUCA CUGAUGAG X CGAA AUUUAGAG	1199	CUCUAAAUU UGACCUGG	1900
1830	GCCAGGUC CUGAUGAG X CGAA AAUUUAGA	1200	UCUAAAUUU GACCUGGC	1901
1846	CUUGGAAA CUGAUGAG X CGAA AUUGGUUG	1201	CAACCAAUA UUUCCAAG	1902
1848	AGCUUGGA CUGAUGAG X CGAA AUAUUGGU	1202	ACCAAUAUU UCCAAGCU	1903
1849	GAGCUUGG CUGAUGAG X CGAA AAUAUUGG	1203	CCAAUAUUU CCAAGCUC	1904
1850	CGAGCUUG CUGAUGAG X CGAA AAAUAUUG	1204	CAAUAUUUC CAAGCUCG	1905
1857	CAUCUUCC CUGAUGAG X CGAA AGCUUGGA	1205	UCCAAGCUC GGAAGAUG	1906
1869	CAACAUAA CUGAUGAG X CGAA AGUCAUCU	1206	AGAUGACUU UUAUGUUG	1907
1870	UCAACAUA CUGAUGAG X CGAA AAGUCAUC	1207	GAUGACUUU UAUGUUGA	1908
1871	UUCAACAU CUGAUGAG X CGAA AAAGUCAU	1208	AUGACUUUU AUGUUGAA	1909
1872	CUUCAACA CUGAUGAG X CGAA AAAAGUCA	1209	UGACUUUUA UGUUGAAG	1910
1876	UCCACUUC CUGAUGAG X CGAA ACAUAAAA	1210	UUUUAUGUU GAAGUGGA	1911
1893	UUUGCACA CUGAUGAG X CGAA ACCUUCUC	1211	GAGAAGGUC UGUGCAAA	1912
1910	AUUCUGCU CUGAUGAG X CGAA AUCACUUU	1212	AAAGUGAUC AGCAGAAU	1913
1919	AACUUUAA CUGAUGAG X CGAA AUUCUGCU	1213	AGCAGAAUA UUAAAGUU	1914

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1921	GGAACUUU CUGAUGAG X CGAA AUAUUCUG	1214	CAGAAUAUU AAAGUUCC	1915
1922	UGGAACUU CUGAUGAG X CGAA AAUAUUCU	1215	AGAAUAUUA AAGUUCCA	1916
1927	UUGCCUGG CUGAUGAG X CGAA ACUUUAAU	1216	AUUAAAGUU CCAGGCAA	1917
1928	GUUGCCUG CUGAUGAG X CGAA AACUUUAA	1217	UUAAAGUUC CAGGCAAC	1918
1938	CCGAAGUC CUGAUGAG X CGAA AGUUGCCU	1218	AGGCAACUU GACUUCGG	1919
1943	UAGCACCG CUGAUGAG X CGAA AGUCAAGU	1219	ACUUGACUU CGGUGCUA	1920
1944	GUAGCACC CUGAUGAG X CGAA AAGUCAAG	1220	CUUGACUUC GGUGCUAC	1921
1951	UUGUUAAG CUGAUGAG X CGAA AGCACCGA	1221	UCGGUGCUA CUUAACAA	1922
1954	AAGUUGUU CUGAUGAG X CGAA AGUAGCAC	1222	GUGCUACUU AACAACUU	1923
1955	UAAGUUGU CUGAUGAG X CGAA AAGUAGCA	1223	UGCUACUUA ACAACUUA	1924
1962	UGGGAUGU CUGAUGAG X CGAA AGUUGUUA	1224	UAACAACUU ACAUCCCA	1925
1963	CUGGGAUG CUGAUGAG X CGAA AAGUUGUU	1225	AACAACUUA CAUCCCAG	1926
1967	CUCCCUGG CUGAUGAG X CGAA AUGUAAGU	1226	ACUUACAUC CCAGGGAG	1927
1980	GGACCACG CUGAUGAG X CGAA ACUGCUCC	1227	GGAGCAGUA CGUGGUCC	1928
1987	CUAGCUCG CUGAUGAG X CGAA ACCACGUA	1228	UACGUGGUC CGAGCUAG	1929
1994	GUUGACUC CUGAUGAG X CGAA AGCUCGGA	1229	UCCGAGCUA GAGUCAAC	1930

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1999	UUGGUGUU CUGAUGAG X CGAA ACUCUAGC	1230	GCUAGAGUC AACACCAA	1931
2033	AGCAGUGA CUGAUGAG X CGAA AUCUUCAC	1231	GUGAAGAUC UCACUGCU	1932
2035	CAAGCAGU CUGAUGAG X CGAA AGAUCUUC	1232	GAAGAUCUC ACUGCUUG	1933
2042	AAGGGUCC CUGAUGAG X CGAA AGCAGUGA	1233	UCACUGCUU GGACCCUU	1934
2050	AUGUCACU CUGAUGAG X CGAA AGGGUCCA	1234	UGGACCCUU AGUGACAU	1935
2051	AAUGUCAC CUGAUGAG X CGAA AAGGGUCC	1235	GGACCCUUA GUGACAUU	1936
2059	GGAGGAAG CUGAUGAG X CGAA AUGUCACU	1236	AGUGACAUU CUUCCUCC	1937
2060	AGGAGGAA CUGAUGAG X CGAA AAUGUCAC	1237	GUGACAUUC UUCCUCCU	1938
2062	UGAGGAGG CUGAUGAG X CGAA AGAAUGUC	1238	GACAUUCUU CCUCCUCA	1939
2063	UUGAGGAG CUGAUGAG X CGAA AAGAAUGU	1239	ACAUUCUUC CUCCUCAA	1940
2066	UGGUUGAG CUGAUGAG X CGAA AGGAAGAA	1240	UUCUUCCUC CUCAACCA	1941
2069	UUCUGGUU CUGAUGAG X CGAA AGGAGGAA	1241	UUCCUCCUC AACCAGAA	1942
2083	GAAAUCUU CUGAUGAG X CGAA AUGUUUUC	1242	GAAAACAUC AAGAUUUC	1943
2089	AUGUUGGA CUGAUGAG X CGAA AUCUUGAU	1243	AUCAAGAUU UCCAACAU	1944
2090	AAUGUUGG CUGAUGAG X CGAA AAUCUUGA	1244	UCAAGAUUU CCAACAUU	1945
2091	UAAUGUUG CUGAUGAG X CGAA AAAUCUUG	1245	CAAGAUUUC CAACAUUA	1946

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2098	GAGUGUGU CUGAUGAG X CGAA AUGUUGGA	1246	UCCAACAUU ACACACUC	1947
2099	GGAGUGUG CUGAUGAG X CGAA AAUGUUGG	1247	CCAACAUUA CACACUCC	1948
2106	CAGCCGAG CUGAUGAG X CGAA AGUGUGUA	1248	UACACACUC CUCGGCUG	1949
2109	UCACAGCC CUGAUGAG X CGAA AGGAGUGU	1249	ACACUCCUC GGCUGUGA	1950
2119	GUCCAAGA CUGAUGAG X CGAA AUCACAGC	1250	GCUGUGAUU UCUUGGAC	1951
2120	UGUCCAAG CUGAUGAG X CGAA AAUCACAG	1251	CUGUGAUUU CUUGGACA	1952
2121	UUGUCCAA CUGAUGAG X CGAA AAAUCACA	1252	UGUGAUUUC UUGGACAA	1953
2123	UAUUGUCC CUGAUGAG X CGAA AGAAAUCA	1253	UGAUUUCUU GGACAAUA	1954
2131	CCAUCCAA CUGAUGAG X CGAA AUUGUCCA	1254	UGGACAAUA UUGGAUGG	1955
2133	AGCCAUCC CUGAUGAG X CGAA AUAUUGUC	1255	GACAAUAUU GGAUGGCU	1956
2142	AAAUAGAA CUGAUGAG X CGAA AGCCAUCC	1256	GGAUGGCUA UUCUAUUU	1957
2144	AGAAAUAG CUGAUGAG X CGAA AUAGCCAU	1257	AUGGCUAUU CUAUUUCU	1958
2145	AAGAAAUA CUGAUGAG X CGAA AAUAGCCA	1258	UGGCUAUUC UAUUUCUU	1959
2147	AGAAGAAA CUGAUGAG X CGAA AGAAUAGC	1259	GCUAUUCUA UUUCUUCU	1960
2149	AUAGAAGA CUGAUGAG X CGAA AUAGAAUA	1260	UAUUCUAUU UCUUCUAU	1961
2150	AAUAGAAG CUGAUGAG X CGAA AAUAGAAU	1261	AUUCUAUUU CUUCUAUU	1962

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2151	UAAUAGAA CUGAUGAG X CGAA AAAUAGAA	1262	UUCUAUUUC UUCUAUUA	1963
2153	AGUAAUAG CUGAUGAG X CGAA AGAAAUAG	1263	CUAUUUCUU CUAUUACU	1964
2154	UAGUAAUA CUGAUGAG X CGAA AAGAAAUA	1264	UAUUUCUUC UAUUACUA	1965
2156	GAUAGUAA CUGAUGAG X CGAA AGAAGAAA	1265	UUUCUUCUA UUACUAUC	1966
2158	CGGAUAGU CUGAUGAG X CGAA AUAGAAGA	1266	UCUUCUAUU ACUAUCCG	1967
2159	ACGGAUAG CUGAUGAG X CGAA AAUAGAAG	1267	CUUCUAUUA CUAUCCGU	1968
2162	GUAACGGA CUGAUGAG X CGAA AGUAAUAG	1268	CUAUUACUA UCCGUUAC	1969
2164	UUGUAACG CUGAUGAG X CGAA AUAGUAAU	1269	AUUACUAUC CGUUACAA	1970
2168	AACCUUGU CUGAUGAG X CGAA ACGGAUAG	1270	CUAUCCGUU ACAAGGUU	1971
2169	GAACCUUG CUGAUGAG X CGAA AACGGAUA	1271	UAUCCGUUA CAAGGUUC	1972
2176	UUGCCUUG CUGAUGAG X CGAA ACCUUGUA	1272	UACAAGGUU CAAGGCAA	1973
2177	CUUGCCUU CUGAUGAG X CGAA AACCUUGU	1273	ACAAGGUUC AAGGCAAG	1974
2203	UUCACAUC CUGAUGAG X CGAA ACGUGCUG	1274	CAGCACGUU GAUGUGAA	1975
2215	GCAUUCUU CUGAUGAG X CGAA AUCUUCAC	1275	GUGAAGAUA AAGAAUGC	1976
2230	UACUGAAU CUGAUGAG X CGAA AUGGUGGC	1276	GCCACCAUC AUUCAGUA	1977
2233	UGAUACUG CUGAUGAG X CGAA AUGAUGGU	1277	ACCAUCAUU CAGUAUCA	1978

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2234	CUGAUACU CUGAUGAG X CGAA AAUGAUGG	1278	CCAUCAUUC AGUAUCAG	1979
2238	UGAGCUGA CUGAUGAG X CGAA ACUGAAUG	1279	CAUUCAGUA UCAGCUCA	1980
2240	CUUGAGCU CUGAUGAG X CGAA AUACUGAA	1280	UUCAGUAUC AGCUCAAG	1981
2245	AGGCCCUU CUGAUGAG X CGAA AGCUGAUA	1281	UAUCAGCUC AAGGGCCU	1982
2254	UCAGGCUC CUGAUGAG X CGAA AGGCCCUU	1282	AAGGGCCUA GAGCCUGA	1983
2271	CCACCUGG CUGAUGAG X CGAA AUGCUGUU	1283	AACAGCAUA CCAGGUGG	1984
2284	UCUGCAAA CUGAUGAG X CGAA AUGUCCAC	1284	GUGGACAUU UUUGCAGA	1985
2285	CUCUGCAA CUGAUGAG X CGAA AAUGUCCA	1285	UGGACAUUU UUGCAGAG	1986
2286	UCUCUGCA CUGAUGAG X CGAA AAAUGUCC	1286	GGACAUUUU UGCAGAGA	1987
2287	UUCUCUGC CUGAUGAG X CGAA AAAAUGUC	1287	GACAUUUUU GCAGAGAA	1988
2302	CUUGACCC CUGAUGAG X CGAA AUGUUGUU	1288	AACAACAUA GGGUCAAG	1989
2307	GGUUGCUU CUGAUGAG X CGAA ACCCUAUG	1289	CAUAGGGUC AAGCAACC	1990
2322	CAUGAGAA CUGAUGAG X CGAA AGGCUGGG	1290	CCCAGCCUU UUCUCAUG	1991
2323	UCAUGAGA CUGAUGAG X CGAA AAGGCUGG	1291	CCAGCCUUU UCUCAUGA	1992
2324	UUCAUGAG CUGAUGAG X CGAA AAAGGCUG	1292	CAGCCUUUU CUCAUGAA	1993
2325	GUUCAUGA CUGAUGAG X CGAA AAAAGGCU	1293	AGCCUUUUC UCAUGAAC	1994

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2327	CAGUUCAU CUGAUGAG X CGAA AGAAAAGG	1294	CCUUUUCUC AUGAACUG	1995
2344	GAUUCUGG CUGAUGAG X CGAA AGGGUCAC	1295	GUGACCCUC CCAGAAUC	1996
2352	GUGCUUGA CUGAUGAG X CGAA AUUCUGGG	1296	CCCAGAAUC UCAAGCAC	1997
2354	UGGUGCUU CUGAUGAG X CGAA AGAUUCUG	1297	CAGAAUCUC AAGCACCA	1998
2371	CCCCCUCC CUGAUGAG X CGAA AGGUCCGC	1298	GCGGACCUC GGAGGGGG	1999
2392	AUGGCUAU CUGAUGAG X CGAA AGCAGCAU	1299	AUGCUGCUU AUAGCCAU	2000
2393	GAUGGCUA CUGAUGAG X CGAA AAGCAGCA	1300	UGCUGCUUA UAGCCAUC	2001
2395	AGGAUGGC CUGAUGAG X CGAA AUAAGCAG	1301	CUGCUUAUA GCCAUCCU	2002
2401	GAGCCAAG CUGAUGAG X CGAA AUGGCUAU	1302	AUAGCCAUC CUUGGCUC	2003
2404	GCAGAGCC CUGAUGAG X CGAA AGGAUGGC	1303	GCCAUCCUU GGCUCUGC	2004
2409	UUCCAGCA CUGAUGAG X CGAA AGCCAAGG	1304	CCUUGGCUC UGCUGGAA	2005
2439	GAAAGGCC CUGAUGAG X CGAA ACAGCACA	1305	UGUGCUGUU GGCCUUUC	2006
2445	UGAUCAGA CUGAUGAG X CGAA AGGCCAAC	1306	GUUGGCCUU UCUGAUCA	2007
2446	AUGAUCAG CUGAUGAG X CGAA AAGGCCAA	1307	UUGGCCUUU CUGAUCAU	2008
2447	UAUGAUCA CUGAUGAG X CGAA AAAGGCCA	1308	UGGCCUUUC UGAUCAUA	2009
2452	UGCAAUAU CUGAUGAG X CGAA AUCAGAAA	1309	UUUCUGAUC AUAUUGCA	2010

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2455	AAUUGCAA CUGAUGAG X CGAA AUGAUCAG	1310	CUGAUCAUA UUGCAAUU	2011
2457	UCAAUUGC CUGAUGAG X CGAA AUAUGAUC	1311	GAUCAUAUU GCAAUUGA	2012
2463	CCCUCUUC CUGAUGAG X CGAA AUUGCAAU	1312	AUUGCAAUU GAAGAGGG	2013
2502	CGUUUUGG CUGAUGAG X CGAA AGGCUUGG	1313	CCAAGCCUU CCAAAACG	2014
2503	ACGUUUUG CUGAUGAG X CGAA AAGGCUUG	1314	CAAGCCUUC CAAAACGU	2015
2535	CUGAGUUG CUGAUGAG X CGAA ACUGCACA	1315	UGUGCAGUU CAACUCAG	2016
2536	CCUGAGUU CUGAUGAG X CGAA AACUGCAC	1316	GUGCAGUUC AACUCAGG	2017
2541	GAGUCCCU CUGAUGAG X CGAA AGUUGAAC	1317	GUUCAACUC AGGGACUC	2018
2549	UAGGGCCA CUGAUGAG X CGAA AGUCCCUG	1318	CAGGGACUC UGGCCCUA	2019
2557	UUCCUGUU CUGAUGAG X CGAA AGGGCCAG	1319	CUGGCCCUA AACAGGAA	2020
2569	UUGUUUUU CUGAUGAG X CGAA ACCUUCCU	1320	AGGAAGGUC AAAAACAA	2021
2585	AAUUGUAG CUGAUGAG X CGAA AUCUGGGU	1321	ACCCAGAUC CUACAAUU	2022
2588	AUAAAUUG CUGAUGAG X CGAA AGGAUCUG	1322	CAGAUCCUA CAAUUUAU	2023
2593	ACUGGAUA CUGAUGAG X CGAA AUUGUAGG	1323	CCUACAAUU UAUCCAGU	2024
2594	CACUGGAU CUGAUGAG X CGAA AAUUGUAG	1324	CUACAAUUU AUCCAGUG	2025
2595	GCACUGGA CUGAUGAG X CGAA AAAUUGUA	1325	UACAAUUUA UCCAGUGC	2026

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2597	AAGCACUG CUGAUGAG X CGAA AUAAAUUG	1326	CAAUUUAUC CAGUGCUU	2027
2605	UUCCAGUC CUGAUGAG X CGAA AGCACUGG	1327	CCAGUGCUU GACUGGAA	2028
2620	UGAAAUUU CUGAUGAG X CGAA AUGUCAUU	1328	AAUGACAUC AAAUUUCA	2029
2625	CAUCUUGA CUGAUGAG X CGAA AUUUGAUG	1329	CAUCAAAUU UCAAGAUG	2030
2626	ACAUCUUG CUGAUGAG X CGAA AAUUUGAU	1330	AUCAAAUUU CAAGAUGU	2031
2627	CACAUCUU CUGAUGAG X CGAA AAAUUUGA	1331	UCAAAUUUC AAGAUGUG	2032
2638	CCCUCCCC CUGAUGAG X CGAA AUCACAUC	1332	GAUGUGAUU GGGGAGGG	2033
2651	UUGGCCAA CUGAUGAG X CGAA AUUGCCCU	1333	AGGGCAAUU UUGGCCAA	2034
2652	CUUGGCCA CUGAUGAG X CGAA AAUUGCCC	1334	GGGCAAUUU UGGCCAAG	2035
2653	ACUUGGCC CUGAUGAG X CGAA AAAUUGCC	1335	GGCAAUUUU GGCCAAGU	2036
2662	GCCUUAAG CUGAUGAG X CGAA ACUUGGCC	1336	GGCCAAGUU CUUAAGGC	2037
2663	CGCCUUAA CUGAUGAG X CGAA AACUUGGC	1337	GCCAAGUUC UUAAGGCG	2038
2665	CGCGCCUU CUGAUGAG X CGAA AGAACUUG	1338	CAAGUUCUU AAGGCGCG	2039
2666	GCGCGCCU CUGAUGAG X CGAA AAGAACUU	1339	AAGUUCUUA AGGCGCGC	2040
2677	UCCUUCUU CUGAUGAG X CGAA AUGCGCGC	1340	GCGCGCAUC AAGAAGGA	2041
2691	CCAUCCGU CUGAUGAG X CGAA ACCCAUCC	1341	GGAUGGGUU ACGGAUGG	2042

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2692	UCCAUCCG CUGAUGAG X CGAA AACCCAUC	1342	GAUGGGUUA CGGAUGGA	2043
2710	AUUCUUUU CUGAUGAG X CGAA AUGGCAGC	1343	GCUGCCAUC AAAAGAAU	2044
2727	UGGAGGCA CUGAUGAG X CGAA AUUCUUUC	1344	GAAAGAAUA UGCCUCCA	2045
2733	CAUCUUUG CUGAUGAG X CGAA AGGCAUAU	1345	AUAUGCCUC CAAAGAUG	2046
2744	GUCCCUGU CUGAUGAG X CGAA AUCAUCUU	1346	AAGAUGAUC ACAGGGAC	2047
2754	CUCCUGCA CUGAUGAG X CGAA AGUCCCUG	1347	CAGGGACUU UGCAGGAG	2048
2755	UCUCCUGC CUGAUGAG X CGAA AAGUCCCU	1348	AGGGACUUU GCAGGAGA	2049
2773	UUACAAAG CUGAUGAG X CGAA ACUUCCAG	1349	CUGGAAGUU CUUUGUAA	2050
2774	UUUACAAA CUGAUGAG X CGAA AACUUCCA	1350	UGGAAGUUC UUUGUAAA	2051
2776	AGUUUACA CUGAUGAG X CGAA AGAACUUC	1351	GAAGUUCUU UGUAAACU	2052
2777	AAGUUUAC CUGAUGAG X CGAA AAGAACUU	1352	AAGUUCUUU GUAAACUU	2053
2780	UCCAAGUU CUGAUGAG X CGAA ACAAAGAA	1353	UUCUUUGUA AACUUGGA	2054
2785	UGGUGUCC CUGAUGAG X CGAA AGUUUACA	1354	UGUAAACUU GGACACCA	2055
2795	GAUGUUUG CUGAUGAG X CGAA AUGGUGUC	1355	GACACCAUC CAAACAUC	2056
2803	AGAUUGAU CUGAUGAG X CGAA AUGUUUGG	1356	CCAAACAUC AUCAAUCU	2057
2806	AAGAGAUU CUGAUGAG X CGAA AUGAUGUU	1357	AACAUCAUC AAUCUCUU	2058

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2810	UCCUAAGA CUGAUGAG X CGAA AUUGAUGA	1358	UCAUCAAUC UCUUAGGA	2059
2812	GCUCCUAA CUGAUGAG X CGAA AGAUUGAU	1359	AUCAAUCUC UUAGGAGC	2060
2814	AUGCUCCU CUGAUGAG X CGAA AGAGAUUG	1360	CAAUCUCUU AGGAGCAU	2061
2815	CAUGCUCC CUGAUGAG X CGAA AAGAGAUU	1361	AAUCUCUUA GGAGCAUG	2062
2831	GUAGCCUC CUGAUGAG X CGAA AUGUUCAC	1362	GUGAACAUC GAGGCUAC	2063
2838	GGUACAAG CUGAUGAG X CGAA AGCCUCGA	1363	UCGAGGCUA CUUGUACC	2064
2841	CCAGGUAC CUGAUGAG X CGAA AGUAGCCU	1364	AGGCUACUU GUACCUGG	2065
2844	UGGCCAGG CUGAUGAG X CGAA ACAAGUAG	1365	CUACUUGUA CCUGGCCA	2066
2854	GCGUACUC CUGAUGAG X CGAA AUGGCCAG	1366	CUGGCCAUU GAGUACGC	2067
2859	GGGGCGCG CUGAUGAG X CGAA ACUCAAUG	1367	CAUUGAGUA CGCGCCCC	2068
2878	AAGUCCAG CUGAUGAG X CGAA AGGUUUCC	1368	GGAAACCUU CUGGACUU	2069
2879	GAAGUCCA CUGAUGAG X CGAA AAGGUUUC	1369	GAAACCUUC UGGACUUC	2070
2886	UGCGAAGG CUGAUGAG X CGAA AGUCCAGA	1370	UCUGGACUU CCUUCGCA	2071
2887	UUGCGAAG CUGAUGAG X CGAA AAGUCCAG	1371	CUGGACUUC CUUCGCAA	2072
2890	CUCUUGCG CUGAUGAG X CGAA AGGAAGUC	1372	GACUUCCUU CGCAAGAG	2073
2891	GCUCUUGC CUGAUGAG X CGAA AAGGAAGU	1373	ACUUCCUUC GCAAGAGC	2074

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2925	CAAUGGCA CUGAUGAG X CGAA AUGCUGGG	1374	CCCAGCAUU UGCCAUUG	2075
2926	GCAAUGGC CUGAUGAG X CGAA AAUGCUGG	1375	CCAGCAUUU GCCAUUGC	2076
2932	CUAUUGGC CUGAUGAG X CGAA AUGGCAAA	1376	UUUGCCAUU GCCAAUAG	2077
2939	CGCGGUGC CUGAUGAG X CGAA AUUGGCAA	1377	UUGCCAAUA GCACCGCG	2078
2949	ACAGUGUG CUGAUGAG X CGAA ACGCGGUG	1378	CACCGCGUC CACACUGU	2079
2958	GCUGGGAG CUGAUGAG X CGAA ACAGUGUG	1379	CACACUGUC CUCCCAGC	2080
2961	GCUGCUGG CUGAUGAG X CGAA AGGACAGU	1380	ACUGUCCUC CCAGCAGC	2081
2971	AAGUGAAG CUGAUGAG X CGAA AGCUGCUG	1381	CAGCAGCUC CUUCACUU	2082
2974	GCGAAGUG CUGAUGAG X CGAA AGGAGCUG	1382	CAGCUCCUU CACUUCGC	2083
2975	AGCGAAGU CUGAUGAG X CGAA AAGGAGCU	1383	AGCUCCUUC ACUUCGCU	2084
2979	CGGCAGCG CUGAUGAG X CGAA AGUGAAGG	1384	CCUUCACUU CGCUGCCG	2085
2980	UCGGCAGC CUGAUGAG X CGAA AAGUGAAG	1385	CUUCACUUC GCUGCCGA	2086
3009	GGCUCAAG CUGAUGAG X CGAA AGUCCAUG	1386	CAUGGACUA CUUGAGCC	2087
3012	UUUGGCUC CUGAUGAG X CGAA AGUAGUCC	1387	GGACUACUU GAGCCAAA	2088
3027	UGUGGAUA CUGAUGAG X CGAA ACUGUUUU	1388	AAAACAGUU UAUCCACA	2089
3028	CUGUGGAU CUGAUGAG X CGAA AACUGUUU	1389	AAACAGUUU AUCCACAG	2090

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3029	CCUGUGGA CUGAUGAG X CGAA AAACUGUU	1390	AACAGUUUA UCCACAGG	2091
3031	UCCCUGUG CUGAUGAG X CGAA AUAAACUG	1391	CAGUUUAUC CACAGGGA	2092
3041	GGCAGCCA CUGAUGAG X CGAA AUCCCUGU	1392	ACAGGGAUC UGGCUGCC	2093
3058	CCAACUAA CUGAUGAG X CGAA AUGUUUCU	1393	AGAAACAUU UUAGUUGG	2094
3059	ACCAACUA CUGAUGAG X CGAA AAUGUUUC	1394	GAAACAUUU UAGUUGGU	2095
3060	CACCAACU CUGAUGAG X CGAA AAAUGUUU	1395	AAACAUUUU AGUUGGUG	2096
3061	UCACCAAC CUGAUGAG X CGAA AAAAUGUU	1396	AACAUUUUA GUUGGUGA	2097
3064	UUUUCACC CUGAUGAG X CGAA ACUAAAAU	1397	AUUUUAGUU GGUGAAAA	2098
3075	UUGCCACA CUGAUGAG X CGAA AGUUUUCA	1398	UGAAAACUA UGUGGCAA	2099
3088	AAAUCUGC CUGAUGAG X CGAA AUUUUUGC	1399	GCAAAAAUA GCAGAUUU	2100
3095	CAAUCCAA CUGAUGAG X CGAA AUCUGCUA	1400	UAGCAGAUU UUGGAUUG	2101
3096	ACAAUCCA CUGAUGAG X CGAA AAUCUGCU	1401	AGCAGAUUU UGGAUUGU	2102
3097	GACAAUCC CUGAUGAG X CGAA AAAUCUGC	1402	GCAGAUUUU GGAUUGUC	2103
3102	CUCGGGAC CUGAUGAG X CGAA AUCCAAAA	1403	UUUUGGAUU GUCCCGAG	2104
3105	GACCUCGG CUGAUGAG X CGAA ACAAUCCA	1404	UGGAUUGUC CCGAGGUC	2105
3113	CACCUCUU CUGAUGAG X CGAA ACCUCGGG	1405	CCCGAGGUC AAGAGGUG	2106

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3123	UUUUCACG CUGAUGAG X CGAA ACACCUCU	1406	AGAGGUGUA CGUGAAAA	2107
3148	CGCACUGG CUGAUGAG X CGAA AGCCUUCC	1407	GGAAGGCUC CCAGUGCG	2108
3169	AGUGACUC CUGAUGAG X CGAA AUGGCCAU	1408	AUGGCCAUC GAGUCACU	2109
3174	AAUUCAGU CUGAUGAG X CGAA ACUCGAUG	1409	CAUCGAGUC ACUGAAUU	2110
3182	CACACUGU CUGAUGAG X CGAA AUUCAGUG	1410	CACUGAAUU ACAGUGUG	2111
3183	ACACACUG CUGAUGAG X CGAA AAUUCAGU	1411	ACUGAAUUA CAGUGUGU	2112
3192	UGGUUGUG CUGAUGAG X CGAA ACACACUG	1412	CAGUGUGUA CACAACCA	2113
3211	UAGGACCA CUGAUGAG X CGAA ACAUCACU	1413	AGUGAUGUA UGGUCCUA	2114
3216	CACCAUAG CUGAUGAG X CGAA ACCAUACA	1414	UGUAUGGUC CUAUGGUG	2115
3219	ACACACCA CUGAUGAG X CGAA AGGACCAU	1415	AUGGUCCUA UGGUGUGU	2116
3228	CCCAUAGU CUGAUGAG X CGAA ACACACCA	1416	UGGUGUGUU ACUAUGGG	2117
3229	UCCCAUAG CUGAUGAG X CGAA AACACACC	1417	GGUGUGUUA CUAUGGGA	2118
3232	AUCUCCCA CUGAUGAG X CGAA AGUAACAC	1418	GUGUUACUA UGGGAGAU	2119
3241	AAGCUAAC CUGAUGAG X CGAA AUCUCCCA	1419	UGGGAGAUU GUUAGCUU	2120
3244	CCUAAGCU CUGAUGAG X CGAA ACAAUCUC	1420	GAGAUUGUU AGCUUAGG	2121
3245	UCCUAAGC CUGAUGAG X CGAA AACAAUCU	1421	AGAUUGUUA GCUUAGGA	2122

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3249	UGCCUCCU CUGAUGAG X CGAA AGCUAACA	1422	UGUUAGCUU AGGAGGCA	2123
3250	GUGCCUCC CUGAUGAG X CGAA AAGCUAAC	1423	GUUAGCUUA GGAGGCAC	2124
3264	UCCCGCAG CUGAUGAG X CGAA AGGGUGUG	1424	CACACCCUA CUGCGGGA	2125
3278	UUCUGCAC CUGAUGAG X CGAA AGUCAUCC	1425	GGAUGACUU GUGCAGAA	2126
3289	UUCUCGUA CUGAUGAG X CGAA AGUUCUGC	1426	GCAGAACUC UACGAGAA	2127
3291	GCUUCUCG CUGAUGAG X CGAA AGAGUUCU	1427	AGAACUCUA CGAGAAGC	2128
3312	CCAGUCUG CUGAUGAG X CGAA AGCCCUGG	1428	CCAGGGCUA CAGACUGG	2129
3351	UUAGAUCA CUGAUGAG X CGAA ACACCUCA	1429	UGAGGUGUA UGAUCUAA	2130
3356	UCUCAUUA CUGAUGAG X CGAA AUCAUACA	1430	UGUAUGAUC UAAUGAGA	2131
3358	UGUCUCAU CUGAUGAG X CGAA AGAUCAUA	1431	UAUGAUCUA AUGAGACA	2132
3386	CCUCUCAU CUGAUGAG X CGAA AGGCUUCU	1432	AGAAGCCUU AUGAGAGG	2133
3387	GCCUCUCA CUGAUGAG X CGAA AAGGCUUC	1433	GAAGCCUUA UGAGAGGC	2134
3399	GGGCAAAU CUGAUGAG X CGAA AUGGCCUC	1434	GAGGCCAUC AUUUGCCC	2135
3402	UCUGGGCA CUGAUGAG X CGAA AUGAUGGC	1435	GCCAUCAUU UGCCCAGA	2136
3403	AUCUGGGC CUGAUGAG X CGAA AAUGAUGG	1436	CCAUCAUUU GCCCAGAU	2137
3412	GACACCAA CUGAUGAG X CGAA AUCUGGGC	1437	GCCCAGAUA UUGGUGUC	2138

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3414	AGGACACC CUGAUGAG X CGAA AUAUCUGG	1438	CCAGAUAUU GGUGUCCU	2139
3420	UGUUUAAG CUGAUGAG X CGAA ACACCAAU	1439	AUUGGUGUC CUUAAACA	2140
3423	UUCUGUUU CUGAUGAG X CGAA AGGACACC	1440	GGUGUCCUU AAACAGAA	2141
3424	AUUCUGUU CUGAUGAG X CGAA AAGGACAC	1441	GUGUCCUUA AACAGAAU	2142
3435	GCUCCUCU CUGAUGAG X CGAA ACAUUCUG	1442	CAGAAUGUU AGAGGAGC	2143
3436	CGCUCCUC CUGAUGAG X CGAA AACAUUCU	1443	AGAAUGUUA GAGGAGCG	2144
3453	UAUUCACG CUGAUGAG X CGAA AGGUCUUU	1444	AAAGACCUA CGUGAAUA	2145
3461	AAGCGUGG CUGAUGAG X CGAA AUUCACGU	1445	ACGUGAAUA CCACGCUU	2146
3469	UUCUCAUA CUGAUGAG X CGAA AGCGUGGU	1446	ACCACGCUU UAUGAGAA	2147
3470	CUUCUCAU CUGAUGAG X CGAA AAGCGUGG	1447	CCACGCUUU AUGAGAAG	2148
3471	ACUUCUCA CUGAUGAG X CGAA AAAGCGUG	1448	CACGCUUUA UGAGAAGU	2149
3480	CAUAAGUA CUGAUGAG X CGAA ACUUCUCA	1449	UGAGAAGUU UACUUAUG	2150
3481	GCAUAAGU CUGAUGAG X CGAA AACUUCUC	1450	GAGAAGUUU ACUUAUGC	2151
3482	UGCAUAAG CUGAUGAG X CGAA AAACUUCU	1451	AGAAGUUUA CUUAUGCA	2152
3485	UCCUGCAU CUGAUGAG X CGAA AGUAAACU	1452	AGUUUACUU AUGCAGGA	2153
3486	UUCCUGCA CUGAUGAG X CGAA AAGUAAAC	1453	GUUUACUUA UGCAGGAA	2154

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3496	GAACAGUC CUGAUGAG X CGAA AUUCCUGC	1454	GCAGGAAUU GACUGUUC	2155
3503	UUCAGCAG CUGAUGAG X CGAA ACAGUCAA	1455	UUGACUGUU CUGCUGAA	2156
3504	CUUCAGCA CUGAUGAG X CGAA AACAGUCA	1456	UGACUGUUC UGCUGAAG	2157
3522	UUCUGUCC CUGAUGAG X CGAA AGGCCGCU	1457	AGCGGCCUA GGACAGAA	2158
3534	GGUAUACA CUGAUGAG X CGAA AUGUUCUG	1458	CAGAACAUC UGUAUACC	2159
3538	AGAGGGUA CUGAUGAG X CGAA ACAGAUGU	1459	ACAUCUGUA UACCCUCU	2160
3540	ACAGAGGG CUGAUGAG X CGAA AUACAGAU	1460	AUCUGUAUA CCCUCUGU	2161
3545	GGGAAACA CUGAUGAG X CGAA AGGGUAUA	1461	UAUACCCUC UGUUUCCC	2162
3549	GAAAGGGA CUGAUGAG X CGAA ACAGAGGG	1462	CCCUCUGUU UCCCUUUC	2163
3550	UGAAAGGG CUGAUGAG X CGAA AACAGAGG	1463	CCUCUGUUU CCCUUUCA	2164
3551	GUGAAAGG CUGAUGAG X CGAA AAACAGAG	1464	CUCUGUUUC CCUUUCAC	2165
3555	GCCAGUGA CUGAUGAG X CGAA AGGGAAAC	1465	GUUUCCCUU UCACUGGC	2166
3556	UGCCAGUG CUGAUGAG X CGAA AAGGGAAA	1466	UUUCCCUUU CACUGGCA	2167
3557	AUGCCAGU CUGAUGAG X CGAA AAAGGGAA	1467	UUCCCUUUC ACUGGCAU	2168
3576	CAGUUGUC CUGAUGAG X CGAA AGGGUCUC	1468	GAGACCCUU GACAACUG	2169
3601	CUUUGGCA CUGAUGAG X CGAA AGGCAUGU	1469	ACAUGCCUC UGCCAAAG	2170

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3618	CACUUAUA CUGAUGAG X CGAA AUCACAUC	1470	GAUGUGAUA UAUAAGUG	2171
3620	UACACUUA CUGAUGAG X CGAA AUAUCACA	1471	UGUGAUAUA UAAGUGUA	2172
3622	UGUACACU CUGAUGAG X CGAA AUAUAUCA	1472	UGAUAUAUA AGUGUACA	2173
3628	CACAUAUG CUGAUGAG X CGAA ACACUUAU	1473	AUAAGUGUA CAUAUGUG	2174
3632	CCAGCACA CUGAUGAG X CGAA AUGUACAC	1474	GUGUACAUA UGUGCUGG	2175
3644	CUUGUUAG CUGAUGAG X CGAA AUUCCAGC	1475	GCUGGAAUU CUAACAAG	2176
3645	ACUUGUUA CUGAUGAG X CGAA AAUUCCAG	1476	CUGGAAUUC UAACAAGU	2177
3647	UGACUUGU CUGAUGAG X CGAA AGAAUUCC	1477	GGAAUUCUA ACAAGUCA	2178
3654	UAACCUAU CUGAUGAG X CGAA ACUUGUUA	1478	UAACAAGUC AUAGGUUA	2179
3657	UAUUAACC CUGAUGAG X CGAA AUGACUUG	1479	CAAGUCAUA GGUUAAUA	2180
3661	UAAAUAUU CUGAUGAG X CGAA ACCUAUGA	1480	UCAUAGGUU AAUAUUUA	2181
3662	UUAAAUAU CUGAUGAG X CGAA AACCUAUG	1481	CAUAGGUUA AUAUUUAA	2182
3665	GUCUUAAA CUGAUGAG X CGAA AUUAACCU	1482	AGGUUAAUA UUUAAGAC	2183
3667	GUGUCUUA CUGAUGAG X CGAA AUAUUAAC	1483	GUUAAUAUU UAAGACAC	2184
3668	AGUGUCUU CUGAUGAG X CGAA AAUAUUAA	1484	UUAAUAUUU AAGACACU	2185
3669	CAGUGUCU CUGAUGAG X CGAA AAAUAUUA	1485	UAAUAUUUA AGACACUG	2186

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3684	AUCACUUA CUGAUGAG X CGAA AUUUUUCA	1486	UGAAAAAUC UAAGUGAU	2187
3686	AUAUCACU CUGAUGAG X CGAA AGAUUUUU	1487	AAAAAUCUA AGUGAUAU	2188
3693	CUGAUUUA CUGAUGAG X CGAA AUCACUUA	1488	UAAGUGAUA UAAAUCAG	2189
3695	AUCUGAUU CUGAUGAG X CGAA AUAUCACU	1489	AGUGAUAUA AAUCAGAU	2190
3699	AAGAAUCU CUGAUGAG X CGAA AUUUAUAU	1490	AUAUAAAUC AGAUUCUU	2191
3704	GAGAGAAG CUGAUGAG X CGAA AUCUGAUU	1491	AAUCAGAUU CUUCUCUC	2192
3705	AGAGAGAA CUGAUGAG X CGAA AAUCUGAU	1492	AUCAGAUUC UUCUCUCU	2193
3707	UGAGAGAG CUGAUGAG X CGAA AGAAUCUG	1493	CAGAUUCUU CUCUCUCA	2194
3708	AUGAGAGA CUGAUGAG X CGAA AAGAAUCU	1494	AGAUUCUUC UCUCUCAU	2195
3710	AAAUGAGA CUGAUGAG X CGAA AGAAGAAU	1495	AUUCUUCUC UCUCAUUU	2196
3712	UAAAAUGA CUGAUGAG X CGAA AGAGAAGA	1496	UCUUCUCUC UCAUUUUA	2197
3714	GAUAAAAU CUGAUGAG X CGAA AGAGAGAA	1497	UUCUCUCUC AUUUUAUC	2198
3717	AGGGAUAA CUGAUGAG X CGAA AUGAGAGA	1498	UCUCUCAUU UUAUCCCU	2199
3718	GAGGGAUA CUGAUGAG X CGAA AAUGAGAG	1499	CUCUCAUUU UAUCCCUC	2200
3719	UGAGGGAU CUGAUGAG X CGAA AAAUGAGA	1500	UCUCAUUUU AUCCCUCA	2201
3720	GUGAGGGA CUGAUGAG X CGAA AAAAUGAG	1501	CUCAUUUUA UCCCUCAC	2202

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3722	AGGUGAGG CUGAUGAG X CGAA AUAAAAUG	1502	CAUUUUAUC CCUCACCU	2203
3726	CUACAGGU CUGAUGAG X CGAA AGGGAUAA	1503	UUAUCCCUC ACCUGUAG	2204
3733	UGGCAUGC CUGAUGAG X CGAA ACAGGUGA	1504	UCACCUGUA GCAUGCCA	2205
3744	UGAAACGG CUGAUGAG X CGAA ACUGGCAU	1505	AUGCCAGUC CCGUUUCA	2206
3749	CUAAAUGA CUGAUGAG X CGAA ACGGGACU	1506	AGUCCCGUU UCAUUUAG	2207
3750	ACUAAAUG CUGAUGAG X CGAA AACGGGAC	1507	GUCCCGUUU CAUUUAGU	2208
3751	GACUAAAU CUGAUGAG X CGAA AAACGGGA	1508	UCCCGUUUC AUUUAGUC	2209
3754	CAUGACUA CUGAUGAG X CGAA AUGAAACG	1509	CGUUUCAUU UAGUCAUG	2210
3755	ACAUGACU CUGAUGAG X CGAA AAUGAAAC	1510	GUUUCAUUU AGUCAUGU	2211
3756	CACAUGAC CUGAUGAG X CGAA AAAUGAAA	1511	UUUCAUUUA GUCAUGUG	2212
3759	GGUCACAU CUGAUGAG X CGAA ACUAAAUG	1512	CAUUUAGUC AUGUGACC	2213
3771	ACAAGACA CUGAUGAG X CGAA AGUGGUCA	1513	UGACCACUC UGUCUUGU	2214
3775	AAACACAA CUGAUGAG X CGAA ACAGAGUG	1514	CACUCUGUC UUGUGUUU	2215
3777	GGAAACAC CUGAUGAG X CGAA AGACAGAG	1515	CUCUGUCUU GUGUUUCC	2216
3782	GCUGUGGA CUGAUGAG X CGAA ACACAAGA	1516	UCUUGUGUU UCCACAGC	2217
3783	GGCUGUGG CUGAUGAG X CGAA AACACAAG	1517	CUUGUGUUU CCACAGCC	2218

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3784	AGGCUGUG CUGAUGAG X CGAA AAACACAA	1518	UUGUGUUUC CACAGCCU	2219
3799	CUGGACUG CUGAUGAG X CGAA ACUUGCAG	1519	CUGCAAGUU CAGUCCAG	2220
3800	CCUGGACU CUGAUGAG X CGAA AACUUGCA	1520	UGCAAGUUC AGUCCAGG	2221
3804	GCAUCCUG CUGAUGAG X CGAA ACUGAACU	1521	AGUUCAGUC CAGGAUGC	2222
3814	UUAGAUGU CUGAUGAG X CGAA AGCAUCCU	1522	AGGAUGCUA ACAUCUAA	2223
3819	UAUUUUUA CUGAUGAG X CGAA AUGUUAGC	1523	GCUAACAUC UAAAAAUA	2224
3821	UCUAUUUU CUGAUGAG X CGAA AGAUGUUA	1524	UAACAUCUA AAAAUAGA	2225
3827	UUUAAGUC CUGAUGAG X CGAA AUUUUUAG	1525	CUAAAAAUA GACUUAAA	2226
3832	UGAGAUUU CUGAUGAG X CGAA AGUCUAUU	1526	AAUAGACUU AAAUCUCA	2227
3833	AUGAGAUU CUGAUGAG X CGAA AAGUCUAU	1527	AUAGACUUA AAUCUCAU	2228
3837	AGCAAUGA CUGAUGAG X CGAA AUUUAAGU	1528	ACUUAAAUC UCAUUGCU	2229
3839	UAAGCAAU CUGAUGAG X CGAA AGAUUUAA	1529	UUAAAUCUC AUUGCUUA	2230
3842	UUGUAAGC CUGAUGAG X CGAA AUGAGAUU	1530	AAUCUCAUU GCUUACAA	2231
3846	AGGCUUGU CUGAUGAG X CGAA AGCAAUGA	1531	UCAUUGCUU ACAAGCCU	2232
3847	UAGGCUUG CUGAUGAG X CGAA AAGCAAUG	1532	CAUUGCUUA CAAGCCUA	2233
3855	AAGAUUCU CUGAUGAG X CGAA AGGCUUGU	1533	ACAAGCCUA AGAAUCUU	2234

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3861	UCUCUAAA CUGAUGAG X CGAA AUUCUUAG	1534	CUAAGAAUC UUUAGAGA	2235
3863	CUUCUCUA CUGAUGAG X CGAA AGAUUCUU	1535	AAGAAUCUU UAGAGAAG	2236
3864	ACUUCUCU CUGAUGAG X CGAA AAGAUUCU	1536	AGAAUCUUU AGAGAAGU	2237
3865	UACUUCUC CUGAUGAG X CGAA AAAGAUUC	1537	GAAUCUUUA GAGAAGUA	2238
3873	CUUAUGUA CUGAUGAG X CGAA ACUUCUCU	1538	AGAGAAGUA UACAUAAG	2239
3875	AACUUAUG CUGAUGAG X CGAA AUACUUCU	1539	AGAAGUAUA CAUAAGUU	2240
3879	CCUAAACU CUGAUGAG X CGAA AUGUAUAC	1540	GUAUACAUA AGUUUAGG	2241
3883	UUAUCCUA CUGAUGAG X CGAA ACUUAUGU	1541	ACAUAAGUU UAGGAUAA	2242
3884	UUUAUCCU CUGAUGAG X CGAA AACUUAUG	1542	CAUAAGUUU AGGAUAAA	2243
3885	UUUUAUCC CUGAUGAG X CGAA AAACUUAU	1543	AUAAGUUUA GGAUAAAA	2244
3890	CAUUAUUU CUGAUGAG X CGAA AUCCUAAA	1544	UUUAGGAUA AAAUAAUG	2245
3895	AAUCCCAU CUGAUGAG X CGAA AUUUUAUC	1545	GAUAAAAUA AUGGGAUU	2246
3903	GAAAAGAA CUGAUGAG X CGAA AUCCCAUU	1546	AAUGGGAUU UUCUUUUC	2247
3904	AGAAAAGA CUGAUGAG X CGAA AAUCCCAU	1547	AUGGGAUUU UCUUUUCU	2248
3905	AAGAAAAG CUGAUGAG X CGAA AAAUCCCA	1548	UGGGAUUUU CUUUUCUU	2249
3906	AAAGAAAA CUGAUGAG X CGAA AAAAUCCC	1549	GGGAUUUUC UUUUCUUU	2250

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3908	GAAAAGAA CUGAUGAG X CGAA AGAAAAUC	1550	GAUUUUCUU UUCUUUUC	2251
3909	AGAAAAGA CUGAUGAG X CGAA AAGAAAAU	1551	AUUUUCUUU UCUUUUCU	2252
3910	GAGAAAAG CUGAUGAG X CGAA AAAGAAAA	1552	UUUUCUUUU CUUUUCUC	2253
3911	AGAGAAAA CUGAUGAG X CGAA AAAAGAAA	1553	UUUCUUUUC UUUUCUCU	2254
3913	CCAGAGAA CUGAUGAG X CGAA AGAAAAGA	1554	UCUUUUCUU UUCUCUGG	2255
3914	ACCAGAGA CUGAUGAG X CGAA AAGAAAAG	1555	CUUUUCUUU UCUCUGGU	2256
3915	UACCAGAG CUGAUGAG X CGAA AAAGAAAA	1556	UUUUCUUUU CUCUGGUA	2257
3916	UUACCAGA CUGAUGAG X CGAA AAAAGAAA	1557	UUUCUUUUC UCUGGUAA	2258
3918	UAUUACCA CUGAUGAG X CGAA AGAAAAGA	1558	UCUUUUCUC UGGUAAUA	2259
3923	GUCAAUAU CUGAUGAG X CGAA ACCAGAGA	1559	UCUCUGGUA AUAUUGAC	2260
3926	CAAGUCAA CUGAUGAG X CGAA AUUACCAG	1560	CUGGUAAUA UUGACUUG	2261
3928	UACAAGUC CUGAUGAG X CGAA AUAUUACC	1561	GGUAAUAUU GACUUGUA	2262
3933	AAAUAUAC CUGAUGAG X CGAA AGUCAAUA	1562	UAUUGACUU GUAUAUUU	2263
3936	UUAAAAUA CUGAUGAG X CGAA ACAAGUCA	1563	UGACUUGUA UAUUUUAA	2264
3938	UCUUAAAA CUGAUGAG X CGAA AUACAAGU	1564	ACUUGUAUA UUUUAAGA	2265
3940	UUUCUUAA CUGAUGAG X CGAA AUAUACAA	1565	UUGUAUAUU UUAAGAAA	2266

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3941	AUUUCUUA CUGAUGAG X CGAA AAUAUACA	1566	UGUAUAUUU UAAGAAAU	2267
3942	UAUUUCUU CUGAUGAG X CGAA AAAUAUAC	1567	GUAUAUUUU AAGAAAUA	2268
3943	UUAUUUCU CUGAUGAG X CGAA AAAAUAUA	1568	UAUAUUUUA AGAAAUAA	2269
3950	CUUUCUGU CUGAUGAG X CGAA AUUUCUUA	1569	UAAGAAAUA ACAGAAAG	2270
3971	GUCUCCCA CUGAUGAG X CGAA AUGUCACC	1570	GGUGACAUU UGGGAGAC	2271
3972	UGUCUCCC CUGAUGAG X CGAA AAUGUCAC	1571	GUGACAUUU GGGAGACA	2272
3989	AAUAUAUA CUGAUGAG X CGAA AUGUCACA	1572	UGUGACAUU UAUAUAUU	2273
3990	CAAUAUAU CUGAUGAG X CGAA AAUGUCAC	1573	GUGACAUUU AUAUAUUG	2274
3991	UCAAUAUA CUGAUGAG X CGAA AAAUGUCA	1574	UGACAUUUA UAUAUUGA	2275
3993	AUUCAAUA CUGAUGAG X CGAA AUAAAUGU	1575	ACAUUUAUA UAUUGAAU	2276
3995	UAAUUCAA CUGAUGAG X CGAA AUAUAAAU	1576	AUUUAUAUA UUGAAUUA	2277
3997	AUUAAUUC CUGAUGAG X CGAA AUAUAUAA	1577	UUAUAUAUU GAAUUAAU	2278
4002	GGGAUAUU CUGAUGAG X CGAA AUUCAAUA	1578	UAUUGAAUU AAUAUCCC	2279
4003	AGGGAUAU CUGAUGAG X CGAA AAUUCAAU	1579	AUUGAAUUA AUAUCCCU	2280
4006	UGUAGGGA CUGAUGAG X CGAA AUUAAUUC	1580	GAAUUAAUA UCCCUACA	2281
4008	CAUGUAGG CUGAUGAG X CGAA AUAUUAAU	1581	AUUAAUAUC CCUACAUG	2282

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4012	AAUACAUG CUGAUGAG X CGAA AGGGAUAU	1582	AUAUCCCUA CAUGUAUU	2283
4018	AUGUGCAA CUGAUGAG X CGAA ACAUGUAG	1583	CUACAUGUA UUGCACAU	2284
4020	CAAUGUGC CUGAUGAG X CGAA AUACAUGU	1584	ACAUGUAUU GCACAUUG	2285
4027	CUUUUUAC CUGAUGAG X CGAA AUGUGCAA	1585	UUGCACAUU GUAAAAAG	2286
4030	AAACUUUU CUGAUGAG X CGAA ACAAUGUG	1586	CACAUUGUA AAAAGUUU	2287
4037	AAAACUAA CUGAUGAG X CGAA ACUUUUUA	1587	UAAAAAGUU UUAGUUUU	2288
4038	CAAAACUA CUGAUGAG X CGAA AACUUUUU	1588	AAAAAGUUU UAGUUUUG	2289
4039	UCAAAACU CUGAUGAG X CGAA AAACUUUU	1589	AAAAGUUUU AGUUUUGA	2290
4040	AUCAAAAC CUGAUGAG X CGAA AAAACUUU	1590	AAAGUUUUA GUUUUGAU	2291
4043	CUCAUCAA CUGAUGAG X CGAA ACUAAAAC	1591	GUUUUAGUU UUGAUGAG	2292
4044	ACUCAUCA CUGAUGAG X CGAA AACUAAAA	1592	UUUUAGUUU UGAUGAGU	2293
4045	AACUCAUC CUGAUGAG X CGAA AAACUAAA	1593	UUUAGUUUU GAUGAGUU	2294
4053	AAACUCAC CUGAUGAG X CGAA ACUCAUCA	1594	UGAUGAGUU GUGAGUUU	2295
4060	ACAAGGUA CUGAUGAG X CGAA ACUCACAA	1595	UUGUGAGUU UACCUUGU	2296
4061	UACAAGGU CUGAUGAG X CGAA AACUCACA	1596	UGUGAGUUU ACCUUGUA	2297
4062	AUACAAGG CUGAUGAG X CGAA AAACUCAC	1597	GUGAGUUUA CCUUGUAU	2298

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4066	CAGUAUAC CUGAUGAG X CGAA AGGUAAAC	1598	GUUUACCUU GUAUACUG	2299
4069	CUACAGUA CUGAUGAG X CGAA ACAAGGUA	1599	UACCUUGUA UACUGUAG	2300
4071	GCCUACAG CUGAUGAG X CGAA AUACAAGG	1600	CCUUGUAUA CUGUAGGC	2301
4076	AGUGUGCC CUGAUGAG X CGAA ACAGUAUA	1601	UAUACUGUA GGCACACU	2302
4085	UCAGUGCA CUGAUGAG X CGAA AGUGUGCC	1602	GGCACACUU UGCACUGA	2303
4086	AUCAGUGC CUGAUGAG X CGAA AAGUGUGC	1603	GCACACUUU GCACUGAU	2304
4095	UCAUGAUA CUGAUGAG X CGAA AUCAGUGC	1604	GCACUGAUA UAUCAUGA	2305
4097	ACUCAUGA CUGAUGAG X CGAA AUAUCAGU	1605	ACUGAUAUA UCAUGAGU	2306
4099	UCACUCAU CUGAUGAG X CGAA AUAUAUCA	1606	UGAUAUAUC AUGAGUGA	2307
4110	AAGACAUU CUGAUGAG X CGAA AUUCACUC	1607	GAGUGAAUA AAUGUCUU	2308
4116	GUAGGCAA CUGAUGAG X CGAA ACAUUUAU	1608	AUAAAUGUC UUGCCUAC	2309
4118	GAGUAGGC CUGAUGAG X CGAA AGACAUUU	1609	AAAUGUCUU GCCUACUC	2310
4123	UUUUUGAG CUGAUGAG X CGAA AGGCAAGA	1610	UCUUGCCUA CUCAAAAA	2311
4126	UUUUUUUU CUGAUGAG X CGAA AGUAGGCA	1611	UGCCUACUC AAAAAAAA	2312

TABLE VI: HAIRPIN RIZOZYMES AND TRARGET SITES FOR TIE-2

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
10	AGAAGG AGAA GCAC ACCAGAGAAACA X GUACAUUACCUGGUA	2313	GUGCU GUU CCUUCU	2381
76	AAACCC AGAA GUUU ACCAGAGAAACA X GUACAUUACCUGGUA	2314	AAACC GCU GGGUUU	2382
164	GAACUA AGAA GGCU ACCAGAGAAACA X GUACAUUACCUGGUA	2315	AGCCA GCU UAGUUC	2383
185	GGAGCA AGAA GACU ACCAGAGAAACA X GUACAUUACCUGGUA	2316	AGUCA GCU UGCUCC	2384
256	UUCAGC AGAA GAUA ACCAGAGAAACA X GUACAUUACCUGGUA	2317	UAUCU GAU GCUGAA	2385
360	ACUUCC AGAA GAUC ACCAGAGAAACA X GUACAUUACCUGGUA	2318	GAUCC GCU GGAAGU	2386
681	GCAUGA AGAA GGUG ACCAGAGAAACA X GUACAUUACCUGGUA	2319	CACCU GCC UCAUGC	2387
693	UCCUGG AGAA GAGC ACCAGAGAAACA X GUACAUUACCUGGUA	2320	GCUCA GCC CCAGGA	2388
751	GGUGAA AGAA GAGG ACCAGAGAAACA X GUACAUUACCUGGUA	2321	CCUCG GCC UUCACC	2389
818	AAGCAG AGAA GAGA ACCAGAGAAACA X GUACAUUACCUGGUA	2322	UCUCU GUA CUGCUU	2390
823	CAUACA AGAA GUAC ACCAGAGAAACA X GUACAUUACCUGGUA	2323	GUACU GCU UGUAUG	2391
986	CAGGGA AGAA GAAC ACCAGAGAAACA X GUACAUUACCUGGUA	2324	GUUCU GUC UCCCUG	2392
994	AUAGGG AGAA GGGA ACCAGAGAAACA X GUACAUUACCUGGUA	2325	UCCCU GAC CCCUAU	2393
1075	CUUACA AGAA GGCC ACCAGAGAAACA X GUACAUUACCUGGUA	2326	GGCCA GAU UGUAAG	2394
1094	UGUUGC AGAA GCAC ACCAGAGAAACA X GUACAUUACCUGGUA	2327	GUGCA GCU GCAACA	2395

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1139	CUGGAG AGAA GAGA ACCAGAGAAACA X GUACAUUACCUGGUA	2328	UCUCU GCU CUCCAG	2396
1216	UAUAUG AGAA GGCA ACCAGAGAAACA X GUACAUUACCUGGUA	2329	UGCCA GAU CAUAUA	2397
1312	UGUCCC AGAA GGCU ACCAGAGAAACA X GUACAUUACCUGGUA	2330	AGCCG GAU GGGACA	2398
1351	GAAAUG AGAA GUAU ACCAGAGAAACA X GUACAUUACCUGGUA	2331	AUACG GAU CAUUUC	2399
1363	UAUGGC AGAA GAGA ACCAGAGAAACA X GUACAUUACCUGGUA	2332	UCUCA GUA GCCAUA	2400
1386	GGGAGG AGAA GGUG ACCAGAGAAACA X GUACAUUACCUGGUA	2333	CACCG GAU CCUCCC	2401
1399	UCCUGA AGAA GGGG ACCAGAGAAACA X GUACAUUACCUGGUA	2334	CCCCU GAC UCAGGA	2402
1544	GCUCAG AGAA GAUG ACCAGAGAAACA X GUACAUUACCUGGUA	2335	CAUCA GCU CUGAGC	2403
1709	CUCCAC AGAA GACC ACCAGAGAAACA X GUACAUUACCUGGUA	2336	GGUCC GUC GUGGAG	2404
1762	GAUAGA AGAA GUUG ACCAGAGAAACA X GUACAUUACCUGGUA	2337	CAACA GCU UCUAUC	2405
1772	GAGGGA AGAA GAUA ACCAGAGAAACA X GUACAUUACCUGGUA	2338	UAUCG GAC UCCCUC	2406
1803	CUUUUA AGAA GGAG ACCAGAGAAACA X GUACAUUACCUGGUA	2339	CUCCU GCC UAAAAG	2407
1815	AGAGUG AGAA GACU ACCAGAGAAACA X GUACAUUACCUGGUA	2340	AGUCA GAC CACUCU	2408
1977	ACCACG AGAA GCUC ACCAGAGAAACA X GUACAUUACCUGGUA	2341	GAGCA GUA CGUGGU	2409
2038	GGUCCA AGAA GUGA ACCAGAGAAACA X GUACAUUACCUGGUA	2342	UCACU GCU UGGACC	2410
2110	AAUCAC AGAA GAGG ACCAGAGAAACA X GUACAUUACCUGGUA	2343	CCUCG GCU GUGAUU	2411

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2235	AGCUGA AGAA GAAU ACCAGAGAAACA X GUACAUUACCUGGUA	2344	AUUCA GUA UCAGCU	2412
2241	CCCUUG AGAA GAUA ACCAGAGAAACA X GUACAUUACCUGGUA	2345	UAUCA GCU CAAGGG	2413
2317	AGAAAA AGAA GGGU ACCAGAGAAACA X GUACAUUACCUGGUA	2346	ACCCA GCC UUUUCU	2414
2365	UCCGAG AGAA GCUG ACCAGAGAAACA X GUACAUUACCUGGUA	2347	CAGCG GAC CUCGGA	2415
2388	GCUAUA AGAA GCAU ACCAGAGAAACA X GUACAUUACCUGGUA	2348	AUGCU GCU UAUAGC	2416
2410	CAUUCC AGAA GAGC ACCAGAGAAACA X GUACAUUACCUGGUA	2349	GCUCU GCU GGAAUG	2417
2423	CAGUCA AGAA GGUC ACCAGAGAAACA X GUACAUUACCUGGUA	2350	GACCU GCC UGACUG	2418
2427	AGCACA AGAA GGCA ACCAGAGAAACA X GUACAUUACCUGGUA	2351	UGCCU GAC UGUGCU	2419
2436	AAGGCC AGAA GCAC ACCAGAGAAACA X GUACAUUACCUGGUA	2352	GUGCU GUU GGCCUU	2420
2448	AAUAUG AGAA GAAA ACCAGAGAAACA X GUACAUUACCUGGUA	2353	UUUCU GAU CAUAUU	2421
2524	CUGCAC AGAA GGUU ACCAGAGAAACA X GUACAUUACCUGGUA	2354	AACCA GCU GUGCAG	2422
2532	GAGUUG AGAA GCAC ACCAGAGAAACA X GUACAUUACCUGGUA	2355	GUGCA GUU CAACUC	2423
2581	UGUAGG AGAA GGGU ACCAGAGAAACA X GUACAUUACCUGGUA	2356	ACCCA GAU CCUACA	2424
2694	GCAUCC AGAA GUAA ACCAGAGAAACA X GUACAUUACCUGGUA	2357	UUACG GAU GGAUGC	2425
2914	UGCUGG AGAA GUCU ACCAGAGAAACA X GUACAUUACCUGGUA	2358	AGACG GAC CCAGCA	2426
2955	UGGGAG AGAA GUGU ACCAGAGAAACA X GUACAUUACCUGGUA	2359	ACACU GUC CUCCCA	2427

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2967	UGAAGG AGAA GCUG ACCAGAGAAACA X GUACAUUACCUGGUA	2360	CAGCA GCU CCUUCA	2428
2983	CACGUC AGAA GCGA ACCAGAGAAACA X GUACAUUACCUGGUA	2361	UCGCU GCC GACGUG	2429
2986	GGCCAC AGAA GCAG ACCAGAGAAACA X GUACAUUACCUGGUA	2362	CUGCC GAC GUGGCC	2430
3024	UGGAUA AGAA GUUU ACCAGAGAAACA X GUACAUUACCUGGUA	2363	AAACA GUU UAUCCA	2431
3091	UCCAAA AGAA GCUA ACCAGAGAAACA X GUACAUUACCUGGUA	2364	UAGCA GAU UUUGGA	2432
3300	CCCUGG AGAA GCUU ACCAGAGAAACA X GUACAUUACCUGGUA	2365	AAGCU GCC CCAGGG	2433
3314	UCUCCA AGAA GUAG ACCAGAGAAACA X GUACAUUACCUGGUA	2366	CUACA GAC UGGAGA	2434
3500	CAGCAG AGAA GUCA ACCAGAGAAACA X GUACAUUACCUGGUA	2367	UGACU GUU CUGCUG	2435
3505	UUCUUC AGAA GAAC ACCAGAGAAACA X GUACAUUACCUGGUA	2368	GUUCU GCU GAAGAA	2436
3517	GUCCUA AGAA GCUU ACCAGAGAAACA X GUACAUUACCUGGUA	2369	AAGCG GCC UAGGAC	2437
3535	AGGGUA AGAA GAUG ACCAGAGAAACA X GUACAUUACCUGGUA	2370	CAUCU GUA UACCCU	2438
3546	AAGGGA AGAA GAGG ACCAGAGAAACA X GUACAUUACCUGGUA	2371	CCUCU GUU UCCCUU	2439
3583	UUUCUC AGAA GUUG ACCAGAGAAACA X GUACAUUACCUGGUA	2372	CAACU GCU GAGAAA	2440
3700	AGAAGA AGAA GAUU ACCAGAGAAACA X GUACAUUACCUGGUA	2373	AAUCA GAU UCUUCU	2441
3730	GCAUGC AGAA GGUG ACCAGAGAAACA X GUACAUUACCUGGUA	2374	CACCU GUA GCAUGC	2442
3741	AAACGG AGAA GGCA ACCAGAGAAACA X GUACAUUACCUGGUA	2375	UGCCA GUC CCGUUU	2443

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3746	AAAUGA AGAA GGAC ACCAGAGAAACA X GUACAUUACCUGGUA	2376	GUCCC GUU UCAUUU	2444
3772	ACACAA AGAA GAGU ACCAGAGAAACA X GUACAUUACCUGGUA	2377	ACUCU GUC UUGUGU	2445
3788	CUUGCA AGAA GUGG ACCAGAGAAACA X GUACAUUACCUGGUA	2378	CCACA GCC UGCAAG	2446
3801	AUCCUG AGAA GAAC ACCAGAGAAACA X GUACAUUACCUGGUA	2379	GUUCA GUC CAGGAU	2447
4073	UGUGCC AGAA GUAU ACCAGAGAAACA X GUACAUUACCUGGUA	2380	AUACU GUA GGCACA	2448

TABLE VII: HAMMERHEAD RIBOZYME AND TARGET SITE SEQUENCES FOR INTEGRIN ALPHA 6 SUBUNIT

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
11	ACCCCCGG CUGAUGAG X CGAA ACGGUCGC	2449	GCGACCGUC CCGGGGGU	3588
63	GCUGCUGC CUGAUGAG X CGAA ACCGCAGC	2450	GCUGCGGUA GCAGCAGC	3589
82	CUGGGUCC CUGAUGAG X CGAA AGGCUGCC	2451	GGCAGCCUC GGACCCAG	3590
119	GGAGCGGG CUGAUGAG X CGAA ACCUGCAG	2452	CUGCAGGUC CCCGCUCC	3591
126	GGGGAGGG CUGAUGAG X CGAA AGCGGGGA	2453	UCCCCGCUC CCCUCCCC	3592
131	CGCACGGG CUGAUGAG X CGAA AGGGGAGC	2454	GCUCCCCUC CCCGUGCG	3593
141	CAUGGGCG CUGAUGAG X CGAA ACGCACGG	2455	CCGUGCGUC CGCCCAUG	3594
172	GGUAGAGC CUGAUGAG X CGAA AGCACAGC	2456	GCUGUGCUU GCUCUACC	3595
176	GACAGGUA CUGAUGAG X CGAA AGCAAGCA	2457	UGCUUGCUC UACCUGUC	3596
178	CCGACAGG CUGAUGAG X CGAA AGAGCAAG	2458	CUUGCUCUA CCUGUCGG	3597
184	GCCCCGCC CUGAUGAG X CGAA ACAGGUAG	2459	CUACCUGUC GGCGGGGC	3598
194	CGGGACAG CUGAUGAG X CGAA AGCCCCGC	2460	GCGGGGCUC CUGUCCCG	3599
199	CGAGCCGG CUGAUGAG X CGAA ACAGGAGC	2461	GCUCCUGUC CCGGCUCG	3600
206	GCUGCGCC CUGAUGAG X CGAA AGCCGGGA	2462	UCCCGGCUC GGCGCAGC	3601
217	CCAAGUUG CUGAUGAG X CGAA AGGCUGCG	2463	CGCAGCCUU CAACUUGG	3602

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
218	UCCAAGUU CUGAUGAG X CGAA AAGGCUGC	2464	GCAGCCUUC AACUUGGA	3603
223	GAGUGUCC CUGAUGAG X CGAA AGUUGAAG	2465	CUUCAACUU GGACACUC	3604
231	GUCCUCCC CUGAUGAG X CGAA AGUGUCCA	2466	UGGACACUC GGGAGGAC	3605
248	UAUUUCCG CUGAUGAG X CGAA AUCACGUU	2467	AACGUGAUC CGGAAAUA	3606
256	GGUCUCCA CUGAUGAG X CGAA AUUUCCGG	2468	CCGGAAAUA UGGAGACC	3607
275	AAGCCGAA CUGAUGAG X CGAA AGGCUCCC	2469	GGGAGCCUC UUCGGCUU	3608
277	AGAAGCCG CUGAUGAG X CGAA AGAGGCUC	2470	GAGCCUCUU CGGCUUCU	3609
278	GAGAAGCC CUGAUGAG X CGAA AAGAGGCU	2471	AGCCUCUUC GGCUUCUC	3610
283	CCAGCGAG CUGAUGAG X CGAA AGCCGAAG	2472	CUUCGGCUU CUCGCUGG	3611
284	GCCAGCGA CUGAUGAG X CGAA AAGCCGAA	2473	UUCGGCUUC UCGCUGGC	3612
286	UGGCCAGC CUGAUGAG X CGAA AGAAGCCG	2474	CGGCUUCUC GCUGGCCA	3613
331	CCACGAGC CUGAUGAG X CGAA ACAGCCGC	2475	GCGGCUGUU GCUCGUGG	3614
335	GCCCCCAC CUGAUGAG X CGAA AGCAACAG	2476	CUGUUGCUC GUGGGGGC	3615
362	UGCAGUGG CUGAUGAG X CGAA AGCGCUUC	2477	GAAGCGCUU CCACUGCA	3616
363	CUGCAGUG CUGAUGAG X CGAA AAGCGCUU	2478	AAGCGCUUC CACUGCAG	3617
397	CGCAGCUG CUGAUGAG X CGAA ACAGCCCU	2479	AGGGCUGUA CAGCUGCG	3618

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
410	CGGGCGGU CUGAUGAG X CGAA AUGUCGCA	2480	UGCGACAUC ACCGCCCG	3619
437	UCAAACUC CUGAUGAG X CGAA AUCCGCGU	2481	ACGCGGAUC GAGUUUGA	3620
442	CGUUAUCA CUGAUGAG X CGAA ACUCGAUC	2482	GAUCGAGUU UGAUAACG	3621
443	UCGUUAUC CUGAUGAG X CGAA AACUCGAU	2483	AUCGAGUUU GAUAACGA	3622
447	AGCAUCGU CUGAUGAG X CGAA AUCAAACU	2484	AGUUUGAUA ACGAUGCU	3623
466	UGCUUUCU CUGAUGAG X CGAA ACGUGGGG	2485	CCCCACGUC AGAAAGCA	3624
483	CAUCCACU CUGAUGAG X CGAA AUCUUCCU	2486	AGGAAGAUC AGUGGAUG	3625
497	UGGACGGU CUGAUGAG X CGAA ACCCCCAU	2487	AUGGGGGUC ACCGUCCA	3626
503	UGGCUCUG CUGAUGAG X CGAA ACGGUGAC	2488	GUCACCGUC CAGAGCCA	3627
516	GCCCCCUG CUGAUGAG X CGAA ACCUUGGC	2489	GCCAAGGUC CAGGGGGC	3628
530	CAUGUCAC CUGAUGAG X CGAA ACCUUGCC	2490	GGCAAGGUC GUGACAUG	3629
543	AUAUCGGU CUGAUGAG X CGAA AGCACAUG	2491	CAUGUGCUC ACCGAUAU	3630
550	UUUUUUCA CUGAUGAG X CGAA AUCGGUGA	2492	UCACCGAUA UGAAAAAA	3631
569	UUCGUAUU CUGAUGAG X CGAA ACAUGCUG	2493	CAGCAUGUU AAUACGAA	3632
570	CUUCGUAU CUGAUGAG X CGAA AACAUGCU	2494	AGCAUGUUA AUACGAAG	3633
573	CUGCUUCG CUGAUGAG X CGAA AUUAACAU	2495	AUGUUAAUA CGAAGCAG	3634

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
586	UGUCUCGG CUGAUGAG X CGAA AUUCCUGC	2496	GCAGGAAUC CCGAGACA	3635
596	CGCCCAAA CUGAUGAG X CGAA AUGUCUCG	2497	CGAGACAUC UUUGGGCG	3636
598	ACCGCCCA CUGAUGAG X CGAA AGAUGUCU	2498	AGACAUCUU UGGGCGGU	3637
599	CACCGCCC CUGAUGAG X CGAA AAGAUGUC	2499	GACAUCUUU GGGCGGUG	3638
609	CAGGACAU CUGAUGAG X CGAA ACACCGCC	2500	GGCGGUGUU AUGUCCUG	3639
610	UCAGGACA CUGAUGAG X CGAA AACACCGC	2501	GCGGUGUUA UGUCCUGA	3640
614	UGACUCAG CUGAUGAG X CGAA ACAUAACA	2502	UGUUAUGUC CUGAGUCA	3641
621	GAGAUUCU CUGAUGAG X CGAA ACUCAGGA	2503	UCCUGAGUC AGAAUCUC	3642
627	AAUCCUGA CUGAUGAG X CGAA AUUCUGAC	2504	GUCAGAAUC UCAGGAUU	3643
629	UCAAUCCU CUGAUGAG X CGAA AGAUUCUG	2505	CAGAAUCUC AGGAUUGA	3644
635	UCGUCUUC CUGAUGAG X CGAA AUCCUGAG	2506	CUCAGGAUU GAAGACGA	3645
645	CCCAUCCA CUGAUGAG X CGAA AUCGUCUU	2507	AAGACGAUA UGGAUGGG	3646
660	AAAGCUCC CUGAUGAG X CGAA AUCUCCCC	2508	GGGGAGAUU GGAGCUUU	3647
667	CAUCACAA CUGAUGAG X CGAA AGCUCCAA	2509	UUGGAGCUU UUGUGAUG	3648
668	CCAUCACA CUGAUGAG X CGAA AAGCUCCA	2510	UGGAGCUUU UGUGAUGG	3649
669	CCCAUCAC CUGAUGAG X CGAA AAAGCUCC	2511	GGAGCUUUU GUGAUGGG	3650

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
682	GGCCUCUC CUGAUGAG X CGAA AUCGCCCA	2512	UGGGCGAUU GAGAGGCC	3651
700	AAGAGCCA CUGAUGAG X CGAA AUUUCUCA	2513	UGAGAAAUU UGGCUCUU	3652
701	CAAGAGCC CUGAUGAG X CGAA AAUUUCUC	2514	GAGAAAUUU GGCUCUUG	3653
706	GCUGGCAA CUGAUGAG X CGAA AGCCAAAU	2515	AUUUGGCUC UUGCCAGC	3654
708	UUGCUGGC CUGAUGAG X CGAA AGAGCCAA	2516	UUGGCUCUU GCCAGCAA	3655
722	GUAGCUGC CUGAUGAG X CGAA ACACCUUG	2517	CAAGGUGUA GCAGCUAC	3656
729	AGUAAAAG CUGAUGAG X CGAA AGCUGCUA	2518	UAGCAGCUA CUUUUACU	3657
732	UUUAGUAA CUGAUGAG X CGAA AGUAGCUG	2519	CAGCUACUU UUACUAAA	3658
733	CUUUAGUA CUGAUGAG X CGAA AAGUAGCU	2520	AGCUACUUU UACUAAAG	3659
734	UCUUUAGU CUGAUGAG X CGAA AAAGUAGC	2521	GCUACUUUU ACUAAAGA	3660
735	GUCUUUAG CUGAUGAG X CGAA AAAAGUAG	2522	CUACUUUUA CUAAAGAC	3661
738	AAAGUCUU CUGAUGAG X CGAA AGUAAAAG	2523	CUUUUACUA AAGACUUU	3662
745	UGUAAUGA CUGAUGAG X CGAA AGUCUUUA	2524	UAAAGACUU UCAUUACA	3663
746	AUGUAAUG CUGAUGAG X CGAA AAGUCUUU	2525	AAAGACUUU CAUUACAU	3664
747	AAUGUAAU CUGAUGAG X CGAA AAAGUCUU	2526	AAGACUUUC AUUACAUU	3665
750	UACAAUGU CUGAUGAG X CGAA AUGAAAGU	2527	ACUUUCAUU ACAUUGUA	3666

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
751	AUACAAUG CUGAUGAG X CGAA AAUGAAAG	2528	CUUUCAUUA CAUUGUAU	3667
755	CCAAAUAC CUGAUGAG X CGAA AUGUAAUG	2529	CAUUACAUU GUAUUUGG	3668
758	GCUCCAAA CUGAUGAG X CGAA ACAAUGUA	2530	UACAUUGUA UUUGGAGC	3669
760	GGGCUCCA CUGAUGAG X CGAA AUACAAUG	2531	CAUUGUAUU UGGAGCCC	3670
761	GGGGCUCC CUGAUGAG X CGAA AAUACAAU	2532	AUUGUAUUU GGAGCCCC	3671
774	GUUAUAAG CUGAUGAG X CGAA ACCCGGGG	2533	CCCCGGGUA CUUAUAAC	3672
777	CCAGUUAU CUGAUGAG X CGAA AGUACCCG	2534	CGGGUACUU AUAACUGG	3673
778	UCCAGUUA CUGAUGAG X CGAA AAGUACCC	2535	GGGUACUUA UAACUGGA	3674
780	UUUCCAGU CUGAUGAG X CGAA AUAAGUAC	2536	GUACUUAUA ACUGGAAA	3675
794	ACACGAAC CUGAUGAG X CGAA AUCCCUUU	2537	AAAGGGAUU GUUCGUGU	3676
797	UCUACACG CUGAUGAG X CGAA ACAAUCCC	2538	GGGAUUGUU CGUGUAGA	3677
798	CUCUACAC CUGAUGAG X CGAA AACAAUCC	2539	GGAUUGUUC GUGUAGAG	3678
803	UUUUGCUC CUGAUGAG X CGAA ACACGAAC	2540	GUUCGUGUA GAGCAAAA	3679
816	AAAAGUGU CUGAUGAG X CGAA AUUCUUUU	2541	AAAAGAAUA ACACUUUU	3680
822	GUCAAAAA CUGAUGAG X CGAA AGUGUUAU	2542	AUAACACUU UUUUUGAC	3681
823	UGUCAAAA CUGAUGAG X CGAA AAGUGUUA	2543	UAACACUUU UUUUGACA	3682

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
824	AUGUCAAA CUGAUGAG X CGAA AAAGUGUU	2544	AACACUUUU UUUGACAU	3683
825	CAUGUCAA CUGAUGAG X CGAA AAAAGUGU	2545	ACACUUUUU UUGACAUG	3684
826	UCAUGUCA CUGAUGAG X CGAA AAAAAGUG	2546	CACUUUUUU UGACAUGA	3685
827	UUCAUGUC CUGAUGAG X CGAA AAAAAAGU	2547	ACUUUUUUU GACAUGAA	3686
839	UCUUCAAA CUGAUGAG X CGAA AUGUUCAU	2548	AUGAACAUC UUUGAAGA	3687
841	CAUCUUCA CUGAUGAG X CGAA AGAUGUUC	2549	GAACAUCUU UGAAGAUG	3688
842	CCAUCUUC CUGAUGAG X CGAA AAGAUGUU	2550	AACAUCUUU GAAGAUGG	3689
855	AACUUCAU CUGAUGAG X CGAA AGGCCCAU	2551	AUGGGCCUU AUGAAGUU	3690
856	CAACUUCA CUGAUGAG X CGAA AAGGCCCA	2552	UGGGCCUUA UGAAGUUG	3691
863	UCUCCACC CUGAUGAG X CGAA ACUUCAUA	2553	UAUGAAGUU GGUGGAGA	3692
891	AGGAACGA CUGAUGAG X CGAA ACUUUCAU	2554	AUGAAAGUC UCGUUCCU	3693
893	ACAGGAAC CUGAUGAG X CGAA AGACUUUC	2555	GAAAGUCUC GUUCCUGU	3694
896	GGAACAGG CUGAUGAG X CGAA ACGAGACU	2556	AGUCUCGUU CCUGUUCC	3695
897	AGGAACAG CUGAUGAG X CGAA AACGAGAC	2557	GUCUCGUUC CUGUUCCU	3696
902	UUAGCAGG CUGAUGAG X CGAA ACAGGAAC	2558	GUUCCUGUU CCUGCUAA	3697
903	GUUAGCAG CUGAUGAG X CGAA AACAGGAA	2559	UUCCUGUUC CUGCUAAC	3698

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
909	GUAACUGU CUGAUGAG X CGAA AGCAGGAA	2560	UUCCUGCUA ACAGUUAC	3699
915	ACCUAAGU CUGAUGAG X CGAA ACUGUUAG	2561	CUAACAGUU ACUUAGGU	3700
916	AACCUAAG CUGAUGAG X CGAA AACUGUUA	2562	UAACAGUUA CUUAGGUU	3701
919	AAAAACCU CUGAUGAG X CGAA AGUAACUG	2563	CAGUUACUU AGGUUUUU	3702
920	GAAAAACC CUGAUGAG X CGAA AAGUAACU	2564	AGUUACUUA GGUUUUUC	3703
924	CAAAGAAA CUGAUGAG X CGAA ACCUAAGU	2565	ACUUAGGUU UUUCUUUG	3704
925	CCAAAGAA CUGAUGAG X CGAA AACCUAAG	2566	CUUAGGUUU UUCUUUGG	3705
926	UCCAAAGA CUGAUGAG X CGAA AAACCUAA	2567	UUAGGUUUU UCUUUGGA	3706
927	GUCCAAAG CUGAUGAG X CGAA AAAACCUA	2568	UAGGUUUUU CUUUGGAC	3707
928	AGUCCAAA CUGAUGAG X CGAA AAAAACCU	2569	AGGUUUUUC UUUGGACU	3708
930	UGAGUCCA CUGAUGAG X CGAA AGAAAAAC	2570	GUUUUUCUU UGGACUCA	3709
931	CUGAGUCC CUGAUGAG X CGAA AAGAAAAA	2571	UUUUUCUUU GGACUCAG	3710
937	CUUUCCCU CUGAUGAG X CGAA AGUCCAAA	2572	UUUGGACUC AGGGAAAG	3711
948	AGAAACAA CUGAUGAG X CGAA ACCUUUCC	2573	GGAAAGGUA UUGUUUCU	3712
950	UUAGAAAC CUGAUGAG X CGAA AUACCUUU	2574	AAAGGUAUU GUUUCUAA	3713
953	UCUUUAGA CUGAUGAG X CGAA ACAAUACC	2575	GGUAUUGUU UCUAAAGA	3714

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
954	AUCUUUAG CUGAUGAG X CGAA AACAAUAC	2576	GUAUUGUUU CUAAAGAU	3715
955	CAUCUUUA CUGAUGAG X CGAA AAACAAUA	2577	UAUUGUUUC UAAAGAUG	3716
957	CUCAUCUU CUGAUGAG X CGAA AGAAACAA	2578	UUGUUUCUA AAGAUGAG	3717
968	ACAAAAGU CUGAUGAG X CGAA AUCUCAUC	2579	GAUGAGAUC ACUUUUGU	3718
972	AGAUACAA CUGAUGAG X CGAA AGUGAUCU	2580	AGAUCACUU UUGUAUCU	3719
973	CAGAUACA CUGAUGAG X CGAA AAGUGAUC	2581	GAUCACUUU UGUAUCUG	3720
974	CCAGAUAC CUGAUGAG X CGAA AAAGUGAU	2582	AUCACUUUU GUAUCUGG	3721
977	GCACCAGA CUGAUGAG X CGAA ACAAAAGU	2583	ACUUUUGUA UCUGGUGC	3722
979	GAGCACCA CUGAUGAG X CGAA AUACAAAA	2584	UUUUGUAUC UGGUGCUC	3723
987	GGCUCUGG CUGAUGAG X CGAA AGCACCAG	2585	CUGGUGCUC CCAGAGCC	3724
999	UCCACUGU CUGAUGAG X CGAA AUUGGCUC	2586	GAGCCAAUC ACAGUGGA	3725
1016	UUCAGCAA CUGAUGAG X CGAA ACCACGGC	2587	GCCGUGGUU UUGCUGAA	3726
1017	CUUCAGCA CUGAUGAG X CGAA AACCACGG	2588	CCGUGGUUU UGCUGAAG	3727
1018	UCUUCAGC CUGAUGAG X CGAA AAACCACG	2589	CGUGGUUUU GCUGAAGA	3728
1039	GAUGUGCA CUGAUGAG X CGAA ACUUCAUG	2590	CAUGAAGUC UGCACAUC	3729
1047	AGGGAGGA CUGAUGAG X CGAA AUGUGCAG	2591	CUGCACAUC UCCUCCCU	3730

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1049	UCAGGGAG CUGAUGAG X CGAA AGAUGUGC	2592	GCACAUCUC CUCCCUGA	3731
1052	UGCUCAGG CUGAUGAG X CGAA AGGAGAUG	2593	CAUCUCCUC CCUGAGCA	3732
1064	CCAUCGAA CUGAUGAG X CGAA AUGUGCUC	2594	GAGCACAUA UUCGAUGG	3733
1066	CUCCAUCG CUGAUGAG X CGAA AUAUGUGC	2595	GCACAUAUU CGAUGGAG	3734
1067	UCUCCAUC CUGAUGAG X CGAA AAUAUGUG	2596	CACAUAUUC GAUGGAGA	3735
1080	AGAGGCCA CUGAUGAG X CGAA ACCUUCUC	2597	GAGAAGGUC UGGCCUCU	3736
1087	CAAAUGAA CUGAUGAG X CGAA AGGCCAGA	2598	UCUGGCCUC UUCAUUUG	3737
1089	GCCAAAUG CUGAUGAG X CGAA AGAGGCCA	2599	UGGCCUCUU CAUUUGGC	3738
1090	AGCCAAAU CUGAUGAG X CGAA AAGAGGCC	2600	GGCCUCUUC AUUUGGCU	3739
1093	CAUAGCCA CUGAUGAG X CGAA AUGAAGAG	2601	CUCUUCAUU UGGCUAUG	3740
1094	UCAUAGCC CUGAUGAG X CGAA AAUGAAGA	2602	UCUUCAUUU GGCUAUGA	3741
1099	CCACAUCA CUGAUGAG X CGAA AGCCAAAU	2603	AUUUGGCUA UGAUGUGG	3742
1121	UCCUUGUU CUGAUGAG X CGAA AGGUCCAC	2604	GUGGACCUC AACAAGGA	3743
1143	AAUAACUA CUGAUGAG X CGAA AUCUUGCC	2605	GGCAAGAUA UAGUUAUU	3744
1145	CCAAUAAC CUGAUGAG X CGAA AUAUCUUG	2606	CAAGAUAUA GUUAUUGG	3745
1148	GCUCCAAU CUGAUGAG X CGAA ACUAUAUC	2607	GAUAUAGUU AUUGGAGC	3746

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1149	GGCUCCAA CUGAUGAG X CGAA AACUAUAU	2608	AUAUAGUUA UUGGAGCC	3747
1151	GGGGCUCC CUGAUGAG X CGAA AUAACUAU	2609	AUAGUUAUU GGAGCCCC	3748
1165	UAUCAAAA CUGAUGAG X CGAA ACUGUGGG	2610	CCCACAGUA UUUUGAUA	3749
1167	UCUAUCAA CUGAUGAG X CGAA AUACUGUG	2611	CACAGUAUU UUGAUAGA	3750
1168	CUCUAUCA CUGAUGAG X CGAA AAUACUGU	2612	ACAGUAUUU UGAUAGAG	3751
1169	UCUCUAUC CUGAUGAG X CGAA AAAUACUG	2613	CAGUAUUUU GAUAGAGA	3752
1173	UCCAUCUC CUGAUGAG X CGAA AUCAAAAU	2614	AUUUUGAUA GAGAUGGA	3753
1187	GCACCUCC CUGAUGAG X CGAA ACUUCUCC	2615	GGAGAAGUU GGAGGUGC	3754
1201	UGUAGACA CUGAUGAG X CGAA ACACUGCA	2616	UGCAGUGUA UGUCUACA	3755
1205	UUCAUGUA CUGAUGAG X CGAA ACAUACAC	2617	GUGUAUGUC UACAUGAA	3756
1207	GGUUCAUG CUGAUGAG X CGAA AGACAUAC	2618	GUAUGUCUA CAUGAACC	3757
1233	CUUCACAU CUGAUGAG X CGAA AUUCCAUC	2619	GAUGGAAUA AUGUGAAG	3758
1247	UUAAGACG CUGAUGAG X CGAA AUUGGCUU	2620	AAGCCAAUU CGUCUUAA	3759
1248	AUUAAGAC CUGAUGAG X CGAA AAUUGGCU	2621	AGCCAAUUC GUCUUAAU	3760
1251	UCCAUUAA CUGAUGAG X CGAA ACGAAUUG	2622	CAAUUCGUC UUAAUGGA	3761
1253	GUUCCAUU CUGAUGAG X CGAA AGACGAAU	2623	AUUCGUCUU AAUGGAAC	3762

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1254	GGUUCCAU CUGAUGAG X CGAA AAGACGAA	2624	UUCGUCUUA AUGGAACC	3763
1269	AAACAUAG CUGAUGAG X CGAA AUCUUUGG	2625	CCAAAGAUU CUAUGUUU	3764
1270	CAAACAUA CUGAUGAG X CGAA AAUCUUUG	2626	CAAAGAUUC UAUGUUUG	3765
1272	GCCAAACA CUGAUGAG X CGAA AGAAUCUU	2627	AAGAUUCUA UGUUUGGC	3766
1276	CAAUGCCA CUGAUGAG X CGAA ACAUAGAA	2628	UUCUAUGUU UGGCAUUG	3767
1277	GCAAUGCC CUGAUGAG X CGAA AACAUAGA	2629	UCUAUGUUU GGCAUUGC	3768
1283	UUUACUGC CUGAUGAG X CGAA AUGCCAAA	2630	UUUGGCAUU GCAGUAAA	3769
1289	AUAUUUUU CUGAUGAG X CGAA ACUGCAAU	2631	AUUGCAGUA AAAAAUAU	3770
1296	AUCUCCAA CUGAUGAG X CGAA AUUUUUUA	2632	UAAAAAAUA UUGGAGAU	3771
1298	AUAUCUCC CUGAUGAG X CGAA AUAUUUUU	2633	AAAAAUAUU GGAGAUAU	3772
1305	UUGAUUAA CUGAUGAG X CGAA AUCUCCAA	2634	UUGGAGAUA UUAAUCAA	3773
1307	UCUUGAUU CUGAUGAG X CGAA AUAUCUCC	2635	GGAGAUAUU AAUCAAGA	3774
1308	AUCUUGAU CUGAUGAG X CGAA AAUAUCUC	2636	GAGAUAUUA AUCAAGAU	3775
1311	GCCAUCUU CUGAUGAG X CGAA AUUAAUAU	2637	AUAUUAAUC AAGAUGGC	3776
1321	UAUCUGGG CUGAUGAG X CGAA AGCCAUCU	2638	AGAUGGCUA CCCAGAUA	3777
1329	AACUGCAA CUGAUGAG X CGAA AUCUGGGU	2639	ACCCAGAUA UUGCAGUU	3778

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1331	CCAACUGC CUGAUGAG X CGAA AUAUCUGG	2640	CCAGAUAUU GCAGUUGG	3779
1337	GGAGCUCC CUGAUGAG X CGAA ACUGCAAU	2641	AUUGCAGUU GGAGCUCC	3780
1344	AUCAUACG CUGAUGAG X CGAA AGCUCCAA	2642	UUGGAGCUC CGUAUGAU	3781
1348	AGUCAUCA CUGAUGAG X CGAA ACGGAGCU	2643	AGCUCCGUA UGAUGACU	3782
1357	CCUUUCCC CUGAUGAG X CGAA AGUCAUCA	2644	UGAUGACUU GGGAAAGG	3783
1367	UAGAUAAA CUGAUGAG X CGAA ACCUUUCC	2645	GGAAAGGUU UUUAUCUA	3784
1368	AUAGAUAA CUGAUGAG X CGAA AACCUUUC	2646	GAAAGGUUU UUAUCUAU	3785
1369	GAUAGAUA CUGAUGAG X CGAA AAACCUUU	2647	AAAGGUUUU UAUCUAUC	3786
1370	UGAUAGAU CUGAUGAG X CGAA AAAACCUU	2648	AAGGUUUUU AUCUAUCA	3787
1371	AUGAUAGA CUGAUGAG X CGAA AAAAACCU	2649	AGGUUUUUA UCUAUCAU	3788
1373	CCAUGAUA CUGAUGAG X CGAA AUAAAAAC	2650	GUUUUUAUC UAUCAUGG	3789
1375	AUCCAUGA CUGAUGAG X CGAA AGAUAAAA	2651	UUUUAUCUA UCAUGGAU	3790
1377	AGAUCCAU CUGAUGAG X CGAA AUAGAUAA	2652	UUAUCUAUC AUGGAUCU	3791
1384	CAUUUGCA CUGAUGAG X CGAA AUCCAUGA	2653	UCAUGGAUC UGCAAAUG	3792
1397	UUGGUAUU CUGAUGAG X CGAA AUUCCAUU	2654	AAUGGAAUA AAUACCAA	3793
1401	UGGUUUGG CUGAUGAG X CGAA AUUUAUUC	2655	GAAUAAAUA CCAAACCA	3794

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1418	CCCUUGAG CUGAUGAG X CGAA ACCUGUGU	2656	ACACAGGUU CUCAAGGG	3795
1419	ACCCUUGA CUGAUGAG X CGAA AACCUGUG	2657	CACAGGUUC UCAAGGGU	3796
1421	AUACCCUU CUGAUGAG X CGAA AGAACCUG	2658	CAGGUUCUC AAGGGUAU	3797
1428	AGGUGAUA CUGAUGAG X CGAA ACCCUUGA	2659	UCAAGGGUA UAUCACCU	3798
1430	UAAGGUGA CUGAUGAG X CGAA AUACCCUU	2660	AAGGGUAUA UCACCUUA	3799
1432	AAUAAGGU CUGAUGAG X CGAA AUAUACCC	2661	GGGUAUAUC ACCUUAUU	3800
1437	UCCAAAAU CUGAUGAG X CGAA AGGUGAUA	2662	UAUCACCUU AUUUUGGA	3801
1438	AUCCAAAA CUGAUGAG X CGAA AAGGUGAU	2663	AUCACCUUA UUUUGGAU	3802
1440	AUAUCCAA CUGAUGAG X CGAA AUAAGGUG	2664	CACCUUAUU UUGGAUAU	3803
1441	AAUAUCCA CUGAUGAG X CGAA AAUAAGGU	2665	ACCUUAUUU UGGAUAUU	3804
1442	GAAUAUCC CUGAUGAG X CGAA AAAUAAGG	2666	CCUUAUUUU GGAUAUUC	3805
1447	CAAUUGAA CUGAUGAG X CGAA AUCCAAAA	2667	UUUUGGAUA UUCAAUUG	3806
1449	AGCAAUUG CUGAUGAG X CGAA AUAUCCAA	2668	UUGGAUAUU CAAUUGCU	3807
1450	CAGCAAUU CUGAUGAG X CGAA AAUAUCCA	2669	UGGAUAUUC AAUUGCUG	3808
1454	UUUCCAGC CUGAUGAG X CGAA AUUGAAUA	2670	UAUUCAAUU GCUGGAAA	3809
1472	UUUCGAUC CUGAUGAG X CGAA AGGUCCAU	2671	AUGGACCUU GAUCGAAA	3810

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1476	GGAAUUUC CUGAUGAG X CGAA AUCAAGGU	2672	ACCUUGAUC GAAAUUCC	3811
1482	AGGGUAGG CUGAUGAG X CGAA AUUUCGAU	2673	AUCGAAAUU CCUACCCU	3812
1483	CAGGGUAG CUGAUGAG X CGAA AAUUUCGA	2674	UCGAAAUUC CUACCCUG	3813
1486	CAUCAGGG CUGAUGAG X CGAA AGGAAUUU	2675	AAAUUCCUA CCCUGAUG	3814
1496	CCAACAGC CUGAUGAG X CGAA ACAUCAGG	2676	CCUGAUGUU GCUGUUGG	3815
1502	AGGGAACC CUGAUGAG X CGAA ACAGCAAC	2677	GUUGCUGUU GGUUCCCU	3816
1506	UGAGAGGG CUGAUGAG X CGAA ACCAACAG	2678	CUGUUGGUU CCCUCUCA	3817
1507	CUGAGAGG CUGAUGAG X CGAA AACCAACA	2679	UGUUGGUUC CCUCUCAG	3818
1511	GAAUCUGA CUGAUGAG X CGAA AGGGAACC	2680	GGUUCCCUC UCAGAUUC	3819
1513	CUGAAUCU CUGAUGAG X CGAA AGAGGGAA	2681	UUCCCUCUC AGAUUCAG	3820
1518	AGUUACUG CUGAUGAG X CGAA AUCUGAGA	2682	UCUCAGAUU CAGUAACU	3821
1519	UAGUUACU CUGAUGAG X CGAA AAUCUGAG	2683	CUCAGAUUC AGUAACUA	3822
1523	AAAAUAGU CUGAUGAG X CGAA ACUGAAUC	2684	GAUUCAGUA ACUAUUUU	3823
1527	UCUGAAAA CUGAUGAG X CGAA AGUUACUG	2685	CAGUAACUA UUUUCAGA	3824
1529	GAUCUGAA CUGAUGAG X CGAA AUAGUUAC	2686	GUAACUAUU UUCAGAUC	3825
1530	GGAUCUGA CUGAUGAG X CGAA AAUAGUUA	2687	UAACUAUUU UCAGAUCC	3826

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1531	GGGAUCUG CUGAUGAG X CGAA AAAUAGUU	2688	AACUAUUUU CAGAUCCC	3827
1532	CGGGAUCU CUGAUGAG X CGAA AAAAUAGU	2689	ACUAUUUUC AGAUCCCG	3828
1537	CAGGCCGG CUGAUGAG X CGAA AUCUGAAA	2690	UUUCAGAUC CCGGCCUG	3829
1550	UGAAUAUU CUGAUGAG X CGAA AUCACAGG	2691	CCUGUGAUU AAUAUUCA	3830
1551	CUGAAUAU CUGAUGAG X CGAA AAUCACAG	2692	CUGUGAUUA AUAUUCAG	3831
1554	UUUCUGAA CUGAUGAG X CGAA AUUAAUCA	2693	UGAUUAAUA UUCAGAAA	3832
1556	GUUUUCUG CUGAUGAG X CGAA AUAUUAAU	2694	AUUAAUAUU CAGAAAAC	3833
1557	GGUUUUCU CUGAUGAG X CGAA AAUAUUAA	2695	UUAAUAUUC AGAAAACC	3834
1568	GUUACUGU CUGAUGAG X CGAA AUGGUUUU	2696	AAAACCAUC ACAGUAAC	3835
1574	UUAGGAGU CUGAUGAG X CGAA ACUGUGAU	2697	AUCACAGUA ACUCCUAA	3836
1578	UCUGUUAG CUGAUGAG X CGAA AGUUACUG	2698	CAGUAACUC CUAACAGA	3837
1581	AAUUCUGU CUGAUGAG X CGAA AGGAGUUA	2699	UAACUCCUA ACAGAAUU	3838
1589	CGGAGGUC CUGAUGAG X CGAA AUUCUGUU	2700	AACAGAAUU GACCUCCG	3839
1595	UUCUGGCG CUGAUGAG X CGAA AGGUCAAU	2701	AUUGACCUC CGCCAGAA	3840
1623	UAUCCCAC CUGAUGAG X CGAA AGGCGCCC	2702	GGGCGCCUA GUGGGAUA	3841
1631	UGGAGGCA CUGAUGAG X CGAA AUCCCACU	2703	AGUGGGAUA UGCCUCCA	3842

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1637	UUAACCUG CUGAUGAG X CGAA AGGCAUAU	2704	AUAUGCCUC CAGGUUAA	3843
1643	CAGGAUUU CUGAUGAG X CGAA ACCUGGAG	2705	CUCCAGGUU AAAUCCUG	3844
1644	ACAGGAUU CUGAUGAG X CGAA AACCUGGA	2706	UCCAGGUUA AAUCCUGU	3845
1648	CAAAACAG CUGAUGAG X CGAA AUUUAACC	2707	GGUUAAAUC CUGUUUUG	3846
1653	AUAUUCAA CUGAUGAG X CGAA ACAGGAUU	2708	AAUCCUGUU UUGAAUAU	3847
1654	UAUAUUCA CUGAUGAG X CGAA AACAGGAU	2709	AUCCUGUUU UGAAUAUA	3848
1655	GUAUAUUC CUGAUGAG X CGAA AAACAGGA	2710	UCCUGUUUU GAAUAUAC	3849
1660	UAGCAGUA CUGAUGAG X CGAA AUUCAAAA	2711	UUUUGAAUA UACUGCUA	3850
1662	GUUAGCAG CUGAUGAG X CGAA AUAUUCAA	2712	UUGAAUAUA CUGCUAAC	3851
1668	AGCGGGGU CUGAUGAG X CGAA AGCAGUAU	2713	AUACUGCUA ACCCCGCU	3852
1680	AGGAUUAU CUGAUGAG X CGAA ACCAGCGG	2714	CCGCUGGUU AUAAUCCU	3853
1681	AAGGAUUA CUGAUGAG X CGAA AACCAGCG	2715	CGCUGGUUA UAAUCCUU	3854
1683	UGAAGGAU CUGAUGAG X CGAA AUAACCAG	2716	CUGGUUAUA AUCCUUCA	3855
1686	UAUUGAAG CUGAUGAG X CGAA AUUAUAAC	2717	GUUAUAAUC CUUCAAUA	3856
1689	UGAUAUUG CUGAUGAG X CGAA AGGAUUAU	2718	AUAAUCCUU CAAUAUCA	3857
1690	UUGAUAUU CUGAUGAG X CGAA AAGGAUUA	2719	UAAUCCUUC AAUAUCAA	3858

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1694	ACAAUUGA CUGAUGAG X CGAA AUUGAAGG	2720	CCUUCAAUA UCAAUUGU	3859
1696	CCACAAUU CUGAUGAG X CGAA AUAUUGAA	2721	UUCAAUAUC AAUUGUGG	3860
1700	GUGCCCAC CUGAUGAG X CGAA AUUGAUAU	2722	AUAUCAAUU GUGGGCAC	3861
1712	UCAGCUUC CUGAUGAG X CGAA AGUGUGCC	2723	GGCACACUU GAAGCUGA	3862
1738	AUAGCCCA CUGAUGAG X CGAA AUUUUCUU	2724	AAGAAAAUC UGGGCUAU	3863
1745	CUUGAGGA CUGAUGAG X CGAA AGCCCAGA	2725	UCUGGGCUA UCCUCAAG	3864
1747	CUCUUGAG CUGAUGAG X CGAA AUAGCCCA	2726	UGGGCUAUC CUCAAGAG	3865
1750	GAACUCUU CUGAUGAG X CGAA AGGAUAGC	2727	GCUAUCCUC AAGAGUUC	3866
1757	CGAAACUG CUGAUGAG X CGAA ACUCUUGA	2728	UCAAGAGUU CAGUUUCG	3867
1758	UCGAAACU CUGAUGAG X CGAA AACUCUUG	2729	CAAGAGUUC AGUUUCGA	3868
1762	GGUUUCGA CUGAUGAG X CGAA ACUGAACU	2730	AGUUCAGUU UCGAAACC	3869
1763	UGGUUUCG CUGAUGAG X CGAA AACUGAAC	2731	GUUCAGUUU CGAAACCA	3870
1764	UUGGUUUC CUGAUGAG X CGAA AAACUGAA	2732	UUCAGUUUC GAAACCAA	3871
1776	GGGCUCAG CUGAUGAG X CGAA ACCUUGGU	2733	ACCAAGGUU CUGAGCCC	3872
1777	UGGGCUCA CUGAUGAG X CGAA AACCUUGG	2734	CCAAGGUUC UGAGCCCA	3873
1789	CUUGAGUA CUGAUGAG X CGAA AUUUGGGC	2735	GCCCAAAUA UACUCAAG	3874

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1791	UUCUUGAG CUGAUGAG X CGAA AUAUUUGG	2736	CCAAAUAUA CUCAAGAA	3875
1794	UAGUUCUU CUGAUGAG X CGAA AGUAUAUU	2737	AAUAUACUC AAGAACUA	3876
1802	UUCAGAGU CUGAUGAG X CGAA AGUUCUUG	2738	CAAGAACUA ACUCUGAA	3877
1806	CCUCUUCA CUGAUGAG X CGAA AGUUAGUU	2739	AACUAACUC UGAAGAGG	3878
1853	UUAUCCUG CUGAUGAG X CGAA AGCCACAG	2740	CUGUGGCUA CAGGAUAA	3879
1860	UCUGAUAU CUGAUGAG X CGAA AUCCUGUA	2741	UACAGGAUA AUAUCAGA	3880
1863	AUCUCUGA CUGAUGAG X CGAA AUUAUCCU	2742	AGGAUAAUA UCAGAGAU	3881
1865	UUAUCUCU CUGAUGAG X CGAA AUAUUAUC	2743	GAUAAUAUC AGAGAUAA	3882
1872	ACGCAGUU CUGAUGAG X CGAA AUCUCUGA	2744	UCAGAGAUA AACUGCGU	3883
1881	GGGAAUGG CUGAUGAG X CGAA ACGCAGUU	2745	AACUGCGUC CCAUUCCC	3884
1886	GUUAUGGG CUGAUGAG X CGAA AUGGGACG	2746	CGUCCCAUU CCCAUAAC	3885
1887	AGUUAUGG CUGAUGAG X CGAA AAUGGGAC	2747	GUCCCAUUC CCAUAACU	3886
1892	GAGGCAGU CUGAUGAG X CGAA AUGGGAAU	2748	AUUCCCAUA ACUGCCUC	3887
1900	UCUCCACU CUGAUGAG X CGAA AGGCAGUU	2749	AACUGCCUC AGUGGAGA	3888
1910	GGCUCUUG CUGAUGAG X CGAA AUCUCCAC	2750	GUGGAGAUC CAAGAGCC	3889
1924	GCCUACGA CUGAUGAG X CGAA AGCUUGGC	2751	GCCAAGCUC UCGUAGGC	3890

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1926	UCGCCUAC CUGAUGAG X CGAA AGAGCUUG	2752	CAAGCUCUC GUAGGCGA	3891
1929	CACUCGCC CUGAUGAG X CGAA ACGAGAGC	2753	GCUCUCGUA GGCGAGUG	3892
1941	UGGAAGUG CUGAUGAG X CGAA AUUCACUC	2754	GAGUGAAUU CACUUCCA	3893
1942	CUGGAAGU CUGAUGAG X CGAA AAUUCACU	2755	AGUGAAUUC ACUUCCAG	3894
1946	ACUUCUGG CUGAUGAG X CGAA AGUGAAUU	2756	AAUUCACUU CCAGAAGU	3895
1947	AACUUCUG CUGAUGAG X CGAA AAGUGAAU	2757	AUUCACUUC CAGAAGUU	3896
1955	AUUGGAAG CUGAUGAG X CGAA ACUUCUGG	2758	CCAGAAGUU CUUCCAAU	3897
1956	AAUUGGAA CUGAUGAG X CGAA AACUUCUG	2759	CAGAAGUUC UUCCAAUU	3898
1958	AGAAUUGG CUGAUGAG X CGAA AGAACUUC	2760	GAAGUUCUU CCAAUUCU	3899
1959	CAGAAUUG CUGAUGAG X CGAA AAGAACUU	2761	AAGUUCUUC CAAUUCUG	3900
1964	GAAUUCAG CUGAUGAG X CGAA AUUGGAAG	2762	CUUCCAAUU CUGAAUUC	3901
1965	UGAAUUCA CUGAUGAG X CGAA AAUUGGAA	2763	UUCCAAUUC UGAAUUCA	3902
1971	UUCAUCUG CUGAUGAG X CGAA AUUCAGAA	2764	UUCUGAAUU CAGAUGAA	3903
1972	GUUCAUCU CUGAUGAG X CGAA AAUUCAGA	2765	UCUGAAUUC AGAUGAAC	3904
1992	AUCAAUAU CUGAUGAG X CGAA AGCUGUCU	2766	AGACAGCUC AUAUUGAU	3905
1995	AACAUCAA CUGAUGAG X CGAA AUGAGCUG	2767	CAGCUCAUA UUGAUGUU	3906

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1997	UGAACAUC CUGAUGAG X CGAA AUAUGAGC	2768	GCUCAUAUU GAUGUUCA	3907
2003	AAGAAGUG CUGAUGAG X CGAA ACAUCAAU	2769	AUUGAUGUU CACUUCUU	3908
2004	UAAGAAGU CUGAUGAG X CGAA AACAUCAA	2770	UUGAUGUUC ACUUCUUA	3909
2008	CUUUUAAG CUGAUGAG X CGAA AGUGAACA	2771	UGUUCACUU CUUAAAAG	3910
2009	UCUUUUAA CUGAUGAG X CGAA AAGUGAAC	2772	GUUCACUUC UUAAAAGA	3911
2011	CCUCUUUU CUGAUGAG X CGAA AGAAGUGA	2773	UCACUUCUU AAAAGAGG	3912
2012	CCCUCUUU CUGAUGAG X CGAA AAGAAGUG	2774	CACUUCUUA AAAGAGGG	3913
2039	CUGUUACA CUGAUGAG X CGAA ACAUUGUC	2775	GACAAUGUA UGUAACAG	3914
2043	GUUGCUGU CUGAUGAG X CGAA ACAUACAU	2776	AUGUAUGUA ACAGCAAC	3915
2054	UCUAGUUU CUGAUGAG X CGAA AGGUUGCU	2777	AGCAACCUU AAACUAGA	3916
2055	UUCUAGUU CUGAUGAG X CGAA AAGGUUGC	2778	GCAACCUUA AACUAGAA	3917
2060	UUAUAUUC CUGAUGAG X CGAA AGUUUAAG	2779	CUUAAACUA GAAUAUAA	3918
2065	AAAAUUUA CUGAUGAG X CGAA AUUCUAGU	2780	ACUAGAAUA UAAAUUUU	3919
2067	GCAAAAUU CUGAUGAG X CGAA AUAUUCUA	2781	UAGAAUAUA AAUUUUGC	3920
2071	GGGUGCAA CUGAUGAG X CGAA AUUUAUAU	2782	AUAUAAAUU UUGCACCC	3921
2072	CGGGUGCA CUGAUGAG X CGAA AAUUUAUA	2783	UAUAAAUUU UGCACCCG	3922

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2073	UCGGGUGC CUGAUGAG X CGAA AAAUUUAU	2784	AUAAAUUUU GCACCCGA	3923
2091	UUUGUCUU CUGAUGAG X CGAA AUUUCCUU	2785	AAGGAAAUC AAGACAAA	3924
2101	AAUAAGAA CUGAUGAG X CGAA AUUUGUCU	2786	AGACAAAUU UUCUUAUU	3925
2102	AAAUAAGA CUGAUGAG X CGAA AAUUUGUC	2787	GACAAAUUU UCUUAUUU	3926
2103	UAAAUAAG CUGAUGAG X CGAA AAAUUUGU	2788	ACAAAUUUU CUUAUUUA	3927
2104	GUAAAUAA CUGAUGAG X CGAA AAAAUUUG	2789	CAAAUUUUC UUAUUUAC	3928
2106	UGGUAAAU CUGAUGAG X CGAA AGAAAAUU	2790	AAUUUUCUU AUUUACCA	3929
2107	UUGGUAAA CUGAUGAG X CGAA AAGAAAAU	2791	AUUUUCUUA UUUACCAA	3930
2109	AAUUGGUA CUGAUGAG X CGAA AUAAGAAA	2792	UUUCUUAUU UACCAAUU	3931
2110	GAAUUGGU CUGAUGAG X CGAA AAUAAGAA	2793	UUCUUAUUU ACCAAUUC	3932
2111	UGAAUUGG CUGAUGAG X CGAA AAAUAAGA	2794	UCUUAUUUA CCAAUUCA	3933
2117	CCUUUUUG CUGAUGAG X CGAA AUUGGUAA	2795	UUACCAAUU CAAAAAGG	3934
2118	ACCUUUUU CUGAUGAG X CGAA AAUUGGUA	2796	UACCAAUUC AAAAAGGU	3935
2129	AGUUCUGG CUGAUGAG X CGAA ACACCUUU	2797	AAAGGUGUA CCAGAACU	3936
2138	UUUAGAAC CUGAUGAG X CGAA AGUUCUGG	2798	CCAGAACUA GUUCUAAA	3937
2141	UCUUUUAG CUGAUGAG X CGAA ACUAGUUC	2799	GAACUAGUU CUAAAAGA	3938

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2142	AUCUUUUA CUGAUGAG X CGAA AACUAGUU	2800	AACUAGUUC UAAAAGAU	3939
2144	UGAUCUUU CUGAUGAG X CGAA AGAACUAG	2801	CUAGUUCUA AAAGAUCA	3940
2151	AUCCUUCU CUGAUGAG X CGAA AUCUUUUA	2802	UAAAAGAUC AGAAGGAU	3941
2160	UAAAGCAA CUGAUGAG X CGAA AUCCUUCU	2803	AGAAGGAUA UUGCUUUA	3942
2162	UCUAAAGC CUGAUGAG X CGAA AUAUCCUU	2804	AAGGAUAUU GCUUUAGA	3943
2166	UAUUUCUA CUGAUGAG X CGAA AGCAAUAU	2805	AUAUUGCUU UAGAAAUA	3944
2167	UUAUUUCU CUGAUGAG X CGAA AAGCAAUA	2806	UAUUGCUUU AGAAAUAA	3945
2168	GUUAUUUC CUGAUGAG X CGAA AAAGCAAU	2807	AUUGCUUUA GAAAUAAC	3946
2174	GUCACUGU CUGAUGAG X CGAA AUUUCUAA	2808	UUAGAAAUA ACAGUGAC	3947
2193	UGGGUUGG CUGAUGAG X CGAA AGGGCUGU	2809	ACAGCCCUU CCAACCCA	3948
2194	UUGGGUUG CUGAUGAG X CGAA AAGGGCUG	2810	CAGCCCUUC CAACCCAA	3949
2208	UUUUGUGG CUGAUGAG X CGAA AUUCCUUG	2811	CAAGGAAUC CCACAAAA	3950
2241	AAUCAGUU CUGAUGAG X CGAA AGCCUCAU	2812	AUGAGGCUA AACUGAUU	3951
2249	AACGUUGC CUGAUGAG X CGAA AUCAGUUU	2813	AAACUGAUU GCAACGUU	3952
2257	UGUCUGGA CUGAUGAG X CGAA ACGUUGCA	2814	UGCAACGUU UCCAGACA	3953
2258	GUGUCUGG CUGAUGAG X CGAA AACGUUGC	2815	GCAACGUUU CCAGACAC	3954

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2259	AGUGUCUG CUGAUGAG X CGAA AAACGUUG	2816	CAACGUUUC CAGACACU	3955
2268	AUAGGUUA CUGAUGAG X CGAA AGUGUCUG	2817	CAGACACUU UAACCUAU	3956
2269	AAUAGGUU CUGAUGAG X CGAA AAGUGUCU	2818	AGACACUUU AACCUAUU	3957
2270	GAAUAGGU CUGAUGAG X CGAA AAAGUGUC	2819	GACACUUUA ACCUAUUC	3958
2275	AUGCAGAA CUGAUGAG X CGAA AGGUUAAA	2820	UUUAACCUA UUCUGCAU	3959
2277	AUAUGCAG CUGAUGAG X CGAA AUAGGUUA	2821	UAACCUAUU CUGCAUAU	3960
2278	UAUAUGCA CUGAUGAG X CGAA AAUAGGUU	2822	AACCUAUUC UGCAUAUA	3961
2284	GUUCUCUA CUGAUGAG X CGAA AUGCAGAA	2823	UUCUGCAUA UAGAGAAC	3962
2286	CAGUUCUC CUGAUGAG X CGAA AUAUGCAG	2824	CUGCAUAUA GAGAACUG	3963
2301	CUCAGGGA CUGAUGAG X CGAA AGCCCUCA	2825	UGAGGGCUU UCCCUGAG	3964
2302	UCUCAGGG CUGAUGAG X CGAA AAGCCCUC	2826	GAGGGCUUU CCCUGAGA	3965
2303	UUCUCAGG CUGAUGAG X CGAA AAAGCCCU	2827	AGGGCUUUC CCUGAGAA	3966
2317	CACAACUC CUGAUGAG X CGAA ACUGUUUC	2828	GAAACAGUU GAGUUGUG	3967
2322	GGCAACAC CUGAUGAG X CGAA ACUCAACU	2829	AGUUGAGUU GUGUUGCC	3968
2327	UGGUUGGC CUGAUGAG X CGAA ACACAACU	2830	AGUUGUGUU GCCAACCA	3969
2344	CAGCUUGC CUGAUGAG X CGAA AGCCAUUC	2831	GAAUGGCUC GCAAGCUG	3970

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2363	GGAUUUCC CUGAUGAG X CGAA AGCUCACA	2832	UGUGAGCUC GGAAAUCC	3971
2370	UUUAAAAG CUGAUGAG X CGAA AUUUCCGA	2833	UCGGAAAUC CUUUUAAA	3972
2373	UCUUUUAA CUGAUGAG X CGAA AGGAUUUC	2834	GAAAUCCUU UUAAAAGA	3973
2374	UUCUUUUA CUGAUGAG X CGAA AAGGAUUU	2835	AAAUCCUUU UAAAAGAA	3974
2375	UUUCUUUU CUGAUGAG X CGAA AAAGGAUU	2836	AAUCCUUUU AAAAGAAA	3975
2376	AUUUCUUU CUGAUGAG X CGAA AAAAGGAU	2837	AUCCUUUUA AAAGAAAU	3976
2385	GACAUUUG CUGAUGAG X CGAA AUUUCUUU	2838	AAAGAAAUU CAAAUGUC	3977
2386	UGACAUUU CUGAUGAG X CGAA AAUUUCUU	2839	AAGAAAUUC AAAUGUCA	3978
2393	UAAAAAGU CUGAUGAG X CGAA ACAUUUGA	2840	UCAAAUGUC ACUUUUUA	3979
2397	CAAAUAAA CUGAUGAG X CGAA AGUGACAU	2841	AUGUCACUU UUUAUUUG	3980
2398	CCAAAUAA CUGAUGAG X CGAA AAGUGACA	2842	UGUCACUUU UUAUUUGG	3981
2399	ACCAAAUA CUGAUGAG X CGAA AAAGUGAC	2843	GUCACUUUU UAUUUGGU	3982
2400	AACCAAAU CUGAUGAG X CGAA AAAAGUGA	2844	UCACUUUUU AUUUGGUU	3983
2401	AAACCAAA CUGAUGAG X CGAA AAAAAGUG	2845	CACUUUUUA UUUGGUUU	3984
2403	UAAAACCA CUGAUGAG X CGAA AUAAAAAG	2846	CUUUUUAUU UGGUUUUA	3985
2404	UUAAAACC CUGAUGAG X CGAA AAUAAAAA	2847	UUUUUAUUU GGUUUUAA	3986

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2408	GUACUUAA CUGAUGAG X CGAA ACCAAAUA	2848	UAUUUGGUU UUAAGUAC	3987
2409	UGUACUUA CUGAUGAG X CGAA AACCAAAU	2849	AUUUGGUUU UAAGUACA	3988
2410	UUGUACUU CUGAUGAG X CGAA AAACCAAA	2850	UUUGGUUUU AAGUACAA	3989
2411	GUUGUACU CUGAUGAG X CGAA AAAACCAA	2851	UUGGUUUUA AGUACAAC	3990
2415	UUCAGUUG CUGAUGAG X CGAA ACUUAAAA	2852	UUUUAAGUA CAACUGAA	3991
2426	UCAAAGGU CUGAUGAG X CGAA ACUUCAGU	2853	ACUGAAGUC ACCUUUGA	3992
2431	GGGUGUCA CUGAUGAG X CGAA AGGUGACU	2854	AGUCACCUU UGACACCC	3993
2432	GGGGUGUC CUGAUGAG X CGAA AAGGUGAC	2855	GUCACCUUU GACACCCC	3994
2443	UAUCCAGA CUGAUGAG X CGAA AUGGGGUG	2856	CACCCCAUA UCUGGAUA	3995
2445	AAUAUCCA CUGAUGAG X CGAA AUAUGGGG	2857	CCCCAUAUC UGGAUAUU	3996
2451	CAGAUUAA CUGAUGAG X CGAA AUCCAGAU	2858	AUCUGGAUA UUAAUCUG	3997
2453	UUCAGAUU CUGAUGAG X CGAA AUAUCCAG	2859	CUGGAUAUU AAUCUGAA	3998
2454	CUUCAGAU CUGAUGAG X CGAA AAUAUCCA	2860	UGGAUAUUA AUCUGAAG	3999
2457	UAACUUCA CUGAUGAG X CGAA AUUAAUAU	2861	AUAUUAAUC UGAAGUUA	4000
2464	UUGUUUCU CUGAUGAG X CGAA ACUUCAGA	2862	UCUGAAGUU AGAAACAA	4001
2465	GUUGUUUC CUGAUGAG X CGAA AACUUCAG	2863	CUGAAGUUA GAAACAAC	4002

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2481	AUUAUCUU CUGAUGAG X CGAA AUUGCUUG	2864	CAAGCAAUC AAGAUAAU	4003
2487	AGCCAAAU CUGAUGAG X CGAA AUCUUGAU	2865	AUCAAGAUA AUUUGGCU	4004
2490	UGGAGCCA CUGAUGAG X CGAA AUUAUCUU	2866	AAGAUAAUU UGGCUCCA	4005
2491	UUGGAGCC CUGAUGAG X CGAA AAUUAUCU	2867	AGAUAAUUU GGCUCCAA	4006
2496	UGUAAUUG CUGAUGAG X CGAA AGCCAAAU	2868	AUUUGGCUC CAAUUACA	4007
2501	UUAGCUGU CUGAUGAG X CGAA AUUGGAGC	2869	GCUCCAAUU ACAGCUAA	4008
2502	UUUAGCUG CUGAUGAG X CGAA AAUUGGAG	2870	CUCCAAUUA CAGCUAAA	4009
2508	UUUUGCUU CUGAUGAG X CGAA AGCUGUAA	2871	UUACAGCUA AAGCAAAA	4010
2522	AGUUCAAU CUGAUGAG X CGAA ACCACUUU	2872	AAAGUGGUU AUUGAACU	4011
2523	CAGUUCAA CUGAUGAG X CGAA AACCACUU	2873	AAGUGGUUA UUGAACUG	4012
2525	AGCAGUUC CUGAUGAG X CGAA AUAACCAC	2874	GUGGUUAUU GAACUGCU	4013
2534	ACCGAUAA CUGAUGAG X CGAA AGCAGUUC	2875	GAACUGCUU UUAUCGGU	4014
2535	GACCGAUA CUGAUGAG X CGAA AAGCAGUU	2876	AACUGCUUU UAUCGGUC	4015
2536	AGACCGAU CUGAUGAG X CGAA AAAGCAGU	2877	ACUGCUUUU AUCGGUCU	4016
2537	GAGACCGA CUGAUGAG X CGAA AAAAGCAG	2878	CUGCUUUUA UCGGUCUC	4017
2539	CCGAGACC CUGAUGAG X CGAA AUAAAAGC	2879	GCUUUUAUC GGUCUCGG	4018

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2543	ACUCCCGA CUGAUGAG X CGAA ACCGAUAA	2880	UUAUCGGUC UCGGGAGU	4019
2545	CAACUCCC CUGAUGAG X CGAA AGACCGAU	2881	AUCGGUCUC GGGAGUUG	4020
2552	GGUUUAGC CUGAUGAG X CGAA ACUCCCGA	2882	UCGGGAGUU GCUAAACC	4021
2556	GGAAGGUU CUGAUGAG X CGAA AGCAACUC	2883	GAGUUGCUA AACCUUCC	4022
2562	CACCUGGG CUGAUGAG X CGAA AGGUUUAG	2884	CUAAACCUU CCCAGGUG	4023
2563	ACACCUGG CUGAUGAG X CGAA AAGGUUUA	2885	UAAACCUUC CCAGGUGU	4024
2572	CUCCAAAA CUGAUGAG X CGAA ACACCUGG	2886	CCAGGUGUA UUUUGGAG	4025
2574	ACCUCCAA CUGAUGAG X CGAA AUACACCU	2887	AGGUGUAUU UUGGAGGU	4026
2575	UACCUCCA CUGAUGAG X CGAA AAUACACC	2888	GGUGUAUUU UGGAGGUA	4027
2576	GUACCUCC CUGAUGAG X CGAA AAAUACAC	2889	GUGUAUUUU GGAGGUAC	4028
2583	AACAACUG CUGAUGAG X CGAA ACCUCCAA	2890	UUGGAGGUA CAGUUGUU	4029
2588	UCGCCAAC CUGAUGAG X CGAA ACUGUACC	2891	GGUACAGUU GUUGGCGA	4030
2591	UGCUCGCC CUGAUGAG X CGAA ACAACUGU	2892	ACAGUUGUU GGCGAGCA	4031
2604	AGAUUUCA CUGAUGAG X CGAA AGCUUGCU	2893	AGCAAGCUA UGAAAUCU	4032
2611	CAUCUUCA CUGAUGAG X CGAA AUUUCAUA	2894	UAUGAAAUC UGAAGAUG	4033
2631	CUCUAUUA CUGAUGAG X CGAA ACUUCCCA	2895	UGGGAAGUU UAAUAGAG	4034

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2632	ACUCUAUU CUGAUGAG X CGAA AACUUCCC	2896	GGGAAGUUU AAUAGAGU	4035
2633	UACUCUAU CUGAUGAG X CGAA AAACUUCC	2897	GGAAGUUUA AUAGAGUA	4036
2636	UCAUACUC CUGAUGAG X CGAA AUUAAACU	2898	AGUUUAAUA GAGUAUGA	4037
2641	UGAAUUCA CUGAUGAG X CGAA ACUCUAUU	2899	AAUAGAGUA UGAAUUCA	4038
2647	UUACCCUG CUGAUGAG X CGAA AUUCAUAC	2900	GUAUGAAUU CAGGGUAA	4039
2648	AUUACCCU CUGAUGAG X CGAA AAUUCAUA	2901	UAUGAAUUC AGGGUAAU	4040
2654	AAGUUUAU CUGAUGAG X CGAA ACCCUGAA	2902	UUCAGGGUA AUAAACUU	4041
2657	CCUAAGUU CUGAUGAG X CGAA AUUACCCU	2903	AGGGUAAUA AACUUAGG	4042
2662	GUUUACCU CUGAUGAG X CGAA AGUUUAUU	2904	AAUAAACUU AGGUAAAC	4043
2663	GGUUUACC CUGAUGAG X CGAA AAGUUUAU	2905	AUAAACUUA GGUAAACC	4044
2667	AAGAGGUU CUGAUGAG X CGAA ACCUAAGU	2906	ACUUAGGUA AACCUCUU	4045
2673	GUUUGUAA CUGAUGAG X CGAA AGGUUUAC	2907	GUAAACCUC UUACAAAC	4046
2675	AGGUUUGU CUGAUGAG X CGAA AGAGGUUU	2908	AAACCUCUU ACAAACCU	4047
2676	GAGGUUUG CUGAUGAG X CGAA AAGAGGUU	2909	AACCUCUUA CAAACCUC	4048
2684	GCUGUGCC CUGAUGAG X CGAA AGGUUUGU	2910	ACAAACCUC GGCACAGC	4049
2698	GAAUGUUC CUGAUGAG X CGAA AGGUUGCU	2911	AGCAACCUU GAACAUUC	4050

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2705	GGCCACUG CUGAUGAG X CGAA AUGUUCAA	2912	UUGAACAUU CAGUGGCC	4051
2706	UGGCCACU CUGAUGAG X CGAA AAUGUUCA	2913	UGAACAUUC AGUGGCCA	4052
2723	CCAUUGCU CUGAUGAG X CGAA AUUUCUUU	2914	AAAGAAAUU AGCAAUGG	4053
2724	CCCAUUGC CUGAUGAG X CGAA AAUUUCUU	2915	AAGAAAUUA GCAAUGGG	4054
2740	AAUAAAGC CUGAUGAG X CGAA ACCAUUUC	2916	GAAAUGGUU GCUUUAUU	4055
2744	ACCAAAUA CUGAUGAG X CGAA AGCAACCA	2917	UGGUUGCUU UAUUUGGU	4056
2745	CACCAAAU CUGAUGAG X CGAA AAGCAACC	2918	GGUUGCUUU AUUUGGUG	4057
2746	UCACCAAA CUGAUGAG X CGAA AAAGCAAC	2919	GUUGCUUUA UUUGGUGA	4058
2748	UUUCACCA CUGAUGAG X CGAA AUAAAGCA	2920	UGCUUUAUU UGGUGAAA	4059
2749	CUUUCACC CUGAUGAG X CGAA AAUAAAGC	2921	GCUUUAUUU GGUGAAAG	4060
2759	UUGGAUUC CUGAUGAG X CGAA ACUUUCAC	2922	GUGAAAGUA GAAUCCAA	4061
2764	AUCCUUUG CUGAUGAG X CGAA AUUCUACU	2923	AGUAGAAUC CAAAGGAU	4062
2773	CCUUUUCC CUGAUGAG X CGAA AUCCUUUG	2924	CAAAGGAUU GGAAAAGG	4063
2783	UCACAAGU CUGAUGAG X CGAA ACCUUUUC	2925	GAAAAGGUA ACUUGUGA	4064
2787	UGGCUCAC CUGAUGAG X CGAA AGUUACCU	2926	AGGUAACUU GUGAGCCA	4065
2807	AGGGAGUU CUGAUGAG X CGAA AUCUCCUU	2927	AAGGAGAUA AACUCCCU	4066

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2812	GGUUCAGG CUGAUGAG X CGAA AGUUUAUC	2928	GAUAAACUC CCUGAACC	4067
2822	GACUCCGU CUGAUGAG X CGAA AGGUUCAG	2929	CUGAACCUA ACGGAGUC	4068
2830	AGUUGUGA CUGAUGAG X CGAA ACUCCGUU	2930	AACGGAGUC UCACAACU	4069
2832	UGAGUUGU CUGAUGAG X CGAA AGACUCCG	2931	CGGAGUCUC ACAACUCA	4070
2839	UCUUUCUU CUGAUGAG X CGAA AGUUGUGA	2932	UCACAACUC AAGAAAGA	4071
2858	UUUUCAGU CUGAUGAG X CGAA AUUUCCCG	2933	CGGGAAAUU ACUGAAAA	4072
2859	UUUUUCAG CUGAUGAG X CGAA AAUUUCCC	2934	GGGAAAUUA CUGAAAAA	4073
2873	UUAUCAUC CUGAUGAG X CGAA AUCUGUUU	2935	AAACAGAUA GAUGAUAA	4074
2880	UUUUCUGU CUGAUGAG X CGAA AUCAUCUA	2936	UAGAUGAUA ACAGAAAA	4075
2890	AUAAAGAA CUGAUGAG X CGAA AUUUUCUG	2937	CAGAAAAUU UUCUUUAU	4076
2891	AAUAAAGA CUGAUGAG X CGAA AAUUUUCU	2938	AGAAAAUUU UCUUUAUU	4077
2892	AAAUAAAG CUGAUGAG X CGAA AAAUUUUC	2939	GAAAAUUUU CUUUAUUU	4078
2893	CAAAUAAA CUGAUGAG X CGAA AAAAUUUU	2940	AAAAUUUUC UUUAUUUG	4079
2895	AGCAAAUA CUGAUGAG X CGAA AGAAAAUU	2941	AAUUUUCUU UAUUUGCU	4080
2896	CAGCAAAU CUGAUGAG X CGAA AAGAAAAU	2942	AUUUUCUUU AUUUGCUG	4081
2897	UCAGCAAA CUGAUGAG X CGAA AAAGAAAA	2943	UUUUCUUUA UUUGCUGA	4082

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2899	UUUCAGCA CUGAUGAG X CGAA AUAAAGAA	2944	UUCUUUAUU UGCUGAAA	4083
2900	CUUUCAGC CUGAUGAG X CGAA AAUAAAGA	2945	UCUUUAUUU GCUGAAAG	4084
2914	GAGUCUGG CUGAUGAG X CGAA AUUUUCUU	2946	AAGAAAAUA CCAGACUC	4085
2922	ACAGUUAA CUGAUGAG X CGAA AGUCUGGU	2947	ACCAGACUC UUAACUGU	4086
2924	CUACAGUU CUGAUGAG X CGAA AGAGUCUG	2948	CAGACUCUU AACUGUAG	4087
2925	GCUACAGU CUGAUGAG X CGAA AAGAGUCU	2949	AGACUCUUA ACUGUAGC	4088
2931	GUUCACGC CUGAUGAG X CGAA ACAGUUAA	2950	UUAACUGUA GCGUGAAC	4089
2957	GGGCAUCU CUGAUGAG X CGAA AUGUUCAC	2951	GUGAACAUC AGAUGCCC	4090
2992	AAAUAAGA CUGAUGAG X CGAA ACGCCUUG	2952	CAAGGCGUC UCUUAUUU	4091
2994	CAAAAUAA CUGAUGAG X CGAA AGACGCCU	2953	AGGCGUCUC UUAUUUUG	4092
2996	CGCAAAAU CUGAUGAG X CGAA AGAGACGC	2954	GCGUCUCUU AUUUUGCG	4093
2997	GCGCAAAA CUGAUGAG X CGAA AAGAGACG	2955	CGUCUCUUA UUUUGCGC	4094
2999	GAGCGCAA CUGAUGAG X CGAA AUAAGAGA	2956	UCUCUUAUU UUGCGCUC	4095
3000	CGAGCGCA CUGAUGAG X CGAA AAUAAGAG	2957	CUCUUAUUU UGCGCUCG	4096
3001	UCGAGCGC CUGAUGAG X CGAA AAAUAAGA	2958	UCUUAUUUU GCGCUCGA	4097
3007	AUAACCUC CUGAUGAG X CGAA AGCGCAAA	2959	UUUGCGCUC GAGGUUAU	4098

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3013	UGUUCCAU CUGAUGAG X CGAA ACCUCGAG	2960	CUCGAGGUU AUGGAACA	4099
3014	CUGUUCCA CUGAUGAG X CGAA AACCUCGA	2961	UCGAGGUUA UGGAACAG	4100
3028	CCUCUAGA CUGAUGAG X CGAA AUGUGCUG	2962	CAGCACAUU UCUAGAGG	4101
3029	UCCUCUAG CUGAUGAG X CGAA AAUGUGCU	2963	AGCACAUUU CUAGAGGA	4102
3030	UUCCUCUA CUGAUGAG X CGAA AAAUGUGC	2964	GCACAUUUC UAGAGGAA	4103
3032	UAUUCCUC CUGAUGAG X CGAA AGAAAUGU	2965	ACAUUUCUA GAGGAAUA	4104
3040	GUUUGGAA CUGAUGAG X CGAA AUUCCUCU	2966	AGAGGAAUA UUCCAAAC	4105
3042	CAGUUUGG CUGAUGAG X CGAA AUAUUCCU	2967	AGGAAUAUU CCAAACUG	4106
3043	UCAGUUUG CUGAUGAG X CGAA AAUAUUCC	2968	GGAAUAUUC CAAACUGA	4107
3055	UGUCCAAG CUGAUGAG X CGAA AGUUCAGU	2969	ACUGAACUA CUUGGACA	4108
3058	GAAUGUCC CUGAUGAG X CGAA AGUAGUUC	2970	GAACUACUU GGACAUUC	4109
3065	CGCAUGAG CUGAUGAG X CGAA AUGUCCAA	2971	UUGGACAUU CUCAUGCG	4110
3066	UCGCAUGA CUGAUGAG X CGAA AAUGUCCA	2972	UGGACAUUC UCAUGCGA	4111
3068	GCUCGCAU CUGAUGAG X CGAA AGAAUGUC	2973	GACAUUCUC AUGCGAGC	4112
3079	CAUCAAUG CUGAUGAG X CGAA AGGCUCGC	2974	GCGAGCCUU CAUUGAUG	4113
3080	ACAUCAAU CUGAUGAG X CGAA AAGGCUCG	2975	CGAGCCUUC AUUGAUGU	4114

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3083	GUCACAUC CUGAUGAG X CGAA AUGAAGGC	2976	GCCUUCAUU GAUGUGAC	4115
3108	CAGCCUGA CUGAUGAG X CGAA AUUUUCGG	2977	CCGAAAAUA UCAGGCUG	4116
3110	GGCAGCCU CUGAUGAG X CGAA AUAUUUUC	2978	GAAAAUAUC AGGCUGCC	4117
3132	UCGAACCU CUGAUGAG X CGAA AGUGCCUG	2979	CAGGCACUC AGGUUCGA	4118
3137	GUCACUCG CUGAUGAG X CGAA ACCUGAGU	2980	ACUCAGGUU CGAGUGAC	4119
3138	AGUCACUC CUGAUGAG X CGAA AACCUGAG	2981	CUCAGGUUC GAGUGACU	4120
3151	UUGAGGGA CUGAUGAG X CGAA ACACAGUC	2982	GACUGUGUU UCCCUCAA	4121
3152	UUUGAGGG CUGAUGAG X CGAA AACACAGU	2983	ACUGUGUUU CCCUCAAA	4122
3153	CUUUGAGG CUGAUGAG X CGAA AAACACAG	2984	CUGUGUUUC CCUCAAAG	4123
3157	CAGUCUUU CUGAUGAG X CGAA AGGGAAAC	2985	GUUUCCCUC AAAGACUG	4124
3167	UACUGAGC CUGAUGAG X CGAA ACAGUCUU	2986	AAGACUGUA GCUCAGUA	4125
3171	CGAAUACU CUGAUGAG X CGAA AGCUACAG	2987	CUGUAGCUC AGUAUUCG	4126
3175	CUCCCGAA CUGAUGAG X CGAA ACUGAGCU	2988	AGCUCAGUA UUCGGGAG	4127
3177	UACUCCCG CUGAUGAG X CGAA AUACUGAG	2989	CUCAGUAUU CGGGAGUA	4128
3178	GUACUCCC CUGAUGAG X CGAA AAUACUGA	2990	UCAGUAUUC GGGAGUAC	4129
3185	CACCAAGG CUGAUGAG X CGAA ACUCCCGA	2991	UCGGGAGUA CCUUGGUG	4130

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3189	GAUCCACC CUGAUGAG X CGAA AGGUACUC	2992	GAGUACCUU GGUGGAUC	4131
3197	ACUAGGAU CUGAUGAG X CGAA AUCCACCA	2993	UGGUGGAUC AUCCUAGU	4132
3200	GCCACUAG CUGAUGAG X CGAA AUGAUCCA	2994	UGGAUCAUC CUAGUGGC	4133
3203	AUAGCCAC CUGAUGAG X CGAA AGGAUGAU	2995	AUCAUCCUA GUGGCUAU	4134
3210	AGCGAGAA CUGAUGAG X CGAA AGCCACUA	2996	UAGUGGCUA UUCUCGCU	4135
3212	CCAGCGAG CUGAUGAG X CGAA AUAGCCAC	2997	GUGGCUAUU CUCGCUGG	4136
3213	CCCAGCGA CUGAUGAG X CGAA AAUAGCCA	2998	UGGCUAUUC UCGCUGGG	4137
3215	AUCCCAGC CUGAUGAG X CGAA AGAAUAGC	2999	GCUAUUCUC GCUGGGAU	4138
3224	AGCAUCAA CUGAUGAG X CGAA AUCCCAGC	3000	GCUGGGAUC UUGAUGCU	4139
3226	CAAGCAUC CUGAUGAG X CGAA AGAUCCCA	3001	UGGGAUCUU GAUGCUUG	4140
3233	AAUAAAGC CUGAUGAG X CGAA AGCAUCAA	3002	UUGAUGCUU GCUUUAUU	4141
3237	CACUAAUA CUGAUGAG X CGAA AGCAAGCA	3003	UGCUUGCUU UAUUAGUG	4142
3238	ACACUAAU CUGAUGAG X CGAA AAGCAAGC	3004	GCUUGCUUU AUUAGUGU	4143
3239	AACACUAA CUGAUGAG X CGAA AAAGCAAG	3005	CUUGCUUUA UUAGUGUU	4144
3241	UAAACACU CUGAUGAG X CGAA AUAAAGCA	3006	UGCUUUAUU AGUGUUUA	4145
3242	AUAAACAC CUGAUGAG X CGAA AAUAAAGC	3007	GCUUUAUUA GUGUUUAU	4146

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3247	AUAGUAUA CUGAUGAG X CGAA ACACUAAU	3008	AUUAGUGUU UAUACUAU	4147
3248	CAUAGUAU CUGAUGAG X CGAA AACACUAA	3009	UUAGUGUUU AUACUAUG	4148
3249	CCAUAGUA CUGAUGAG X CGAA AAACACUA	3010	UAGUGUUUA UACUAUGG	4149
3251	UUCCAUAG CUGAUGAG X CGAA AUAAACAC	3011	GUGUUUAUA CUAUGGAA	4150
3254	CACUUCCA CUGAUGAG X CGAA AGUAUAAA	3012	UUUAUACUA UGGAAGUG	4151
3267	CUUGAAGA CUGAUGAG X CGAA ACCACACU	3013	AGUGUGGUU UCUUCAAG	4152
3268	UCUUGAAG CUGAUGAG X CGAA AACCACAC	3014	GUGUGGUUU CUUCAAGA	4153
3269	CUCUUGAA CUGAUGAG X CGAA AAACCACA	3015	UGUGGUUUC UUCAAGAG	4154
3271	UUCUCUUG CUGAUGAG X CGAA AGAAACCA	3016	UGGUUUCUU CAAGAGAA	4155
3272	UUUCUCUU CUGAUGAG X CGAA AAGAAACC	3017	GGUUUCUUC AAGAGAAA	4156
3282	AUCUUUCU CUGAUGAG X CGAA AUUUCUCU	3018	AGAGAAAUA AGAAAGAU	4157
3291	AUCAUAAU CUGAUGAG X CGAA AUCUUUCU	3019	AGAAAGAUC AUUAUGAU	4158
3294	GGCAUCAU CUGAUGAG X CGAA AUGAUCUU	3020	AAGAUCAUU AUGAUGCC	4159
3295	UGGCAUCA CUGAUGAG X CGAA AAUGAUCU	3021	AGAUCAUUA UGAUGCCA	4160
3307	CCUUGUGA CUGAUGAG X CGAA AUGUGGCA	3022	UGCCACAUA UCACAAGG	4161
3309	AGCCUUGU CUGAUGAG X CGAA AUAUGUGG	3023	CCACAUAUC ACAAGGCU	4162

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3323	UGAGCAUG CUGAUGAG X CGAA AUCUCAGC	3024	GCUGAGAUC CAUGCUCA	4163
3330	AGAUGGCU CUGAUGAG X CGAA AGCAUGGA	3025	UCCAUGCUC AGCCAUCU	4164
3337	CUUUAUCA CUGAUGAG X CGAA AUGGCUGA	3026	UCAGCCAUC UGAUAAAG	4165
3342	CCUCUCUU CUGAUGAG X CGAA AUCAGAUG	3027	CAUCUGAUA AAGAGAGG	4166
3353	UCAGAAGU CUGAUGAG X CGAA AGCCUCUC	3028	GAGAGGCUU ACUUCUGA	4167
3354	AUCAGAAG CUGAUGAG X CGAA AAGCCUCU	3029	AGAGGCUUA CUUCUGAU	4168
3357	UGCAUCAG CUGAUGAG X CGAA AGUAAGCC	3030	GGCUUACUU CUGAUGCA	4169
3358	AUGCAUCA CUGAUGAG X CGAA AAGUAAGC	3031	GCUUACUUC UGAUGCAU	4170
3367	AUCAAUAC CUGAUGAG X CGAA AUGCAUCA	3032	UGAUGCAUA GUAUUGAU	4171
3370	UAGAUCAA CUGAUGAG X CGAA ACUAUGCA	3033	UGCAUAGUA UUGAUCUA	4172
3372	AGUAGAUC CUGAUGAG X CGAA AUACUAUG	3034	CAUAGUAUU GAUCUACU	4173
3376	CAGAAGUA CUGAUGAG X CGAA AUCAAUAC	3035	GUAUUGAUC UACUUCUG	4174
3378	UACAGAAG CUGAUGAG X CGAA AGAUCAAU	3036	AUUGAUCUA CUUCUGUA	4175
3381	AAUUACAG CUGAUGAG X CGAA AGUAGAUC	3037	GAUCUACUU CUGUAAUU	4176
3382	CAAUUACA CUGAUGAG X CGAA AAGUAGAU	3038	AUCUACUUC UGUAAUUG	4177
3386	CACACAAU CUGAUGAG X CGAA ACAGAAGU	3039	ACUUCUGUA AUUGUGUG	4178

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3389	AUCCACAC CUGAUGAG X CGAA AUUACAGA	3040	UCUGUAAUU GUGUGGAU	4179
3398	GUUUAAAG CUGAUGAG X CGAA AUCCACAC	3041	GUGUGGAUU CUUUAAAC	4180
3399	CGUUUAAA CUGAUGAG X CGAA AAUCCACA	3042	UGUGGAUUC UUUAAACG	4181
3401	AGCGUUUA CUGAUGAG X CGAA AGAAUCCA	3043	UGGAUUCUU UAAACGCU	4182
3402	GAGCGUUU CUGAUGAG X CGAA AAGAAUCC	3044	GGAUUCUUU AAACGCUC	4183
3403	AGAGCGUU CUGAUGAG X CGAA AAAGAAUC	3045	GAUUCUUUA AACGCUCU	4184
3410	CGUACCUA CUGAUGAG X CGAA AGCGUUUA	3046	UAAACGCUC UAGGUACG	4185
3412	AUCGUACC CUGAUGAG X CGAA AGAGCGUU	3047	AACGCUCUA GGUACGAU	4186
3416	UGUCAUCG CUGAUGAG X CGAA ACCUAGAG	3048	CUCUAGGUA CGAUGACA	4187
3429	UAUCGGGG CUGAUGAG X CGAA ACACUGUC	3049	GACAGUGUU CCCCGAUA	4188
3430	GUAUCGGG CUGAUGAG X CGAA AACACUGU	3050	ACAGUGUUC CCCGAUAC	4189
3437	CAGCAUGG CUGAUGAG X CGAA AUCGGGGA	3051	UCCCCGAUA CCAUGCUG	4190
3447	CGGAUCCU CUGAUGAG X CGAA ACAGCAUG	3052	CAUGCUGUA AGGAUCCG	4191
3453	UCUUUCCG CUGAUGAG X CGAA AUCCUUAC	3053	GUAAGGAUC CGGAAAGA	4192
3474	UCAUCUUU CUGAUGAG X CGAA AUCUCUCG	3054	CGAGAGAUC AAAGAUGA	4193
3488	UAUCAAUA CUGAUGAG X CGAA ACUUUUCA	3055	UGAAAAGUA UAUUGAUA	4194

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3490	GUUAUCAA CUGAUGAG X CGAA AUACUUUU	3056	AAAAGUAUA UUGAUAAC	4195
3492	AGGUUAUC CUGAUGAG X CGAA AUAUACUU	3057	AAGUAUAUU GAUAACCU	4196
3496	UUCAAGGU CUGAUGAG X CGAA AUCAAUAU	3058	AUAUUGAUA ACCUUGAA	4197
3501	UUUUUUUC CUGAUGAG X CGAA AGGUUAUC	3059	GAUAACCUU GAAAAAAA	4198
3519	CACUUUGU CUGAUGAG X CGAA AUCCACUG	3060	CAGUGGAUC ACAAAGUG	4199
3545	GCUAUGAG CUGAUGAG X CGAA AGCUUUCA	3061	UGAAAGCUA CUCAUAGC	4200
3548	CCCGCUAU CUGAUGAG X CGAA AGUAGCUU	3062	AAGCUACUC AUAGCGGG	4201
3551	GCCCCCGC CUGAUGAG X CGAA AUGAGUAG	3063	CUACUCAUA GCGGGGGC	4202
3562	UUUUUUUU CUGAUGAG X CGAA AGGCCCCC	3064	GGGGGCCUA AAAAAAAA	4203
3577	GUACUGUG CUGAUGAG X CGAA AGCUUUUU	3065	AAAAAGCUU CACAGUAC	4204
3578	GGUACUGU CUGAUGAG X CGAA AAGCUUUU	3066	AAAAGCUUC ACAGUACC	4205
3584	AGUUUGGG CUGAUGAG X CGAA ACUGUGAA	3067	UUCACAGUA CCCAAACU	4206
3596	GUUGGAAA CUGAUGAG X CGAA AGCAGUUU	3068	AAACUGCUU UUUCCAAC	4207
3597	AGUUGGAA CUGAUGAG X CGAA AAGCAGUU	3069	AACUGCUUU UUCCAACU	4208
3598	GAGUUGGA CUGAUGAG X CGAA AAAGCAGU	3070	ACUGCUUUU UCCAACUC	4209
3599	UGAGUUGG CUGAUGAG X CGAA AAAAGCAG	3071	CUGCUUUUU CCAACUCA	4210

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3600	CUGAGUUG CUGAUGAG X CGAA AAAAAGCA	3072	UGCUUUUUC CAACUCAG	4211
3606	GAAUUUCU CUGAUGAG X CGAA AGUUGGAA	3073	UUCCAACUC AGAAAUUC	4212
3613	CCAAAUUG CUGAUGAG X CGAA AUUUCUGA	3074	UCAGAAAUU CAAUUUGG	4213
3614	UCCAAAUU CUGAUGAG X CGAA AAUUUCUG	3075	CAGAAAUUC AAUUUGGA	4214
3618	UAAAUCCA CUGAUGAG X CGAA AUUGAAUU	3076	AAUUCAAUU UGGAUUUA	4215
3619	UUAAAUCC CUGAUGAG X CGAA AAUUGAAU	3077	AUUCAAUUU GGAUUUAA	4216
3624	GGCUUUUA CUGAUGAG X CGAA AUCCAAAU	3078	AUUUGGAUU UAAAAGCC	4217
3625	AGGCUUUU CUGAUGAG X CGAA AAUCCAAA	3079	UUUGGAUUU AAAAGCCU	4218
3626	CAGGCUUU CUGAUGAG X CGAA AAAUCCAA	3080	UUGGAUUUA AAAGCCUG	4219
3637	CAGGGAUU CUGAUGAG X CGAA AGCAGGCU	3081	AGCCUGCUC AAUCCCUG	4220
3641	UCCUCAGG CUGAUGAG X CGAA AUUGAGCA	3082	UGCUCAAUC CCUGAGGA	4221
3655	CACUCUGA CUGAUGAG X CGAA AUCAGUCC	3083	GGACUGAUU UCAGAGUG	4222
3656	UCACUCUG CUGAUGAG X CGAA AAUCAGUC	3084	GACUGAUUU CAGAGUGA	4223
3657	GUCACUCU CUGAUGAG X CGAA AAAUCAGU	3085	ACUGAUUUC AGAGUGAC	4224
3667	ACUGUGUG CUGAUGAG X CGAA AGUCACUC	3086	GAGUGACUA CACACAGU	4225
3676	UAGGUUCG CUGAUGAG X CGAA ACUGUGUG	3087	CACACAGUA CGAACCUA	4226

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3684	UAAAACUG CUGAUGAG X CGAA AGGUUCGU	3088	ACGAACCUA CAGUUUUA	4227
3689	ACAGUUAA CUGAUGAG X CGAA ACUGUAGG	3089	CCUACAGUU UUAACUGU	4228
3690	CACAGUUA CUGAUGAG X CGAA AACUGUAG	3090	CUACAGUUU UAACUGUG	4229
3691	CCACAGUU CUGAUGAG X CGAA AAACUGUA	3091	UACAGUUUU AACUGUGG	4230
3692	UCCACAGU CUGAUGAG X CGAA AAAACUGU	3092	ACAGUUUUA ACUGUGGA	4231
3702	CGUAACAA CUGAUGAG X CGAA AUCCACAG	3093	CUGUGGAUA UUGUUACG	4232
3704	UACGUAAC CUGAUGAG X CGAA AUAUCCAC	3094	GUGGAUAUU GUUACGUA	4233
3707	GGCUACGU CUGAUGAG X CGAA ACAAUAUC	3095	GAUAUUGUU ACGUAGCC	4234
3708	AGGCUACG CUGAUGAG X CGAA AACAAUAU	3096	AUAUUGUUA CGUAGCCU	4235
3712	CCUUAGGC CUGAUGAG X CGAA ACGUAACA	3097	UGUUACGUA GCCUAAGG	4236
3717	AGGAGCCU CUGAUGAG X CGAA AGGCUACG	3098	CGUAGCCUA AGGCUCCU	4237
3723	CAAAACAG CUGAUGAG X CGAA AGCCUUAG	3099	CUAAGGCUC CUGUUUUG	4238
3728	CUGUGCAA CUGAUGAG X CGAA ACAGGAGC	3100	GCUCCUGUU UUGCACAG	4239
3729	GCUGUGCA CUGAUGAG X CGAA AACAGGAG	3101	CUCCUGUUU UGCACAGC	4240
3730	GGCUGUGC CUGAUGAG X CGAA AAACAGGA	3102	UCCUGUUUU GCACAGCC	4241
3743	CAGUUUUA CUGAUGAG X CGAA AUUUGGCU	3103	AGCCAAAUU UAAAACUG	4242

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3744	ACAGUUUU CUGAUGAG X CGAA AAUUUGGC	3104	GCCAAAUUU AAAACUGU	4243
3745	AACAGUUU CUGAUGAG X CGAA AAAUUUGG	3105	CCAAAUUUA AAACUGUU	4244
3753	UCCAUUCC CUGAUGAG X CGAA ACAGUUUU	3106	AAAACUGUU GGAAUGGA	4245
3763	UAAAGAAA CUGAUGAG X CGAA AUCCAUUC	3107	GAAUGGAUU UUUCUUUA	4246
3764	UUAAAGAA CUGAUGAG X CGAA AAUCCAUU	3108	AAUGGAUUU UUCUUUAA	4247
3765	GUUAAAGA CUGAUGAG X CGAA AAAUCCAU	3109	AUGGAUUUU UCUUUAAC	4248
3766	AGUUAAAG CUGAUGAG X CGAA AAAAUCCA	3110	UGGAUUUUU CUUUAACU	4249
3767	CAGUUAAA CUGAUGAG X CGAA AAAAAUCC	3111	GGAUUUUUC UUUAACUG	4250
3769	GGCAGUUA CUGAUGAG X CGAA AGAAAAAU	3112	AUUUUUCUU UAACUGCC	4251
3770	CGGCAGUU CUGAUGAG X CGAA AAGAAAAA	3113	UUUUUCUUU AACUGCCG	4252
3771	ACGGCAGU CUGAUGAG X CGAA AAAGAAAA	3114	UUUUCUUUA ACUGCCGU	4253
3780	AGUUAAAU CUGAUGAG X CGAA ACGGCAGU	3115	ACUGCCGUA AUUUAACU	4254
3783	GAAAGUUA CUGAUGAG X CGAA AUUACGGC	3116	GCCGUAAUU UAACUUUC	4255
3784	AGAAAGUU CUGAUGAG X CGAA AAUUACGG	3117	CCGUAAUUU AACUUUCU	4256
3785	CAGAAAGU CUGAUGAG X CGAA AAAUUACG	3118	CGUAAUUUA ACUUUCUG	4257
3789	AACCCAGA CUGAUGAG X CGAA AGUUAAAU	3119	AUUUAACUU UCUGGGUU	4258

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3790	CAACCCAG CUGAUGAG X CGAA AAGUUAAA	3120	UUUAACUUU CUGGGUUG	4259
3791	GCAACCCA CUGAUGAG X CGAA AAAGUUAA	3121	UUAACUUUC UGGGUUGC	4260
3797	ACAAAGGC CUGAUGAG X CGAA ACCCAGAA	3122	UUCUGGGUU GCCUUUGU	4261
3802	CAAAAACA CUGAUGAG X CGAA AGGCAACC	3123	GGUUGCCUU UGUUUUUG	4262
3803	CCAAAAAC CUGAUGAG X CGAA AAGGCAAC	3124	GUUGCCUUU GUUUUUGG	4263
3806	ACGCCAAA CUGAUGAG X CGAA ACAAAGGC	3125	GCCUUUGUU UUUGGCGU	4264
3807	CACGCCAA CUGAUGAG X CGAA AACAAAGG	3126	CCUUUGUUU UUGGCGUG	4265
3808	CCACGCCA CUGAUGAG X CGAA AAACAAAG	3127	CUUUGUUUU UGGCGUGG	4266
3809	GCCACGCC CUGAUGAG X CGAA AAAACAAA	3128	UUUGUUUUU GGCGUGGC	4267
3823	CAUGAUGU CUGAUGAG X CGAA AGUCAGCC	3129	GGCUGACUU ACAUCAUG	4268
3824	ACAUGAUG CUGAUGAG X CGAA AAGUCAGC	3130	GCUGACUUA CAUCAUGU	4269
3828	CAACACAU CUGAUGAG X CGAA AUGUAAGU	3131	ACUUACAUC AUGUGUUG	4270
3835	CCUUCCCC CUGAUGAG X CGAA ACACAUGA	3132	UCAUGUGUU GGGGAAGG	4271
3855	CUGAGUGC CUGAUGAG X CGAA ACUGGGCA	3133	UGCCCAGUU GCACUCAG	4272
3861	UGUCACCU CUGAUGAG X CGAA AGUGCAAC	3134	GUUGCACUC AGGUGACA	4273
3871	AUCUGGAG CUGAUGAG X CGAA AUGUCACC	3135	GGUGACAUC CUCCAGAU	4274

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3874	ACUAUCUG CUGAUGAG X CGAA AGGAUGUC	3136	GACAUCCUC CAGAUAGU	4275
3880	AGCUACAC CUGAUGAG X CGAA AUCUGGAG	3137	CUCCAGAUA GUGUAGCU	4276
3885	UCCUCAGC CUGAUGAG X CGAA ACACUAUC	3138	GAUAGUGUA GCUGAGGA	4277
3901	GGUGAGUG CUGAUGAG X CGAA AGGUGCCU	3139	AGGCACCUA CACUCACC	4278
3906	GUGCAGGU CUGAUGAG X CGAA AGUGUAGG	3140	CCUACACUC ACCUGCAC	4279
3916	CACUCUGU CUGAUGAG X CGAA AGUGCAGG	3141	CCUGCACUA ACAGAGUG	4280
3930	GAGGUUAG CUGAUGAG X CGAA ACGGCCAC	3142	GUGGCCGUC CUAACCUC	4281
3933	CCCGAGGU CUGAUGAG X CGAA AGGACGGC	3143	GCCGUCCUA ACCUCGGG	4282
3938	GCAGGCCC CUGAUGAG X CGAA AGGUUAGG	3144	CCUAACCUC GGGCCUGC	4283
3958	ACGUGAUG CUGAUGAG X CGAA ACGUCUGC	3145	GCAGACGUC CAUCACGU	4284
3962	GCUAACGU CUGAUGAG X CGAA AUGGACGU	3146	ACGUCCAUC ACGUUAGC	4285
3967	GGACAGCU CUGAUGAG X CGAA ACGUGAUG	3147	CAUCACGUU AGCUGUCC	4286
3968	GGGACAGC CUGAUGAG X CGAA AACGUGAU	3148	AUCACGUUA GCUGUCCC	4287
3974	UGAUGUGG CUGAUGAG X CGAA ACAGCUAA	3149	UUAGCUGUC CCACAUCA	4288
3981	AGUCUUGU CUGAUGAG X CGAA AUGUGGGA	3150	UCCCACAUC ACAAGACU	4289
3990	CAAUGGCA CUGAUGAG X CGAA AGUCUUGU	3151	ACAAGACUA UGCCAUUG	4290

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3997	ACUACCCC CUGAUGAG X CGAA AUGGCAUA	3152	UAUGCCAUU GGGGUAGU	4291
4003	AACACAAC CUGAUGAG X CGAA ACCCCAAU	3153	AUUGGGGUA GUUGUGUU	4292
4006	UGAAACAC CUGAUGAG X CGAA ACUACCCC	3154	GGGGUAGUU GUGUUUCA	4293
4011	UCCGUUGA CUGAUGAG X CGAA ACACAACU	3155	AGUUGUGUU UCAACGGA	4294
4012	UUCCGUUG CUGAUGAG X CGAA AACACAAC	3156	GUUGUGUUU CAACGGAA	4295
4013	UUUCCGUU CUGAUGAG X CGAA AAACACAA	3157	UUGUGUUUC AACGGAAA	4296
4029	UAGUUUAA CUGAUGAG X CGAA ACAGCACU	3158	AGUGCUGUC UUAAACUA	4297
4031	UUUAGUUU CUGAUGAG X CGAA AGACAGCA	3159	UGCUGUCUU AAACUAAA	4298
4032	AUUUAGUU CUGAUGAG X CGAA AAGACAGC	3160	GCUGUCUUA AACUAAAU	4299
4037	UGCACAUU CUGAUGAG X CGAA AGUUUAAG	3161	CUUAAACUA AAUGUGCA	4300
4048	UCACCUUC CUGAUGAG X CGAA AUUGCACA	3162	UGUGCAAUA GAAGGUGA	4301
4060	AGGAUGGC CUGAUGAG X CGAA ACAUCACC	3163	GGUGAUGUU GCCAUCCU	4302
4066	GACGGUAG CUGAUGAG X CGAA AUGGCAAC	3164	GUUGCCAUC CUACCGUC	4303
4069	AAAGACGG CUGAUGAG X CGAA AGGAUGGC	3165	GCCAUCCUA CCGUCUUU	4304
4074	CAGGAAAA CUGAUGAG X CGAA ACGGUAGG	3166	CCUACCGUC UUUUCCUG	4305
4076	AACAGGAA CUGAUGAG X CGAA AGACGGUA	3167	UACCGUCUU UUCCUGUU	4306

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4077	AAACAGGA CUGAUGAG X CGAA AAGACGGU	3168	ACCGUCUUU UCCUGUUU	4307
4078	GAAACAGG CUGAUGAG X CGAA AAAGACGG	3169	CCGUCUUUU CCUGUUUC	4308
4079	GGAAACAG CUGAUGAG X CGAA AAAAGACG	3170	CGUCUUUUC CUGUUUCC	4309
4084	AGCUAGGA CUGAUGAG X CGAA ACAGGAAA	3171	UUUCCUGUU UCCUAGCU	4310
4085	CAGCUAGG CUGAUGAG X CGAA AACAGGAA	3172	UUCCUGUUU CCUAGCUG	4311
4086	ACAGCUAG CUGAUGAG X CGAA AAACAGGA	3173	UCCUGUUUC CUAGCUGU	4312
4089	CACACAGC CUGAUGAG X CGAA AGGAAACA	3174	UGUUUCCUA GCUGUGUG	4313
4101	UGAGCAGG CUGAUGAG X CGAA AUUCACAC	3175	GUGUGAAUA CCUGCUCA	4314
4108	UUUGACGU CUGAUGAG X CGAA AGCAGGUA	3176	UACCUGCUC ACGUCAAA	4315
4113	AUGCAUUU CUGAUGAG X CGAA ACGUGAGC	3177	GCUCACGUC AAAUGCAU	4316
4122	GAAACUUG CUGAUGAG X CGAA AUGCAUUU	3178	AAAUGCAUA CAAGUUUC	4317
4128	GAGAAUGA CUGAUGAG X CGAA ACUUGUAU	3179	AUACAAGUU UCAUUCUC	4318
4129	GGAGAAUG CUGAUGAG X CGAA AACUUGUA	3180	UACAAGUUU CAUUCUCC	4319
4130	GGGAGAAU CUGAUGAG X CGAA AAACUUGU	3181	ACAAGUUUC AUUCUCCC	4320
4133	AAAGGGAG CUGAUGAG X CGAA AUGAAACU	3182	AGUUUCAUU CUCCCUUU	4321
4134	GAAAGGGA CUGAUGAG X CGAA AAUGAAAC	3183	GUUUCAUUC UCCCUUUC	4322

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4136	GUGAAAGG CUGAUGAG X CGAA AGAAUGAA	3184	UUCAUUCUC CCUUUCAC	4323
4140	UUUAGUGA CUGAUGAG X CGAA AGGGAGAA	3185	UUCUCCCUU UCACUAAA	4324
4141	UUUUAGUG CUGAUGAG X CGAA AAGGGAGA	3186	UCUCCCUUU CACUAAAA	4325
4142	UUUUUAGU CUGAUGAG X CGAA AAAGGGAG	3187	CUCCCUUUC ACUAAAAA	4326
4146	UGUGUUUU CUGAUGAG X CGAA AGUGAAAG	3188	CUUUCACUA AAAACACA	4327
4170	UAGCAUUC CUGAUGAG X CGAA AGUCUGUU	3189	AACAGACUU GAAUGCUA	4328
4178	AGUAUAAC CUGAUGAG X CGAA AGCAUUCA	3190	UGAAUGCUA GUUAUACU	4329
4181	AUAAGUAU CUGAUGAG X CGAA ACUAGCAU	3191	AUGCUAGUU AUACUUAU	4330
4182	AAUAAGUA CUGAUGAG X CGAA AACUAGCA	3192	UGCUAGUUA UACUUAUU	4331
4184	CAAAUAAG CUGAUGAG X CGAA AUAACUAG	3193	CUAGUUAUA CUUAUUUG	4332
4187	AUACAAAU CUGAUGAG X CGAA AGUAUAAC	3194	GUUAUACUU AUUUGUAU	4333
4188	UAUACAAA CUGAUGAG X CGAA AAGUAUAA	3195	UUAUACUUA UUUGUAUA	4334
4190	CAUAUACA CUGAUGAG X CGAA AUAAGUAU	3196	AUACUUAUU UGUAUAUG	4335
4191	CCAUAUAC CUGAUGAG X CGAA AAUAAGUA	3197	UACUUAUUU GUAUAUGG	4336
4194	AUACCAUA CUGAUGAG X CGAA ACAAAUAA	3198	UUAUUUGUA UAUGGUAU	4337
4196	AAAUACCA CUGAUGAG X CGAA AUACAAAU	3199	AUUUGUAUA UGGUAUUU	4338

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4201	AAAAUAAA CUGAUGAG X CGAA ACCAUAUA	3200	UAUAUGGUA UUUAUUUU	4339
4203	AAAAAAUA CUGAUGAG X CGAA AUACCAUA	3201	UAUGGUAUU UAUUUUUU	4340
4204	GAAAAAAU CUGAUGAG X CGAA AAUACCAU	3202	AUGGUAUUU AUUUUUUC	4341
4205	AGAAAAAA CUGAUGAG X CGAA AAAUACCA	3203	UGGUAUUUA UUUUUUCU	4342
4207	AAAGAAAA CUGAUGAG X CGAA AUAAAUAC	3204	GUAUUUAUU UUUUCUUU	4343
4208	AAAAGAAA CUGAUGAG X CGAA AAUAAAUA	3205	UAUUUAUUU UUUCUUUU	4344
4209	GAAAAGAA CUGAUGAG X CGAA AAAUAAAU	3206	AUUUAUUUU UUCUUUUC	4345
4210	AGAAAAGA CUGAUGAG X CGAA AAAAUAAA	3207	UUUAUUUUU UCUUUUCU	4346
4211	AAGAAAAG CUGAUGAG X CGAA AAAAAUAA	3208	UUAUUUUUU CUUUUCUU	4347
4212	AAAGAAAA CUGAUGAG X CGAA AAAAAAUA	3209	UAUUUUUUC UUUUCUUU	4348
4214	GUAAAGAA CUGAUGAG X CGAA AGAAAAAA	3210	UUUUUUCUU UUCUUUAC	4349
4215	UGUAAAGA CUGAUGAG X CGAA AAGAAAAA	3211	UUUUUCUUU UCUUUACA	4350
4216	UUGUAAAG CUGAUGAG X CGAA AAAGAAAA	3212	UUUUCUUUU CUUUACAA	4351
4217	UUUGUAAA CUGAUGAG X CGAA AAAAGAAA	3213	UUUCUUUUC UUUACAAA	4352
4219	GGUUUGUA CUGAUGAG X CGAA AGAAAAGA	3214	UCUUUUCUU UACAAACC	4353
4220	UGGUUUGU CUGAUGAG X CGAA AAGAAAAG	3215	CUUUUCUUU ACAAACCA	4354

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4221	AUGGUUUG CUGAUGAG X CGAA AAAGAAAA	3216	UUUUCUUUA CAAACCAU	4355
4230	AAUAACAA CUGAUGAG X CGAA AUGGUUUG	3217	CAAACCAUU UUGUUAUU	4356
4231	CAAUAACA CUGAUGAG X CGAA AAUGGUUU	3218	AAACCAUUU UGUUAUUG	4357
4232	UCAAUAAC CUGAUGAG X CGAA AAAUGGUU	3219	AACCAUUUU GUUAUUGA	4358
4235	UAGUCAAU CUGAUGAG X CGAA ACAAAAUG	3220	CAUUUUGUU AUUGACUA	4359
4236	UUAGUCAA CUGAUGAG X CGAA AACAAAAU	3221	AUUUUGUUA UUGACUAA	4360
4238	UGUUAGUC CUGAUGAG X CGAA AUAACAAA	3222	UUUGUUAUU GACUAACA	4361
4243	UGGCCUGU CUGAUGAG X CGAA AGUCAAUA	3223	UAUUGACUA ACAGGCCA	4362
4258	AAACUGGA CUGAUGAG X CGAA ACUCUUUG	3224	CAAAGAGUC UCCAGUUU	4363
4260	GUAAACUG CUGAUGAG X CGAA AGACUCUU	3225	AAGAGUCUC CAGUUUAC	4364
4265	GAAGGGUA CUGAUGAG X CGAA ACUGGAGA	3226	UCUCCAGUU UACCCUUC	4365
4266	UGAAGGGU CUGAUGAG X CGAA AACUGGAG	3227	CUCCAGUUU ACCCUUCA	4366
4267	CUGAAGGG CUGAUGAG X CGAA AAACUGGA	3228	UCCAGUUUA CCCUUCAG	4367
4272	CCAACCUG CUGAUGAG X CGAA AGGGUAAA	3229	UUUACCCUU CAGGUUGG	4368
4273	ACCAACCU CUGAUGAG X CGAA AAGGGUAA	3230	UUACCCUUC AGGUUGGU	4369
4278	AUUAAACC CUGAUGAG X CGAA ACCUGAAG	3231	CUUCAGGUU GGUUUAAU	4370

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4282	AUUGAUUA CUGAUGAG X CGAA ACCAACCU	3232	AGGUUGGUU UAAUCAAU	4371
4283	GAUUGAUU CUGAUGAG X CGAA AACCAACC	3233	GGUUGGUUU AAUCAAUC	4372
4284	UGAUUGAU CUGAUGAG X CGAA AAACCAAC	3234	GUUGGUUUA AUCAAUCA	4373
4287	UUCUGAUU CUGAUGAG X CGAA AUUAAACC	3235	GGUUUAAUC AAUCAGAA	4374
4291	CUAAUUCU CUGAUGAG X CGAA AUUGAUUA	3236	UAAUCAAUC AGAAUUAG	4375
4297	CUAAUUCU CUGAUGAG X CGAA AUUCUGAU	3237	AUCAGAAUU AGAAUUAG	4376
4298	UCUAAUUC CUGAUGAG X CGAA AAUUCUGA	3238	UCAGAAUUA GAAUUAGA	4377
4303	CAUGCUCU CUGAUGAG X CGAA AUUCUAAU	3239	AUUAGAAUU AGAGCAUG	4378
4304	CCAUGCUC CUGAUGAG X CGAA AAUUCUAA	3240	UUAGAAUUA GAGCAUGG	4379
4319	AUAGUGAU CUGAUGAG X CGAA ACCCUCCC	3241	GGGAGGGUC AUCACUAU	4380
4322	GUCAUAGU CUGAUGAG X CGAA AUGACCCU	3242	AGGGUCAUC ACUAUGAC	4381
4326	UUAGGUCA CUGAUGAG X CGAA AGUGAUGA	3243	UCAUCACUA UGACCUAA	4382
4333	AAAUAAUU CUGAUGAG X CGAA AGGUCAUA	3244	UAUGACCUA AAUUAUUU	4383
4337	CAGUAAAU CUGAUGAG X CGAA AUUUAGGU	3245	ACCUAAAUU AUUUACUG	4384
4338	GCAGUAAA CUGAUGAG X CGAA AAUUUAGG	3246	CCUAAAUUA UUUACUGC	4385
4340	UUGCAGUA CUGAUGAG X CGAA AUAAUUUA	3247	UAAAUUAUU UACUGCAA	4386

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4341	UUUGCAGU CUGAUGAG X CGAA AAUAAUUU	3248	AAAUUAUUU ACUGCAAA	4387
4342	UUUUGCAG CUGAUGAG X CGAA AAAUAAUU	3249	AAUUAUUUA CUGCAAAA	4388
4358	UUUAUAAA CUGAUGAG X CGAA AUUUUCUU	3250	AAGAAAAUC UUUAUAAA	4389
4360	CAUUUAUA CUGAUGAG X CGAA AGAUUUUC	3251	GAAAAUCUU UAUAAAUG	4390
4361	ACAUUUAU CUGAUGAG X CGAA AAGAUUUU	3252	AAAAUCUUU AUAAAUGU	4391
4362	UACAUUUA CUGAUGAG X CGAA AAAGAUUU	3253	AAAUCUUUA UAAAUGUA	4392
4364	GGUACAUU CUGAUGAG X CGAA AUAAAGAU	3254	AUCUUUAUA AAUGUACC	4393
4370	CUCUCUGG CUGAUGAG X CGAA ACAUUUAU	3255	AUAAAUGUA CCAGAGAG	4394
4382	AUUAAAAC CUGAUGAG X CGAA ACUCUCUC	3256	GAGAGAGUU GUUUUAAU	4395
4385	GUUAUUAA CUGAUGAG X CGAA ACAACUCU	3257	AGAGUUGUU UUAAUAAC	4396
4386	AGUUAUUA CUGAUGAG X CGAA AACAACUC	3258	GAGUUGUUU UAAUAACU	4397
4387	AAGUUAUU CUGAUGAG X CGAA AAACAACU	3259	AGUUGUUUU AAUAACUU	4398
4388	UAAGUUAU CUGAUGAG X CGAA AAAACAAC	3260	GUUGUUUUA AUAACUUA	4399
4391	AGAUAAGU CUGAUGAG X CGAA AUUAAAAC	3261	GUUUUAAUA ACUUAUCU	4400
4395	UUAUAGAU CUGAUGAG X CGAA AGUUAUUA	3262	UAAUAACUU AUCUAUAA	4401
4396	UUUAUAGA CUGAUGAG X CGAA AAGUUAUU	3263	AAUAACUUA UCUAUAAA	4402

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4398	AGUUUAUA CUGAUGAG X CGAA AUAAGUUA	3264	UAACUUAUC UAUAAACU	4403
4400	AUAGUUUA CUGAUGAG X CGAA AGAUAAGU	3265	ACUUAUCUA UAAACUAU	4404
4402	UUAUAGUU CUGAUGAG X CGAA AUAGAUAA	3266	UUAUCUAUA AACUAUAA	4405
4407	AGAGGUUA CUGAUGAG X CGAA AGUUUAUA	3267	UAUAAACUA UAACCUCU	4406
4409	GGAGAGGU CUGAUGAG X CGAA AUAGUUUA	3268	UAAACUAUA ACCUCUCC	4407
4414	AUGAAGGA CUGAUGAG X CGAA AGGUUAUA	3269	UAUAACCUC UCCUUCAU	4408
4416	UCAUGAAG CUGAUGAG X CGAA AGAGGUUA	3270	UAACCUCUC CUUCAUGA	4409
4419	CUGUCAUG CUGAUGAG X CGAA AGGAGAGG	3271	CCUCUCCUU CAUGACAG	4410
4420	GCUGUCAU CUGAUGAG X CGAA AAGGAGAG	3272	CUCUCCUUC AUGACAGC	4411
4431	GUGGGGUG CUGAUGAG X CGAA AGGCUGUC	3273	GACAGCCUC CACCCCAC	4412
4452	AUUUCUUA CUGAUGAG X CGAA ACCUUUUG	3274	CAAAAGGUU UAAGAAAU	4413
4453	UAUUUCUU CUGAUGAG X CGAA AACCUUUU	3275	AAAAGGUUU AAGAAAUA	4414
4454	CUAUUUCU CUGAUGAG X CGAA AAACCUUU	3276	AAAGGUUUA AGAAAUAG	4415
4461	UAUAAUUC CUGAUGAG X CGAA AUUUCUUA	3277	UAAGAAAUA GAAUUAUA	4416
4466	ACAGUUAU CUGAUGAG X CGAA AUUCUAUU	3278	AAUAGAAUU AUAACUGU	4417
4467	UACAGUUA CUGAUGAG X CGAA AAUUCUAU	3279	AUAGAAUUA UAACUGUA	4418

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4469	UUUACAGU CUGAUGAG X CGAA AUAAUUCU	3280	AGAAUUAUA ACUGUAAA	4419
4475	AACAUCUU CUGAUGAG X CGAA ACAGUUAU	3281	AUAACUGUA AAGAUGUU	4420
4483	CUGAAAUA CUGAUGAG X CGAA ACAUCUUU	3282	AAAGAUGUU UAUUUCAG	4421
4484	CCUGAAAU CUGAUGAG X CGAA AACAUCUU	3283	AAGAUGUUU AUUUCAGG	4422
4485	GCCUGAAA CUGAUGAG X CGAA AAACAUCU	3284	AGAUGUUUA UUUCAGGC	4423
4487	AUGCCUGA CUGAUGAG X CGAA AUAAACAU	3285	AUGUUUAUU UCAGGCAU	4424
4488	AAUGCCUG CUGAUGAG X CGAA AAUAAACA	3286	UGUUUAUUU CAGGCAUU	4425
4489	CAAUGCCU CUGAUGAG X CGAA AAAUAAAC	3287	GUUUAUUUC AGGCAUUG	4426
4496	AAAUAUCC CUGAUGAG X CGAA AUGCCUGA	3288	UCAGGCAUU GGAUAUUU	4427
4501	GUAAAAAA CUGAUGAG X CGAA AUCCAAUG	3289	CAUUGGAUA UUUUUUAC	4428
4503	AAGUAAAA CUGAUGAG X CGAA AUAUCCAA	3290	UUGGAUAUU UUUUACUU	4429
4504	AAAGUAAA CUGAUGAG X CGAA AAUAUCCA	3291	UGGAUAUUU UUUACUUU	4430
4505	UAAAGUAA CUGAUGAG X CGAA AAAUAUCC	3292	GGAUAUUUU UUACUUUA	4431
4506	CUAAAGUA CUGAUGAG X CGAA AAAAUAUC	3293	GAUAUUUUU UACUUUAG	4432
4507	UCUAAAGU CUGAUGAG X CGAA AAAAAUAU	3294	AUAUUUUUU ACUUUAGA	4433
4508	UUCUAAAG CUGAUGAG X CGAA AAAAAAUA	3295	UAUUUUUUA CUUUAGAA	4434

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4511	GGCUUCUA CUGAUGAG X CGAA AGUAAAAA	3296	UUUUUACUU UAGAAGCC	4435
4512	AGGCUUCU CUGAUGAG X CGAA AAGUAAAA	3297	UUUUACUUU AGAAGCCU	4436
4513	CAGGCUUC CUGAUGAG X CGAA AAAGUAAA	3298	UUUACUUUA GAAGCCUG	4437
4525	AGAAACAU CUGAUGAG X CGAA AUGCAGGC	3299	GCCUGCAUA AUGUUUCU	4438
4530	AAUCCAGA CUGAUGAG X CGAA ACAUUAUG	3300	CAUAAUGUU UCUGGAUU	4439
4531	AAAUCCAG CUGAUGAG X CGAA AACAUUAU	3301	AUAAUGUUU CUGGAUUU	4440
4532	UAAAUCCA CUGAUGAG X CGAA AAACAUUA	3302	UAAUGUUUC UGGAUUUA	4441
4538	AGUAUGUA CUGAUGAG X CGAA AUCCAGAA	3303	UUCUGGAUU UACAUACU	4442
4539	CAGUAUGU CUGAUGAG X CGAA AAUCCAGA	3304	UCUGGAUUU ACAUACUG	4443
4540	ACAGUAUG CUGAUGAG X CGAA AAAUCCAG	3305	CUGGAUUUA CAUACUGU	4444
4544	UGUUACAG CUGAUGAG X CGAA AUGUAAAU	3306	AUUUACAUA CUGUAACA	4445
4549	CUGAAUGU CUGAUGAG X CGAA ACAGUAUG	3307	CAUACUGUA ACAUUCAG	4446
4554	AAUUCCUG CUGAUGAG X CGAA AUGUUACA	3308	UGUAACAUU CAGGAAUU	4447
4555	GAAUUCCU CUGAUGAG X CGAA AAUGUUAC	3309	GUAACAUUC AGGAAUUC	4448
4562	UCUCCAAG CUGAUGAG X CGAA AUUCCUGA	3310	UCAGGAAUU CUUGGAGA	4449
4563	UUCUCCAA CUGAUGAG X CGAA AAUUCCUG	3311	CAGGAAUUC UUGGAGAA	4450

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4565	UCUUCUCC CUGAUGAG X CGAA AGAAUUCC	3312	GGAAUUCUU GGAGAAGA	4451
4579	AGUGAAUA CUGAUGAG X CGAA ACCCAUCU	3313	AGAUGGGUU UAUUCACU	4452
4580	CAGUGAAU CUGAUGAG X CGAA AACCCAUC	3314	GAUGGGUUU AUUCACUG	4453
4581	UCAGUGAA CUGAUGAG X CGAA AAACCCAU	3315	AUGGGUUUA UUCACUGA	4454
4583	GUUCAGUG CUGAUGAG X CGAA AUAAACCC	3316	GGGUUUAUU CACUGAAC	4455
4584	AGUUCAGU CUGAUGAG X CGAA AAUAAACC	3317	GGUUUAUUC ACUGAACU	4456
4593	CCGCACUA CUGAUGAG X CGAA AGUUCAGU	3318	ACUGAACUC UAGUGCGG	4457
4595	AACCGCAC CUGAUGAG X CGAA AGAGUUCA	3319	UGAACUCUA GUGCGGUU	4458
4603	AGUGAGUA CUGAUGAG X CGAA ACCGCACU	3320	AGUGCGGUU UACUCACU	4459
4604	CAGUGAGU CUGAUGAG X CGAA AACCGCAC	3321	GUGCGGUUU ACUCACUG	4460
4605	GCAGUGAG CUGAUGAG X CGAA AAACCGCA	3322	UGCGGUUUA CUCACUGC	4461
4608	GCAGCAGU CUGAUGAG X CGAA AGUAAACC	3323	GGUUUACUC ACUGCUGC	4462
4621	AUAUACAG CUGAUGAG X CGAA AUUUGCAG	3324	CUGCAAAUA CUGUAUAU	4463
4626	CCUGAAUA CUGAUGAG X CGAA ACAGUAUU	3325	AAUACUGUA UAUUCAGG	4464
4628	GUCCUGAA CUGAUGAG X CGAA AUACAGUA	3326	UACUGUAUA UUCAGGAC	4465
4630	AAGUCCUG CUGAUGAG X CGAA AUAUACAG	3327	CUGUAUAUU CAGGACUU	4466

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4631	CAAGUCCU CUGAUGAG X CGAA AAUAUACA	3328	UGUAUAUUC AGGACUUG	4467
4638	UUUCUUUC CUGAUGAG X CGAA AGUCCUGA	3329	UCAGGACUU GAAAGAAA	4468
4659	UAGUUCCA CUGAUGAG X CGAA AGGCAUUC	3330	GAAUGCCUA UGGAACUA	4469
4667	GGAUCCAC CUGAUGAG X CGAA AGUUCCAU	3331	AUGGAACUA GUGGAUCC	4470
4674	UCAGUUUG CUGAUGAG X CGAA AUCCACUA	3332	UAGUGGAUC CAAACUGA	4471
4684	UUAUACUG CUGAUGAG X CGAA AUCAGUUU	3333	AAACUGAUC CAGUAUAA	4472
4689	UAGUCUUA CUGAUGAG X CGAA ACUGGAUC	3334	GAUCCAGUA UAAGACUA	4473
4691	AGUAGUCU CUGAUGAG X CGAA AUACUGGA	3335	UCCAGUAUA AGACUACU	4474
4697	AGAUUCAG CUGAUGAG X CGAA AGUCUUAU	3336	AUAAGACUA CUGAAUCU	4475
4704	UGGUAGCA CUGAUGAG X CGAA AUUCAGUA	3337	UACUGAAUC UGCUACCA	4476
4709	UGUUUUGG CUGAUGAG X CGAA AGCAGAUU	3338	AAUCUGCUA CCAAAACA	4477
4720	CACUGAUU CUGAUGAG X CGAA ACUGUUUU	3339	AAAACAGUU AAUCAGUG	4478
4721	UCACUGAU CUGAUGAG X CGAA AACUGUUU	3340	AAACAGUUA AUCAGUGA	4479
4724	GACUCACU CUGAUGAG X CGAA AUUAACUG	3341	CAGUUAAUC AGUGAGUC	4480
4732	GAACACUC CUGAUGAG X CGAA ACUCACUG	3342	CAGUGAGUC GAGUGUUC	4481
4739	AAAAAUAG CUGAUGAG X CGAA ACACUCGA	3343	UCGAGUGUU CUAUUUUU	4482

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4740	AAAAAAUA CUGAUGAG X CGAA AACACUCG	3344	CGAGUGUUC UAUUUUUU	4483
4742	ACAAAAAA CUGAUGAG X CGAA AGAACACU	3345	AGUGUUCUA UUUUUUGU	4484
4744	AAACAAAA CUGAUGAG X CGAA AUAGAACA	3346	UGUUCUAUU UUUUGUUU	4485
4745	AAAACAAA CUGAUGAG X CGAA AAUAGAAC	3347	GUUCUAUUU UUUGUUUU	4486
4746	CAAAACAA CUGAUGAG X CGAA AAAUAGAA	3348	UUCUAUUUU UUGUUUUG	4487
4747	ACAAAACA CUGAUGAG X CGAA AAAAUAGA	3349	UCUAUUUUU UGUUUUGU	4488
4748	AACAAAAC CUGAUGAG X CGAA AAAAAUAG	3350	CUAUUUUUU GUUUUGUU	4489
4751	GGAAACAA CUGAUGAG X CGAA ACAAAAAA	3351	UUUUUUGUU UUGUUUCC	4490
4752	AGGAAACA CUGAUGAG X CGAA AACAAAAA	3352	UUUUUGUUU UGUUUCCU	4491
4753	GAGGAAAC CUGAUGAG X CGAA AAACAAAA	3353	UUUUGUUUU GUUUCCUC	4492
4756	GGGGAGGA CUGAUGAG X CGAA ACAAAACA	3354	UGUUUUGUU UCCUCCCC	4493
4757	AGGGGAGG CUGAUGAG X CGAA AACAAAAC	3355	GUUUUGUUU CCUCCCCU	4494
4758	UAGGGGAG CUGAUGAG X CGAA AAACAAAA	3356	UUUUGUUUC CUCCCCUA	4495
4761	AGAUAGGG CUGAUGAG X CGAA AGGAAACA	3357	UGUUUCCUC CCCUAUCU	4496
4766	AAUACAGA CUGAUGAG X CGAA AGGGGAGG	3358	CCUCCCCUA UCUGUAUU	4497
4768	GGAAUACA CUGAUGAG X CGAA AUAGGGGA	3359	UCCCCUAUC UGUAUUCC	4498

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4772	UUUGGGAA CUGAUGAG X CGAA ACAGAUAG	3360	CUAUCUGUA UUCCCAAA	4499
4774	UUUUUGGG CUGAUGAG X CGAA AUACAGAU	3361	AUCUGUAUU CCCAAAAA	4500
4775	AUUUUUGG CUGAUGAG X CGAA AAUACAGA	3362	UCUGUAUUC CCAAAAAU	4501
4784	CCCAAAGU CUGAUGAG X CGAA AUUUUUGG	3363	CCAAAAAUU ACUUUGGG	4502
4785	CCCCAAAG CUGAUGAG X CGAA AAUUUUUG	3364	CAAAAAUUA CUUUGGGG	4503
4788	UAGCCCCA CUGAUGAG X CGAA AGUAAUUU	3365	AAAUUACUU UGGGGCUA	4504
4789	UUAGCCCC CUGAUGAG X CGAA AAGUAAUU	3366	AAUUACUUU GGGGCUAA	4505
4796	UGUUAAAU CUGAUGAG X CGAA AGCCCCAA	3367	UUGGGGCUA AUUUAACA	4506
4799	UCUUGUUA CUGAUGAG X CGAA AUUAGCCC	3368	GGGCUAAUU UAACAAGA	4507
4800	UUCUUGUU CUGAUGAG X CGAA AAUUAGCC	3369	GGCUAAUUU AACAAGAA	4508
4801	GUUCUUGU CUGAUGAG X CGAA AAAUUAGC	3370	GCUAAUUUA ACAAGAAC	4509
4811	ACAAUUUA CUGAUGAG X CGAA AGUUCUUG	3371	CAAGAACUU UAAAUUGU	4510
4812	CACAAUUU CUGAUGAG X CGAA AAGUUCUU	3372	AAGAACUUU AAAUUGUG	4511
4813	ACACAAUU CUGAUGAG X CGAA AAAGUUCU	3373	AGAACUUUA AAUUGUGU	4512
4817	UAAAACAC CUGAUGAG X CGAA AUUUAAAG	3374	CUUUAAAUU GUGUUUUA	4513
4822	ACAAUUAA CUGAUGAG X CGAA ACACAAUU	3375	AAUUGUGUU UUAAUUGU	4514

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4823	UACAAUUA CUGAUGAG X CGAA AACACAAU	3376	AUUGUGUUU UAAUUGUA	4515
4824	UUACAAUU CUGAUGAG X CGAA AAACACAA	3377	UUGUGUUUU AAUUGUAA	4516
4825	UUUACAAU CUGAUGAG X CGAA AAAACACA	3378	UGUGUUUUA AUUGUAAA	4517
4828	AUUUUUAC CUGAUGAG X CGAA AUUAAAAC	3379	GUUUUAAUU GUAAAAAU	4518
4831	GCCAUUUU CUGAUGAG X CGAA ACAAUUAA	3380	UUAAUUGUA AAAAUGGC	4519
4852	AGAGUAAU CUGAUGAG X CGAA AUUCCACC	3381	GGUGGAAUU AUUACUCU	4520
4853	UAGAGUAA CUGAUGAG X CGAA AAUUCCAC	3382	GUGGAAUUA UUACUCUA	4521
4855	UAUAGAGU CUGAUGAG X CGAA AUAAUUCC	3383	GGAAUUAUU ACUCUAUA	4522
4856	GUAUAGAG CUGAUGAG X CGAA AAUAAUUC	3384	GAAUUAUUA CUCUAUAC	4523
4859	AAUGUAUA CUGAUGAG X CGAA AGUAAUAA	3385	UUAUUACUC UAUACAUU	4524
4861	UGAAUGUA CUGAUGAG X CGAA AGAGUAAU	3386	AUUACUCUA UACAUUCA	4525
4863	GUUGAAUG CUGAUGAG X CGAA AUAGAGUA	3387	UACUCUAUA CAUUCAAC	4526
4867	CUCUGUUG CUGAUGAG X CGAA AUGUAUAG	3388	CUAUACAUU CAACAGAG	4527
4868	UCUCUGUU CUGAUGAG X CGAA AAUGUAUA	3389	UAUACAUUC AACAGAGA	4528
4883	UUCAUAUC CUGAUGAG X CGAA AUUCAGUC	3390	GACUGAAUA GAUAUGAA	4529
4887	AGCUUUCA CUGAUGAG X CGAA AUCUAUUC	3391	GAAUAGAUA UGAAAGCU	4530

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4899	UUAAAAAA CUGAUGAG X CGAA AUCAGCUU	3392	AAGCUGAUU UUUUUUAA	4531
4900	AUUAAAAA CUGAUGAG X CGAA AAUCAGCU	3393	AGCUGAUUU UUUUUAAU	4532
4901	AAUUAAAA CUGAUGAG X CGAA AAAUCAGC	3394	GCUGAUUUU UUUUAAUU	4533
4902	UAAUUAAA CUGAUGAG X CGAA AAAAUCAG	3395	CUGAUUUUU UUUAAUUA	4534
4903	GUAAUUAA CUGAUGAG X CGAA AAAAAUCA	3396	UGAUUUUUU UUAAUUAC	4535
4904	GGUAAUUA CUGAUGAG X CGAA AAAAAAUC	3397	GAUUUUUUU UAAUUACC	4536
4905	UGGUAAUU CUGAUGAG X CGAA AAAAAAAU	3398	AUUUUUUUU AAUUACCA	4537
4906	AUGGUAAU CUGAUGAG X CGAA AAAAAAAA	3399	UUUUUUUUA AUUACCAU	4538
4909	AGCAUGGU CUGAUGAG X CGAA AUUAAAAA	3400	UUUUUAAUU ACCAUGCU	4539
4910	AAGCAUGG CUGAUGAG X CGAA AAUUAAAA	3401	UUUUAAUUA CCAUGCUU	4540
4918	ACAUUGUG CUGAUGAG X CGAA AGCAUGGU	3402	ACCAUGCUU CACAAUGU	4541
4919	AACAUUGU CUGAUGAG X CGAA AAGCAUGG	3403	CCAUGCUUC ACAAUGUU	4542
4927	UAUAACUU CUGAUGAG X CGAA ACAUUGUG	3404	CACAAUGUU AAGUUAUA	4543
4928	AUAUAACU CUGAUGAG X CGAA AACAUUGU	3405	ACAAUGUUA AGUUAUAU	4544
4932	CCCCAUAU CUGAUGAG X CGAA ACUUAACA	3406	UGUUAAGUU AUAUGGGG	4545
4933	UCCCCAUA CUGAUGAG X CGAA AACUUAAC	3407	GUUAAGUUA UAUGGGGA	4546

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4935	GCUCCCCA CUGAUGAG X CGAA AUAACUUA	3408	UAAGUUAUA UGGGGAGC	4547
4961	AAACAAAU CUGAUGAG X CGAA AGCACCUG	3409	CAGGUGCUA AUUUGUUU	4548
4964	CCAAAACA CUGAUGAG X CGAA AUUAGCAC	3410	GUGCUAAUU UGUUUUGG	4549
4965	UCCAAAAC CUGAUGAG X CGAA AAUUAGCA	3411	UGCUAAUUU GUUUUGGA	4550
4968	AUAUCCAA CUGAUGAG X CGAA ACAAAUUA	3412	UAAUUUGUU UUGGAUAU	4551
4969	UAUAUCCA CUGAUGAG X CGAA AACAAAUU	3413	AAUUUGUUU UGGAUAUA	4552
4970	CUAUAUCC CUGAUGAG X CGAA AAACAAAU	3414	AUUUGUUUU GGAUAUAG	4553
4975	UUAUACUA CUGAUGAG X CGAA AUCCAAAA	3415	UUUUGGAUA UAGUAUAA	4554
4977	GCUUAUAC CUGAUGAG X CGAA AUAUCCAA	3416	UUGGAUAUA GUAUAAGC	4555
4980	ACUGCUUA CUGAUGAG X CGAA ACUAUAUC	3417	GAUAUAGUA UAAGCAGU	4556
4982	ACACUGCU CUGAUGAG X CGAA AUACUAUA	3418	UAUAGUAUA AGCAGUGU	4557
4991	AAAACACA CUGAUGAG X CGAA ACACUGCU	3419	AGCAGUGUC UGUGUUUU	4558
4997	UCUUUCAA CUGAUGAG X CGAA ACACAGAC	3420	GUCUGUGUU UUGAAAGA	4559
4998	UUCUUUCA CUGAUGAG X CGAA AACACAGA	3421	UCUGUGUUU UGAAAGAA	4560
4999	AUUCUUUC CUGAUGAG X CGAA AAACACAG	3422	CUGUGUUUU GAAAGAAU	4561
5008	CUGUGUUC CUGAUGAG X CGAA AUUCUUUC	3423	GAAAGAAUA GAACACAG	4562

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
5018	GCACUACA CUGAUGAG X CGAA ACUGUGUU	3424	AACACAGUU UGUAGUGC	4563
5019	GGCACUAC CUGAUGAG X CGAA AACUGUGU	3425	ACACAGUUU GUAGUGCC	4564
5022	AGUGGCAC CUGAUGAG X CGAA ACAAACUG	3426	CAGUUUGUA GUGCCACU	4565
5033	CCCAAAAC CUGAUGAG X CGAA ACAGUGGC	3427	GCCACUGUU GUUUUGGG	4566
5036	CCCCCCAA CUGAUGAG X CGAA ACAACAGU	3428	ACUGUUGUU UUGGGGGG	4567
5037	CCCCCCCA CUGAUGAG X CGAA AACAACAG	3429	CUGUUGUUU UGGGGGGG	4568
5038	CCCCCCCC CUGAUGAG X CGAA AAACAACA	3430	UGUUGUUUU GGGGGGGG	4569
5049	AAGAAAAA CUGAUGAG X CGAA AGCCCCCC	3431	GGGGGGCUU UUUUUCUU	4570
5050	AAAGAAAA CUGAUGAG X CGAA AAGCCCCC	3432	GGGGGCUUU UUUUCUUU	4571
5051	AAAAGAAA CUGAUGAG X CGAA AAAGCCCC	3433	GGGGCUUUU UUUCUUUU	4572
5052	AAAAAGAA CUGAUGAG X CGAA AAAAGCCC	3434	GGGCUUUUU UUCUUUUU	4573
5053	GAAAAAGA CUGAUGAG X CGAA AAAAAGCC	3435	GGCUUUUUU UCUUUUUC	4574
5054	GGAAAAAG CUGAUGAG X CGAA AAAAAAGC	3436	GCUUUUUUU CUUUUUCC	4575
5055	CGGAAAAA CUGAUGAG X CGAA AAAAAAAG	3437	CUUUUUUUC UUUUUCCG	4576
5057	UCCGGAAA CUGAUGAG X CGAA AGAAAAAA	3438	UUUUUUCUU UUUCCGGA	4577
5058	UUCCGGAA CUGAUGAG X CGAA AAGAAAAA	3439	UUUUUCUUU UUCCGGAA	4578

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
5059	UUUCCGGA CUGAUGAG X CGAA AAAGAAAA	3440	UUUUCUUUU UCCGGAAA	4579
5060	UUUUCCGG CUGAUGAG X CGAA AAAAGAAA	3441	UUUCUUUUU CCGGAAAA	4580
5061	AUUUUCCG CUGAUGAG X CGAA AAAAAGAA	3442	UUCUUUUUC CGGAAAAU	4581
5070	GGUUUAAG CUGAUGAG X CGAA AUUUUCCG	3443	CGGAAAAUC CUUAAACC	4582
5073	UAAGGUUU CUGAUGAG X CGAA AGGAUUUU	3444	AAAAUCCUU AAACCUUA	4583
5074	UUAAGGUU CUGAUGAG X CGAA AAGGAUUU	3445	AAAUCCUUA AACCUUAA	4584
5080	AGUAUCUU CUGAUGAG X CGAA AGGUUUAA	3446	UUAAACCUU AAGAUACU	4585
5081	UAGUAUCU CUGAUGAG X CGAA AAGGUUUA	3447	UAAACCUUA AGAUACUA	4586
5086	GUCCUUAG CUGAUGAG X CGAA AUCUUAAG	3448	CUUAAGAUA CUAAGGAC	4587
5089	AACGUCCU CUGAUGAG X CGAA AGUAUCUU	3449	AAGAUACUA AGGACGUU	4588
5097	ACCAAAAC CUGAUGAG X CGAA ACGUCCUU	3450	AAGGACGUU GUUUUGGU	4589
5100	ACAACCAA CUGAUGAG X CGAA ACAACGUC	3451	GACGUUGUU UUGGUUGU	4590
5101	UACAACCA CUGAUGAG X CGAA AACAACGU	3452	ACGUUGUUU UGGUUGUA	4591
5102	GUACAACC CUGAUGAG X CGAA AAACAACG	3453	CGUUGUUUU GGUUGUAC	4592
5106	CCAAGUAC CUGAUGAG X CGAA ACCAAAAC	3454	GUUUUGGUU GUACUUGG	4593
5109	AUUCCAAG CUGAUGAG X CGAA ACAACCAA	3455	UUGGUUGUA CUUGGAAU	4594

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
5112	AGAAUUCC CUGAUGAG X CGAA AGUACAAC	3456	GUUGUACUU GGAAUUCU	4595
5118	UGACUAAG CUGAUGAG X CGAA AUUCCAAG	3457	CUUGGAAUU CUUAGUCA	4596
5119	GUGACUAA CUGAUGAG X CGAA AAUUCCAA	3458	UUGGAAUUC UUAGUCAC	4597
5121	UUGUGACU CUGAUGAG X CGAA AGAAUUCC	3459	GGAAUUCUU AGUCACAA	4598
5122	UUUGUGAC CUGAUGAG X CGAA AAGAAUUC	3460	GAAUUCUUA GUCACAAA	4599
5125	UAUUUUGU CUGAUGAG X CGAA ACUAAGAA	3461	UUCUUAGUC ACAAAAUA	4600
5133	ACAAAAUA CUGAUGAG X CGAA AUUUUGUG	3462	CACAAAAUA UAUUUUGU	4601
5135	AAACAAAA CUGAUGAG X CGAA AUAUUUUG	3463	CAAAAUAUA UUUUGUUU	4602
5137	GUAAACAA CUGAUGAG X CGAA AUAUAUUU	3464	AAAUAUAUU UUGUUUAC	4603
5138	UGUAAACA CUGAUGAG X CGAA AAUAUAUU	3465	AAUAUAUUU UGUUUACA	4604
5139	UUGUAAAC CUGAUGAG X CGAA AAAUAUAU	3466	AUAUAUUUU GUUUACAA	4605
5142	UUUUUGUA CUGAUGAG X CGAA ACAAAAUA	3467	UAUUUUGUU UACAAAAA	4606
5143	AUUUUUGU CUGAUGAG X CGAA AACAAAAU	3468	AUUUUGUUU ACAAAAAU	4607
5144	AAUUUUUG CUGAUGAG X CGAA AAACAAAA	3469	UUUUGUUUA CAAAAAUU	4608
5152	UUUACAGA CUGAUGAG X CGAA AUUUUUGU	3470	ACAAAAAUU UCUGUAAA	4609
5153	UUUUACAG CUGAUGAG X CGAA AAUUUUUG	3471	CAAAAAUUU CUGUAAAA	4610

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
5154	GUUUUACA CUGAUGAG X CGAA AAAUUUUU	3472	AAAAAUUUC UGUAAAAC	4611
5158	ACCUGUUU CUGAUGAG X CGAA ACAGAAAU	3473	AUUUCUGUA AAACAGGU	4612
5167	ACUGUUAU CUGAUGAG X CGAA ACCUGUUU	3474	AAACAGGUU AUAACAGU	4613
5168	CACUGUUA CUGAUGAG X CGAA AACCUGUU	3475	AACAGGUUA UAACAGUG	4614
5170	AACACUGU CUGAUGAG X CGAA AUAACCUG	3476	CAGGUUAUA ACAGUGUU	4615
5178	AGACUUUA CUGAUGAG X CGAA ACACUGUU	3477	AACAGUGUU UAAAGUCU	4616
5179	GAGACUUU CUGAUGAG X CGAA AACACUGU	3478	ACAGUGUUU AAAGUCUC	4617
5180	UGAGACUU CUGAUGAG X CGAA AAACACUG	3479	CAGUGUUUA AAGUCUCA	4618
5185	GAAACUGA CUGAUGAG X CGAA ACUUUAAA	3480	UUUAAAGUC UCAGUUUC	4619
5187	AAGAAACU CUGAUGAG X CGAA AGACUUUA	3481	UAAAGUCUC AGUUUCUU	4620
5191	AAGCAAGA CUGAUGAG X CGAA ACUGAGAC	3482	GUCUCAGUU UCUUGCUU	4621
5192	CAAGCAAG CUGAUGAG X CGAA AACUGAGA	3483	UCUCAGUUU CUUGCUUG	4622
5193	CCAAGCAA CUGAUGAG X CGAA AAACUGAG	3484	CUCAGUUUC UUGCUUGG	4623
5195	CCCCAAGC CUGAUGAG X CGAA AGAAACUG	3485	CAGUUUCUU GCUUGGGG	4624
5199	AGUUCCCC CUGAUGAG X CGAA AGCAAGAA	3486	UUCUUGCUU GGGGAACU	4625
5208	AGGGACAC CUGAUGAG X CGAA AGUUCCCC	3487	GGGGAACUU GUGUCCCU	4626

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
5213	ACAUUAGG CUGAUGAG X CGAA ACACAAGU	3488	ACUUGUGUC CCUAAUGU	4627
5217	UAACACAU CUGAUGAG X CGAA AGGGACAC	3489	GUGUCCCUA AUGUGUUA	4628
5224	AGCAAUCU CUGAUGAG X CGAA ACACAUUA	3490	UAAUGUGUU AGAUUGCU	4629
5225	UAGCAAUC CUGAUGAG X CGAA AACACAUU	3491	AAUGUGUUA GAUUGCUA	4630
5229	AAUCUAGC CUGAUGAG X CGAA AUCUAACA	3492	UGUUAGAUU GCUAGAUU	4631
5233	UAGCAAUC CUGAUGAG X CGAA AGCAAUCU	3493	AGAUUGCUA GAUUGCUA	4632
5237	UCCUUAGC CUGAUGAG X CGAA AUCUAGCA	3494	UGCUAGAUU GCUAAGGA	4633
5241	CAGCUCCU CUGAUGAG X CGAA AGCAAUCU	3495	AGAUUGCUA AGGAGCUG	4634
5252	CUGUCAAG CUGAUGAG X CGAA AUCAGCUC	3496	GAGCUGAUA CUUGACAG	4635
5255	AAACUGUC CUGAUGAG X CGAA AGUAUCAG	3497	CUGAUACUU GACAGUUU	4636
5262	GUCUAAAA CUGAUGAG X CGAA ACUGUCAA	3498	UUGACAGUU UUUUAGAC	4637
5263	GGUCUAAA CUGAUGAG X CGAA AACUGUCA	3499	UGACAGUUU UUUAGACC	4638
5264	AGGUCUAA CUGAUGAG X CGAA AAACUGUC	3500	GACAGUUUU UUAGACCU	4639
5265	CAGGUCUA CUGAUGAG X CGAA AAAACUGU	3501	ACAGUUUUU UAGACCUG	4640
5266	ACAGGUCU CUGAUGAG X CGAA AAAAACUG	3502	CAGUUUUUU AGACCUGU	4641
5267	CACAGGUC CUGAUGAG X CGAA AAAAAACU	3503	AGUUUUUUA GACCUGUG	4642

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
5277	UUUUUAGU CUGAUGAG X CGAA ACACAGGU	3504	ACCUGUGUU ACUAAAAA	4643
5278	UUUUUUAG CUGAUGAG X CGAA AACACAGG	3505	CCUGUGUUA CUAAAAAA	4644
5281	CUUUUUUU CUGAUGAG X CGAA AGUAACAC	3506	GUGUUACUA AAAAAAAG	4645
5298	CCUUUUCC CUGAUGAG X CGAA ACAUUCAU	3507	AUGAAUGUC GGAAAAGG	4646
5311	ACCCUCCC CUGAUGAG X CGAA ACACCCUU	3508	AAGGGUGUU GGGAGGGU	4647
5323	UCUUUGUU CUGAUGAG X CGAA ACCACCCU	3509	AGGGUGGUC AACAAAGA	4648
5343	AACACCAU CUGAUGAG X CGAA ACAUCUUU	3510	AAAGAUGUU AUGGUGUU	4649
5344	AAACACCA CUGAUGAG X CGAA AACAUCUU	3511	AAGAUGUUA UGGUGUUU	4650
5351	UAAGUCUA CUGAUGAG X CGAA ACACCAUA	3512	UAUGGUGUU UAGACUUA	4651
5352	AUAAGUCU CUGAUGAG X CGAA AACACCAU	3513	AUGGUGUUU AGACUUAU	4652
5353	CAUAAGUC CUGAUGAG X CGAA AAACACCA	3514	UGGUGUUUA GACUUAUG	4653
5358	ACAACCAU CUGAUGAG X CGAA AGUCUAAA	3515	UUUAGACUU AUGGUUGU	4654
5359	AACAACCA CUGAUGAG X CGAA AAGUCUAA	3516	UUAGACUUA UGGUUGUU	4655
5364	UUUUUAAC CUGAUGAG X CGAA ACCAUAAG	3517	CUUAUGGUU GUUAAAAA	4656
5367	ACAUUUUU CUGAUGAG X CGAA ACAACCAU	3518	AUGGUUGUU AAAAAUGU	4657
5368	GACAUUUU CUGAUGAG X CGAA AACAACCA	3519	UGGUUGUUA AAAAUGUC	4658

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
5376	CUUGAGAU CUGAUGAG X CGAA ACAUUUUU	3520	AAAAAUGUC AUCUCAAG	4659
5379	UGACUUGA CUGAUGAG X CGAA AUGACAUU	3521	AAUGUCAUC UCAAGUCA	4660
5381	CUUGACUU CUGAUGAG X CGAA AGAUGACA	3522	UGUCAUCUC AAGUCAAG	4661
5386	AGUGACUU CUGAUGAG X CGAA ACUUGAGA	3523	UCUCAAGUC AAGUCACU	4662
5391	AGACCAGU CUGAUGAG X CGAA ACUUGACU	3524	AGUCAAGUC ACUGGUCU	4663
5398	UGCAAACA CUGAUGAG X CGAA ACCAGUGA	3525	UCACUGGUC UGUUUGCA	4664
5402	CAAAUGCA CUGAUGAG X CGAA ACAGACCA	3526	UGGUCUGUU UGCAUUUG	4665
5403	UCAAAUGC CUGAUGAG X CGAA AACAGACC	3527	GGUCUGUUU GCAUUUGA	4666
5408	AUGUAUCA CUGAUGAG X CGAA AUGCAAAC	3528	GUUUGCAUU UGAUACAU	4667
5409	AAUGUAUC CUGAUGAG X CGAA AAUGCAAA	3529	UUUGCAUUU GAUACAUU	4668
5413	CAAAAAUG CUGAUGAG X CGAA AUCAAAUG	3530	CAUUUGAUA CAUUUUUG	4669
5417	AGUACAAA CUGAUGAG X CGAA AUGUAUCA	3531	UGAUACAUU UUUGUACU	4670
5418	UAGUACAA CUGAUGAG X CGAA AAUGUAUC	3532	GAUACAUUU UUGUACUA	4671
5419	UUAGUACA CUGAUGAG X CGAA AAAUGUAU	3533	AUACAUUUU UGUACUAA	4672
5420	GUUAGUAC CUGAUGAG X CGAA AAAAUGUA	3534	UACAUUUUU GUACUAAC	4673
5423	CUAGUUAG CUGAUGAG X CGAA ACAAAAAU	3535	AUUUUUGUA CUAACUAG	4674

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
5426	AUGCUAGU CUGAUGAG X CGAA AGUACAAA	3536	UUUGUACUA ACUAGCAU	4675
5430	UACAAUGC CUGAUGAG X CGAA AGUUAGUA	3537	UACUAACUA GCAUUGUA	4676
5435	AAUUUUAC CUGAUGAG X CGAA AUGCUAGU	3538	ACUAGCAUU GUAAAAUU	4677
5438	AAUAAUUU CUGAUGAG X CGAA ACAAUGCU	3539	AGCAUUGUA AAAUUAUU	4678
5443	CAUGAAAU CUGAUGAG X CGAA AUUUUACA	3540	UGUAAAAUU AUUUCAUG	4679
5444	UCAUGAAA CUGAUGAG X CGAA AAUUUUAC	3541	GUAAAAUUA UUUCAUGA	4680
5446	AAUCAUGA CUGAUGAG X CGAA AUAAUUUU	3542	AAAAUUAUU UCAUGAUU	4681
5447	UAAUCAUG CUGAUGAG X CGAA AAUAAUUU	3543	AAAUUAUUU CAUGAUUA	4682
5448	CUAAUCAU CUGAUGAG X CGAA AAAUAAUU	3544	AAUUAUUUC AUGAUUAG	4683
5454	UAAUUUCU CUGAUGAG X CGAA AUCAUGAA	3545	UUCAUGAUU AGAAAUUA	4684
5455	GUAAUUUC CUGAUGAG X CGAA AAUCAUGA	3546	UCAUGAUUA GAAAUUAC	4685
5461	CCACAGGU CUGAUGAG X CGAA AUUUCUAA	3547	UUAGAAAUU ACCUGUGG	4686
5462	UCCACAGG CUGAUGAG X CGAA AAUUUCUA	3548	UAGAAAUUA CCUGUGGA	4687
5472	UAUACAAA CUGAUGAG X CGAA AUCCACAG	3549	CUGUGGAUA UUUGUAUA	4688
5474	UUUAUACA CUGAUGAG X CGAA AUAUCCAC	3550	GUGGAUAUU UGUAUAAA	4689
5475	UUUUAUAC CUGAUGAG X CGAA AAUAUCCA	3551	UGGAUAUUU GUAUAAAA	4690

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
5478	CACUUUUA CUGAUGAG X CGAA ACAAAUAU	3552	AUAUUUGUA UAAAAGUG	4691
5480	CACACUUU CUGAUGAG X CGAA AUACAAAU	3553	AUUUGUAUA AAAGUGUG	4692
5493	AAAAAAUU CUGAUGAG X CGAA AUUUCACA	3554	UGUGAAAUA AAUUUUUU	4693
5497	UUAUAAAA CUGAUGAG X CGAA AUUUAUUU	3555	AAAUAAAUU UUUUAUAA	4694
5498	UUUAUAAA CUGAUGAG X CGAA AAUUUAUU	3556	AAUAAAUUU UUUAUAAA	4695
5499	UUUUAUAA CUGAUGAG X CGAA AAAUUUAU	3557	AUAAAUUUU UUAUAAAA	4696
5500	CUUUUAUA CUGAUGAG X CGAA AAAAUUUA	3558	UAAAUUUUU UAUAAAAG	4697
5501	ACUUUUAU CUGAUGAG X CGAA AAAAAUUU	3559	AAAUUUUUU AUAAAAGU	4698
5502	CACUUUUA CUGAUGAG X CGAA AAAAAAUU	3560	AAUUUUUUA UAAAAGUG	4699
5504	AACACUUU CUGAUGAG X CGAA AUAAAAAA	3561	UUUUUUAUA AAAGUGUU	4700
5512	AAACAAUG CUGAUGAG X CGAA ACACUUUU	3562	AAAAGUGUU CAUUGUUU	4701
5513	GAAACAAU CUGAUGAG X CGAA AACACUUU	3563	AAAGUGUUC AUUGUUUC	4702
5516	UACGAAAC CUGAUGAG X CGAA AUGAACAC	3564	GUGUUCAUU GUUUCGUA	4703
5519	UGUUACGA CUGAUGAG X CGAA ACAAUGAA	3565	UUCAUUGUU UCGUAACA	4704
5520	GUGUUACG CUGAUGAG X CGAA AACAAUGA	3566	UCAUUGUUU CGUAACAC	4705
5521	UGUGUUAC CUGAUGAG X CGAA AAACAAUG	3567	CAUUGUUUC GUAACACA	4706

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
5524	UGCUGUGU CUGAUGAG X CGAA ACGAAACA	3568	UGUUUCGUA ACACAGCA	4707
5534	ACAUAUAC CUGAUGAG X CGAA AUGCUGUG	3569	CACAGCAUU GUAUAUGU	4708
5537	UUCACAUA CUGAUGAG X CGAA ACAAUGCU	3570	AGCAUUGUA UAUGUGAA	4709
5539	GCUUCACA CUGAUGAG X CGAA AUACAAUG	3571	CAUUGUAUA UGUGAAGC	4710
5553	UAAUUUUA CUGAUGAG X CGAA AGUUUGCU	3572	AGCAAACUC UAAAAUUA	4711
5555	UAUAAUUU CUGAUGAG X CGAA AGAGUUUG	3573	CAAACUCUA AAAUUAUA	4712
5560	UCAUUUAU CUGAUGAG X CGAA AUUUUAGA	3574	UCUAAAAUU AUAAAUGA	4713
5561	GUCAUUUA CUGAUGAG X CGAA AAUUUUAG	3575	CUAAAAUUA UAAAUGAC	4714
5563	UUGUCAUU CUGAUGAG X CGAA AUAAUUUU	3576	AAAAUUAUA AAUGACAA	4715
5579	AAAUAGAU CUGAUGAG X CGAA AUUCAGGU	3577	ACCUGAAUU AUCUAUUU	4716
5580	GAAAUAGA CUGAUGAG X CGAA AAUUCAGG	3578	CCUGAAUUA UCUAUUUC	4717
5582	AUGAAAUA CUGAUGAG X CGAA AUAAUUCA	3579	UGAAUUAUC UAUUUCAU	4718
5584	UGAUGAAA CUGAUGAG X CGAA AGAUAAUU	3580	AAUUAUCUA UUUCAUCA	4719
5586	UUUGAUGA CUGAUGAG X CGAA AUAGAUAA	3581	UUAUCUAUU UCAUCAAA	4720
5587	UUUUGAUG CUGAUGAG X CGAA AAUAGAUA	3582	UAUCUAUUU CAUCAAAA	4721
5588	UUUUUGAU CUGAUGAG X CGAA AAAUAGAU	3583	AUCUAUUUC AUCAAAAA	4722

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
5591	UUUUUUUU CUGAUGAG X CGAA AUGAAAUA	3584	UAUUUCAUC AAAAAAAA	4723
5614	UGCCCAUA CUGAUGAG X CGAA AGUUUUUU	3585	AAAAAACUU UAUGGGCA	4724
5615	GUGCCCAU CUGAUGAG X CGAA AAGUUUUU	3586	AAAAACUUU AUGGGCAC	4725
5616	UGUGCCCA CUGAUGAG X CGAA AAAGUUUU	3587	AAAACUUUA UGGGCACA	4726

TABLE VIII: HAIRPIN RIBOZYME AND TARGET SEQUENCES FOR INTEGRIN ALPHA 6 SUBUNIT

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No
8	CCCCGG AGAA GUCG ACCAGAGAAACA X GUACAUUACCUGGUA	4727	CGACC GUC CCGGGG	4821
60	UGCUGC AGAA GCAG ACCAGAGAAACA X GUACAUUACCUGGUA	4728	CUGCG GUA GCAGCA	4822
77	GUCCGA AGAA GCCG ACCAGAGAAACA X GUACAUUACCUGGUA	4729	CGGCA GCC UCGGAC	4823
83	GGCUGG AGAA GAGG ACCAGAGAAACA X GUACAUUACCUGGUA	4730	CCUCG GAC CCAGCC	4824
89	GCUCCG AGAA GGGU ACCAGAGAAACA X GUACAUUACCUGGUA	4731	ACCCA GCC CGGAGC	4825
106	UGCAGC AGAA GCCC ACCAGAGAAACA X GUACAUUACCUGGUA	4732	GGGCG GCC GCUGCA	4826
109	ACCUGC AGAA GCCG ACCAGAGAAACA X GUACAUUACCUGGUA	4733	CGGCC GCU GCAGGU	4827
122	GAGGGG AGAA GGGA ACCAGAGAAACA X GUACAUUACCUGGUA	4734	UCCCC GCU CCCCUC	4828
142	GCCAUG AGAA GACG ACCAGAGAAACA X GUACAUUACCUGGUA	4735	CGUCC GCC CAUGGC	4829
152	CCCGGC AGAA GCCA ACCAGAGAAACA X GUACAUUACCUGGUA	4736	UGGCC GCC GCCGGG	4830

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No
155	CUGCCC AGAA GCGG ACCAGAGAAACA X GUACAUUACCUGGUA	4737	CCGCC GCC GGGCAG	4831
163	AAGCAC AGAA GCCC ACCAGAGAAACA X GUACAUUACCUGGUA	4738	GGGCA GCU GUGCUU	4832
181	CCCGCC AGAA GGUA ACCAGAGAAACA X GUACAUUACCUGGUA	4739	UACCU GUC GGCGGG	4833
196	AGCCGG AGAA GGAG ACCAGAGAAACA X GUACAUUACCUGGUA	4740	CUCCU GUC CCGGCU	4834
202	GCGCCG AGAA GGGA ACCAGAGAAACA X GUACAUUACCUGGUA	4741	UCCCG GCU CGGCGC	4835
212	GUUGAA AGAA GCGC ACCAGAGAAACA X GUACAUUACCUGGUA	4742	GCGCA GCC UUCAAC	4836
279	GCGAGA AGAA GAAG ACCAGAGAAACA X GUACAUUACCUGGUA	4743	CUUCG GCU UCUCGC	4837
310	UCCUCG AGAA GCAG ACCAGAGAAACA X GUACAUUACCUGGUA	4744	CUGCA GCC CGAGGA	4838
325	AGCAAC AGAA GCUU ACCAGAGAAACA X GUACAUUACCUGGUA	4745	AAGCG GCU GUUGCU	4839
328	ACGAGC AGAA GCCG ACCAGAGAAACA X GUACAUUACCUGGUA	4746	CGGCU GUU GCUCGU	4840

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No
394	CAGCUG AGAA GCCC ACCAGAGAAACA X GUACAUUACCUGGUA	4747	GGGCU GUA CAGCUG	4841
399	UGUCGC AGAA GUAC ACCAGAGAAACA X GUACAUUACCUGGUA	4748	GUACA GCU GCGACA	4842
413	CCCCCG AGAA GUGA ACCAGAGAAACA X GUACAUUACCUGGUA	4749	UCACC GCC CGGGGG	4843
433	AACUCG AGAA GCGU ACCAGAGAAACA X GUACAUUACCUGGUA	4750	ACGCG GAU CGAGUU	4844
455	CGUGGG AGAA GCAU ACCAGAGAAACA X GUACAUUACCUGGUA	4751	AUGCU GAC CCCACG	4845
500	GCUCUG AGAA GUGA ACCAGAGAAACA X GUACAUUACCUGGUA	4752	UCACC GUC CAGAGC	4846
899	AGCAGG AGAA GGAA ACCAGAGAAACA X GUACAUUACCUGGUA	4753	UUCCU GUU CCUGCU	4847
1162	UCAAAA AGAA GUGG ACCAGAGAAACA X GUACAUUACCUGGUA	4754	CCACA GUA UUUUGA	4848
1224	UAUUCC AGAA GCCU ACCAGAGAAACA X GUACAUUACCUGGUA	4755	AGGCA GAU GGAAUA	4849
1334	AGCUCC AGAA GCAA ACCAGAGAAACA X GUACAUUACCUGGUA	4756	UUGCA GUU GGAGCU	4850

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No
1345	UCAUCA AGAA GAGC ACCAGAGAAACA X GUACAUUACCUGGUA	4757	GCUCC GUA UGAUGA	4851
1490	AGCAAC AGAA GGGU ACCAGAGAAACA X GUACAUUACCUGGUA	4758	ACCCU GAU GUUGCU	4852
1499	GGAACC AGAA GCAA ACCAGAGAAACA X GUACAUUACCUGGUA	4759	UUGCU GUU GGUUCC	4853
1514	UACUGA AGAA GAGA ACCAGAGAAACA X GUACAUUACCUGGUA	4760	UCUCA GAU UCAGUA	4854
1533	GCCGGG AGAA GAAA ACCAGAGAAACA X GUACAUUACCUGGUA	4761	UUUCA GAU CCCGGC	4855
1540	AUCACA AGAA GGGA ACCAGAGAAACA X GUACAUUACCUGGUA	4762	UCCCG GCC UGUGAU	4856
1650	AUUCAA AGAA GGAU ACCAGAGAAACA X GUACAUUACCUGGUA	4763	AUCCU GUU UUGAAU	4857
1673	AUAACC AGAA GGGU ACCAGAGAAACA X GUACAUUACCUGGUA	4764	ACCCC GCU GGUUAU	4858
1759	UUUCGA AGAA GAAC ACCAGAGAAACA X GUACAUUACCUGGUA	4765	GUUCA GUU UCGAAA	4859
1895	CACUGA AGAA GUUA ACCAGAGAAACA X GUACAUUACCUGGUA	4766	UAACU GCC UCAGUG	4860

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No
1973	GGGUUC AGAA GAAU ACCAGAGAAACA X GUACAUUACCUGGUA	4767	AUUCA GAU GAACCC	4861
1988	AAUAUG AGAA GUCU ACCAGAGAAACA X GUACAUUACCUGGUA	4768	AGACA GCU CAUAUU	4862
2187	UGGAAG AGAA GUUU ACCAGAGAAACA X GUACAUUACCUGGUA	4769	AAACA GCC CUUCCA	4863
2245	GUUGCA AGAA GUUU ACCAGAGAAACA X GUACAUUACCUGGUA	4770	AAACU GAU UGCAAC	4864
2314	CAACUC AGAA GUUU ACCAGAGAAACA X GUACAUUACCUGGUA	4771	AAACA GUU GAGUUG	4865
2351	CUCACA AGAA GCUU ACCAGAGAAACA X GUACAUUACCUGGUA	4772	AAGCU GAC UGUGAG	4866
2530	GAUAAA AGAA GUUC ACCAGAGAAACA X GUACAUUACCUGGUA	4773	GAACU GCU UUUAUC	4867
2540	UCCCGA AGAA GAUA ACCAGAGAAACA X GUACAUUACCUGGUA	4774	UAUCG GUC UCGGGA	4868
2585	GCCAAC AGAA GUAC ACCAGAGAAACA X GUACAUUACCUGGUA	4775	GUACA GUU GUUGGC	4869
2917	UUAAGA AGAA GGUA ACCAGAGAAACA X GUACAUUACCUGGUA	4776	UACCA GAC UCUUAA	4870

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No
2928	UCACGC AGAA GUUA ACCAGAGAAACA X GUACAUUACCUGGUA	4777	UAACU GUA GCGUGA	4871
2958	GCGGGC AGAA GAUG ACCAGAGAAACA X GUACAUUACCUGGUA	4778	CAUCA GAU GCCCGC	4872
2965	CCCCGC AGAA GGCA ACCAGAGAAACA X GUACAUUACCUGGUA	4779	UGCCC GCU GCGGGG	4873
3092	GGCAGC AGAA GUCA ACCAGAGAAACA X GUACAUUACCUGGUA	4780	UGACU GCU GCUGCC	4874
3095	UUCGGC AGAA GCAG ACCAGAGAAACA X GUACAUUACCUGGUA	4781	CUGCU GCU GCCGAA	4875
3098	AUUUUC AGAA GCAG ACCAGAGAAACA X GUACAUUACCUGGUA	4782	CUGCU GCC GAAAAU	4876
3164	CUGAGC AGAA GUCU ACCAGAGAAACA X GUACAUUACCUGGUA	4783	AGACU GUA GCUCAG	4877
3172	CCCGAA AGAA GAGC ACCAGAGAAACA X GUACAUUACCUGGUA	4784	GCUCA GUA UUCGGG	4878
3359	CUAUGC AGAA GAAG ACCAGAGAAACA X GUACAUUACCUGGUA	4785	CUUCU GAU GCAUAG	4879
3581	UUUGGG AGAA GUGA ACCAGAGAAACA X GUACAUUACCUGGUA	4786	UCACA GUA CCCAAA	4880

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No
3592	GGAAAA AGAA GUUU ACCAGAGAAACA X GUACAUUACCUGGUA	4787	AAACU GCU UUUUCC	4881
3633	GGAUUG AGAA GGCU ACCAGAGAAACA X GUACAUUACCUGGUA	4788	AGCCU GCU CAAUCC	4882
3651	UCUGAA AGAA GUCC ACCAGAGAAACA X GUACAUUACCUGGUA	4789	GGACU GAU UUCAGA	4883
3673	GGUUCG AGAA GUGU ACCAGAGAAACA X GUACAUUACCUGGUA	4790	ACACA GUA CGAACC	4884
3686	AGUUAA AGAA GUAG ACCAGAGAAACA X GUACAUUACCUGGUA	4791	CUACA GUU UUAACU	4885
3725	GUGCAA AGAA GGAG ACCAGAGAAACA X GUACAUUACCUGGUA	4792	CUCCU GUU UUGCAC	4886
3750	CAUUCC AGAA GUUU ACCAGAGAAACA X GUACAUUACCUGGUA	4793	AAACU GUU GGAAUG	4887
3774	AAUUAC AGAA GUUA ACCAGAGAAACA X GUACAUUACCUGGUA	4794	UAACU GCC GUAAUU	4888
3818	AUGUAA AGAA GCCA ACCAGAGAAACA X GUACAUUACCUGGUA	4795	UGGCU GAC UUACAU	4889
3847	CAACUG AGAA GGCC ACCAGAGAAACA X GUACAUUACCUGGUA	4796	GGCCU GCC CAGUUG	4890

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No
3852	GAGUGC AGAA GGGC ACCAGAGAAACA X GUACAUUACCUGGUA	4797	GCCCA GUU GCACUC	4891
3927	GGUUAG AGAA GCCA ACCAGAGAAACA X GUACAUUACCUGGUA	4798	UGGCC GUC CUAACC	4892
3944	CUGCGC AGAA GGCC ACCAGAGAAACA X GUACAUUACCUGGUA	4799	GGCCU GCU GCGCAG	4893
3952	AUGGAC AGAA GCGC ACCAGAGAAACA X GUACAUUACCUGGUA	4800	GCGCA GAC GUCCAU	4894
3971	AUGUGG AGAA GCUA ACCAGAGAAACA X GUACAUUACCUGGUA	4801	UAGCU GUC CCACAU	4895
4026	GUUUAA AGAA GCAC ACCAGAGAAACA X GUACAUUACCUGGUA	4802	GUGCU GUC UUAAAC	4896
4071	GGAAAA AGAA GUAG ACCAGAGAAACA X GUACAUUACCUGGUA	4803	CUACC GUC UUUUCC	4897
4081	CUAGGA AGAA GGAA ACCAGAGAAACA X GUACAUUACCUGGUA	4804	UUCCU GUU UCCUAG	4898
4104	GACGUG AGAA GGUA ACCAGAGAAACA X GUACAUUACCUGGUA	4805	UACCU GCU CACGUC	4899
4165	AUUCAA AGAA GUUG ACCAGAGAAACA X GUACAUUACCUGGUA	4806	CAACA GAC UUGAAU	4900

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No
4262	AGGGUA AGAA GGAG ACCAGAGAAACA X GUACAUUACCUGGUA	4807	CUCCA GUU UACCCU	4901
4426	GGUGGA AGAA GUCA ACCAGAGAAACA X GUACAUUACCUGGUA	4808	UGACA GCC UCCACC	4902
4600	UGAGUA AGAA GCAC ACCAGAGAAACA X GUACAUUACCUGGUA	4809	GUGCG GUU UACUCA	4903
4611	AUUUGC AGAA GUGA ACCAGAGAAACA X GUACAUUACCUGGUA	4810	UCACU GCU GCAAAU	4904
4623	UGAAUA AGAA GUAU ACCAGAGAAACA X GUACAUUACCUGGUA	4811	AUACU GUA UAUUCA	4905
4680	UACUGG AGAA GUUU ACCAGAGAAACA X GUACAUUACCUGGUA	4812	AAACU GAU CCAGUA	4906
4686	GUCUUA AGAA GGAU ACCAGAGAAACA X GUACAUUACCUGGUA	4813	AUCCA GUA UAAGAC	4907
4769	UGGGAA AGAA GAUA ACCAGAGAAACA X GUACAUUACCUGGUA	4814	UAUCU GUA UUCCCA	4908
4895	AAAAAA AGAA GCUU ACCAGAGAAACA X GUACAUUACCUGGUA	4815	AAGCU GAU UUUUUU	4909
5015	ACUACA AGAA GUGU ACCAGAGAAACA X GUACAUUACCUGGUA	4816	ACACA GUU UGUAGU	4910

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No
5030	CAAAAC AGAA GUGG ACCAGAGAAACA X GUACAUUACCUGGUA	4817	CCACU GUU GUUUUG	4911
5188	GCAAGA AGAA GAGA ACCAGAGAAACA X GUACAUUACCUGGUA	4818	UCUCA GUU UCUUGC	4912
5259	CUAAAA AGAA GUCA ACCAGAGAAACA X GUACAUUACCUGGUA	4819	UGACA GUU UUUUAG	4913
5399	AAUGCA AGAA GACC ACCAGAGAAACA X GUACAUUACCUGGUA	4820	GGUCU GUU UGCAUU	4914

TABLE IX: HAMMERHEAD RIBOZYME AND TARGET SEQUENCES FOR INTEGRIN SUBUNIT BETA 3

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
17	GAGGGCAA CUGAUGAG X CGAA ACCACAUC	4915	GAUGUGGUC UUGCCCUC	5702
19	UUGAGGGC CUGAUGAG X CGAA AGACCACA	4916	UGUGGUCUU GCCCUCAA	5703
25	UACCUGUU CUGAUGAG X CGAA AGGGCAAG	4917	CUUGCCCUC AACAGGUA	5704
33	AGACUACC CUGAUGAG X CGAA ACCUGUUG	4918	CAACAGGUA GGUAGUCU	5705
37	CGGUAGAC CUGAUGAG X CGAA ACCUACCU	4919	AGGUAGGUA GUCUACCG	5706
40	UUCCGGUA CUGAUGAG X CGAA ACUACCUA	4920	UAGGUAGUC UACCGGAA	5707
42	UUUUCCGG CUGAUGAG X CGAA AGACUACC	4921	GGUAGUCUA CCGGAAAA	5708
58	UCUUGCCU CUGAUGAG X CGAA AGUUUGGU	4922	ACCAAACUA AGGCAAGA	5709
74	UAUUCACU CUGAUGAG X CGAA AUUUUUUU	4923	AAAAAAAUU AGUGAAUA	5710
75	UUAUUCAC CUGAUGAG X CGAA AAUUUUUU	4924	AAAAAAUUA GUGAAUAA	5711
82	UCCUUUAU CUGAUGAG X CGAA AUUCACUA	4925	UAGUGAAUA AUAAAGGA	5712
85	CAGUCCUU CUGAUGAG X CGAA AUUAUUCA	4926	UGAAUAAUA AAGGACUG	5713
101	CUUCUCUG CUGAUGAG X CGAA ACCGGUUC	4927	GAACCGGUU CAGAGAAG	5714
102	CCUUCUCU CUGAUGAG X CGAA AACCGGUU	4928	AACCGGUUC AGAGAAGG	5715
114	AUCUGCUG CUGAUGAG X CGAA AUGCCUUC	4929	GAAGGCAUU CAGCAGAU	5716

Posi-tion	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
115	CAUCUGCU CUGAUGAG X CGAA AAUGCCUU	4930	AAGGCAUUC AGCAGAUG	5717
125	GACUGGCA CUGAUGAG X CGAA ACAUCUGC	4931	GCAGAUGUU UGCCAGUC	5718
126	UGACUGGC CUGAUGAG X CGAA AACAUCUG	4932	CAGAUGUUU GCCAGUCA	5719
133	AUUCAUUU CUGAUGAG X CGAA ACUGGCAA	4933	UUGCCAGUC AAAUGAAU	5720
142	CACACUUU CUGAUGAG X CGAA AUUCAUUU	4934	AAAUGAAUU AAAGUGUG	5721
143	UCACACUU CUGAUGAG X CGAA AAUUCAUU	4935	AAUGAAUUA AAGUGUGA	5722
164	ACUACCUC CUGAUGAG X CGAA AGUUUCAU	4936	AUGAAACUC GAGGUAGU	5723
170	UCACCCAC CUGAUGAG X CGAA ACCUCGAG	4937	CUCGAGGUA GUGGGUGA	5724
185	AUUCUUGG CUGAUGAG X CGAA ACACAUUC	4938	GAAUGUGUC CCAAGAAU	5725
194	UUUCGCUG CUGAUGAG X CGAA AUUCUUGG	4939	CCAAGAAUC CAGCGAAA	5726
209	UCCUGGGA CUGAUGAG X CGAA ACCCUGUU	4940	AACAGGGUC UCCCAGGA	5727
211	CCUCCUGG CUGAUGAG X CGAA AGACCCUG	4941	CAGGGUCUC CCAGGAGG	5728
235	CCUCUCCG CUGAUGAG X CGAA ACCCUUCC	4942	GGAAGGGUC CGGAGAGG	5729
255	AAGGCCAG CUGAUGAG X CGAA AGCCUGUG	4943	CACAGGCUC CUGGCCUU	5730
263	UGCUUAGA CUGAUGAG X CGAA AGGCCAGG	4944	CCUGGCCUU UCUAAGCA	5731
264	GUGCUUAG CUGAUGAG X CGAA AAGGCCAG	4945	CUGGCCUUU CUAAGCAC	5732

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
265	UGUGCUUA CUGAUGAG X CGAA AAAGGCCA	4946	UGGCCUUUC UAAGCACA	5733
267	GGUGUGCU CUGAUGAG X CGAA AGAAAGGC	4947	GCCUUUCUA AGCACACC	5734
287	GGGUCCGC CUGAUGAG X CGAA ACUGGGCA	4948	UGCCCAGUC GCGGACCC	5735
337	CCCACGAG CUGAUGAG X CGAA ACCCGCCU	4949	AGGCGGGUC CUCGUGGG	5736
340	UCGCCCAC CUGAUGAG X CGAA AGGACCCG	4950	CGGGUCCUC GUGGGCGA	5737
378	UGGGAAAC CUGAUGAG X CGAA AUUGCUCC	4951	GGAGCAAUA GUUUCCCA	5738
381	CGGUGGGA CUGAUGAG X CGAA ACUAUUGC	4952	GCAAUAGUU UCCCACCG	5739
382	GCGGUGGG CUGAUGAG X CGAA AACUAUUG	4953	CAAUAGUUU CCCACCGC	5740
383	AGCGGUGG CUGAUGAG X CGAA AAACUAUU	4954	AAUAGUUUC CCACCGCU	5741
392	CUGAGAGG CUGAUGAG X CGAA AGCGGUGG	4955	CCACCGCUC CCUCUCAG	5742
396	GCGCCUGA CUGAUGAG X CGAA AGGGAGCG	4956	CGCUCCCUC UCAGGCGC	5743
398	CUGCGCCU CUGAUGAG X CGAA AGAGGGAG	4957	CUCCCUCUC AGGCGCAG	5744
410	CUUCUCUA CUGAUGAG X CGAA ACCCUGCG	4958	CGCAGGGUC UAGAGAAG	5745
412	CGCUUCUC CUGAUGAG X CGAA AGACCCUG	4959	CAGGGUCUA GAGAAGCG	5746
430	CUUCUCUA CUGAUGAG X CGAA AUCCCCUC	4960	GAGGGGAUC UAGAGAAG	5747
432	GGCUUCUC CUGAUGAG X CGAA AGAUCCCC	4961	GGGGAUCUA GAGAAGCC	5748

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
461	GGGCCGCG CUGAUGAG X CGAA ACUCGCGC	4962	GCGCGAGUC CGCGGCCC	5749
477	UGGGACGC CUGAUGAG X CGAA ACGGGGCG	4963	CGCCCCGUU GCGUCCCA	5750
482	GUGGGUGG CUGAUGAG X CGAA ACGCAACG	4964	CGUUGCGUC CCACCCAC	5751
496	GGGGAGGG CUGAUGAG X CGAA ACGCGGUG	4965	CACCGCGUC CCCUCCCC	5752
501	GGGGAGGG CUGAUGAG X CGAA AGGGGACG	4966	CGUCCCCUC CCCUCCCC	5753
506	CGGGAGGG CUGAUGAG X CGAA AGGGGAGG	4967	CCUCCCCUC CCCUCCCG	5754
511	CGCAGCGG CUGAUGAG X CGAA AGGGGAGG	4968	CCUCCCCUC CCGCUGCG	5755
614	GUCGCCCA CUGAUGAG X CGAA AGCGGCCG	4969	CGGCCGCUC UGGGCGAC	5756
653	CCUACGCC CUGAUGAG X CGAA ACGCCCGC	4970	GCGGGCGUU GGCGUAGG	5757
659	UCACCUCC CUGAUGAG X CGAA ACGCCAAC	4971	GUUGGCGUA GGAGGUGA	5758
676	CCGAGCCG CUGAUGAG X CGAA AGCCUCAC	4972	GUGAGGCUC CGGCUCGG	5759
682	ACGCUGCC CUGAUGAG X CGAA AGCCGGAG	4973	CUCCGGCUC GGCAGCGU	5760
691	GCAGCUGC CUGAUGAG X CGAA ACGCUGCC	4974	GGCAGCGUC GCAGCUGC	5761
708	GGGGCGCA CUGAUGAG X CGAA AUCCUGGG	4975	CCCAGGAUC UGCGCCCC	5762
720	CGCAACUU CUGAUGAG X CGAA ACCGGGGC	4976	GCCCCGGUC AAGUUGCG	5763
725	AAGUCCGC CUGAUGAG X CGAA ACUUGACC	4977	GGUCAAGUU GCGGACUU	5764

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
733	CCGGCUCC CUGAUGAG X CGAA AGUCCGCA	4978	UGCGGACUUGGAGCCGG	5765
760	GACGNGCG CUGAUGAG X CGAA ACCAGUCC	4979	GGACUGGUCCGCNCGUC	5766
768	CCCACGCA CUGAUGAG X CGAA ACGNGCGG	4980	CCGCNCGUCUGCGUGGG	5767
780	GACACGNG CUGAUGAG X CGAA AUUCCCAC	4981	GUGGGAAUNCNCGUGUC	5768
788	CCAGCCAG CUGAUGAG X CGAA ACACGNGN	4982	NCNCGUGUCCUGGCUGG	5769
803	CCGGNUCC CUGAUGAG X CGAA ACCGNGCC	4983	GGCNCGGUCGGANCCGG	5770
825	GGGCCAGG CUGAUGAG X CGAA AGGUNCCC	4984	GGGNACCUUCCUGGCCC	5771
826	CGGGCCAG CUGAUGAG X CGAA AAGGUNCC	4985	GGNACCUUCCUGGCCCG	5772
877	UCUCGGAG CUGAUGAG X CGAA ACCCGCUC	4986	GAGCGGGUCCUCCGAGA	5773
880	GCGUCUCG CUGAUGAG X CGAA AGGACCCG	4987	CGGGUCCUCCGAGACGC	5774
898	GCCUGGCU CUGAUGAG X CGAA AUGGCUUC	4988	GAAGCCAUCAGCCAGGC	5775
916	CGGCCGGG CUGAUGAG X CGAA AGGNNNUC	4989	GANNNCCUUCCCGGCCG	5776
917	GCGGCCGG CUGAUGAG X CGAA AAGGNNNU	4990	ANNNCCUUCCCGGCCGC	5777
954	GGCUCAGA CUGAUGAG X CGAA AUGCGCCC	4991	GGGCGCAUCUCUGAGCC	5778
956	GGGGCUCA CUGAUGAG X CGAA AGAUGCGC	4992	GCGCAUCUCUGAGCCCC	5779
970	CCCCGGGU CUGAUGAG X CGAA AGCGCGGG	4993	CCCGCGCUCACCCGGGG	5780

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
989	NCACCCGC CUGAUGAG X CGAA ACGCGCGC	4994	GCGCGCGUC GCGGGUGN	5781
999	CCGACCAG CUGAUGAG X CGAA ANCACCCG	4995	CGGGUGNUC CUGGUCGG	5782
1005	CUUGGNCC CUGAUGAG X CGAA ACCAGGAN	4996	NUCCUGGUC GGNCCAAG	5783
1048	ACCCCCGG CUGAUGAG X CGAA AGCCCCAC	4997	GUGGGGCUU CCGGGGGU	5784
1049	AACCCCCG CUGAUGAG X CGAA AAGCCCCA	4998	UGGGGCUUC CGGGGGUU	5785
1057	GCGGGAAC CUGAUGAG X CGAA ACCCCCGG	4999	CCGGGGGUU GUUCCCGC	5786
1060	GGGGCGGG CUGAUGAG X CGAA ACAACCCC	5000	GGGGUUGUU CCCGCCCC	5787
1061	AGGGGCGG CUGAUGAG X CGAA AACAACCC	5001	GGGUUGUUC CCGCCCCU	5788
1070	CCUCUGCC CUGAUGAG X CGAA AGGGGCGG	5002	CCGCCCCUU GGCAGAGG	5789
1089	CAGGAAGU CUGAUGAG X CGAA ACAGGGCA	5003	UGCCCUGUA ACUUCCUG	5790
1093	CACCCAGG CUGAUGAG X CGAA AGUUACAG	5004	CUGUAACUU CCUGGGUG	5791
1094	UCACCCAG CUGAUGAG X CGAA AAGUUACA	5005	UGUAACUUC CUGGGUGA	5792
1123	GAAAUGUA CUGAUGAG X CGAA ACCCGCGC	5006	GCGCGGGUU UACAUUUC	5793
1124	GGAAAUGU CUGAUGAG X CGAA AACCCGCG	5007	CGCGGGUUU ACAUUUCC	5794
1125	GGGAAAUG CUGAUGAG X CGAA AAACCCGC	5008	GCGGGUUUA CAUUUCCC	5795
1129	UGUGGGGA CUGAUGAG X CGAA AUGUAAAC	5009	GUUUACAUU UCCCCACA	5796

Posi-tion	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1130	AUGUGGGG CUGAUGAG X CGAA AAUGUAAA	5010	UUUACAUUU CCCCACAU	5797
1131	AAUGUGGG CUGAUGAG X CGAA AAAUGUAA	5011	UUACAUUUC CCCACAUU	5798
1139	AAAUUGGA CUGAUGAG X CGAA AUGUGGGG	5012	CCCCACAUU UCCAAUUU	5799
1140	GAAAUUGG CUGAUGAG X CGAA AAUGUGGG	5013	CCCACAUUU CCAAUUUC	5800
1141	AGAAAUUG CUGAUGAG X CGAA AAAUGUGG	5014	CCACAUUUC CAAUUUCU	5801
1146	ACAGGAGA CUGAUGAG X CGAA AUUGGAAA	5015	UUUCCAAUU UCUCCUGU	5802
1147	AACAGGAG CUGAUGAG X CGAA AAUUGGAA	5016	UUCCAAUUU CUCCUGUU	5803
1148	UAACAGGA CUGAUGAG X CGAA AAAUUGGA	5017	UCCAAUUUC UCCUGUUA	5804
1150	CGUAACAG CUGAUGAG X CGAA AGAAAUUG	5018	CAAUUUCUC CUGUUACG	5805
1155	GAAAGCGU CUGAUGAG X CGAA ACAGGAGA	5019	UCUCCUGUU ACGCUUUC	5806
1156	AGAAAGCG CUGAUGAG X CGAA AACAGGAG	5020	CUCCUGUUA CGCUUUCU	5807
1161	UCUGGAGA CUGAUGAG X CGAA AGCGUAAC	5021	GUUACGCUU UCUCCAGA	5808
1162	UUCUGGAG CUGAUGAG X CGAA AAGCGUAA	5022	UUACGCUUU CUCCAGAA	5809
1163	CUUCUGGA CUGAUGAG X CGAA AAAGCGUA	5023	UACGCUUUC UCCAGAAG	5810
1165	ACCUUCUG CUGAUGAG X CGAA AGAAAGCG	5024	CGCUUUCUC CAGAAGGU	5811
1174	AAAGAAAA CUGAUGAG X CGAA ACCUUCUG	5025	CAGAAGGUU UUUUCUUU	5812

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1175	GAAAGAAA CUGAUGAG X CGAA AACCUUCU	5026	AGAAGGUUU UUUCUUUC	5813
1176	GGAAAGAA CUGAUGAG X CGAA AAACCUUC	5027	GAAGGUUUU UUCUUUCC	5814
1177	AGGAAAGA CUGAUGAG X CGAA AAAACCUU	5028	AAGGUUUUU UCUUUCCU	5815
1178	AAGGAAAG CUGAUGAG X CGAA AAAAACCU	5029	AGGUUUUUU CUUUCCUU	5816
1179	AAAGGAAA CUGAUGAG X CGAA AAAAAACC	5030	GGUUUUUUC UUUCCUUU	5817
1181	AAAAAGGA CUGAUGAG X CGAA AGAAAAAA	5031	UUUUUUCUU UCCUUUUU	5818
1182	AAAAAAGG CUGAUGAG X CGAA AAGAAAAA	5032	UUUUUCUUU CCUUUUUU	5819
1183	GAAAAAAG CUGAUGAG X CGAA AAAGAAAA	5033	UUUUCUUUC CUUUUUUC	5820
1186	AAAGAAAA CUGAUGAG X CGAA AGGAAAGA	5034	UCUUUCCUU UUUUCUUU	5821
1187	GAAAGAAA CUGAUGAG X CGAA AAGGAAAG	5035	CUUUCCUUU UUUCUUUC	5822
1188	AGAAAGAA CUGAUGAG X CGAA AAAGGAAA	5036	UUUCCUUUU UUCUUUCU	5823
1189	AAGAAAGA CUGAUGAG X CGAA AAAAGGAA	5037	UUCCUUUUU UCUUUCUU	5824
1190	AAAGAAAG CUGAUGAG X CGAA AAAAAGGA	5038	UCCUUUUUU CUUUCUUU	5825
1191	GAAAGAAA CUGAUGAG X CGAA AAAAAAGG	5039	CCUUUUUUC UUUCUUUC	5826
1193	AAGAAAGA CUGAUGAG X CGAA AGAAAAAA	5040	UUUUUUCUU UCUUUCUU	5827
1194	AAAGAAAG CUGAUGAG X CGAA AAGAAAAA	5041	UUUUUCUUU CUUUCUUU	5828

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1195	GAAAGAAA CUGAUGAG X CGAA AAAGAAAA	5042	UUUUCUUUC UUUCUUUC	5829
1197	AAGAAAGA CUGAUGAG X CGAA AGAAAGAA	5043	UUCUUUCUU UCUUUCUU	5830
1198	AAAGAAAG CUGAUGAG X CGAA AAGAAAGA	5044	UCUUUCUUU CUUUCUUU	5831
1199	AAAAGAAA CUGAUGAG X CGAA AAAGAAAG	5045	CUUUCUUUC UUUCUUUU	5832
1201	AAAAAAGA CUGAUGAG X CGAA AGAAAGAA	5046	UUCUUUCUU UCUUUUUU	5833
1202	AAAAAAAG CUGAUGAG X CGAA AAGAAAGA	5047	UCUUUCUUU CUUUUUUU	5834
1203	UAAAAAAA CUGAUGAG X CGAA AAAGAAAG	5048	CUUUCUUUC UUUUUUUA	5835
1205	GGUAAAAA CUGAUGAG X CGAA AGAAAGAA	5049	UUCUUUCUU UUUUUACC	5836
1206	AGGUAAAA CUGAUGAG X CGAA AAGAAAGA	5050	UCUUUCUUU UUUUACCU	5837
1207	AAGGUAAA CUGAUGAG X CGAA AAAGAAAG	5051	CUUUCUUUU UUUACCUU	5838
1208	GAAGGUAA CUGAUGAG X CGAA AAAAGAAA	5052	UUUCUUUUU UUACCUUC	5839
1209	UGAAGGUA CUGAUGAG X CGAA AAAAAGAA	5053	UUCUUUUUU UACCUUCA	5840
1210	UUGAAGGU CUGAUGAG X CGAA AAAAAAGA	5054	UCUUUUUUU ACCUUCAA	5841
1211	GUUGAAGG CUGAUGAG X CGAA AAAAAAAG	5055	CUUUUUUUA CCUUCAAC	5842
1215	GUAUGUUG CUGAUGAG X CGAA AGGUAAAA	5056	UUUUACCUU CAACAUAC	5843
1216	AGUAUGUU CUGAUGAG X CGAA AAGGUAAA	5057	UUUACCUUC AACAUACU	5844

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1222	CGCAGGAG CUGAUGAG X CGAA AUGUUGAA	5058	UUCAACAUA CUCCUGCG	5845
1225	CCCCGCAG CUGAUGAG X CGAA AGUAUGUU	5059	AACAUACUC CUGCGGGG	5846
1235	UCCAAAAC CUGAUGAG X CGAA ACCCCGCA	5060	UGCGGGGUU GUUUUGGA	5847
1238	UGCUCCAA CUGAUGAG X CGAA ACAACCCC	5061	GGGGUUGUU UUGGAGCA	5848
1239	CUGCUCCA CUGAUGAG X CGAA AACAACCC	5062	GGGUUGUUU UGGAGCAG	5849
1240	CCUGCUCC CUGAUGAG X CGAA AAACAACC	5063	GGUUGUUUU GGAGCAGG	5850
1257	AGGAGGCA CUGAUGAG X CGAA AGCCUCAU	5064	AUGAGGCUU UGCCUCCU	5851
1258	GAGGAGGC CUGAUGAG X CGAA AAGCCUCA	5065	UGAGGCUUU GCCUCCUC	5852
1263	CACUGGAG CUGAUGAG X CGAA AGGCAAAG	5066	CUUUGCCUC CUCCAGUG	5853
1266	GGACACUG CUGAUGAG X CGAA AGGAGGCA	5067	UGCCUCCUC CAGUGUCC	5854
1273	CACCUGGG CUGAUGAG X CGAA ACACUGGA	5068	UCCAGUGUC CCCAGGUG	5855
1294	UGGGAGCA CUGAUGAG X CGAA AGGCACCG	5069	CGGUGCCUC UGCUCCCA	5856
1299	UGCCCUGG CUGAUGAG X CGAA AGCAGAGG	5070	CCUCUGCUC CCAGGGCA	5857
1327	ACACUAGA CUGAUGAG X CGAA AUUUUUCG	5071	CGAAAAAUC UCUAGUGU	5858
1329	AUACACUA CUGAUGAG X CGAA AGAUUUUU	5072	AAAAAUCUC UAGUGUAU	5859
1331	GAAUACAC CUGAUGAG X CGAA AGAGAUUU	5073	AAAUCUCUA GUGUAUUC	5860

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1336	UCCCCGAA CUGAUGAG X CGAA ACACUAGA	5074	UCUAGUGUA UUCGGGGA	5861
1338	GUUCCCCG CUGAUGAG X CGAA AUACACUA	5075	UAGUGUAUU CGGGGAAC	5862
1339	GGUUCCCC CUGAUGAG X CGAA AAUACACU	5076	AGUGUAUUC GGGGAACC	5863
1359	GCCCAAGG CUGAUGAG X CGAA AGCCUUUU	5077	AAAAGGCUC CCUUGGGC	5864
1363	ACCGGCCC CUGAUGAG X CGAA AGGGAGCC	5078	GGCUCCCUU GGGCCGGU	5865
1377	AAGCCAAG CUGAUGAG X CGAA AUCCCACC	5079	GGUGGGAUC CUUGGCUU	5866
1380	ACAAAGCC CUGAUGAG X CGAA AGGAUCCC	5080	GGGAUCCUU GGCUUUGU	5867
1385	CAGAGACA CUGAUGAG X CGAA AGCCAAGG	5081	CCUUGGCUU UGUCUCUG	5868
1386	CCAGAGAC CUGAUGAG X CGAA AAGCCAAG	5082	CUUGGCUUU GUCUCUGG	5869
1389	CAGCCAGA CUGAUGAG X CGAA ACAAAGCC	5083	GGCUUUGUC UCUGGCUG	5870
1391	AGCAGCCA CUGAUGAG X CGAA AGACAAAG	5084	CUUUGUCUC UGGCUGCU	5871
1411	UGACGGCU CUGAUGAG X CGAA ACGGUGUG	5085	CACACCGUC AGCCGUCA	5872
1418	AUUGCCCU CUGAUGAG X CGAA ACGGCUGA	5086	UCAGCCGUC AGGGCAAU	5873
1427	CGAAUGCC CUGAUGAG X CGAA AUUGCCCU	5087	AGGGCAAUU GGCAUUCG	5874
1433	AGAGGCCG CUGAUGAG X CGAA AUGCCAAU	5088	AUUGGCAUU CGGCCUCU	5875
1434	AAGAGGCC CUGAUGAG X CGAA AAUGCCAA	5089	UUGGCAUUC GGCCUCUU	5876

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1440	GUACCAAA CUGAUGAG X CGAA AGGCCGAA	5090	UUCGGCCUC UUUGGUAC	5877
1442	CAGUACCA CUGAUGAG X CGAA AGAGGCCG	5091	CGGCCUCUU UGGUACUG	5878
1443	CCAGUACC CUGAUGAG X CGAA AAGAGGCC	5092	GGCCUCUUU GGUACUGG	5879
1447	GUCCCCAG CUGAUGAG X CGAA ACCAAAGA	5093	UCUUUGGUA CUGGGGAC	5880
1491	CGGGCAGC CUGAUGAG X CGAA ACCCCGGG	5094	CCCGGGGUU GCUGCCCG	5881
1504	UCAGAGAG CUGAUGAG X CGAA ACCACGGG	5095	CCCGUGGUC CUCUCUGA	5882
1507	GACUCAGA CUGAUGAG X CGAA AGGACCAC	5096	GUGGUCCUC UCUGAGUC	5883
1509	AGGACUCA CUGAUGAG X CGAA AGAGGACC	5097	GGUCCUCUC UGAGUCCU	5884
1515	UCACCAAG CUGAUGAG X CGAA ACUCAGAG	5098	CUCUGAGUC CUUGGUGA	5885
1518	AAAUCACC CUGAUGAG X CGAA AGGACUCA	5099	UGAGUCCUU GGUGAUUU	5886
1525	CCAGGCAA CUGAUGAG X CGAA AUCACCAA	5100	UUGGUGAUU UUGCCUGG	5887
1526	CCCAGGCA CUGAUGAG X CGAA AAUCACCA	5101	UGGUGAUUU UGCCUGGG	5888
1527	GCCCAGGC CUGAUGAG X CGAA AAAUCACC	5102	GGUGAUUUU GCCUGGGC	5889
1554	CAGACCAG CUGAUGAG X CGAA AGCCAGGG	5103	CCCUGGCUC CUGGUCUG	5890
1560	CCCCAGCA CUGAUGAG X CGAA ACCAGGAG	5104	CUCCUGGUC UGCUGGGG	5891
1575	CUGAGGCA CUGAUGAG X CGAA AGGCGGCC	5105	GGCCGCCUC UGCCUCAG	5892

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1581	CAUCCUCU CUGAUGAG X CGAA AGGCAGAG	5106	CUCUGCCUC AGAGGAUG	5893
1606	AAAAUACU CUGAUGAG X CGAA ACAUGCAC	5107	GUGCAUGUA AGUAUUUU	5894
1610	AUUAAAAA CUGAUGAG X CGAA ACUUACAU	5108	AUGUAAGUA UUUUUAAU	5895
1612	UUAUUAAA CUGAUGAG X CGAA AUACUUAC	5109	GUAAGUAUU UUUAAUAA	5896
1613	UUUAUUAA CUGAUGAG X CGAA AAUACUUA	5110	UAAGUAUUU UUAAUAAA	5897
1614	UUUUAUUA CUGAUGAG X CGAA AAAUACUU	5111	AAGUAUUUU UAAUAAAA	5898
1615	UUUUUAUU CUGAUGAG X CGAA AAAAUACU	5112	AGUAUUUUU AAUAAAAA	5899
1616	GUUUUUAU CUGAUGAG X CGAA AAAAAUAC	5113	GUAUUUUUA AUAAAAAC	5900
1619	ACAGUUUU CUGAUGAG X CGAA AUUAAAAA	5114	UUUUUAAUA AAAACUGU	5901
1628	ACGAGUAC CUGAUGAG X CGAA ACAGUUUU	5115	AAAACUGUA GUACUCGU	5902
1631	UUUACGAG CUGAUGAG X CGAA ACUACAGU	5116	ACUGUAGUA CUCGUAAA	5903
1634	UGUUUUAC CUGAUGAG X CGAA AGUACUAC	5117	GUAGUACUC GUAAAACA	5904
1637	GAUUGUUU CUGAUGAG X CGAA ACGAGUAC	5118	GUACUCGUA AAACAAUC	5905
1645	AGGGUGUA CUGAUGAG X CGAA AUUGUUUU	5119	AAAACAAUC UACACCCU	5906
1647	GCAGGGUG CUGAUGAG X CGAA AGAUUGUU	5120	AACAAUCUA CACCCUGC	5907
1665	AAAUAACA CUGAUGAG X CGAA AUCCCUUC	5121	GAAGGGAUU UGUUAUUU	5908

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1666	AAAAUAAC CUGAUGAG X CGAA AAUCCCUU	5122	AAGGGAUUU GUUAUUUU	5909
1669	AAUAAAAU CUGAUGAG X CGAA ACAAAUCC	5123	GGAUUUGUU AUUUUAUU	5910
1670	AAAUAAAA CUGAUGAG X CGAA AACAAAUC	5124	GAUUUGUUA UUUUAUUU	5911
1672	UAAAAUAA CUGAUGAG X CGAA AUAACAAA	5125	UUUGUUAUU UUAUUUUA	5912
1673	AUAAAAUA CUGAUGAG X CGAA AAUAACAA	5126	UUGUUAUUU UAUUUUAU	5913
1674	AAUAAAAU CUGAUGAG X CGAA AAAUAACA	5127	UGUUAUUUU AUUUUAUU	5914
1675	UAAUAAAA CUGAUGAG X CGAA AAAAUAAC	5128	GUUAUUUUA UUUUAUUA	5915
1677	AAUAAUAA CUGAUGAG X CGAA AUAAAAUA	5129	UAUUUUAUU UUAUUAUU	5916
1678	AAAUAAUA CUGAUGAG X CGAA AAUAAAAU	5130	AUUUUAUUU UAUUAUUU	5917
1679	UAAAUAAU CUGAUGAG X CGAA AAAUAAAA	5131	UUUUAUUUU AUUAUUUA	5918
1680	AUAAAUAA CUGAUGAG X CGAA AAAAUAAA	5132	UUUAUUUUA UUAUUUAU	5919
1682	AAAUAAAU CUGAUGAG X CGAA AUAAAAUA	5133	UAUUUUAUU AUUUAUUU	5920
1683	UAAAUAAA CUGAUGAG X CGAA AAUAAAAU	5134	AUUUUAUUA UUUAUUUA	5921
1685	AAUAAAUA CUGAUGAG X CGAA AUAAUAAA	5135	UUUAUUAUU UAUUUAUU	5922
1686	AAAUAAAU CUGAUGAG X CGAA AAUAAUAA	5136	UUAUUAUUU AUUUAUUU	5923
1687	UAAAUAAA CUGAUGAG X CGAA AAAUAAUA	5137	UAUUAUUUA UUUAUUUA	5924

Posi-tion	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1689	AAUAAAUA CUGAUGAG X CGAA AUAAAUAA	5138	UUAUUUAUU UAUUUAUU	5925
1690	AAAUAAAU CUGAUGAG X CGAA AAUAAAUA	5139	UAUUUAUUU AUUUAUUU	5926
1691	UAAAUAAA CUGAUGAG X CGAA AAAUAAAU	5140	AUUUAUUUA UUUAUUUA	5927
1693	AAUAAAUA CUGAUGAG X CGAA AUAAAUAA	5141	UUAUUUAUU UAUUUAUU	5928
1694	AAAUAAAU CUGAUGAG X CGAA AAUAAAUA	5142	UAUUUAUUU AUUUAUUU	5929
1695	UAAAUAAA CUGAUGAG X CGAA AAAUAAAU	5143	AUUUAUUUA UUUAUUUA	5930
1697	AAUAAAUA CUGAUGAG X CGAA AUAAAUAA	5144	UUAUUUAUU UAUUUAUU	5931
1698	AAAUAAAU CUGAUGAG X CGAA AAUAAAUA	5145	UAUUUAUUU AUUUAUUU	5932
1699	AAAAUAAA CUGAUGAG X CGAA AAAUAAAU	5146	AUUUAUUUA UUUAUUUU	5933
1701	CAAAAAUA CUGAUGAG X CGAA AUAAAUAA	5147	UUAUUUAUU UAUUUUUG	5934
1702	UCAAAAAU CUGAUGAG X CGAA AAUAAAUA	5148	UAUUUAUUU AUUUUUGA	5935
1703	CUCAAAAA CUGAUGAG X CGAA AAAUAAAU	5149	AUUUAUUUA UUUUUGAG	5936
1705	GUCUCAAA CUGAUGAG X CGAA AUAAAUAA	5150	UUAUUUAUU UUUGAGAC	5937
1706	CGUCUCAA CUGAUGAG X CGAA AAUAAAUA	5151	UAUUUAUUU UUGAGACG	5938
1707	CCGUCUCA CUGAUGAG X CGAA AAAUAAAU	5152	AUUUAUUUU UGAGACGG	5939
1708	UCCGUCUC CUGAUGAG X CGAA AAAAUAAA	5153	UUUAUUUUU GAGACGGA	5940

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1719	CAGAGCAA CUGAUGAG X CGAA ACUCCGUC	5154	GACGGAGUC UUGCUCUG	5941
1721	GACAGAGC CUGAUGAG X CGAA AGACUCCG	5155	CGGAGUCUU GCUCUGUC	5942
1725	GGGCGACA CUGAUGAG X CGAA AGCAAGAC	5156	GUCUUGCUC UGUCGCCC	5943
1729	GCCUGGGC CUGAUGAG X CGAA ACAGAGCA	5157	UGCUCUGUC GCCCAGGC	5944
1756	GAGCCGAG CUGAUGAG X CGAA ACCCACCA	5158	UGGUGGGUU CUCGGCUC	5945
1757	UGAGCCGA CUGAUGAG X CGAA AACCCACC	5159	GGUGGGUUC UCGGCUCA	5946
1759	AGUGAGCC CUGAUGAG X CGAA AGAACCCA	5160	UGGGUUCUC GGCUCACU	5947
1764	GUUGCAGU CUGAUGAG X CGAA AGCCGAGA	5161	UCUCGGCUC ACUGCAAC	5948
1774	GGAGGCAG CUGAUGAG X CGAA AGUUGCAG	5162	CUGCAACUU CUGCCUCC	5949
1775	AGGAGGCA CUGAUGAG X CGAA AAGUUGCA	5163	UGCAACUUC UGCCUCCU	5950
1781	AAACCCAG CUGAUGAG X CGAA AGGCAGAA	5164	UUCUGCCUC CUGGGUUU	5951
1788	AUCGCUUA CUGAUGAG X CGAA ACCCAGGA	5165	UCCUGGGUU UAAGCGAU	5952
1789	AAUCGCUU CUGAUGAG X CGAA AACCCAGG	5166	CCUGGGUUU AAGCGAUU	5953
1790	GAAUCGCU CUGAUGAG X CGAA AAACCCAG	5167	CUGGGUUUA AGCGAUUC	5954
1797	GCCAGAAG CUGAUGAG X CGAA AUCGCUUA	5168	UAAGCGAUU CUUCUGGC	5955
1798	AGCCAGAA CUGAUGAG X CGAA AAUCGCUU	5169	AAGCGAUUC UUCUGGCU	5956

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1800	UGAGCCAG CUGAUGAG X CGAA AGAAUCGC	5170	GCGAUUCUU CUGGCUCA	5957
1801	CUGAGCCA CUGAUGAG X CGAA AAGAAUCG	5171	CGAUUCUUC UGGCUCAG	5958
1807	GGGAGGCU CUGAUGAG X CGAA AGCCAGAA	5172	UUCUGGCUC AGCCUCCC	5959
1813	CUACUCGG CUGAUGAG X CGAA AGGCUGAG	5173	CUCAGCCUC CCGAGUAG	5960
1820	AUCCCAGC CUGAUGAG X CGAA ACUCGGGA	5174	UCCCGAGUA GCUGGGAU	5961
1829	GCGCCUGU CUGAUGAG X CGAA AUCCCAGC	5175	GCUGGGAUU ACAGGCGC	5962
1830	GGCGCCUG CUGAUGAG X CGAA AAUCCCAG	5176	CUGGGAUUA CAGGCGCC	5963
1856	ACAAAAAU CUGAUGAG X CGAA AGCCGGCC	5177	GGCCGGCUA AUUUUUGU	5964
1859	AAUACAAA CUGAUGAG X CGAA AUUAGCCG	5178	CGGCUAAUU UUUGUAUU	5965
1860	AAAUACAA CUGAUGAG X CGAA AAUUAGCC	5179	GGCUAAUUU UUGUAUUU	5966
1861	AAAAUACA CUGAUGAG X CGAA AAAUUAGC	5180	GCUAAUUUU UGUAUUUU	5967
1862	AAAAAUAC CUGAUGAG X CGAA AAAAUUAG	5181	CUAAUUUUU GUAUUUUU	5968
1865	ACUAAAAA CUGAUGAG X CGAA ACAAAAAU	5182	AUUUUUGUA UUUUUAGU	5969
1867	CUACUAAA CUGAUGAG X CGAA AUACAAAA	5183	UUUUGUAUU UUUAGUAG	5970
1868	UCUACUAA CUGAUGAG X CGAA AAUACAAA	5184	UUUGUAUUU UUAGUAGA	5971
1869	CUCUACUA CUGAUGAG X CGAA AAAUACAA	5185	UUGUAUUUU UAGUAGAG	5972

Posi-tion	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1870	UCUCUACU CUGAUGAG X CGAA AAAAUACA	5186	UGUAUUUUU AGUAGAGA	5973
1871	GUCUCUAC CUGAUGAG X CGAA AAAAAUAC	5187	GUAUUUUUA GUAGAGAC	5974
1874	CGCGUCUC CUGAUGAG X CGAA ACUAAAAA	5188	UUUUUAGUA GAGACGCG	5975
1885	CAUGGUGA CUGAUGAG X CGAA ACCGCGUC	5189	GACGCGGUU UCACCAUG	5976
1886	ACAUGGUG CUGAUGAG X CGAA AACCGCGU	5190	ACGCGGUUU CACCAUGU	5977
1887	AACAUGGU CUGAUGAG X CGAA AAACCGCG	5191	CGCGGUUUC ACCAUGUU	5978
1895	GCCUGGCC CUGAUGAG X CGAA ACAUGGUG	5192	CACCAUGUU GGCCAGGC	5979
1908	GAGCUCCA CUGAUGAG X CGAA ACCAGCCU	5193	AGGCUGGUC UGGAGCUC	5980
1916	GAGGCCAG CUGAUGAG X CGAA AGCUCCAG	5194	CUGGAGCUC CUGGCCUC	5981
1924	GAUCACUU CUGAUGAG X CGAA AGGCCAGG	5195	CCUGGCCUC AAGUGAUC	5982
1932	GGUGGGCG CUGAUGAG X CGAA AUCACUUG	5196	CAAGUGAUC CGCCCACC	5983
1942	GGGAGGCU CUGAUGAG X CGAA AGGUGGGC	5197	GCCCACCUC AGCCUCCC	5984
1948	CACUUUGG CUGAUGAG X CGAA AGGCUGAG	5198	CUCAGCCUC CCAAAGUG	5985
1965	CACGCCUG CUGAUGAG X CGAA AUUCCCAG	5199	CUGGGAAUA CAGGCGUG	5986
1996	UUAAAAUA CUGAUGAG X CGAA AUCCUGGC	5200	GCCAGGAUU UAUUUUAA	5987
1997	UUUAAAAU CUGAUGAG X CGAA AAUCCUGG	5201	CCAGGAUUU AUUUUAAA	5988

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1998	UUUUAAAA CUGAUGAG X CGAA AAAUCCUG	5202	CAGGAUUUA UUUUAAAA	5989
2000	CUUUUUAA CUGAUGAG X CGAA AUAAAUCC	5203	GGAUUUAUU UUAAAAAG	5990
2001	CCUUUUUA CUGAUGAG X CGAA AAUAAAUC	5204	GAUUUAUUU UAAAAAGG	5991
2002	CCCUUUUU CUGAUGAG X CGAA AAAUAAAU	5205	AUUUAUUUU AAAAAGGG	5992
2003	UCCCUUUU CUGAUGAG X CGAA AAAAUAAA	5206	UUUAUUUUA AAAAGGGA	5993
2016	UAUCAACA CUGAUGAG X CGAA AUCUUCCC	5207	GGGAAGAUU UGUUGAUA	5994
2017	UUAUCAAC CUGAUGAG X CGAA AAUCUUCC	5208	GGAAGAUUU GUUGAUAA	5995
2020	AAUUUAUC CUGAUGAG X CGAA ACAAAUCU	5209	AGAUUUGUU GAUAAAUU	5996
2024	AGUGAAUU CUGAUGAG X CGAA AUCAACAA	5210	UUGUUGAUA AAUUCACU	5997
2028	UUGAAGUG CUGAUGAG X CGAA AUUUAUCA	5211	UGAUAAAUU CACUUCAA	5998
2029	UUUGAAGU CUGAUGAG X CGAA AAUUUAUC	5212	GAUAAAUUC ACUUCAAA	5999
2033	UAUCUUUG CUGAUGAG X CGAA AGUGAAUU	5213	AAUUCACUU CAAAGAUA	6000
2034	UUAUCUUU CUGAUGAG X CGAA AAGUGAAU	5214	AUUCACUUC AAAGAUAA	6001
2041	GAAUAGUU CUGAUGAG X CGAA AUCUUUGA	5215	UCAAAGAUA AACUAUUC	6002
2046	UUUUCGAA CUGAUGAG X CGAA AGUUUAUC	5216	GAUAAACUA UUCGAAAA	6003
2048	UAUUUUCG CUGAUGAG X CGAA AUAGUUUA	5217	UAAACUAUU CGAAAAUA	6004

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2049	GUAUUUUC CUGAUGAG X CGAA AAUAGUUU	5218	AAACUAUUC GAAAAUAC	6005
2056	CACUAAAG CUGAUGAG X CGAA AUUUUCGA	5219	UCGAAAAUA CUUUAGUG	6006
2059	AAUCACUA CUGAUGAG X CGAA AGUAUUUU	5220	AAAAUACUU UAGUGAUU	6007
2060	GAAUCACU CUGAUGAG X CGAA AAGUAUUU	5221	AAAUACUUU AGUGAUUC	6008
2061	GGAAUCAC CUGAUGAG X CGAA AAAGUAUU	5222	AAUACUUUA GUGAUUCC	6009
2067	UUGACGGG CUGAUGAG X CGAA AUCACUAA	5223	UUAGUGAUU CCCGUCAA	6010
2068	CUUGACGG CUGAUGAG X CGAA AAUCACUA	5224	UAGUGAUUC CCGUCAAG	6011
2073	AGAGUCUU CUGAUGAG X CGAA ACGGGAAU	5225	AUUCCCGUC AAGACUCU	6012
2080	ACACAGAA CUGAUGAG X CGAA AGUCUUGA	5226	UCAAGACUC UUCUGUGU	6013
2082	AUACACAG CUGAUGAG X CGAA AGAGUCUU	5227	AAGACUCUU CUGUGUAU	6014
2083	CAUACACA CUGAUGAG X CGAA AAGAGUCU	5228	AGACUCUUC UGUGUAUG	6015
2089	UCUAUACA CUGAUGAG X CGAA ACACAGAA	5229	UUCUGUGUA UGUAUAGA	6016
2093	UACGUCUA CUGAUGAG X CGAA ACAUACAC	5230	GUGUAUGUA UAGACGUA	6017
2095	UAUACGUC CUGAUGAG X CGAA AUACAUAC	5231	GUAUGUAUA GACGUAUA	6018
2101	AUGAGUUA CUGAUGAG X CGAA ACGUCUAU	5232	AUAGACGUA UAACUCAU	6019
2103	GAAUGAGU CUGAUGAG X CGAA AUACGUCU	5233	AGACGUAUA ACUCAUUC	6020

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2107	UCCAGAAU CUGAUGAG X CGAA AGUUAUAC	5234	GUAUAACUC AUUCUGGA	6021
2110	CUGUCCAG CUGAUGAG X CGAA AUGAGUUA	5235	UAACUCAUU CUGGACAG	6022
2111	CCUGUCCA CUGAUGAG X CGAA AAUGAGUU	5236	AACUCAUUC UGGACAGG	6023
2128	AAAAAAGA CUGAUGAG X CGAA AUCCUUGC	5237	GCAAGGAUA UCUUUUUU	6024
2130	CAAAAAAA CUGAUGAG X CGAA AUAUCCUU	5238	AAGGAUAUC UUUUUUUG	6025
2132	AACAAAAA CUGAUGAG X CGAA AGAUAUCC	5239	GGAUAUCUU UUUUUGUU	6026
2133	AAACAAAA CUGAUGAG X CGAA AAGAUAUC	5240	GAUAUCUUU UUUUGUUU	6027
2134	CAAACAAA CUGAUGAG X CGAA AAAGAUAU	5241	AUAUCUUUU UUUGUUUG	6028
2135	ACAAACAA CUGAUGAG X CGAA AAAAGAUA	5242	UAUCUUUUU UUGUUUGU	6029
2136	AACAAACA CUGAUGAG X CGAA AAAAAGAU	5243	AUCUUUUUU UGUUUGUU	6030
2137	AAACAAAC CUGAUGAG X CGAA AAAAAAGA	5244	UCUUUUUUU GUUUGUUU	6031
2140	AACAAACA CUGAUGAG X CGAA ACAAAAAA	5245	UUUUUUGUU UGUUUGUU	6032
2141	AAACAAAC CUGAUGAG X CGAA AACAAAAA	5246	UUUUUGUUU GUUUGUUU	6033
2144	AACAAACA CUGAUGAG X CGAA ACAAACAA	5247	UUGUUUGUU UGUUUGUU	6034
2145	AAACAAAC CUGAUGAG X CGAA AACAAACA	5248	UGUUUGUUU GUUUGUUU	6035
2148	UCAAAACA CUGAUGAG X CGAA ACAAACAA	5249	UUGUUUGUU UGUUUUGA	6036

Posi-tion	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2149	CUCAAAAC CUGAUGAG X CGAA AACAAACA	5250	UGUUUGUUU GUUUUGAG	6037
2152	CAUCUCAA CUGAUGAG X CGAA ACAAACAA	5251	UUGUUUGUU UUGAGAUG	6038
2153	CCAUCUCA CUGAUGAG X CGAA AACAAACA	5252	UGUUUGUUU UGAGAUGG	6039
2154	UCCAUCUC CUGAUGAG X CGAA AAACAAAC	5253	GUUUGUUUU GAGAUGGA	6040
2165	GACAGCGA CUGAUGAG X CGAA AGUCCAUC	5254	GAUGGACUC UCGCUGUC	6041
2167	GCGACAGC CUGAUGAG X CGAA AGAGUCCA	5255	UGGACUCUC GCUGUCGC	6042
2173	AGCCUGGC CUGAUGAG X CGAA ACAGCGAG	5256	CUCGCUGUC GCCAGGCU	6043
2182	CUGCACUC CUGAUGAG X CGAA AGCCUGGC	5257	GCCAGGCUA GAGUGCAG	6044
2200	UGAGCUGA CUGAUGAG X CGAA AUCGCGCC	5258	GGCGCGAUU UCAGCUCA	6045
2201	GUGAGCUG CUGAUGAG X CGAA AAUCGCGC	5259	GCGCGAUUU CAGCUCAC	6046
2202	AGUGAGCU CUGAUGAG X CGAA AAAUCGCG	5260	CGCGAUUUC AGCUCACU	6047
2207	GUUGCAGU CUGAUGAG X CGAA AGCUGAAA	5261	UUUCAGCUC ACUGCAAC	6048
2218	GGGAAGCG CUGAUGAG X CGAA AGGUUGCA	5262	UGCAACCUC CGCUUCCC	6049
2223	AACCCGGG CUGAUGAG X CGAA AGCGGAGG	5263	CCUCCGCUU CCCGGGUU	6050
2224	GAACCCGG CUGAUGAG X CGAA AAGCGGAG	5264	CUCCGCUUC CCGGGUUC	6051
2231	AUCGCUUG CUGAUGAG X CGAA ACCCGGGA	5265	UCCCGGGUU CAAGCGAU	6052

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2232	AAUCGCUU CUGAUGAG X CGAA AACCCGGG	5266	CCCGGGUUC AAGCGAUU	6053
2240	GGCAGGAG CUGAUGAG X CGAA AUCGCUUG	5267	CAAGCGAUU CUCCUGCC	6054
2241	AGGCAGGA CUGAUGAG X CGAA AAUCGCUU	5268	AAGCGAUUC UCCUGCCU	6055
2243	UGAGGCAG CUGAUGAG X CGAA AGAAUCGC	5269	GCGAUUCUC CUGCCUCA	6056
2250	GGGAGGCU CUGAUGAG X CGAA AGGCAGGA	5270	UCCUGCCUC AGCCUCCC	6057
2256	CUACUCGG CUGAUGAG X CGAA AGGCUGAG	5271	CUCAGCCUC CCGAGUAG	6058
2263	AUCCCAGC CUGAUGAG X CGAA ACUCGGGA	5272	UCCCGAGUA GCUGGGAU	6059
2272	GUGCCUGU CUGAUGAG X CGAA AUCCCAGC	5273	GCUGGGAUU ACAGGCAC	6060
2273	CGUGCCUG CUGAUGAG X CGAA AAUCCCAG	5274	CUGGGAUUA CAGGCACG	6061
2296	AAAAUUAG CUGAUGAG X CGAA AGGGCGUG	5275	CACGCCCUA CUAAUUUU	6062
2299	UCAAAAAU CUGAUGAG X CGAA AGUAGGGC	5276	GCCCUACUA AUUUUUGA	6063
2302	AAAUCAAA CUGAUGAG X CGAA AUUAGUAG	5277	CUACUAAUU UUUGAUUU	6064
2303	AAAAUCAA CUGAUGAG X CGAA AAUUAGUA	5278	UACUAAUUU UUGAUUUU	6065
2304	AAAAAUCA CUGAUGAG X CGAA AAAUUAGU	5279	ACUAAUUUU UGAUUUUU	6066
2305	UAAAAAUC CUGAUGAG X CGAA AAAAUUAG	5280	CUAAUUUUU GAUUUUUA	6067
2309	CUACUAAA CUGAUGAG X CGAA AUCAAAAA	5281	UUUUUGAUU UUUAGUAG	6068

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2310	UCUACUAA CUGAUGAG X CGAA AAUCAAAA	5282	UUUUGAUUU UUAGUAGA	6069
2311	CUCUACUA CUGAUGAG X CGAA AAAUCAAA	5283	UUUGAUUUU UAGUAGAG	6070
2312	UCUCUACU CUGAUGAG X CGAA AAAAUCAA	5284	UUGAUUUUU AGUAGAGA	6071
2313	GUCUCUAC CUGAUGAG X CGAA AAAAAUCA	5285	UGAUUUUUA GUAGAGAC	6072
2316	CCCGUCUC CUGAUGAG X CGAA ACUAAAAA	5286	UUUUUAGUA GAGACGGG	6073
2327	CAUGGGGA CUGAUGAG X CGAA AUCCCGUC	5287	GACGGGAUU UCCCCAUG	6074
2328	ACAUGGGG CUGAUGAG X CGAA AAUCCCGU	5288	ACGGGAUUU CCCCAUGU	6075
2329	AACAUGGG CUGAUGAG X CGAA AAAUCCCG	5289	CGGGAUUUC CCCAUGUU	6076
2337	UCCUGGCC CUGAUGAG X CGAA ACAUGGGG	5290	CCCCAUGUU GGCCAGGA	6077
2350	GAGAUCGA CUGAUGAG X CGAA AUCAUCCU	5291	AGGAUGAUC UCGAUCUC	6078
2352	AAGAGAUC CUGAUGAG X CGAA AGAUCAUC	5292	GAUGAUCUC GAUCUCUU	6079
2356	GGUCAAGA CUGAUGAG X CGAA AUCGAGAU	5293	AUCUCGAUC UCUUGACC	6080
2358	GGGGUCAA CUGAUGAG X CGAA AGAUCGAG	5294	CUCGAUCUC UUGACCCC	6081
2360	ACGGGGUC CUGAUGAG X CGAA AGAGAUCG	5295	CGAUCUCUU GACCCCGU	6082
2372	GGCAGGCU CUGAUGAG X CGAA AUCACGGG	5296	CCCGUGAUC AGCCUGCC	6083
2382	GGGAGGCC CUGAUGAG X CGAA AGGCAGGC	5297	GCCUGCCUU GGCCUCCC	6084

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2388	CACUUUGG CUGAUGAG X CGAA AGGCCAAG	5298	CUUGGCCUC CCAAAGUG	6085
2404	ACGCCUGU CUGAUGAG X CGAA AUCCCAGC	5299	GCUGGGAUU ACAGGCGU	6086
2405	CACGCCUG CUGAUGAG X CGAA AAUCCCAG	5300	CUGGGAUUA CAGGCGUG	6087
2437	CUUCAAGA CUGAUGAG X CGAA ACCCUUGG	5301	CCAAGGGUA UCUUGAAG	6088
2439	UCCUUCAA CUGAUGAG X CGAA AUACCCUU	5302	AAGGGUAUC UUGAAGGA	6089
2441	CCUCCUUC CUGAUGAG X CGAA AGAUACCC	5303	GGGUAUCUU GAAGGAGG	6090
2453	UCAACUGU CUGAUGAG X CGAA AUCCCUCC	5304	GGAGGGAUU ACAGUUGA	6091
2454	AUCAACUG CUGAUGAG X CGAA AAUCCCUC	5305	GAGGGAUUA CAGUUGAU	6092
2459	UACAUAUC CUGAUGAG X CGAA ACUGUAAU	5306	AUUACAGUU GAUAUGUA	6093
2463	CCUCUACA CUGAUGAG X CGAA AUCAACUG	5307	CAGUUGAUA UGUAGAGG	6094
2467	UAUUCCUC CUGAUGAG X CGAA ACAUAUCA	5308	UGAUAUGUA GAGGAAUA	6095
2475	CACUGCAA CUGAUGAG X CGAA AUUCCUCU	5309	AGAGGAAUA UUGCAGUG	6096
2477	ACCACUGC CUGAUGAG X CGAA AUAUUCCU	5310	AGGAAUAUU GCAGUGGU	6097
2486	GCAGCAAU CUGAUGAG X CGAA ACCACUGC	5311	GCAGUGGUU AUUGCUGC	6098
2487	UGCAGCAA CUGAUGAG X CGAA AACCACUG	5312	CAGUGGUUA UUGCUGCA	6099
2489	AAUGCAGC CUGAUGAG X CGAA AUAACCAC	5313	GUGGUUAUU GCUGCAUU	6100

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2497	ACAUAGGA CUGAUGAG X CGAA AUGCAGCA	5314	UGCUGCAUU UCCUAUGU	6101
2498	CACAUAGG CUGAUGAG X CGAA AAUGCAGC	5315	GCUGCAUUU CCUAUGUG	6102
2499	UCACAUAG CUGAUGAG X CGAA AAAUGCAG	5316	CUGCAUUUC CUAUGUGA	6103
2502	CAGUCACA CUGAUGAG X CGAA AGGAAAUG	5317	CAUUUCCUA UGUGACUG	6104
2516	AUCUGUUU CUGAUGAG X CGAA AGUCCCAG	5318	CUGGGACUA AAACAGAU	6105
2525	UAUCAGCU CUGAUGAG X CGAA AUCUGUUU	5319	AAACAGAUC AGCUGAUA	6106
2533	GCUAACAC CUGAUGAG X CGAA AUCAGCUG	5320	CAGCUGAUA GUGUUAGC	6107
2538	UGCACGCU CUGAUGAG X CGAA ACACUAUC	5321	GAUAGUGUU AGCGUGCA	6108
2539	CUGCACGC CUGAUGAG X CGAA AACACUAU	5322	AUAGUGUUA GCGUGCAG	6109
2556	AGUCAUCA CUGAUGAG X CGAA ACUGCUCA	5323	UGAGCAGUC UGAUGACU	6110
2565	CUGUGUCA CUGAUGAG X CGAA AGUCAUCA	5324	UGAUGACUA UGACACAG	6111
2578	GAGAUUCU CUGAUGAG X CGAA AUUUCUGU	5325	ACAGAAAUA AGAAUCUC	6112
2584	AUGCUGGA CUGAUGAG X CGAA AUUCUUAU	5326	AUAAGAAUC UCCAGCAU	6113
2586	GAAUGCUG CUGAUGAG X CGAA AGAUUCUU	5327	AAGAAUCUC CAGCAUUC	6114
2593	CAGGGCAG CUGAUGAG X CGAA AUGCUGGA	5328	UCCAGCAUU CUGCCCUG	6115
2594	CCAGGGCA CUGAUGAG X CGAA AAUGCUGG	5329	CCAGCAUUC UGCCCUGG	6116

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2617	UCUGACCC CUGAUGAG X CGAA AGGCUCCA	5330	UGGAGCCUU GGGUCAGA	6117
2622	CAGCAUCU CUGAUGAG X CGAA ACCCAAGG	5331	CCUUGGGUC AGAUGCUG	6118
2637	GGCAUCAA CUGAUGAG X CGAA AGCCAGCA	5332	UGCUGGCUA UUGAUGCC	6119
2639	CCGGCAUC CUGAUGAG X CGAA AUAGCCAG	5333	CUGGCUAUU GAUGCCGG	6120
2660	CCCUGGUG CUGAUGAG X CGAA AUUUCUCC	5334	GGAGAAAUC CACCAGGG	6121
2674	UUUUUACU CUGAUGAG X CGAA AGUUGCCC	5335	GGGCAACUC AGUAAAAA	6122
2678	UUAUUUUU CUGAUGAG X CGAA ACUGAGUU	5336	AACUCAGUA AAAAAUAA	6123
2685	UAUUUAUU CUGAUGAG X CGAA AUUUUUUA	5337	UAAAAAAUA AAUAAAUA	6124
2689	UAUUUAUU CUGAUGAG X CGAA AUUUAUUU	5338	AAAUAAAUA AAUAAAUA	6125
2693	UAUUUAUU CUGAUGAG X CGAA AUUUAUUU	5339	AAAUAAAUA AAUAAAUA	6126
2697	UAUUUAUU CUGAUGAG X CGAA AUUUAUUU	5340	AAAUAAAUA AAUAAAUA	6127
2701	UAUUUAUU CUGAUGAG X CGAA AUUUAUUU	5341	AAAUAAAUA AAUAAAUA	6128
2705	UAUUUAUU CUGAUGAG X CGAA AUUUAUUU	5342	AAAUAAAUA AAUAAAUA	6129
2709	UAAUUAUU CUGAUGAG X CGAA AUUUAUUU	5343	AAAUAAAUA AAUAAUUA	6130
2713	UUUUUAAU CUGAUGAG X CGAA AUUUAUUU	5344	AAAUAAAUA AUUAAAAA	6131
2716	CUUUUUUU CUGAUGAG X CGAA AUUAUUUA	5345	UAAAUAAUU AAAAAAAG	6132

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2717	CCUUUUUU CUGAUGAG X CGAA AAUUAUUU	5346	AAAUAAUUA AAAAAAGG	6133
2728	GACAAGGA CUGAUGAG X CGAA ACCCUUUU	5347	AAAAGGGUA UCCUUGUC	6134
2730	AGGACAAG CUGAUGAG X CGAA AUACCCUU	5348	AAGGGUAUC CUUGUCCU	6135
2733	GACAGGAC CUGAUGAG X CGAA AGGAUACC	5349	GGUAUCCUU GUCCUGUC	6136
2736	CUGGACAG CUGAUGAG X CGAA ACAAGGAU	5350	AUCCUUGUC CUGUCCAG	6137
2741	UCAUCCUG CUGAUGAG X CGAA ACAGGACA	5351	UGUCCUGUC CAGGAUGA	6138
2756	AUGGAAGC CUGAUGAG X CGAA AGCAUCUC	5352	GAGAUGCUU GCUUCCAU	6139
2760	GUGCAUGG CUGAUGAG X CGAA AGCAAGCA	5353	UGCUUGCUU CCAUGCAC	6140
2761	AGUGCAUG CUGAUGAG X CGAA AAGCAAGC	5354	GCUUGCUUC CAUGCACU	6141
2770	AUUGUCGU CUGAUGAG X CGAA AGUGCAUG	5355	CAUGCACUU ACGACAAU	6142
2771	AAUUGUCG CUGAUGAG X CGAA AAGUGCAU	5356	AUGCACUUA CGACAAUU	6143
2779	ACAGCAAA CUGAUGAG X CGAA AUUGUCGU	5357	ACGACAAUU UUUGCUGU	6144
2780	GACAGCAA CUGAUGAG X CGAA AAUUGUCG	5358	CGACAAUUU UUGCUGUC	6145
2781	UGACAGCA CUGAUGAG X CGAA AAAUUGUC	5359	GACAAUUUU UGCUGUCA	6146
2782	AUGACAGC CUGAUGAG X CGAA AAAAUUGU	5360	ACAAUUUUU GCUGUCAU	6147
2788	UUUUUAAU CUGAUGAG X CGAA ACAGCAAA	5361	UUUGCUGUC AUUAAAAA	6148

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2791	AAUUUUUU CUGAUGAG X CGAA AUGACAGC	5362	GCUGUCAUU AAAAAAUU	6149
2792	AAAUUUUU CUGAUGAG X CGAA AAUGACAG	5363	CUGUCAUUA AAAAAUUU	6150
2799	AAUGUGAA CUGAUGAG X CGAA AUUUUUUA	5364	UAAAAAAUU UUCACAUU	6151
2800	GAAUGUGA CUGAUGAG X CGAA AAUUUUUU	5365	AAAAAAUUU UCACAUUC	6152
2801	UGAAUGUG CUGAUGAG X CGAA AAAUUUUU	5366	AAAAAUUUU CACAUUCA	6153
2802	GUGAAUGU CUGAUGAG X CGAA AAAAUUUU	5367	AAAAUUUUC ACAUUCAC	6154
2807	AGACUGUG CUGAUGAG X CGAA AUGUGAAA	5368	UUUCACAUU CACAGUCU	6155
2808	AAGACUGU CUGAUGAG X CGAA AAUGUGAA	5369	UUCACAUUC ACAGUCUU	6156
2814	AUUUAGAA CUGAUGAG X CGAA ACUGUGAA	5370	UUCACAGUC UUCUAAAU	6157
2816	GAAUUUAG CUGAUGAG X CGAA AGACUGUG	5371	CACAGUCUU CUAAAUUC	6158
2817	UGAAUUUA CUGAUGAG X CGAA AAGACUGU	5372	ACAGUCUUC UAAAUUCA	6159
2819	AGUGAAUU CUGAUGAG X CGAA AGAAGACU	5373	AGUCUUCUA AAUUCACU	6160
2823	CCAAAGUG CUGAUGAG X CGAA AUUUAGAA	5374	UUCUAAAUU CACUUUGG	6161
2824	UCCAAAGU CUGAUGAG X CGAA AAUUUAGA	5375	UCUAAAUUC ACUUUGGA	6162
2828	ACACUCCA CUGAUGAG X CGAA AGUGAAUU	5376	AAUUCACUU UGGAGUGU	6163
2829	UACACUCC CUGAUGAG X CGAA AAGUGAAU	5377	AUUCACUUU GGAGUGUA	6164

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2837	GAAUCCAA CUGAUGAG X CGAA ACACUCCA	5378	UGGAGUGUA UUGGAUUC	6165
2839	UGGAAUCC CUGAUGAG X CGAA AUACACUC	5379	GAGUGUAUU GGAUUCCA	6166
2844	UGCAGUGG CUGAUGAG X CGAA AUCCAAUA	5380	UAUUGGAUU CCACUGCA	6167
2845	AUGCAGUG CUGAUGAG X CGAA AAUCCAAU	5381	AUUGGAUUC CACUGCAU	6168
2854	CGUAUGUC CUGAUGAG X CGAA AUGCAGUG	5382	CACUGCAUU GACAUACG	6169
2860	AACUUACG CUGAUGAG X CGAA AUGUCAAU	5383	AUUGACAUA CGUAAGUU	6170
2864	UGCAAACU CUGAUGAG X CGAA ACGUAUGU	5384	ACAUACGUA AGUUUGCA	6171
2868	UUAAUGCA CUGAUGAG X CGAA ACUUACGU	5385	ACGUAAGUU UGCAUUAA	6172
2869	UUUAAUGC CUGAUGAG X CGAA AACUUACG	5386	CGUAAGUUU GCAUUAAA	6173
2874	GAUCUUUU CUGAUGAG X CGAA AUGCAAAC	5387	GUUUGCAUU AAAAGAUC	6174
2875	GGAUCUUU CUGAUGAG X CGAA AAUGCAAA	5388	UUUGCAUUA AAAGAUCC	6175
2882	UCUUAAAG CUGAUGAG X CGAA AUCUUUUA	5389	UAAAAGAUC CUUUAAGA	6176
2885	AUAUCUUA CUGAUGAG X CGAA AGGAUCUU	5390	AAGAUCCUU UAAGAUAU	6177
2886	GAUAUCUU CUGAUGAG X CGAA AAGGAUCU	5391	AGAUCCUUU AAGAUAUC	6178
2887	AGAUAUCU CUGAUGAG X CGAA AAAGGAUC	5392	GAUCCUUUA AGAUAUCU	6179
2892	UGACCAGA CUGAUGAG X CGAA AUCUUAAA	5393	UUUAAGAUA UCUGGUCA	6180

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2894	CCUGACCA CUGAUGAG X CGAA AUAUCUUA	5394	UAAGAUAUC UGGUCAGG	6181
2899	CCGUGCCU CUGAUGAG X CGAA ACCAGAUA	5395	UAUCUGGUC AGGCACGG	6182
2913	ACAGGCGU CUGAUGAG X CGAA AGCCACCG	5396	CGGUGGCUC ACGCCUGU	6183
2922	GCUGGGAU CUGAUGAG X CGAA ACAGGCGU	5397	ACGCCUGUA AUCCCAGC	6184
2925	AGUGCUGG CUGAUGAG X CGAA AUUACAGG	5398	CCUGUAAUC CCAGCACU	6185
2934	ACUUCCCA CUGAUGAG X CGAA AGUGCUGG	5399	CCAGCACUU UGGGAAGU	6186
2935	CACUUCCC CUGAUGAG X CGAA AAGUGCUG	5400	CAGCACUUU GGGAAGUG	6187
2949	AAUCCUUC CUGAUGAG X CGAA ACCUCCAC	5401	GUGGAGGUA GAAGGAUU	6188
2957	GCUCAAGC CUGAUGAG X CGAA AUCCUUCU	5402	AGAAGGAUU GCUUGAGC	6189
2961	CUGGGCUC CUGAUGAG X CGAA AGCAAUCC	5403	GGAUUGCUU GAGCCCAG	6190
2974	UGGUCUCG CUGAUGAG X CGAA ACUCCUGG	5404	CCAGGAGUU CGAGACCA	6191
2975	CUGGUCUC CUGAUGAG X CGAA AACUCCUG	5405	CAGGAGUUC GAGACCAG	6192
2986	UGUUGCCC CUGAUGAG X CGAA AGCUGGUC	5406	GACCAGCUU GGGCAACA	6193
2996	GGUCUCAC CUGAUGAG X CGAA AUGUUGCC	5407	GGCAACAUA GUGAGACC	6194
3006	GUAGAGAU CUGAUGAG X CGAA AGGUCUCA	5408	UGAGACCUA AUCUCUAC	6195
3009	UUAGUAGA CUGAUGAG X CGAA AUUAGGUC	5409	GACCUAAUC UCUACUAA	6196

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3011	UUUUAGUA CUGAUGAG X CGAA AGAUUAGG	5410	CCUAAUCUC UACUAAAA	6197
3013	AUUUUUAG CUGAUGAG X CGAA AGAGAUUA	5411	UAAUCUCUA CUAAAAAU	6198
3016	UUAAUUUU CUGAUGAG X CGAA AGUAGAGA	5412	UCUCUACUA AAAAUUAA	6199
3022	UUUUUUUU CUGAUGAG X CGAA AUUUUUAG	5413	CUAAAAAUU AAAAAAAA	6200
3023	UUUUUUUU CUGAUGAG X CGAA AAUUUUUA	5414	UAAAAAUUA AAAAAAAA	6201
3033	CGCCUAAG CUGAUGAG X CGAA AUUUUUUU	5415	AAAAAAAUC CUUAGGCG	6202
3036	GAUCGCCU CUGAUGAG X CGAA AGGAUUUU	5416	AAAAUCCUU AGGCGAUC	6203
3037	AGAUCGCC CUGAUGAG X CGAA AAGGAUUU	5417	AAAUCCUUA GGCGAUCU	6204
3044	UGUGAACA CUGAUGAG X CGAA AUCGCCUA	5418	UAGGCGAUC UGUUCACA	6205
3048	AAUCUGUG CUGAUGAG X CGAA ACAGAUCG	5419	CGAUCUGUU CACAGAUU	6206
3049	UAAUCUGU CUGAUGAG X CGAA AACAGAUC	5420	GAUCUGUUC ACAGAUUA	6207
3056	ACAAGAUU CUGAUGAG X CGAA AUCUGUGA	5421	UCACAGAUU AAUCUUGU	6208
3057	CACAAGAU CUGAUGAG X CGAA AAUCUGUG	5422	CACAGAUUA AUCUUGUG	6209
3060	AAUCACAA CUGAUGAG X CGAA AUUAAUCU	5423	AGAUUAAUC UUGUGAUU	6210
3062	CCAAUCAC CUGAUGAG X CGAA AGAUUAAU	5424	AUUAAUCUU GUGAUUGG	6211
3068	AUCGCCCC CUGAUGAG X CGAA AUCACAAG	5425	CUUGUGAUU GGGGCGAU	6212

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3077	ACUUCUGG CUGAUGAG X CGAA AUCGCCCC	5426	GGGGCGAUU CCAGAAGU	6213
3078	CACUUCUG CUGAUGAG X CGAA AAUCGCCC	5427	GGGCGAUUC CAGAAGUG	6214
3096	CUCAGCAC CUGAUGAG X CGAA ACCCAUCA	5428	UGAUGGGUU GUGCUGAG	6215
3107	UGUGGGGC CUGAUGAG X CGAA AGCUCAGC	5429	GCUGAGCUA GCCCCACA	6216
3118	CUCAGAGA CUGAUGAG X CGAA AGUGUGGG	5430	CCCACACUC UCUCUGAG	6217
3120	UUCUCAGA CUGAUGAG X CGAA AGAGUGUG	5431	CACACUCUC UCUGAGAA	6218
3122	GCUUCUCA CUGAUGAG X CGAA AGAGAGUG	5432	CACUCUCUC UGAGAAGC	6219
3136	CACUACUG CUGAUGAG X CGAA ACACUGCU	5433	AGCAGUGUA CAGUAGUG	6220
3141	UUAAACAC CUGAUGAG X CGAA ACUGUACA	5434	UGUACAGUA GUGUUUAA	6221
3146	UGCCCUUA CUGAUGAG X CGAA ACACUACU	5435	AGUAGUGUU UAAGGGCA	6222
3147	CUGCCCUU CUGAUGAG X CGAA AACACUAC	5436	GUAGUGUUU AAGGGCAG	6223
3148	CCUGCCCU CUGAUGAG X CGAA AAACACUA	5437	UAGUGUUUA AGGGCAGG	6224
3161	UGACUUUA CUGAUGAG X CGAA AGCCCCUG	5438	CAGGGGCUC UAAAGUCA	6225
3163	UCUGACUU CUGAUGAG X CGAA AGAGCCCC	5439	GGGGCUCUA AAGUCAGA	6226
3168	GGAAGUCU CUGAUGAG X CGAA ACUUUAGA	5440	UCUAAAGUC AGACUUCC	6227
3174	UACUCUGG CUGAUGAG X CGAA AGUCUGAC	5441	GUCAGACUU CCAGAGUA	6228

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3175	UUACUCUG CUGAUGAG X CGAA AAGUCUGA	5442	UCAGACUUC CAGAGUAA	6229
3182	GGGGGUAU CUGAUGAG X CGAA ACUCUGGA	5443	UCCAGAGUA AUACCCCC	6230
3185	GGGGGGGG CUGAUGAG X CGAA AUUACUCU	5444	AGAGUAAUA CCCCCCCC	6231
3203	UGAUUUGU CUGAUGAG X CGAA AGGUUGGG	5445	CCCAACCUC ACAAAUCA	6232
3210	UAGAAACU CUGAUGAG X CGAA AUUUGUGA	5446	UCACAAAUC AGUUUCUA	6233
3214	AUAGUAGA CUGAUGAG X CGAA ACUGAUUU	5447	AAAUCAGUU UCUACUAU	6234
3215	UAUAGUAG CUGAUGAG X CGAA AACUGAUU	5448	AAUCAGUUU CUACUAUA	6235
3216	AUAUAGUA CUGAUGAG X CGAA AAACUGAU	5449	AUCAGUUUC UACUAUAU	6236
3218	AAAUAUAG CUGAUGAG X CGAA AGAAACUG	5450	CAGUUUCUA CUAUAUUU	6237
3221	UAUAAAUA CUGAUGAG X CGAA AGUAGAAA	5451	UUUCUACUA UAUUUAUA	6238
3223	GAUAUAAA CUGAUGAG X CGAA AUAGUAGA	5452	UCUACUAUA UUUAUAUC	6239
3225	CAGAUAUA CUGAUGAG X CGAA AUAUAGUA	5453	UACUAUAUU UAUAUCUG	6240
3226	GCAGAUAU CUGAUGAG X CGAA AAUAUAGU	5454	ACUAUAUUU AUAUCUGC	6241
3227	GGCAGAUA CUGAUGAG X CGAA AAAUAUAG	5455	CUAUAUUUA UAUCUGCC	6242
3229	AUGGCAGA CUGAUGAG X CGAA AUAAAUAU	5456	AUAUUUAUA UCUGCCAU	6243
3231	GGAUGGCA CUGAUGAG X CGAA AUAUAAAU	5457	AUUUAUAUC UGCCAUCC	6244

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3238	AACACUGG CUGAUGAG X CGAA AUGGCAGA	5458	UCUGCCAUC CCAGUGUU	6245
3246	CUACCACC CUGAUGAG X CGAA ACACUGGG	5459	CCCAGUGUU GGUGGUAG	6246
3253	GAAGACCC CUGAUGAG X CGAA ACCACCAA	5460	UUGGUGGUA GGGUCUUC	6247
3258	GAUCUGAA CUGAUGAG X CGAA ACCCUACC	5461	GGUAGGGUC UUCAGAUC	6248
3260	GGGAUCUG CUGAUGAG X CGAA AGACCCUA	5462	UAGGGUCUU CAGAUCCC	6249
3261	AGGGAUCU CUGAUGAG X CGAA AAGACCCU	5463	AGGGUCUUC AGAUCCCU	6250
3266	UCCCCAGG CUGAUGAG X CGAA AUCUGAAG	5464	CUUCAGAUC CCUGGGGA	6251
3296	AACUCUCC CUGAUGAG X CGAA ACUCUCAU	5465	AUGAGAGUA GGAGAGUU	6252
3304	CCCAACAC CUGAUGAG X CGAA ACUCUCCU	5466	AGGAGAGUU GUGUUGGG	6253
3309	GGAGUCCC CUGAUGAG X CGAA ACACAACU	5467	AGUUGUGUU GGGACUCC	6254
3316	AACACUUG CUGAUGAG X CGAA AGUCCCAA	5468	UUGGGACUC CAAGUGUU	6255
3324	GCCCCUUC CUGAUGAG X CGAA ACACUUGG	5469	CCAAGUGUU GAAGGGGC	6256
3362	UCUGGGAC CUGAUGAG X CGAA ACCUCUCU	5470	AGAGAGGUU GUCCCAGA	6257
3365	UACUCUGG CUGAUGAG X CGAA ACAACCUC	5471	GAGGUUGUC CCAGAGUA	6258
3373	GACUCCGC CUGAUGAG X CGAA ACUCUGGG	5472	CCCAGAGUA GCGGAGUC	6259
3381	CCAAAGCA CUGAUGAG X CGAA ACUCCGCU	5473	AGCGGAGUC UGCUUUGG	6260

Posi-tion	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3386	UCUCCCCA CUGAUGAG X CGAA AGCAGACU	5474	AGUCUGCUU UGGGGAGA	6261
3387	UUCUCCCC CUGAUGAG X CGAA AAGCAGAC	5475	GUCUGCUUU GGGGAGAA	6262
3403	CCUCAGUC CUGAUGAG X CGAA AUCUCUCU	5476	AGAGAGAUU GACUGAGG	6263
3414	CUUGAUGC CUGAUGAG X CGAA AUCCUCAG	5477	CUGAGGAUA GCAUCAAG	6264
3419	AAAAACUU CUGAUGAG X CGAA AUGCUAUC	5478	GAUAGCAUC AAGUUUUU	6265
3424	AAAUAAAA CUGAUGAG X CGAA ACUUGAUG	5479	CAUCAAGUU UUUUAUUU	6266
3425	AAAAUAAA CUGAUGAG X CGAA AACUUGAU	5480	AUCAAGUUU UUUAUUUU	6267
3426	UAAAAUAA CUGAUGAG X CGAA AAACUUGA	5481	UCAAGUUUU UUAUUUUA	6268
3427	AUAAAAUA CUGAUGAG X CGAA AAAACUUG	5482	CAAGUUUUU UAUUUUAU	6269
3428	CAUAAAAU CUGAUGAG X CGAA AAAAACUU	5483	AAGUUUUUU AUUUUAUG	6270
3429	ACAUAAAA CUGAUGAG X CGAA AAAAAACU	5484	AGUUUUUUA UUUUAUGU	6271
3431	GUACAUAA CUGAUGAG X CGAA AUAAAAAA	5485	UUUUUUAUU UUAUGUAC	6272
3432	UGUACAUA CUGAUGAG X CGAA AAUAAAAA	5486	UUUUUAUUU UAUGUACA	6273
3433	UUGUACAU CUGAUGAG X CGAA AAAUAAAA	5487	UUUUAUUUU AUGUACAA	6274
3434	UUUGUACA CUGAUGAG X CGAA AAAAUAAA	5488	UUUAUUUUA UGUACAAA	6275
3438	CAUCUUUG CUGAUGAG X CGAA ACAUAAAA	5489	UUUUAUGUA CAAAGAUG	6276

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3449	GCUAAAAA CUGAUGAG X CGAA AUCAUCUU	5490	AAGAUGAUC UUUUUAGC	6277
3451	AAGCUAAA CUGAUGAG X CGAA AGAUCAUC	5491	GAUGAUCUU UUUAGCUU	6278
3452	GAAGCUAA CUGAUGAG X CGAA AAGAUCAU	5492	AUGAUCUUU UUAGCUUC	6279
3453	UGAAGCUA CUGAUGAG X CGAA AAAGAUCA	5493	UGAUCUUUU UAGCUUCA	6280
3454	GUGAAGCU CUGAUGAG X CGAA AAAAGAUC	5494	GAUCUUUUU AGCUUCAC	6281
3455	GGUGAAGC CUGAUGAG X CGAA AAAAAGAU	5495	AUCUUUUUA GCUUCACC	6282
3459	CCUGGGUG CUGAUGAG X CGAA AGCUAAAA	5496	UUUUAGCUU CACCCAGG	6283
3460	UCCUGGGU CUGAUGAG X CGAA AAGCUAAA	5497	UUUAGCUUC ACCCAGGA	6284
3472	AAAACCCA CUGAUGAG X CGAA ACUUCCUG	5498	CAGGAAGUA UGGGUUUU	6285
3478	AGACACAA CUGAUGAG X CGAA ACCCAUAC	5499	GUAUGGGUU UUGUGUCU	6286
3479	AAGACACA CUGAUGAG X CGAA AACCCAUA	5500	UAUGGGUUU UGUGUCUU	6287
3480	GAAGACAC CUGAUGAG X CGAA AAACCCAU	5501	AUGGGUUUU GUGUCUUC	6288
3485	ACGAGGAA CUGAUGAG X CGAA ACACAAAA	5502	UUUUGUGUC UUCCUCGU	6289
3487	ACACGAGG CUGAUGAG X CGAA AGACACAA	5503	UUGUGUCUU CCUCGUGU	6290
3488	AACACGAG CUGAUGAG X CGAA AAGACACA	5504	UGUGUCUUC CUCGUGUU	6291
3491	CUAAACAC CUGAUGAG X CGAA AGGAAGAC	5505	GUCUUCCUC GUGUUUAG	6292

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3496	AAAACCUA CUGAUGAG X CGAA ACACGAGG	5506	CCUCGUGUU UAGGUUUU	6293
3497	AAAAACCU CUGAUGAG X CGAA AACACGAG	5507	CUCGUGUUU AGGUUUUU	6294
3498	UAAAAACC CUGAUGAG X CGAA AAACACGA	5508	UCGUGUUUA GGUUUUUA	6295
3502	AGAAUAAA CUGAUGAG X CGAA ACCUAAAC	5509	GUUUAGGUU UUUAUUCU	6296
3503	CAGAAUAA CUGAUGAG X CGAA AACCUAAA	5510	UUUAGGUUU UUAUUCUG	6297
3504	UCAGAAUA CUGAUGAG X CGAA AAACCUAA	5511	UUAGGUUUU UAUUCUGA	6298
3505	GUCAGAAU CUGAUGAG X CGAA AAAACCUA	5512	UAGGUUUUU AUUCUGAC	6299
3506	GGUCAGAA CUGAUGAG X CGAA AAAAACCU	5513	AGGUUUUUA UUCUGACC	6300
3508	UAGGUCAG CUGAUGAG X CGAA AUAAAAAC	5514	GUUUUUAUU CUGACCUA	6301
3509	UUAGGUCA CUGAUGAG X CGAA AAUAAAAA	5515	UUUUUAUUC UGACCUAA	6302
3516	GACCUAAU CUGAUGAG X CGAA AGGUCAGA	5516	UCUGACCUA AUUAGGUC	6303
3519	UUAGACCU CUGAUGAG X CGAA AUUAGGUC	5517	GACCUAAUU AGGUCUAA	6304
3520	CUUAGACC CUGAUGAG X CGAA AAUUAGGU	5518	ACCUAAUUA GGUCUAAG	6305
3524	UCAGCUUA CUGAUGAG X CGAA ACCUAAUU	5519	AAUUAGGUC UAAGCUGA	6306
3526	CCUCAGCU CUGAUGAG X CGAA AGACCUAA	5520	UUAGGUCUA AGCUGAGG	6307
3539	AGAGAAAU CUGAUGAG X CGAA AGCACCUC	5521	GAGGUGCUU AUUUCUCU	6308

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3540	AAGAGAAA CUGAUGAG X CGAA AAGCACCU	5522	AGGUGCUUA UUUCUCUU	6309
3542	AGAAGAGA CUGAUGAG X CGAA AUAAGCAC	5523	GUGCUUAUU UCUCUUCU	6310
3543	CAGAAGAG CUGAUGAG X CGAA AAUAAGCA	5524	UGCUUAUUU CUCUUCUG	6311
3544	CCAGAAGA CUGAUGAG X CGAA AAAUAAGC	5525	GCUUAUUUC UCUUCUGG	6312
3546	CUCCAGAA CUGAUGAG X CGAA AGAAAUAA	5526	UUAUUUCUC UUCUGGAG	6313
3548	AACUCCAG CUGAUGAG X CGAA AGAGAAAU	5527	AUUUCUCUU CUGGAGUU	6314
3549	AAACUCCA CUGAUGAG X CGAA AAGAGAAA	5528	UUUCUCUUC UGGAGUUU	6315
3556	AGGAUAUA CUGAUGAG X CGAA ACUCCAGA	5529	UCUGGAGUU UAUAUCCU	6316
3557	UAGGAUAU CUGAUGAG X CGAA AACUCCAG	5530	CUGGAGUUU AUAUCCUA	6317
3558	CUAGGAUA CUGAUGAG X CGAA AAACUCCA	5531	UGGAGUUUA UAUCCUAG	6318
3560	UUCUAGGA CUGAUGAG X CGAA AUAAACUC	5532	GAGUUUAUA UCCUAGAA	6319
3562	GCUUCUAG CUGAUGAG X CGAA AUAUAAAC	5533	GUUUAUAUC CUAGAAGC	6320
3565	AGAGCUUC CUGAUGAG X CGAA AGGAUAUA	5534	UAUAUCCUA GAAGCUCU	6321
3572	CGAUUGGA CUGAUGAG X CGAA AGCUUCUA	5535	UAGAAGCUC UCCAAUCG	6322
3574	UUCGAUUG CUGAUGAG X CGAA AGAGCUUC	5536	GAAGCUCUC CAAUCGAA	6323
3579	AGGGCUUC CUGAUGAG X CGAA AUUGGAGA	5537	UCUCCAAUC GAAGCCCU	6324

Posi-tion	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3588	UACCUGCA CUGAUGAG X CGAA AGGGCUUC	5538	GAAGCCCUC UGCAGGUA	6325
3596	CCUGAGGA CUGAUGAG X CGAA ACCUGCAG	5539	CUGCAGGUA UCCUCAGG	6326
3598	GACCUGAG CUGAUGAG X CGAA AUACCUGC	5540	GCAGGUAUC CUCAGGUC	6327
3601	CAGGACCU CUGAUGAG X CGAA AGGAUACC	5541	GGUAUCCUC AGGUCCUG	6328
3606	UUCUCCAG CUGAUGAG X CGAA ACCUGAGG	5542	CCUCAGGUC CUGGAGAA	6329
3631	AAGCCAAC CUGAUGAG X CGAA AGCCUUCC	5543	GGAAGGCUU GUUGGCUU	6330
3634	CCGAAGCC CUGAUGAG X CGAA ACAAGCCU	5544	AGGCUUGUU GGCUUCGG	6331
3639	CCUUUCCG CUGAUGAG X CGAA AGCCAACA	5545	UGUUGGCUU CGGAAAGG	6332
3640	CCCUUUCC CUGAUGAG X CGAA AAGCCAAC	5546	GUUGGCUUC GGAAAGGG	6333
3655	UUAAACCA CUGAUGAG X CGAA AGCCCUCC	5547	GGAGGGCUA UGGUUUAA	6334
3660	UGGCUUUA CUGAUGAG X CGAA ACCAUAGC	5548	GCUAUGGUU UAAAGCCA	6335
3661	CUGGCUUU CUGAUGAG X CGAA AACCAUAG	5549	CUAUGGUUU AAAGCCAG	6336
3662	ACUGGCUU CUGAUGAG X CGAA AAACCAUA	5550	UAUGGUUUA AAGCCAGU	6337
3671	CCACAUCU CUGAUGAG X CGAA ACUGGCUU	5551	AAGCCAGUA AGAUGUGG	6338
3682	AAGAAUCA CUGAUGAG X CGAA ACCCACAU	5552	AUGUGGGUU UGAUUCUU	6339
3683	CAAGAAUC CUGAUGAG X CGAA AACCCACA	5553	UGUGGGUUU GAUUCUUG	6340

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3687	AAGUCAAG CUGAUGAG X CGAA AUCAAACC	5554	GGUUUGAUU CUUGACUU	6341
3688	AAAGUCAA CUGAUGAG X CGAA AAUCAAAC	5555	GUUUGAUUC UUGACUUU	6342
3690	ACAAAGUC CUGAUGAG X CGAA AGAAUCAA	5556	UUGAUUCUU GACUUUGU	6343
3695	AGGAGACA CUGAUGAG X CGAA AGUCAAGA	5557	UCUUGACUU UGUCUCCU	6344
3696	CAGGAGAC CUGAUGAG X CGAA AAGUCAAG	5558	CUUGACUUU GUCUCCUG	6345
3699	CUACAGGA CUGAUGAG X CGAA ACAAAGUC	5559	GACUUUGUC UCCUGUAG	6346
3701	GCCUACAG CUGAUGAG X CGAA AGACAAAG	5560	CUUUGUCUC CUGUAGGC	6347
3706	ACACAGCC CUGAUGAG X CGAA ACAGGAGA	5561	UCUCCUGUA GGCUGUGU	6348
3720	ACUUAUUU CUGAUGAG X CGAA AGGCCACA	5562	UGUGGCCUU AAAUAAGU	6349
3721	AACUUAUU CUGAUGAG X CGAA AAGGCCAC	5563	GUGGCCUUA AAUAAGUU	6350
3725	AGGUAACU CUGAUGAG X CGAA AUUUAAGG	5564	CCUUAAAUA AGUUACCU	6351
3729	GAUUAGGU CUGAUGAG X CGAA ACUUAUUU	5565	AAAUAAGUU ACCUAAUC	6352
3730	AGAUUAGG CUGAUGAG X CGAA AACUUAUU	5566	AAUAAGUUA CCUAAUCU	6353
3734	CAAGAGAU CUGAUGAG X CGAA AGGUAACU	5567	AGUUACCUA AUCUCUUG	6354
3737	ACUCAAGA CUGAUGAG X CGAA AUUAGGUA	5568	UACCUAAUC UCUUGAGU	6355
3739	GGACUCAA CUGAUGAG X CGAA AGAUUAGG	5569	CCUAAUCUC UUGAGUCC	6356

Posi-tion	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3741	GAGGACUC CUGAUGAG X CGAA AGAGAUUA	5570	UAAUCUCUU GAGUCCUC	6357
3746	AAACUGAG CUGAUGAG X CGAA ACUCAAGA	5571	UCUUGAGUC CUCAGUUU	6358
3749	AGGAAACU CUGAUGAG X CGAA AGGACUCA	5572	UGAGUCCUC AGUUUCCU	6359
3753	AAUGAGGA CUGAUGAG X CGAA ACUGAGGA	5573	UCCUCAGUU UCCUCAUU	6360
3754	AAAUGAGG CUGAUGAG X CGAA AACUGAGG	5574	CCUCAGUUU CCUCAUUU	6361
3755	CAAAUGAG CUGAUGAG X CGAA AAACUGAG	5575	CUCAGUUUC CUCAUUUG	6362
3758	UUACAAAU CUGAUGAG X CGAA AGGAAACU	5576	AGUUUCCUC AUUUGUAA	6363
3761	GCCUUACA CUGAUGAG X CGAA AUGAGGAA	5577	UUCCUCAUU UGUAAGGC	6364
3762	UGCCUUAC CUGAUGAG X CGAA AAUGAGGA	5578	UCCUCAUUU GUAAGGCA	6365
3765	CUCUGCCU CUGAUGAG X CGAA ACAAAUGA	5579	UCAUUUGUA AGGCAGAG	6366
3786	CAUAAUCA CUGAUGAG X CGAA AGGCAUUG	5580	CAAUGCCUA UGAUUAUG	6367
3791	AUCAGCAU CUGAUGAG X CGAA AUCAUAGG	5581	CCUAUGAUU AUGCUGAU	6368
3792	AAUCAGCA CUGAUGAG X CGAA AAUCAUAG	5582	CUAUGAUUA UGCUGAUU	6369
3800	UUUCAUUU CUGAUGAG X CGAA AUCAGCAU	5583	AUGCUGAUU AAAUGAAA	6370
3801	GUUUCAUU CUGAUGAG X CGAA AAUCAGCA	5584	UGCUGAUUA AAUGAAAC	6371
3823	UAAACACU CUGAUGAG X CGAA AUUUUGUG	5585	CACAAAAUA AGUGUUUA	6372

Posi-tion	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3829	AUUCAUUA CUGAUGAG X CGAA ACACUUAU	5586	AUAAGUGUU UAAUGAAU	6373
3830	CAUUCAUU CUGAUGAG X CGAA AACACUUA	5587	UAAGUGUUU AAUGAAUG	6374
3831	UCAUUCAU CUGAUGAG X CGAA AAACACUU	5588	AAGUGUUUA AUGAAUGA	6375
3845	GACAAUAG CUGAUGAG X CGAA AGUUGUCA	5589	UGACAACUA CUAUUGUC	6376
3848	AAUGACAA CUGAUGAG X CGAA AGUAGUUG	5590	CAACUACUA UUGUCAUU	6377
3850	AUAAUGAC CUGAUGAG X CGAA AUAGUAGU	5591	ACUACUAUU GUCAUUAU	6378
3853	AGAAUAAU CUGAUGAG X CGAA ACAAUAGU	5592	ACUAUUGUC AUUAUUCU	6379
3856	GGAAGAAU CUGAUGAG X CGAA AUGACAAU	5593	AUUGUCAUU AUUCUUCC	6380
3857	AGGAAGAA CUGAUGAG X CGAA AAUGACAA	5594	UUGUCAUUA UUCUUCCU	6381
3859	AUAGGAAG CUGAUGAG X CGAA AUAAUGAC	5595	GUCAUUAUU CUUCCUAU	6382
3860	GAUAGGAA CUGAUGAG X CGAA AAUAAUGA	5596	UCAUUAUUC UUCCUAUC	6383
3862	UGGAUAGG CUGAUGAG X CGAA AGAAUAAU	5597	AUUAUUCUU CCUAUCCA	6384
3863	AUGGAUAG CUGAUGAG X CGAA AAGAAUAA	5598	UUAUUCUUC CUAUCCAU	6385
3866	AGCAUGGA CUGAUGAG X CGAA AGGAAGAA	5599	UUCUUCCUA UCCAUGCU	6386
3868	AUAGCAUG CUGAUGAG X CGAA AUAGGAAG	5600	CUUCCUAUC CAUGCUAU	6387
3875	AUGGCAGA CUGAUGAG X CGAA AGCAUGGA	5601	UCCAUGCUA UCUGCCAU	6388

Posi-tion	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3877	ACAUGGCA CUGAUGAG X CGAA AUAGCAUG	5602	CAUGCUAUC UGCCAUGU	6389
3886	GCCUCCAA CUGAUGAG X CGAA ACAUGGCA	5603	UGCCAUGUA UUGGAGGC	6390
3888	UUGCCUCC CUGAUGAG X CGAA AUACAUGG	5604	CCAUGUAUU GGAGGCAA	6391
3904	GAAGUAGU CUGAUGAG X CGAA ACAGCUUU	5605	AAAGCUGUU ACUACUUC	6392
3905	UGAAGUAG CUGAUGAG X CGAA AACAGCUU	5606	AAGCUGUUA CUACUUCA	6393
3908	GCAUGAAG CUGAUGAG X CGAA AGUAACAG	5607	CUGUUACUA CUUCAUGC	6394
3911	UAUGCAUG CUGAUGAG X CGAA AGUAGUAA	5608	UUACUACUU CAUGCAUA	6395
3912	AUAUGCAU CUGAUGAG X CGAA AAGUAGUA	5609	UACUACUUC AUGCAUAU	6396
3919	AUAGCGCA CUGAUGAG X CGAA AUGCAUGA	5610	UCAUGCAUA UGCGCUAU	6397
3926	AGCCUGCA CUGAUGAG X CGAA AGCGCAUA	5611	UAUGCGCUA UGCAGGCU	6398
3935	CAUUCUGG CUGAUGAG X CGAA AGCCUGCA	5612	UGCAGGCUU CCAGAAUG	6399
3936	UCAUUCUG CUGAUGAG X CGAA AAGCCUGC	5613	GCAGGCUUC CAGAAUGA	6400
3957	GGGAAAGG CUGAUGAG X CGAA ACCCCAUC	5614	GAUGGGGUC CCUUUCCC	6401
3961	GUGGGGGA CUGAUGAG X CGAA AGGGACCC	5615	GGGUCCCUU UCCCCCAC	6402
3962	UGUGGGGG CUGAUGAG X CGAA AAGGGACC	5616	GGUCCCUUU CCCCCACA	6403
3963	AUGUGGGG CUGAUGAG X CGAA AAAGGGAC	5617	GUCCCUUUC CCCCACAU	6404

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
3972	CUCUCACA CUGAUGAG X CGAA AUGUGGGG	5618	CCCCACAUA UGUGAGAG	6405
3986	AUAAGAGG CUGAUGAG X CGAA ACCCCCUC	5619	GAGGGGGUC CCUCUUAU	6406
3990	UGAAAUAA CUGAUGAG X CGAA AGGGACCC	5620	GGGUCCCUC UUAUUUCA	6407
3992	GUUGAAAU CUGAUGAG X CGAA AGAGGGAC	5621	GUCCCUCUU AUUUCAAC	6408
3993	AGUUGAAA CUGAUGAG X CGAA AAGAGGGA	5622	UCCCUCUUA UUUCAACU	6409
3995	CGAGUUGA CUGAUGAG X CGAA AUAAGAGG	5623	CCUCUUAUU UCAACUCG	6410
3996	ACGAGUUG CUGAUGAG X CGAA AAUAAGAG	5624	CUCUUAUUU CAACUCGU	6411
3997	AACGAGUU CUGAUGAG X CGAA AAAUAAGA	5625	UCUUAUUUC AACUCGUU	6412
4002	UGAGGAAC CUGAUGAG X CGAA AGUUGAAA	5626	UUUCAACUC GUUCCUCA	6413
4005	CAAUGAGG CUGAUGAG X CGAA ACGAGUUG	5627	CAACUCGUU CCUCAUUG	6414
4006	GCAAUGAG CUGAUGAG X CGAA AACGAGUU	5628	AACUCGUUC CUCAUUGC	6415
4009	CCAGCAAU CUGAUGAG X CGAA AGGAACGA	5629	UCGUUCCUC AUUGCUGG	6416
4012	AAACCAGC CUGAUGAG X CGAA AUGAGGAA	5630	UUCCUCAUU GCUGGUUU	6417
4019	AUAUGCCA CUGAUGAG X CGAA ACCAGCAA	5631	UUGCUGGUU UGGCAUAU	6418
4020	GAUAUGCC CUGAUGAG X CGAA AACCAGCA	5632	UGCUGGUUU GGCAUAUC	6419
4026	AGCUGAGA CUGAUGAG X CGAA AUGCCAAA	5633	UUUGGCAUA UCUCAGCU	6420

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4028	GUAGCUGA CUGAUGAG X CGAA AUAUGCCA	5634	UGGCAUAUC UCAGCUAC	6421
4030	GAGUAGCU CUGAUGAG X CGAA AGAUAUGC	5635	GCAUAUCUC AGCUACUC	6422
4035	GGUUAGAG CUGAUGAG X CGAA AGCUGAGA	5636	UCUCAGCUA CUCUAACC	6423
4038	CCGGGUUA CUGAUGAG X CGAA AGUAGCUG	5637	CAGCUACUC UAACCCGG	6424
4040	UGCCGGGU CUGAUGAG X CGAA AGAGUAGC	5638	GCUACUCUA ACCCGGCA	6425
4054	CUUCUGUG CUGAUGAG X CGAA AUUCUUGC	5639	GCAAGAAUC CACAGAAG	6426
4084	AAAUGUAU CUGAUGAG X CGAA AGCCUUUU	5640	AAAAGGCUU AUACAUUU	6427
4085	CAAAUGUA CUGAUGAG X CGAA AAGCCUUU	5641	AAAGGCUUA UACAUUUG	6428
4087	AGCAAAUG CUGAUGAG X CGAA AUAAGCCU	5642	AGGCUUAUA CAUUUGCU	6429
4091	GUAAAGCA CUGAUGAG X CGAA AUGUAUAA	5643	UUAUACAUU UGCUUUAC	6430
4092	GGUAAAGC CUGAUGAG X CGAA AAUGUAUA	5644	UAUACAUUU GCUUUACC	6431
4096	UAUGGGUA CUGAUGAG X CGAA AGCAAAUG	5645	CAUUUGCUU UACCCAUA	6432
4097	UUAUGGGU CUGAUGAG X CGAA AAGCAAAU	5646	AUUUGCUUU ACCCAUAA	6433
4098	CUUAUGGG CUGAUGAG X CGAA AAAGCAAA	5647	UUUGCUUUA CCCAUAAG	6434
4104	GGUUUUCU CUGAUGAG X CGAA AUGGGUAA	5648	UUACCCAUA AGAAAACC	6435
4114	CAGGGCUU CUGAUGAG X CGAA AGGUUUUC	5649	GAAAACCUC AAGCCCUG	6436

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4124	UUUUCAGA CUGAUGAG X CGAA ACAGGGCU	5650	AGCCCUGUA UCUGAAAA	6437
4126	UUUUUUCA CUGAUGAG X CGAA AUACAGGG	5651	CCCUGUAUC UGAAAAAA	6438
4144	GAUCCUUU CUGAUGAG X CGAA AUCUUCCU	5652	AGGAAGAUA AAAGGAUC	6439
4152	GUCUUAUA CUGAUGAG X CGAA AUCCUUUU	5653	AAAAGGAUC UAUAAGAC	6440
4154	AAGUCUUA CUGAUGAG X CGAA AGAUCCUU	5654	AAGGAUCUA UAAGACUU	6441
4156	UGAAGUCU CUGAUGAG X CGAA AUAGAUCC	5655	GGAUCUAUA AGACUUCA	6442
4162	GGAACUUG CUGAUGAG X CGAA AGUCUUAU	5656	AUAAGACUU CAAGUUCC	6443
4163	UGGAACUU CUGAUGAG X CGAA AAGUCUUA	5657	UAAGACUUC AAGUUCCA	6444
4168	UCUCAUGG CUGAUGAG X CGAA ACUUGAAG	5658	CUUCAAGUU CCAUGAGA	6445
4169	UUCUCAUG CUGAUGAG X CGAA AACUUGAA	5659	UUCAAGUUC CAUGAGAA	6446
4189	ACAAAAUA CUGAUGAG X CGAA ACAUGUCC	5660	GGACAUGUC UAUUUUGU	6447
4191	GAACAAAA CUGAUGAG X CGAA AGACAUGU	5661	ACAUGUCUA UUUUGUUC	6448
4193	UUGAACAA CUGAUGAG X CGAA AUAGACAU	5662	AUGUCUAUU UUGUUCAA	6449
4194	AUUGAACA CUGAUGAG X CGAA AAUAGACA	5663	UGUCUAUUU UGUUCAAU	6450
4195	UAUUGAAC CUGAUGAG X CGAA AAAUAGAC	5664	GUCUAUUUU GUUCAAUA	6451
4198	GAGUAUUG CUGAUGAG X CGAA ACAAAAUA	5665	UAUUUUGUU CAAUACUC	6452

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4199	AGAGUAUU CUGAUGAG X CGAA AACAAAAU	5666	AUUUUGUUC AAUACUCU	6453
4203	GCAUAGAG CUGAUGAG X CGAA AUUGAACA	5667	UGUUCAAUA CUCUAUGC	6454
4206	UGGGCAUA CUGAUGAG X CGAA AGUAUUGA	5668	UCAAUACUC UAUGCCCA	6455
4208	AGUGGGCA CUGAUGAG X CGAA AGAGUAUU	5669	AAUACUCUA UGCCCACU	6456
4228	UUGCUGCC CUGAUGAG X CGAA AUGUGCCA	5670	UGGCACAUA GGCAGCAA	6457
4244	UCCACAGA CUGAUGAG X CGAA AUUUGUUU	5671	AAACAAAUA UCUGUGGA	6458
4246	AUUCCACA CUGAUGAG X CGAA AUAUUUGU	5672	ACAAAUAUC UGUGGAAU	6459
4258	CCUUUACA CUGAUGAG X CGAA AGCAUUCC	5673	GGAAUGCUA UGUAAAGG	6460
4262	GAUGCCUU CUGAUGAG X CGAA ACAUAGCA	5674	UGCUAUGUA AAGGCAUC	6461
4270	CAUCUAUA CUGAUGAG X CGAA AUGCCUUU	5675	AAAGGCAUC UAUAGAUG	6462
4272	AUCAUCUA CUGAUGAG X CGAA AGAUGCCU	5676	AGGCAUCUA UAGAUGAU	6463
4274	ACAUCAUC CUGAUGAG X CGAA AUAGAUGC	5677	GCAUCUAUA GAUGAUGU	6464
4287	CUUAAAGG CUGAUGAG X CGAA AGGCACAU	5678	AUGUGCCUC CCUUUAAG	6465
4291	GUUUCUUA CUGAUGAG X CGAA AGGGAGGC	5679	GCCUCCCUU UAAGAAAC	6466
4292	GGUUUCUU CUGAUGAG X CGAA AAGGGAGG	5680	CCUCCCUUU AAGAAACC	6467
4293	GGGUUUCU CUGAUGAG X CGAA AAAGGGAG	5681	CUCCCUUUA AGAAACCC	6468

Posi-tion	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4305	UAUUCAAA CUGAUGAG X CGAA AUUGGGUU	5682	AACCCAAUA UUUGAAUA	6469
4307	AAUAUUCA CUGAUGAG X CGAA AUAUUGGG	5683	CCCAAUAUU UGAAUAUU	6470
4308	AAAUAUUC CUGAUGAG X CGAA AAUAUUGG	5684	CCAAUAUUU GAAUAUUU	6471
4313	AGUGCAAA CUGAUGAG X CGAA AUUCAAAU	5685	AUUUGAAUA UUUGCACU	6472
4315	UGAGUGCA CUGAUGAG X CGAA AUAUUCAA	5686	UUGAAUAUU UGCACUCA	6473
4316	AUGAGUGC CUGAUGAG X CGAA AAUAUUCA	5687	UGAAUAUUU GCACUCAU	6474
4322	GUAUGAAU CUGAUGAG X CGAA AGUGCAAA	5688	UUUGCACUC AUUCAUAC	6475
4325	CUUGUAUG CUGAUGAG X CGAA AUGAGUGC	5689	GCACUCAUU CAUACAAG	6476
4326	UCUUGUAU CUGAUGAG X CGAA AAUGAGUG	5690	CACUCAUUC AUACAAGA	6477
4329	GGAUCUUG CUGAUGAG X CGAA AUGAAUGA	5691	UCAUUCAUA CAAGAUCC	6478
4336	CACUUGAG CUGAUGAG X CGAA AUCUUGUA	5692	UACAAGAUC CUCAAGUG	6479
4339	GAGCACUU CUGAUGAG X CGAA AGGAUCUU	5693	AAGAUCCUC AAGUGCUC	6480
4347	UCCAAACG CUGAUGAG X CGAA AGCACUUG	5694	CAAGUGCUC CGUUUGGA	6481
4351	AUUAUCCA CUGAUGAG X CGAA ACGGAGCA	5695	UGCUCCGUU UGGAUAAU	6482
4352	GAUUAUCC CUGAUGAG X CGAA AACGGAGC	5696	GCUCCGUUU GGAUAAUC	6483
4357	CUCCAGAU CUGAUGAG X CGAA AUCCAAAC	5697	GUUUGGAUA AUCUGGAG	6484

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4360	ACCCUCCA CUGAUGAG X CGAA AUUAUCCA	5698	UGGAUAAUC UGGAGGGU	6485
4369	UGUUUUCA CUGAUGAG X CGAA ACCCUCCA	5699	UGGAGGGUA UGAAAACA	6486
4379	AUCUUGGC CUGAUGAG X CGAA AUGUUUUC	5700	GAAAACAUA GCCAAGAU	6487
4388	GAAUUCAU CUGAUGAG X CGAA AUCUUGGC	5701	GCCAAGAUC AUGAAUUC	6488

TABLE X: HAIRPIN RIBOZYME AND TARGET SEQUENCES FOR INTEGRIN SUBUNIT BETA 3

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
98	UCUCUG AGAA GGUU ACCAGAGAAACA X GUACAUUACCUGGUA	6489	AACCG GUU CAGAGA	6569
119	GCAAAC AGAA GCUG ACCAGAGAAACA X GUACAUUACCUGGUA	6490	CAGCA GAU GUUUGC	6570
284	GUCCGC AGAA GGGC ACCAGAGAAACA X GUACAUUACCUGGUA	6491	GCCCA GUC GCGGAC	6571
290	CCGGGG AGAA GCGA ACCAGAGAAACA X GUACAUUACCUGGUA	6492	UCGCG GAC CCCCGG	6572
313	CGGGUC AGAA GCGC ACCAGAGAAACA X GUACAUUACCUGGUA	6493	GCGCU GAC GACCCG	6573
322	CCUGCC AGAA GGGU ACCAGAGAAACA X GUACAUUACCUGGUA	6494	ACCCG GCU GGCAGG	6574
388	AGAGGG AGAA GUGG ACCAGAGAAACA X GUACAUUACCUGGUA	6495	CCACC GCU CCCUCU	6575
465	GGGGCG AGAA GCGG ACCAGAGAAACA X GUACAUUACCUGGUA	6496	CCGCG GCC CGCCCC	6576
469	CAACGG AGAA GGCC ACCAGAGAAACA X GUACAUUACCUGGUA	6497	GGCCC GCC CCGUUG	6577
474	GGACGC AGAA GGGC ACCAGAGAAACA X GUACAUUACCUGGUA	6498	GCCCC GUU GCGUCC	6578
513	UUCCGC AGAA GGAG ACCAGAGAAACA X GUACAUUACCUGGUA	6499	CUCCC GCU GCGGAA	6579
527	GCCCGC AGAA GCUU ACCAGAGAAACA X GUACAUUACCUGGUA	6500	AAGCG GCC GCGGGC	6580
578	CAUCUC AGAA GCCU ACCAGAGAAACA X GUACAUUACCUGGUA	6501	AGGCG GAC GAGAUG	6581
595	GGCCGC AGAA GCGC ACCAGAGAAACA X GUACAUUACCUGGUA	6502	GCGCG GCC GCGGCC	6582
601	GGCCGG AGAA GCGG ACCAGAGAAACA X GUACAUUACCUGGUA	6503	CCGCG GCC CCGGCC	6583

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
607	CAGAGC AGAA GGGG ACCAGAGAAACA X GUACAUUACCUGGUA	6504	CCCCG GCC GCUCUG	6584
610	GCCCAG AGAA GCCG ACCAGAGAAACA X GUACAUUACCUGGUA	6505	CGGCC GCU CUGGGC	6585
678	CUGCCG AGAA GGAG ACCAGAGAAACA X GUACAUUACCUGGUA	6506	CUCCG GCU CGGCAG	6586
694	UGGGGC AGAA GCGA ACCAGAGAAACA X GUACAUUACCUGGUA	6507	UCGCA GCU GCCCCA	6587
697	UCCUGG AGAA GCUG ACCAGAGAAACA X GUACAUUACCUGGUA	6508	CAGCU GCC CCAGGA	6588
728	CUCCAA AGAA GCAA ACCAGAGAAACA X GUACAUUACCUGGUA	6509	UUGCG GAC UUGGAG	6589
800	GGUCC AGAA GGC ACCAGAGAAACA X GUACAUUACCUGGUA	6510	GCNCG GUC GGANCC	6590
920	CGCGGC AGAA GGGA ACCAGAGAAACA X GUACAUUACCUGGUA	6511	UCCCG GCC GCCGCG	6591
923	CGCCGC AGAA GCCG ACCAGAGAAACA X GUACAUUACCUGGUA	6512	CGGCC GCC GCGGCG	6592
1006	UCCUUG AGAA GACC ACCAGAGAAACA X GUACAUUACCUGGUA	6513	GGUCG GNC CAAGGA	6593
1020	UUCCUG AGAA GUCG ACCAGAGAAACA X GUACAUUACCUGGUA	6514	CGACU GCC CAGGAA	6594
1063	CCAAGG AGAA GGAA ACCAGAGAAACA X GUACAUUACCUGGUA	6515	UUCCC GCC CCUUGG	6595
1295	CCUGGG AGAA GAGG ACCAGAGAAACA X GUACAUUACCUGGUA	6516	CCUCU GCU CCCAGG	6596
1307	UGCAGG AGAA GCCC ACCAGAGAAACA X GUACAUUACCUGGUA	6517	GGGCA GAC CCUGCA	6597
1396	GUGCGC AGAA GCCA ACCAGAGAAACA X GUACAUUACCUGGUA	6518	UGGCU GCU GCGCAC	6598
1412	CCUGAC AGAA GACG ACCAGAGAAACA X GUACAUUACCUGGUA	6519	CGUCA GCC GUCAGG	6599

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
1435	CAAAGA AGAA GAAU ACCAGAGAAACA X GUACAUUACCUGGUA	6520	AUUCG GCC UCUUUG	6600
1481	ACCCCG AGAA GUGC ACCAGAGAAACA X GUACAUUACCUGGUA	6521	GCACA GCC CGGGGU	6601
1494	ACCACG AGAA GCAA ACCAGAGAAACA X GUACAUUACCUGGUA	6522	UUGCU GCC CGUGGU	6602
1561	GGCCCC AGAA GACC ACCAGAGAAACA X GUACAUUACCUGGUA	6523	GGUCU GCU GGGGCC	6603
1570	GGCAGA AGAA GCCC ACCAGAGAAACA X GUACAUUACCUGGUA	6524	GGGCC GCC UCUGCC	6604
1576	CUCUGA AGAA GAGG ACCAGAGAAACA X GUACAUUACCUGGUA	6525	CCUCU GCC UCAGAG	6605
1625	GAGUAC AGAA GUUU ACCAGAGAAACA X GUACAUUACCUGGUA	6526	AAACU GUA GUACUC	6606
1726	CUGGGC AGAA GAGC ACCAGAGAAACA X GUACAUUACCUGGUA	6527	GCUCU GUC GCCCAG	6607
1760	GCAGUG AGAA GAGA ACCAGAGAAACA X GUACAUUACCUGGUA	6528	UCUCG GCU CACUGC	6608
1776	CCAGGA AGAA GAAG ACCAGAGAAACA X GUACAUUACCUGGUA	6529	CUUCU GCC UCCUGG	6609
1808	UCGGGA AGAA GAGC ACCAGAGAAACA X GUACAUUACCUGGUA	6530	GCUCA GCC UCCCGA	6610
1848	UUAGCC AGAA GUGG ACCAGAGAAACA X GUACAUUACCUGGUA	6531	CCACG GCC GGCUAA	6611
1882	UGGUGA AGAA GCGU ACCAGAGAAACA X GUACAUUACCUGGUA	6532	ACGCG GUU UCACCA	6612
1933	GAGGUG AGAA GAUC ACCAGAGAAACA X GUACAUUACCUGGUA	6533	GAUCC GCC CACCUC	6613
1943	UUGGGA AGAA GAGG ACCAGAGAAACA X GUACAUUACCUGGUA	6534	CCUCA GCC UCCCAA	6614
2170	CCUGGC AGAA GCGA ACCAGAGAAACA X GUACAUUACCUGGUA	6535	UCGCU GUC GCCAGG	6615

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2203	GCAGUG AGAA GAAA ACCAGAGAAACA X GUACAUUACCUGGUA	6536	UUUCA GCU CACUGC	6616
2219	CCGGGA AGAA GAGG ACCAGAGAAACA X GUACAUUACCUGGUA	6537	CCUCC GCU UCCCGG	6617
2245	GGCUGA AGAA GGAG ACCAGAGAAACA X GUACAUUACCUGGUA	6538	CUCCU GCC UCAGCC	6618
2251	UCGGGA AGAA GAGG ACCAGAGAAACA X GUACAUUACCUGGUA	6539	CCUCA GCC UCCCGA	6619
2373	AAGGCA AGAA GAUC ACCAGAGAAACA X GUACAUUACCUGGUA	6540	GAUCA GCC UGCCUU	6620
2377	GGCCAA AGAA GGCU ACCAGAGAAACA X GUACAUUACCUGGUA	6541	AGCCU GCC UUGGCC	6621
2456	CAUAUC AGAA GUAA ACCAGAGAAACA X GUACAUUACCUGGUA	6542	UUACA GUU GAUAUG	6622
2521	CAGCUG AGAA GUUU ACCAGAGAAACA X GUACAUUACCUGGUA	6543	AAACA GAU CAGCUG	6623
2526	ACUAUC AGAA GAUC ACCAGAGAAACA X GUACAUUACCUGGUA	6544	GAUCA GCU GAUAGU	6624
2553	UCAUCA AGAA GCUC ACCAGAGAAACA X GUACAUUACCUGGUA	6545	GAGCA GUC UGAUGA	6625
2557	AUAGUC AGAA GACU ACCAGAGAAACA X GUACAUUACCUGGUA	6546	AGUCU GAU GACUAU	6626
2595	UCCCAG AGAA GAAU ACCAGAGAAACA X GUACAUUACCUGGUA	6547	AUUCU GCC CUGGGA	6627
2623	AGCAGC AGAA GACC ACCAGAGAAACA X GUACAUUACCUGGUA	6548	GGUCA GAU GCUGCU	6628
2629	AUAGCC AGAA GCAU ACCAGAGAAACA X GUACAUUACCUGGUA	6549	AUGCU GCU GGCUAU	6629
2738	AUCCUG AGAA GGAC ACCAGAGAAACA X GUACAUUACCUGGUA	6550	GUCCU GUC CAGGAU	6630
2811	UUAGAA AGAA GUGA ACCAGAGAAACA X GUACAUUACCUGGUA	6551	UCACA GUC UUCUAA	6631

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
2982	UGCCCA AGAA GGUC ACCAGAGAAACA X GUACAUUACCUGGUA	6552	GACCA GCU UGGGCA	6632
3045	UCUGUG AGAA GAUC ACCAGAGAAACA X GUACAUUACCUGGUA	6553	GAUCU GUU CACAGA	6633
3052	AGAUUA AGAA GUGA ACCAGAGAAACA X GUACAUUACCUGGUA	6554	UCACA GAU UAAUCU	6634
3138	AAACAC AGAA GUAC ACCAGAGAAACA X GUACAUUACCUGGUA	6555	GUACA GUA GUGUUU	6635
3169	CUGGAA AGAA GACU ACCAGAGAAACA X GUACAUUACCUGGUA	6556	AGUCA GAC UUCCAG	6636
3211	AGUAGA AGAA GAUU ACCAGAGAAACA X GUACAUUACCUGGUA	6557	AAUCA GUU UCUACU	6637
3262	CCAGGG AGAA GAAG ACCAGAGAAACA X GUACAUUACCUGGUA	6558	CUUCA GAU CCCUGG	6638
3278	CCCACC AGAA GCUU ACCAGAGAAACA X GUACAUUACCUGGUA	6559	AAGCA GAU GGUGGG	6639
3382	CCCCAA AGAA GACU ACCAGAGAAACA X GUACAUUACCUGGUA	6560	AGUCU GCU UUGGGG	6640
3510	AAUUAG AGAA GAAU ACCAGAGAAACA X GUACAUUACCUGGUA	6561	AUUCU GAC CUAAUU	6641
3703	ACAGCC AGAA GGAG ACCAGAGAAACA X GUACAUUACCUGGUA	6562	CUCCU GUA GGCUGU	6642
3750	UGAGGA AGAA GAGG ACCAGAGAAACA X GUACAUUACCUGGUA	6563	CCUCA GUU UCCUCA	6643
3796	CAUUUA AGAA GCAU ACCAGAGAAACA X GUACAUUACCUGGUA	6564	AUGCU GAU UAAAUG	6644
3948	GACCCC AGAA GUUU ACCAGAGAAACA X GUACAUUACCUGGUA	6565	AAACU GAU GGGGUC	6645
4121	UUCAGA AGAA GGGC ACCAGAGAAACA X GUACAUUACCUGGUA	6566	GCCCU GUA UCUGAA	6646
4216	GUGCCA AGAA GUGG ACCAGAGAAACA X GUACAUUACCUGGUA	6567	CCACU GCC UGGCAC	6647

Position	RZ	Seq. I.D. No.	Substrate	Seq. I.D. No.
4348	UAUCCA AGAA GAGC ACCAGAGAAACA X GUACAUUACCUGGUA	6568	GCUCC GUU UGGAUA	6648

Claims

1. An enzymatic nucleic acid molecule with RNA cleaving activity, wherein said enzymatic nucleic acid molecule specifically cleaves RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene.

2. An enzymatic nucleic acid molecule with RNA cleaving activity, wherein said enzymatic nucleic acid molecules specifically cleaves RNA encoded by an integrin subunit beta 3 (β3) gene.

3. An enzymatic nucleic acid molecule with RNA cleaving activity, wherein said enzymatic nucleic acid molecules cleaves RNA encoded by a integrin subunit alpha 6 (α6) gene.

4. An enzymatic nucleic acid molecule with RNA cleaving activity, wherein said enzymatic nucleic acid molecules cleaves RNA encoded by a Tie-2 gene.

5. The enzymatic nucleic acid molecule of any of claims 1-4, wherein said enzymatic nucleic acid molecule is in a hammerhead configuration.

6. The enzymatic nucleic acid molecule of claim 5, wherein said enzymatic nucleic acid molecule comprises a stem II region of length greater than or equal to 2 base pairs.

7. The enzymatic nucleic acid molecule of any of claims 1-4, wherein said enzymatic nucleic acid molecule is in a hairpin configuration.

8. The enzymatic nucleic acid molecule of any of claims 1-4, wherein said enzymatic nucleic acid is in a hepatitis delta virus, group I intron, group II intron, VS nucleic acid or RNase P nucleic acid configuration.

9. The enzymatic nucleic acid molecule of any of claims 1-4, wherein said enzymatic nucleic molecule is a DNAzyme.

10. The enzymatic nucleic acid of claim 7, wherein said enzymatic nucleic acid molecule comprises a stem II region of length between three and seven base-pairs.

11. The enzymatic nucleic acid molecule of any of claims 1-4, wherein said enzymatic nucleic acid molecule comprises between 12 and 100 bases complementary to said RNA.

12. The enzymatic nucleic acid molecule of any of claims 1-4, wherein said enzymatic nucleic acid molecule comprises between 14 and 24 bases complementary to said mRNA.

13. The enzymatic nucleic acid molecule of claim 5 wherein said enzymatic nucleic acid molecule consists essentially of any sequence defined as Seq. I.D. Nos 1-393, 911-1611, 2449-3587, and 4915-5701.

14 The enzymatic nucleic acid molecule of claim 7, wherein said enzymatic nucleic acid molecule consists essentially of any sequence defined as Seq. ID 787-848, 2313-2380, 4727-4820 and 6489-6568.

15. A mammalian cell including an enzymatic nucleic acid molecule of any of claims 1-4.

16. The mammalian cell of claim 15, wherein said mammalian cell is a human cell.

17. An expression vector comprising nucleic acid sequence encoding at least one enzymatic nucleic acid molecule of any of claims 1-4 in a manner which allows expression of that enzymatic nucleic acid molecule.

18. A mammalian cell including an expression vector of claim 17.

19. The mammalian cell of claim 18, wherein said mammalian cell is a human cell.

20. A method for treatment of cancer, diabetic retinopathy, age related macular degeneration (ARMD), inflammation, and arthritis comprising the step of administering to a patient an enzymatic nucleic acid molecule of any of claims 1-4.

21. A method for treatment of cancer comprising the step of administering to a patient, an expression vector of claim 17.

22. A method for the treatment of cancer, diabetic retinopathy, age related macular degeneration (ARMD), inflammation, and arthritis comprising the step of administering to a patient an expression vector of claim 17.

23. A method for treatment of cancer comprising the steps of: a) isolating cells from a patient; b) administering to said cells an enzymatic nucleic acid molecule of any of claims 1-4; and c) introducing said cells back into said patient.

24. A pharmaceutical composition comprising the enzymatic nucleic acid molecule of any of claims 1-4.

25. A method of treatment of a patient having a condition associated with an elevated level of aryl hydrocarbon nuclear transporter (ARNT), comprising the step of administration to said patient an enzymatic nucleic acid molecule of claim 1.

26. A method of treatment of a patient having a condition associated with the level of Tie-2 comprising the step of administration to said patient an enzymatic nucleic acid molecule of claim 2.

27. A method of treatment of a patient having a condition associated with the level of integrin subunit alpha 6, comprising the step of administration to said patient an enzymatic nucleic acid molecule of claim 3.

28. A method of treatment of a patient having a condition associated with the level of integrin subunit beta 3 comprising the step of administration to said patient an enzymatic nucleic acid molecule of claim 4.

29. A method of treatment of a patient having a condition associated with the level of aryl hydrocarbon nuclear transporter (ARNT), comprising the steps of: (a)contacting cells of said patient with an enzymatic nucleic acid molecule of claim 1; and (b) administering to said patient one or more additional drugs.

30. A method of treatment of a patient having a condition associated with the level of Tie-2, comprising the steps of: (a)contacting cells of said patient with an enzymatic nucleic acid molecule of claim 2; and (b)

administering to said patient one or more additional drugs.

31. A method of treatment of a patient having a condition associated with the level of integrin subunit alpha 6, comprising the steps of: (a)contacting cells of said patient with an enzymatic nucleic acid molecule of claim 3; and (b) administering to said patient one or more additional drugs.

32. A method of treatment of a patient having a condition associated with the level of integrin subunit beta 3, comprising the steps of: (a)contacting cells of said patient with an enzymatic nucleic acid molecule of claim 4; and (b) administering to said patient one or more additional drugs.

33. The enzymatic nucleic acid molecule of claim 5, wherein said enzymatic nucleic acid molecule comprises at least five ribose residues, phosphorothioate linkages in at least three of the 5' terminal nucleotides, a 2'-*C*-allyl modification at position No. 4 of said nucleic acid, at least ten 2'-*O*-methyl modifications, and a 3′- end modification.

34. The enzymatic nucleic acid of claim 33, wherein said enzymatic nucleic acid comprises a 3'-3' linked inverted ribose moiety at said 3' end.

35. The enzymatic nucleic acid molecule of claim 5, wherein said enzymatic nucleic acid molecule comprises at least five ribose residues; phosphorothioate linkages at least three of the 5' terminal nucleotides 2'-amino modification at position No. 4 and/or at position No. 7 of

said enzymatic nucleic acid molecule; at least ten 2'-*O*-methyl modifications; and a 3′- end modification.

36. The enzymatic nucleic acid molecule of claim 5, wherein said enzymatic nucleic acid molecule comprises at least five ribose residues; phosphorothioate linkages at least three of the 5' terminal nucleotides, abasic substitution at position No. 4 and/or at position No. 7 of said enzymatic nucleic acid molecule; at least ten 2'-*O*-methyl modifications; comprises a 3'-end modification.

37. The enzymatic nucleic acid molecule of claim 5, wherein said enzymatic nucleic acid molecule comprises of at least five ribose residues; phosphorothioate linkages at least three of the 5' terminal nucleotides; a 6-methyl uridine substitution at position No. 4 and/or at position No. 7 of said enzymatic nucleic acid molecule; at least ten 2'-*O*-methyl modifications; and comprises a 3' end modification.

38. A method for modulating expression of ARNT gene in a mammalian cell comprising the step of administering to said cell an enzymatic nucleic acid molecule of claim 1.

39. A method for modulating expression of integrin subunit beta 3 in a mammalian cell comprising the step of administering to said cell an enzymatic nucleic acid molecule of claim 2.

40. A method for modulating expression of integrin subunit alpha 6 in a mammalian cell comprising the step of administering to said cell an enzymatic nucleic acid molecule of claim 3.

41. A method for modulating expression of Tie-2 in a mammalian cell comprising the step of administering to said cell an enzymatic nucleic acid molecule of claim 4.

42. A method of cleaving an ARNT RNA molecule comprising the step of, contacting the enzymatic nucleic acid molecule of claim 1 with said ARNT RNA molecule under conditions suitable for the cleavage of said ARNT RNA molecule.

43. A method of cleaving a integrin subunit beta 3 RNA molecule comprising the step of, contacting the enzymatic nucleic acid molecule of claim 2 with said integrin subunit beta 3 RNA molecule under conditions suitable for the cleavage of said integrin subunit beta 3 RNA molecule.

44. A method of cleaving a integrin subunit alpha 6 RNA molecule comprising the step of, contacting the enzymatic nucleic acid molecule of claim 3 with said integrin subunit alpha 6 RNA molecule under conditions suitable for the cleavage of said integrin subunit alpha 6 RNA molecule.

45. A method of cleaving a Tie-2 RNA molecule comprising the step of, contacting the enzymatic nucleic acid molecule of claim 4 with said Tie-2 RNA molecule under conditions suitable for the cleavage of said Tie-2 RNA molecule.

46. The method of any of claims 42-45, wherein said cleavage is carried out in the presence of a divalent cation.

47. The method of claim 46, wherein said divalent cation is Mg^{2+}.

48. The enzymatic nucleic acid molecule of any of claims 1-4, wherein said enzymatic nucleic acid molecule is chemically synthesized.

49. The expression vector of claim 17, wherein said expression vector comprises:

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.

50. The expression vector of claim 17, wherein said 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.

51. The expression vector of claim 17, wherein said 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.

52. The expression vector of claim 18, wherein said 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.

53. The enzymatic nucleic acid molecule of claim 1, wherein said enzymatic nucleic acid comprises sequences that are complementary to any of sequences defined as Seq ID Nos **394-786 and 849-910.**

54. The enzymatic nucleic acid molecule of claim 2, wherein said enzymatic nucleic acid comprises sequences that are complementary to any of sequences defined as Seq ID Nos **5702-6488 and 6569-6648.**

55. The enzymatic nucleic acid molecule of claim 3, wherein said enzymatic nucleic acid comprises sequences

that are complementary to any of sequences defined as Seq ID Nos **3588-4726 and 4821-4914**.

56. The enzymatic nucleic acid molecule of claim 4, wherein said enzymatic nucleic acid comprises sequences that are complementary to any of sequences defined as Seq ID Nos **1612-2312 and 2381-2448**.

57. The enzymatic nucleic acid molecule of any of claims 1-4, wherein said enzymatic nucleic acid comprises at least one 2′-sugar modification.

58. The enzymatic nucleic acid molecule of any of claims 1-4, wherein said enzymatic nucleic acid comprises at least one nucleic acid base modification.

59. The enzymatic nucleic acid molecule of any of claims 1-4, wherein said enzymatic nucleic acid comprises at least one phosphorothioate modification.

Figure 1: Ribozyme Motifs

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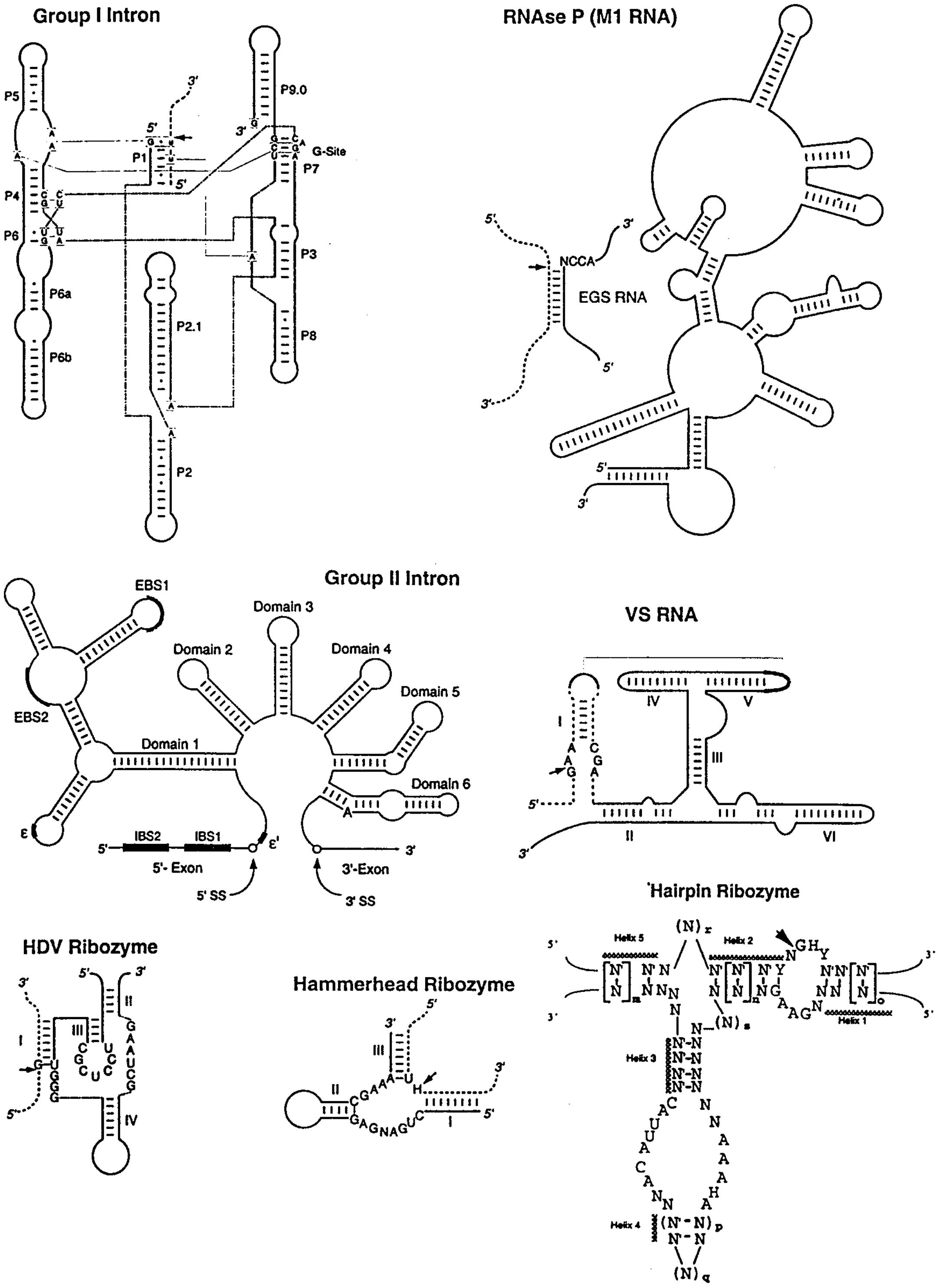

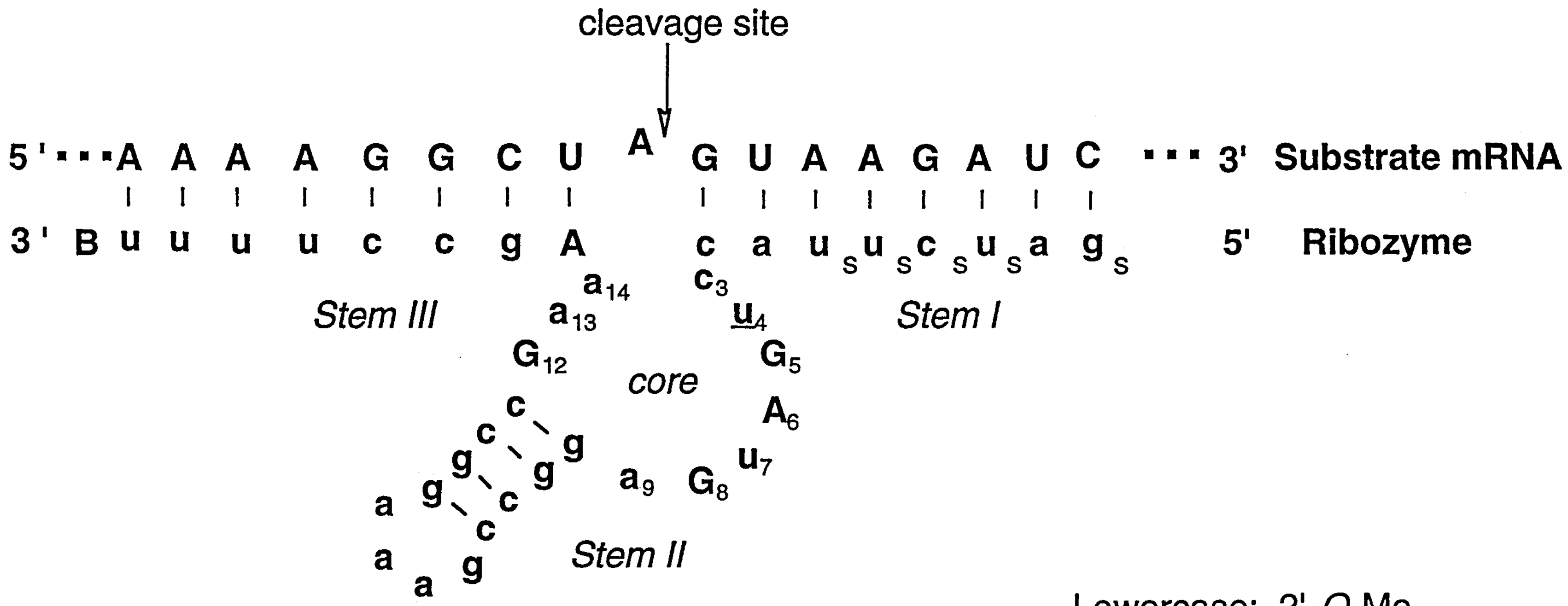

Lowercase: 2'-*O*-Me
Uppercase: ribonucleotide
B: inverted deoxy abasic
s: phosphorothioate
<u>u</u>: c-allyl modification

Figure (2). Structure of ribozyme directed to Tie-2 position 428 and its substrate RNA sequence

SEQUENCE LISTING

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Jaiswal, Sudhir K.

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Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr
 30                  35                  40                  45

tgc agt gcc agc tca agt gta agt tac atg cac tgg ttc cag cag aag      193
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys
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Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr
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Cys His Gln Arg Thr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys
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ctt gag atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg      433
Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
                130                 135                 140

cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg      481
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
            145                 150                 155

ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat      529
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
        160                 165                 170

aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac      577
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
    175                 180                 185

agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa      625
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
190                 195                 200                 205

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Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
                210                 215                 220

ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt          718
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Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln
            100                 105                 110
Arg Thr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
        115                 120                 125
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
    130                 135                 140
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145                 150                 155                 160
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
                165                 170                 175
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
            180                 185                 190
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
        195                 200                 205
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
    210                 215                 220
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235

      <210> 3
      <211> 1476
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (24)...(1472)

      <400> 3
ggatctatcg attcccgggt acc atg gga tct aaa cct ttt ttg tct ctt ctt     53
                          Met Gly Ser Lys Pro Phe Leu Ser Leu Leu
                           1               5                   10

tca ttg tca ttg ctt ttg ttt aca tct act agt ttg gca ggg gtc cag      101
Ser Leu Ser Leu Leu Leu Phe Thr Ser Thr Ser Leu Ala Gly Val Gln
                 15                  20                  25

ctt cag cag tca gga cct gac ctg gtg aaa cct ggg gcc tca gtg aag      149
Leu Gln Gln Ser Gly Pro Asp Leu Val Lys Pro Gly Ala Ser Val Lys
             30                  35                  40

ata tcc tgc aag gct tct gga tac aca ttc act gac tac aac ata cac      197
Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Asn Ile His
         45                  50                  55

tgg gtg aag cag agc cgt gga aag agc ctt gag tgg att gga tat att      245
Trp Val Lys Gln Ser Arg Gly Lys Ser Leu Glu Trp Ile Gly Tyr Ile
     60                  65                  70

tat cct tac aat ggt aat act tac tac aac cag aag ttc aag aac aag      293
Tyr Pro Tyr Asn Gly Asn Thr Tyr Tyr Asn Gln Lys Phe Lys Asn Lys
 75                  80                  85                  90

gcc aca ttg act gta gac aat tcc tcc acc tca gcc tac atg gag ctc      341
```

```
Ala Thr Leu Thr Val Asp Asn Ser Ser Thr Ser Ala Tyr Met Glu Leu
                 95                 100                 105

cgc agc ctg aca tct gag gac tct gca gtc tat tac tgt gca acc tac       389
Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Thr Tyr
            110                 115                 120

ttt gac tac tgg ggc caa ggc acc act ctc aca gtg agc tca gca tcc       437
Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser
        125                 130                 135

ccg acc agc ccc aag gtc ttc ccg ctg agc ctc gac agc acc ccc caa       485
Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Asp Ser Thr Pro Gln
    140                 145                 150

gat ggg aac gtg gtc gtc gca tgc ctg gtc cag ggc ttc ttc ccc cag       533
Asp Gly Asn Val Val Val Ala Cys Leu Val Gln Gly Phe Phe Pro Gln
155                 160                 165                 170

gag cca ctc agt gtg acc tgg agc gaa agc gga cag aac gtg acc gcc       581
Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Asn Val Thr Ala
                175                 180                 185

aga aac ttc cca cct agc cag gat gcc tcc ggg gac ctg tac acc acg       629
Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr Thr Thr
            190                 195                 200

agc agc cag ctg acc ctg ccg gcc aca cag tgc cca gac ggc aag tcc       677
Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Pro Asp Gly Lys Ser
        205                 210                 215

gtg aca tgc cac gtg aag cac tac acg aat tcc agc cag gat gtg act       725
Val Thr Cys His Val Lys His Tyr Thr Asn Ser Ser Gln Asp Val Thr
    220                 225                 230

gtg ccc tgc cga gtt ccc cca cct ccc cca tgc tgc cac ccc cga ctg       773
Val Pro Cys Arg Val Pro Pro Pro Pro Pro Cys Cys His Pro Arg Leu
235                 240                 245                 250

tcg ctg cac cga ccg gcc ctc gag gac ctg ctc tta ggt tca gaa gcg       821
Ser Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala
                255                 260                 265

aac ctc acg tgc aca ctg acc ggc ctg aga gat gcc tct ggt gcc acc       869
Asn Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Ala Thr
            270                 275                 280

ttc acc tgg acg ccc tca agt ggg aag agc gct gtt caa gga cca cct       917
Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro
        285                 290                 295

gag cgt gac ctc tgt ggc tgc tac agc gtg tcc aga gta ctt cct ggc       965
Glu Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Arg Val Leu Pro Gly
    300                 305                 310
```

```
tgt gcc cag cca tgg aac cat ggg gag acc ttc acc tgc act gct gcc        1013
Cys Ala Gln Pro Trp Asn His Gly Glu Thr Phe Thr Cys Thr Ala Ala
315                 320                 325                 330

cac ccc gag ttg aag acc cca cta acc gcc aac atc aca aaa tcc gga        1061
His Pro Glu Leu Lys Thr Pro Leu Thr Ala Asn Ile Thr Lys Ser Gly
                335                 340                 345

aac aca ttc cgg ccc gag gtc cac ctg ctg ccg ccg ccg tcg gag gag        1109
Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu
            350                 355                 360

ctg gcc ctg aac gag ctg gtg acg ctg acg tgc ctg gca cgt ggc ttc        1157
Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe
        365                 370                 375

agc ccc aag gat gtg ctg gtt cgc tgg ctg cag ggg tca cag gag ctg        1205
Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu
    380                 385                 390

ccc cgc gag aag tac ctg act tgg gca tcc cgg cag gag ccc agc cag        1253
Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln
395                 400                 405                 410

ggc acc acc acc tat gct gtg acc agc ata ctg cgc gtg gca gcc gag        1301
Gly Thr Thr Thr Tyr Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu
                415                 420                 425

gac tgg aag aag ggg gag acc ttc tcc tgc atg gtg ggc cac gag gcc        1349
Asp Trp Lys Lys Gly Glu Thr Phe Ser Cys Met Val Gly His Glu Ala
            430                 435                 440

ctg ccg ctg gcc ttc aca cag aag acc atc gac cgc ttg gcg ggt aaa        1397
Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys
        445                 450                 455

ccc acc cat atc aat gtg tct gtt gtc atg gcg gag gcg gac ggc acc        1445
Pro Thr His Ile Asn Val Ser Val Val Met Ala Glu Ala Asp Gly Thr
    460                 465                 470

tgc tac aga tct gaa aag gat gaa ctt taga                               1476
Cys Tyr Arg Ser Glu Lys Asp Glu Leu
475                 480


      <210> 4
      <211> 483
      <212> PRT
      <213> Homo sapiens

      <400> 4
Met Gly Ser Lys Pro Phe Leu Ser Leu Leu Ser Leu Ser Leu Leu Leu
 1               5                  10                  15
```

```
Phe Thr Ser Thr Ser Leu Ala Gly Val Gln Leu Gln Gln Ser Gly Pro
            20                  25                  30
Asp Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser
        35                  40                  45
Gly Tyr Thr Phe Thr Asp Tyr Asn Ile His Trp Val Lys Gln Ser Arg
    50                  55                  60
Gly Lys Ser Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn
65                  70                  75                  80
Thr Tyr Tyr Asn Gln Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp
                85                  90                  95
Asn Ser Ser Thr Ser Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu
            100                 105                 110
Asp Ser Ala Val Tyr Tyr Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln
        115                 120                 125
Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Pro Thr Ser Pro Lys Val
    130                 135                 140
Phe Pro Leu Ser Leu Asp Ser Thr Pro Gln Asp Gly Asn Val Val Val
145                 150                 155                 160
Ala Cys Leu Val Gln Gly Phe Phe Pro Gln Glu Pro Leu Ser Val Thr
                165                 170                 175
Trp Ser Glu Ser Gly Gln Asn Val Thr Ala Arg Asn Phe Pro Pro Ser
            180                 185                 190
Gln Asp Ala Ser Gly Asp Leu Tyr Thr Thr Ser Ser Gln Leu Thr Leu
        195                 200                 205
Pro Ala Thr Gln Cys Pro Asp Gly Lys Ser Val Thr Cys His Val Lys
    210                 215                 220
His Tyr Thr Asn Ser Ser Gln Asp Val Thr Val Pro Cys Arg Val Pro
225                 230                 235                 240
Pro Pro Pro Pro Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala
                245                 250                 255
Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn Leu Thr Cys Thr Leu
            260                 265                 270
Thr Gly Leu Arg Asp Ala Ser Gly Ala Thr Phe Thr Trp Thr Pro Ser
        275                 280                 285
Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Glu Arg Asp Leu Cys Gly
    290                 295                 300
Cys Tyr Ser Val Ser Arg Val Leu Pro Gly Cys Ala Gln Pro Trp Asn
305                 310                 315                 320
His Gly Glu Thr Phe Thr Cys Thr Ala Ala His Pro Glu Leu Lys Thr
                325                 330                 335
Pro Leu Thr Ala Asn Ile Thr Lys Ser Gly Asn Thr Phe Arg Pro Glu
            340                 345                 350
Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn Glu Leu
        355                 360                 365
Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp Val Leu
    370                 375                 380
Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu
385                 390                 395                 400
Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr Tyr Ala
                405                 410                 415
Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys Gly Glu
            420                 425                 430
Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala Phe Thr
        435                 440                 445
```

```
Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro Thr His Ile Asn Val
    450                 455                 460
Ser Val Val Met Ala Glu Ala Asp Gly Thr Cys Tyr Arg Ser Glu Lys
465                 470                 475                 480
Asp Glu Leu


      <210> 5
      <211> 504
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (25)...(501)

      <400> 5
aggatctatc gattcccggg tacc atg gag aac cat ttg ctt ttc tgg gga        51
                           Met Glu Asn His Leu Leu Phe Trp Gly
                            1               5

gtc ctg gcg gtt ttt att aag gct gtt cat gtg aaa gcc caa gaa gat       99
Val Leu Ala Val Phe Ile Lys Ala Val His Val Lys Ala Gln Glu Asp
 10                  15                  20                  25

gaa agg att gtt ctt gtt gac aac aaa tgt aag tgt gcc cgg att act      147
Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys Cys Ala Arg Ile Thr
                 30                  35                  40

tcc agg atc atc cgt tct tcc gaa gat cct aat gag gac att gtg gag      195
Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn Glu Asp Ile Val Glu
             45                  50                  55

aga aac atc cga att att gtt cct ctg aac aac agg gag aat atc tct      243
Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg Glu Asn Ile Ser
         60                  65                  70

gat ccc acc tca cca ttg aga acc aga ttt gtg tac cat ttg tct gac      291
Asp Pro Thr Ser Pro Leu Arg Thr Arg Phe Val Tyr His Leu Ser Asp
     75                  80                  85

ctc tgt aaa aaa tgt gat cct aca gaa gtg gag ctg gat aat cag ata      339
Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu Asp Asn Gln Ile
 90                  95                 100                 105

gtt act gct acc cag agc aat atc tgt gat gaa gac agt gct aca gag      387
Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp Ser Ala Thr Glu
                110                 115                 120

acc tgc tac act tat gac aga aac aag tgc tac aca gct gtg gtc cca      435
Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Ala Val Val Pro
            125                 130                 135

ctc gta tat ggt ggt gag acc aaa atg gtg gaa aca gcc tta acc cca      483
```

```
Leu Val Tyr Gly Gly Glu Thr Lys Met Val Glu Thr Ala Leu Thr Pro
        140                 145                 150

gat gcc tgc tat cct gac tga                                         504
Asp Ala Cys Tyr Pro Asp
    155


      <210> 6
      <211> 159
      <212> PRT
      <213> Homo sapiens

      <400> 6
Met Glu Asn His Leu Leu Phe Trp Gly Val Leu Ala Val Phe Ile Lys
 1               5                  10                  15
Ala Val His Val Lys Ala Gln Glu Asp Glu Arg Ile Val Leu Val Asp
            20                  25                  30
Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser
        35                  40                  45
Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val
    50                  55                  60
Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg
65                  70                  75                  80
Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro
                85                  90                  95
Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn
            100                 105                 110
Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg
        115                 120                 125
Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr
    130                 135                 140
Lys Met Val Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp
145                 150                 155

      <210> 7
      <211> 1841
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (18)...(1838)

      <400> 7
gtcgattccc gggtacc atg gtg ctc ttc gtg ctc acc tgc ctg ctg gcg      50
                   Met Val Leu Phe Val Leu Thr Cys Leu Leu Ala
                    1               5                  10

gtc ttc cca gcc atc tcc acg aag agt ccc ata ttt ggt ccc gag gag     98
Val Phe Pro Ala Ile Ser Thr Lys Ser Pro Ile Phe Gly Pro Glu Glu
            15                  20                  25

gtg aat agt gtg gaa ggt aac tca gtg tcc atc acg tgc tac tac cca    146
```

```
Val Asn Ser Val Glu Gly Asn Ser Val Ser Ile Thr Cys Tyr Tyr Pro
         30                  35                  40

ccc acc tct gtc aac cgg cac acc cgg aag tac tgg tgc cgg cag gga        194
Pro Thr Ser Val Asn Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly
     45                  50                  55

gct aga ggt ggc tgc ata acc ctc atc tcc tcg gag ggc tac gtc tcc        242
Ala Arg Gly Gly Cys Ile Thr Leu Ile Ser Ser Glu Gly Tyr Val Ser
 60                  65                  70                  75

agc aaa tat gca ggc agg gct aac ctc acc aac ttc ccg gag aac ggc        290
Ser Lys Tyr Ala Gly Arg Ala Asn Leu Thr Asn Phe Pro Glu Asn Gly
                 80                  85                  90

aca ttt gtg gtg aac att gcc cag ctg agc cag gat gac tcc ggg cgc        338
Thr Phe Val Val Asn Ile Ala Gln Leu Ser Gln Asp Asp Ser Gly Arg
             95                 100                 105

tac aag tgt ggc ctg ggc atc aat agc cga ggc ctg tcc ttt gat gtc        386
Tyr Lys Cys Gly Leu Gly Ile Asn Ser Arg Gly Leu Ser Phe Asp Val
        110                 115                 120

agc ctg gag gtc agc cag ggt cct ggg ctc cta aat gac act aaa gtc        434
Ser Leu Glu Val Ser Gln Gly Pro Gly Leu Leu Asn Asp Thr Lys Val
    125                 130                 135

tac aca gtg gac ctg ggc aga acg gtg acc atc aac tgc cct ttc aag        482
Tyr Thr Val Asp Leu Gly Arg Thr Val Thr Ile Asn Cys Pro Phe Lys
140                 145                 150                 155

act gag aat gct caa aag agg aag tcc ttg tac aag cag ata ggc ctg        530
Thr Glu Asn Ala Gln Lys Arg Lys Ser Leu Tyr Lys Gln Ile Gly Leu
                160                 165                 170

tac cct gtg ctg gtc atc gac tcc agt ggt tat gtg aat ccc aac tat        578
Tyr Pro Val Leu Val Ile Asp Ser Ser Gly Tyr Val Asn Pro Asn Tyr
            175                 180                 185

aca gga aga ata cgc ctt gat att cag ggt act ggc cag tta ctg ttc        626
Thr Gly Arg Ile Arg Leu Asp Ile Gln Gly Thr Gly Gln Leu Leu Phe
        190                 195                 200

agc gtt gtc atc aac caa ctc agg ctc agc gat gct ggg cag tat ctc        674
Ser Val Val Ile Asn Gln Leu Arg Leu Ser Asp Ala Gly Gln Tyr Leu
    205                 210                 215

tgc cag gct ggg gat gat tcc aat agt aat aag aag aat gct gac ctc        722
Cys Gln Ala Gly Asp Asp Ser Asn Ser Asn Lys Lys Asn Ala Asp Leu
220                 225                 230                 235

caa gtg cta aag ccc gag ccc gag ctg gtt tat gaa gac ctg agg ggc        770
Gln Val Leu Lys Pro Glu Pro Glu Leu Val Tyr Glu Asp Leu Arg Gly
                240                 245                 250
```

```
tca gtg acc ttc cac tgt gcc ctg ggc cct gag gtg gca aac gtg gcc       818
Ser Val Thr Phe His Cys Ala Leu Gly Pro Glu Val Ala Asn Val Ala
            255                 260                 265

aaa ttt ctg tgc cga cag agc agt ggg gaa aac tgt gac gtg gtc gtc       866
Lys Phe Leu Cys Arg Gln Ser Ser Gly Glu Asn Cys Asp Val Val Val
        270                 275                 280

aac acc ctg ggg aag agg gcc cca gcc ttt gag ggc agg atc ctg ctc       914
Asn Thr Leu Gly Lys Arg Ala Pro Ala Phe Glu Gly Arg Ile Leu Leu
    285                 290                 295

aac ccc cag gac aag gat ggc tca ttc agt gtg gtg atc aca ggc ctg       962
Asn Pro Gln Asp Lys Asp Gly Ser Phe Ser Val Val Ile Thr Gly Leu
300                 305                 310                 315

agg aag gag gat gca ggg cgc tac ctg tgt gga gcc cat tcg gat ggt      1010
Arg Lys Glu Asp Ala Gly Arg Tyr Leu Cys Gly Ala His Ser Asp Gly
                320                 325                 330

cag ctg cag gaa ggc tcg cct atc cag gcc tgg caa ctc ttc gtc aat      1058
Gln Leu Gln Glu Gly Ser Pro Ile Gln Ala Trp Gln Leu Phe Val Asn
            335                 340                 345

gag gag tcc acg att ccc cgc agc ccc act gtg gtg aag ggg gtg gca      1106
Glu Glu Ser Thr Ile Pro Arg Ser Pro Thr Val Val Lys Gly Val Ala
        350                 355                 360

gga agc tct gtg gcc gtg ctc tgc ccc tac aac cgt aag gaa agc aaa      1154
Gly Ser Ser Val Ala Val Leu Cys Pro Tyr Asn Arg Lys Glu Ser Lys
    365                 370                 375

agc atc aag tac tgg tgt ctc tgg gaa ggg gcc cag aat ggc cgc tgc      1202
Ser Ile Lys Tyr Trp Cys Leu Trp Glu Gly Ala Gln Asn Gly Arg Cys
380                 385                 390                 395

ccc ctg ctg gtg gac agc gag ggg tgg gtt aag gcc cag tac gag ggc      1250
Pro Leu Leu Val Asp Ser Glu Gly Trp Val Lys Ala Gln Tyr Glu Gly
                400                 405                 410

cgc ctc tcc ctg ctg gag gag cca ggc aac ggc acc ttc act gtc atc      1298
Arg Leu Ser Leu Leu Glu Glu Pro Gly Asn Gly Thr Phe Thr Val Ile
            415                 420                 425

ctc aac cag ctc acc agc cgg gac gcc ggc ttc tac tgg tgt ctg acc      1346
Leu Asn Gln Leu Thr Ser Arg Asp Ala Gly Phe Tyr Trp Cys Leu Thr
        430                 435                 440

aac ggc gat act ctc tgg agg acc acc gtg gag atc aag att atc gaa      1394
Asn Gly Asp Thr Leu Trp Arg Thr Thr Val Glu Ile Lys Ile Ile Glu
    445                 450                 455

gga gaa cca aac ctc aag gtt ccc ggg aat gtc acg gct gtg ctg gga      1442
```

```
Gly Glu Pro Asn Leu Lys Val Pro Gly Asn Val Thr Ala Val Leu Gly
460                 465                 470                 475

gag act ctc aag gtc ccc tgt cac ttt cca tgc aaa ttc tcc tcg tac       1490
Glu Thr Leu Lys Val Pro Cys His Phe Pro Cys Lys Phe Ser Ser Tyr
                480                 485                 490

gag aaa tac tgg tgc aag tgg aat aac acg ggc tgc cag gcc ctg ccc       1538
Glu Lys Tyr Trp Cys Lys Trp Asn Asn Thr Gly Cys Gln Ala Leu Pro
            495                 500                 505

agc caa gac gaa ggc ccc agc aag gcc ttc gtg aac tgt gac gag aac       1586
Ser Gln Asp Glu Gly Pro Ser Lys Ala Phe Val Asn Cys Asp Glu Asn
        510                 515                 520

agc cgg ctt gtc tcc ctg acc ctg aac ctg gtg acc agg gct gat gag       1634
Ser Arg Leu Val Ser Leu Thr Leu Asn Leu Val Thr Arg Ala Asp Glu
    525                 530                 535

ggc tgg tac tgg tgt gga gtg aag cag ggc cac ttc tat gga gag act       1682
Gly Trp Tyr Trp Cys Gly Val Lys Gln Gly His Phe Tyr Gly Glu Thr
540                 545                 550                 555

gca gcc gtc tat gtg gca gtt gaa gag agg aag gca gcg ggg tcc cgc       1730
Ala Ala Val Tyr Val Ala Val Glu Glu Arg Lys Ala Ala Gly Ser Arg
                560                 565                 570

gat gtc agc cta gcg aag gca gac gct gct cct gat gag aag gtg cta       1778
Asp Val Ser Leu Ala Lys Ala Asp Ala Ala Pro Asp Glu Lys Val Leu
            575                 580                 585

gac tct ggt ttt cgg gag att gag aac aaa gcc att cag gat ccc agg       1826
Asp Ser Gly Phe Arg Glu Ile Glu Asn Lys Ala Ile Gln Asp Pro Arg
        590                 595                 600

ctt ttt gca gag tga                                                   1841
Leu Phe Ala Glu
    605


      <210> 8
      <211> 607
      <212> PRT
      <213> Homo sapiens

      <400> 8
Met Val Leu Phe Val Leu Thr Cys Leu Leu Ala Val Phe Pro Ala Ile
 1              5                   10                  15
Ser Thr Lys Ser Pro Ile Phe Gly Pro Glu Glu Val Asn Ser Val Glu
            20                  25                  30
Gly Asn Ser Val Ser Ile Thr Cys Tyr Tyr Pro Pro Thr Ser Val Asn
        35                  40                  45
Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Arg Gly Gly Cys
    50                  55                  60
```

```
Ile Thr Leu Ile Ser Ser Glu Gly Tyr Val Ser Ser Lys Tyr Ala Gly
65                  70                  75                  80
Arg Ala Asn Leu Thr Asn Phe Pro Glu Asn Gly Thr Phe Val Val Asn
                85                  90                  95
Ile Ala Gln Leu Ser Gln Asp Asp Ser Gly Arg Tyr Lys Cys Gly Leu
            100                 105                 110
Gly Ile Asn Ser Arg Gly Leu Ser Phe Asp Val Ser Leu Glu Val Ser
        115                 120                 125
Gln Gly Pro Gly Leu Leu Asn Asp Thr Lys Val Tyr Thr Val Asp Leu
    130                 135                 140
Gly Arg Thr Val Thr Ile Asn Cys Pro Phe Lys Thr Glu Asn Ala Gln
145                 150                 155                 160
Lys Arg Lys Ser Leu Tyr Lys Gln Ile Gly Leu Tyr Pro Val Leu Val
                165                 170                 175
Ile Asp Ser Ser Gly Tyr Val Asn Pro Asn Tyr Thr Gly Arg Ile Arg
            180                 185                 190
Leu Asp Ile Gln Gly Thr Gly Gln Leu Leu Phe Ser Val Val Ile Asn
        195                 200                 205
Gln Leu Arg Leu Ser Asp Ala Gly Gln Tyr Leu Cys Gln Ala Gly Asp
    210                 215                 220
Asp Ser Asn Ser Asn Lys Lys Asn Ala Asp Leu Gln Val Leu Lys Pro
225                 230                 235                 240
Glu Pro Glu Leu Val Tyr Glu Asp Leu Arg Gly Ser Val Thr Phe His
                245                 250                 255
Cys Ala Leu Gly Pro Glu Val Ala Asn Val Ala Lys Phe Leu Cys Arg
            260                 265                 270
Gln Ser Ser Gly Glu Asn Cys Asp Val Val Val Asn Thr Leu Gly Lys
        275                 280                 285
Arg Ala Pro Ala Phe Glu Gly Arg Ile Leu Leu Asn Pro Gln Asp Lys
    290                 295                 300
Asp Gly Ser Phe Ser Val Val Ile Thr Gly Leu Arg Lys Glu Asp Ala
305                 310                 315                 320
Gly Arg Tyr Leu Cys Gly Ala His Ser Asp Gly Gln Leu Gln Glu Gly
                325                 330                 335
Ser Pro Ile Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile
            340                 345                 350
Pro Arg Ser Pro Thr Val Val Lys Gly Val Ala Gly Ser Ser Val Ala
        355                 360                 365
Val Leu Cys Pro Tyr Asn Arg Lys Glu Ser Lys Ser Ile Lys Tyr Trp
    370                 375                 380
Cys Leu Trp Glu Gly Ala Gln Asn Gly Arg Cys Pro Leu Leu Val Asp
385                 390                 395                 400
Ser Glu Gly Trp Val Lys Ala Gln Tyr Glu Gly Arg Leu Ser Leu Leu
                405                 410                 415
Glu Glu Pro Gly Asn Gly Thr Phe Thr Val Ile Leu Asn Gln Leu Thr
            420                 425                 430
Ser Arg Asp Ala Gly Phe Tyr Trp Cys Leu Thr Asn Gly Asp Thr Leu
        435                 440                 445
Trp Arg Thr Thr Val Glu Ile Lys Ile Ile Glu Gly Glu Pro Asn Leu
    450                 455                 460
Lys Val Pro Gly Asn Val Thr Ala Val Leu Gly Glu Thr Leu Lys Val
465                 470                 475                 480
Pro Cys His Phe Pro Cys Lys Phe Ser Ser Tyr Glu Lys Tyr Trp Cys
                485                 490                 495
```

```
Lys Trp Asn Asn Thr Gly Cys Gln Ala Leu Pro Ser Gln Asp Glu Gly
            500                 505                 510
Pro Ser Lys Ala Phe Val Asn Cys Asp Glu Asn Ser Arg Leu Val Ser
        515                 520                 525
Leu Thr Leu Asn Leu Val Thr Arg Ala Asp Glu Gly Trp Tyr Trp Cys
    530                 535                 540
Gly Val Lys Gln Gly His Phe Tyr Gly Glu Thr Ala Ala Val Tyr Val
545                 550                 555                 560
Ala Val Glu Glu Arg Lys Ala Ala Gly Ser Arg Asp Val Ser Leu Ala
                565                 570                 575
Lys Ala Asp Ala Ala Pro Asp Glu Lys Val Leu Asp Ser Gly Phe Arg
            580                 585                 590
Glu Ile Glu Asn Lys Ala Ile Gln Asp Pro Arg Leu Phe Ala Glu
        595                 600                 605
```