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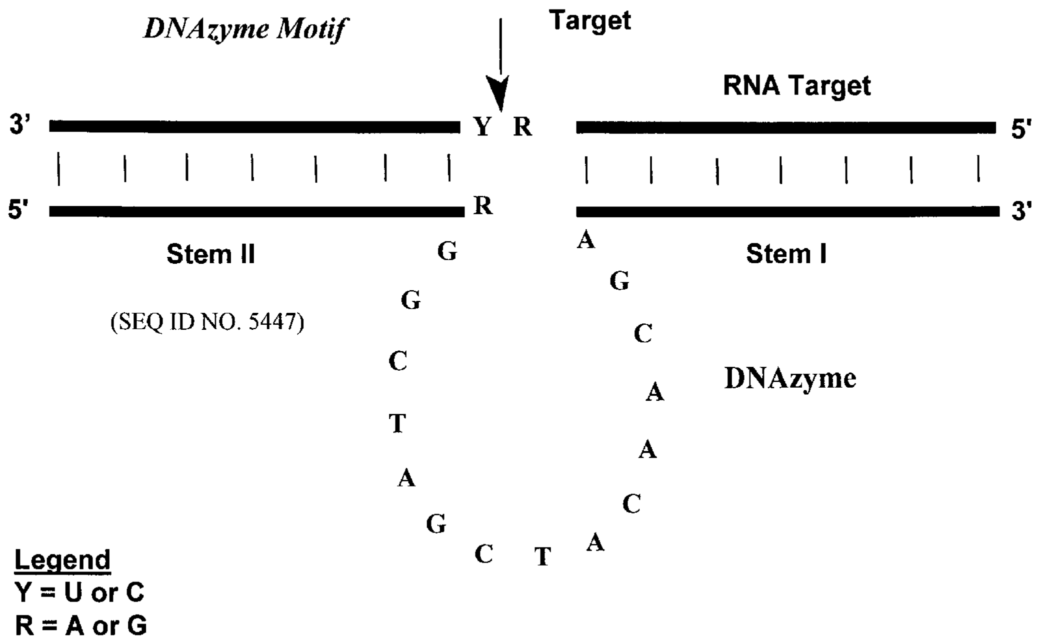
(54) Title: METHOD AND REAGENT FOR THE INHIBITION OF CALCIUM ACTIVATED CHLORIDE CHANNEL-1 (CLCA-1)



(57) **Abstract:** Nucleic acid molecules, including antisense and enzymatic nucleic acid molecules, such as hammerhead ribozymes, DNAzymes, and GeneBlocs, which modulate the expression of calcium activated chloride channels (CLCA1, CLCA2, CLCA3, and CLCA4).

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DESCRIPTION

METHOD AND REAGENT FOR THE INHIBITION OF CALCIUM ACTIVATED CHLORIDE CHANNEL-1 (CLCA-1)

Background Of The Invention

The present invention concerns compounds, compositions, and methods for the study, diagnosis, and treatment of conditions and diseases related to the expression of CLCA (Cl^- Channel Ca^{2+}-Activated) genes.

The following is a brief description of the current understanding of CLCAs. The discussion is not meant to be complete and is provided only for understanding the invention that follows. The summary is not an admission that any of the work described below is prior art to the claimed invention.

CLCA proteins are emerging as a new class of channel proteins that mediate Ca^{2+}-activated Cl^- conductance in a variety of tissues. Members of the CLCA family have been cloned, isolated, and partially characterized from human, bovine, and murine species. These proteins demonstrate a high degree of homology in their size, sequence, and predicted structure yet can vary considerably in tissue distribution. Bovine CLCA1 (bCLCA1 or CaCC) was the first reported CLCA homolog. The bCLCA1 protein, which was isolated from and is exclusively detected in trachial epithelial cells, functions as a Ca^{2+}-activated Cl^- channel (Ran and Benos, 1992, *J. Biol. Chem.*, 267, 3618-3625; Cunningham *et al.*, 1995, *J. Biol. Chem.*, 270, 31016-31026). Another bovine homolog, bovine lung-endothelial cell adhesion molecule-1 (Lu-ECAM-1), appears to have involvement in the preferential metastasis of melanoma cells to the lung. Lu-ECAM-1 shares 92% nucleotide identity to bCLCA1 and is expressed in vascular endothelial cells (Elble *et al.*, 1997, *J. Biol. Chem.*, 272, 27853-27861). It has been shown that Lu-ECAM-1, can mediate the binding of lung-metastatic mouse B16F10 melanoma cells to endothelial cells (Zhu *et al.*, 1992, *J. Clin. Invest.*, 89, 1718-1724), however, due to sequence similarity to bCLCA1, the role of Lu-ECAM-1 as a chloride channel has been suggested (Elble *et al.*, *supra*). The mouse homolog, mCLCA1, appears to have an expression pattern similar to the cystic fibrosis transmembrane conductance regulator (CFTR), with expression seen in various secretory epithelial cells, squamous epithelia, and in some lymphocytes (Gruber *et al.*, 1998, *Histochem. Cell Biol.*, 110, 43-49).

The three human CLCA homologs (hCLCA1, hCLCA2, and hCLCA3) thus far cloned, isolated, and partially characterized, all retain sequence homology, similar cDNA length, and are all located on the short arm of chromosome 1 (1p22-p31). Human CLCA proteins show a restricted pattern of expression in differing secretory tissues. Human CLCA1 was the first reported calcium activated chloride channel in humans. The 31,902-bp hCLCA1 gene is located on chromosome 1p22-p31, contains 14 introns, and is preceded by a canonic promoter region that contains an L1 transposable element. Expression of hCLCA1 is predominant in intestinal basal crypt epithelia and goblet cells. A protein processing model has been proposed for hCLCA1 in which the primary translation product (125-kDa) is cleaved to a 90-kDa and a group of 37- to 41-kDa proteins, the latter apparently representing different glycosylation products of the same polypeptide (Gruber *et al.,* 1998, *Genomics,* 54, 200-214). Transient expression of hCLCA1 cDNA in HEK 293 cells is associated with an increase in whole-cell Ca^{2+}-activated Cl^- conductance that is susceptible to inhibition with anion channel blocking compounds. Cell attached patch recordings of transfected cells in this study revealed single channels with a slope conductance of 13.4 pS (Gruber *et al., supra*).

The hCLCA2 homolog is processed in a similar manner as is hCLCA1, resulting in the formation of a heterodimer consisting of a 90-kDa amino terminal and an approximately 35-kDa carboxy terminal subunit with anchorage to the plasma membrane via four or five transmembrane domains. Expression of hCLCA2 is somewhat less restricted than that of hCLCA1, being expressed from human lung, trachea, and breast tissue (Gruber *et al.,* 1999, *Am. J. Physiol.,* 276, C1261-C1270). Human CLCA2 is expressed in normal breast epithelium but not in breast tumors of different stages of progression, suggesting that hCLCA2 may act as a tumor suppressor in breast cancer (Gruber *et al.,* 1999, *Cancer Res.,* 59, 5488-5491). Human CLCA3 is a truncated, secreted member of the CLCA family which is expressed in numerous tissues including lung, trachea, spleen, thymus, and breast tissue. Unlike hCLCA1 and hCLCA2 which are processed into heterodimers, hCLCA3 mRNA encodes a 37-kDa glycoprotein that corresponds to the N-terminal extracellular domain of its homologs. When hCLCA3 is expressed in HEK 293 or CHO cells, the 37-kDa glycoprotein is secreted (Gruber and Pauli, 1999, *Biochem. Biophys. Acta,* 1444, 418-423).

Holroyd *et al.,* International PCT publication No. WO/9944620, describe a calcium-activated chloride channel that is induced by IL-9.

Summary Of The Invention

The invention features novel nucleic acid-based techniques [e.g., enzymatic nucleic acid molecules (ribozymes), antisense nucleic acids, 2-5A antisense chimeras, triplex DNA, antisense nucleic acids containing RNA cleaving chemical groups] and methods for their use to modulate the expression of CLCA (Cl^- Channel Ca^{2+}-Activated) genes.

In a preferred embodiment, the invention features the use of one or more of the nucleic acid-based techniques independently or in combination to inhibit the expression of the genes encoding hCLCA1, hCLCA2, hCLCA3, and hCLCA4. Specifically, the invention features the use of nucleic acid-based techniques to specifically inhibit the expression of CLCA1 (GenBank accession Nos. NM_001285, AF039400, AF039401, AF127036), CLCA2 (GenBank accession No. NM_006536), CLCA3 (GenBank accession No. NM_004921), and CLCA4 (GenBank accession No. NM_012128) genes. In yet another preferred embodiment, the invention features the inhibition of CLCA1 gene using the nucleic acid-based techniques of the instant invention.

In another preferred embodiment, the invention features the use of an enzymatic nucleic acid molecule, preferably in the hammerhead, NCH (Inozyme), G-cleaver, amberzyme, zinzyme and/or DNAzyme motif, to inhibit the expression of CLCA genes.

By "inhibit" it is meant that the activity of CLCA1 or level of RNAs or equivalent RNAs encoding one or more protein subunits of CLCA1 is reduced below that observed in the absence of the nucleic acid molecules of the invention. In one embodiment, inhibition with enzymatic nucleic acid molecules preferably is below that level observed in the presence of an enzymatically inactive or attenuated molecule that is able to bind to the same site on the target RNA, but is unable to cleave that RNA. In another embodiment, inhibition with antisense oligonucleotides is preferably below that level observed in the presence of, for example, an oligonucleotide with scrambled sequence or with mismatches. In another embodiment, inhibition of CLCA1 genes with the nucleic acid molecule of the instant invention is greater than in the presence of the nucleic acid molecule than in its absence, or the presence of a control, irrelevant, or non-inhibitory oligonucleotide.

By "enzymatic nucleic acid molecule" it is meant a nucleic acid molecule which has complementarity in a substrate binding region to a specified gene target, and also has an enzymatic activity which is active to specifically cleave target RNA. That is, the enzymatic nucleic acid molecule is able to intermolecularly cleave RNA and thereby inactivate a target RNA molecule. These complementary regions allow sufficient hybridization of the enzymatic nucleic acid molecule to the target RNA and thus permit cleavage. One hundred percent 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, aptazyme or aptamer-binding ribozyme, regulatable ribozyme, 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 "nucleic acid molecule" as used herein is meant a molecule having nucleotides. The nucleic acid can be single, double, or multiple stranded and may comprise modified or unmodified nucleotides or non-nucleotides or various mixtures and combinations thereof.

By "enzymatic portion" or "catalytic domain" is meant that portion/region of the enzymatic nucleic acid molecule essential for cleavage of a nucleic acid substrate (for example, see **Figures 1-4**).

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. Examples of such arms are shown generally in **Figures 1-4**. 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 and of sufficient length to stably interact with the target RNA; 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 "NCH" or "Inozyme" motif is meant, an enzymatic nucleic acid molecule comprising a motif as described in Ludwig *et al.*, USSN No. 09/406,643, filed September 27, 1999, entitled "COMPOSITIONS HAVING RNA CLEAVING ACTIVITY", and International PCT publication Nos. WO 98/58058 and WO 98/58057, all incorporated by reference herein in their entirety including the drawings.

By "G-cleaver" motif is meant, an enzymatic nucleic acid molecule comprising a motif as described in Eckstein *et al.*, International PCT publication No. WO 99/16871, incorporated by reference herein in its entirety including the drawings.

By "zinzyme" motif is meant, a class II enzymatic nucleic acid molecule comprising a motif as described in Beigelman *et al.*, International PCT publication No. WO 99/55857, incorporated by reference herein in its entirety including the drawings. Zinzymes represent a non-limiting example of an enzymatic nucleic acid molecule that does not require a ribonucleotide (2'-OH) group within its own nucleic acid sequence for activity.

By "amberzyme" motif is meant, a class I enzymatic nucleic acid molecule comprising a motif as described in Beigelman *et al.*, International PCT publication No. WO 99/55857, incorporated by reference herein in its entirety including the drawings. Amberzymes represent a non-limiting example of an enzymatic nucleic acid molecule that does not require a ribonucleotide (2'-OH) group within its own nucleic acid sequence for activity.

By 'DNAzyme' is meant, an enzymatic nucleic acid molecule that does not require the presence of a ribonucleotide (2'-OH) group within the DNAzyme molecule for its activity. In particular embodiments the enzymatic nucleic acid molecule may have an attached linker(s) or other attached or associated groups, moieties, or chains containing one or more nucleotides with 2'-OH groups.

DNAzyme can be synthesized chemically or expressed endogenously *in vivo,* by means of a single stranded DNA vector or equivalent thereof.

By "sufficient length" is meant an oligonucleotide of greater than or equal to 3 nucleotides that is of a length great enough to provide the intended function under the expected condition. For example, for binding arms of enzymatic nucleic acid "sufficient length" means that the binding arm sequence is long enough to provide stable binding to a target site under the expected binding conditions. Preferably, the binding arms are not so long as to prevent useful turnover.

By "stably interact" is meant, interaction of the oligonucleotides with target nucleic acid (*e.g.,* by forming hydrogen bonds with complementary nucleotides in the target under physiological conditions).

By "equivalent" RNA to CLCA1 is meant to include those naturally occurring RNA molecules having homology (partial or complete) to CLCA1 proteins or encoding for proteins with similar function as CLCA1 in various organisms, including human, rodent, primate, rabbit, pig, protozoans, fungi, plants, and other microorganisms and parasites. 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 "antisense nucleic acid", it is meant a non-enzymatic nucleic acid molecule that binds to target RNA by means of RNA-RNA or RNA-DNA or RNA-PNA (protein nucleic acid; Egholm *et al.,* 1993 *Nature* 365, 566) interactions and alters the activity of the target RNA (for a review, see Stein and Cheng, 1993 *Science* 261, 1004 and Woolf *et al.,* US patent No. 5,849,902). Typically, antisense molecules will be complementary to a target sequence along a single contiguous sequence of the antisense molecule. However, in certain embodiments, an antisense molecule may bind to substrate such that the substrate molecule forms a loop, and/or an antisense molecule may bind such that the antisense molecule forms a loop. Thus, the antisense molecule may be complementary to two (or even more) non-contiguous substrate sequences or two (or even more) non-contiguous sequence portions of an antisense molecule may be complementary to a target sequence or both. For a review of current antisense strategies, see Schmajuk *et al.,* 1999, *J. Biol. Chem.,* 274, 21783-21789, Delihas *et al.,* 1997, *Nature,* 15, 751-753, Stein *et al.,* 1997, *Antisense N. A. Drug Dev.*, 7, 151, Crooke, 1998, *Biotech. Genet. Eng. Rev.*, 15, 121-157, Crooke, 1997, *Ad. Pharmacol.*, 40, 1-49. In addition, antisense DNA can be used to target RNA by means of DNA-RNA interactions, thereby activating RNase H, which digests the target RNA in the duplex. Antisense DNA can be synthesized chemically or expressed via the use of a single stranded DNA expression vector or equivalent thereof.

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

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

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

By "complementarity" is meant that a nucleic acid can form hydrogen bond(s) with another RNA sequence by either traditional Watson-Crick or other non-traditional types. In reference to the nucleic molecules of the present invention, the binding free energy for a nucleic acid molecule with its target or complementary sequence is sufficient to allow the relevant function of the nucleic acid to proceed, e.g., ribozyme cleavage, antisense or triple helix inhibition. Determination of binding free energies for nucleic acid molecules is well known in the art (see, e.g., Turner et al., 1987, *CSH Symp. Quant. Biol.* LII pp.123-133; Frier *et al.*, 1986, *Proc. Nat. Acad. Sci. USA* 83:9373-9377; Turner *et al.*, 1987, *J. Am. Chem. Soc.* 109:3783-3785). A percent complementarity indicates the percentage of contiguous residues in a nucleic acid molecule which can form hydrogen bonds (e.g., Watson-Crick base pairing) with a second nucleic acid sequence (e.g., 5, 6, 7, 8, 9, 10 out of 10 being 50%, 60%, 70%, 80%, 90%, and 100% complementary). "Perfectly complementary" means that all the contiguous residues of a nucleic acid sequence will hydrogen bond with the same number of contiguous residues in a second nucleic acid sequence.

At least seven basic varieties of naturally occurring enzymatic nucleic acids are known presently. Each can catalyze the hydrolysis of RNA phosphodiester bonds in *trans* (and thus can cleave other RNA molecules) under physiological conditions. **Table I** summarizes some of the characteristics 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 a 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. Thus, a single ribozyme molecule is able to cleave many molecules of target RNA. In addition, the ribozyme is a highly specific inhibitor of gene expression, 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 completely eliminate catalytic activity of a ribozyme.

The enzymatic nucleic acid molecule that cleave the specified sites in CLCA1-specific RNAs represent a novel therapeutic approach to treat Chronic Obstructive Pulmonary Diseases (COPDs), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome, and other indications that may respond to the level of CLCA1.

In one of the preferred embodiments of the inventions described herein, the enzymatic nucleic acid molecule is formed in a hammerhead or hairpin motif, but may also be formed in the motif of a hepatitis delta virus, group I intron, group II intron or RNase P RNA (in association with an RNA guide sequence), *Neurospora* VS RNA, DNAzymes, NCH cleaving motifs, or G-cleavers. Examples of such hammerhead motifs are described by Dreyfus, *supra,* Rossi *et al.*, 1992, *AIDS Research and Human Retroviruses* 8, 183; Examples of hairpin motifs are described 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, Hampel *et al.*, 1990 *Nucleic Acids Res.* 18, 299; Chowrira & McSwiggen, US. Patent No. 5,631,359. The hepatitis delta virus motif is described by Perrotta and Been, 1992 *Biochemistry* 31, 16. The RNase P motif is described 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. The Group I intron is described by Cech *et al.*, U.S. Patent 4,987,071. DNAzymes are described by Usman *et al.*, International PCT Publication No. WO 95/11304; Chartrand *et al.*, 1995, *NAR* 23, 4092; Breaker *et al.*, 1995, *Chem. Bio.* 2, 655; Santoro *et al.*, 1997, *PNAS* 94, 4262. NCH cleaving motifs are described in Ludwig & Sproat, International PCT Publication No. WO 98/58058; and G-cleavers are described in Kore *et al.*, 1998, *Nucleic Acids Research* 26, 4116-4120 and Eckstein *et al.*, International PCT Publication No. WO 99/16871. Additional motifs such as the Aptazyme (Breaker *et al.*, WO 98/43993), Amberzyme (Class I motif; Figure 3; Beigelman *et al.*, International PCT publication No. WO 99/55857) and Zinzyme (Beigelman *et al.*, International PCT publication No. WO 99/55857), all these references are incorporated by reference herein in their totalities, including drawings and can also be used in the present invention. These specific motifs are not limiting in the invention. and those skilled in the art will recognize that all that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target gene RNA regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart an RNA cleaving activity to the molecule (Cech *et al.*, U.S. Patent No. 4,987,071).

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

In a preferred embodiment, the invention provides a method for producing a class of nucleic acid–based gene inhibiting agents which exhibit a high degree of specificity for the RNA of a desired target. For example, the enzymatic nucleic acid molecule is preferably targeted to a highly conserved sequence region of target RNAs encoding CLCA proteins (for example, CLCA1, CLCA2, CLCA3 and/or CLCA4) such that specific treatment of a disease or condition can be provided with either one or several nucleic acid molecules of the invention. Such nucleic acid molecules can be delivered exogenously to specific tissue or cellular targets as required. Alternatively, the nucleic acid molecules (*e.g.*, ribozymes and antisense) can be expressed from DNA and/or RNA vectors that are delivered to specific cells.

In a preferred embodiment, the invention features the use of nucleic acid-based inhibitors of the invention to specifically target genes that share homology with the CLCA1 gene.

As used herein "cell" is used in its usual biological sense, and does not refer to an entire multicellular organism, e.g., specifically does not refer to a human. The cell may be present in a non-human multicellular organism, e.g., birds, plants and mammals such as cows, sheep, apes, monkeys, swine, dogs, and cats.

By "CLCA proteins" is meant, a protein or a mutant protein derivative thereof, comprising a calcium activated chloride channel protein.

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

The nucleic acid-based inhibitors of CLCA1 expression are useful for the prevention and/or treatment of diseases and conditions including Chronic Obstructive Pulmonary Disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome, and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue, alone or in combination with other therapies.

By "related" is meant that the reduction of CLCA1 expression (specifically CLCA1 gene) RNA levels and thus reduction in the level of the respective protein will relieve, to some extent, the symptoms of the disease or condition.

The nucleic acid-based inhibitors of the invention are added directly, or can be complexed with cationic lipids, packaged within liposomes, or otherwise delivered to target cells or tissues. 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 preferred embodiments, the enzymatic nucleic acid inhibitors comprise sequences, which are complementary to the substrate sequences in **Tables III to IX**. Examples of such enzymatic nucleic acid molecules also are shown in **Tables III to IX**. Examples of such enzymatic nucleic acid molecules consist essentially of sequences defined in these Tables.

In yet another embodiment, the invention features antisense nucleic acid molecules and 2-5A chimera including sequences complementary to the substrate sequences shown in **Tables III to IX**. Such nucleic acid molecules can include sequences as shown for the binding arms of the enzymatic nucleic acid molecules in **Tables III to VIII** and sequences shown as GeneBloc™ sequences in **Table IX**. Similarly, triplex molecules can be provided targeted to the corresponding DNA target regions, and containing the DNA equivalent of a target sequence or a sequence complementary to the specified target (substrate) sequence. Typically, antisense molecules will be complementary to a target sequence along a single contiguous sequence of the antisense molecule. However, in certain embodiments, an antisense molecule may bind to substrate such that the substrate molecule forms a loop, and/or an antisense molecule may bind such that the antisense molecule forms a loop. Thus, the antisense molecule may be complementary to two (or even more) non-contiguous substrate sequences or two (or even more) non-contiguous sequence portions of an antisense molecule may be complementary to a target sequence or both.

By "consists essentially of" is meant that the active nucleic acid molecule of the invention, for example, an enzymatic nucleic acid molecule, contains an enzymatic center or core equivalent to those in the examples, and binding arms able to bind RNA such that cleavage at the target site occurs. Other sequences can be present which do not interfere with such cleavage. Thus, a core region can, for example, include one or more loop, stem-loop structure, or linker which does not prevent enzymatic activity. Thus, the underlined regions in the sequences in **Tables III, IV** and **VIII** can be such a loop, stem-loop, nucleotide linker, and/or non-nucleotide linker and can be represented generally as sequence "X". For example, a core sequence for a hammerhead enzymatic nucleic acid can comprise a conserved sequence, such as 5'-CUGAUGAG-3' and 5'-CGAA-3' connected by "X", where X is 5'-GCCGUUAGGC-3' (SEQ ID NO 5450), or any other Stem II region known in the art.

In another aspect of the invention, ribozymes or antisense molecules that interact with target RNA molecules and inhibit CLCA1 (specifically CLCA1 gene) activity are expressed from transcription units inserted into DNA or RNA vectors. The recombinant vectors are preferably DNA plasmids or viral vectors. Ribozyme or antisense 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 or antisense are delivered as described above, and persist in target cells. Alternatively, viral vectors may be used that provide for transient expression of ribozymes or antisense. Such vectors can be repeatedly administered as necessary. Once expressed, the ribozymes or antisense bind to the target RNA and inhibit its function or expression. Delivery of ribozyme or antisense expressing vectors can 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. Antisense DNA can be expressed endogenously via the use of a single stranded DNA intracellular expression vector.

By RNA is meant a molecule comprising at least one ribonucleotide residue. By "ribonucleotide" is meant a nucleotide with a hydroxyl group at the 2' position of a β-D-ribo-furanose moiety.

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

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 the nucleic acid molecules of the invention can be administered. Preferably, a patient is a mammal or mammalian cells. More preferably, a patient is a human or human cells.

The nucleic acid molecules of the instant invention, 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 the levels of CLCA1, the patient may be treated, or other appropriate cells may be treated, as is evident to those skilled in the art, individually or in combination with one or more drugs under conditions suitable for the treatment.

In a further embodiment, the described molecules, such as antisense or ribozymes, can be used in combination with other known treatments to treat conditions or diseases discussed above. For example, the described molecules could be used in combination with one or more known therapeutic agents to treat Chronic Obstructive Pulmonary Diseases (COPDs), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome, and/or other disease states or conditions which respond to the modulation of CLCA1 expression.

In another preferred embodiment, the invention features nucleic acid-based inhibitors (*e.g.,* enzymatic nucleic acid molecules (ribozymes), antisense nucleic acids, 2-5A antisense chimeras, triplex DNA, antisense nucleic acids containing RNA cleaving chemical groups) and methods for their use to down regulate or inhibit the expression of genes (*e.g.,* CLCA1) capable of progression and/or maintenance of Chronic Obstructive Pulmonary Diseases (COPDs), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome, and/or other disease states or conditions which respond to the modulation of CLCA1 expression.

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

The foregoing description of the various aspects and embodiments is provided with reference to the exemplary calcium activated chloride channel gene CLCA1, which is also referred to as CaCC1 or ICACC-1. However, the various aspects and embodiments are also directed to other genes which express CLCA1 or CaCC1-like proteins (for example hCLCA2, hCLCA3, hCLCA4, CaCC2, and CaCC3). Those additional genes can be analyzed for target sites using the methods described for CLCA1. Thus, the inhibition and the effects of such inhibition of the other genes can be performed as described herein.

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

First the drawings will be described briefly.

Drawings

Figure 1 shows examples of chemically stabilized ribozyme motifs. **HH Rz**, represents hammerhead ribozyme motif (Usman *et al.*, 1996, *Curr. Op. Struct. Bio.*, 1, 527); **NCH Rz** represents the NCH ribozyme motif (Ludwig & Sproat, International PCT Publication No. WO 98/58058); **G-Cleaver**, represents G-cleaver ribozyme motif (Kore *et al.*, 1998, *Nucleic Acids Research* 26, 4116-4120). **N** or **n**, represent independently a nucleotide which may be same or different and have complementarity to each other; **rI**, represents ribo-Inosine nucleotide; arrow indicates the site of cleavage within the target. Position 4 of the HH Rz and the NCH Rz is shown as having 2'-*C*-allyl modification, but those skilled in the art will recognize that this position can be modified with other modifications well known in the art, so long as such modifications do not significantly inhibit the activity of the ribozyme.

Figure 2 shows an example of the Amberzyme ribozyme motif that is chemically stabilized (see, for example, Beigelman *et al.*, International PCT publication No. WO 99/55857, incorporated by reference herein; also referred to as Class I Motif). The Amberzyme motif is a class of enzymatic nucleic molecules that do not require the presence of a ribonucleotide (2'-OH) group for its activity.

Figure 3 shows an example of the Zinzyme A ribozyme motif that is chemically stabilized (Beigelman *et al.*, International PCT publication No. WO 99/55857, incorporated by reference herein; also referred to as Class A or Class II Motif). The Zinzyme motif is a class of enzymatic nucleic molecules that do not require the presence of a ribonucleotide (2'-OH) group for its activity.

Figure 4 shows an example of a DNAzyme motif described by Santoro *et al.*, 1997, *PNAS*, 94, 4262.

Figures 5A and 5B are diagrammatic schemes representative of the process used for Target Discovery in the instant invention. The process for Target Discovery is described in Jarvis *et al.*, International PCT publication No. WO 98/50530, incorporated by reference herein in its entirety including the Figures.

Mechanism of action of Nucleic Acid Molecules of the Invention

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

In addition, binding of single stranded DNA to RNA may result in nuclease degradation of the heteroduplex (Wu-Pong, *supra*; Crooke, *supra*). To date, the only backbone modified DNA chemistry which will act as substrates for RNase H are phosphorothioates, phosphorodithioates, and borontrifluoridates. Recently it has been reported that 2'-arabino and 2'-fluoro arabino- containing oligos can also activate RNase H activity.

A number of antisense molecules have been described that utilize novel configurations of chemically modified nucleotides, secondary structure, and/or RNase H substrate domains (Woolf *et al.*, International PCT Publication No. WO 98/13526; Thompson *et al.*, International PCT Publication No. WO 99/54459; Hartmann *et al.*, USSN 60/101,174 which was filed on September 21, 1998) all of these are incorporated by reference herein in their entirety.

In addition, antisense deoxyoligoribonucleotides can be used to target RNA by means of DNA-RNA interactions, thereby activating RNase H, which digests the target RNA in the duplex. Antisense DNA can be expressed endogenously *in vivo* via the use of a single stranded DNA intracellular expression vector or equivalents and variations thereof.

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

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

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

Enzymatic Nucleic Acid: Seven basic varieties of naturally occurring enzymatic RNAs are presently known. 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.

Nucleic acid molecules of this invention will block to some extent CLCA1 protein expression and can be used to treat disease or diagnose disease associated with the levels of CLCA1.

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

Nucleic acid molecules having an endonuclease enzymatic activity are able to repeatedly cleave other separate RNA molecules in a nucleotide base sequence-specific manner. Such enzymatic nucleic acid molecules can be targeted to virtually any RNA transcript, and achieve efficient cleavage *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 and 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 (Warashina *et al.*, 1999, *Chemistry and Biology*, 6, 237-250).

The nucleic acid molecules of the instant invention are also referred to as GeneBloc reagents, which are essentially nucleic acid molecules (e.g.; ribozymes, antisense) capable of down-regulating gene expression.

GeneBlocs are modified oligonucleotides including ribozymes and modified antisense oligonucleotides that bind to and target specific mRNA molecules. Because GeneBlocs can be designed to target any specific mRNA, their potential applications are quite broad. Traditional antisense approaches have often relied heavily on the use of phosphorothioate modifications to enhance stability in biological samples, leading to a myriad of specificity problems stemming from non-specific protein binding and general cytotoxicity (Stein, 1995, *Nature Medicine*, 1, 1119). In contrast, GeneBlocs contain a number of modifications that confer nuclease resistance while making minimal use of phosphorothioate linkages, which reduces toxicity, increases binding affinity and minimizes non-specific effects compared with traditional antisense oligonucleotides. Similar reagents have recently been utilized successfully in various cell culture systems (Vassar, *et al.*, 1999, *Science*, 286, 735) and in vivo (Jarvis et al., manuscript in preparation). In addition, novel cationic lipids can be utilized to enhance cellular uptake in the presence of serum. Since ribozymes and antisense oligonucleotides regulate gene expression at the RNA level, the ability to maintain a steady-state dose of GeneBloc over several days was important for target protein and phenotypic analysis. The advances in resistance to nuclease degradation and prolonged activity in vitro have supported the use of GeneBlocs in target validation applications.

<u>Target sites</u>

Targets for useful ribozymes and antisense nucleic acids 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. All of these publications are hereby incorporated by reference herein in their totality. Other examples include the following PCT applications, which concern inactivation of expression of disease-related genes: WO 95/23225, WO 95/13380, WO 94/02595, all of which are incorporated by reference herein. Rather than repeat the guidance provided in those documents here, specific examples of such methods are provided herein, not limiting to those in the art. Ribozymes and antisense to such targets are designed as described in those applications and synthesized to be tested *in vitro* and *in vivo*, as also described. The sequences of human CLCA1 RNAs were screened for optimal enzymatic nucleic acid and antisense target sites using a computer-folding algorithm. Antisense, hammerhead, DNAzyme, NCH, amberzyme, zinzyme, or G-Cleaver ribozyme binding/cleavage sites were identified. These sites are shown in **Tables III to IX** (all sequences are 5' to 3' in the tables; the underlined region can be any base-paired sequence, the actual sequence is not relevant here). The nucleotide base position is noted in the Tables as that site to be cleaved by the designated type of enzymatic nucleic acid molecule. While human sequences can be screened and enzymatic nucleic acid molecule and/or antisense thereafter designed, as discussed in Stinchcomb *et al.,* WO 95/23225, mouse targeted ribozymes may be useful to test efficacy of action of the enzymatic nucleic acid molecule and/or antisense prior to testing in humans.

Antisense, hammerhead, DNAzyme, NCH, amberzyme, zinzyme or G-Cleaver ribozyme binding/cleavage sites were identified. The nucleic acid molecules are individually analyzed by computer folding (Jaeger *et al.,* 1989 *Proc. Natl. Acad. Sci. USA*, 86, 7706) to assess whether the sequences fold into the appropriate secondary structure. Those nucleic acid molecules with unfavorable intramolecular interactions such as between the binding arms and the catalytic core are eliminated from consideration. Varying binding arm lengths can be chosen to optimize activity.

Antisense, hammerhead, DNAzyme, NCH, amberzyme, zinzyme or G-Cleaver ribozyme binding/cleavage sites were identified and were designed to anneal to various sites in the RNA target. The binding arms are complementary to the target site sequences described above. The nucleic acid molecules were chemically synthesized. The method of synthesis used follows the procedure for normal DNA/RNA synthesis as described below and in Usman *et al.*, 1987 *J. Am. Chem. Soc.*, 109, 7845; Scaringe *et al.*, 1990 *Nucleic Acids Res.*, 18, 5433; Wincott *et al.*, 1995 *Nucleic Acids Res.* 23, 2677-2684; and Caruthers *et al.*, 1992, *Methods in Enzymology* 211,3-19.

Synthesis of Nucleic acid Molecules

Synthesis of nucleic acids greater than 100 nucleotides in length is difficult using automated methods, and the therapeutic cost of such molecules is prohibitive. In this invention, small nucleic acid motifs ("small refers to nucleic acid motifs no more than 100 nucleotides in length, preferably no more than 80 nucleotides in length, and most preferably no more than 50 nucleotides in length; *e.g.*, antisense oligonucleotides, hammerhead or the NCH ribozymes) are preferably used for exogenous delivery. The simple structure of these molecules increases the ability of the nucleic acid to invade targeted regions of RNA structure. Exemplary molecules of the instant invention are chemically synthesized, and others can similarly be synthesized.

Oligonucleotides (e.g.; antisense GeneBlocs) are synthesized using protocols known in the art as described in Caruthers *et al.*, 1992, *Methods in Enzymology* 211, 3-19, Thompson *et al.,* International PCT Publication No. WO 99/54459, Wincott *et al.,* 1995, *Nucleic Acids Res.* 23, 2677-2684, Wincott *et al.,* 1997, *Methods Mol. Bio.*, 74, 59, Brennan *et al.,* 1998, *Biotechnol Bioeng.,* 61, 33-45, and Brennan, US patent No. 6,001,311. All of these references are incorporated herein by reference. The synthesis of oligonucleotides makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. In a non-limiting example, small scale syntheses are conducted on a 394 Applied Biosystems, Inc. synthesizer using a 0.2 μmol scale protocol with a 2.5 min coupling step for 2'-O-methylated nucleotides and a 45 sec coupling step for 2'-deoxy nucleotides. **Table II** outlines the amounts and the contact times of the reagents used in the synthesis cycle. Alternatively, syntheses at the 0.2 μmol scale can be performed on a 96-well plate synthesizer, such as the instrument produced by Protogene (Palo Alto, CA) with minimal modification to the cycle. A 33-fold excess (60 μL of 0.11 M = 6.6 μmol) of 2'-O-methyl phosphoramidite and a 105-fold excess of S-ethyl tetrazole (60 μL of 0.25 M = 15 μmol) can be used in each coupling cycle of 2'-O-methyl residues relative to polymer-bound 5'-hydroxyl. A 22-fold excess (40 μL of 0.11 M = 4.4 μmol) of deoxy phosphoramidite and a 70-fold excess of S-ethyl tetrazole (40 μL of 0.25 M = 10 μmol) can be used in each coupling cycle of deoxy residues relative to polymer-bound 5'-hydroxyl. Average coupling yields on the 394 Applied Biosystems, Inc. synthesizer, determined by colorimetric quantitation of the trityl fractions, are typically 97.5-99%. Other oligonucleotide synthesis reagents for the 394 Applied Biosystems, Inc. synthesizer include; detritylation solution is 3% TCA in methylene chloride (ABI); capping is performed with 16% *N*-methyl imidazole in THF (ABI) and 10% acetic anhydride/10% 2,6-lutidine in THF (ABI); and oxidation solution is 16.9 mM I_2, 49 mM pyridine, 9% water in THF (PERSEPTIVE™). Burdick & Jackson Synthesis Grade acetonitrile is used directly from the reagent bottle. S-Ethyltetrazole solution (0.25 M in acetonitrile) is made up from the solid obtained from American International Chemical, Inc. Alternately, for the introduction of phosphorothioate linkages, Beaucage reagent (3H-1,2-Benzodithiol-3-one 1,1-dioxide, 0.05 M in acetonitrile) is used.

Deprotection of the antisense oligonucleotides is performed as follows: the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 40% aq. methylamine (1 mL) at 65 °C for 10 min. After cooling to –20 °C, the supernatant is removed from the polymer support. The support is washed three times with 1.0 mL of EtOH:MeCN:H2O/3:1:1, vortexed and the supernatant is then added to the first supernatant. The combined supernatants, containing the oligoribonucleotide, are dried to a white powder.

The method of synthesis used for normal RNA including certain enzymatic nucleic acid molecules follows the procedure as described in Usman *et al.,* 1987, *J. Am. Chem. Soc.*, 109, 7845; Scaringe *et al.,* 1990, *Nucleic Acids Res.*, 18, 5433; Wincott *et al.,* 1995, *Nucleic Acids Res.* 23, 2677-2684 and Wincott *et al.,* 1997, *Methods Mol. Bio.*, 74, 59, and makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. In a non-limiting example, small scale syntheses are conducted on a 394 Applied Biosystems, Inc. synthesizer using a 0.2 μmol scale protocol with a 7.5 min coupling step for alkylsilyl protected nucleotides and a 2.5 min coupling step for 2'-O-methylated nucleotides. **Table II** outlines the amounts and the contact times of the reagents used in the synthesis cycle. Alternatively, syntheses at the 0.2 μmol scale can be done on a 96-well plate synthesizer, such as the instrument produced by Protogene (Palo Alto, CA) with minimal modification to the cycle. A 33-fold excess

(60 µL of 0.11 M = 6.6 µmol) of 2'-O-methyl phosphoramidite and a 75-fold excess of S-ethyl tetrazole (60 µL of 0.25 M = 15 µmol) can be used in each coupling cycle of 2'-O-methyl residues relative to polymer-bound 5'-hydroxyl. A 66-fold excess (120 µL of 0.11 M = 13.2 µmol) of alkylsilyl (ribo) protected phosphoramidite and a 150-fold excess of S-ethyl tetrazole (120 µL of 0.25 M = 30 µmol) can be used in each coupling cycle of ribo residues relative to polymer-bound 5'-hydroxyl. Average coupling yields on the 394 Applied Biosystems, Inc. synthesizer, determined by colorimetric quantitation of the trityl fractions, are typically 97.5-99%. Other oligonucleotide synthesis reagents for the 394 Applied Biosystems, Inc. synthesizer include; detritylation solution is 3% TCA in methylene chloride (ABI); capping is performed with 16% *N*-methyl imidazole in THF (ABI) and 10% acetic anhydride/10% 2,6-lutidine in THF (ABI); oxidation solution is 16.9 mM I_2, 49 mM pyridine, 9% water in THF (PERSEPTIVE™). Burdick & Jackson Synthesis Grade acetonitrile is used directly from the reagent bottle. S-Ethyltetrazole solution (0.25 M in acetonitrile) is made up from the solid obtained from American International Chemical, Inc. Alternately, for the introduction of phosphorothioate linkages, Beaucage reagent (3H-1,2-Benzodithiol-3-one 1,1-dioxide0.05 M in acetonitrile) is used.

Deprotection of the RNA is performed using either a two-pot or one-pot protocol. For the two-pot protocol, the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 40% aq. methylamine (1 mL) at 65 °C for 10 min. After cooling to –20 °C, the supernatant is removed from the polymer support. The support is washed three times with 1.0 mL of EtOH:MeCN:H2O/3:1:1, vortexed and the supernatant is then added to the first supernatant. The combined supernatants, containing the oligoribonucleotide, are dried to a white powder. The base deprotected oligoribonucleotide is resuspended in anhydrous TEA/HF/NMP solution (300 µL of a solution of 1.5 mL N-methylpyrrolidinone, 750 µL TEA and 1 mL TEA•3HF to provide a 1.4 M HF concentration) and heated to 65 °C. After 1.5 h, the oligomer is quenched with 1.5 M NH_4HCO_3.

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

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

Inactive hammerhead ribozymes or binding attenuated control (BAC) oligonucleotides) are 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). Similarly, one or more nucleotide substitutions can be introduced in other enzymatic nucleic acid molecules to inactivate the molecule and such molecules can serve as a negative control.

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

Alternatively, the nucleic acid molecules of the present invention can be synthesized separately and joined together post-synthetically, for example by ligation (Moore *et al.*, 1992, *Science* 256, 9923; Draper *et al.*, International PCT publication No. WO 93/23569; Shabarova *et al.*, 1991, *Nucleic Acids Research* 19, 4247; Bellon *et al.,* 1997, *Nucleosides & Nucleotides*, 16, 951; Bellon *et al.,* 1997, *Bioconjugate Chem.* 8, 204).

The nucleic acid molecules of the present invention are modified extensively 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; Usman *et al.,* 1994, *Nucleic Acids Symp. Ser.* 31, 163). Ribozymes are purified by gel electrophoresis using general methods or are purified by high pressure liquid chromatography (HPLC; See Wincott *et al., supra*, the totality of which is hereby incorporated herein by reference) and are re-suspended in water.

The sequences of the ribozymes and antisense constructs that are chemically synthesized, useful in this study, are shown in **Tables III to IX**. 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. The ribozyme and antisense construct sequences listed in **Tables III to IX** may be formed of ribonucleotides or other nucleotides or non-nucleotides. Such ribozymes with enzymatic activity are equivalent to the ribozymes described specifically in the Tables.

Optimizing Activity of the nucleic acid molecule of the invention.

Chemically synthesizing nucleic acid molecules with modifications (base, sugar and/or phosphate) that prevent their degradation by serum ribonucleases may increase their potency (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; 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 the nucleic acid molecules described herein. All these references are incorporated by reference herein. Modifications which enhance their efficacy in cells, and removal of bases from nucleic acid molecules to shorten oligonucleotide synthesis times and reduce chemical requirements are desired.

There are several examples in the art describing sugar, base and phosphate modifications that can be introduced into nucleic acid molecules with significant enhancement in their nuclease stability and efficacy. For example, oligonucleotides are modified to enhance stability and/or enhance biological 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 modifications of 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; Beigelman *et al.,* International PCT publication No. WO 97/26270; Beigelman *et al.,* US Patent No. 5,716,824; Usman *et al.,* US patent No. 5,627,053; Woolf *et al.*, International PCT Publication No. WO 98/13526; Thompson *et al.*, USSN 60/082,404 which was filed on April 20, 1998; Karpeisky *et al.,* 1998, *Tetrahedron Lett.,* 39, 1131; Earnshaw and Gait, 1998, *Biopolymers (Nucleic acid Sciences),* 48, 39-55; Verma and Eckstein, 1998, *Annu. Rev. Biochem.,* 67, 99-134; and Burlina *et al.*, 1997, *Bioorg. Med. Chem.*, 5, 1999-2010; all of the references are hereby incorporated by reference herein in their totalities). 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. In view of such teachings, similar modifications can be used as described herein to modify the nucleic acid molecules of the instant invention.

While chemical modification of oligonucleotide internucleotide linkages with phosphorothioate, phosphorothioate, and/or 5'-methylphosphonate linkages improves stability, too many of these modifications may cause some toxicity. Therefore when designing nucleic acid molecules the amount of these internucleotide linkages should be minimized. The reduction in the concentration of these linkages should lower toxicity resulting in increased efficacy and higher specificity of these molecules.

Nucleic acid molecules having chemical modifications which maintain or enhance 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. Therapeutic nucleic acid molecules 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, nucleic acid molecules must be resistant to nucleases in order to function as effective intracellular therapeutic agents. Improvements in the chemical synthesis of RNA and DNA (Wincott *et al.*, 1995 *Nucleic Acids Res.* 23, 2677; Caruthers *et al.*, 1992, *Methods in Enzymology* 211,3-19 (incorporated by reference herein) have expanded the ability to modify nucleic acid molecules by introducing nucleotide modifications to enhance their nuclease stability as described above.

Use of these the nucleic acid-based molecules of the invention will lead to better treatment of the disease progression by affording the possibility of combination therapies (*e.g.*, multiple antisense or enzymatic nucleic acid molecules targeted to different genes, nucleic acid molecules coupled with known small molecule inhibitors, or intermittent treatment with combinations of molecules (including different motifs) and/or other chemical or biological molecules). The treatment of patients with nucleic acid molecules may also include combinations of different types of nucleic acid molecules.

Therapeutic nucleic acid molecules (*e.g.*, enzymatic nucleic acid molecules and antisense nucleic acid molecules) 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, these nucleic acid molecules must be resistant to nucleases in order to function as effective intracellular therapeutic agents. Improvements in the chemical synthesis of nucleic acid molecules described in the instant invention and in the art have expanded the ability to modify nucleic acid molecules by introducing nucleotide modifications to enhance their nuclease stability as described above.

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

In yet another preferred embodiment, 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 of an all RNA ribozyme.

In another aspect the nucleic acid molecules comprise a 5' and/or a 3'- cap structure.

By "cap structure" is meant chemical modifications, which have been incorporated at either terminus of the oligonucleotide (see, for example, Wincott *et al.*, WO 97/26270, incorporated by reference herein). These terminal modifications protect the nucleic acid molecule from exonuclease degradation, and may help in delivery and/or localization within a cell. The cap may be present at the 5'-terminus (5'-cap) or at the 3'-terminus (3'-cap) or may be present on both termini. In non-limiting examples the 5'-cap is selected from the group comprising inverted abasic residue (moiety), 4',5'-methylene nucleotide; 1-(beta-D-erythrofuranosyl) nucleotide, 4'-thio nucleotide, carbocyclic nucleotide; 1,5-anhydrohexitol nucleotide; L-nucleotides; alpha-nucleotides; modified base nucleotide; phosphorodithioate linkage; *threo*-pentofuranosyl nucleotide; acyclic 3',4'-seco nucleotide; acyclic 3,4-dihydroxybutyl nucleotide; acyclic 3,5-dihydroxypentyl nucleotide, 3'-3'-inverted nucleotide moiety; 3'-3'-inverted abasic moiety; 3'-2'-inverted nucleotide moiety; 3'-2'-inverted abasic moiety; 1,4-butanediol phosphate; 3'-phosphoramidate; hexylphosphate; aminohexyl phosphate; 3'-phosphate; 3'-phosphorothioate; phosphorodithioate; or bridging or non-bridging methylphosphonate moiety (for more details see Wincott *et al.,* International PCT publication No. WO 97/26270, incorporated by reference herein).

In yet another preferred embodiment, the 3'-cap is selected from a group comprising, 4',5'-methylene nucleotide; 1-(beta-D-erythrofuranosyl) nucleotide; 4'-thio nucleotide, carbocyclic nucleotide; 5'-amino-alkyl phosphate; 1,3-diamino-2-propyl phosphate, 3-aminopropyl phosphate; 6-aminohexyl phosphate; 1,2-aminododecyl phosphate; hydroxypropyl phosphate; 1,5-anhydrohexitol nucleotide; L-nucleotide; alpha-nucleotide; modified base nucleotide; phosphorodithioate; *threo*-pentofuranosyl nucleotide; acyclic 3',4'-seco nucleotide; 3,4-dihydroxybutyl nucleotide; 3,5-dihydroxypentyl nucleotide, 5'-5'-inverted nucleotide moiety; 5'-5'-inverted abasic moiety; 5'-phosphoramidate; 5'-phosphorothioate; 1,4-butanediol phosphate; 5'-amino; bridging and/or non-bridging 5'-phosphoramidate, phosphorothioate and/or phosphorodithioate, bridging or non bridging methylphosphonate and 5'-mercapto moieties (for more details, see Beaucage and Iyer, 1993, *Tetrahedron* 49, 1925; incorporated by reference herein).

By the term "non-nucleotide" is meant any group or compound which can be incorporated into a nucleic acid chain in the place of one or more nucleotide units, including either sugar and/or phosphate substitutions, and allows the remaining bases to exhibit their enzymatic activity. The group or compound is abasic in that it does not contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine.

An "alkyl" group refers to a saturated aliphatic hydrocarbon, including straight-chain, branched-chain, and cyclic alkyl groups. Preferably, the alkyl group has 1 to 12 carbons. More preferably it is a lower alkyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO_2 or $N(CH_3)_2$, amino, or SH. The term also includes alkenyl groups which are unsaturated hydrocarbon groups containing at least one carbon-carbon double bond, including straight-chain, branched-chain, and cyclic groups. Preferably, the alkenyl group has 1 to 12 carbons. More preferably it is a lower alkenyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkenyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO_2, halogen, $N(CH_3)_2$, amino, or SH. The term "alkyl" also includes alkynyl groups which have an unsaturated hydrocarbon group containing at least one carbon-carbon triple bond, including straight-chain, branched-chain, and cyclic groups. Preferably, the alkynyl group has 1 to 12 carbons. More preferably it is a lower alkynyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkynyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO_2 or $N(CH_3)_2$, amino or SH.

Such alkyl groups may also include aryl, alkylaryl, carbocyclic aryl, heterocyclic aryl, amide and ester groups. An "aryl" group refers to an aromatic group which has at least one ring having a conjugated π electron system and includes carbocyclic aryl, heterocyclic aryl and biaryl groups, all of which may be optionally substituted. The preferred substituent(s) of aryl groups are halogen, trihalomethyl, hydroxyl, SH, OH, cyano, alkoxy, alkyl, alkenyl, alkynyl, and amino groups. An "alkylaryl" group refers to an alkyl group (as described above) covalently joined to an aryl group (as described above). Carbocyclic aryl groups are groups wherein the ring atoms on the aromatic ring are all carbon atoms. The carbon atoms are optionally substituted. Heterocyclic aryl groups are groups having from 1 to 3 heteroatoms as ring atoms in the aromatic ring and the remainder of the ring atoms are carbon atoms. Suitable heteroatoms include oxygen, sulfur, and nitrogen, and include furanyl, thienyl, pyridyl, pyrrolyl, N-lower alkyl pyrrolo, pyrimidyl, pyrazinyl, imidazolyl and the like, all optionally substituted. An "amide" refers to an -C(O)-NH-R, where R is either alkyl, aryl, alkylaryl or hydrogen. An "ester" refers to an -C(O)-OR', where R is either alkyl, aryl, alkylaryl or hydrogen.

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 nucleotide sugar moiety. Nucleotides 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; Uhlmann & Peyman, 1990, *Chemical Reviews,* 90, 4, 544-579, all are hereby incorporated by reference herein). There are several examples of modified nucleic acid bases known in the art as 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 nucleic acid molecules 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), propyne, and others (Burgin *et al.*, 1996, *Biochemistry*, 35, 14090; Uhlman & Peyman, *supra*). 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 at any position, for example, within the catalytic core of an enzymatic nucleic acid molecule and/or in the substrate-binding regions of the nucleic acid molecule.

In a preferred embodiment, the invention features modified ribozymes with phosphate backbone modifications comprising one or more phosphorothioate, phosphorodithioate, methylphosphonate, morpholino, amidate carbamate, carboxymethyl, acetamidate, polyamide, sulfonate, sulfonamide, sulfamate, formacetal, thioformacetal, and/or alkylsilyl, substitutions. For a review of oligonucleotide backbone modifications see Hunziker and Leumann, 1995, *Nucleic Acid Analogues: Synthesis and Properties,* in *Modern Synthetic Methods,* VCH, 331-417, and Mesmaeker *et al.,* 1994, *Novel Backbone Replacements for Oligonucleotides,* in *Carbohydrate Modifications in Antisense Research,* ACS, 24-39. These references are hereby incorporated by reference herein.

By "abasic" is meant sugar moieties lacking a base or having other chemical groups in place of a base at the 1' position, (for more details, see Wincott *et al.,* International PCT publication No. WO 97/26270).

By "unmodified nucleoside" is meant one of the bases adenine, cytosine, guanine, thymine, uracil joined to the 1' carbon of β-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.

In connection with 2'-modified nucleotides as described for the present invention, by "amino" is meant 2'-NH_2 or 2'-*O*- NH_2, which may be modified or unmodified. Such modified groups are described, for example, in Eckstein *et al.*, U.S. Patent 5,672,695 and Matulic-Adamic *et al.*, WO 98/28317, respectively, which are both incorporated by reference herein in their entireties.

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

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

Administration of Nucleic Acid Molecules

Methods for the delivery of nucleic acid molecules are described in Akhtar *et al.*, 1992, *Trends Cell Bio.*, 2, 139; and *Delivery Strategies for Antisense Oligonucleotide Therapeutics*, ed. Akhtar, 1995 which are both incorporated herein by reference. Sullivan *et al.*, PCT WO 94/02595, further describes the general methods for delivery of enzymatic RNA molecules. These protocols may be utilized for the delivery of virtually any nucleic acid molecule. Nucleic acid molecules may be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres. For some indications, nucleic acid molecules may be directly delivered *ex vivo* to cells or tissues with or without the aforementioned vehicles. Alternatively, the nucleic acid/vehicle combination is locally delivered by direct injection or by use of a catheter, infusion pump or stent. Other routes of delivery include, but are not limited to, intravascular, intramuscular, subcutaneous or joint injection, aerosol inhalation, oral (tablet or pill form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed descriptions of nucleic acid delivery and administration are provided in Sullivan *et al.*, supra, Draper *et al.*, PCT WO93/23569, Beigelman *et al.,* PCT WO99/05094, and Klimuk *et al.,* PCT WO99/04819 all of which have been incorporated by reference herein.

In addition, the nucleic acid molecules of the instant invention, used to treat pulmonary diseases and disorders, may be administered directly to the lungs via pulmonary delivery. The pulmonary delivery of oligonucleotides is described by Bennett *et al.*, International PCT publication Nos. WO/9960166 and WO/9960010; Danahay *et al.*, 1999, *Pharm. Res.*, 16(10), 1542-1549; Metzger and Nyce, 1999, *J. Allergy Clin. Immunol.*, 104(2, Pt. 1), 260-266; Nicklin *et al.*, 1998, *Pharm. Res.*, 15(4), 583-591; Illum and Watts, International PCT publication No. WO/9735562; and Nyce, 1997, *Expert Opin. Invest. Drugs*, 6(9), 1149-1156.

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 other compositions known in the art.

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, including 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 from reaching 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 that lead to systemic absorption include, without limitations:

intravenous, subcutaneous, intraperitoneal, inhalation, oral, intrapulmonary and intramuscular. Each of these administration routes exposes 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 that 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 cancer cells.

By pharmaceutically acceptable formulation is meant, a composition or formulation that allows for the effective distribution of the nucleic acid molecules of the instant invention in the physical location most suitable for their desired activity. Non-limiting examples of agents suitable for formulation with the nucleic acid molecules of the instant invention include: P-glycoprotein inhibitors (such as Pluronic P85) which can enhance entry of drugs into the CNS (Jolliet-Riant and Tillement, 1999, *Fundam. Clin. Pharmacol.*, 13, 16-26); biodegradable polymers, such as poly (DL-lactide-coglycolide) microspheres for sustained release delivery after intracerebral implantation (Emerich, DF *et al*, 1999, *Cell Transplant*, 8, 47-58) Alkermes, Inc. Cambridge, MA; and loaded nanoparticles, such as those made of polybutylcyanoacrylate, which can deliver drugs across the blood brain barrier and can alter neuronal uptake mechanisms (*Prog Neuropsychopharmacol Biol Psychiatry*, 23, 941-949, 1999). Other non-limiting examples of delivery strategies for the nucleic acid molecules of the instant invention include material described in Boado *et al.*, 1998, *J. Pharm. Sci.*, 87, 1308-1315; Tyler *et al.*, 1999, *FEBS Lett.*, 421, 280-284; Pardridge *et al.*, 1995, *PNAS USA.*, 92, 5592-5596; Boado, 1995, *Adv. Drug Delivery Rev.*, 15, 73-107; Aldrian-Herrada *et al.*, 1998, *Nucleic Acids Res.*, 26, 4910-4916; and Tyler *et al.*, 1999, *PNAS USA.*, 96, 7053-7058.

The invention also features the use of the composition comprising surface-modified liposomes containing poly (ethylene glycol) lipids (PEG-modified, or long-circulating liposomes or stealth liposomes). These formulations offer a 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). All incorporated by reference herein. 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). All incorporated by reference herein. 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 which 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.

In addition, the invention features the use of methods to deliver the nucleic acid molecules of the instant invention to hematopoietic cells, including monocytes and lymphocytes. These methods are described in detail by Hartmann *et al.*, 1998, *J. Phamacol. Exp. Ther.*, 285(2), 920-928; Kronenwett *et al.*, 1998, *Blood*, 91(3), 852-862; Filion and Phillips, 1997, *Biochim. Biophys. Acta.*, 1329(2), 345-356; Ma and Wei, 1996, *Leuk. Res.*, 20(11/12), 925-930; and Bongartz *et al.*, 1994, *Nucleic Acids Research*, 22(22), 4681-8. Such methods, as described above, include the use of free oligonucleotide, cationic lipid formulations, liposome formulations including pH sensitive liposomes and immunoliposomes, and bioconjugates including oligonucleotides conjugated to fusogenic peptides, for the transfection of hematopoietic cells with oligonucleotides.

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. These include sodium benzoate, sorbic acid and esters of *p*-hydroxybenzoic acid. In addition, antioxidants and suspending agents may be used.

A pharmaceutically effective dose is that dose required to prevent, inhibit the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state. The pharmaceutically effective dose depends on the type of disease, the composition used, the route of administration, the type of mammal being treated, the physical characteristics of the specific mammal under consideration, concurrent medication, and other factors which those skilled in the medical arts will recognize. Generally, an amount between 0.1 mg/kg and 100 mg/kg body weight/day of active ingredients is administered dependent upon potency of the negatively charged polymer.

The nucleic acid molecules of the present invention may also be administered to a patient in combination with other therapeutic compounds to increase the overall therapeutic effect. The use of multiple compounds to treat an indication may increase the beneficial effects while reducing the presence of side effects. Oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylcysteine, mucokinetic agents, and DNase (Pulmozyme) are non-limiting examples of compounds and/or methods that can be combined with or used in conjunction with the nucleic acid molecules (*e.g.* ribozymes and antisense molecules) of the instant invention. Those skilled in the art will recognize that other drug compounds and therapies can be similarly and readily combined with the nucleic acid molecules of the instant invention (*e.g.* ribozymes and antisense molecules) and are, therefore, within the scope of the instant invention.

Alternatively, certain of the 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 these references are hereby incorporated in their totalities by reference herein).

In another aspect of the invention, RNA molecules of the present invention are preferably 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 nucleic acid molecules are delivered as described above, and persist in target cells. Alternatively, viral vectors may be used that provide for transient expression of nucleic acid molecules. Such vectors might be repeatedly administered as necessary. Once expressed, the nucleic acid molecule binds to the target mRNA. Delivery of nucleic acid molecule expressing vectors could be systemic, such as by intravenous or intra-muscular 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 a nucleic acid sequence encoding at least one of the nucleic acid molecules disclosed in the instant invention. The nucleic acid sequence encoding the nucleic acid molecule of the instant invention is operably linked in a manner which allows expression of that nucleic acid molecule.

In another aspect, the invention features an expression vector comprising: a) 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 nucleic acid sequence encoding at least one of the nucleic acid catalyst of the instant invention; and wherein said sequence 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 sequence encoding the nucleic acid catalyst of the invention; and/or an intron (intervening sequences).

Transcription of the nucleic acid molecule 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). All of these references are incorporated by reference herein.

Several investigators have demonstrated that nucleic acid molecules, such as 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; and 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; and 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 a nucleic acid sequence encoding at least one of the nucleic acid molecules 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 nucleic acid sequence encoding at least one said nucleic acid molecule; and wherein said sequence 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 nucleic acid sequence encoding at least one said nucleic acid molecule, wherein said sequence is operably linked to the 3'-end of said open reading frame; and wherein said sequence 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 nucleic acid sequence encoding at least one said nucleic acid molecule; and wherein said sequence 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 nucleic acid sequence encoding at least one said nucleic acid molecule, wherein said sequence is operably linked to the 3'-end of said open reading frame; and wherein said sequence 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 nucleic acids of the instant invention.

The following examples demonstrate the selection and design of Antisense, hammerhead, DNAzyme, NCH, Amberzyme, Zinzyme, or G-Cleaver ribozyme molecules and binding/cleavage sites within CLCA1 RNA.

Example 1: Reporter System

Applicant used a target discovery and target validation approach to finding genes that are involved in chronic mucous hypersecretion. In order to discover genes playing a role in the expression of mucins, a readily assayable reporter system was devised. The reporter system consists of a plasmid construct, termed pMUC5AC-EGFP, bearing a gene coding for Green Fluorescent Protein (GFP). The promoter region of the GFP gene is replaced by a portion of the Mucin 5AC promoter sufficient to direct efficient transcription of the GFP gene. The plasmid also contains the neomycin drug resistance gene.

Example 2: Host Cell Line for Target Discovery

The cell line selected as host for these studies, NCI-H292 (ATCC CRL-1848), is derived from a human lung mucoepidermoid carcinoma. The cells retain mucoepidermoid characteristics in culture and endogenously express mucin 5AC and mucin 2. The pMUC5AC-EGFP plasmid was transfected into NCI-H292 using a cationic lipid formulation. Following transfection, the cells were subjected to limiting dilution cloning under selection by 600 μg/mL Geneticin. Cells retaining the pMUC5AC-EGFP plasmid survive the Geneticin treatment and form colonies derived from single surviving cells.The resulting clonal cell lines were screened by flow cytometry for the capacity to upregulate GFP production directed by the Mucin 5AC promoter. Treating the cells with sterilized M9 bacterial medium in which Pseudomonas aeruginosa had been cultured (Pseudomonas conditioned medium, PCM) induced the mucin promoter. The PCM is supplemented with phorbol myristate acetate (PMA).

A clonal cell line highly responsive to mucin promoter induction, designated H292/MUC5AC/EGFP Clone8 (H292 Clone 8) was selected as the reporter line for subsequent studies. The process for Target Discovery is described in Jarvis *et al.*, International PCT publication No. WO 98/50530, incorporated by reference herein in its entirety including the Figures.

Example 3: Ribozyme Library Construction

A ribozyme library was constructed with oligonucletides containing ribozymes with two randomized regions comprising six-nucleotide binding "arms" (Stem I and Stem III of a ribozyme-substrate complex). Oligo sequence 5' and 3' of the ribozyme contains restriction endonuclease cleavage sites for cloning. The 3' trailing sequence forms a stem-loop for priming DNA polymerase extension to form a double stranded molecule. The double-stranded ribozyme library was cloned into the U6+27 transcription unit located in the 5' LTR region of a retroviral vector containing the human nerve growth factor receptor (hNGFr) reporter gene. Positioning the U6+27/ribozyme transcription unit in the 5' LTR results in a duplication of the transcription unit when the vector integrates into the host cell genome. As a result, the ribozyme is transcribed by RNA polymerase III from U6+27 and by RNA polymerase II activity directed by the 5' LTR. The ribozyme library was packaged into retroviral particles that were used to infect and transduce H292 Clone 8 cells. Assay of the hNGFr reporter indicated that 50% to 60% of Clone 8 cells incorporated the ribozyme construct. Figure 5A and 5B describe the generalized scheme used in the ribozyme library construction and target discovery. By "randomized region" is meant a region of completely random sequence and/or partially random sequence. By completely random sequence is meant a sequence wherein theoretically there is equal representation of A, T, G and C nucleotides or modified derivatives thereof, at each position in the sequence. By partially random sequence is meant a sequence wherein there is an unequal representation of A, T, G and C nucleotides or modified derivatives thereof, at each position in the sequence. A partially random sequence can therefore have one or more positions of complete randomness and one or more positions with defined nucleotides.

Example 4: Enriching for Non-responders to Mucin Induction

Sorting of ribozyme library-containing cells was performed to enrich for cells that produce less GFP after treatment with PCM and PMA. Lower GFP production may be due to ribozyme action upon genes involved in the activation of the mucin promoter. Alternatively, ribozymes may directly target the mucin/GFP transcript resulting in reduced GFP expression.

Cells were seeded at a density of 1 x 10^6 per 150 cm^2 style cell culture flasks. After 72 hours the standard cell culture medium was replaced with medium without fetal bovine serum. After 24 hours of serum deprivation the cells were treated with serum-containing medium supplemented with PCM (to 40%) and PMA (to 50 nM) to induced GFP production via the mucin promoter. After 20 to 22 hours, cells were monitored for GFP level on a FACStar Plus cell sorter.

Sorting was performed if 90% of ribozyme library cells from an unsorted control sample were induced to produce GFP above background levels. Two cell fractions were collected in each round of sorting.

In the initial sort the M1 gate collected cells in luminescence channels 1 to 4.5; those cells with the lowest GFP signal (5% of the induced population). The M2 sort gate collected cells in luminescence channels 4.5 to 20; cells with low GFP signal (10% of the induced population). The M1 and M2 fractions together represented the 15% of the induced population responding least to the GFP induction treatment. In order to assure that the diversity of the ribozyme library was represented 2.3 X 10^6 cells were collected in the M1 fraction and 4.6 x 10^6 cells were collected in the M2 fraction. The M1 and M2 fractions wee cultured separately and representative portions of each were cryopreserved after each round of sorting.

When treated with PCM and PMA prior to a second round of sorting, cells from both the M1 and M2 fractions responded as before with >90% of the cells producing elevated levels of GFP. The same sorting criteria and sort gates were used in the second round. As in the first round of sorting the M1 sort gate collected 5% of the treated cells (those with little or no GFP) and the M2 gate collected 10% of the cells. Two more rounds of sorting were performed using the same sorting criteria.

Prior to the third round of sorting the M1 fraction showed a three-fold enrichment of GFP negative cells. Prior to the fourth round of sorting both the M1 and M2 fractions were significantly enriched in cells unresponsive to the GFP induction treatment.

Following the third round of sorting the M1 fraction was selected to generate a database of ribozymes present in the sorted cells.

Example 5: Recovery of Ribozyme Sequence from Sorted Cells

Genomic DNA was obtained from sorted ribozyme library cells by standard methods. Nested polymerase chain reaction (PCR) primers (Sequence ID Nos. 5468 and 5469) that hybridized to the retroviral vector 5' and 3' of the ribozyme were used to recover and amplify the ribozyme sequences from the Clone 8 library cell DNA. The PCR product was ligated into a bacterial cloning vector. Two methods were developed to use the recovered ribozyme library, in plasmid form, to generate a database of ribozyme binding arm sequences. In the first approach the library was cloned into *E. coli*. DNA was prepared by plasmid isolation from bacterial colonies or by direct colony PCR and ribozyme arm sequence was determined. Over 450 sequences have been obtained by this method. A second method used the ribozyme library to transfect H292 Clone 8 cells. Clonal lines of stably transfected cells were established and induced with PCM and PMA. Those lines which failed to respond to GFP induction were probed by PCR for single ribozyme integration events. Over 300 sequences were obtained in this manner. The unique ribozyme sequences obtained by both methods were added to a Target Sequence Tag (TST) database.

Example 6: Bioinformatics

After sequencing 760 recovered ribozymes 171 unique sequences were found. Of the unique sequences, 91 have been recovered once and 80 have been found multiple times. Most of the repeated sequences have been found 2 to 11 times. One sequence has been recovered 145 times. The diversity of the sequences obtained indicates that the sorted cells are a promising source of information leading to target discovery.

Ribozyme binding arm sequences were compared to public and private gene data banks. Gene matches were compiled according to perfect and imperfect matches. Potential gene targets were categorized by the number of different ribozyme sequences matching each gene. Multiple ribozyme matches have been found for 180 genes. Genes with more than one perfect ribozyme match were given close attention. A total of 34 genes have been verified to date to have multiple perfect ribozyme matches. Of those at least 17 have protein products of known function.

Two perfect ribozyme matches were found for human calcium activated chloride channel-1 (hCLCA1). Each ribozyme matches at two sites in the hCLCA1 gene. A third sorted library ribozyme sequence "hits" hCLCA1 but has a single nucleotide mismatch.

Example 7: Selection of hCLCA1 for Validation

The selection of hCLCA1 as a candidate for target validation was based on bioinformatics and on emerging data in murine models of mucous hypersecretion in the trachea and lung. Two ribozymes (Seq. ID Nos. 2332 and 2273) recovered from cells that no longer respond to mucin promoter/GFP induction match perfectly to hCLCA1. A third has a single mismatch. Evidence from two murine models indicates a correlation between mucous hypersecretion in the lung and strong upregulation of gob-5 (GenBank ABO17156), a murine homologue of hCLCA1.

Example 8: Validation of hCLCA1

To validate hCLCA1 as a regulator of MUC5AC expression, GeneBloc reagents were designed (Table IX) to the hCLCA1 cDNA sequence (GenBank AF039400). GeneBloc reagents are complexed with a cationic lipid formulation prior to administration to H292/MUC5AC/GFP Clone 8 cells. Concentrations of the GeneBloc reagents administered range from 30 nM to 120 nM at cationic lipid concentrations of 4-6 μg/mL. Cells are treated with GeneBloc reagents for 72 to 96 hours. Before the termination of GeneBloc treatment, PCM (to 40 %) and PMA (to 50 nM) are added to induce the MUC5AC promoter. After twenty hours of induction the cells are harvested and assayed for phenotypic and molecular parameters. Reduced GFP expression in GeneBloc treated cells (measured by flow cytometry) is taken as evidence for validation of hCLCA1. Knockdown of hCLCA1

RNA in GeneBloc treated cells can correlate with reduced endogenous MUC5AC RNA and reduced GFP RNA (from the MUC5AC/GFP construct) to complete validation of hCLCA1.

Example 9: Identification of Potential Target Sites in Human CLCA1 RNA

The sequence of human CLCA1 is screened for accessible sites using a computer-folding algorithm. Regions of the RNA are identified that do not form secondary folding structures. These regions contain potential ribozyme and/or antisense binding/cleavage sites. The sequences of these binding/cleavage sites are shown in **Tables III-IX.**

Example 10: Selection of Enzymatic Nucleic Acid Cleavage Sites in Human CLCA1 RNA

Ribozyme target sites are chosen by analyzing sequences of Human CLCA1 (GenBank accession numbers: NM_001285 and AF039400) and prioritizing the sites on the basis of folding. Ribozymes are designed that could bind each target and are 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 are 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.

Example 11: Chemical Synthesis and Purification of Ribozymes and Antisense for Efficient Cleavage and/or blocking of CLCA1 RNA

Ribozymes and antisense constructs are designed to anneal to various sites in the RNA message. The binding arms of the ribozymes are complementary to the target site sequences described above, while the antisense constructs are fully complimentary to the target site sequences described above. The ribozymes and antisense constructs were chemically synthesized. The method of synthesis used followed the procedure for normal RNA synthesis as described above and 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 typically >98%.

Ribozymes and antisense constructs are also synthesized from DNA templates using bacteriophage T7 RNA polymerase (Milligan and Uhlenbeck, 1989, *Methods Enzymol.* 180, 51). Ribozymes and antisense constructs are purified by gel electrophoresis using general methods or are purified by high pressure liquid chromatography (HPLC; see Wincott *et al.*, *supra*; the totality of which is hereby incorporated herein by reference) and are resuspended in water. The sequences of the chemically synthesized ribozymes and antisense constructs used in this study are shown below in **Table III-IX.**

Indications

Particular conditions and disease states that can be associated with CLCA1 expression modulation include but are not limited to Chronic Obstructive Pulmonary Disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome, and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue, alone or in combination with other therapies.

The present body of knowledge in CLCA1 research indicates the need for methods to assay CLCA1 activity and for compounds that can regulate CLCA1 expression for research, diagnostic, and therapeutic use.

The nucleic acid molecules of the present invention may also be administered to a patient in combination with other therapeutic compounds to increase the overall therapeutic effect. The use of multiple compounds to treat an indication may increase the beneficial effects while reducing the presence of side effects. Oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylcysteine, mucokinetic agents, and DNase (Pulmozyme), are non-limiting examples of methods and/or treatments that can be used in combination with nucleic acid molecules of the invention. Those skilled in the art will recognize that other drug compounds and therapies can be similarly and readily combined with the nucleic acid molecules of the instant invention (*e.g.* ribozymes and antisense molecules) and are, therefore, within the scope of the instant invention.

Cell Culture

The cell culture system described in Example 8 can be used to evaluate nucleic acid molecules of the invention for efficacy in CLCA1 and mucin modulation.

Animal Models

Numerous reports can be found which describe animal models relevant to disease states such as COPD and cystic fibrosis. These models can be used to determine efficacy of the nucleic acid molecules of the instant invention targeting such disease states or conditions. Animal models for chronic pulmonary disease (COPD) are described by Shapiro, 2000, *Am. J. Respir. Cell Mol. Biol.*, 22(1), 4-7; Hogg, 1998, *Ika Daigaku Zasshi,* 56(3), 429-432; and Garssen *et al.*, 1997, *Inhalation Toxicol.*, 9(6), 581-599. Animal models for cystic fibrosis are described by Kent *et al.*, 1997, *J. Clin. Invest.*, 100(12), 3060-3069; Hill *et al.*, 1997, 62(1), 113-122; Grubb and Gabriel, 1997, *Am. J. Physiol.*, 272, G258-G266; Rozmahel, 1996, *From: Diss. Abstr. Int. B 1997*, 57(8), 4863; Van Doorninck *et al.*, 1995, *EMBO J.*, 14(18), 4403-11; and Zeiher *et al.*, 1995, *J. Clin. Invest.*, 96(4), 2051-64.

Diagnostic uses

The nucleic acid molecules of this invention (*e.g., ribozymes)* may be used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 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 mRNAs associated with CLCA1-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 can 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.*, CLCA1) 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 enzymatic nucleic acid molecule is ideal for cleavage of RNAs of unknown sequence. Applicant describes the use of nucleic acid molecules to down-regulate gene expression of target genes in bacterial, microbial, fungal, viral, and eukaryotic systems including plant, or mammalian cells.

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

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

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

The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of" and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments, optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the description and the appended claims.

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

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 [[i],[ii]].
- Complete kinetic framework established for one ribozyme [[iii],[iv],[v],[vi]].
- Studies of ribozyme folding and substrate docking underway [[vii],[viii],[ix]].
- Chemical modification investigation of important residues well established [[x],[xi]].
- The small (4-6 nt) binding site may make this ribozyme too non-specific for targeted RNA cleavage, however, the Tetrahymena group I intron has been used to repair a "defective" □-galactosidase message by the ligation of new □-galactosidase sequences onto the defective message [[xii]].

RNAse P RNA (M1 RNA)

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

Group II Introns

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

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

Neurospora VS RNA

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

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

Hairpin Ribozyme

- Size: ~50 nucleotides.
- Requires the target sequence GUC immediately 3' of the cleavage site.
- Binds 4-6 nucleotides at the 5'-side of the cleavage site and a variable number to the 3'-side of the cleavage site.
- Reaction mechanism: attack by 2′-OH 5′ to the scissile bond to generate cleavage products with 2′,3′-cyclic phosphate and 5′-OH ends.

- 3 known members of this class. Found in three plant pathogen (satellite RNAs of the tobacco ringspot virus, arabis mosaic virus and chicory yellow mottle virus) which uses RNA as the infectious agent.
- Essential structural features largely defined [xxxi,xxxii,xxxiii,xxxiv]
- Ligation activity (in addition to cleavage activity) makes ribozyme amenable to engineering through *in vitro* selection [xxxv]
- Complete kinetic framework established for one ribozyme [xxxvi].
- Chemical modification investigation of important residues begun [xxxvii,xxxviii].

Hepatitis Delta Virus (HDV) Ribozyme

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

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Table II:

A. 2.5 µmol Synthesis Cycle ABI 394 Instrument

Reagent	Equivalents	Amount	Wait Time* DNA	Wait Time* 2'-O-methyl	Wait Time* RNA
Phosphoramidites	6.5	163 µL	45 sec	2.5 min	7.5 min
S-Ethyl Tetrazole	23.8	238 µL	45 sec	2.5 min	7.5 min
Acetic Anhydride	100	233 µL	5 sec	5 sec	5 sec
N-Methyl Imidazole	186	233 µL	5 sec	5 sec	5 sec
TCA	176	2.3 mL	21 sec	21 sec	21 sec
Iodine	11.2	1.7 mL	45 sec	45 sec	45 sec
Beaucage	12.9	645 µL	100 sec	300 sec	300 sec
Acetonitrile	NA	6.67 mL	NA	NA	NA

B. 0.2 µmol Synthesis Cycle ABI 394 Instrument

Reagent	Equivalents	Amount	Wait Time* DNA	Wait Time* 2'-O-methyl	Wait Time* RNA
Phosphoramidites	15	31 µL	45 sec	233 sec	465 sec
S-Ethyl Tetrazole	38.7	31 µL	45 sec	233 min	465 sec
Acetic Anhydride	655	124 µL	5 sec	5 sec	5 sec
N-Methyl Imidazole	1245	124 µL	5 sec	5 sec	5 sec
TCA	700	732 µL	10 sec	10 sec	10 sec
Iodine	20.6	244 µL	15 sec	15 sec	15 sec
Beaucage	7.7	232 µL	100 sec	300 sec	300 sec

52

Acetonitrile	NA	2.64 mL	NA	NA	NA

C. 0.2 μmol Synthesis Cycle 96 well Instrument

Reagent	Equivalents DNA/2'-O-methyl/Ribo	Amount DNA/2'-O-methyl/Ribo	Wait Time* DNA	Wait Time* 2'-O-methyl	Wait Time* Ribo
Phosphoramidites	22/33/66	40/60/120 μL	60 sec	180 sec	360sec
S-Ethyl Tetrazole	70/105/210	40/60/120 μL	60 sec	180 min	360 sec
Acetic Anhydride	265/265/265	50/50/50 μL	10 sec	10 sec	10 sec
N-Methyl Imidazole	502/502/502	50/50/50 μL	10 sec	10 sec	10 sec
TCA	238/475/475	250/500/500 μL	15 sec	15 sec	15 sec
Iodine	6.8/6.8/6.8	80/80/80 μL	30 sec	30 sec	30 sec
Beaucage	34/51/51	80/120/120	100 sec	200 sec	200 sec
Acetonitrile	NA	1150/1150/1150 μL	NA	NA	NA

*** Wait time does not include contact time during delivery.**

Table III: Human CLCA1 Hammerhead Ribozyme and Target Sequence 249.021

Pos	Substrate	Seq ID No.	Ribozyme	Rz Seq ID No.
11	CUAAUGCU U UUGGUACA	1	UGUACCAA CUGAUGAG GCCGUUAGGC CGAA AGCAUUAG	2190
12	UAAUGCUU U UGGUACAA	2	UUGUACCA CUGAUGAG GCCGUUAGGC CGAA AAGCAUUA	2191
13	AAUGCUUU U GGUACAAA	3	UUUGUACC CUGAUGAG GCCGUUAGGC CGAA AAAGCAUU	2192
17	CUUUUGGU A CAAAUGGA	4	UCCAUUUG CUGAUGAG GCCGUUAGGC CGAA ACCAAAAG	2193
34	UGUGGAAU A UAAUUGAA	5	UUCAAUUA CUGAUGAG GCCGUUAGGC CGAA AUUCCACA	2194
36	UGGAAUAU A AUUGAAUA	6	UAUUCAAU CUGAUGAG GCCGUUAGGC CGAA AUAUUCCA	2195
39	AAUAUAAU U GAAUAUUU	7	AAAUAUUC CUGAUGAG GCCGUUAGGC CGAA AUUAUAUU	2196
44	AAUUGAAU A UUUUCUUG	8	CAAGAAAA CUGAUGAG GCCGUUAGGC CGAA AUUCAAUU	2197
46	UUGAAUAU U UUCUUGUU	9	AACAAGAA CUGAUGAG GCCGUUAGGC CGAA AUAUUCAA	2198
47	UGAAUAUU U UCUUGUUU	10	AAACAAGA CUGAUGAG GCCGUUAGGC CGAA AAUAUUCA	2199
48	GAAUAUUU U CUUGUUUA	11	UAAACAAG CUGAUGAG GCCGUUAGGC CGAA AAAUAUUC	2200
49	AAUAUUUU C UUGUUUAA	12	UUAAACAA CUGAUGAG GCCGUUAGGC CGAA AAAAUAUU	2201
51	UAUUUUCU U GUUUAAGG	13	CCUUAAAC CUGAUGAG GCCGUUAGGC CGAA AGAAAAUA	2202
54	UUUCUUGU U UAAGGGGA	14	UCCCCUUA CUGAUGAG GCCGUUAGGC CGAA ACAAGAAA	2203
55	UUCUUGUU U AAGGGGAG	15	CUCCCCUU CUGAUGAG GCCGUUAGGC CGAA AACAAGAA	2204
56	UCUUGUUU A AGGGGAGC	16	GCUCCCCU CUGAUGAG GCCGUUAGGC CGAA AAACAAGA	2205
77	AGAGGUGU U GAGGUUAU	17	AUAACCUC CUGAUGAG GCCGUUAGGC CGAA ACACCUCU	2206
83	GUUGAGGU U AUGUCAAG	18	CUUGACAU CUGAUGAG GCCGUUAGGC CGAA ACCUCAAC	2207
84	UUGAGGUU A UGUCAAGC	19	GCUUGACA CUGAUGAG GCCGUUAGGC CGAA AACCUCAA	2208
88	GGUUAUGU C AAGCAUCU	20	AGAUGCUU CUGAUGAG GCCGUUAGGC CGAA ACAUAACC	2209
95	UCAAGCAU C UGGCACAG	21	CUGUGCCA CUGAUGAG GCCGUUAGGC CGAA AUGCUUGA	2210
122	AUGGAAAU A UUUACAAG	22	CUUGUAAA CUGAUGAG GCCGUUAGGC CGAA AUUUCCAU	2211
124	GGAAAUAU U UACAAGUA	23	UACUUGUA CUGAUGAG GCCGUUAGGC CGAA AUAUUUCC	2212
125	GAAAUAUU U ACAAGUAC	24	GUACUUGU CUGAUGAG GCCGUUAGGC CGAA AAUAUUUC	2213
126	AAAUAUUU A CAAGUACG	25	CGUACUUG CUGAUGAG GCCGUUAGGC CGAA AAAUAUUU	2214
132	UUACAAGU A CGCAAUUU	26	AAAUUGCG CUGAUGAG GCCGUUAGGC CGAA ACUUGUAA	2215
139	UACGCAAU U UGAGACUA	27	UAGUCUCA CUGAUGAG GCCGUUAGGC CGAA AUUGCGUA	2216
140	ACGCAAUU U GAGACUAA	28	UUAGUCUC CUGAUGAG GCCGUUAGGC CGAA AAUUGCGU	2217
147	UUGAGACU A AGAUAUUG	29	CAAUAUCU CUGAUGAG GCCGUUAGGC CGAA AGUCUCAA	2218
152	ACUAAGAU A UUGUUAUC	30	GAUAACAA CUGAUGAG GCCGUUAGGC CGAA AUCUUAGU	2219
154	UAAGAUAU U GUUAUCAU	31	AUGAUAAC CUGAUGAG GCCGUUAGGC CGAA AUAUCUUA	2220
157	GAUAUUGU U AUCAUUCU	32	AGAAUGAU CUGAUGAG GCCGUUAGGC CGAA ACAAUAUC	2221
158	AUAUUGUU A UCAUUCUC	33	GAGAAUGA CUGAUGAG GCCGUUAGGC CGAA AACAAUAU	2222
160	AUUGUUAU C AUUCUCCU	34	AGGAGAAU CUGAUGAG GCCGUUAGGC CGAA AUAACAAU	2223
163	GUUAUCAU U CUCCUAUU	35	AAUAGGAG CUGAUGAG GCCGUUAGGC CGAA AUGAUAAC	2224
164	UUAUCAUU C UCCUAUUG	36	CAAUAGGA CUGAUGAG GCCGUUAGGC CGAA AAUGAUAA	2225
166	AUCAUUCU C CUAUUGAA	37	UUCAAUAG CUGAUGAG GCCGUUAGGC CGAA AGAAUGAU	2226
169	AUUCUCCU A UUGAAGAC	38	GUCUUCAA CUGAUGAG GCCGUUAGGC CGAA AGGAGAAU	2227
171	UCUCCUAU U GAAGACAA	39	UUGUCUUC CUGAUGAG GCCGUUAGGC CGAA AUAGGAGA	2228
187	AGAGCAAU A GUAAAACA	40	UGUUUUAC CUGAUGAG GCCGUUAGGC CGAA AUUGCUCU	2229
190	GCAAUAGU A AAACACAU	41	AUGUGUUU CUGAUGAG GCCGUUAGGC CGAA ACUAUUGC	2230
199	AAACACAU C AGGUCAGG	42	CCUGACCU CUGAUGAG GCCGUUAGGC CGAA AUGUGUUU	2231
204	CAUCAGGU C AGGGGGUU	43	AACCCCCU CUGAUGAG GCCGUUAGGC CGAA ACCUGAUG	2232
212	CAGGGGGU U AAAGACCU	44	AGGUCUUU CUGAUGAG GCCGUUAGGC CGAA ACCCCCUG	2233
213	AGGGGGUU A AAGACCUG	45	CAGGUCUU CUGAUGAG GCCGUUAGGC CGAA AACCCCCU	2234
226	CCUGUGAU A AACCACUU	46	AAGUGGUU CUGAUGAG GCCGUUAGGC CGAA AUCACAGG	2235
234	AAACCACU U CCGAUAAG	47	CUUAUCGG CUGAUGAG GCCGUUAGGC CGAA AGUGGUUU	2236
235	AACCACUU C CGAUAAGU	48	ACUUAUCG CUGAUGAG GCCGUUAGGC CGAA AAGUGGUU	2237
240	CUUCCGAU A AGUUGGAA	49	UUCCAACU CUGAUGAG GCCGUUAGGC CGAA AUCGGAAG	2238
244	CGAUAAGU U GGAAACGU	50	ACGUUUCC CUGAUGAG GCCGUUAGGC CGAA ACUUAUCG	2239
257	ACGUGUGU C UAUAUUUU	51	AAAAUAUA CUGAUGAG GCCGUUAGGC CGAA ACACACGU	2240
259	GUGUGUCU A UAUUUUCA	52	UGAAAAUA CUGAUGAG GCCGUUAGGC CGAA AGACACAC	2241

261	GUGUCUAU A UUUUCAUA	53	UAUGAAAA CUGAUGAG GCCGUUAGGC CGAA AUAGACAC	2242
263	GUCUAUAU U UUCAUAUC	54	GAUAUGAA CUGAUGAG GCCGUUAGGC CGAA AUAUAGAC	2243
264	UCUAUAUU U UCAUAUCU	55	AGAUAUGA CUGAUGAG GCCGUUAGGC CGAA AAUAUAGA	2244
265	CUAUAUUU U CAUAUCUG	56	CAGAUAUG CUGAUGAG GCCGUUAGGC CGAA AAAUAUAG	2245
266	UAUAUUUU C AUAUCUGU	57	ACAGAUAU CUGAUGAG GCCGUUAGGC CGAA AAAAUAUA	2246
269	AUUUUCAU A UCUGUAUA	58	UAUACAGA CUGAUGAG GCCGUUAGGC CGAA AUGAAAAU	2247
271	UUUCAUAU C UGUAUAUA	59	UAUAUACA CUGAUGAG GCCGUUAGGC CGAA AUAUGAAA	2248
275	AUAUCUGU A UAUAUAUA	60	UAUAUAUA CUGAUGAG GCCGUUAGGC CGAA ACAGAUAU	2249
277	AUCUGUAU A UAUAUAAU	61	AUUAUAUA CUGAUGAG GCCGUUAGGC CGAA AUACAGAU	2250
279	CUGUAUAU A UAUAAUGG	62	CCAUUAUA CUGAUGAG GCCGUUAGGC CGAA AUAUACAG	2251
281	GUAUAUAU A UAAUGGUA	63	UACCAUUA CUGAUGAG GCCGUUAGGC CGAA AUAUAUAC	2252
283	AUAUAUAU A AUGGUAAA	64	UUUACCAU CUGAUGAG GCCGUUAGGC CGAA AUAUAUAU	2253
289	AUAAUGGU A AAGAAAGA	65	UCUUUCUU CUGAUGAG GCCGUUAGGC CGAA ACCAUUAU	2254
303	AGACACCU U CGUAACCC	66	GGGUUACG CUGAUGAG GCCGUUAGGC CGAA AGGUGUCU	2255
304	GACACCUU C GUAACCCG	67	CGGGUUAC CUGAUGAG GCCGUUAGGC CGAA AAGGUGUC	2256
307	ACCUUCGU A ACCCGCAU	68	AUGCGGGU CUGAUGAG GCCGUUAGGC CGAA ACGAAGGU	2257
316	ACCCGCAU U UUCCAAAG	69	CUUUGGAA CUGAUGAG GCCGUUAGGC CGAA AUGCGGGU	2258
317	CCCGCAUU U UCCAAAGA	70	UCUUUGGA CUGAUGAG GCCGUUAGGC CGAA AAUGCGGG	2259
318	CCGCAUUU U CCAAAGAG	71	CUCUUUGG CUGAUGAG GCCGUUAGGC CGAA AAAUGCGG	2260
319	CGCAUUUU C CAAAGAGA	72	UCUCUUUG CUGAUGAG GCCGUUAGGC CGAA AAAAUGCG	2261
333	AGAGGAAU C ACAGGGAG	73	CUCCCUGU CUGAUGAG GCCGUUAGGC CGAA AUUCCUCU	2262
346	GGAGAUGU A CAGCAAUG	74	CAUUGCUG CUGAUGAG GCCGUUAGGC CGAA ACAUCUCC	2263
362	GGGGCCAU U UAAGAGUU	75	AACUCUUA CUGAUGAG GCCGUUAGGC CGAA AUGGCCCC	2264
363	GGGCCAUU U AAGAGUUC	76	GAACUCUU CUGAUGAG GCCGUUAGGC CGAA AAUGGCCC	2265
364	GGCCAUUU A AGAGUUCU	77	AGAACUCU CUGAUGAG GCCGUUAGGC CGAA AAAUGGCC	2266
370	UUAAGAGU U CUGUGUUC	78	GAACACAG CUGAUGAG GCCGUUAGGC CGAA ACUCUUAA	2267
371	UAAGAGUU C UGUGUUCA	79	UGAACACA CUGAUGAG GCCGUUAGGC CGAA AACUCUUA	2268
377	UUCUGUGU U CAUCUUGA	80	UCAAGAUG CUGAUGAG GCCGUUAGGC CGAA ACACAGAA	2269
378	UCUGUGUU C AUCUUGAU	81	AUCAAGAU CUGAUGAG GCCGUUAGGC CGAA AACACAGA	2270
381	GUGUUCAU C UUGAUUCU	82	AGAAUCAA CUGAUGAG GCCGUUAGGC CGAA AUGAACAC	2271
383	GUUCAUCU U GAUUCUUC	83	GAAGAAUC CUGAUGAG GCCGUUAGGC CGAA AGAUGAAC	2272
387	AUCUUGAU U CUUCACCU	84	AGGUGAAG CUGAUGAG GCCGUUAGGC CGAA AUCAAGAU	2273
388	UCUUGAUU C UUCACCUU	85	AAGGUGAA CUGAUGAG GCCGUUAGGC CGAA AAUCAAGA	2274
390	UUGAUUCU U CACCUUCU	86	AGAAGGUG CUGAUGAG GCCGUUAGGC CGAA AGAAUCAA	2275
391	UGAUUCUU C ACCUUCUA	87	UAGAAGGU CUGAUGAG GCCGUUAGGC CGAA AAGAAUCA	2276
396	CUUCACCU U CUAGAAGG	88	CCUUCUAG CUGAUGAG GCCGUUAGGC CGAA AGGUGAAG	2277
397	UUCACCUU C UAGAAGGG	89	CCCUUCUA CUGAUGAG GCCGUUAGGC CGAA AAGGUGAA	2278
399	CACCUUCU A GAAGGGGC	90	GCCCCUUC CUGAUGAG GCCGUUAGGC CGAA AGAAGGUG	2279
415	CCCUGAGU A AUUCACUC	91	GAGUGAAU CUGAUGAG GCCGUUAGGC CGAA ACUCAGGG	2280
418	UGAGUAAU U CACUCAUU	92	AAUGAGUG CUGAUGAG GCCGUUAGGC CGAA AUUACUCA	2281
419	GAGUAAUU C ACUCAUUC	93	GAAUGAGU CUGAUGAG GCCGUUAGGC CGAA AAUUACUC	2282
423	AAUUCACU C AUUCAGCU	94	AGCUGAAU CUGAUGAG GCCGUUAGGC CGAA AGUGAAUU	2283
426	UCACUCAU U CAGCUGAA	95	UUCAGCUG CUGAUGAG GCCGUUAGGC CGAA AUGAGUGA	2284
427	CACUCAUU C AGCUGAAC	96	GUUCAGCU CUGAUGAG GCCGUUAGGC CGAA AAUGAGUG	2285
446	CAAUGGCU A UGAAGGCA	97	UGCCUUCA CUGAUGAG GCCGUUAGGC CGAA AGCCAUUG	2286
456	GAAGGCAU U GUCGUUGC	98	GCAACGAC CUGAUGAG GCCGUUAGGC CGAA AUGCCUUC	2287
459	GGCAUUGU C GUUGCAAU	99	AUUGCAAC CUGAUGAG GCCGUUAGGC CGAA ACAAUGCC	2288
462	AUUGUCGU U GCAAUCGA	100	UCGAUUGC CUGAUGAG GCCGUUAGGC CGAA ACGACAAU	2289
468	GUUGCAAU C GACCCCAA	101	UUGGGGUC CUGAUGAG GCCGUUAGGC CGAA AUUGCAAC	2290
498	GAAACACU C AUUCAACA	102	UGUUGAAU CUGAUGAG GCCGUUAGGC CGAA AGUGUUUC	2291
501	ACACUCAU U CAACAAAU	103	AUUUGUUG CUGAUGAG GCCGUUAGGC CGAA AUGAGUGU	2292
502	CACUCAUU C AACAAAUA	104	UAUUUGUU CUGAUGAG GCCGUUAGGC CGAA AAUGAGUG	2293
510	CAACAAAU A AAGGACAU	105	AUGUCCUU CUGAUGAG GCCGUUAGGC CGAA AUUUGUUG	2294
533	CCAGGCAU C UCUGUAUC	106	GAUACAGA CUGAUGAG GCCGUUAGGC CGAA AUGCCUGG	2295
535	AGGCAUCU C UGUAUCUG	107	CAGAUACA CUGAUGAG GCCGUUAGGC CGAA AGAUGCCU	2296
539	AUCUCUGU A UCUGUUUG	108	CAAACAGA CUGAUGAG GCCGUUAGGC CGAA ACAGAGAU	2297

541	CUCUGUAU C UGUUUGAA	109	UUCAAACA CUGAUGAG GCCGUUAGGC CGAA AUACAGAG	2298
545	GUAUCUGU U UGAAGCUA	110	UAGCUUCA CUGAUGAG GCCGUUAGGC CGAA ACAGAUAC	2299
546	UAUCUGUU U GAAGCUAC	111	GUAGCUUC CUGAUGAG GCCGUUAGGC CGAA AACAGAUA	2300
553	UUGAAGCU A CAGGAAAG	112	CUUUCCUG CUGAUGAG GCCGUUAGGC CGAA AGCUUCAA	2301
566	AAAGCGAU U UUAUUUCA	113	UGAAAUAA CUGAUGAG GCCGUUAGGC CGAA AUCGCUUU	2302
567	AAGCGAUU U UAUUUCAA	114	UUGAAAUA CUGAUGAG GCCGUUAGGC CGAA AAUCGCUU	2303
568	AGCGAUUU U AUUUCAAA	115	UUUGAAAU CUGAUGAG GCCGUUAGGC CGAA AAAUCGCU	2304
569	GCGAUUUU A UUUCAAAA	116	UUUUGAAA CUGAUGAG GCCGUUAGGC CGAA AAAAUCGC	2305
571	GAUUUUAU U UCAAAAAU	117	AUUUUUGA CUGAUGAG GCCGUUAGGC CGAA AUAAAAUC	2306
572	AUUUUAUU U CAAAAAUG	118	CAUUUUUG CUGAUGAG GCCGUUAGGC CGAA AAUAAAAU	2307
573	UUUUAUUU C AAAAAUGU	119	ACAUUUUU CUGAUGAG GCCGUUAGGC CGAA AAAUAAAA	2308
582	AAAAAUGU U GCCAUUUU	120	AAAAUGGC CUGAUGAG GCCGUUAGGC CGAA ACAUUUUU	2309
588	GUUGCCAU U UUGAUUCC	121	GGAAUCAA CUGAUGAG GCCGUUAGGC CGAA AUGGCAAC	2310
589	UUGCCAUU U UGAUUCCU	122	AGGAAUCA CUGAUGAG GCCGUUAGGC CGAA AAUGGCAA	2311
590	UGCCAUUU U GAUUCCUG	123	CAGGAAUC CUGAUGAG GCCGUUAGGC CGAA AAAUGGCA	2312
594	AUUUUGAU U CCUGAAAC	124	GUUUCAGG CUGAUGAG GCCGUUAGGC CGAA AUCAAAAU	2313
595	UUUUGAUU C CUGAAACA	125	UGUUUCAG CUGAUGAG GCCGUUAGGC CGAA AAUCAAAA	2314
623	GGCUGACU A UGUGAGAC	126	GUCUCACA CUGAUGAG GCCGUUAGGC CGAA AGUCAGCC	2315
639	CCAAAACU U GAGACCUA	127	UAGGUCUC CUGAUGAG GCCGUUAGGC CGAA AGUUUUGG	2316
647	UGAGACCU A CAAAAAUG	128	CAUUUUUG CUGAUGAG GCCGUUAGGC CGAA AGGUCUCA	2317
663	GCUGAUGU U CUGGUUGC	129	GCAACCAG CUGAUGAG GCCGUUAGGC CGAA ACAUCAGC	2318
664	CUGAUGUU C UGGUUGCU	130	AGCAACCA CUGAUGAG GCCGUUAGGC CGAA AACAUCAG	2319
669	GUUCUGGU U GCUGAGUC	131	GACUCAGC CUGAUGAG GCCGUUAGGC CGAA ACCAGAAC	2320
677	UGCUGAGU C UACUCCUC	132	GAGGAGUA CUGAUGAG GCCGUUAGGC CGAA ACUCAGCA	2321
679	CUGAGUCU A CUCCUCCA	133	UGGAGGAG CUGAUGAG GCCGUUAGGC CGAA AGACUCAG	2322
682	AGUCUACU C CUCCAGGU	134	ACCUGGAG CUGAUGAG GCCGUUAGGC CGAA AGUAGACU	2323
685	CUACUCCU C CAGGUAAU	135	AUUACCUG CUGAUGAG GCCGUUAGGC CGAA AGGAGUAG	2324
691	CUCCAGGU A AUGAUGAA	136	UUCAUCAU CUGAUGAG GCCGUUAGGC CGAA ACCUGGAG	2325
704	UGAACCCU A CACUGAGC	137	GCUCAGUG CUGAUGAG GCCGUUAGGC CGAA AGGGUUCA	2326
747	GAAAGGAU C CACCUCAC	138	GUGAGGUG CUGAUGAG GCCGUUAGGC CGAA AUCCUUUC	2327
753	AUCCACCU C ACUCCUGA	139	UCAGGAGU CUGAUGAG GCCGUUAGGC CGAA AGGUGGAU	2328
757	ACCUCACU C CUGAUUUC	140	GAAAUCAG CUGAUGAG GCCGUUAGGC CGAA AGUGAGGU	2329
763	CUCCUGAU U UCAUUGCA	141	UGCAAUGA CUGAUGAG GCCGUUAGGC CGAA AUCAGGAG	2330
764	UCCUGAUU U CAUUGCAG	142	CUGCAAUG CUGAUGAG GCCGUUAGGC CGAA AAUCAGGA	2331
765	CCUGAUUU C AUUGCAGG	143	CCUGCAAU CUGAUGAG GCCGUUAGGC CGAA AAAUCAGG	2332
768	GAUUUCAU U GCAGGAAA	144	UUUCCUGC CUGAUGAG GCCGUUAGGC CGAA AUGAAAUC	2333
782	AAAAAAGU U AGCUGAAU	145	AUUCAGCU CUGAUGAG GCCGUUAGGC CGAA ACUUUUUU	2334
783	AAAAAGUU A GCUGAAUA	146	UAUUCAGC CUGAUGAG GCCGUUAGGC CGAA AACUUUUU	2335
791	AGCUGAAU A UGGACCAC	147	GUGGUCCA CUGAUGAG GCCGUUAGGC CGAA AUUCAGCU	2336
805	CACAAGGU A AGGCAUUU	148	AAAUGCCU CUGAUGAG GCCGUUAGGC CGAA ACCUUGUG	2337
812	UAAGGCAU U UGUCCAUG	149	CAUGGACA CUGAUGAG GCCGUUAGGC CGAA AUGCCUUA	2338
813	AAGGCAUU U GUCCAUGA	150	UCAUGGAC CUGAUGAG GCCGUUAGGC CGAA AAUGCCUU	2339
816	GCAUUUGU C CAUGAGUG	151	CACUCAUG CUGAUGAG GCCGUUAGGC CGAA ACAAAUGC	2340
829	AGUGGGCU C AUCUACGA	152	UCGUAGAU CUGAUGAG GCCGUUAGGC CGAA AGCCCACU	2341
832	GGGCUCAU C UACGAUGG	153	CCAUCGUA CUGAUGAG GCCGUUAGGC CGAA AUGAGCCC	2342
834	GCUCAUCU A CGAUGGGG	154	CCCCAUCG CUGAUGAG GCCGUUAGGC CGAA AGAUGAGC	2343
846	UGGGGAGU A UUUGACGA	155	UCGUCAAA CUGAUGAG GCCGUUAGGC CGAA ACUCCCCA	2344
848	GGGAGUAU U UGACGAGU	156	ACUCGUCA CUGAUGAG GCCGUUAGGC CGAA AUACUCCC	2345
849	GGAGUAUU U GACGAGUA	157	UACUCGUC CUGAUGAG GCCGUUAGGC CGAA AAUACUCC	2346
857	UGACGAGU A CAAUAAUG	158	CAUUAUUG CUGAUGAG GCCGUUAGGC CGAA ACUCGUCA	2347
862	AGUACAAU A AUGAUGAG	159	CUCAUCAU CUGAUGAG GCCGUUAGGC CGAA AUUGUACU	2348
875	UGAGAAAU U CUACUUAU	160	AUAAGUAG CUGAUGAG GCCGUUAGGC CGAA AUUUCUCA	2349
876	GAGAAAUU C UACUUAUC	161	GAUAAGUA CUGAUGAG GCCGUUAGGC CGAA AAUUUCUC	2350
878	GAAAUUCU A CUUAUCCA	162	UGGAUAAG CUGAUGAG GCCGUUAGGC CGAA AGAAUUUC	2351
881	AUUCUACU U AUCCAAUG	163	CAUUGGAU CUGAUGAG GCCGUUAGGC CGAA AGUAGAAU	2352
882	UUCUACUU A UCCAAUGG	164	CCAUUGGA CUGAUGAG GCCGUUAGGC CGAA AAGUAGAA	2353

884	CUACUUAU C CAAUGGAA	165	UUCCAUUG CUGAUGAG GCCGUUAGGC CGAA AUAAGUAG	2354
897	GGAAGAAU A CAAGCAGU	166	ACUGCUUG CUGAUGAG GCCGUUAGGC CGAA AUUCUUCC	2355
906	CAAGCAGU A AGAUGUUC	167	GAACAUCU CUGAUGAG GCCGUUAGGC CGAA ACUGCUUG	2356
913	UAAGAUGU U CAGCAGGU	168	ACCUGCUG CUGAUGAG GCCGUUAGGC CGAA ACAUCUUA	2357
914	AAGAUGUU C AGCAGGUA	169	UACCUGCU CUGAUGAG GCCGUUAGGC CGAA AACAUCUU	2358
922	CAGCAGGU A UUACUGGU	170	ACCAGUAA CUGAUGAG GCCGUUAGGC CGAA ACCUGCUG	2359
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925	CAGGUAUU A CUGGUACA	172	UGUACCAG CUGAUGAG GCCGUUAGGC CGAA AAUACCUG	2361
931	UUACUGGU A CAAAUGUA	173	UACAUUUG CUGAUGAG GCCGUUAGGC CGAA ACCAGUAA	2362
939	ACAAAUGU A GUAAAGAA	174	UUCUUUAC CUGAUGAG GCCGUUAGGC CGAA ACAUUUGU	2363
942	AAUGUAGU A AAGAAGUG	175	CACUUCUU CUGAUGAG GCCGUUAGGC CGAA ACUACAUU	2364
952	AGAAGUGU C AGGGAGGC	176	GCCUCCCU CUGAUGAG GCCGUUAGGC CGAA ACACUUCU	2365
967	GCAGCUGU U ACACCAAA	177	UUUGGUGU CUGAUGAG GCCGUUAGGC CGAA ACAGCUGC	2366
968	CAGCUGUU A CACCAAAA	178	UUUUGGUG CUGAUGAG GCCGUUAGGC CGAA AACAGCUG	2367
986	AUGCACAU U CAAUAAAG	179	CUUUAUUG CUGAUGAG GCCGUUAGGC CGAA AUGUGCAU	2368
987	UGCACAUU C AAUAAAGU	180	ACUUUAUU CUGAUGAG GCCGUUAGGC CGAA AAUGUGCA	2369
991	CAUUCAAU A AAGUUACA	181	UGUAACUU CUGAUGAG GCCGUUAGGC CGAA AUUGAAUG	2370
996	AAUAAAGU U ACAGGACU	182	AGUCCUGU CUGAUGAG GCCGUUAGGC CGAA ACUUUAUU	2371
997	AUAAAGUU A CAGGACUC	183	GAGUCCUG CUGAUGAG GCCGUUAGGC CGAA AACUUUAU	2372
1005	ACAGGACU C UAUGAAAA	184	UUUUCAUA CUGAUGAG GCCGUUAGGC CGAA AGUCCUGU	2373
1007	AGGACUCU A UGAAAAAG	185	CUUUUUCA CUGAUGAG GCCGUUAGGC CGAA AGAGUCCU	2374
1025	AUGUGAGU U UGUUCUCC	186	GGAGAACA CUGAUGAG GCCGUUAGGC CGAA ACUCACAU	2375
1026	UGUGAGUU U GUUCUCCA	187	UGGAGAAC CUGAUGAG GCCGUUAGGC CGAA AACUCACA	2376
1029	GAGUUUGU U CUCCAAUC	188	GAUUGGAG CUGAUGAG GCCGUUAGGC CGAA ACAAACUC	2377
1030	AGUUUGUU C UCCAAUCC	189	GGAUUGGA CUGAUGAG GCCGUUAGGC CGAA AACAAACU	2378
1032	UUUGUUCU C CAAUCCCG	190	CGGGAUUG CUGAUGAG GCCGUUAGGC CGAA AGAACAAA	2379
1037	UCUCCAAU C CCGCCAGA	191	UCUGGCGG CUGAUGAG GCCGUUAGGC CGAA AUUGGAGA	2380
1057	AGAAGGCU U CUAUAAUG	192	CAUUAUAG CUGAUGAG GCCGUUAGGC CGAA AGCCUUCU	2381
1058	GAAGGCUU C UAUAAUGU	193	ACAUUAUA CUGAUGAG GCCGUUAGGC CGAA AAGCCUUC	2382
1060	AGGCUUCU A UAAUGUUU	194	AAACAUUA CUGAUGAG GCCGUUAGGC CGAA AGAAGCCU	2383
1062	GCUUCUAU A AUGUUUGC	195	GCAAACAU CUGAUGAG GCCGUUAGGC CGAA AUAGAAGC	2384
1067	UAUAAUGU U UGCACAAC	196	GUUGUGCA CUGAUGAG GCCGUUAGGC CGAA ACAUUAUA	2385
1068	AUAAUGUU U GCACAACA	197	UGUUGUGC CUGAUGAG GCCGUUAGGC CGAA AACAUUAU	2386
1080	CAACAUGU U GAUUCUAU	198	AUAGAAUC CUGAUGAG GCCGUUAGGC CGAA ACAUGUUG	2387
1084	AUGUUGAU U CUAUAGUU	199	AACUAUAG CUGAUGAG GCCGUUAGGC CGAA AUCAACAU	2388
1085	UGUUGAUU C UAUAGUUG	200	CAACUAUA CUGAUGAG GCCGUUAGGC CGAA AAUCAACA	2389
1087	UUGAUUCU A UAGUUGAA	201	UUCAACUA CUGAUGAG GCCGUUAGGC CGAA AGAAUCAA	2390
1089	GAUUCUAU A GUUGAAUU	202	AAUUCAAC CUGAUGAG GCCGUUAGGC CGAA AUAGAAUC	2391
1092	UCUAUAGU U GAAUUCUG	203	CAGAAUUC CUGAUGAG GCCGUUAGGC CGAA ACUAUAGA	2392
1097	AGUUGAAU U CUGUACAG	204	CUGUACAG CUGAUGAG GCCGUUAGGC CGAA AUUCAACU	2393
1098	GUUGAAUU C UGUACAGA	205	UCUGUACA CUGAUGAG GCCGUUAGGC CGAA AAUUCAAC	2394
1102	AAUUCUGU A CAGAACAA	206	UUGUUCUG CUGAUGAG GCCGUUAGGC CGAA ACAGAAUU	2395
1129	AAGAAGCU C CAAACAAG	207	CUUGUUUG CUGAUGAG GCCGUUAGGC CGAA AGCUUCUU	2396
1144	AGCAAAAU C AAAAAUGC	208	GCAUUUUU CUGAUGAG GCCGUUAGGC CGAA AUUUUGCU	2397
1156	AAUGCAAU C UCCGAAGC	209	GCUUCGGA CUGAUGAG GCCGUUAGGC CGAA AUUGCAUU	2398
1158	UGCAAUCU C CGAAGCAC	210	GUGCUUCG CUGAUGAG GCCGUUAGGC CGAA AGAUUGCA	2399
1179	GAAGUGAU C CGUGAUUC	211	GAAUCACG CUGAUGAG GCCGUUAGGC CGAA AUCACUUC	2400
1186	UCCGUGAU U CUGAGGAC	212	GUCCUCAG CUGAUGAG GCCGUUAGGC CGAA AUCACGGA	2401
1187	CCGUGAUU C UGAGGACU	213	AGUCCUCA CUGAUGAG GCCGUUAGGC CGAA AAUCACGG	2402
1196	UGAGGACU U UAAGAAAA	214	UUUUCUUA CUGAUGAG GCCGUUAGGC CGAA AGUCCUCA	2403
1197	GAGGACUU U AAGAAAAC	215	GUUUUCUU CUGAUGAG GCCGUUAGGC CGAA AAGUCCUC	2404
1198	AGGACUUU A AGAAAACC	216	GGUUUUCU CUGAUGAG GCCGUUAGGC CGAA AAAGUCCU	2405
1210	AAACCACU C CUAUGACA	217	UGUCAUAG CUGAUGAG GCCGUUAGGC CGAA AGUGGUUU	2406
1213	CCACUCCU A UGACAACA	218	UGUUGUCA CUGAUGAG GCCGUUAGGC CGAA AGGAGUGG	2407
1234	CACCAAAU C CCACCUUC	219	GAAGGUGG CUGAUGAG GCCGUUAGGC CGAA AUUUGGUG	2408
1241	UCCCACCU U CUCAUUGC	220	GCAAUGAG CUGAUGAG GCCGUUAGGC CGAA AGGUGGGA	2409

1242	CCCACCUU C UCAUUGCU	221	AGCAAUGA CUGAUGAG GCCGUUAGGC CGAA AAGGUGGG	2410
1244	CACCUUCU C AUUGCUGC	222	GCAGCAAU CUGAUGAG GCCGUUAGGC CGAA AGAAGGUG	2411
1247	CUUCUCAU U GCUGCAGA	223	UCUGCAGC CUGAUGAG GCCGUUAGGC CGAA AUGAGAAG	2412
1257	CUGCAGAU U GGACAAAG	224	CUUUGUCC CUGAUGAG GCCGUUAGGC CGAA AUCUGCAG	2413
1269	CAAAGAAU U GUGUGUUU	225	AAACACAC CUGAUGAG GCCGUUAGGC CGAA AUUCUUUG	2414
1276	UUGUGUGU U UAGUCCUU	226	AAGGACUA CUGAUGAG GCCGUUAGGC CGAA ACACACAA	2415
1277	UGUGUGUU U AGUCCUUG	227	CAAGGACU CUGAUGAG GCCGUUAGGC CGAA AACACACA	2416
1278	GUGUGUUU A GUCCUUGA	228	UCAAGGAC CUGAUGAG GCCGUUAGGC CGAA AAACACAC	2417
1281	UGUUUAGU C CUUGACAA	229	UUGUCAAG CUGAUGAG GCCGUUAGGC CGAA ACUAAACA	2418
1284	UUAGUCCU U GACAAAUC	230	GAUUUGUC CUGAUGAG GCCGUUAGGC CGAA AGGACUAA	2419
1292	UGACAAAU C UGGAAGCA	231	UGCUUCCA CUGAUGAG GCCGUUAGGC CGAA AUUUGUCA	2420
1312	CGACUGGU A ACCGCCUC	232	GAGGCGGU CUGAUGAG GCCGUUAGGC CGAA ACCAGUCG	2421
1320	AACCGCCU C AAUCGACU	233	AGUCGAUU CUGAUGAG GCCGUUAGGC CGAA AGGCGGUU	2422
1324	GCCUCAAU C GACUGAAU	234	AUUCAGUC CUGAUGAG GCCGUUAGGC CGAA AUUGAGGC	2423
1333	GACUGAAU C AAGCAGGC	235	GCCUGCUU CUGAUGAG GCCGUUAGGC CGAA AUUCAGUC	2424
1347	GGCCAGCU U UUCCUGCU	236	AGCAGGAA CUGAUGAG GCCGUUAGGC CGAA AGCUGGCC	2425
1348	GCCAGCUU U UCCUGCUG	237	CAGCAGGA CUGAUGAG GCCGUUAGGC CGAA AAGCUGGC	2426
1349	CCAGCUUU U CCUGCUGC	238	GCAGCAGG CUGAUGAG GCCGUUAGGC CGAA AAAGCUGG	2427
1350	CAGCUUUU C CUGCUGCA	239	UGCAGCAG CUGAUGAG GCCGUUAGGC CGAA AAAAGCUG	2428
1365	CAGACAGU U GAGCUGGG	240	CCCAGCUC CUGAUGAG GCCGUUAGGC CGAA ACUGUCUG	2429
1376	GCUGGGGU C CUGGGUUG	241	CAACCCAG CUGAUGAG GCCGUUAGGC CGAA ACCCCAGC	2430
1383	UCCUGGGU U GGGAUGGU	242	ACCAUCCC CUGAUGAG GCCGUUAGGC CGAA ACCCAGGA	2431
1397	GGUGACAU U UGACAGUG	243	CACUGUCA CUGAUGAG GCCGUUAGGC CGAA AUGUCACC	2432
1398	GUGACAUU U GACAGUGC	244	GCACUGUC CUGAUGAG GCCGUUAGGC CGAA AAUGUCAC	2433
1416	GCCCAUGU A CAAAGUGA	245	UCACUUUG CUGAUGAG GCCGUUAGGC CGAA ACAUGGGC	2434
1428	AGUGAACU C AUACAGAU	246	AUCUGUAU CUGAUGAG GCCGUUAGGC CGAA AGUUCACU	2435
1431	GAACUCAU A CAGAUAAA	247	UUUAUCUG CUGAUGAG GCCGUUAGGC CGAA AUGAGUUC	2436
1437	AUACAGAU A AACAGUGG	248	CCACUGUU CUGAUGAG GCCGUUAGGC CGAA AUCUGUAU	2437
1464	GACACACU C GCCAAAAG	249	CUUUUGGC CUGAUGAG GCCGUUAGGC CGAA AGUGUGUC	2438
1475	CAAAAGAU U ACCUGCAG	250	CUGCAGGU CUGAUGAG GCCGUUAGGC CGAA AUCUUUUG	2439
1476	AAAAGAUU A CCUGCAGC	251	GCUGCAGG CUGAUGAG GCCGUUAGGC CGAA AAUCUUUU	2440
1489	CAGCAGCU U CAGGAGGG	252	CCCUCCUG CUGAUGAG GCCGUUAGGC CGAA AGCUGCUG	2441
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1506	ACGUCCAU C UGCAGCGG	255	CCGCUGCA CUGAUGAG GCCGUUAGGC CGAA AUGGACGU	2444
1518	AGCGGGCU U CGAUCGGC	256	GCCGAUCG CUGAUGAG GCCGUUAGGC CGAA AGCCCGCU	2445
1519	GCGGGCUU C GAUCGGCA	257	UGCCGAUC CUGAUGAG GCCGUUAGGC CGAA AAGCCCGC	2446
1523	GCUUCGAU C GGCAUUUA	258	UAAAUGCC CUGAUGAG GCCGUUAGGC CGAA AUCGAAGC	2447
1529	AUCGGCAU U UACUGUGA	259	UCACAGUA CUGAUGAG GCCGUUAGGC CGAA AUGCCGAU	2448
1530	UCGGCAUU U ACUGUGAU	260	AUCACAGU CUGAUGAG GCCGUUAGGC CGAA AAUGCCGA	2449
1531	CGGCAUUU A CUGUGAUU	261	AAUCACAG CUGAUGAG GCCGUUAGGC CGAA AAAUGCCG	2450
1539	ACUGUGAU U AGGAAGAA	262	UUCUUCCU CUGAUGAG GCCGUUAGGC CGAA AUCACAGU	2451
1540	CUGUGAUU A GGAAGAAA	263	UUUCUUCC CUGAUGAG GCCGUUAGGC CGAA AAUCACAG	2452
1550	GAAGAAAU A UCCAACUG	264	CAGUUGGA CUGAUGAG GCCGUUAGGC CGAA AUUUCUUC	2453
1552	AGAAAUAU C CAACUGAU	265	AUCAGUUG CUGAUGAG GCCGUUAGGC CGAA AUAUUUCU	2454
1565	UGAUGGAU C UGAAAUUG	266	CAAUUUCA CUGAUGAG GCCGUUAGGC CGAA AUCCAUCA	2455
1572	UCUGAAAU U GUGCUGCU	267	AGCAGCAC CUGAUGAG GCCGUUAGGC CGAA AUUUCAGA	2456
1603	ACAACACU A UAAGUGGG	268	CCCACUUA CUGAUGAG GCCGUUAGGC CGAA AGUGUUGU	2457
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1616	UGGGUGCU U UAACGAGG	270	CCUCGUUA CUGAUGAG GCCGUUAGGC CGAA AGCACCCA	2459
1617	GGGUGCUU U AACGAGGU	271	ACCUCGUU CUGAUGAG GCCGUUAGGC CGAA AAGCACCC	2460
1618	GGUGCUUU A ACGAGGUC	272	GACCUCGU CUGAUGAG GCCGUUAGGC CGAA AAAGCACC	2461
1626	AACGAGGU C AAACAAAG	273	CUUUGUUU CUGAUGAG GCCGUUAGGC CGAA ACCUCGUU	2462
1644	GGUGCCAU C AUCCACAC	274	GUGUGGAU CUGAUGAG GCCGUUAGGC CGAA AUGGCACC	2463
1647	GCCAUCAU C CACACAGU	275	ACUGUGUG CUGAUGAG GCCGUUAGGC CGAA AUGAUGGC	2464
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1660	CAGUCGCU U UGGGGCCC	277	GGGCCCCA CUGAUGAG GCCGUUAGGC CGAA AGCGACUG	2466
1661	AGUCGCUU U GGGGCCCU	278	AGGGCCCC CUGAUGAG GCCGUUAGGC CGAA AAGCGACU	2467
1670	GGGGCCCU C UGCAGCUC	279	GAGCUGCA CUGAUGAG GCCGUUAGGC CGAA AGGGCCCC	2468
1678	CUGCAGCU C AAGAACUA	280	UAGUUCUU CUGAUGAG GCCGUUAGGC CGAA AGCUGCAG	2469
1686	CAAGAACU A GAGGAGCU	281	AGCUCCUC CUGAUGAG GCCGUUAGGC CGAA AGUUCUUG	2470
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1714	CAGGAGGU U UACAGACA	283	UGUCUGUA CUGAUGAG GCCGUUAGGC CGAA ACCUCCUG	2472
1715	AGGAGGUU U ACAGACAU	284	AUGUCUGU CUGAUGAG GCCGUUAGGC CGAA AACCUCCU	2473
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1724	ACAGACAU A UGCUUCAG	286	CUGAAGCA CUGAUGAG GCCGUUAGGC CGAA AUGUCUGU	2475
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1741	AUCAAGUU C AGAACAAU	291	AUUGUUCU CUGAUGAG GCCGUUAGGC CGAA AACUUGAU	2480
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1911	UUUCUUAU C ACCUGGAC	319	GUCCAGGU CUGAUGAG GCCGUUAGGC CGAA AUAAGAAA	2508
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1976	AGGUGGCU U UGUAGUGG	326	CCACUACA CUGAUGAG GCCGUUAGGC CGAA AGCCACCU	2515
1977	GGUGGCUU U GUAGUGGA	327	UCCACUAC CUGAUGAG GCCGUUAGGC CGAA AAGCCACC	2516
1980	GGCUUUGU A GUGGACAA	328	UUGUCCAC CUGAUGAG GCCGUUAGGC CGAA ACAAAGCC	2517
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2010	GCCUACCU C CAAAUCCC	330	GGGAUUUG CUGAUGAG GCCGUUAGGC CGAA AGGUAGGC	2519
2016	CUCCAAAU C CCAGGCAU	331	AUGCCUGG CUGAUGAG GCCGUUAGGC CGAA AUUUGGAG	2520
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2048	UUGGAAAU A CAGUCUGC	336	GCAGACUG CUGAUGAG GCCGUUAGGC CGAA AUUUCCAA	2525
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2134	CAGUGACU U CCAAAACG	347	CGUUUUGG CUGAUGAG GCCGUUAGGC CGAA AGUCACUG	2536
2135	AGUGACUU C CAAAACGA	348	UCGUUUUG CUGAUGAG GCCGUUAGGC CGAA AAGUCACU	2537
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2191	AUGCAAAU A UUCGCCAA	356	UUGGCGAA CUGAUGAG GCCGUUAGGC CGAA AUUUGCAU	2545
2193	GCAAAUAU U CGCCAAGG	357	CCUUGGCG CUGAUGAG GCCGUUAGGC CGAA AUAUUUGC	2546
2194	CAAAUAUU C GCCAAGGA	358	UCCUUGGC CUGAUGAG GCCGUUAGGC CGAA AAUAUUUG	2547
2207	AGGAGCCU C CCCAAUUC	359	GAAUUGGG CUGAUGAG GCCGUUAGGC CGAA AGGCUCCU	2548
2214	UCCCCAAU U CUCAGGGC	360	GCCCUGAG CUGAUGAG GCCGUUAGGC CGAA AUUGGGGA	2549
2215	CCCCAAUU C UCAGGGCC	361	GGCCCUGA CUGAUGAG GCCGUUAGGC CGAA AAUUGGGG	2550
2217	CCAAUUCU C AGGGCCAG	362	CUGGCCCU CUGAUGAG GCCGUUAGGC CGAA AGAAUUGG	2551
2229	GCCAGUGU C ACAGCCCU	363	AGGGCUGU CUGAUGAG GCCGUUAGGC CGAA ACACUGGC	2552
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2246	GAUUGAAU C AGUGAAUG	365	CAUUCACU CUGAUGAG GCCGUUAGGC CGAA AUUCAAUC	2554
2265	AAAACAGU U ACCUUGGA	366	UCCAAGGU CUGAUGAG GCCGUUAGGC CGAA ACUGUUUU	2555
2266	AAACAGUU A CCUUGGAA	367	UUCCAAGG CUGAUGAG GCCGUUAGGC CGAA AACUGUUU	2556
2270	AGUUACCU U GGAACUAC	368	GUAGUUCC CUGAUGAG GCCGUUAGGC CGAA AGGUAACU	2557
2277	UUGGAACU A CUGGAUAA	369	UUAUCCAG CUGAUGAG GCCGUUAGGC CGAA AGUUCCAA	2558
2284	UACUGGAU A AUGGAGCA	370	UGCUCCAU CUGAUGAG GCCGUUAGGC CGAA AUCCAGUA	2559
2305	CUGAUGCU A CUAAGGAU	371	AUCCUUAG CUGAUGAG GCCGUUAGGC CGAA AGCAUCAG	2560
2308	AUGCUACU A AGGAUGAC	372	GUCAUCCU CUGAUGAG GCCGUUAGGC CGAA AGUAGCAU	2561
2322	GACGGUGU C UACUCAAG	373	CUUGAGUA CUGAUGAG GCCGUUAGGC CGAA ACACCGUC	2562
2324	CGGUGUCU A CUCAAGGU	374	ACCUUGAG CUGAUGAG GCCGUUAGGC CGAA AGACACCG	2563
2327	UGUCUACU C AAGGUAUU	375	AAUACCUU CUGAUGAG GCCGUUAGGC CGAA AGUAGACA	2564
2333	CUCAAGGU A UUUCACAA	376	UUGUGAAA CUGAUGAG GCCGUUAGGC CGAA ACCUUGAG	2565
2335	CAAGGUAU U UCACAACU	377	AGUUGUGA CUGAUGAG GCCGUUAGGC CGAA AUACCUUG	2566
2336	AAGGUAUU U CACAACUU	378	AAGUUGUG CUGAUGAG GCCGUUAGGC CGAA AAUACCUU	2567
2337	AGGUAUUU C ACAACUUA	379	UAAGUUGU CUGAUGAG GCCGUUAGGC CGAA AAAUACCU	2568
2344	UCACAACU U AUGACACG	380	CGUGUCAU CUGAUGAG GCCGUUAGGC CGAA AGUUGUGA	2569
2345	CACAACUU A UGACACGA	381	UCGUGUCA CUGAUGAG GCCGUUAGGC CGAA AAGUUGUG	2570
2359	CGAAUGGU A GAUACAGU	382	ACUGUAUC CUGAUGAG GCCGUUAGGC CGAA ACCAUUCG	2571
2363	UGGUAGAU A CAGUGUAA	383	UUACACUG CUGAUGAG GCCGUUAGGC CGAA AUCUACCA	2572
2370	UACAGUGU A AAAGUGCG	384	CGCACUUU CUGAUGAG GCCGUUAGGC CGAA ACACUGUA	2573
2383	UGCGGGCU C UGGGAGGA	385	UCCUCCCA CUGAUGAG GCCGUUAGGC CGAA AGCCCGCA	2574
2394	GGAGGAGU U AACGCAGC	386	GCUGCGUU CUGAUGAG GCCGUUAGGC CGAA ACUCCUCC	2575
2395	GAGGAGUU A ACGCAGCC	387	GGCUGCGU CUGAUGAG GCCGUUAGGC CGAA AACUCCUC	2576
2418	AGAGUGAU A CCCCAGCA	388	UGCUGGGG CUGAUGAG GCCGUUAGGC CGAA AUCACUCU	2577

2441	AGCACUGU A CAUACCUG	389	CAGGUAUG CUGAUGAG GCCGUUAGGC CGAA ACAGUGCU	2578
2445	CUGUACAU A CCUGGCUG	390	CAGCCAGG CUGAUGAG GCCGUUAGGC CGAA AUGUACAG	2579
2457	GGCUGGAU U GAGAAUGA	391	UCAUUCUC CUGAUGAG GCCGUUAGGC CGAA AUCCAGCC	2580
2472	GAUGAAAU A CAAUGGAA	392	UUCCAUUG CUGAUGAG GCCGUUAGGC CGAA AUUUCAUC	2581
2482	AAUGGAAU C CACCAAGA	393	UCUUGGUG CUGAUGAG GCCGUUAGGC CGAA AUUCCAUU	2582
2499	CCUGAAAU U AAUAAGGA	394	UCCUUAUU CUGAUGAG GCCGUUAGGC CGAA AUUUCAGG	2583
2500	CUGAAAUU A AUAAGGAU	395	AUCCUUAU CUGAUGAG GCCGUUAGGC CGAA AAUUUCAG	2584
2503	AAAUUAAU A AGGAUGAU	396	AUCAUCCU CUGAUGAG GCCGUUAGGC CGAA AUUAAUUU	2585
2514	GAUGAUGU U CAACACAA	397	UUGUGUUG CUGAUGAG GCCGUUAGGC CGAA ACAUCAUC	2586
2515	AUGAUGUU C AACACAAG	398	CUUGUGUU CUGAUGAG GCCGUUAGGC CGAA AACAUCAU	2587
2533	AAGUGUGU U UCAGCAGA	399	UCUGCUGA CUGAUGAG GCCGUUAGGC CGAA ACACACUU	2588
2534	AGUGUGUU U CAGCAGAA	400	UUCUGCUG CUGAUGAG GCCGUUAGGC CGAA AACACACU	2589
2535	GUGUGUUU C AGCAGAAC	401	GUUCUGCU CUGAUGAG GCCGUUAGGC CGAA AAACACAC	2590
2546	CAGAACAU C CUCGGGAG	402	CUCCCGAG CUGAUGAG GCCGUUAGGC CGAA AUGUUCUG	2591
2549	AACAUCCU C GGGAGGCU	403	AGCCUCCC CUGAUGAG GCCGUUAGGC CGAA AGGAUGUU	2592
2558	GGGAGGCU C AUUUGUGG	404	CCACAAAU CUGAUGAG GCCGUUAGGC CGAA AGCCUCCC	2593
2561	AGGCUCAU U UGUGGCUU	405	AAGCCACA CUGAUGAG GCCGUUAGGC CGAA AUGAGCCU	2594
2562	GGCUCAUU U GUGGCUUC	406	GAAGCCAC CUGAUGAG GCCGUUAGGC CGAA AAUGAGCC	2595
2569	UUGUGGCU U CUGAUGUC	407	GACAUCAG CUGAUGAG GCCGUUAGGC CGAA AGCCACAA	2596
2570	UGUGGCUU C UGAUGUCC	408	GGACAUCA CUGAUGAG GCCGUUAGGC CGAA AAGCCACA	2597
2577	UCUGAUGU C CCAAAUGC	409	GCAUUUGG CUGAUGAG GCCGUUAGGC CGAA ACAUCAGA	2598
2587	CAAAUGCU C CCAUACCU	410	AGGUAUGG CUGAUGAG GCCGUUAGGC CGAA AGCAUUUG	2599
2592	GCUCCCAU A CCUGAUCU	411	AGAUCAGG CUGAUGAG GCCGUUAGGC CGAA AUGGGAGC	2600
2599	UACCUGAU C UCUUCCCA	412	UGGGAAGA CUGAUGAG GCCGUUAGGC CGAA AUCAGGUA	2601
2601	CCUGAUCU C UUCCCACC	413	GGUGGGAA CUGAUGAG GCCGUUAGGC CGAA AGAUCAGG	2602
2603	UGAUCUCU U CCCACCUG	414	CAGGUGGG CUGAUGAG GCCGUUAGGC CGAA AGAGAUCA	2603
2604	GAUCUCUU C CCACCUGG	415	CCAGGUGG CUGAUGAG GCCGUUAGGC CGAA AAGAGAUC	2604
2619	GGCCAAAU C ACCGACCU	416	AGGUCGGU CUGAUGAG GCCGUUAGGC CGAA AUUUGGCC	2605
2640	GCGGAAAU U CACGGGGG	417	CCCCCGUG CUGAUGAG GCCGUUAGGC CGAA AUUUCCGC	2606
2641	CGGAAAUU C ACGGGGGC	418	GCCCCCGU CUGAUGAG GCCGUUAGGC CGAA AAUUUCCG	2607
2653	GGGGCAGU C UCAUUAAU	419	AUUAAUGA CUGAUGAG GCCGUUAGGC CGAA ACUGCCCC	2608
2655	GGCAGUCU C AUUAAUCU	420	AGAUUAAU CUGAUGAG GCCGUUAGGC CGAA AGACUGCC	2609
2658	AGUCUCAU U AAUCUGAC	421	GUCAGAUU CUGAUGAG GCCGUUAGGC CGAA AUGAGACU	2610
2659	GUCUCAUU A AUCUGACU	422	AGUCAGAU CUGAUGAG GCCGUUAGGC CGAA AAUGAGAC	2611
2662	UCAUUAAU C UGACUUGG	423	CCAAGUCA CUGAUGAG GCCGUUAGGC CGAA AUUAAUGA	2612
2668	AUCUGACU U GGACAGCU	424	AGCUGUCC CUGAUGAG GCCGUUAGGC CGAA AGUCAGAU	2613
2677	GGACAGCU C CUGGGGAU	425	AUCCCCAG CUGAUGAG GCCGUUAGGC CGAA AGCUGUCC	2614
2689	GGGAUGAU U AUGACCAU	426	AUGGUCAU CUGAUGAG GCCGUUAGGC CGAA AUCAUCCC	2615
2690	GGAUGAUU A UGACCAUG	427	CAUGGUCA CUGAUGAG GCCGUUAGGC CGAA AAUCAUCC	2616
2707	GAACAGCU C ACAAGUAU	428	AUACUUGU CUGAUGAG GCCGUUAGGC CGAA AGCUGUUC	2617
2714	UCACAAGU A UAUCAUUC	429	GAAUGAUA CUGAUGAG GCCGUUAGGC CGAA ACUUGUGA	2618
2716	ACAAGUAU A UCAUUCGA	430	UCGAAUGA CUGAUGAG GCCGUUAGGC CGAA AUACUUGU	2619
2718	AAGUAUAU C AUUCGAAU	431	AUUCGAAU CUGAUGAG GCCGUUAGGC CGAA AUAUACUU	2620
2721	UAUAUCAU U CGAAUAAG	432	CUUAUUCG CUGAUGAG GCCGUUAGGC CGAA AUGAUAUA	2621
2722	AUAUCAUU C GAAUAAGU	433	ACUUAUUC CUGAUGAG GCCGUUAGGC CGAA AAUGAUAU	2622
2727	AUUCGAAU A AGUACAAG	434	CUUGUACU CUGAUGAG GCCGUUAGGC CGAA AUUCGAAU	2623
2731	GAAUAAGU A CAAGUAUU	435	AAUACUUG CUGAUGAG GCCGUUAGGC CGAA ACUUAUUC	2624
2737	GUACAAGU A UUCUUGAU	436	AUCAAGAA CUGAUGAG GCCGUUAGGC CGAA ACUUGUAC	2625
2739	ACAAGUAU U CUUGAUCU	437	AGAUCAAG CUGAUGAG GCCGUUAGGC CGAA AUACUUGU	2626
2740	CAAGUAUU C UUGAUCUC	438	GAGAUCAA CUGAUGAG GCCGUUAGGC CGAA AAUACUUG	2627
2742	AGUAUUCU U GAUCUCAG	439	CUGAGAUC CUGAUGAG GCCGUUAGGC CGAA AGAAUACU	2628
2746	UUCUUGAU C UCAGAGAC	440	GUCUCUGA CUGAUGAG GCCGUUAGGC CGAA AUCAAGAA	2629
2748	CUUGAUCU C AGAGACAA	441	UUGUCUCU CUGAUGAG GCCGUUAGGC CGAA AGAUCAAG	2630
2759	AGACAAGU U CAAUGAAU	442	AUUCAUUG CUGAUGAG GCCGUUAGGC CGAA ACUUGUCU	2631
2760	GACAAGUU C AAUGAAUC	443	GAUUCAUU CUGAUGAG GCCGUUAGGC CGAA AACUUGUC	2632
2768	CAAUGAAU C UCUUCAAG	444	CUUGAAGA CUGAUGAG GCCGUUAGGC CGAA AUUCAUUG	2633

2770	AUGAAUCU C UUCAAGUG	445	CACUUGAA CUGAUGAG GCCGUUAGGC CGAA AGAUUCAU	2634
2772	GAAUCUCU U CAAGUGAA	446	UUCACUUG CUGAUGAG GCCGUUAGGC CGAA AGAGAUUC	2635
2773	AAUCUCUU C AAGUGAAU	447	AUUCACUU CUGAUGAG GCCGUUAGGC CGAA AAGAGAUU	2636
2782	AAGUGAAU A CUACUGCU	448	AGCAGUAG CUGAUGAG GCCGUUAGGC CGAA AUUCACUU	2637
2785	UGAAUACU A CUGCUCUC	449	GAGAGCAG CUGAUGAG GCCGUUAGGC CGAA AGUAUUCA	2638
2791	CUACUGCU C UCAUCCCA	450	UGGGAUGA CUGAUGAG GCCGUUAGGC CGAA AGCAGUAG	2639
2793	ACUGCUCU C AUCCCAAA	451	UUUGGGAU CUGAUGAG GCCGUUAGGC CGAA AGAGCAGU	2640
2796	GCUCUCAU C CCAAAGGA	452	UCCUUUGG CUGAUGAG GCCGUUAGGC CGAA AUGAGAGC	2641
2813	AGCCAACU C UGAGGAAG	453	CUUCCUCA CUGAUGAG GCCGUUAGGC CGAA AGUUGGCU	2642
2823	GAGGAAGU C UUUUUGUU	454	AACAAAAA CUGAUGAG GCCGUUAGGC CGAA ACUUCCUC	2643
2825	GGAAGUCU U UUUGUUUA	455	UAAACAAA CUGAUGAG GCCGUUAGGC CGAA AGACUUCC	2644
2826	GAAGUCUU U UUGUUUAA	456	UUAAACAA CUGAUGAG GCCGUUAGGC CGAA AAGACUUC	2645
2827	AAGUCUUU U UGUUUAAA	457	UUUAAACA CUGAUGAG GCCGUUAGGC CGAA AAAGACUU	2646
2828	AGUCUUUU U GUUUAAAC	458	GUUUAAAC CUGAUGAG GCCGUUAGGC CGAA AAAAGACU	2647
2831	CUUUUUGU U UAAACCAG	459	CUGGUUUA CUGAUGAG GCCGUUAGGC CGAA ACAAAAAG	2648
2832	UUUUUGUU U AAACCAGA	460	UCUGGUUU CUGAUGAG GCCGUUAGGC CGAA AACAAAAA	2649
2833	UUUUGUUU A AACCAGAA	461	UUCUGGUU CUGAUGAG GCCGUUAGGC CGAA AAACAAAA	2650
2847	GAAAACAU U ACUUUUGA	462	UCAAAAGU CUGAUGAG GCCGUUAGGC CGAA AUGUUUUC	2651
2848	AAAACAUU A CUUUUGAA	463	UUCAAAAG CUGAUGAG GCCGUUAGGC CGAA AAUGUUUU	2652
2851	ACAUUACU U UUGAAAAU	464	AUUUUCAA CUGAUGAG GCCGUUAGGC CGAA AGUAAUGU	2653
2852	CAUUACUU U UGAAAAUG	465	CAUUUUCA CUGAUGAG GCCGUUAGGC CGAA AAGUAAUG	2654
2853	AUUACUUU U GAAAAUGG	466	CCAUUUUC CUGAUGAG GCCGUUAGGC CGAA AAAGUAAU	2655
2869	GCACAGAU C UUUUCAUU	467	AAUGAAAA CUGAUGAG GCCGUUAGGC CGAA AUCUGUGC	2656
2871	ACAGAUCU U UUCAUUGC	468	GCAAUGAA CUGAUGAG GCCGUUAGGC CGAA AGAUCUGU	2657
2872	CAGAUCUU U UCAUUGCU	469	AGCAAUGA CUGAUGAG GCCGUUAGGC CGAA AAGAUCUG	2658
2873	AGAUCUUU U CAUUGCUA	470	UAGCAAUG CUGAUGAG GCCGUUAGGC CGAA AAAGAUCU	2659
2874	GAUCUUUU C AUUGCUAU	471	AUAGCAAU CUGAUGAG GCCGUUAGGC CGAA AAAAGAUC	2660
2877	CUUUUCAU U GCUAUUCA	472	UGAAUAGC CUGAUGAG GCCGUUAGGC CGAA AUGAAAAG	2661
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2912	UCUGAAAU C AGAAAUAU	480	AUAUUUCU CUGAUGAG GCCGUUAGGC CGAA AUUUCAGA	2669
2919	UCAGAAAU A UCCAACAU	481	AUGUUGGA CUGAUGAG GCCGUUAGGC CGAA AUUUCUGA	2670
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2928	UCCAACAU U GCACGAGU	483	ACUCGUGC CUGAUGAG GCCGUUAGGC CGAA AUGUUGGA	2672
2937	GCACGAGU A UCUUUGUU	484	AACAAAGA CUGAUGAG GCCGUUAGGC CGAA ACUCGUGC	2673
2939	ACGAGUAU C UUUGUUUA	485	UAAACAAA CUGAUGAG GCCGUUAGGC CGAA AUACUCGU	2674
2941	GAGUAUCU U UGUUUAUU	486	AAUAAACA CUGAUGAG GCCGUUAGGC CGAA AGAUACUC	2675
2942	AGUAUCUU U GUUUAUUC	487	GAAUAAAC CUGAUGAG GCCGUUAGGC CGAA AAGAUACU	2676
2945	AUCUUUGU U UAUUCCUC	488	GAGGAAUA CUGAUGAG GCCGUUAGGC CGAA ACAAAGAU	2677
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2977	AGACACCU A GUCCUGAU	495	AUCAGGAC CUGAUGAG GCCGUUAGGC CGAA AGGUGUCU	2684
2980	CACCUAGU C CUGAUGAA	496	UUCAUCAG CUGAUGAG GCCGUUAGGC CGAA ACUAGGUG	2685
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3007	CUUGUCCU A AUAUUCAU	501	AUGAAUAU CUGAUGAG GCCGUUAGGC CGAA AGGACAAG	2690
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3013	CUAAUAUU C AUAUCAAC	504	GUUGAUAU CUGAUGAG GCCGUUAGGC CGAA AAUAUUAG	2693
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3107	CUGAAUUU U UGUCAGAU	523	AUCUGACA CUGAUGAG GCCGUUAGGC CGAA AAAUUCAG	2712
3108	UGAAUUUU U GUCAGAUA	524	UAUCUGAC CUGAUGAG GCCGUUAGGC CGAA AAAAUUCA	2713
3111	AUUUUUGU C AGAUAAAU	525	AUUUAUCU CUGAUGAG GCCGUUAGGC CGAA ACAAAAAU	2714
3116	UGUCAGAU A AAUAAAAU	526	AUUUUAUU CUGAUGAG GCCGUUAGGC CGAA AUCUGACA	2715
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3129	AAAUAAAU C AUUCAUCC	529	GGAUGAAU CUGAUGAG GCCGUUAGGC CGAA AUUUAUUU	2718
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3133	AAAUCAUU C AUCCUUUU	531	AAAAGGAU CUGAUGAG GCCGUUAGGC CGAA AAUGAUUU	2720
3136	UCAUUCAU C CUUUUUUU	532	AAAAAAAG CUGAUGAG GCCGUUAGGC CGAA AUGAAUGA	2721
3139	UUCAUCCU U UUUUUGAU	533	AUCAAAAA CUGAUGAG GCCGUUAGGC CGAA AGGAUGAA	2722
3140	UCAUCCUU U UUUUGAUU	534	AAUCAAAA CUGAUGAG GCCGUUAGGC CGAA AAGGAUGA	2723
3141	CAUCCUUU U UUUGAUUA	535	UAAUCAAA CUGAUGAG GCCGUUAGGC CGAA AAAGGAUG	2724
3142	AUCCUUUU U UUGAUUAU	536	AUAAUCAA CUGAUGAG GCCGUUAGGC CGAA AAAAGGAU	2725
3143	UCCUUUUU U UGAUUAUA	537	UAUAAUCA CUGAUGAG GCCGUUAGGC CGAA AAAAAGGA	2726
3144	CCUUUUUU U GAUUAUAA	538	UUAUAAUC CUGAUGAG GCCGUUAGGC CGAA AAAAAAGG	2727
3148	UUUUUGAU U AUAAAAUU	539	AAUUUUAU CUGAUGAG GCCGUUAGGC CGAA AUCAAAAA	2728
3149	UUUUGAUU A UAAAAUUU	540	AAAUUUUA CUGAUGAG GCCGUUAGGC CGAA AAUCAAAA	2729
3151	UUGAUUAU A AAAUUUUC	541	GAAAAUUU CUGAUGAG GCCGUUAGGC CGAA AUAAUCAA	2730
3156	UAUAAAAU U UUCUAAAA	542	UUUUAGAA CUGAUGAG GCCGUUAGGC CGAA AUUUUAUA	2731
3157	AUAAAAUU U UCUAAAAU	543	AUUUUAGA CUGAUGAG GCCGUUAGGC CGAA AAUUUUAU	2732
3158	UAAAAUUU U CUAAAAUG	544	CAUUUUAG CUGAUGAG GCCGUUAGGC CGAA AAAUUUUA	2733
3159	AAAAUUUU C UAAAAUGU	545	ACAUUUUA CUGAUGAG GCCGUUAGGC CGAA AAAAUUUU	2734
3161	AAUUUUCU A AAAUGUAU	546	AUACAUUU CUGAUGAG GCCGUUAGGC CGAA AGAAAAUU	2735
3168	UAAAAUGU A UUUUAGAC	547	GUCUAAAA CUGAUGAG GCCGUUAGGC CGAA ACAUUUUA	2736
3170	AAAUGUAU U UUAGACUU	548	AAGUCUAA CUGAUGAG GCCGUUAGGC CGAA AUACAUUU	2737
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3171	AAUGUAUU U UAGACUUC	549	GAAGUCUA CUGAUGAG GCCGUUAGGC CGAA AAUACAUU	2738
3261	AAUGUAUU U UAGACUUC	549	GAAGUCUA CUGAUGAG GCCGUUAGGC CGAA AAUACAUU	2738
3172	AUGUAUUU U AGACUUCC	550	GGAAGUCU CUGAUGAG GCCGUUAGGC CGAA AAAUACAU	2739
3262	AUGUAUUU U AGACUUCC	550	GGAAGUCU CUGAUGAG GCCGUUAGGC CGAA AAAUACAU	2739
3173	UGUAUUUU A GACUUCCU	551	AGGAAGUC CUGAUGAG GCCGUUAGGC CGAA AAAAUACA	2740
3263	UGUAUUUU A GACUUCCU	551	AGGAAGUC CUGAUGAG GCCGUUAGGC CGAA AAAAUACA	2740
3178	UUUAGACU U CCUGUAGG	552	CCUACAGG CUGAUGAG GCCGUUAGGC CGAA AGUCUAAA	2741

3268	UUUAGACU U CCUGUAGG	552	CCUACAGG CUGAUGAG GCCGUUAGGC CGAA AGUCUAAA	2741
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3269	UUAGACUU C CUGUAGGG	553	CCCUACAG CUGAUGAG GCCGUUAGGC CGAA AAGUCUAA	2742
3184	CUUCCUGU A GGGGGCGA	554	UCGCCCCC CUGAUGAG GCCGUUAGGC CGAA ACAGGAAG	2743
3274	CUUCCUGU A GGGGGCGA	554	UCGCCCCC CUGAUGAG GCCGUUAGGC CGAA ACAGGAAG	2743
3194	GGGGCGAU A UACUAAAU	555	AUUUAGUA CUGAUGAG GCCGUUAGGC CGAA AUCGCCCC	2744
3247	GGGGCGAU A UACUAAAU	555	AUUUAGUA CUGAUGAG GCCGUUAGGC CGAA AUCGCCCC	2744
3196	GGCGAUAU A CUAAAUGU	556	ACAUUUAG CUGAUGAG GCCGUUAGGC CGAA AUAUCGCC	2745
3249	GGCGAUAU A CUAAAUGU	556	ACAUUUAG CUGAUGAG GCCGUUAGGC CGAA AUAUCGCC	2745
3199	GAUAUACU A AAUGUAUA	557	UAUACAUU CUGAUGAG GCCGUUAGGC CGAA AGUAUAUC	2746
3205	CUAAAUGU A UAUAGUAC	558	GUACUAUA CUGAUGAG GCCGUUAGGC CGAA ACAUUUAG	2747
3207	AAAUGUAU A UAGUACAU	559	AUGUACUA CUGAUGAG GCCGUUAGGC CGAA AUACAUUU	2748
3209	AUGUAUAU A GUACAUUU	560	AAAUGUAC CUGAUGAG GCCGUUAGGC CGAA AUAUACAU	2749
3212	UAUAUAGU A CAUUUAUA	561	UAUAAAUG CUGAUGAG GCCGUUAGGC CGAA ACUAUAUA	2750
3216	UAGUACAU U UAUACUAA	562	UUAGUAUA CUGAUGAG GCCGUUAGGC CGAA AUGUACUA	2751
3217	AGUACAUU U AUACUAAA	563	UUUAGUAU CUGAUGAG GCCGUUAGGC CGAA AAUGUACU	2752
3218	GUACAUUU A UACUAAAU	564	AUUUAGUA CUGAUGAG GCCGUUAGGC CGAA AAAUGUAC	2753
3220	ACAUUUAU A CUAAAUGU	565	ACAUUUAG CUGAUGAG GCCGUUAGGC CGAA AUAAAUGU	2754
3223	UUUAUACU A AAUGUAUU	566	AAUACAUU CUGAUGAG GCCGUUAGGC CGAA AGUAUAAA	2755
3229	CUAAAUGU A UUCCUGUA	567	UACAGGAA CUGAUGAG GCCGUUAGGC CGAA ACAUUUAG	2756
3231	AAAUGUAU U CCUGUAGG	568	CCUACAGG CUGAUGAG GCCGUUAGGC CGAA AUACAUUU	2757
3232	AAUGUAUU C CUGUAGGG	569	CCCUACAG CUGAUGAG GCCGUUAGGC CGAA AAUACAUU	2758
3237	AUUCCUGU A GGGGGCGA	570	UCGCCCCC CUGAUGAG GCCGUUAGGC CGAA ACAGGAAU	2759
3252	GAUAUACU A AAUGUAUU	571	AAUACAUU CUGAUGAG GCCGUUAGGC CGAA AGUAUAUC	2760
3258	CUAAAUGU A UUUUAGAC	572	GUCUAAAA CUGAUGAG GCCGUUAGGC CGAA ACAUUUAG	2761
3284	GGGGCGAU A AAAUAAAA	573	UUUUAUUU CUGAUGAG GCCGUUAGGC CGAA AUCGCCCC	2762
3289	GAUAAAAU A AAAUGCUA	574	UAGCAUUU CUGAUGAG GCCGUUAGGC CGAA AUUUUAUC	2763
3297	AAAAUGCU A AACAACUG	575	CAGUUGUU CUGAUGAG GCCGUUAGGC CGAA AGCAUUUU	2764

Input Sequence = NM_001285. Cut Site = UH/.
Arm Length = 8. Core Sequence = CUGAUGAG GCCGUUAGGC CGAA
Underlined region can be any X sequence or linker, as described herein.
NM_001285 (Homo sapiens chloride channel, calcium activated, 1 (CLCA1) mRNA, 3311 bp)

Table IV: Human CLCA1 Inozyme and Target Sequence 249.021

Pos	Substrate	Seq ID No.	Inozyme	Rz Seq ID No.
10	GCUAAUGC U UUUGGUAC	576	GUACCAAA CUGAUGAG GCCGUUAGGC CGAA ICAUUAGC	2765
19	UUUGGUAC A AAUGGAUG	577	CAUCCAUU CUGAUGAG GCCGUUAGGC CGAA IUACCAAA	2766
50	AUAUUUUC U UGUUUAAG	578	CUUAAACA CUGAUGAG GCCGUUAGGC CGAA IAAAAUAU	2767
65	AGGGGAGC A UGAAGAGG	579	CCUCUUCA CUGAUGAG GCCGUUAGGC CGAA ICUCCCCU	2768
89	GUUAUGUC A AGCAUCUG	580	CAGAUGCU CUGAUGAG GCCGUUAGGC CGAA IACAUAAC	2769
93	UGUCAAGC A UCUGGCAC	581	GUGCCAGA CUGAUGAG GCCGUUAGGC CGAA ICUUGACA	2770
96	CAAGCAUC U GGCACAGC	582	GCUGUGCC CUGAUGAG GCCGUUAGGC CGAA IAUGCUUG	2771
100	CAUCUGGC A CAGCUGAA	583	UUCAGCUG CUGAUGAG GCCGUUAGGC CGAA ICCAGAUG	2772
102	UCUGGCAC A GCUGAAGG	584	CCUUCAGC CUGAUGAG GCCGUUAGGC CGAA IUGCCAGA	2773
105	GGCACAGC U GAAGGCAG	585	CUGCCUUC CUGAUGAG GCCGUUAGGC CGAA ICUGUGCC	2774
112	CUGAAGGC A GAUGGAAA	586	UUUCCAUC CUGAUGAG GCCGUUAGGC CGAA ICCUUCAG	2775
128	AUAUUUAC A AGUACGCA	587	UGCGUACU CUGAUGAG GCCGUUAGGC CGAA IUAAAUAU	2776
136	AAGUACGC A AUUUGAGA	588	UCUCAAAU CUGAUGAG GCCGUUAGGC CGAA ICGUACUU	2777
146	UUUGAGAC U AAGAUAUU	589	AAUAUCUU CUGAUGAG GCCGUUAGGC CGAA IUCUCAAA	2778
161	UUGUUAUC A UUCUCCUA	590	UAGGAGAA CUGAUGAG GCCGUUAGGC CGAA IAUAACAA	2779
165	UAUCAUUC U CCUAUUGA	591	UCAAUAGG CUGAUGAG GCCGUUAGGC CGAA IAAUGAUA	2780
167	UCAUUCUC C UAUUGAAG	592	CUUCAAUA CUGAUGAG GCCGUUAGGC CGAA IAGAAUGA	2781
168	CAUUCUCC U AUUGAAGA	593	UCUUCAAU CUGAUGAG GCCGUUAGGC CGAA IGAGAAUG	2782
178	UUGAAGAC A AGAGCAAU	594	AUUGCUCU CUGAUGAG GCCGUUAGGC CGAA IUCUUCAA	2783
184	ACAAGAGC A AUAGUAAA	595	UUUACUAU CUGAUGAG GCCGUUAGGC CGAA ICUCUUGU	2784
195	AGUAAAAC A CAUCAGGU	596	ACCUGAUG CUGAUGAG GCCGUUAGGC CGAA IUUUUACU	2785
197	UAAAACAC A UCAGGUCA	597	UGACCUGA CUGAUGAG GCCGUUAGGC CGAA IUGUUUUA	2786
200	AACACAUC A GGUCAGGG	598	CCCUGACC CUGAUGAG GCCGUUAGGC CGAA IAUGUGUU	2787
205	AUCAGGUC A GGGGGUUA	599	UAACCCCC CUGAUGAG GCCGUUAGGC CGAA IACCUGAU	2788
219	UUAAAGAC C UGUGAUAA	600	UUAUCACA CUGAUGAG GCCGUUAGGC CGAA IUCUUUAA	2789
220	UAAAGACC U GUGAUAAA	601	UUUAUCAC CUGAUGAG GCCGUUAGGC CGAA IGUCUUUA	2790
230	UGAUAAAC C ACUUCCGA	602	UCGGAAGU CUGAUGAG GCCGUUAGGC CGAA IUUUAUCA	2791
231	GAUAAACC A CUUCCGAU	603	AUCGGAAG CUGAUGAG GCCGUUAGGC CGAA IGUUUAUC	2792
233	UAAACCAC U UCCGAUAA	604	UUAUCGGA CUGAUGAG GCCGUUAGGC CGAA IUGGUUUA	2793
236	ACCACUUC C GAUAAGUU	605	AACUUAUC CUGAUGAG GCCGUUAGGC CGAA IAAGUGGU	2794

258	CGUGUGUC U AUAUUUUC	606	GAAAAUAU CUGAUGAG GCCGUUAGGC CGAA IACACACG	2795
267	AUAUUUUC A UAUCUGUA	607	UACAGAUA CUGAUGAG GCCGUUAGGC CGAA IAAAAUAU	2796
272	UUCAUAUC U GUAUAUAU	608	AUAUAUAC CUGAUGAG GCCGUUAGGC CGAA IAUAUGAA	2797
299	AGAAAGAC A CCUUCGUA	609	UACGAAGG CUGAUGAG GCCGUUAGGC CGAA IUCUUUCU	2798
301	AAAGACAC C UUCGUAAC	610	GUUACGAA CUGAUGAG GCCGUUAGGC CGAA IUGUCUUU	2799
302	AAGACACC U UCGUAACC	611	GGUUACGA CUGAUGAG GCCGUUAGGC CGAA IGUGUCUU	2800
310	UUCGUAAC C CGCAUUUU	612	AAAAUGCG CUGAUGAG GCCGUUAGGC CGAA IUUACGAA	2801
311	UCGUAACC C GCAUUUUC	613	GAAAAUGC CUGAUGAG GCCGUUAGGC CGAA IGUUACGA	2802
314	UAACCCGC A UUUUCCAA	614	UUGGAAAA CUGAUGAG GCCGUUAGGC CGAA ICGGGUUA	2803
320	GCAUUUUC C AAAGAGAG	615	CUCUCUUU CUGAUGAG GCCGUUAGGC CGAA IAAAAUGC	2804
321	CAUUUUCC A AAGAGAGG	616	CCUCUCUU CUGAUGAG GCCGUUAGGC CGAA IGAAAAUG	2805
334	GAGGAAUC A CAGGGAGA	617	UCUCCCUG CUGAUGAG GCCGUUAGGC CGAA IAUUCCUC	2806
336	GGAAUCAC A GGGAGAUG	618	CAUCUCCC CUGAUGAG GCCGUUAGGC CGAA IUGAUUCC	2807
348	AGAUGUAC A GCAAUGGG	619	CCCAUUGC CUGAUGAG GCCGUUAGGC CGAA IUACAUCU	2808
351	UGUACAGC A AUGGGGCC	620	GGCCCCAU CUGAUGAG GCCGUUAGGC CGAA ICUGUACA	2809
359	AAUGGGGC C AUUUAAGA	621	UCUUAAAU CUGAUGAG GCCGUUAGGC CGAA ICCCCAUU	2810
360	AUGGGGCC A UUUAAGAG	622	CUCUUAAA CUGAUGAG GCCGUUAGGC CGAA IGCCCCAU	2811
372	AAGAGUUC U GUGUUCAU	623	AUGAACAC CUGAUGAG GCCGUUAGGC CGAA IAACUCUU	2812
379	CUGUGUUC A UCUUGAUU	624	AAUCAAGA CUGAUGAG GCCGUUAGGC CGAA IAACACAG	2813
382	UGUUCAUC U UGAUUCUU	625	AAGAAUCA CUGAUGAG GCCGUUAGGC CGAA IAUGAACA	2814
389	CUUGAUUC U UCACCUUC	626	GAAGGUGA CUGAUGAG GCCGUUAGGC CGAA IAAUCAAG	2815
392	GAUUCUUC A CCUUCUAG	627	CUAGAAGG CUGAUGAG GCCGUUAGGC CGAA IAAGAAUC	2816
394	UUCUUCAC C UUCUAGAA	628	UUCUAGAA CUGAUGAG GCCGUUAGGC CGAA IUGAAGAA	2817
395	UCUUCACC U UCUAGAAG	629	CUUCUAGA CUGAUGAG GCCGUUAGGC CGAA IGUGAAGA	2818
398	UCACCUUC U AGAAGGGG	630	CCCCUUCU CUGAUGAG GCCGUUAGGC CGAA IAAGGUGA	2819
408	GAAGGGGC C CUGAGUAA	631	UUACUCAG CUGAUGAG GCCGUUAGGC CGAA ICCCCUUC	2820
409	AAGGGGCC C UGAGUAAU	632	AUUACUCA CUGAUGAG GCCGUUAGGC CGAA IGCCCCUU	2821
410	AGGGGCCC U GAGUAAUU	633	AAUUACUC CUGAUGAG GCCGUUAGGC CGAA IGGCCCCU	2822
420	AGUAAUUC A CUCAUUCA	634	UGAAUGAG CUGAUGAG GCCGUUAGGC CGAA IAAUUACU	2823
422	UAAUUCAC U CAUUCAGC	635	GCUGAAUG CUGAUGAG GCCGUUAGGC CGAA IUGAAUUA	2824
424	AUUCACUC A UUCAGCUG	636	CAGCUGAA CUGAUGAG GCCGUUAGGC CGAA IAGUGAAU	2825
428	ACUCAUUC A GCUGAACA	637	UGUUCAGC CUGAUGAG GCCGUUAGGC CGAA IAAUGAGU	2826
431	CAUUCAGC U GAACAACA	638	UGUUGUUC CUGAUGAG GCCGUUAGGC CGAA ICUGAAUG	2827
436	AGCUGAAC A ACAAUGGC	639	GCCAUUGU CUGAUGAG GCCGUUAGGC CGAA IUUCAGCU	2828

439	UGAACAAC A AUGGCUAU	640	AUAGCCAU CUGAUGAG GCCGUUAGGC CGAA IUUGUUCA	2829
445	ACAAUGGC U AUGAAGGC	641	GCCUUCAU CUGAUGAG GCCGUUAGGC CGAA ICCAUUGU	2830
454	AUGAAGGC A UUGUCGUU	642	AACGACAA CUGAUGAG GCCGUUAGGC CGAA ICCUUCAU	2831
465	GUCGUUGC A AUCGACCC	643	GGGUCGAU CUGAUGAG GCCGUUAGGC CGAA ICAACGAC	2832
472	CAAUCGAC C CCAAUGUG	644	CACAUUGG CUGAUGAG GCCGUUAGGC CGAA IUCGAUUG	2833
473	AAUCGACC C CAAUGUGC	645	GCACAUUG CUGAUGAG GCCGUUAGGC CGAA IGUCGAUU	2834
474	AUCGACCC C AAUGUGCC	646	GGCACAUU CUGAUGAG GCCGUUAGGC CGAA IGGUCGAU	2835
475	UCGACCCC A AUGUGCCA	647	UGGCACAU CUGAUGAG GCCGUUAGGC CGAA IGGGUCGA	2836
482	CAAUGUGC C AGAAGAUG	648	CAUCUUCU CUGAUGAG GCCGUUAGGC CGAA ICACAUUG	2837
483	AAUGUGCC A GAAGAUGA	649	UCAUCUUC CUGAUGAG GCCGUUAGGC CGAA IGCACAUU	2838
495	GAUGAAAC A CUCAUUCA	650	UGAAUGAG CUGAUGAG GCCGUUAGGC CGAA IUUUCAUC	2839
497	UGAAACAC U CAUUCAAC	651	GUUGAAUG CUGAUGAG GCCGUUAGGC CGAA IUGUUUCA	2840
499	AAACACUC A UUCAACAA	652	UUGUUGAA CUGAUGAG GCCGUUAGGC CGAA IAGUGUUU	2841
503	ACUCAUUC A ACAAAUAA	653	UUAUUUGU CUGAUGAG GCCGUUAGGC CGAA IAAUGAGU	2842
506	CAUUCAAC A AAUAAAGG	654	CCUUUAUU CUGAUGAG GCCGUUAGGC CGAA IUUGAAUG	2843
517	UAAAGGAC A UGGUGACC	655	GGUCACCA CUGAUGAG GCCGUUAGGC CGAA IUCCUUUA	2844
525	AUGGUGAC C CAGGCAUC	656	GAUGCCUG CUGAUGAG GCCGUUAGGC CGAA IUCACCAU	2845
526	UGGUGACC C AGGCAUCU	657	AGAUGCCU CUGAUGAG GCCGUUAGGC CGAA IGUCACCA	2846
527	GGUGACCC A GGCAUCUC	658	GAGAUGCC CUGAUGAG GCCGUUAGGC CGAA IGGUCACC	2847
531	ACCCAGGC A UCUCUGUA	659	UACAGAGA CUGAUGAG GCCGUUAGGC CGAA ICCUGGGU	2848
534	CAGGCAUC U CUGUAUCU	660	AGAUACAG CUGAUGAG GCCGUUAGGC CGAA IAUGCCUG	2849
536	GGCAUCUC U GUAUCUGU	661	ACAGAUAC CUGAUGAG GCCGUUAGGC CGAA IAGAUGCC	2850
542	UCUGUAUC U GUUUGAAG	662	CUUCAAAC CUGAUGAG GCCGUUAGGC CGAA IAUACAGA	2851
552	UUUGAAGC U ACAGGAAA	663	UUUCCUGU CUGAUGAG GCCGUUAGGC CGAA ICUUCAAA	2852
555	GAAGCUAC A GGAAAGCG	664	CGCUUUCC CUGAUGAG GCCGUUAGGC CGAA IUAGCUUC	2853
574	UUUAUUUC A AAAAUGUU	665	AACAUUUU CUGAUGAG GCCGUUAGGC CGAA IAAAUAAA	2854
585	AAUGUUGC C AUUUUGAU	666	AUCAAAAU CUGAUGAG GCCGUUAGGC CGAA ICAACAUU	2855
586	AUGUUGCC A UUUUGAUU	667	AAUCAAAA CUGAUGAG GCCGUUAGGC CGAA IGCAACAU	2856
596	UUUGAUUC C UGAAACAU	668	AUGUUUCA CUGAUGAG GCCGUUAGGC CGAA IAAUCAAA	2857
597	UUGAUUCC U GAAACAUG	669	CAUGUUUC CUGAUGAG GCCGUUAGGC CGAA IGAAUCAA	2858
603	CCUGAAAC A UGGAAGAC	670	GUCUUCCA CUGAUGAG GCCGUUAGGC CGAA IUUUCAGG	2859
612	UGGAAGAC A AAGGCUGA	671	UCAGCCUU CUGAUGAG GCCGUUAGGC CGAA IUCUUCCA	2860
618	ACAAAGGC U GACUAUGU	672	ACAUAGUC CUGAUGAG GCCGUUAGGC CGAA ICCUUUGU	2861
622	AGGCUGAC U AUGUGAGA	673	UCUCACAU CUGAUGAG GCCGUUAGGC CGAA IUCAGCCU	2862

632	UGUGAGAC C AAAACUUG	674	CAAGUUUU CUGAUGAG GCCGUUAGGC CGAA IUCUCACA	2863
633	GUGAGACC A AAACUUGA	675	UCAAGUUU CUGAUGAG GCCGUUAGGC CGAA IGUCUCAC	2864
638	ACCAAAAC U UGAGACCU	676	AGGUCUCA CUGAUGAG GCCGUUAGGC CGAA IUUUUGGU	2865
645	CUUGAGAC C UACAAAAA	677	UUUUUGUA CUGAUGAG GCCGUUAGGC CGAA IUCUCAAG	2866
646	UUGAGACC U ACAAAAAU	678	AUUUUUGU CUGAUGAG GCCGUUAGGC CGAA IGUCUCAA	2867
649	AGACCUAC A AAAAUGCU	679	AGCAUUUU CUGAUGAG GCCGUUAGGC CGAA IUAGGUCU	2868
657	AAAAAUGC U GAUGUUCU	680	AGAACAUC CUGAUGAG GCCGUUAGGC CGAA ICAUUUUU	2869
665	UGAUGUUC U GGUUGCUG	681	CAGCAACC CUGAUGAG GCCGUUAGGC CGAA IAACAUCA	2870
672	CUGGUUGC U GAGUCUAC	682	GUAGACUC CUGAUGAG GCCGUUAGGC CGAA ICAACCAG	2871
678	GCUGAGUC U ACUCCUCC	683	GGAGGAGU CUGAUGAG GCCGUUAGGC CGAA IACUCAGC	2872
681	GAGUCUAC U CCUCCAGG	684	CCUGGAGG CUGAUGAG GCCGUUAGGC CGAA IUAGACUC	2873
683	GUCUACUC C UCCAGGUA	685	UACCUGGA CUGAUGAG GCCGUUAGGC CGAA IAGUAGAC	2874
684	UCUACUCC U CCAGGUAA	686	UUACCUGG CUGAUGAG GCCGUUAGGC CGAA IGAGUAGA	2875
686	UACUCCUC C AGGUAAUG	687	CAUUACCU CUGAUGAG GCCGUUAGGC CGAA IAGGAGUA	2876
687	ACUCCUCC A GGUAAUGA	688	UCAUUACC CUGAUGAG GCCGUUAGGC CGAA IGAGGAGU	2877
701	UGAUGAAC C CUACACUG	689	CAGUGUAG CUGAUGAG GCCGUUAGGC CGAA IUUCAUCA	2878
702	GAUGAACC C UACACUGA	690	UCAGUGUA CUGAUGAG GCCGUUAGGC CGAA IGUUCAUC	2879
703	AUGAACCC U ACACUGAG	691	CUCAGUGU CUGAUGAG GCCGUUAGGC CGAA IGGUUCAU	2880
706	AACCCUAC A CUGAGCAG	692	CUGCUCAG CUGAUGAG GCCGUUAGGC CGAA IUAGGGUU	2881
708	CCCUACAC U GAGCAGAU	693	AUCUGCUC CUGAUGAG GCCGUUAGGC CGAA IUGUAGGG	2882
713	CACUGAGC A GAUGGGCA	694	UGCCCAUC CUGAUGAG GCCGUUAGGC CGAA ICUCAGUG	2883
721	AGAUGGGC A ACUGUGGA	695	UCCACAGU CUGAUGAG GCCGUUAGGC CGAA ICCCAUCU	2884
724	UGGGCAAC U GUGGAGAG	696	CUCUCCAC CUGAUGAG GCCGUUAGGC CGAA IUUGCCCA	2885
748	AAAGGAUC C ACCUCACU	697	AGUGAGGU CUGAUGAG GCCGUUAGGC CGAA IAUCCUUU	2886
749	AAGGAUCC A CCUCACUC	698	GAGUGAGG CUGAUGAG GCCGUUAGGC CGAA IGAUCCUU	2887
751	GGAUCCAC C UCACUCCU	699	AGGAGUGA CUGAUGAG GCCGUUAGGC CGAA IUGGAUCC	2888
752	GAUCCACC U CACUCCUG	700	CAGGAGUG CUGAUGAG GCCGUUAGGC CGAA IGUGGAUC	2889
754	UCCACCUC A CUCCUGAU	701	AUCAGGAG CUGAUGAG GCCGUUAGGC CGAA IAGGUGGA	2890
756	CACCUCAC U CCUGAUUU	702	AAAUCAGG CUGAUGAG GCCGUUAGGC CGAA IUGAGGUG	2891
758	CCUCACUC C UGAUUUCA	703	UGAAAUCA CUGAUGAG GCCGUUAGGC CGAA IAGUGAGG	2892
759	CUCACUCC U GAUUUCAU	704	AUGAAAUC CUGAUGAG GCCGUUAGGC CGAA IGAGUGAG	2893
766	CUGAUUUC A UUGCAGGA	705	UCCUGCAA CUGAUGAG GCCGUUAGGC CGAA IAAAUCAG	2894
771	UUCAUUGC A GGAAAAAA	706	UUUUUUCC CUGAUGAG GCCGUUAGGC CGAA ICAAUGAA	2895
786	AAGUUAGC U GAAUAUGG	707	CCAUAUUC CUGAUGAG GCCGUUAGGC CGAA ICUAACUU	2896

797	AUAUGGAC C ACAAGGUA	708	UACCUUGU CUGAUGAG GCCGUUAGGC CGAA IUCCAUAU	2897
798	UAUGGACC A CAAGGUAA	709	UUACCUUG CUGAUGAG GCCGUUAGGC CGAA IGUCCAUA	2898
800	UGGACCAC A AGGUAAGG	710	CCUUACCU CUGAUGAG GCCGUUAGGC CGAA IUGGUCCA	2899
810	GGUAAGGC A UUUGUCCA	711	UGGACAAA CUGAUGAG GCCGUUAGGC CGAA ICCUUACC	2900
817	CAUUUGUC C AUGAGUGG	712	CCACUCAU CUGAUGAG GCCGUUAGGC CGAA IACAAAUG	2901
818	AUUUGUCC A UGAGUGGG	713	CCCACUCA CUGAUGAG GCCGUUAGGC CGAA IGACAAAU	2902
828	GAGUGGGC U CAUCUACG	714	CGUAGAUG CUGAUGAG GCCGUUAGGC CGAA ICCCACUC	2903
830	GUGGGCUC A UCUACGAU	715	AUCGUAGA CUGAUGAG GCCGUUAGGC CGAA IAGCCCAC	2904
833	GGCUCAUC U ACGAUGGG	716	CCCAUCGU CUGAUGAG GCCGUUAGGC CGAA IAUGAGCC	2905
859	ACGAGUAC A AUAAUGAU	717	AUCAUUAU CUGAUGAG GCCGUUAGGC CGAA IUACUCGU	2906
877	AGAAAUUC U ACUUAUCC	718	GGAUAAGU CUGAUGAG GCCGUUAGGC CGAA IAAUUUCU	2907
880	AAUUCUAC U UAUCCAAU	719	AUUGGAUA CUGAUGAG GCCGUUAGGC CGAA IUAGAAUU	2908
885	UACUUAUC C AAUGGAAG	720	CUUCCAUU CUGAUGAG GCCGUUAGGC CGAA IAUAAGUA	2909
886	ACUUAUCC A AUGGAAGA	721	UCUUCCAU CUGAUGAG GCCGUUAGGC CGAA IGAUAAGU	2910
899	AAGAAUAC A AGCAGUAA	722	UUACUGCU CUGAUGAG GCCGUUAGGC CGAA IUAUUCUU	2911
903	AUACAAGC A GUAAGAUG	723	CAUCUUAC CUGAUGAG GCCGUUAGGC CGAA ICUUGUAU	2912
915	AGAUGUUC A GCAGGUAU	724	AUACCUGC CUGAUGAG GCCGUUAGGC CGAA IAACAUCU	2913
918	UGUUCAGC A GGUAUUAC	725	GUAAUACC CUGAUGAG GCCGUUAGGC CGAA ICUGAACA	2914
927	GGUAUUAC U GGUACAAA	726	UUUGUACC CUGAUGAG GCCGUUAGGC CGAA IUAAUACC	2915
933	ACUGGUAC A AAUGUAGU	727	ACUACAUU CUGAUGAG GCCGUUAGGC CGAA IUACCAGU	2916
953	GAAGUGUC A GGGAGGCA	728	UGCCUCCC CUGAUGAG GCCGUUAGGC CGAA IACACUUC	2917
961	AGGGAGGC A GCUGUUAC	729	GUAACAGC CUGAUGAG GCCGUUAGGC CGAA ICCUCCCU	2918
964	GAGGCAGC U GUUACACC	730	GGUGUAAC CUGAUGAG GCCGUUAGGC CGAA ICUGCCUC	2919
970	GCUGUUAC A CCAAAAGA	731	UCUUUUGG CUGAUGAG GCCGUUAGGC CGAA IUAACAGC	2920
972	UGUUACAC C AAAAGAUG	732	CAUCUUUU CUGAUGAG GCCGUUAGGC CGAA IUGUAACA	2921
973	GUUACACC A AAAGAUGC	733	GCAUCUUU CUGAUGAG GCCGUUAGGC CGAA IGUGUAAC	2922
982	AAAGAUGC A CAUUCAAU	734	AUUGAAUG CUGAUGAG GCCGUUAGGC CGAA ICAUCUUU	2923
984	AGAUGCAC A UUCAAUAA	735	UUAUUGAA CUGAUGAG GCCGUUAGGC CGAA IUGCAUCU	2924
988	GCACAUUC A AUAAAGUU	736	AACUUUAU CUGAUGAG GCCGUUAGGC CGAA IAAUGUGC	2925
999	AAAGUUAC A GGACUCUA	737	UAGAGUCC CUGAUGAG GCCGUUAGGC CGAA IUAACUUU	2926
1004	UACAGGAC U CUAUGAAA	738	UUUCAUAG CUGAUGAG GCCGUUAGGC CGAA IUCCUGUA	2927
1006	CAGGACUC U AUGAAAAA	739	UUUUUCAU CUGAUGAG GCCGUUAGGC CGAA IAGUCCUG	2928
1031	GUUUGUUC U CCAAUCCC	740	GGGAUUGG CUGAUGAG GCCGUUAGGC CGAA IAACAAAC	2929
1033	UUGUUCUC C AAUCCCGC	741	GCGGGAUU CUGAUGAG GCCGUUAGGC CGAA IAGAACAA	2930

1034	UGUUCUCC A AUCCCGCC	742	GGCGGGAU CUGAUGAG GCCGUUAGGC CGAA IGAGAACA	2931
1038	CUCCAAUC C CGCCAGAC	743	GUCUGGCG CUGAUGAG GCCGUUAGGC CGAA IAUUGGAG	2932
1039	UCCAAUCC C GCCAGACG	744	CGUCUGGC CUGAUGAG GCCGUUAGGC CGAA IGAUUGGA	2933
1042	AAUCCCGC C AGACGGAG	745	CUCCGUCU CUGAUGAG GCCGUUAGGC CGAA ICGGGAUU	2934
1043	AUCCCGCC A GACGGAGA	746	UCUCCGUC CUGAUGAG GCCGUUAGGC CGAA IGCGGGAU	2935
1056	GAGAAGGC U UCUAUAAU	747	AUUAUAGA CUGAUGAG GCCGUUAGGC CGAA ICCUUCUC	2936
1059	AAGGCUUC U AUAAUGUU	748	AACAUUAU CUGAUGAG GCCGUUAGGC CGAA IAAGCCUU	2937
1071	AUGUUUGC A CAACAUGU	749	ACAUGUUG CUGAUGAG GCCGUUAGGC CGAA ICAAACAU	2938
1073	GUUUGCAC A ACAUGUUG	750	CAACAUGU CUGAUGAG GCCGUUAGGC CGAA IUGCAAAC	2939
1076	UGCACAAC A UGUUGAUU	751	AAUCAACA CUGAUGAG GCCGUUAGGC CGAA IUUGUGCA	2940
1086	GUUGAUUC U AUAGUUGA	752	UCAACUAU CUGAUGAG GCCGUUAGGC CGAA IAAUCAAC	2941
1099	UUGAAUUC U GUACAGAA	753	UUCUGUAC CUGAUGAG GCCGUUAGGC CGAA IAAUUCAA	2942
1104	UUCUGUAC A GAACAAAA	754	UUUUGUUC CUGAUGAG GCCGUUAGGC CGAA IUACAGAA	2943
1109	UACAGAAC A AAACCACA	755	UGUGGUUU CUGAUGAG GCCGUUAGGC CGAA IUUCUGUA	2944
1114	AACAAAAC C ACAACAAA	756	UUUGUUGU CUGAUGAG GCCGUUAGGC CGAA IUUUUGUU	2945
1115	ACAAAACC A CAACAAAG	757	CUUUGUUG CUGAUGAG GCCGUUAGGC CGAA IGUUUUGU	2946
1117	AAAACCAC A ACAAAGAA	758	UUCUUUGU CUGAUGAG GCCGUUAGGC CGAA IUGGUUUU	2947
1120	ACCACAAC A AAGAAGCU	759	AGCUUCUU CUGAUGAG GCCGUUAGGC CGAA IUUGUGGU	2948
1128	AAAGAAGC U CCAAACAA	760	UUGUUUGG CUGAUGAG GCCGUUAGGC CGAA ICUUCUUU	2949
1130	AGAAGCUC C AAACAAGC	761	GCUUGUUU CUGAUGAG GCCGUUAGGC CGAA IAGCUUCU	2950
1131	GAAGCUCC A AACAAGCA	762	UGCUUGUU CUGAUGAG GCCGUUAGGC CGAA IGAGCUUC	2951
1135	CUCCAAAC A AGCAAAAU	763	AUUUUGCU CUGAUGAG GCCGUUAGGC CGAA IUUUGGAG	2952
1139	AAACAAGC A AAAUCAAA	764	UUUGAUUU CUGAUGAG GCCGUUAGGC CGAA ICUUGUUU	2953
1145	GCAAAAUC A AAAAUGCA	765	UGCAUUUU CUGAUGAG GCCGUUAGGC CGAA IAUUUUGC	2954
1153	AAAAAUGC A AUCUCCGA	766	UCGGAGAU CUGAUGAG GCCGUUAGGC CGAA ICAUUUUU	2955
1157	AUGCAAUC U CCGAAGCA	767	UGCUUCGG CUGAUGAG GCCGUUAGGC CGAA IAUUGCAU	2956
1159	GCAAUCUC C GAAGCACA	768	UGUGCUUC CUGAUGAG GCCGUUAGGC CGAA IAGAUUGC	2957
1165	UCCGAAGC A CAUGGGAA	769	UUCCCAUG CUGAUGAG GCCGUUAGGC CGAA ICUUCGGA	2958
1167	CGAAGCAC A UGGGAAGU	770	ACUUCCCA CUGAUGAG GCCGUUAGGC CGAA IUGCUUCG	2959
1180	AAGUGAUC C GUGAUUCU	771	AGAAUCAC CUGAUGAG GCCGUUAGGC CGAA IAUCACUU	2960
1188	CGUGAUUC U GAGGACUU	772	AAGUCCUC CUGAUGAG GCCGUUAGGC CGAA IAAUCACG	2961
1195	CUGAGGAC U UUAAGAAA	773	UUUCUUAA CUGAUGAG GCCGUUAGGC CGAA IUCCUCAG	2962
1206	AAGAAAAC C ACUCCUAU	774	AUAGGAGU CUGAUGAG GCCGUUAGGC CGAA IUUUUCUU	2963
1207	AGAAAACC A CUCCUAUG	775	CAUAGGAG CUGAUGAG GCCGUUAGGC CGAA IGUUUUCU	2964

1209	AAAACCAC U CCUAUGAC	776	GUCAUAGG CUGAUGAG GCCGUUAGGC CGAA IUGGUUUU	2965
1211	AACCACUC C UAUGACAA	777	UUGUCAUA CUGAUGAG GCCGUUAGGC CGAA IAGUGGUU	2966
1212	ACCACUCC U AUGACAAC	778	GUUGUCAU CUGAUGAG GCCGUUAGGC CGAA IGAGUGGU	2967
1218	CCUAUGAC A ACACAGCC	779	GGCUGUGU CUGAUGAG GCCGUUAGGC CGAA IUCAUAGG	2968
1221	AUGACAAC A CAGCCACC	780	GGUGGCUG CUGAUGAG GCCGUUAGGC CGAA IUUGUCAU	2969
1223	GACAACAC A GCCACCAA	781	UUGGUGGC CUGAUGAG GCCGUUAGGC CGAA IUGUUGUC	2970
1226	AACACAGC C ACCAAAUC	782	GAUUUGGU CUGAUGAG GCCGUUAGGC CGAA ICUGUGUU	2971
1227	ACACAGCC A CCAAAUCC	783	GGAUUUGG CUGAUGAG GCCGUUAGGC CGAA IGCUGUGU	2972
1229	ACAGCCAC C AAAUCCCA	784	UGGGAUUU CUGAUGAG GCCGUUAGGC CGAA IUGGCUGU	2973
1230	CAGCCACC A AAUCCCAC	785	GUGGGAUU CUGAUGAG GCCGUUAGGC CGAA IGUGGCUG	2974
1235	ACCAAAUC C CACCUUCU	786	AGAAGGUG CUGAUGAG GCCGUUAGGC CGAA IAUUUGGU	2975
1236	CCAAAUCC C ACCUUCUC	787	GAGAAGGU CUGAUGAG GCCGUUAGGC CGAA IGAUUUGG	2976
1237	CAAAUCCC A CCUUCUCA	788	UGAGAAGG CUGAUGAG GCCGUUAGGC CGAA IGGAUUUG	2977
1239	AAUCCCAC C UUCUCAUU	789	AAUGAGAA CUGAUGAG GCCGUUAGGC CGAA IUGGGAUU	2978
1240	AUCCCACC U UCUCAUUG	790	CAAUGAGA CUGAUGAG GCCGUUAGGC CGAA IGUGGGAU	2979
1243	CCACCUUC U CAUUGCUG	791	CAGCAAUG CUGAUGAG GCCGUUAGGC CGAA IAAGGUGG	2980
1245	ACCUUCUC A UUGCUGCA	792	UGCAGCAA CUGAUGAG GCCGUUAGGC CGAA IAGAAGGU	2981
1250	CUCAUUGC U GCAGAUUG	793	CAAUCUGC CUGAUGAG GCCGUUAGGC CGAA ICAAUGAG	2982
1253	AUUGCUGC A GAUUGGAC	794	GUCCAAUC CUGAUGAG GCCGUUAGGC CGAA ICAGCAAU	2983
1262	GAUUGGAC A AAGAAUUG	795	CAAUUCUU CUGAUGAG GCCGUUAGGC CGAA IUCCAAUC	2984
1282	GUUUAGUC C UUGACAAA	796	UUUGUCAA CUGAUGAG GCCGUUAGGC CGAA IACUAAAC	2985
1283	UUUAGUCC U UGACAAAU	797	AUUUGUCA CUGAUGAG GCCGUUAGGC CGAA IGACUAAA	2986
1288	UCCUUGAC A AAUCUGGA	798	UCCAGAUU CUGAUGAG GCCGUUAGGC CGAA IUCAAGGA	2987
1293	GACAAAUC U GGAAGCAU	799	AUGCUUCC CUGAUGAG GCCGUUAGGC CGAA IAUUUGUC	2988
1300	CUGGAAGC A UGGCGACU	800	AGUCGCCA CUGAUGAG GCCGUUAGGC CGAA ICUUCCAG	2989
1308	AUGGCGAC U GGUAACCG	801	CGGUUACC CUGAUGAG GCCGUUAGGC CGAA IUCGCCAU	2990
1315	CUGGUAAC C GCCUCAAU	802	AUUGAGGC CUGAUGAG GCCGUUAGGC CGAA IUUACCAG	2991
1318	GUAACCGC C UCAAUCGA	803	UCGAUUGA CUGAUGAG GCCGUUAGGC CGAA ICGGUUAC	2992
1319	UAACCGCC U CAAUCGAC	804	GUCGAUUG CUGAUGAG GCCGUUAGGC CGAA IGCGGUUA	2993
1321	ACCGCCUC A AUCGACUG	805	CAGUCGAU CUGAUGAG GCCGUUAGGC CGAA IAGGCGGU	2994
1328	CAAUCGAC U GAAUCAAG	806	CUUGAUUC CUGAUGAG GCCGUUAGGC CGAA IUCGAUUG	2995
1334	ACUGAAUC A AGCAGGCC	807	GGCCUGCU CUGAUGAG GCCGUUAGGC CGAA IAUUCAGU	2996
1338	AAUCAAGC A GGCCAGCU	808	AGCUGGCC CUGAUGAG GCCGUUAGGC CGAA ICUUGAUU	2997
1342	AAGCAGGC C AGCUUUUC	809	GAAAAGCU CUGAUGAG GCCGUUAGGC CGAA ICCUGCUU	2998

1343	AGCAGGCC A GCUUUUCC	810	GGAAAAGC CUGAUGAG GCCGUUAGGC CGAA IGCCUGCU	2999
1346	AGGCCAGC U UUUCCUGC	811	GCAGGAAA CUGAUGAG GCCGUUAGGC CGAA ICUGGCCU	3000
1351	AGCUUUUC C UGCUGCAG	812	CUGCAGCA CUGAUGAG GCCGUUAGGC CGAA IAAAAGCU	3001
1352	GCUUUUCC U GCUGCAGA	813	UCUGCAGC CUGAUGAG GCCGUUAGGC CGAA IGAAAAGC	3002
1355	UUUCCUGC U GCAGACAG	814	CUGUCUGC CUGAUGAG GCCGUUAGGC CGAA ICAGGAAA	3003
1358	CCUGCUGC A GACAGUUG	815	CAACUGUC CUGAUGAG GCCGUUAGGC CGAA ICAGCAGG	3004
1362	CUGCAGAC A GUUGAGCU	816	AGCUCAAC CUGAUGAG GCCGUUAGGC CGAA IUCUGCAG	3005
1370	AGUUGAGC U GGGGUCCU	817	AGGACCCC CUGAUGAG GCCGUUAGGC CGAA ICUCAACU	3006
1377	CUGGGGUC C UGGGUUGG	818	CCAACCCA CUGAUGAG GCCGUUAGGC CGAA IACCCCAG	3007
1378	UGGGGUCC U GGGUUGGG	819	CCCAACCC CUGAUGAG GCCGUUAGGC CGAA IGACCCCA	3008
1395	AUGGUGAC A UUUGACAG	820	CUGUCAAA CUGAUGAG GCCGUUAGGC CGAA IUCACCAU	3009
1402	CAUUUGAC A GUGCUGCC	821	GGCAGCAC CUGAUGAG GCCGUUAGGC CGAA IUCAAAUG	3010
1407	GACAGUGC U GCCCAUGU	822	ACAUGGGC CUGAUGAG GCCGUUAGGC CGAA ICACUGUC	3011
1410	AGUGCUGC C CAUGUACA	823	UGUACAUG CUGAUGAG GCCGUUAGGC CGAA ICAGCACU	3012
1411	GUGCUGCC C AUGUACAA	824	UUGUACAU CUGAUGAG GCCGUUAGGC CGAA IGCAGCAC	3013
1412	UGCUGCCC A UGUACAAA	825	UUUGUACA CUGAUGAG GCCGUUAGGC CGAA IGGCAGCA	3014
1418	CCAUGUAC A AAGUGAAC	826	GUUCACUU CUGAUGAG GCCGUUAGGC CGAA IUACAUGG	3015
1427	AAGUGAAC U CAUACAGA	827	UCUGUAUG CUGAUGAG GCCGUUAGGC CGAA IUUCACUU	3016
1429	GUGAACUC A UACAGAUA	828	UAUCUGUA CUGAUGAG GCCGUUAGGC CGAA IAGUUCAC	3017
1433	ACUCAUAC A GAUAAACA	829	UGUUUAUC CUGAUGAG GCCGUUAGGC CGAA IUAUGAGU	3018
1441	AGAUAAAC A GUGGCAGU	830	ACUGCCAC CUGAUGAG GCCGUUAGGC CGAA IUUUAUCU	3019
1447	ACAGUGGC A GUGACAGG	831	CCUGUCAC CUGAUGAG GCCGUUAGGC CGAA ICCACUGU	3020
1453	GCAGUGAC A GGGACACA	832	UGUGUCCC CUGAUGAG GCCGUUAGGC CGAA IUCACUGC	3021
1459	ACAGGGAC A CACUCGCC	833	GGCGAGUG CUGAUGAG GCCGUUAGGC CGAA IUCCCUGU	3022
1461	AGGGACAC A CUCGCCAA	834	UUGGCGAG CUGAUGAG GCCGUUAGGC CGAA IUGUCCCU	3023
1463	GGACACAC U CGCCAAAA	835	UUUUGGCG CUGAUGAG GCCGUUAGGC CGAA IUGUGUCC	3024
1467	ACACUCGC C AAAAGAUU	836	AAUCUUUU CUGAUGAG GCCGUUAGGC CGAA ICGAGUGU	3025
1468	CACUCGCC A AAAGAUUA	837	UAAUCUUU CUGAUGAG GCCGUUAGGC CGAA IGCGAGUG	3026
1478	AAGAUUAC C UGCAGCAG	838	CUGCUGCA CUGAUGAG GCCGUUAGGC CGAA IUAAUCUU	3027
1479	AGAUUACC U GCAGCAGC	839	GCUGCUGC CUGAUGAG GCCGUUAGGC CGAA IGUAAUCU	3028
1482	UUACCUGC A GCAGCUUC	840	GAAGCUGC CUGAUGAG GCCGUUAGGC CGAA ICAGGUAA	3029
1485	CCUGCAGC A GCUUCAGG	841	CCUGAAGC CUGAUGAG GCCGUUAGGC CGAA ICUGCAGG	3030
1488	GCAGCAGC U UCAGGAGG	842	CCUCCUGA CUGAUGAG GCCGUUAGGC CGAA ICUGCUGC	3031
1491	GCAGCUUC A GGAGGGAC	843	GUCCCUCC CUGAUGAG GCCGUUAGGC CGAA IAAGCUGC	3032

1503	GGGACGUC C AUCUGCAG	844	CUGCAGAU CUGAUGAG GCCGUUAGGC CGAA IACGUCCC	3033
1504	GGACGUCC A UCUGCAGC	845	GCUGCAGA CUGAUGAG GCCGUUAGGC CGAA IGACGUCC	3034
1507	CGUCCAUC U GCAGCGGG	846	CCCGCUGC CUGAUGAG GCCGUUAGGC CGAA IAUGGACG	3035
1510	CCAUCUGC A GCGGGCUU	847	AAGCCCGC CUGAUGAG GCCGUUAGGC CGAA ICAGAUGG	3036
1517	CAGCGGGC U UCGAUCGG	848	CCGAUCGA CUGAUGAG GCCGUUAGGC CGAA ICCCGCUG	3037
1527	CGAUCGGC A UUUACUGU	849	ACAGUAAA CUGAUGAG GCCGUUAGGC CGAA ICCGAUCG	3038
1533	GCAUUUAC U GUGAUUAG	850	CUAAUCAC CUGAUGAG GCCGUUAGGC CGAA IUAAAUGC	3039
1553	GAAAUAUC C AACUGAUG	851	CAUCAGUU CUGAUGAG GCCGUUAGGC CGAA IAUAUUUC	3040
1554	AAAUAUCC A ACUGAUGG	852	CCAUCAGU CUGAUGAG GCCGUUAGGC CGAA IGAUAUUU	3041
1557	UAUCCAAC U GAUGGAUC	853	GAUCCAUC CUGAUGAG GCCGUUAGGC CGAA IUUGGAUA	3042
1566	GAUGGAUC U GAAAUUGU	854	ACAAUUUC CUGAUGAG GCCGUUAGGC CGAA IAUCCAUC	3043
1577	AAUUGUGC U GCUGACGG	855	CCGUCAGC CUGAUGAG GCCGUUAGGC CGAA ICACAAUU	3044
1580	UGUGCUGC U GACGGAUG	856	CAUCCGUC CUGAUGAG GCCGUUAGGC CGAA ICAGCACA	3045
1597	GGGAAGAC A ACACUAUA	857	UAUAGUGU CUGAUGAG GCCGUUAGGC CGAA IUCUUCCC	3046
1600	AAGACAAC A CUAUAAGU	858	ACUUAUAG CUGAUGAG GCCGUUAGGC CGAA IUUGUCUU	3047
1602	GACAACAC U AUAAGUGG	859	CCACUUAU CUGAUGAG GCCGUUAGGC CGAA IUGUUGUC	3048
1615	GUGGGUGC U UUAACGAG	860	CUCGUUAA CUGAUGAG GCCGUUAGGC CGAA ICACCCAC	3049
1627	ACGAGGUC A AACAAAGU	861	ACUUUGUU CUGAUGAG GCCGUUAGGC CGAA IACCUCGU	3050
1631	GGUCAAAC A AAGUGGUG	862	CACCACUU CUGAUGAG GCCGUUAGGC CGAA IUUUGACC	3051
1641	AGUGGUGC C AUCAUCCA	863	UGGAUGAU CUGAUGAG GCCGUUAGGC CGAA ICACCACU	3052
1642	GUGGUGCC A UCAUCCAC	864	GUGGAUGA CUGAUGAG GCCGUUAGGC CGAA IGCACCAC	3053
1645	GUGCCAUC A UCCACACA	865	UGUGUGGA CUGAUGAG GCCGUUAGGC CGAA IAUGGCAC	3054
1648	CCAUCAUC C ACACAGUC	866	GACUGUGU CUGAUGAG GCCGUUAGGC CGAA IAUGAUGG	3055
1649	CAUCAUCC A CACAGUCG	867	CGACUGUG CUGAUGAG GCCGUUAGGC CGAA IGAUGAUG	3056
1651	UCAUCCAC A CAGUCGCU	868	AGCGACUG CUGAUGAG GCCGUUAGGC CGAA IUGGAUGA	3057
1653	AUCCACAC A GUCGCUUU	869	AAAGCGAC CUGAUGAG GCCGUUAGGC CGAA IUGUGGAU	3058
1659	ACAGUCGC U UUGGGGCC	870	GGCCCCAA CUGAUGAG GCCGUUAGGC CGAA ICGACUGU	3059
1667	UUUGGGGC C CUCUGCAG	871	CUGCAGAG CUGAUGAG GCCGUUAGGC CGAA ICCCCAAA	3060
1668	UUGGGGCC C UCUGCAGC	872	GCUGCAGA CUGAUGAG GCCGUUAGGC CGAA IGCCCCAA	3061
1669	UGGGGCCC U CUGCAGCU	873	AGCUGCAG CUGAUGAG GCCGUUAGGC CGAA IGGCCCCA	3062
1671	GGGCCCUC U GCAGCUCA	874	UGAGCUGC CUGAUGAG GCCGUUAGGC CGAA IAGGGCCC	3063
1674	CCCUCUGC A GCUCAAGA	875	UCUUGAGC CUGAUGAG GCCGUUAGGC CGAA ICAGAGGG	3064
1677	UCUGCAGC U CAAGAACU	876	AGUUCUUG CUGAUGAG GCCGUUAGGC CGAA ICUGCAGA	3065
1679	UGCAGCUC A AGAACUAG	877	CUAGUUCU CUGAUGAG GCCGUUAGGC CGAA IAGCUGCA	3066

1685	UCAAGAAC U AGAGGAGC	878	GCUCCUCU CUGAUGAG GCCGUUAGGC CGAA IUUCUUGA	3067
1694	AGAGGAGC U GUCCAAAA	879	UUUUGGAC CUGAUGAG GCCGUUAGGC CGAA ICUCCUCU	3068
1698	GAGCUGUC C AAAAUGAC	880	GUCAUUUU CUGAUGAG GCCGUUAGGC CGAA IACAGCUC	3069
1699	AGCUGUCC A AAAUGACA	881	UGUCAUUU CUGAUGAG GCCGUUAGGC CGAA IGACAGCU	3070
1707	AAAAUGAC A GGAGGUUU	882	AAACCUCC CUGAUGAG GCCGUUAGGC CGAA IUCAUUUU	3071
1718	AGGUUUAC A GACAUAUG	883	CAUAUGUC CUGAUGAG GCCGUUAGGC CGAA IUAAACCU	3072
1722	UUACAGAC A UAUGCUUC	884	GAAGCAUA CUGAUGAG GCCGUUAGGC CGAA IUCUGUAA	3073
1728	ACAUAUGC U UCAGAUCA	885	UGAUCUGA CUGAUGAG GCCGUUAGGC CGAA ICAUAUGU	3074
1731	UAUGCUUC A GAUCAAGU	886	ACUUGAUC CUGAUGAG GCCGUUAGGC CGAA IAAGCAUA	3075
1736	UUCAGAUC A AGUUCAGA	887	UCUGAACU CUGAUGAG GCCGUUAGGC CGAA IAUCUGAA	3076
1742	UCAAGUUC A GAACAAUG	888	CAUUGUUC CUGAUGAG GCCGUUAGGC CGAA IAACUUGA	3077
1747	UUCAGAAC A AUGGCCUC	889	GAGGCCAU CUGAUGAG GCCGUUAGGC CGAA IUUCUGAA	3078
1753	ACAAUGGC C UCAUUGAU	890	AUCAAUGA CUGAUGAG GCCGUUAGGC CGAA ICCAUUGU	3079
1754	CAAUGGCC U CAUUGAUG	891	CAUCAAUG CUGAUGAG GCCGUUAGGC CGAA IGCCAUUG	3080
1756	AUGGCCUC A UUGAUGCU	892	AGCAUCAA CUGAUGAG GCCGUUAGGC CGAA IAGGCCAU	3081
1764	AUUGAUGC U UUUGGGGC	893	GCCCCAAA CUGAUGAG GCCGUUAGGC CGAA ICAUCAAU	3082
1773	UUUGGGGC C CUUUCAUC	894	GAUGAAAG CUGAUGAG GCCGUUAGGC CGAA ICCCCAAA	3083
1774	UUGGGGCC C UUUCAUCA	895	UGAUGAAA CUGAUGAG GCCGUUAGGC CGAA IGCCCCAA	3084
1775	UGGGGCCC U UUCAUCAG	896	CUGAUGAA CUGAUGAG GCCGUUAGGC CGAA IGGCCCCA	3085
1779	GCCCUUUC A UCAGGAAA	897	UUUCCUGA CUGAUGAG GCCGUUAGGC CGAA IAAAGGGC	3086
1782	CUUUCAUC A GGAAAUGG	898	CCAUUUCC CUGAUGAG GCCGUUAGGC CGAA IAUGAAAG	3087
1794	AAUGGAGC U GUCUCUCA	899	UGAGAGAC CUGAUGAG GCCGUUAGGC CGAA ICUCCAUU	3088
1798	GAGCUGUC U CUCAGCGC	900	GCGCUGAG CUGAUGAG GCCGUUAGGC CGAA IACAGCUC	3089
1800	GCUGUCUC U CAGCGCUC	901	GAGCGCUG CUGAUGAG GCCGUUAGGC CGAA IAGACAGC	3090
1802	UGUCUCUC A GCGCUCCA	902	UGGAGCGC CUGAUGAG GCCGUUAGGC CGAA IAGAGACA	3091
1807	CUCAGCGC U CCAUCCAG	903	CUGGAUGG CUGAUGAG GCCGUUAGGC CGAA ICGCUGAG	3092
1809	CAGCGCUC C AUCCAGCU	904	AGCUGGAU CUGAUGAG GCCGUUAGGC CGAA IAGCGCUG	3093
1810	AGCGCUCC A UCCAGCUU	905	AAGCUGGA CUGAUGAG GCCGUUAGGC CGAA IGAGCGCU	3094
1813	GCUCCAUC C AGCUUGAG	906	CUCAAGCU CUGAUGAG GCCGUUAGGC CGAA IAUGGAGC	3095
1814	CUCCAUCC A GCUUGAGA	907	UCUCAAGC CUGAUGAG GCCGUUAGGC CGAA IGAUGGAG	3096
1817	CAUCCAGC U UGAGAGUA	908	UACUCUCA CUGAUGAG GCCGUUAGGC CGAA ICUGGAUG	3097
1836	GGAUUAAC C CUCCAGAA	909	UUCUGGAG CUGAUGAG GCCGUUAGGC CGAA IUUAAUCC	3098
1837	GAUUAACC C UCCAGAAC	910	GUUCUGGA CUGAUGAG GCCGUUAGGC CGAA IGUUAAUC	3099
1838	AUUAACCC U CCAGAACA	911	UGUUCUGG CUGAUGAG GCCGUUAGGC CGAA IGGUUAAU	3100

1840	UAACCCUC C AGAACAGC	912	GCUGUUCU CUGAUGAG GCCGUUAGGC CGAA IAGGGUUA	3101
1841	AACCCUCC A GAACAGCC	913	GGCUGUUC CUGAUGAG GCCGUUAGGC CGAA IGAGGGUU	3102
1846	UCCAGAAC A GCCAGUGG	914	CCACUGGC CUGAUGAG GCCGUUAGGC CGAA IUUCUGGA	3103
1849	AGAACAGC C AGUGGAUG	915	CAUCCACU CUGAUGAG GCCGUUAGGC CGAA ICUGUUCU	3104
1850	GAACAGCC A GUGGAUGA	916	UCAUCCAC CUGAUGAG GCCGUUAGGC CGAA IGCUGUUC	3105
1864	UGAAUGGC A CAGUGAUC	917	GAUCACUG CUGAUGAG GCCGUUAGGC CGAA ICCAUUCA	3106
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1879	UCGUGGAC A GCACCGUG	919	CACGGUGC CUGAUGAG GCCGUUAGGC CGAA IUCCACGA	3108
1882	UGGACAGC A CCGUGGGA	920	UCCCACGG CUGAUGAG GCCGUUAGGC CGAA ICUGUCCA	3109
1884	GACAGCAC C GUGGGAAA	921	UUUCCCAC CUGAUGAG GCCGUUAGGC CGAA IUGCUGUC	3110
1897	GAAAGGAC A CUUUGUUU	922	AAACAAAG CUGAUGAG GCCGUUAGGC CGAA IUCCUUUC	3111
1899	AAGGACAC U UUGUUUCU	923	AGAAACAA CUGAUGAG GCCGUUAGGC CGAA IUGUCCUU	3112
1907	UUUGUUUC U UAUCACCU	924	AGGUGAUA CUGAUGAG GCCGUUAGGC CGAA IAAACAAA	3113
1912	UUCUUAUC A CCUGGACA	925	UGUCCAGG CUGAUGAG GCCGUUAGGC CGAA IAUAAGAA	3114
1914	CUUAUCAC C UGGACAAC	926	GUUGUCCA CUGAUGAG GCCGUUAGGC CGAA IUGAUAAG	3115
1915	UUAUCACC U GGACAACG	927	CGUUGUCC CUGAUGAG GCCGUUAGGC CGAA IGUGAUAA	3116
1920	ACCUGGAC A ACGCAGCC	928	GGCUGCGU CUGAUGAG GCCGUUAGGC CGAA IUCCAGGU	3117
1925	GACAACGC A GCCUCCCC	929	GGGGAGGC CUGAUGAG GCCGUUAGGC CGAA ICGUUGUC	3118
1928	AACGCAGC C UCCCCAAA	930	UUUGGGGA CUGAUGAG GCCGUUAGGC CGAA ICUGCGUU	3119
1929	ACGCAGCC U CCCCAAAU	931	AUUUGGGG CUGAUGAG GCCGUUAGGC CGAA IGCUGCGU	3120
1931	GCAGCCUC C CCAAAUCC	932	GGAUUUGG CUGAUGAG GCCGUUAGGC CGAA IAGGCUGC	3121
1932	CAGCCUCC C CAAAUCCU	933	AGGAUUUG CUGAUGAG GCCGUUAGGC CGAA IGAGGCUG	3122
1933	AGCCUCCC C AAAUCCUU	934	AAGGAUUU CUGAUGAG GCCGUUAGGC CGAA IGGAGGCU	3123
1934	GCCUCCCC A AAUCCUUC	935	GAAGGAUU CUGAUGAG GCCGUUAGGC CGAA IGGGAGGC	3124
1939	CCCAAAUC C UUCUCUGG	936	CCAGAGAA CUGAUGAG GCCGUUAGGC CGAA IAUUUGGG	3125
1940	CCAAAUCC U UCUCUGGG	937	CCCAGAGA CUGAUGAG GCCGUUAGGC CGAA IGAUUUGG	3126
1943	AAUCCUUC U CUGGGAUC	938	GAUCCCAG CUGAUGAG GCCGUUAGGC CGAA IAAGGAUU	3127
1945	UCCUUCUC U GGGAUCCC	939	GGGAUCCC CUGAUGAG GCCGUUAGGC CGAA IAGAAGGA	3128
1952	CUGGGAUC C CAGUGGAC	940	GUCCACUG CUGAUGAG GCCGUUAGGC CGAA IAUCCCAG	3129
1953	UGGGAUCC C AGUGGACA	941	UGUCCACU CUGAUGAG GCCGUUAGGC CGAA IGAUCCCA	3130
1954	GGGAUCCC A GUGGACAG	942	CUGUCCAC CUGAUGAG GCCGUUAGGC CGAA IGGAUCCC	3131
1961	CAGUGGAC A GAAGCAAG	943	CUUGCUUC CUGAUGAG GCCGUUAGGC CGAA IUCCACUG	3132
1967	ACAGAAGC A AGGUGGCU	944	AGCCACCU CUGAUGAG GCCGUUAGGC CGAA ICUUCUGU	3133
1975	AAGGUGGC U UUGUAGUG	945	CACUACAA CUGAUGAG GCCGUUAGGC CGAA ICCACCUU	3134

1987	UAGUGGAC A AAAACACC	946	GGUGUUUU CUGAUGAG GCCGUUAGGC CGAA IUCCACUA	3135
1993	ACAAAAAC A CCAAAAUG	947	CAUUUUGG CUGAUGAG GCCGUUAGGC CGAA IUUUUUGU	3136
1995	AAAAACAC C AAAAUGGC	948	GCCAUUUU CUGAUGAG GCCGUUAGGC CGAA IUGUUUUU	3137
1996	AAAACACC A AAAUGGCC	949	GGCCAUUU CUGAUGAG GCCGUUAGGC CGAA IGUGUUUU	3138
2004	AAAAUGGC C UACCUCCA	950	UGGAGGUA CUGAUGAG GCCGUUAGGC CGAA ICCAUUUU	3139
2005	AAAUGGCC U ACCUCCAA	951	UUGGAGGU CUGAUGAG GCCGUUAGGC CGAA IGCCAUUU	3140
2008	UGGCCUAC C UCCAAAUC	952	GAUUUGGA CUGAUGAG GCCGUUAGGC CGAA IUAGGCCA	3141
2009	GGCCUACC U CCAAAUCC	953	GGAUUUGG CUGAUGAG GCCGUUAGGC CGAA IGUAGGCC	3142
2011	CCUACCUC C AAAUCCCA	954	UGGGAUUU CUGAUGAG GCCGUUAGGC CGAA IAGGUAGG	3143
2012	CUACCUCC A AAUCCCAG	955	CUGGGAUU CUGAUGAG GCCGUUAGGC CGAA IGAGGUAG	3144
2017	UCCAAAUC C CAGGCAUU	956	AAUGCCUG CUGAUGAG GCCGUUAGGC CGAA IAUUUGGA	3145
2018	CCAAAUCC C AGGCAUUG	957	CAAUGCCU CUGAUGAG GCCGUUAGGC CGAA IGAUUUGG	3146
2019	CAAAUCCC A GGCAUUGC	958	GCAAUGCC CUGAUGAG GCCGUUAGGC CGAA IGGAUUUG	3147
2023	UCCCAGGC A UUGCUAAG	959	CUUAGCAA CUGAUGAG GCCGUUAGGC CGAA ICCUGGGA	3148
2028	GGCAUUGC U AAGGUUGG	960	CCAACCUU CUGAUGAG GCCGUUAGGC CGAA ICAAUGCC	3149
2038	AGGUUGGC A CUUGGAAA	961	UUUCCAAG CUGAUGAG GCCGUUAGGC CGAA ICCAACCU	3150
2040	GUUGGCAC U UGGAAAUA	962	UAUUUCCA CUGAUGAG GCCGUUAGGC CGAA IUGCCAAC	3151
2050	GGAAAUAC A GUCUGCAA	963	UUGCAGAC CUGAUGAG GCCGUUAGGC CGAA IUAUUUCC	3152
2054	AUACAGUC U GCAAGCAA	964	UUGCUUGC CUGAUGAG GCCGUUAGGC CGAA IACUGUAU	3153
2057	CAGUCUGC A AGCAAGCU	965	AGCUUGCU CUGAUGAG GCCGUUAGGC CGAA ICAGACUG	3154
2061	CUGCAAGC A AGCUCACA	966	UGUGAGCU CUGAUGAG GCCGUUAGGC CGAA ICUUGCAG	3155
2065	AAGCAAGC U CACAAACC	967	GGUUUGUG CUGAUGAG GCCGUUAGGC CGAA ICUUGCUU	3156
2067	GCAAGCUC A CAAACCUU	968	AAGGUUUG CUGAUGAG GCCGUUAGGC CGAA IAGCUUGC	3157
2069	AAGCUCAC A AACCUUGA	969	UCAAGGUU CUGAUGAG GCCGUUAGGC CGAA IUGAGCUU	3158
2073	UCACAAAC C UUGACCCU	970	AGGGUCAA CUGAUGAG GCCGUUAGGC CGAA IUUUGUGA	3159
2074	CACAAACC U UGACCCUG	971	CAGGGUCA CUGAUGAG GCCGUUAGGC CGAA IGUUUGUG	3160
2079	ACCUUGAC C CUGACUGU	972	ACAGUCAG CUGAUGAG GCCGUUAGGC CGAA IUCAAGGU	3161
2080	CCUUGACC C UGACUGUC	973	GACAGUCA CUGAUGAG GCCGUUAGGC CGAA IGUCAAGG	3162
2081	CUUGACCC U GACUGUCA	974	UGACAGUC CUGAUGAG GCCGUUAGGC CGAA IGGUCAAG	3163
2085	ACCCUGAC U GUCACGUC	975	GACGUGAC CUGAUGAG GCCGUUAGGC CGAA IUCAGGGU	3164
2089	UGACUGUC A CGUCCCGU	976	ACGGGACG CUGAUGAG GCCGUUAGGC CGAA IACAGUCA	3165
2094	GUCACGUC C CGUGCGUC	977	GACGCACG CUGAUGAG GCCGUUAGGC CGAA IACGUGAC	3166
2095	UCACGUCC C GUGCGUCC	978	GGACGCAC CUGAUGAG GCCGUUAGGC CGAA IGACGUGA	3167
2103	CGUGCGUC C AAUGCUAC	979	GUAGCAUU CUGAUGAG GCCGUUAGGC CGAA IACGCACG	3168

2104	GUGCGUCC A AUGCUACC	980	GGUAGCAU CUGAUGAG GCCGUUAGGC CGAA IGACGCAC	3169
2109	UCCAAUGC U ACCCUGCC	981	GGCAGGGU CUGAUGAG GCCGUUAGGC CGAA ICAUUGGA	3170
2112	AAUGCUAC C CUGCCUCC	982	GGAGGCAG CUGAUGAG GCCGUUAGGC CGAA IUAGCAUU	3171
2113	AUGCUACC C UGCCUCCA	983	UGGAGGCA CUGAUGAG GCCGUUAGGC CGAA IGUAGCAU	3172
2114	UGCUACCC U GCCUCCAA	984	UUGGAGGC CUGAUGAG GCCGUUAGGC CGAA IGGUAGCA	3173
2117	UACCCUGC C UCCAAUUA	985	UAAUUGGA CUGAUGAG GCCGUUAGGC CGAA ICAGGGUA	3174
2118	ACCCUGCC U CCAAUUAC	986	GUAAUUGG CUGAUGAG GCCGUUAGGC CGAA IGCAGGGU	3175
2120	CCUGCCUC C AAUUACAG	987	CUGUAAUU CUGAUGAG GCCGUUAGGC CGAA IAGGCAGG	3176
2121	CUGCCUCC A AUUACAGU	988	ACUGUAAU CUGAUGAG GCCGUUAGGC CGAA IGAGGCAG	3177
2127	CCAAUUAC A GUGACUUC	989	GAAGUCAC CUGAUGAG GCCGUUAGGC CGAA IUAAUUGG	3178
2133	ACAGUGAC U UCCAAAAC	990	GUUUUGGA CUGAUGAG GCCGUUAGGC CGAA IUCACUGU	3179
2136	GUGACUUC C AAAACGAA	991	UUCGUUUU CUGAUGAG GCCGUUAGGC CGAA IAAGUCAC	3180
2137	UGACUUCC A AAACGAAC	992	GUUCGUUU CUGAUGAG GCCGUUAGGC CGAA IGAAGUCA	3181
2146	AAACGAAC A AGGACACC	993	GGUGUCCU CUGAUGAG GCCGUUAGGC CGAA IUUCGUUU	3182
2152	ACAAGGAC A CCAGCAAA	994	UUUGCUGG CUGAUGAG GCCGUUAGGC CGAA IUCCUUGU	3183
2154	AAGGACAC C AGCAAAUU	995	AAUUUGCU CUGAUGAG GCCGUUAGGC CGAA IUGUCCUU	3184
2155	AGGACACC A GCAAAUUC	996	GAAUUUGC CUGAUGAG GCCGUUAGGC CGAA IGUGUCCU	3185
2158	ACACCAGC A AAUUCCCC	997	GGGGAAUU CUGAUGAG GCCGUUAGGC CGAA ICUGGUGU	3186
2164	GCAAAUUC C CCAGCCCU	998	AGGGCUGG CUGAUGAG GCCGUUAGGC CGAA IAAUUUGC	3187
2165	CAAAUUCC C CAGCCCUC	999	GAGGGCUG CUGAUGAG GCCGUUAGGC CGAA IGAAUUUG	3188
2166	AAAUUCCC C AGCCCUCU	1000	AGAGGGCU CUGAUGAG GCCGUUAGGC CGAA IGGAAUUU	3189
2167	AAUUCCCC A GCCCUCUG	1001	CAGAGGGC CUGAUGAG GCCGUUAGGC CGAA IGGGAAUU	3190
2170	UCCCCAGC C CUCUGGUA	1002	UACCAGAG CUGAUGAG GCCGUUAGGC CGAA ICUGGGGA	3191
2171	CCCCAGCC C UCUGGUAG	1003	CUACCAGA CUGAUGAG GCCGUUAGGC CGAA IGCUGGGG	3192
2172	CCCAGCCC U CUGGUAGU	1004	ACUACCAG CUGAUGAG GCCGUUAGGC CGAA IGGCUGGG	3193
2174	CAGCCCUC U GGUAGUUU	1005	AAACUACC CUGAUGAG GCCGUUAGGC CGAA IAGGGCUG	3194
2187	GUUUAUGC A AAUAUUCG	1006	CGAAUAUU CUGAUGAG GCCGUUAGGC CGAA ICAUAAAC	3195
2197	AUAUUCGC C AAGGAGCC	1007	GGCUCCUU CUGAUGAG GCCGUUAGGC CGAA ICGAAUAU	3196
2198	UAUUCGCC A AGGAGCCU	1008	AGGCUCCU CUGAUGAG GCCGUUAGGC CGAA IGCGAAUA	3197
2205	CAAGGAGC C UCCCCAAU	1009	AUUGGGGA CUGAUGAG GCCGUUAGGC CGAA ICUCCUUG	3198
2206	AAGGAGCC U CCCCAAUU	1010	AAUUGGGG CUGAUGAG GCCGUUAGGC CGAA IGCUCCUU	3199
2208	GGAGCCUC C CCAAUUCU	1011	AGAAUUGG CUGAUGAG GCCGUUAGGC CGAA IAGGCUCC	3200
2209	GAGCCUCC C CAAUUCUC	1012	GAGAAUUG CUGAUGAG GCCGUUAGGC CGAA IGAGGCUC	3201
2210	AGCCUCCC C AAUUCUCA	1013	UGAGAAUU CUGAUGAG GCCGUUAGGC CGAA IGGAGGCU	3202

2211	GCCUCCCC A AUUCUCAG	1014	CUGAGAAU CUGAUGAG GCCGUUAGGC CGAA IGGGAGGC	3203
2216	CCCAAUUC U CAGGGCCA	1015	UGGCCCUG CUGAUGAG GCCGUUAGGC CGAA IAAUUGGG	3204
2218	CAAUUCUC A GGGCCAGU	1016	ACUGGCCC CUGAUGAG GCCGUUAGGC CGAA IAGAAUUG	3205
2223	CUCAGGGC C AGUGUCAC	1017	GUGACACU CUGAUGAG GCCGUUAGGC CGAA ICCCUGAG	3206
2224	UCAGGGCC A GUGUCACA	1018	UGUGACAC CUGAUGAG GCCGUUAGGC CGAA IGCCCUGA	3207
2230	CCAGUGUC A CAGCCCUG	1019	CAGGGCUG CUGAUGAG GCCGUUAGGC CGAA IACACUGG	3208
2232	AGUGUCAC A GCCCUGAU	1020	AUCAGGGC CUGAUGAG GCCGUUAGGC CGAA IUGACACU	3209
2235	GUCACAGC C CUGAUUGA	1021	UCAAUCAG CUGAUGAG GCCGUUAGGC CGAA ICUGUGAC	3210
2236	UCACAGCC C UGAUUGAA	1022	UUCAAUCA CUGAUGAG GCCGUUAGGC CGAA IGCUGUGA	3211
2237	CACAGCCC U GAUUGAAU	1023	AUUCAAUC CUGAUGAG GCCGUUAGGC CGAA IGGCUGUG	3212
2247	AUUGAAUC A GUGAAUGG	1024	CCAUUCAC CUGAUGAG GCCGUUAGGC CGAA IAUUCAAU	3213
2262	GGAAAAAC A GUUACCUU	1025	AAGGUAAC CUGAUGAG GCCGUUAGGC CGAA IUUUUUCC	3214
2268	ACAGUUAC C UUGGAACU	1026	AGUUCCAA CUGAUGAG GCCGUUAGGC CGAA IUAACUGU	3215
2269	CAGUUACC U UGGAACUA	1027	UAGUUCCA CUGAUGAG GCCGUUAGGC CGAA IGUAACUG	3216
2276	CUUGGAAC U ACUGGAUA	1028	UAUCCAGU CUGAUGAG GCCGUUAGGC CGAA IUUCCAAG	3217
2279	GGAACUAC U GGAUAAUG	1029	CAUUAUCC CUGAUGAG GCCGUUAGGC CGAA IUAGUUCC	3218
2292	AAUGGAGC A GGUGCUGA	1030	UCAGCACC CUGAUGAG GCCGUUAGGC CGAA ICUCCAUU	3219
2298	GCAGGUGC U GAUGCUAC	1031	GUAGCAUC CUGAUGAG GCCGUUAGGC CGAA ICACCUGC	3220
2304	GCUGAUGC U ACUAAGGA	1032	UCCUUAGU CUGAUGAG GCCGUUAGGC CGAA ICAUCAGC	3221
2307	GAUGCUAC U AAGGAUGA	1033	UCAUCCUU CUGAUGAG GCCGUUAGGC CGAA IUAGCAUC	3222
2323	ACGGUGUC U ACUCAAGG	1034	CCUUGAGU CUGAUGAG GCCGUUAGGC CGAA IACACCGU	3223
2326	GUGUCUAC U CAAGGUAU	1035	AUACCUUG CUGAUGAG GCCGUUAGGC CGAA IUAGACAC	3224
2328	GUCUACUC A AGGUAUUU	1036	AAAUACCU CUGAUGAG GCCGUUAGGC CGAA IAGUAGAC	3225
2338	GGUAUUUC A CAACUUAU	1037	AUAAGUUG CUGAUGAG GCCGUUAGGC CGAA IAAAUACC	3226
2340	UAUUUCAC A ACUUAUGA	1038	UCAUAAGU CUGAUGAG GCCGUUAGGC CGAA IUGAAAUA	3227
2343	UUCACAAC U UAUGACAC	1039	GUGUCAUA CUGAUGAG GCCGUUAGGC CGAA IUUGUGAA	3228
2350	CUUAUGAC A CGAAUGGU	1040	ACCAUUCG CUGAUGAG GCCGUUAGGC CGAA IUCAUAAG	3229
2365	GUAGAUAC A GUGUAAAA	1041	UUUUACAC CUGAUGAG GCCGUUAGGC CGAA IUAUCUAC	3230
2382	GUGCGGGC U CUGGGAGG	1042	CCUCCCAG CUGAUGAG GCCGUUAGGC CGAA ICCCGCAC	3231
2384	GCGGGCUC U GGGAGGAG	1043	CUCCUCCC CUGAUGAG GCCGUUAGGC CGAA IAGCCCGC	3232
2400	GUUAACGC A GCCAGACG	1044	CGUCUGGC CUGAUGAG GCCGUUAGGC CGAA ICGUUAAC	3233
2403	AACGCAGC C AGACGGAG	1045	CUCCGUCU CUGAUGAG GCCGUUAGGC CGAA ICUGCGUU	3234
2404	ACGCAGCC A GACGGAGA	1046	UCUCCGUC CUGAUGAG GCCGUUAGGC CGAA IGCUGCGU	3235
2420	AGUGAUAC C CCAGCAGA	1047	UCUGCUGG CUGAUGAG GCCGUUAGGC CGAA IUAUCACU	3236

2421	GUGAUACC C CAGCAGAG	1048	CUCUGCUG CUGAUGAG GCCGUUAGGC CGAA IGUAUCAC	3237
2422	UGAUACCC C AGCAGAGU	1049	ACUCUGCU CUGAUGAG GCCGUUAGGC CGAA IGGUAUCA	3238
2423	GAUACCCC A GCAGAGUG	1050	CACUCUGC CUGAUGAG GCCGUUAGGC CGAA IGGGUAUC	3239
2426	ACCCCAGC A GAGUGGAG	1051	CUCCACUC CUGAUGAG GCCGUUAGGC CGAA ICUGGGGU	3240
2436	AGUGGAGC A CUGUACAU	1052	AUGUACAG CUGAUGAG GCCGUUAGGC CGAA ICUCCACU	3241
2438	UGGAGCAC U GUACAUAC	1053	GUAUGUAC CUGAUGAG GCCGUUAGGC CGAA IUGCUCCA	3242
2443	CACUGUAC A UACCUGGC	1054	GCCAGGUA CUGAUGAG GCCGUUAGGC CGAA IUACAGUG	3243
2447	GUACAUAC C UGGCUGGA	1055	UCCAGCCA CUGAUGAG GCCGUUAGGC CGAA IUAUGUAC	3244
2448	UACAUACC U GGCUGGAU	1056	AUCCAGCC CUGAUGAG GCCGUUAGGC CGAA IGUAUGUA	3245
2452	UACCUGGC U GGAUUGAG	1057	CUCAAUCC CUGAUGAG GCCGUUAGGC CGAA ICCAGGUA	3246
2474	UGAAAUAC A AUGGAAUC	1058	GAUUCCAU CUGAUGAG GCCGUUAGGC CGAA IUAUUUCA	3247
2483	AUGGAAUC C ACCAAGAC	1059	GUCUUGGU CUGAUGAG GCCGUUAGGC CGAA IAUUCCAU	3248
2484	UGGAAUCC A CCAAGACC	1060	GGUCUUGG CUGAUGAG GCCGUUAGGC CGAA IGAUUCCA	3249
2486	GAAUCCAC C AAGACCUG	1061	CAGGUCUU CUGAUGAG GCCGUUAGGC CGAA IUGGAUUC	3250
2487	AAUCCACC A AGACCUGA	1062	UCAGGUCU CUGAUGAG GCCGUUAGGC CGAA IGUGGAUU	3251
2492	ACCAAGAC C UGAAAUUA	1063	UAAUUUCA CUGAUGAG GCCGUUAGGC CGAA IUCUUGGU	3252
2493	CCAAGACC U GAAAUUAA	1064	UUAAUUUC CUGAUGAG GCCGUUAGGC CGAA IGUCUUGG	3253
2516	UGAUGUUC A ACACAAGC	1065	GCUUGUGU CUGAUGAG GCCGUUAGGC CGAA IAACAUCA	3254
2519	UGUUCAAC A CAAGCAAG	1066	CUUGCUUG CUGAUGAG GCCGUUAGGC CGAA IUUGAACA	3255
2521	UUCAACAC A AGCAAGUG	1067	CACUUGCU CUGAUGAG GCCGUUAGGC CGAA IUGUUGAA	3256
2525	ACACAAGC A AGUGUGUU	1068	AACACACU CUGAUGAG GCCGUUAGGC CGAA ICUUGUGU	3257
2536	UGUGUUUC A GCAGAACA	1069	UGUUCUGC CUGAUGAG GCCGUUAGGC CGAA IAAACACA	3258
2539	GUUUCAGC A GAACAUCC	1070	GGAUGUUC CUGAUGAG GCCGUUAGGC CGAA ICUGAAAC	3259
2544	AGCAGAAC A UCCUCGGG	1071	CCCGAGGA CUGAUGAG GCCGUUAGGC CGAA IUUCUGCU	3260
2547	AGAACAUC C UCGGGAGG	1072	CCUCCCGA CUGAUGAG GCCGUUAGGC CGAA IAUGUUCU	3261
2548	GAACAUCC U CGGGAGGC	1073	GCCUCCCG CUGAUGAG GCCGUUAGGC CGAA IGAUGUUC	3262
2557	CGGGAGGC U CAUUUGUG	1074	CACAAAUG CUGAUGAG GCCGUUAGGC CGAA ICCUCCCG	3263
2559	GGAGGCUC A UUUGUGGC	1075	GCCACAAA CUGAUGAG GCCGUUAGGC CGAA IAGCCUCC	3264
2568	UUUGUGGC U UCUGAUGU	1076	ACAUCAGA CUGAUGAG GCCGUUAGGC CGAA ICCACAAA	3265
2571	GUGGCUUC U GAUGUCCC	1077	GGGACAUC CUGAUGAG GCCGUUAGGC CGAA IAAGCCAC	3266
2578	CUGAUGUC C CAAAUGCU	1078	AGCAUUUG CUGAUGAG GCCGUUAGGC CGAA IACAUCAG	3267
2579	UGAUGUCC C AAAUGCUC	1079	GAGCAUUU CUGAUGAG GCCGUUAGGC CGAA IGACAUCA	3268
2580	GAUGUCCC A AAUGCUCC	1080	GGAGCAUU CUGAUGAG GCCGUUAGGC CGAA IGGACAUC	3269
2586	CCAAAUGC U CCCAUACC	1081	GGUAUGGG CUGAUGAG GCCGUUAGGC CGAA ICAUUUGG	3270

2588	AAAUGCUC C CAUACCUG	1082	CAGGUAUG CUGAUGAG GCCGUUAGGC CGAA IAGCAUUU	3271
2589	AAUGCUCC C AUACCUGA	1083	UCAGGUAU CUGAUGAG GCCGUUAGGC CGAA IGAGCAUU	3272
2590	AUGCUCCC A UACCUGAU	1084	AUCAGGUA CUGAUGAG GCCGUUAGGC CGAA IGGAGCAU	3273
2594	UCCCAUAC C UGAUCUCU	1085	AGAGAUCA CUGAUGAG GCCGUUAGGC CGAA IUAUGGGA	3274
2595	CCCAUACC U GAUCUCUU	1086	AAGAGAUC CUGAUGAG GCCGUUAGGC CGAA IGUAUGGG	3275
2600	ACCUGAUC U CUUCCCAC	1087	GUGGGAAG CUGAUGAG GCCGUUAGGC CGAA IAUCAGGU	3276
2602	CUGAUCUC U UCCCACCU	1088	AGGUGGGA CUGAUGAG GCCGUUAGGC CGAA IAGAUCAG	3277
2605	AUCUCUUC C CACCUGGC	1089	GCCAGGUG CUGAUGAG GCCGUUAGGC CGAA IAAGAGAU	3278
2606	UCUCUUCC C ACCUGGCC	1090	GGCCAGGU CUGAUGAG GCCGUUAGGC CGAA IGAAGAGA	3279
2607	CUCUUCCC A CCUGGCCA	1091	UGGCCAGG CUGAUGAG GCCGUUAGGC CGAA IGGAAGAG	3280
2609	CUUCCCAC C UGGCCAAA	1092	UUUGGCCA CUGAUGAG GCCGUUAGGC CGAA IUGGGAAG	3281
2610	UUCCCACC U GGCCAAAU	1093	AUUUGGCC CUGAUGAG GCCGUUAGGC CGAA IGUGGGAA	3282
2614	CACCUGGC C AAAUCACC	1094	GGUGAUUU CUGAUGAG GCCGUUAGGC CGAA ICCAGGUG	3283
2615	ACCUGGCC A AAUCACCG	1095	CGGUGAUU CUGAUGAG GCCGUUAGGC CGAA IGCCAGGU	3284
2620	GCCAAAUC A CCGACCUG	1096	CAGGUCGG CUGAUGAG GCCGUUAGGC CGAA IAUUUGGC	3285
2622	CAAAUCAC C GACCUGAA	1097	UUCAGGUC CUGAUGAG GCCGUUAGGC CGAA IUGAUUUG	3286
2626	UCACCGAC C UGAAGGCG	1098	CGCCUUCA CUGAUGAG GCCGUUAGGC CGAA IUCGGUGA	3287
2627	CACCGACC U GAAGGCGG	1099	CCGCCUUC CUGAUGAG GCCGUUAGGC CGAA IGUCGGUG	3288
2642	GGAAAUUC A CGGGGGCA	1100	UGCCCCCG CUGAUGAG GCCGUUAGGC CGAA IAAUUUCC	3289
2650	ACGGGGGC A GUCUCAUU	1101	AAUGAGAC CUGAUGAG GCCGUUAGGC CGAA ICCCCCGU	3290
2654	GGGCAGUC U CAUUAAUC	1102	GAUUAAUG CUGAUGAG GCCGUUAGGC CGAA IACUGCCC	3291
2656	GCAGUCUC A UUAAUCUG	1103	CAGAUUAA CUGAUGAG GCCGUUAGGC CGAA IAGACUGC	3292
2663	CAUUAAUC U GACUUGGA	1104	UCCAAGUC CUGAUGAG GCCGUUAGGC CGAA IAUUAAUG	3293
2667	AAUCUGAC U UGGACAGC	1105	GCUGUCCA CUGAUGAG GCCGUUAGGC CGAA IUCAGAUU	3294
2673	ACUUGGAC A GCUCCUGG	1106	CCAGGAGC CUGAUGAG GCCGUUAGGC CGAA IUCCAAGU	3295
2676	UGGACAGC U CCUGGGGA	1107	UCCCCAGG CUGAUGAG GCCGUUAGGC CGAA ICUGUCCA	3296
2678	GACAGCUC C UGGGGAUG	1108	CAUCCCCA CUGAUGAG GCCGUUAGGC CGAA IAGCUGUC	3297
2679	ACAGCUCC U GGGGAUGA	1109	UCAUCCCC CUGAUGAG GCCGUUAGGC CGAA IGAGCUGU	3298
2695	AUUAUGAC C AUGGAACA	1110	UGUUCCAU CUGAUGAG GCCGUUAGGC CGAA IUCAUAAU	3299
2696	UUAUGACC A UGGAACAG	1111	CUGUUCCA CUGAUGAG GCCGUUAGGC CGAA IGUCAUAA	3300
2703	CAUGGAAC A GCUCACAA	1112	UUGUGAGC CUGAUGAG GCCGUUAGGC CGAA IUUCCAUG	3301
2706	GGAACAGC U CACAAGUA	1113	UACUUGUG CUGAUGAG GCCGUUAGGC CGAA ICUGUUCC	3302
2708	AACAGCUC A CAAGUAUA	1114	UAUACUUG CUGAUGAG GCCGUUAGGC CGAA IAGCUGUU	3303
2710	CAGCUCAC A AGUAUAUC	1115	GAUAUACU CUGAUGAG GCCGUUAGGC CGAA IUGAGCUG	3304

2719	AGUAUAUC A UUCGAAUA	1116	UAUUCGAA CUGAUGAG GCCGUUAGGC CGAA IAUAUACU	3305
2733	AUAAGUAC A AGUAUUCU	1117	AGAAUACU CUGAUGAG GCCGUUAGGC CGAA IUACUUAU	3306
2741	AAGUAUUC U UGAUCUCA	1118	UGAGAUCA CUGAUGAG GCCGUUAGGC CGAA IAAUACUU	3307
2747	UCUUGAUC U CAGAGACA	1119	UGUCUCUG CUGAUGAG GCCGUUAGGC CGAA IAUCAAGA	3308
2749	UUGAUCUC A GAGACAAG	1120	CUUGUCUC CUGAUGAG GCCGUUAGGC CGAA IAGAUCAA	3309
2755	UCAGAGAC A AGUUCAAU	1121	AUUGAACU CUGAUGAG GCCGUUAGGC CGAA IUCUCUGA	3310
2761	ACAAGUUC A AUGAAUCU	1122	AGAUUCAU CUGAUGAG GCCGUUAGGC CGAA IAACUUGU	3311
2769	AAUGAAUC U CUUCAAGU	1123	ACUUGAAG CUGAUGAG GCCGUUAGGC CGAA IAUUCAUU	3312
2771	UGAAUCUC U UCAAGUGA	1124	UCACUUGA CUGAUGAG GCCGUUAGGC CGAA IAGAUUCA	3313
2774	AUCUCUUC A AGUGAAUA	1125	UAUUCACU CUGAUGAG GCCGUUAGGC CGAA IAAGAGAU	3314
2784	GUGAAUAC U ACUGCUCU	1126	AGAGCAGU CUGAUGAG GCCGUUAGGC CGAA IUAUUCAC	3315
2787	AAUACUAC U GCUCUCAU	1127	AUGAGAGC CUGAUGAG GCCGUUAGGC CGAA IUAGUAUU	3316
2790	ACUACUGC U CUCAUCCC	1128	GGGAUGAG CUGAUGAG GCCGUUAGGC CGAA ICAGUAGU	3317
2792	UACUGCUC U CAUCCCAA	1129	UUGGGAUG CUGAUGAG GCCGUUAGGC CGAA IAGCAGUA	3318
2794	CUGCUCUC A UCCCAAAG	1130	CUUUGGGA CUGAUGAG GCCGUUAGGC CGAA IAGAGCAG	3319
2797	CUCUCAUC C CAAAGGAA	1131	UUCCUUUG CUGAUGAG GCCGUUAGGC CGAA IAUGAGAG	3320
2798	UCUCAUCC C AAAGGAAG	1132	CUUCCUUU CUGAUGAG GCCGUUAGGC CGAA IGAUGAGA	3321
2799	CUCAUCCC A AAGGAAGC	1133	GCUUCCUU CUGAUGAG GCCGUUAGGC CGAA IGGAUGAG	3322
2808	AAGGAAGC C AACUCUGA	1134	UCAGAGUU CUGAUGAG GCCGUUAGGC CGAA ICUUCCUU	3323
2809	AGGAAGCC A ACUCUGAG	1135	CUCAGAGU CUGAUGAG GCCGUUAGGC CGAA IGCUUCCU	3324
2812	AAGCCAAC U CUGAGGAA	1136	UUCCUCAG CUGAUGAG GCCGUUAGGC CGAA IUUGGCUU	3325
2814	GCCAACUC U GAGGAAGU	1137	ACUUCCUC CUGAUGAG GCCGUUAGGC CGAA IAGUUGGC	3326
2824	AGGAAGUC U UUUUGUUU	1138	AAACAAAA CUGAUGAG GCCGUUAGGC CGAA IACUUCCU	3327
2837	GUUUAAAC C AGAAAACA	1139	UGUUUUCU CUGAUGAG GCCGUUAGGC CGAA IUUUAAAC	3328
2838	UUUAAACC A GAAAACAU	1140	AUGUUUUC CUGAUGAG GCCGUUAGGC CGAA IGUUUAAA	3329
2845	CAGAAAAC A UUACUUUU	1141	AAAAGUAA CUGAUGAG GCCGUUAGGC CGAA IUUUUCUG	3330
2850	AACAUUAC U UUUGAAAA	1142	UUUUCAAA CUGAUGAG GCCGUUAGGC CGAA IUAAUGUU	3331
2863	AAAAUGGC A CAGAUCUU	1143	AAGAUCUG CUGAUGAG GCCGUUAGGC CGAA ICCAUUUU	3332
2865	AAUGGCAC A GAUCUUUU	1144	AAAAGAUC CUGAUGAG GCCGUUAGGC CGAA IUGCCAUU	3333
2870	CACAGAUC U UUUCAUUG	1145	CAAUGAAA CUGAUGAG GCCGUUAGGC CGAA IAUCUGUG	3334
2875	AUCUUUUC A UUGCUAUU	1146	AAUAGCAA CUGAUGAG GCCGUUAGGC CGAA IAAAAGAU	3335
2880	UUCAUUGC U AUUCAGGC	1147	GCCUGAAU CUGAUGAG GCCGUUAGGC CGAA ICAAUGAA	3336
2885	UGCUAUUC A GGCUGUUG	1148	CAACAGCC CUGAUGAG GCCGUUAGGC CGAA IAAUAGCA	3337
2889	AUUCAGGC U GUUGAUAA	1149	UUAUCAAC CUGAUGAG GCCGUUAGGC CGAA ICCUGAAU	3338

2906	GGUCGAUC U GAAAUCAG	1150	CUGAUUUC CUGAUGAG GCCGUUAGGC CGAA IAUCGACC	3339
2913	CUGAAAUC A GAAAUAUC	1151	GAUAUUUC CUGAUGAG GCCGUUAGGC CGAA IAUUUCAG	3340
2922	GAAAUAUC C AACAUUGC	1152	GCAAUGUU CUGAUGAG GCCGUUAGGC CGAA IAUAUUUC	3341
2923	AAAUAUCC A ACAUUGCA	1153	UGCAAUGU CUGAUGAG GCCGUUAGGC CGAA IGAUAUUU	3342
2926	UAUCCAAC A UUGCACGA	1154	UCGUGCAA CUGAUGAG GCCGUUAGGC CGAA IUUGGAUA	3343
2931	AACAUUGC A CGAGUAUC	1155	GAUACUCG CUGAUGAG GCCGUUAGGC CGAA ICAAUGUU	3344
2940	CGAGUAUC U UUGUUUAU	1156	AUAAACAA CUGAUGAG GCCGUUAGGC CGAA IAUACUCG	3345
2951	GUUUAUUC C UCCACAGA	1157	UCUGUGGA CUGAUGAG GCCGUUAGGC CGAA IAAUAAAC	3346
2952	UUUAUUCC U CCACAGAC	1158	GUCUGUGG CUGAUGAG GCCGUUAGGC CGAA IGAAUAAA	3347
2954	UAUUCCUC C ACAGACUC	1159	GAGUCUGU CUGAUGAG GCCGUUAGGC CGAA IAGGAAUA	3348
2955	AUUCCUCC A CAGACUCC	1160	GGAGUCUG CUGAUGAG GCCGUUAGGC CGAA IGAGGAAU	3349
2957	UCCUCCAC A GACUCCGC	1161	GCGGAGUC CUGAUGAG GCCGUUAGGC CGAA IUGGAGGA	3350
2961	CCACAGAC U CCGCCAGA	1162	UCUGGCGG CUGAUGAG GCCGUUAGGC CGAA IUCUGUGG	3351
2963	ACAGACUC C GCCAGAGA	1163	UCUCUGGC CUGAUGAG GCCGUUAGGC CGAA IAGUCUGU	3352
2966	GACUCCGC C AGAGACAC	1164	GUGUCUCU CUGAUGAG GCCGUUAGGC CGAA ICGGAGUC	3353
2967	ACUCCGCC A GAGACACC	1165	GGUGUCUC CUGAUGAG GCCGUUAGGC CGAA IGCGGAGU	3354
2973	CCAGAGAC A CCUAGUCC	1166	GGACUAGG CUGAUGAG GCCGUUAGGC CGAA IUCUCUGG	3355
2975	AGAGACAC C UAGUCCUG	1167	CAGGACUA CUGAUGAG GCCGUUAGGC CGAA IUGUCUCU	3356
2976	GAGACACC U AGUCCUGA	1168	UCAGGACU CUGAUGAG GCCGUUAGGC CGAA IGUGUCUC	3357
2981	ACCUAGUC C UGAUGAAA	1169	UUUCAUCA CUGAUGAG GCCGUUAGGC CGAA IACUAGGU	3358
2982	CCUAGUCC U GAUGAAAC	1170	GUUUCAUC CUGAUGAG GCCGUUAGGC CGAA IGACUAGG	3359
2994	GAAACGUC U GCUCCUUG	1171	CAAGGAGC CUGAUGAG GCCGUUAGGC CGAA IACGUUUC	3360
2997	ACGUCUGC U CCUUGUCC	1172	GGACAAGG CUGAUGAG GCCGUUAGGC CGAA ICAGACGU	3361
2999	GUCUGCUC C UUGUCCUA	1173	UAGGACAA CUGAUGAG GCCGUUAGGC CGAA IAGCAGAC	3362
3000	UCUGCUCC U UGUCCUAA	1174	UUAGGACA CUGAUGAG GCCGUUAGGC CGAA IGAGCAGA	3363
3005	UCCUUGUC C UAAUAUUC	1175	GAAUAUUA CUGAUGAG GCCGUUAGGC CGAA IACAAGGA	3364
3006	CCUUGUCC U AAUAUUCA	1176	UGAAUAUU CUGAUGAG GCCGUUAGGC CGAA IGACAAGG	3365
3014	UAAUAUUC A UAUCAACA	1177	UGUUGAUA CUGAUGAG GCCGUUAGGC CGAA IAAUAUUA	3366
3019	UUCAUAUC A ACAGCACC	1178	GGUGCUGU CUGAUGAG GCCGUUAGGC CGAA IAUAUGAA	3367
3022	AUAUCAAC A GCACCAUU	1179	AAUGGUGC CUGAUGAG GCCGUUAGGC CGAA IUUGAUAU	3368
3025	UCAACAGC A CCAUUCCU	1180	AGGAAUGG CUGAUGAG GCCGUUAGGC CGAA ICUGUUGA	3369
3027	AACAGCAC C AUUCCUGG	1181	CCAGGAAU CUGAUGAG GCCGUUAGGC CGAA IUGCUGUU	3370
3028	ACAGCACC A UUCCUGGC	1182	GCCAGGAA CUGAUGAG GCCGUUAGGC CGAA IGUGCUGU	3371
3032	CACCAUUC C UGGCAUUC	1183	GAAUGCCA CUGAUGAG GCCGUUAGGC CGAA IAAUGGUG	3372

3033	ACCAUUCC U GGCAUUCA	1184	UGAAUGCC CUGAUGAG GCCGUUAGGC CGAA IGAAUGGU	3373
3037	UUCCUGGC A UUCACAUU	1185	AAUGUGAA CUGAUGAG GCCGUUAGGC CGAA ICCAGGAA	3374
3041	UGGCAUUC A CAUUUUAA	1186	UUAAAAUG CUGAUGAG GCCGUUAGGC CGAA IAAUGCCA	3375
3043	GCAUUCAC A UUUUAAAA	1187	UUUUAAAA CUGAUGAG GCCGUUAGGC CGAA IUGAAUGC	3376
3077	AGGAGAAC U GCAGCUGU	1188	ACAGCUGC CUGAUGAG GCCGUUAGGC CGAA IUUCUCCU	3377
3080	AGAACUGC A GCUGUCAA	1189	UUGACAGC CUGAUGAG GCCGUUAGGC CGAA ICAGUUCU	3378
3083	ACUGCAGC U GUCAAUAG	1190	CUAUUGAC CUGAUGAG GCCGUUAGGC CGAA ICUGCAGU	3379
3087	CAGCUGUC A AUAGCCUA	1191	UAGGCUAU CUGAUGAG GCCGUUAGGC CGAA IACAGCUG	3380
3093	UCAAUAGC C UAGGGCUG	1192	CAGCCCUA CUGAUGAG GCCGUUAGGC CGAA ICUAUUGA	3381
3094	CAAUAGCC U AGGGCUGA	1193	UCAGCCCU CUGAUGAG GCCGUUAGGC CGAA IGCUAUUG	3382
3100	CCUAGGGC U GAAUUUUU	1194	AAAAAUUC CUGAUGAG GCCGUUAGGC CGAA ICCCUAGG	3383
3112	UUUUUGUC A GAUAAAUA	1195	UAUUUAUC CUGAUGAG GCCGUUAGGC CGAA IACAAAAA	3384
3130	AAUAAAUC A UUCAUCCU	1196	AGGAUGAA CUGAUGAG GCCGUUAGGC CGAA IAUUUAUU	3385
3134	AAUCAUUC A UCCUUUUU	1197	AAAAAGGA CUGAUGAG GCCGUUAGGC CGAA IAAUGAUU	3386
3137	CAUUCAUC C UUUUUUUG	1198	CAAAAAAA CUGAUGAG GCCGUUAGGC CGAA IAUGAAUG	3387
3138	AUUCAUCC U UUUUUUGA	1199	UCAAAAAA CUGAUGAG GCCGUUAGGC CGAA IGAUGAAU	3388
3160	AAAUUUUC U AAAAUGUA	1200	UACAUUUU CUGAUGAG GCCGUUAGGC CGAA IAAAAUUU	3389
3177	UUUUAGAC U UCCUGUAG	1201	CUACAGGA CUGAUGAG GCCGUUAGGC CGAA IUCUAAAA	3390
3267	UUUUAGAC U UCCUGUAG	1201	CUACAGGA CUGAUGAG GCCGUUAGGC CGAA IUCUAAAA	3390
3180	UAGACUUC C UGUAGGGG	1202	CCCCUACA CUGAUGAG GCCGUUAGGC CGAA IAAGUCUA	3391
3270	UAGACUUC C UGUAGGGG	1202	CCCCUACA CUGAUGAG GCCGUUAGGC CGAA IAAGUCUA	3391
3181	AGACUUCC U GUAGGGGG	1203	CCCCCUAC CUGAUGAG GCCGUUAGGC CGAA IGAAGUCU	3392
3271	AGACUUCC U GUAGGGGG	1203	CCCCCUAC CUGAUGAG GCCGUUAGGC CGAA IGAAGUCU	3392
3198	CGAUAUAC U AAAUGUAU	1204	AUACAUUU CUGAUGAG GCCGUUAGGC CGAA IUAUAUCG	3393
3251	CGAUAUAC U AAAUGUAU	1204	AUACAUUU CUGAUGAG GCCGUUAGGC CGAA IUAUAUCG	3393
3214	UAUAGUAC A UUUAUACU	1205	AGUAUAAA CUGAUGAG GCCGUUAGGC CGAA IUACUAUA	3394
3222	AUUUAUAC U AAAUGUAU	1206	AUACAUUU CUGAUGAG GCCGUUAGGC CGAA IUAUAAAU	3395

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3233	AUGUAUUC C UGUAGGGG	1207	CCCCUACA CUGAUGAG GCCGUUAGGC CGAA IAAUACAU	3396
3234	UGUAUUCC U GUAGGGGG	1208	CCCCCUAC CUGAUGAG GCCGUUAGGC CGAA IGAAUACA	3397
3296	UAAAAUGC U AAACAACU	1209	AGUUGUUU CUGAUGAG GCCGUUAGGC CGAA ICAUUUUA	3398
3301	UGCUAAAC A ACUGGGUA	1210	UACCCAGU CUGAUGAG GCCGUUAGGC CGAA IUUUAGCA	3399

Input Sequence = NM_001285. Cut Site = CH/.
Arm Length = 8. Core Sequence = CUGAUGAG GCCGUUAGGC CGAA
Underlined region can be any X sequence or linker, as described herein.
NM_001285 (Homo sapiens chloride channel, calcium activated, 1 (CLCA1) mRNA, 3311 bp)

249.021

Table V: Human CLCA1 G-cleaver Ribozyme and Target Sequence

Pos	Substrate	Seq ID No.	Ribozyme	Rz Seq ID No.
40	AUAUAAUU G AAUAUUUU	1211	AAAAUAUU UGAUG GCAUGCACUAUGC GCG AAUUAUAU	3400
67	GGGAGCAU G AAGAGGUG	1212	CACCUCUU UGAUG GCAUGCACUAUGC GCG AUGCUCCC	3401
78	GAGGUGUU G AGGUUAUG	1213	CAUAACCU UGAUG GCAUGCACUAUGC GCG AACACCUC	3402
106	GCACAGCU G AAGGCAGA	1214	UCUGCCUU UGAUG GCAUGCACUAUGC GCG AGCUGUGC	3403
134	ACAAGUAC G CAAUUUGA	1215	UCAAAUUG UGAUG GCAUGCACUAUGC GCG GUACUUGU	3404
141	CGCAAUUU G AGACUAAG	1216	CUUAGUCU UGAUG GCAUGCACUAUGC GCG AAAUUGCG	3405
172	CUCCUAUU G AAGACAAG	1217	CUUGUCUU UGAUG GCAUGCACUAUGC GCG AAUAGGAG	3406
223	AGACCUGU G AUAAACCA	1218	UGGUUUAU UGAUG GCAUGCACUAUGC GCG ACAGGUCU	3407
237	CCACUUCC G AUAAGUUG	1219	CAACUUAU UGAUG GCAUGCACUAUGC GCG GGAAGUGG	3408
312	CGUAACCC G CAUUUUCC	1220	GGAAAAUG UGAUG GCAUGCACUAUGC GCG GGGUUACG	3409
384	UUCAUCUU G AUUCUUCA	1221	UGAAGAAU UGAUG GCAUGCACUAUGC GCG AAGAUGAA	3410
411	GGGGCCCU G AGUAAUUC	1222	GAAUUACU UGAUG GCAUGCACUAUGC GCG AGGGCCCC	3411
432	AUUCAGCU G AACAACAA	1223	UUGUUGUU UGAUG GCAUGCACUAUGC GCG AGCUGAAU	3412
448	AUGGCUAU G AAGGCAUU	1224	AAUGCCUU UGAUG GCAUGCACUAUGC GCG AUAGCCAU	3413
463	UUGUCGUU G CAAUCGAC	1225	GUCGAUUG UGAUG GCAUGCACUAUGC GCG AACGACAA	3414
469	UUGCAAUC G ACCCCAAU	1226	AUUGGGGU UGAUG GCAUGCACUAUGC GCG GAUUGCAA	3415
480	CCCAAUGU G CCAGAAGA	1227	UCUUCUGG UGAUG GCAUGCACUAUGC GCG ACAUUGGG	3416
490	CAGAAGAU G AAACACUC	1228	GAGUGUUU UGAUG GCAUGCACUAUGC GCG AUCUUCUG	3417
522	GACAUGGU G ACCCAGGC	1229	GCCUGGGU UGAUG GCAUGCACUAUGC GCG ACCAUGUC	3418
547	AUCUGUUU G AAGCUACA	1230	UGUAGCUU UGAUG GCAUGCACUAUGC GCG AAACAGAU	3419
563	AGGAAAGC G AUUUUAUU	1231	AAUAAAAU UGAUG GCAUGCACUAUGC GCG GCUUUCCU	3420
583	AAAAUGUU G CCAUUUUG	1232	CAAAAUGG UGAUG GCAUGCACUAUGC GCG AACAUUUU	3421
591	GCCAUUUU G AUUCCUGA	1233	UCAGGAAU UGAUG GCAUGCACUAUGC GCG AAAAUGGC	3422
598	UGAUUCCU G AAACAUGG	1234	CCAUGUUU UGAUG GCAUGCACUAUGC GCG AGGAAUCA	3423
619	CAAAGGCU G ACUAUGUG	1235	CACAUAGU UGAUG GCAUGCACUAUGC GCG AGCCUUUG	3424
627	GACUAUGU G AGACCAAA	1236	UUUGGUCU UGAUG GCAUGCACUAUGC GCG ACAUAGUC	3425
640	CAAAACUU G AGACCUAC	1237	GUAGGUCU UGAUG GCAUGCACUAUGC GCG AAGUUUUG	3426
655	ACAAAAAU G CUGAUGUU	1238	AACAUCAG UGAUG GCAUGCACUAUGC GCG AUUUUUGU	3427

658	AAAAUGCU G AUGUUCUG	1239	CAGAACAU UGAUG GCAUGCACUAUGC GCG AGCAUUUU	3428
670	UUCUGGUU G CUGAGUCU	1240	AGACUCAG UGAUG GCAUGCACUAUGC GCG AACCAGAA	3429
673	UGGUUGCU G AGUCUACU	1241	AGUAGACU UGAUG GCAUGCACUAUGC GCG AGCAACCA	3430
694	CAGGUAAU G AUGAACCC	1242	GGGUUCAU UGAUG GCAUGCACUAUGC GCG AUUACCUG	3431
697	GUAAUGAU G AACCCUAC	1243	GUAGGGUU UGAUG GCAUGCACUAUGC GCG AUCAUUAC	3432
709	CCUACACU G AGCAGAUG	1244	CAUCUGCU UGAUG GCAUGCACUAUGC GCG AGUGUAGG	3433
739	AGAAGGGU G AAAGGAUC	1245	GAUCCUUU UGAUG GCAUGCACUAUGC GCG ACCCUUCU	3434
760	UCACUCCU G AUUUCAUU	1246	AAUGAAAU UGAUG GCAUGCACUAUGC GCG AGGAGUGA	3435
769	AUUUCAUU G CAGGAAAA	1247	UUUUCCUG UGAUG GCAUGCACUAUGC GCG AAUGAAAU	3436
787	AGUUAGCU G AAUAUGGA	1248	UCCAUAUU UGAUG GCAUGCACUAUGC GCG AGCUAACU	3437
820	UUGUCCAU G AGUGGGCU	1249	AGCCCACU UGAUG GCAUGCACUAUGC GCG AUGGACAA	3438
836	UCAUCUAC G AUGGGGAG	1250	CUCCCCAU UGAUG GCAUGCACUAUGC GCG GUAGAUGA	3439
850	GAGUAUUU G ACGAGUAC	1251	GUACUCGU UGAUG GCAUGCACUAUGC GCG AAAUACUC	3440
853	UAUUUGAC G AGUACAAU	1252	AUUGUACU UGAUG GCAUGCACUAUGC GCG GUCAAAUA	3441
865	ACAAUAAU G AUGAGAAA	1253	UUUCUCAU UGAUG GCAUGCACUAUGC GCG AUUAUUGU	3442
868	AUAAUGAU G AGAAAUUC	1254	GAAUUUCU UGAUG GCAUGCACUAUGC GCG AUCAUUAU	3443
980	CAAAAGAU G CACAUUCA	1255	UGAAUGUG UGAUG GCAUGCACUAUGC GCG AUCUUUUG	3444
1009	GACUCUAU G AAAAAGGA	1256	UCCUUUUU UGAUG GCAUGCACUAUGC GCG AUAGAGUC	3445
1021	AAGGAUGU G AGUUUGUU	1257	AACAAACU UGAUG GCAUGCACUAUGC GCG ACAUCCUU	3446
1040	CCAAUCCC G CCAGACGG	1258	CCGUCUGG UGAUG GCAUGCACUAUGC GCG GGGAUUGG	3447
1069	UAAUGUUU G CACAACAU	1259	AUGUUGUG UGAUG GCAUGCACUAUGC GCG AAACAUUA	3448
1081	AACAUGUU G AUUCUAUA	1260	UAUAGAAU UGAUG GCAUGCACUAUGC GCG AACAUGUU	3449
1093	CUAUAGUU G AAUUCUGU	1261	ACAGAAUU UGAUG GCAUGCACUAUGC GCG AACUAUAG	3450
1151	UCAAAAAU G CAAUCUCC	1262	GGAGAUUG UGAUG GCAUGCACUAUGC GCG AUUUUUGA	3451
1160	CAAUCUCC G AAGCACAU	1263	AUGUGCUU UGAUG GCAUGCACUAUGC GCG GGAGAUUG	3452
1176	UGGGAAGU G AUCCGUGA	1264	UCACGGAU UGAUG GCAUGCACUAUGC GCG ACUUCCCA	3453
1183	UGAUCCGU G AUUCUGAG	1265	CUCAGAAU UGAUG GCAUGCACUAUGC GCG ACGGAUCA	3454
1189	GUGAUUCU G AGGACUUU	1266	AAAGUCCU UGAUG GCAUGCACUAUGC GCG AGAAUCAC	3455
1215	ACUCCUAU G ACAACACA	1267	UGUGUUGU UGAUG GCAUGCACUAUGC GCG AUAGGAGU	3456
1248	UUCUCAUU G CUGCAGAU	1268	AUCUGCAG UGAUG GCAUGCACUAUGC GCG AAUGAGAA	3457
1251	UCAUUGCU G CAGAUUGG	1269	CCAAUCUG UGAUG GCAUGCACUAUGC GCG AGCAAUGA	3458
1285	UAGUCCUU G ACAAAUCU	1270	AGAUUUGU UGAUG GCAUGCACUAUGC GCG AAGGACUA	3459
1305	AGCAUGGC G ACUGGUAA	1271	UUACCAGU UGAUG GCAUGCACUAUGC GCG GCCAUGCU	3460

1316	UGGUAACC G CCUCAAUC	1272	GAUUGAGG UGAUG GCAUGCACUAUGC GCG GGUUACCA	3461
1325	CCUCAAUC G ACUGAAUC	1273	GAUUCAGU UGAUG GCAUGCACUAUGC GCG GAUUGAGG	3462
1329	AAUCGACU G AAUCAAGC	1274	GCUUGAUU UGAUG GCAUGCACUAUGC GCG AGUCGAUU	3463
1353	CUUUUCCU G CUGCAGAC	1275	GUCUGCAG UGAUG GCAUGCACUAUGC GCG AGGAAAAG	3464
1356	UUCCUGCU G CAGACAGU	1276	ACUGUCUG UGAUG GCAUGCACUAUGC GCG AGCAGGAA	3465
1366	AGACAGUU G AGCUGGGG	1277	CCCCAGCU UGAUG GCAUGCACUAUGC GCG AACUGUCU	3466
1392	GGGAUGGU G ACAUUUGA	1278	UCAAAUGU UGAUG GCAUGCACUAUGC GCG ACCAUCCC	3467
1399	UGACAUUU G ACAGUGCU	1279	AGCACUGU UGAUG GCAUGCACUAUGC GCG AAAUGUCA	3468
1405	UUGACAGU G CUGCCCAU	1280	AUGGGCAG UGAUG GCAUGCACUAUGC GCG ACUGUCAA	3469
1408	ACAGUGCU G CCCAUGUA	1281	UACAUGGG UGAUG GCAUGCACUAUGC GCG AGCACUGU	3470
1423	UACAAAGU G AACUCAUA	1282	UAUGAGUU UGAUG GCAUGCACUAUGC GCG ACUUUGUA	3471
1450	GUGGCAGU G ACAGGGAC	1283	GUCCCUGU UGAUG GCAUGCACUAUGC GCG ACUGCCAC	3472
1465	ACACACUC G CCAAAAGA	1284	UCUUUUGG UGAUG GCAUGCACUAUGC GCG GAGUGUGU	3473
1480	GAUUACCU G CAGCAGCU	1285	AGCUGCUG UGAUG GCAUGCACUAUGC GCG AGGUAAUC	3474
1508	GUCCAUCU G CAGCGGGC	1286	GCCCGCUG UGAUG GCAUGCACUAUGC GCG AGAUGGAC	3475
1520	CGGGCUUC G AUCGGCAU	1287	AUGCCGAU UGAUG GCAUGCACUAUGC GCG GAAGCCCG	3476
1536	UUUACUGU G AUUAGGAA	1288	UUCCUAAU UGAUG GCAUGCACUAUGC GCG ACAGUAAA	3477
1558	AUCCAACU G AUGGAUCU	1289	AGAUCCAU UGAUG GCAUGCACUAUGC GCG AGUUGGAU	3478
1567	AUGGAUCU G AAAUUGUG	1290	CACAAUUU UGAUG GCAUGCACUAUGC GCG AGAUCCAU	3479
1575	GAAAUUGU G CUGCUGAC	1291	GUCAGCAG UGAUG GCAUGCACUAUGC GCG ACAAUUUC	3480
1578	AUUGUGCU G CUGACGGA	1292	UCCGUCAG UGAUG GCAUGCACUAUGC GCG AGCACAAU	3481
1581	GUGCUGCU G ACGGAUGG	1293	CCAUCCGU UGAUG GCAUGCACUAUGC GCG AGCAGCAC	3482
1613	AAGUGGGU G CUUUAACG	1294	CGUUAAAG UGAUG GCAUGCACUAUGC GCG ACCCACUU	3483
1621	GCUUUAAC G AGGUCAAA	1295	UUUGACCU UGAUG GCAUGCACUAUGC GCG GUUAAAGC	3484
1639	AAAGUGGU G CCAUCAUC	1296	GAUGAUGG UGAUG GCAUGCACUAUGC GCG ACCACUUU	3485
1657	ACACAGUC G CUUUGGGG	1297	CCCCAAAG UGAUG GCAUGCACUAUGC GCG GACUGUGU	3486
1672	GGCCCUCU G CAGCUCAA	1298	UUGAGCUG UGAUG GCAUGCACUAUGC GCG AGAGGGCC	3487
1704	UCCAAAAU G ACAGGAGG	1299	CCUCCUGU UGAUG GCAUGCACUAUGC GCG AUUUUGGA	3488
1726	AGACAUAU G CUUCAGAU	1300	AUCUGAAG UGAUG GCAUGCACUAUGC GCG AUAUGUCU	3489
1759	GCCUCAUU G AUGCUUUU	1301	AAAAGCAU UGAUG GCAUGCACUAUGC GCG AAUGAGGC	3490
1762	UCAUUGAU G CUUUUGGG	1302	CCCAAAAG UGAUG GCAUGCACUAUGC GCG AUCAAUGA	3491
1805	CUCUCAGC G CUCCAUCC	1303	GGAUGGAG UGAUG GCAUGCACUAUGC GCG GCUGAGAG	3492
1819	UCCAGCUU G AGAGUAAG	1304	CUUACUCU UGAUG GCAUGCACUAUGC GCG AAGCUGGA	3493

1857	CAGUGGAU G AAUGGCAC	1305	GUGCCAUU UGAUG GCAUGCACUAUGC GCG AUCCACUG	3494
1869	GGCACAGU G AUCGUGGA	1306	UCCACGAU UGAUG GCAUGCACUAUGC GCG ACUGUGCC	3495
1923	UGGACAAC G CAGCCUCC	1307	GGAGGCUG UGAUG GCAUGCACUAUGC GCG GUUGUCCA	3496
2026	CAGGCAUU G CUAAGGUU	1308	AACCUUAG UGAUG GCAUGCACUAUGC GCG AAUGCCUG	3497
2055	UACAGUCU G CAAGCAAG	1309	CUUGCUUG UGAUG GCAUGCACUAUGC GCG AGACUGUA	3498
2076	CAAACCUU G ACCCUGAC	1310	GUCAGGGU UGAUG GCAUGCACUAUGC GCG AAGGUUUG	3499
2082	UUGACCCU G ACUGUCAC	1311	GUGACAGU UGAUG GCAUGCACUAUGC GCG AGGGUCAA	3500
2098	CGUCCCGU G CGUCCAAU	1312	AUUGGACG UGAUG GCAUGCACUAUGC GCG ACGGGACG	3501
2107	CGUCCAAU G CUACCCUG	1313	CAGGGUAG UGAUG GCAUGCACUAUGC GCG AUUGGACG	3502
2115	GCUACCCU G CCUCCAAU	1314	AUUGGAGG UGAUG GCAUGCACUAUGC GCG AGGGUAGC	3503
2130	AUUACAGU G ACUUCCAA	1315	UUGGAAGU UGAUG GCAUGCACUAUGC GCG ACUGUAAU	3504
2142	UCCAAAAC G AACAAGGA	1316	UCCUUGUU UGAUG GCAUGCACUAUGC GCG GUUUUGGA	3505
2185	UAGUUUAU G CAAAUAUU	1317	AAUAUUUG UGAUG GCAUGCACUAUGC GCG AUAAACUA	3506
2195	AAAUAUUC G CCAAGGAG	1318	CUCCUUGG UGAUG GCAUGCACUAUGC GCG GAAUAUUU	3507
2238	ACAGCCCU G AUUGAAUC	1319	GAUUCAAU UGAUG GCAUGCACUAUGC GCG AGGGCUGU	3508
2242	CCCUGAUU G AAUCAGUG	1320	CACUGAUU UGAUG GCAUGCACUAUGC GCG AAUCAGGG	3509
2250	GAAUCAGU G AAUGGAAA	1321	UUUCCAUU UGAUG GCAUGCACUAUGC GCG ACUGAUUC	3510
2296	GAGCAGGU G CUGAUGCU	1322	AGCAUCAG UGAUG GCAUGCACUAUGC GCG ACCUGCUC	3511
2299	CAGGUGCU G AUGCUACU	1323	AGUAGCAU UGAUG GCAUGCACUAUGC GCG AGCACCUG	3512
2302	GUGCUGAU G CUACUAAG	1324	CUUAGUAG UGAUG GCAUGCACUAUGC GCG AUCAGCAC	3513
2314	CUAAGGAU G ACGGUGUC	1325	GACACCGU UGAUG GCAUGCACUAUGC GCG AUCCUUAG	3514
2347	CAACUUAU G ACACGAAU	1326	AUUCGUGU UGAUG GCAUGCACUAUGC GCG AUAAGUUG	3515
2352	UAUGACAC G AAUGGUAG	1327	CUACCAUU UGAUG GCAUGCACUAUGC GCG GUGUCAUA	3516
2376	GUAAAAGU G CGGGCUCU	1328	AGAGCCCG UGAUG GCAUGCACUAUGC GCG ACUUUUAC	3517
2398	GAGUUAAC G CAGCCAGA	1329	UCUGGCUG UGAUG GCAUGCACUAUGC GCG GUUAACUC	3518
2415	CGGAGAGU G AUACCCCA	1330	UGGGGUAU UGAUG GCAUGCACUAUGC GCG ACUCUCCG	3519
2458	GCUGGAUU G AGAAUGAU	1331	AUCAUUCU UGAUG GCAUGCACUAUGC GCG AAUCCAGC	3520
2464	UUGAGAAU G AUGAAAUA	1332	UAUUUCAU UGAUG GCAUGCACUAUGC GCG AUUCUCAA	3521
2467	AGAAUGAU G AAAUACAA	1333	UUGUAUUU UGAUG GCAUGCACUAUGC GCG AUCAUUCU	3522
2494	CAAGACCU G AAAUUAAU	1334	AUUAAUUU UGAUG GCAUGCACUAUGC GCG AGGUCUUG	3523
2509	AUAAGGAU G AUGUUCAA	1335	UUGAACAU UGAUG GCAUGCACUAUGC GCG AUCCUUAU	3524
2572	UGGCUUCU G AUGUCCCA	1336	UGGGACAU UGAUG GCAUGCACUAUGC GCG AGAAGCCA	3525
2584	UCCCAAAU G CUCCCAUA	1337	UAUGGGAG UGAUG GCAUGCACUAUGC GCG AUUUGGGA	3526

2596	CCAUACCU G AUCUCUUC	1338	GAAGAGAU UGAUG GCAUGCACUAUGC GCG AGGUAUGG	3527
2623	AAAUCACC G ACCUGAAG	1339	CUUCAGGU UGAUG GCAUGCACUAUGC GCG GGUGAUUU	3528
2628	ACCGACCU G AAGGCGGA	1340	UCCGCCUU UGAUG GCAUGCACUAUGC GCG AGGUCGGU	3529
2664	AUUAAUCU G ACUUGGAC	1341	GUCCAAGU UGAUG GCAUGCACUAUGC GCG AGAUUAAU	3530
2686	CUGGGGAU G AUUAUGAC	1342	GUCAUAAU UGAUG GCAUGCACUAUGC GCG AUCCCCAG	3531
2692	AUGAUUAU G ACCAUGGA	1343	UCCAUGGU UGAUG GCAUGCACUAUGC GCG AUAAUCAU	3532
2723	UAUCAUUC G AAUAAGUA	1344	UACUUAUU UGAUG GCAUGCACUAUGC GCG GAAUGAUA	3533
2743	GUAUUCUU G AUCUCAGA	1345	UCUGAGAU UGAUG GCAUGCACUAUGC GCG AAGAAUAC	3534
2764	AGUUCAAU G AAUCUCUU	1346	AAGAGAUU UGAUG GCAUGCACUAUGC GCG AUUGAACU	3535
2778	CUUCAAGU G AAUACUAC	1347	GUAGUAUU UGAUG GCAUGCACUAUGC GCG ACUUGAAG	3536
2788	AUACUACU G CUCUCAUC	1348	GAUGAGAG UGAUG GCAUGCACUAUGC GCG AGUAGUAU	3537
2815	CCAACUCU G AGGAAGUC	1349	GACUUCCU UGAUG GCAUGCACUAUGC GCG AGAGUUGG	3538
2854	UUACUUUU G AAAAUGGC	1350	GCCAUUUU UGAUG GCAUGCACUAUGC GCG AAAAGUAA	3539
2878	UUUUCAUU G CUAUUCAG	1351	CUGAAUAG UGAUG GCAUGCACUAUGC GCG AAUGAAAA	3540
2893	AGGCUGUU G AUAAGGUC	1352	GACCUUAU UGAUG GCAUGCACUAUGC GCG AACAGCCU	3541
2902	AUAAGGUC G AUCUGAAA	1353	UUUCAGAU UGAUG GCAUGCACUAUGC GCG GACCUUAU	3542
2907	GUCGAUCU G AAAUCAGA	1354	UCUGAUUU UGAUG GCAUGCACUAUGC GCG AGAUCGAC	3543
2929	CCAACAUU G CACGAGUA	1355	UACUCGUG UGAUG GCAUGCACUAUGC GCG AAUGUUGG	3544
2933	CAUUGCAC G AGUAUCUU	1356	AAGAUACU UGAUG GCAUGCACUAUGC GCG GUGCAAUG	3545
2964	CAGACUCC G CCAGAGAC	1357	GUCUCUGG UGAUG GCAUGCACUAUGC GCG GGAGUCUG	3546
2983	CUAGUCCU G AUGAAACG	1358	CGUUUCAU UGAUG GCAUGCACUAUGC GCG AGGACUAG	3547
2986	GUCCUGAU G AAACGUCU	1359	AGACGUUU UGAUG GCAUGCACUAUGC GCG AUCAGGAC	3548
2995	AAACGUCU G CUCCUUGU	1360	ACAAGGAG UGAUG GCAUGCACUAUGC GCG AGACGUUU	3549
3078	GGAGAACU G CAGCUGUC	1361	GACAGCUG UGAUG GCAUGCACUAUGC GCG AGUUCUCC	3550
3101	CUAGGGCU G AAUUUUUG	1362	CAAAAAUU UGAUG GCAUGCACUAUGC GCG AGCCCUAG	3551
3145	CUUUUUUU G AUUAUAAA	1363	UUUAUAAU UGAUG GCAUGCACUAUGC GCG AAAAAAAG	3552
3191	UAGGGGGC G AUAUACUA	1364	UAGUAUAU UGAUG GCAUGCACUAUGC GCG GCCCCCUA	3553
3244	UAGGGGGC G AUAUACUA	1364	UAGUAUAU UGAUG GCAUGCACUAUGC GCG GCCCCCUA	3553
3281	UAGGGGGC G AUAAAAUA	1365	UAUUUUAU UGAUG GCAUGCACUAUGC GCG GCCCCCUA	3554
3294	AAUAAAAU G CUAAACAA	1366	UUGUUUAG UGAUG GCAUGCACUAUGC GCG AUUUUAUU	3555
27	AAAUGGAU G UGGAAUAU	1367	AUAUUCCA UGAUG GCAUGCACUAUGC GCG AUCCAUUU	3556
52	AUUUUCUU G UUUAAGGG	1368	CCCUUAAA UGAUG GCAUGCACUAUGC GCG AAGAAAAU	3557
75	GAAGAGGU G UUGAGGUU	1369	AACCUCAA UGAUG GCAUGCACUAUGC GCG ACCUCUUC	3558

86	GAGGUUAU G UCAAGCAU	1370	AUGCUUGA UGAUG GCAUGCACUAUGC GCG AUAACCUC	3559
155	AAGAUAUU G UUAUCAUU	1371	AAUGAUAA UGAUG GCAUGCACUAUGC GCG AAUAUCUU	3560
221	AAAGACCU G UGAUAAAC	1372	GUUUAUCA UGAUG GCAUGCACUAUGC GCG AGGUCUUU	3561
253	GGAAACGU G UGUCUAUA	1373	UAUAGACA UGAUG GCAUGCACUAUGC GCG ACGUUUCC	3562
255	AAACGUGU G UCUAUAUU	1374	AAUAUAGA UGAUG GCAUGCACUAUGC GCG ACACGUUU	3563
273	UCAUAUCU G UAUAUAUA	1375	UAUAUAUA UGAUG GCAUGCACUAUGC GCG AGAUAUGA	3564
344	AGGGAGAU G UACAGCAA	1376	UUGCUGUA UGAUG GCAUGCACUAUGC GCG AUCUCCCU	3565
373	AGAGUUCU G UGUUCAUC	1377	GAUGAACA UGAUG GCAUGCACUAUGC GCG AGAACUCU	3566
375	AGUUCUGU G UUCAUCUU	1378	AAGAUGAA UGAUG GCAUGCACUAUGC GCG ACAGAACU	3567
457	AAGGCAUU G UCGUUGCA	1379	UGCAACGA UGAUG GCAUGCACUAUGC GCG AAUGCCUU	3568
478	ACCCCAAU G UGCCAGAA	1380	UUCUGGCA UGAUG GCAUGCACUAUGC GCG AUUGGGGU	3569
537	GCAUCUCU G UAUCUGUU	1381	AACAGAUA UGAUG GCAUGCACUAUGC GCG AGAGAUGC	3570
543	CUGUAUCU G UUUGAAGC	1382	GCUUCAAA UGAUG GCAUGCACUAUGC GCG AGAUACAG	3571
580	UCAAAAAU G UUGCCAUU	1383	AAUGGCAA UGAUG GCAUGCACUAUGC GCG AUUUUUGA	3572
625	CUGACUAU G UGAGACCA	1384	UGGUCUCA UGAUG GCAUGCACUAUGC GCG AUAGUCAG	3573
661	AUGCUGAU G UUCUGGUU	1385	AACCAGAA UGAUG GCAUGCACUAUGC GCG AUCAGCAU	3574
725	GGGCAACU G UGGAGAGA	1386	UCUCUCCA UGAUG GCAUGCACUAUGC GCG AGUUGCCC	3575
814	AGGCAUUU G UCCAUGAG	1387	CUCAUGGA UGAUG GCAUGCACUAUGC GCG AAAUGCCU	3576
911	AGUAAGAU G UUCAGCAG	1388	CUGCUGAA UGAUG GCAUGCACUAUGC GCG AUCUUACU	3577
937	GUACAAAU G UAGUAAAG	1389	CUUUACUA UGAUG GCAUGCACUAUGC GCG AUUUGUAC	3578
950	AAAGAAGU G UCAGGGAG	1390	CUCCCUGA UGAUG GCAUGCACUAUGC GCG ACUUCUUU	3579
965	AGGCAGCU G UUACACCA	1391	UGGUGUAA UGAUG GCAUGCACUAUGC GCG AGCUGCCU	3580
1019	AAAAGGAU G UGAGUUUG	1392	CAAACUCA UGAUG GCAUGCACUAUGC GCG AUCCUUUU	3581
1027	GUGAGUUU G UUCUCCAA	1393	UUGGAGAA UGAUG GCAUGCACUAUGC GCG AAACUCAC	3582
1065	UCUAUAAU G UUUGCACA	1394	UGUGCAAA UGAUG GCAUGCACUAUGC GCG AUUAUAGA	3583
1078	CACAACAU G UUGAUUCU	1395	AGAAUCAA UGAUG GCAUGCACUAUGC GCG AUGUUGUG	3584
1100	UGAAUUCU G UACAGAAC	1396	GUUCUGUA UGAUG GCAUGCACUAUGC GCG AGAAUUCA	3585
1270	AAAGAAUU G UGUGUUUA	1397	UAAACACA UGAUG GCAUGCACUAUGC GCG AAUUCUUU	3586
1272	AGAAUUGU G UGUUUAGU	1398	ACUAAACA UGAUG GCAUGCACUAUGC GCG ACAAUUCU	3587
1274	AAUUGUGU G UUUAGUCC	1399	GGACUAAA UGAUG GCAUGCACUAUGC GCG ACACAAUU	3588
1414	CUGCCCAU G UACAAAGU	1400	ACUUUGUA UGAUG GCAUGCACUAUGC GCG AUGGGCAG	3589
1534	CAUUUACU G UGAUUAGG	1401	CCUAAUCA UGAUG GCAUGCACUAUGC GCG AGUAAAUG	3590
1573	CUGAAAUU G UGCUGCUG	1402	CAGCAGCA UGAUG GCAUGCACUAUGC GCG AAUUUCAG	3591

1695	GAGGAGCU G UCCAAAAU	1403	AUUUUGGA UGAUG GCAUGCACUAUGC GCG AGCUCCUC	3592
1795	AUGGAGCU G UCUCUCAG	1404	CUGAGAGA UGAUG GCAUGCACUAUGC GCG AGCUCCAU	3593
1902	GACACUUU G UUUCUUAU	1405	AUAAGAAA UGAUG GCAUGCACUAUGC GCG AAAGUGUC	3594
1978	GUGGCUUU G UAGUGGAC	1406	GUCCACUA UGAUG GCAUGCACUAUGC GCG AAAGCCAC	3595
2086	CCCUGACU G UCACGUCC	1407	GGACGUGA UGAUG GCAUGCACUAUGC GCG AGUCAGGG	3596
2227	GGGCCAGU G UCACAGCC	1408	GGCUGUGA UGAUG GCAUGCACUAUGC GCG ACUGGCCC	3597
2320	AUGACGGU G UCUACUCA	1409	UGAGUAGA UGAUG GCAUGCACUAUGC GCG ACCGUCAU	3598
2368	GAUACAGU G UAAAAGUG	1410	CACUUUUA UGAUG GCAUGCACUAUGC GCG ACUGUAUC	3599
2439	GGAGCACU G UACAUACC	1411	GGUAUGUA UGAUG GCAUGCACUAUGC GCG AGUGCUCC	3600
2512	AGGAUGAU G UUCAACAC	1412	GUGUUGAA UGAUG GCAUGCACUAUGC GCG AUCAUCCU	3601
2529	AAGCAAGU G UGUUUCAG	1413	CUGAAACA UGAUG GCAUGCACUAUGC GCG ACUUGCUU	3602
2531	GCAAGUGU G UUUCAGCA	1414	UGCUGAAA UGAUG GCAUGCACUAUGC GCG ACACUUGC	3603
2563	GCUCAUUU G UGGCUUCU	1415	AGAAGCCA UGAUG GCAUGCACUAUGC GCG AAAUGAGC	3604
2575	CUUCUGAU G UCCCAAAU	1416	AUUUGGGA UGAUG GCAUGCACUAUGC GCG AUCAGAAG	3605
2829	GUCUUUUU G UUUAAACC	1417	GGUUUAAA UGAUG GCAUGCACUAUGC GCG AAAAAGAC	3606
2890	UUCAGGCU G UUGAUAAG	1418	CUUAUCAA UGAUG GCAUGCACUAUGC GCG AGCCUGAA	3607
2943	GUAUCUUU G UUUAUUCC	1419	GGAAUAAA UGAUG GCAUGCACUAUGC GCG AAAGAUAC	3608
3002	UGCUCCUU G UCCUAAUA	1420	UAUUAGGA UGAUG GCAUGCACUAUGC GCG AAGGAGCA	3609
3057	AAAAUUAU G UGGAAGUG	1421	CACUUCCA UGAUG GCAUGCACUAUGC GCG AUAAUUUU	3610
3084	CUGCAGCU G UCAAUAGC	1422	GCUAUUGA UGAUG GCAUGCACUAUGC GCG AGCUGCAG	3611
3109	GAAUUUUU G UCAGAUAA	1423	UUAUCUGA UGAUG GCAUGCACUAUGC GCG AAAAAUUC	3612
3166	UCUAAAAU G UAUUUUAG	1424	CUAAAAUA UGAUG GCAUGCACUAUGC GCG AUUUUAGA	3613
3182	GACUUCCU G UAGGGGGC	1425	GCCCCCUA UGAUG GCAUGCACUAUGC GCG AGGAAGUC	3614
3272	GACUUCCU G UAGGGGGC	1425	GCCCCCUA UGAUG GCAUGCACUAUGC GCG AGGAAGUC	3614
3203	UACUAAAU G UAUAUAGU	1426	ACUAUAUA UGAUG GCAUGCACUAUGC GCG AUUUAGUA	3615
3227	UACUAAAU G UAUUCCUG	1427	CAGGAAUA UGAUG GCAUGCACUAUGC GCG AUUUAGUA	3616
3235	GUAUUCCU G UAGGGGGC	1428	GCCCCCUA UGAUG GCAUGCACUAUGC GCG AGGAAUAC	3617
3256	UACUAAAU G UAUUUUAG	1429	CUAAAAUA UGAUG GCAUGCACUAUGC GCG AUUUAGUA	3618

Input Sequence = NM_001285. Cut Site = YG/M or UG/U.
Arm Length = 8. Core Sequence = UGAUG GCAUGCACUAUGC GCG
NM_001285 (Homo sapiens chloride channel, calcium activated, 1 (CLCA1) mRNA, 3311 bp)

Table VI: Human CLCA1 Zinzyme and Target Sequence 249.021

Pos	Substrate	Seq ID	Zinzyme	Rz Seq ID
134	ACAAGUAC G CAAUUUGA	1215	UCAAAUUG GCCGAAAGGCGAGUGAGGUCU GUACUUGU	3619
312	CGUAACCC G CAUUUUCC	1220	GGAAAAUG GCCGAAAGGCGAGUGAGGUCU GGGUUACG	3620
463	UUGUCGUU G CAAUCGAC	1225	GUCGAUUG GCCGAAAGGCGAGUGAGGUCU AACGACAA	3621
480	CCCAAUGU G CCAGAAGA	1227	UCUUCUGG GCCGAAAGGCGAGUGAGGUCU ACAUUGGG	3622
583	AAAAUGUU G CCAUUUUG	1232	CAAAAUGG GCCGAAAGGCGAGUGAGGUCU AACAUUUU	3623
655	ACAAAAAU G CUGAUGUU	1238	AACAUCAG GCCGAAAGGCGAGUGAGGUCU AUUUUUGU	3624
670	UUCUGGUU G CUGAGUCU	1240	AGACUCAG GCCGAAAGGCGAGUGAGGUCU AACCAGAA	3625
769	AUUUCAUU G CAGGAAAA	1247	UUUUCCUG GCCGAAAGGCGAGUGAGGUCU AAUGAAAU	3626
980	CAAAAGAU G CACAUUCA	1255	UGAAUGUG GCCGAAAGGCGAGUGAGGUCU AUCUUUUG	3627
1040	CCAAUCCC G CCAGACGG	1258	CCGUCUGG GCCGAAAGGCGAGUGAGGUCU GGGAUUGG	3628
1069	UAAUGUUU G CACAACAU	1259	AUGUUGUG GCCGAAAGGCGAGUGAGGUCU AAACAUUA	3629
1151	UCAAAAAU G CAAUCUCC	1262	GGAGAUUG GCCGAAAGGCGAGUGAGGUCU AUUUUUGA	3630
1248	UUCUCAUU G CUGCAGAU	1268	AUCUGCAG GCCGAAAGGCGAGUGAGGUCU AAUGAGAA	3631
1251	UCAUUGCU G CAGAUUGG	1269	CCAAUCUG GCCGAAAGGCGAGUGAGGUCU AGCAAUGA	3632
1316	UGGUAACC G CCUCAAUC	1272	GAUUGAGG GCCGAAAGGCGAGUGAGGUCU GGUUACCA	3633
1353	CUUUUCCU G CUGCAGAC	1275	GUCUGCAG GCCGAAAGGCGAGUGAGGUCU AGGAAAAG	3634
1356	UUCCUGCU G CAGACAGU	1276	ACUGUCUG GCCGAAAGGCGAGUGAGGUCU AGCAGGAA	3635
1405	UUGACAGU G CUGCCCAU	1280	AUGGGCAG GCCGAAAGGCGAGUGAGGUCU ACUGUCAA	3636
1408	ACAGUGCU G CCCAUGUA	1281	UACAUGGG GCCGAAAGGCGAGUGAGGUCU AGCACUGU	3637
1465	ACACACUC G CCAAAAGA	1284	UCUUUUGG GCCGAAAGGCGAGUGAGGUCU GAGUGUGU	3638
1480	GAUUACCU G CAGCAGCU	1285	AGCUGCUG GCCGAAAGGCGAGUGAGGUCU AGGUAAUC	3639
1508	GUCCAUCU G CAGCGGGC	1286	GCCCGCUG GCCGAAAGGCGAGUGAGGUCU AGAUGGAC	3640
1575	GAAAUUGU G CUGCUGAC	1291	GUCAGCAG GCCGAAAGGCGAGUGAGGUCU ACAAUUUC	3641
1578	AUUGUGCU G CUGACGGA	1292	UCCGUCAG GCCGAAAGGCGAGUGAGGUCU AGCACAAU	3642
1613	AAGUGGGU G CUUUAACG	1294	CGUUAAAG GCCGAAAGGCGAGUGAGGUCU ACCCACUU	3643
1639	AAAGUGGU G CCAUCAUC	1296	GAUGAUGG GCCGAAAGGCGAGUGAGGUCU ACCACUUU	3644
1657	ACACAGUC G CUUUGGGG	1297	CCCCAAAG GCCGAAAGGCGAGUGAGGUCU GACUGUGU	3645
1672	GGCCCUCU G CAGCUCAA	1298	UUGAGCUG GCCGAAAGGCGAGUGAGGUCU AGAGGGCC	3646
1726	AGACAUAU G CUUCAGAU	1300	AUCUGAAG GCCGAAAGGCGAGUGAGGUCU AUAUGUCU	3647

1762	UCAUUGAU G CUUUUGGG	1302	CCCAAAAG GCCGAAAGGCGAGUGAGGUCU AUCAAUGA	3648
1805	CUCUCAGC G CUCCAUCC	1303	GGAUGGAG GCCGAAAGGCGAGUGAGGUCU GCUGAGAG	3649
1923	UGGACAAC G CAGCCUCC	1307	GGAGGCUG GCCGAAAGGCGAGUGAGGUCU GUUGUCCA	3650
2026	CAGGCAUU G CUAAGGUU	1308	AACCUUAG GCCGAAAGGCGAGUGAGGUCU AAUGCCUG	3651
2055	UACAGUCU G CAAGCAAG	1309	CUUGCUUG GCCGAAAGGCGAGUGAGGUCU AGACUGUA	3652
2098	CGUCCCGU G CGUCCAAU	1312	AUUGGACG GCCGAAAGGCGAGUGAGGUCU ACGGGACG	3653
2107	CGUCCAAU G CUACCCUG	1313	CAGGGUAG GCCGAAAGGCGAGUGAGGUCU AUUGGACG	3654
2115	GCUACCCU G CCUCCAAU	1314	AUUGGAGG GCCGAAAGGCGAGUGAGGUCU AGGGUAGC	3655
2185	UAGUUUAU G CAAAUAUU	1317	AAUAUUUG GCCGAAAGGCGAGUGAGGUCU AUAAACUA	3656
2195	AAAUAUUC G CCAAGGAG	1318	CUCCUUGG GCCGAAAGGCGAGUGAGGUCU GAAUAUUU	3657
2296	GAGCAGGU G CUGAUGCU	1322	AGCAUCAG GCCGAAAGGCGAGUGAGGUCU ACCUGCUC	3658
2302	GUGCUGAU G CUACUAAG	1324	CUUAGUAG GCCGAAAGGCGAGUGAGGUCU AUCAGCAC	3659
2376	GUAAAAGU G CGGGCUCU	1328	AGAGCCCG GCCGAAAGGCGAGUGAGGUCU ACUUUUAC	3660
2398	GAGUUAAC G CAGCCAGA	1329	UCUGGCUG GCCGAAAGGCGAGUGAGGUCU GUUAACUC	3661
2584	UCCCAAAU G CUCCCAUA	1337	UAUGGGAG GCCGAAAGGCGAGUGAGGUCU AUUUGGGA	3662
2788	AUACUACU G CUCUCAUC	1348	GAUGAGAG GCCGAAAGGCGAGUGAGGUCU AGUAGUAU	3663
2878	UUUUCAUU G CUAUUCAG	1351	CUGAAUAG GCCGAAAGGCGAGUGAGGUCU AAUGAAAA	3664
2929	CCAACAUU G CACGAGUA	1355	UACUCGUG GCCGAAAGGCGAGUGAGGUCU AAUGUUGG	3665
2964	CAGACUCC G CCAGAGAC	1357	GUCUCUGG GCCGAAAGGCGAGUGAGGUCU GGAGUCUG	3666
2995	AAACGUCU G CUCCUUGU	1360	ACAAGGAG GCCGAAAGGCGAGUGAGGUCU AGACGUUU	3667
3078	GGAGAACU G CAGCUGUC	1361	GACAGCUG GCCGAAAGGCGAGUGAGGUCU AGUUCUCC	3668
3294	AAUAAAAU G CUAAACAA	1366	UUGUUUAG GCCGAAAGGCGAGUGAGGUCU AUUUUAUU	3669
27	AAAUGGAU G UGGAAUAU	1367	AUAUUCCA GCCGAAAGGCGAGUGAGGUCU AUCCAUUU	3670
52	AUUUUCUU G UUUAAGGG	1368	CCCUUAAA GCCGAAAGGCGAGUGAGGUCU AAGAAAAU	3671
75	GAAGAGGU G UUGAGGUU	1369	AACCUCAA GCCGAAAGGCGAGUGAGGUCU ACCUCUUC	3672
86	GAGGUUAU G UCAAGCAU	1370	AUGCUUGA GCCGAAAGGCGAGUGAGGUCU AUAACCUC	3673
155	AAGAUAUU G UUAUCAUU	1371	AAUGAUAA GCCGAAAGGCGAGUGAGGUCU AAUAUCUU	3674
221	AAAGACCU G UGAUAAAC	1372	GUUUAUCA GCCGAAAGGCGAGUGAGGUCU AGGUCUUU	3675
253	GGAAACGU G UGUCUAUA	1373	UAUAGACA GCCGAAAGGCGAGUGAGGUCU ACGUUUCC	3676
255	AAACGUGU G UCUAUAUU	1374	AAUAUAGA GCCGAAAGGCGAGUGAGGUCU ACACGUUU	3677
273	UCAUAUCU G UAUAUAUA	1375	UAUAUAUA GCCGAAAGGCGAGUGAGGUCU AGAUAUGA	3678
344	AGGGAGAU G UACAGCAA	1376	UUGCUGUA GCCGAAAGGCGAGUGAGGUCU AUCUCCCU	3679
373	AGAGUUCU G UGUUCAUC	1377	GAUGAACA GCCGAAAGGCGAGUGAGGUCU AGAACUCU	3680

375	AGUUCUGU G UUCAUCUU	1378	AAGAUGAA GCCGAAAGGCGAGUGAGGUCU ACAGAACU	3681
457	AAGGCAUU G UCGUUGCA	1379	UGCAACGA GCCGAAAGGCGAGUGAGGUCU AAUGCCUU	3682
478	ACCCCAAU G UGCCAGAA	1380	UUCUGGCA GCCGAAAGGCGAGUGAGGUCU AUUGGGGU	3683
537	GCAUCUCU G UAUCUGUU	1381	AACAGAUA GCCGAAAGGCGAGUGAGGUCU AGAGAUGC	3684
543	CUGUAUCU G UUUGAAGC	1382	GCUUCAAA GCCGAAAGGCGAGUGAGGUCU AGAUACAG	3685
580	UCAAAAAU G UUGCCAUU	1383	AAUGGCAA GCCGAAAGGCGAGUGAGGUCU AUUUUUGA	3686
625	CUGACUAU G UGAGACCA	1384	UGGUCUCA GCCGAAAGGCGAGUGAGGUCU AUAGUCAG	3687
661	AUGCUGAU G UUCUGGUU	1385	AACCAGAA GCCGAAAGGCGAGUGAGGUCU AUCAGCAU	3688
725	GGGCAACU G UGGAGAGA	1386	UCUCUCCA GCCGAAAGGCGAGUGAGGUCU AGUUGCCC	3689
814	AGGCAUUU G UCCAUGAG	1387	CUCAUGGA GCCGAAAGGCGAGUGAGGUCU AAAUGCCU	3690
911	AGUAAGAU G UUCAGCAG	1388	CUGCUGAA GCCGAAAGGCGAGUGAGGUCU AUCUUACU	3691
937	GUACAAAU G UAGUAAAG	1389	CUUUACUA GCCGAAAGGCGAGUGAGGUCU AUUUGUAC	3692
950	AAAGAAGU G UCAGGGAG	1390	CUCCCUGA GCCGAAAGGCGAGUGAGGUCU ACUUCUUU	3693
965	AGGCAGCU G UUACACCA	1391	UGGUGUAA GCCGAAAGGCGAGUGAGGUCU AGCUGCCU	3694
1019	AAAAGGAU G UGAGUUUG	1392	CAAACUCA GCCGAAAGGCGAGUGAGGUCU AUCCUUUU	3695
1027	GUGAGUUU G UUCUCCAA	1393	UUGGAGAA GCCGAAAGGCGAGUGAGGUCU AAACUCAC	3696
1065	UCUAUAAU G UUUGCACA	1394	UGUGCAAA GCCGAAAGGCGAGUGAGGUCU AUUAUAGA	3697
1078	CACAACAU G UUGAUUCU	1395	AGAAUCAA GCCGAAAGGCGAGUGAGGUCU AUGUUGUG	3698
1100	UGAAUUCU G UACAGAAC	1396	GUUCUGUA GCCGAAAGGCGAGUGAGGUCU AGAAUUCA	3699
1270	AAAGAAUU G UGUGUUUA	1397	UAAACACA GCCGAAAGGCGAGUGAGGUCU AAUUCUUU	3700
1272	AGAAUUGU G UGUUUAGU	1398	ACUAAACA GCCGAAAGGCGAGUGAGGUCU ACAAUUCU	3701
1274	AAUUGUGU G UUUAGUCC	1399	GGACUAAA GCCGAAAGGCGAGUGAGGUCU ACACAAUU	3702
1414	CUGCCCAU G UACAAAGU	1400	ACUUUGUA GCCGAAAGGCGAGUGAGGUCU AUGGGCAG	3703
1534	CAUUUACU G UGAUUAGG	1401	CCUAAUCA GCCGAAAGGCGAGUGAGGUCU AGUAAAUG	3704
1573	CUGAAAUU G UGCUGCUG	1402	CAGCAGCA GCCGAAAGGCGAGUGAGGUCU AAUUUCAG	3705
1695	GAGGAGCU G UCCAAAAU	1403	AUUUUGGA GCCGAAAGGCGAGUGAGGUCU AGCUCCUC	3706
1795	AUGGAGCU G UCUCUCAG	1404	CUGAGAGA GCCGAAAGGCGAGUGAGGUCU AGCUCCAU	3707
1902	GACACUUU G UUUCUUAU	1405	AUAAGAAA GCCGAAAGGCGAGUGAGGUCU AAAGUGUC	3708
1978	GUGGCUUU G UAGUGGAC	1406	GUCCACUA GCCGAAAGGCGAGUGAGGUCU AAAGCCAC	3709
2086	CCCUGACU G UCACGUCC	1407	GGACGUGA GCCGAAAGGCGAGUGAGGUCU AGUCAGGG	3710
2227	GGGCCAGU G UCACAGCC	1408	GGCUGUGA GCCGAAAGGCGAGUGAGGUCU ACUGGCCC	3711
2320	AUGACGGU G UCUACUCA	1409	UGAGUAGA GCCGAAAGGCGAGUGAGGUCU ACCGUCAU	3712
2368	GAUACAGU G UAAAAGUG	1410	CACUUUUA GCCGAAAGGCGAGUGAGGUCU ACUGUAUC	3713

2439	GGAGCACU G UACAUACC	1411	GGUAUGUA GCCGAAAGGCGAGUGAGGUCU AGUGCUCC	3714
2512	AGGAUGAU G UUCAACAC	1412	GUGUUGAA GCCGAAAGGCGAGUGAGGUCU AUCAUCCU	3715
2529	AAGCAAGU G UGUUUCAG	1413	CUGAAACA GCCGAAAGGCGAGUGAGGUCU ACUUGCUU	3716
2531	GCAAGUGU G UUUCAGCA	1414	UGCUGAAA GCCGAAAGGCGAGUGAGGUCU ACACUUGC	3717
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2943	GUAUCUUU G UUUAUUCC	1419	GGAAUAAA GCCGAAAGGCGAGUGAGGUCU AAAGAUAC	3722
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3166	UCUAAAAU G UAUUUUAG	1424	CUAAAAUA GCCGAAAGGCGAGUGAGGUCU AUUUUAGA	3727
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73	AUGAAGAG G UGUUGAGG	1432	CCUCAACA GCCGAAAGGCGAGUGAGGUCU CUCUUCAU	3735
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91	UAUGUCAA G CAUCUGGC	1434	GCCAGAUG GCCGAAAGGCGAGUGAGGUCU UUGACAUA	3737
98	AGCAUCUG G CACAGCUG	1435	CAGCUGUG GCCGAAAGGCGAGUGAGGUCU CAGAUGCU	3738
103	CUGGCACA G CUGAAGGC	1436	GCCUUCAG GCCGAAAGGCGAGUGAGGUCU UGUGCCAG	3739
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182	AGACAAGA G CAAUAGUA	1439	UACUAUUG GCCGAAAGGCGAGUGAGGUCU UCUUGUCU	3742
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3189	UGUAGGGG G CGAUAUAC	1613	GUAUAUCG GCCGAAAGGCGAGUGAGGUCU CCCCUACA	3916
3242	UGUAGGGG G CGAUAUAC	1613	GUAUAUCG GCCGAAAGGCGAGUGAGGUCU CCCCUACA	3916
3210	UGUAUAUA G UACAUUUA	1614	UAAAUGUA GCCGAAAGGCGAGUGAGGUCU UAUAUACA	3917
3279	UGUAGGGG G CGAUAAAA	1615	UUUUAUCG GCCGAAAGGCGAGUGAGGUCU CCCCUACA	3918

Input Sequence = NM_001285. Cut Site = G/Y
Arm Length = 8. Core Sequence = GCcgaaagGCGaGuCaaGGuCu
NM_001285 (Homo sapiens chloride channel, calcium activated, 1 (CLCA1) mRNA, 3311 bp)

Table VII: Human CLCA1 DNAzyme and Target Sequence 249.021

Pos	Substrate	Seq ID No	DNAzyme	Rz Seq ID No
17	CUUUUGGU A CAAAUGGA	4	TCCATTTG GGCTAGCTACAACGA ACCAAAAG	3919
34	UGUGGAAU A UAAUUGAA	5	TTCAATTA GGCTAGCTACAACGA ATTCCACA	3920
44	AAUUGAAU A UUUUCUUG	8	CAAGAAAA GGCTAGCTACAACGA ATTCAATT	3921
84	UUGAGGUU A UGUCAAGC	19	GCTTGACA GGCTAGCTACAACGA AACCTCAA	3922
122	AUGGAAAU A UUUACAAG	22	CTTGTAAA GGCTAGCTACAACGA ATTTCCAT	3923
126	AAAUAUUU A CAAGUACG	25	CGTACTTG GGCTAGCTACAACGA AAATATTT	3924
132	UUACAAGU A CGCAAUUU	26	AAATTGCG GGCTAGCTACAACGA ACTTGTAA	3925
152	ACUAAGAU A UUGUUAUC	30	GATAACAA GGCTAGCTACAACGA ATCTTAGT	3926
158	AUAUUGUU A UCAUUCUC	33	GAGAATGA GGCTAGCTACAACGA AACAATAT	3927
169	AUUCUCCU A UUGAAGAC	38	GTCTTCAA GGCTAGCTACAACGA AGGAGAAT	3928
259	GUGUGUCU A UAUUUUCA	52	TGAAAATA GGCTAGCTACAACGA AGACACAC	3929
261	GUGUCUAU A UUUUCAUA	53	TATGAAAA GGCTAGCTACAACGA ATAGACAC	3930
269	AUUUUCAU A UCUGUAUA	58	TATACAGA GGCTAGCTACAACGA ATGAAAAT	3931
275	AUAUCUGU A UAUAUAUA	60	TATATATA GGCTAGCTACAACGA ACAGATAT	3932
277	AUCUGUAU A UAUAUAAU	61	ATTATATA GGCTAGCTACAACGA ATACAGAT	3933
279	CUGUAUAU A UAUAAUGG	62	CCATTATA GGCTAGCTACAACGA ATATACAG	3934
281	GUAUAUAU A UAAUGGUA	63	TACCATTA GGCTAGCTACAACGA ATATATAC	3935
346	GGAGAUGU A CAGCAAUG	74	CATTGCTG GGCTAGCTACAACGA ACATCTCC	3936
446	CAAUGGCU A UGAAGGCA	97	TGCCTTCA GGCTAGCTACAACGA AGCCATTG	3937
539	AUCUCUGU A UCUGUUUG	108	CAAACAGA GGCTAGCTACAACGA ACAGAGAT	3938
553	UUGAAGCU A CAGGAAAG	112	CTTTCCTG GGCTAGCTACAACGA AGCTTCAA	3939
569	GCGAUUUU A UUUCAAAA	116	TTTTGAAA GGCTAGCTACAACGA AAAATCGC	3940
623	GGCUGACU A UGUGAGAC	126	GTCTCACA GGCTAGCTACAACGA AGTCAGCC	3941
647	UGAGACCU A CAAAAAUG	128	CATTTTTG GGCTAGCTACAACGA AGGTCTCA	3942
679	CUGAGUCU A CUCCUCCA	133	TGGAGGAG GGCTAGCTACAACGA AGACTCAG	3943
704	UGAACCCU A CACUGAGC	137	GCTCAGTG GGCTAGCTACAACGA AGGGTTCA	3944
791	AGCUGAAU A UGGACCAC	147	GTGGTCCA GGCTAGCTACAACGA ATTCAGCT	3945
834	GCUCAUCU A CGAUGGGG	154	CCCCATCG GGCTAGCTACAACGA AGATGAGC	3946
846	UGGGGAGU A UUUGACGA	155	TCGTCAAA GGCTAGCTACAACGA ACTCCCCA	3947
857	UGACGAGU A CAAUAAUG	158	CATTATTG GGCTAGCTACAACGA ACTCGTCA	3948
878	GAAAUUCU A CUUAUCCA	162	TGGATAAG GGCTAGCTACAACGA AGAATTTC	3949
882	UUCUACUU A UCCAAUGG	164	CCATTGGA GGCTAGCTACAACGA AAGTAGAA	3950
897	GGAAGAAU A CAAGCAGU	166	ACTGCTTG GGCTAGCTACAACGA ATTCTTCC	3951
922	CAGCAGGU A UUACUGGU	170	ACCAGTAA GGCTAGCTACAACGA ACCTGCTG	3952
925	CAGGUAUU A CUGGUACA	172	TGTACCAG GGCTAGCTACAACGA AATACCTG	3953
931	UUACUGGU A CAAAUGUA	173	TACATTTG GGCTAGCTACAACGA ACCAGTAA	3954
968	CAGCUGUU A CACCAAAA	178	TTTTGGTG GGCTAGCTACAACGA AACAGCTG	3955
997	AUAAAGUU A CAGGACUC	183	GAGTCCTG GGCTAGCTACAACGA AACTTTAT	3956
1007	AGGACUCU A UGAAAAAG	185	CTTTTTCA GGCTAGCTACAACGA AGAGTCCT	3957
1060	AGGCUUCU A UAAUGUUU	194	AAACATTA GGCTAGCTACAACGA AGAAGCCT	3958
1087	UUGAUUCU A UAGUUGAA	201	TTCAACTA GGCTAGCTACAACGA AGAATCAA	3959
1102	AAUUCUGU A CAGAACAA	206	TTGTTCTG GGCTAGCTACAACGA ACAGAATT	3960
1213	CCACUCCU A UGACAACA	218	TGTTGTCA GGCTAGCTACAACGA AGGAGTGG	3961
1416	GCCCAUGU A CAAAGUGA	245	TCACTTTG GGCTAGCTACAACGA ACATGGGC	3962
1431	GAACUCAU A CAGAUAAA	247	TTTATCTG GGCTAGCTACAACGA ATGAGTTC	3963
1476	AAAAGAUU A CCUGCAGC	251	GCTGCAGG GGCTAGCTACAACGA AATCTTTT	3964
1531	CGGCAUUU A CUGUGAUU	261	AATCACAG GGCTAGCTACAACGA AAATGCCG	3965
1550	GAAGAAAU A UCCAACUG	264	CAGTTGGA GGCTAGCTACAACGA ATTTCTTC	3966
1603	ACAACACU A UAAGUGGG	268	CCCACTTA GGCTAGCTACAACGA AGTGTTGT	3967
1716	GGAGGUUU A CAGACAUA	285	TATGTCTG GGCTAGCTACAACGA AAACCTCC	3968
1724	ACAGACAU A UGCUUCAG	286	CTGAAGCA GGCTAGCTACAACGA ATGTCTGT	3969

1909	UGUUUCUU A UCACCUGG	318	CCAGGTGA GGCTAGCTACAACGA AAGAAACA	3970
2006	AAUGGCCU A CCUCCAAA	329	TTTGGAGG GGCTAGCTACAACGA AGGCCATT	3971
2048	UUGGAAAU A CAGUCUGC	336	GCAGACTG GGCTAGCTACAACGA ATTTCCAA	3972
2110	CCAAUGCU A CCCUGCCU	343	AGGCAGGG GGCTAGCTACAACGA AGCATTGG	3973
2125	CUCCAAUU A CAGUGACU	346	AGTCACTG GGCTAGCTACAACGA AATTGGAG	3974
2183	GGUAGUUU A UGCAAAUA	355	TATTTGCA GGCTAGCTACAACGA AAACTACC	3975
2191	AUGCAAAU A UUCGCCAA	356	TTGGCGAA GGCTAGCTACAACGA ATTTGCAT	3976
2266	AAACAGUU A CCUUGGAA	367	TTCCAAGG GGCTAGCTACAACGA AACTGTTT	3977
2277	UUGGAACU A CUGGAUAA	369	TTATCCAG GGCTAGCTACAACGA AGTTCCAA	3978
2305	CUGAUGCU A CUAAGGAU	371	ATCCTTAG GGCTAGCTACAACGA AGCATCAG	3979
2324	CGGUGUCU A CUCAAGGU	374	ACCTTGAG GGCTAGCTACAACGA AGACACCG	3980
2333	CUCAAGGU A UUUCACAA	376	TTGTGAAA GGCTAGCTACAACGA ACCTTGAG	3981
2345	CACAACUU A UGACACGA	381	TCGTGTCA GGCTAGCTACAACGA AAGTTGTG	3982
2363	UGGUAGAU A CAGUGUAA	383	TTACACTG GGCTAGCTACAACGA ATCTACCA	3983
2418	AGAGUGAU A CCCCAGCA	388	TGCTGGGG GGCTAGCTACAACGA ATCACTCT	3984
2441	AGCACUGU A CAUACCUG	389	CAGGTATG GGCTAGCTACAACGA ACAGTGCT	3985
2445	CUGUACAU A CCUGGCUG	390	CAGCCAGG GGCTAGCTACAACGA ATGTACAG	3986
2472	GAUGAAAU A CAAUGGAA	392	TTCCATTG GGCTAGCTACAACGA ATTTCATC	3987
2592	GCUCCCAU A CCUGAUCU	411	AGATCAGG GGCTAGCTACAACGA ATGGGAGC	3988
2690	GGAUGAUU A UGACCAUG	427	CATGGTCA GGCTAGCTACAACGA AATCATCC	3989
2714	UCACAAGU A UAUCAUUC	429	GAATGATA GGCTAGCTACAACGA ACTTGTGA	3990
2716	ACAAGUAU A UCAUUCGA	430	TCGAATGA GGCTAGCTACAACGA ATACTTGT	3991
2731	GAAUAAGU A CAAGUAUU	435	AATACTTG GGCTAGCTACAACGA ACTTATTC	3992
2737	GUACAAGU A UUCUUGAU	436	ATCAAGAA GGCTAGCTACAACGA ACTTGTAC	3993
2782	AAGUGAAU A CUACUGCU	448	AGCAGTAG GGCTAGCTACAACGA ATTCACTT	3994
2785	UGAAUACU A CUGCUCUC	449	GAGAGCAG GGCTAGCTACAACGA AGTATTCA	3995
2848	AAAACAUU A CUUUUGAA	463	TTCAAAAG GGCTAGCTACAACGA AATGTTTT	3996
2881	UCAUUGCU A UUCAGGCU	473	AGCCTGAA GGCTAGCTACAACGA AGCAATGA	3997
2919	UCAGAAAU A UCCAACAU	481	ATGTTGGA GGCTAGCTACAACGA ATTTCTGA	3998
2937	GCACGAGU A UCUUUGUU	484	AACAAAGA GGCTAGCTACAACGA ACTCGTGC	3999
2947	CUUUGUUU A UUCCUCCA	490	TGGAGGAA GGCTAGCTACAACGA AAACAAAG	4000
3010	GUCCUAAU A UUCAUAUC	502	GATATGAA GGCTAGCTACAACGA ATTAGGAC	4001
3016	AUAUUCAU A UCAACAGC	505	GCTGTTGA GGCTAGCTACAACGA ATGAATAT	4002
3055	UAAAAAUU A UGUGGAAG	516	CTTCCACA GGCTAGCTACAACGA AATTTTTA	4003
3149	UUUUGAUU A UAAAAUUU	540	AAATTTTA GGCTAGCTACAACGA AATCAAAA	4004
3168	UAAAAUGU A UUUUAGAC	547	GTCTAAAA GGCTAGCTACAACGA ACATTTTA	4005
3194	GGGGCGAU A UACUAAAU	555	ATTTAGTA GGCTAGCTACAACGA ATCGCCCC	4006
3247	GGGGCGAU A UACUAAAU	555	ATTTAGTA GGCTAGCTACAACGA ATCGCCCC	4006
3196	GGCGAUAU A CUAAAUGU	556	ACATTTAG GGCTAGCTACAACGA ATATCGCC	4007
3249	GGCGAUAU A CUAAAUGU	556	ACATTTAG GGCTAGCTACAACGA ATATCGCC	4007
3205	CUAAAUGU A UAUAGUAC	558	GTACTATA GGCTAGCTACAACGA ACATTTAG	4008
3207	AAAUGUAU A UAGUACAU	559	ATGTACTA GGCTAGCTACAACGA ATACATTT	4009
3212	UAUAUAGU A CAUUUAUA	561	TATAAATG GGCTAGCTACAACGA ACTATATA	4010
3218	GUACAUUU A UACUAAAU	564	ATTTAGTA GGCTAGCTACAACGA AAATGTAC	4011
3220	ACAUUUAU A CUAAAUGU	565	ACATTTAG GGCTAGCTACAACGA ATAAATGT	4012
3229	CUAAAUGU A UUCCUGUA	567	TACAGGAA GGCTAGCTACAACGA ACATTTAG	4013
3258	CUAAAUGU A UUUUAGAC	572	GTCTAAAA GGCTAGCTACAACGA ACATTTAG	4014
65	AGGGGAGC A UGAAGAGG	579	CCTCTTCA GGCTAGCTACAACGA GCTCCCCT	4015
93	UGUCAAGC A UCUGGCAC	581	GTGCCAGA GGCTAGCTACAACGA GCTTGACA	4016
100	CAUCUGGC A CAGCUGAA	583	TTCAGCTG GGCTAGCTACAACGA GCCAGATG	4017
161	UUGUUAUC A UUCUCCUA	590	TAGGAGAA GGCTAGCTACAACGA GATAACAA	4018
195	AGUAAAAC A CAUCAGGU	596	ACCTGATG GGCTAGCTACAACGA GTTTTACT	4019
197	UAAAACAC A UCAGGUCA	597	TGACCTGA GGCTAGCTACAACGA GTGTTTTA	4020
231	GAUAAACC A CUUCCGAU	603	ATCGGAAG GGCTAGCTACAACGA GGTTTATC	4021
267	AUAUUUUC A UAUCUGUA	607	TACAGATA GGCTAGCTACAACGA GAAAATAT	4022
299	AGAAAGAC A CCUUCGUA	609	TACGAAGG GGCTAGCTACAACGA GTCTTTCT	4023

314	UAACCCGC A UUUUCCAA	614	TTGGAAAA GGCTAGCTACAACGA GCGGGTTA	4024
334	GAGGAAUC A CAGGGAGA	617	TCTCCCTG GGCTAGCTACAACGA GATTCCTC	4025
360	AUGGGGCC A UUUAAGAG	622	CTCTTAAA GGCTAGCTACAACGA GGCCCCAT	4026
379	CUGUGUUC A UCUUGAUU	624	AATCAAGA GGCTAGCTACAACGA GAACACAG	4027
392	GAUUCUUC A CCUUCUAG	627	CTAGAAGG GGCTAGCTACAACGA GAAGAATC	4028
420	AGUAAUUC A CUCAUUCA	634	TGAATGAG GGCTAGCTACAACGA GAATTACT	4029
424	AUUCACUC A UUCAGCUG	636	CAGCTGAA GGCTAGCTACAACGA GAGTGAAT	4030
454	AUGAAGGC A UUGUCGUU	642	AACGACAA GGCTAGCTACAACGA GCCTTCAT	4031
495	GAUGAAAC A CUCAUUCA	650	TGAATGAG GGCTAGCTACAACGA GTTTCATC	4032
499	AAACACUC A UUCAACAA	652	TTGTTGAA GGCTAGCTACAACGA GAGTGTTT	4033
517	UAAAGGAC A UGGUGACC	655	GGTCACCA GGCTAGCTACAACGA GTCCTTTA	4034
531	ACCCAGGC A UCUCUGUA	659	TACAGAGA GGCTAGCTACAACGA GCCTGGGT	4035
586	AUGUUGCC A UUUUGAUU	667	AATCAAAA GGCTAGCTACAACGA GGCAACAT	4036
603	CCUGAAAC A UGGAAGAC	670	GTCTTCCA GGCTAGCTACAACGA GTTTCAGG	4037
706	AACCCUAC A CUGAGCAG	692	CTGCTCAG GGCTAGCTACAACGA GTAGGGTT	4038
749	AAGGAUCC A CCUCACUC	698	GAGTGAGG GGCTAGCTACAACGA GGATCCTT	4039
754	UCCACCUC A CUCCUGAU	701	ATCAGGAG GGCTAGCTACAACGA GAGGTGGA	4040
766	CUGAUUUC A UUGCAGGA	705	TCCTGCAA GGCTAGCTACAACGA GAAATCAG	4041
798	UAUGGACC A CAAGGUAA	709	TTACCTTG GGCTAGCTACAACGA GGTCCATA	4042
810	GGUAAGGC A UUUGUCCA	711	TGGACAAA GGCTAGCTACAACGA GCCTTACC	4043
818	AUUUGUCC A UGAGUGGG	713	CCCACTCA GGCTAGCTACAACGA GGACAAAT	4044
830	GUGGGCUC A UCUACGAU	715	ATCGTAGA GGCTAGCTACAACGA GAGCCCAC	4045
970	GCUGUUAC A CCAAAAGA	731	TCTTTTGG GGCTAGCTACAACGA GTAACAGC	4046
982	AAAGAUGC A CAUUCAAU	734	ATTGAATG GGCTAGCTACAACGA GCATCTTT	4047
984	AGAUGCAC A UUCAAUAA	735	TTATTGAA GGCTAGCTACAACGA GTGCATCT	4048
1071	AUGUUUGC A CAACAUGU	749	ACATGTTG GGCTAGCTACAACGA GCAAACAT	4049
1076	UGCACAAC A UGUUGAUU	751	AATCAACA GGCTAGCTACAACGA GTTGTGCA	4050
1115	ACAAAACC A CAACAAAG	757	CTTTGTTG GGCTAGCTACAACGA GGTTTTGT	4051
1165	UCCGAAGC A CAUGGGAA	769	TTCCCATG GGCTAGCTACAACGA GCTTCGGA	4052
1167	CGAAGCAC A UGGGAAGU	770	ACTTCCCA GGCTAGCTACAACGA GTGCTTCG	4053
1207	AGAAAACC A CUCCUAUG	775	CATAGGAG GGCTAGCTACAACGA GGTTTTCT	4054
1221	AUGACAAC A CAGCCACC	780	GGTGGCTG GGCTAGCTACAACGA GTTGTCAT	4055
1227	ACACAGCC A CCAAAUCC	783	GGATTTGG GGCTAGCTACAACGA GGCTGTGT	4056
1237	CAAAUCCC A CCUUCUCA	788	TGAGAAGG GGCTAGCTACAACGA GGGATTTG	4057
1245	ACCUUCUC A UUGCUGCA	792	TGCAGCAA GGCTAGCTACAACGA GAGAAGGT	4058
1300	CUGGAAGC A UGGCGACU	800	AGTCGCCA GGCTAGCTACAACGA GCTTCCAG	4059
1395	AUGGUGAC A UUUGACAG	820	CTGTCAAA GGCTAGCTACAACGA GTCACCAT	4060
1412	UGCUGCCC A UGUACAAA	825	TTTGTACA GGCTAGCTACAACGA GGGCAGCA	4061
1429	GUGAACUC A UACAGAUA	828	TATCTGTA GGCTAGCTACAACGA GAGTTCAC	4062
1459	ACAGGGAC A CACUCGCC	833	GGCGAGTG GGCTAGCTACAACGA GTCCCTGT	4063
1461	AGGGACAC A CUCGCCAA	834	TTGGCGAG GGCTAGCTACAACGA GTGTCCCT	4064
1504	GGACGUCC A UCUGCAGC	845	GCTGCAGA GGCTAGCTACAACGA GGACGTCC	4065
1527	CGAUCGGC A UUUACUGU	849	ACAGTAAA GGCTAGCTACAACGA GCCGATCG	4066
1600	AAGACAAC A CUAUAAGU	858	ACTTATAG GGCTAGCTACAACGA GTTGTCTT	4067
1642	GUGGUGCC A UCAUCCAC	864	GTGGATGA GGCTAGCTACAACGA GGCACCAC	4068
1645	GUGCCAUC A UCCACACA	865	TGTGTGGA GGCTAGCTACAACGA GATGGCAC	4069
1649	CAUCAUCC A CACAGUCG	867	CGACTGTG GGCTAGCTACAACGA GGATGATG	4070
1651	UCAUCCAC A CAGUCGCU	868	AGCGACTG GGCTAGCTACAACGA GTGGATGA	4071
1722	UUACAGAC A UAUGCUUC	884	GAAGCATA GGCTAGCTACAACGA GTCTGTAA	4072
1756	AUGGCCUC A UUGAUGCU	892	AGCATCAA GGCTAGCTACAACGA GAGGCCAT	4073
1779	GCCCUUUC A UCAGGAAA	897	TTTCCTGA GGCTAGCTACAACGA GAAAGGGC	4074
1810	AGCGCUCC A UCCAGCUU	905	AAGCTGGA GGCTAGCTACAACGA GGAGCGCT	4075
1864	UGAAUGGC A CAGUGAUC	917	GATCACTG GGCTAGCTACAACGA GCCATTCA	4076
1882	UGGACAGC A CCGUGGGA	920	TCCCACGG GGCTAGCTACAACGA GCTGTCCA	4077
1897	GAAAGGAC A CUUUGUUU	922	AAACAAAG GGCTAGCTACAACGA GTCCTTTC	4078
1912	UUCUUAUC A CCUGGACA	925	TGTCCAGG GGCTAGCTACAACGA GATAAGAA	4079

1993	ACAAAAAC A CCAAAAUG	947	CATTTTGG GGCTAGCTACAACGA GTTTTTGT	4080
2023	UCCCAGGC A UUGCUAAG	959	CTTAGCAA GGCTAGCTACAACGA GCCTGGGA	4081
2038	AGGUUGGC A CUUGGAAA	961	TTTCCAAG GGCTAGCTACAACGA GCCAACCT	4082
2067	GCAAGCUC A CAAACCUU	968	AAGGTTTG GGCTAGCTACAACGA GAGCTTGC	4083
2089	UGACUGUC A CGUCCCGU	976	ACGGGACG GGCTAGCTACAACGA GACAGTCA	4084
2152	ACAAGGAC A CCAGCAAA	994	TTTGCTGG GGCTAGCTACAACGA GTCCTTGT	4085
2230	CCAGUGUC A CAGCCCUG	1019	CAGGGCTG GGCTAGCTACAACGA GACACTGG	4086
2338	GGUAUUUC A CAACUUAU	1037	ATAAGTTG GGCTAGCTACAACGA GAAATACC	4087
2350	CUUAUGAC A CGAAUGGU	1040	ACCATTCG GGCTAGCTACAACGA GTCATAAG	4088
2436	AGUGGAGC A CUGUACAU	1052	ATGTACAG GGCTAGCTACAACGA GCTCCACT	4089
2443	CACUGUAC A UACCUGGC	1054	GCCAGGTA GGCTAGCTACAACGA GTACAGTG	4090
2484	UGGAAUCC A CCAAGACC	1060	GGTCTTGG GGCTAGCTACAACGA GGATTCCA	4091
2519	UGUUCAAC A CAAGCAAG	1066	CTTGCTTG GGCTAGCTACAACGA GTTGAACA	4092
2544	AGCAGAAC A UCCUCGGG	1071	CCCGAGGA GGCTAGCTACAACGA GTTCTGCT	4093
2559	GGAGGCUC A UUUGUGGC	1075	GCCACAAA GGCTAGCTACAACGA GAGCCTCC	4094
2590	AUGCUCCC A UACCUGAU	1084	ATCAGGTA GGCTAGCTACAACGA GGGAGCAT	4095
2607	CUCUUCCC A CCUGGCCA	1091	TGGCCAGG GGCTAGCTACAACGA GGGAAGAG	4096
2620	GCCAAAUC A CCGACCUG	1096	CAGGTCGG GGCTAGCTACAACGA GATTTGGC	4097
2642	GGAAAUUC A CGGGGGCA	1100	TGCCCCCG GGCTAGCTACAACGA GAATTTCC	4098
2656	GCAGUCUC A UUAAUCUG	1103	CAGATTAA GGCTAGCTACAACGA GAGACTGC	4099
2696	UUAUGACC A UGGAACAG	1111	CTGTTCCA GGCTAGCTACAACGA GGTCATAA	4100
2708	AACAGCUC A CAAGUAUA	1114	TATACTTG GGCTAGCTACAACGA GAGCTGTT	4101
2719	AGUAUAUC A UUCGAAUA	1116	TATTCGAA GGCTAGCTACAACGA GATATACT	4102
2794	CUGCUCUC A UCCCAAAG	1130	CTTTGGGA GGCTAGCTACAACGA GAGAGCAG	4103
2845	CAGAAAAC A UUACUUUU	1141	AAAAGTAA GGCTAGCTACAACGA GTTTTCTG	4104
2863	AAAAUGGC A CAGAUCUU	1143	AAGATCTG GGCTAGCTACAACGA GCCATTTT	4105
2875	AUCUUUUC A UUGCUAUU	1146	AATAGCAA GGCTAGCTACAACGA GAAAAGAT	4106
2926	UAUCCAAC A UUGCACGA	1154	TCGTGCAA GGCTAGCTACAACGA GTTGGATA	4107
2931	AACAUUGC A CGAGUAUC	1155	GATACTCG GGCTAGCTACAACGA GCAATGTT	4108
2955	AUUCCUCC A CAGACUCC	1160	GGAGTCTG GGCTAGCTACAACGA GGAGGAAT	4109
2973	CCAGAGAC A CCUAGUCC	1166	GGACTAGG GGCTAGCTACAACGA GTCTCTGG	4110
3014	UAAUAUUC A UAUCAACA	1177	TGTTGATA GGCTAGCTACAACGA GAATATTA	4111
3025	UCAACAGC A CCAUUCCU	1180	AGGAATGG GGCTAGCTACAACGA GCTGTTGA	4112
3028	ACAGCACC A UUCCUGGC	1182	GCCAGGAA GGCTAGCTACAACGA GGTGCTGT	4113
3037	UUCCUGGC A UUCACAUU	1185	AATGTGAA GGCTAGCTACAACGA GCCAGGAA	4114
3041	UGGCAUUC A CAUUUUAA	1186	TTAAAATG GGCTAGCTACAACGA GAATGCCA	4115
3043	GCAUUCAC A UUUUAAAA	1187	TTTTAAAA GGCTAGCTACAACGA GTGAATGC	4116
3130	AAUAAAUC A UUCAUCCU	1196	AGGATGAA GGCTAGCTACAACGA GATTTATT	4117
3134	AAUCAUUC A UCCUUUUU	1197	AAAAAGGA GGCTAGCTACAACGA GAATGATT	4118
3214	UAUAGUAC A UUUAUACU	1205	AGTATAAA GGCTAGCTACAACGA GTACTATA	4119
134	ACAAGUAC G CAAUUUGA	1215	TCAAATTG GGCTAGCTACAACGA GTACTTGT	4120
312	CGUAACCC G CAUUUUCC	1220	GGAAAATG GGCTAGCTACAACGA GGGTTACG	4121
463	UUGUCGUU G CAAUCGAC	1225	GTCGATTG GGCTAGCTACAACGA AACGACAA	4122
480	CCCAAUGU G CCAGAAGA	1227	TCTTCTGG GGCTAGCTACAACGA ACATTGGG	4123
583	AAAAUGUU G CCAUUUUG	1232	CAAAATGG GGCTAGCTACAACGA AACATTTT	4124
655	ACAAAAAU G CUGAUGUU	1238	AACATCAG GGCTAGCTACAACGA ATTTTTGT	4125
670	UUCUGGUU G CUGAGUCU	1240	AGACTCAG GGCTAGCTACAACGA AACCAGAA	4126
769	AUUUCAUU G CAGGAAAA	1247	TTTTCCTG GGCTAGCTACAACGA AATGAAAT	4127
980	CAAAAGAU G CACAUUCA	1255	TGAATGTG GGCTAGCTACAACGA ATCTTTTG	4128
1040	CCAAUCCC G CCAGACGG	1258	CCGTCTGG GGCTAGCTACAACGA GGGATTGG	4129
1069	UAAUGUUU G CACAACAU	1259	ATGTTGTG GGCTAGCTACAACGA AAACATTA	4130
1151	UCAAAAAU G CAAUCUCC	1262	GGAGATTG GGCTAGCTACAACGA ATTTTTGA	4131
1248	UUCUCAUU G CUGCAGAU	1268	ATCTGCAG GGCTAGCTACAACGA AATGAGAA	4132
1251	UCAUUGCU G CAGAUUGG	1269	CCAATCTG GGCTAGCTACAACGA AGCAATGA	4133
1316	UGGUAACC G CCUCAAUC	1272	GATTGAGG GGCTAGCTACAACGA GGTTACCA	4134
1353	CUUUUCCU G CUGCAGAC	1275	GTCTGCAG GGCTAGCTACAACGA AGGAAAAG	4135

1356	UUCCUGCU G CAGACAGU	1276	ACTGTCTG GGCTAGCTACAACGA AGCAGGAA	4136
1405	UUGACAGU G CUGCCCAU	1280	ATGGGCAG GGCTAGCTACAACGA ACTGTCAA	4137
1408	ACAGUGCU G CCCAUGUA	1281	TACATGGG GGCTAGCTACAACGA AGCACTGT	4138
1465	ACACACUC G CCAAAAGA	1284	TCTTTTGG GGCTAGCTACAACGA GAGTGTGT	4139
1480	GAUUACCU G CAGCAGCU	1285	AGCTGCTG GGCTAGCTACAACGA AGGTAATC	4140
1508	GUCCAUCU G CAGCGGGC	1286	GCCCGCTG GGCTAGCTACAACGA AGATGGAC	4141
1575	GAAAUUGU G CUGCUGAC	1291	GTCAGCAG GGCTAGCTACAACGA ACAATTTC	4142
1578	AUUGUGCU G CUGACGGA	1292	TCCGTCAG GGCTAGCTACAACGA AGCACAAT	4143
1613	AAGUGGGU G CUUUAACG	1294	CGTTAAAG GGCTAGCTACAACGA ACCCACTT	4144
1639	AAAGUGGU G CCAUCAUC	1296	GATGATGG GGCTAGCTACAACGA ACCACTTT	4145
1657	ACACAGUC G CUUUGGGG	1297	CCCCAAAG GGCTAGCTACAACGA GACTGTGT	4146
1672	GGCCCUCU G CAGCUCAA	1298	TTGAGCTG GGCTAGCTACAACGA AGAGGGCC	4147
1726	AGACAUAU G CUUCAGAU	1300	ATCTGAAG GGCTAGCTACAACGA ATATGTCT	4148
1762	UCAUUGAU G CUUUUGGG	1302	CCCAAAAG GGCTAGCTACAACGA ATCAATGA	4149
1805	CUCUCAGC G CUCCAUCC	1303	GGATGGAG GGCTAGCTACAACGA GCTGAGAG	4150
1923	UGGACAAC G CAGCCUCC	1307	GGAGGCTG GGCTAGCTACAACGA GTTGTCCA	4151
2026	CAGGCAUU G CUAAGGUU	1308	AACCTTAG GGCTAGCTACAACGA AATGCCTG	4152
2055	UACAGUCU G CAAGCAAG	1309	CTTGCTTG GGCTAGCTACAACGA AGACTGTA	4153
2098	CGUCCCGU G CGUCCAAU	1312	ATTGGACG GGCTAGCTACAACGA ACGGGACG	4154
2107	CGUCCAAU G CUACCCUG	1313	CAGGGTAG GGCTAGCTACAACGA ATTGGACG	4155
2115	GCUACCCU G CCUCCAAU	1314	ATTGGAGG GGCTAGCTACAACGA AGGGTAGC	4156
2185	UAGUUUAU G CAAAUAUU	1317	AATATTTG GGCTAGCTACAACGA ATAAACTA	4157
2195	AAAUAUUC G CCAAGGAG	1318	CTCCTTGG GGCTAGCTACAACGA GAATATTT	4158
2296	GAGCAGGU G CUGAUGCU	1322	AGCATCAG GGCTAGCTACAACGA ACCTGCTC	4159
2302	GUGCUGAU G CUACUAAG	1324	CTTAGTAG GGCTAGCTACAACGA ATCAGCAC	4160
2376	GUAAAAGU G CGGGCUCU	1328	AGAGCCCG GGCTAGCTACAACGA ACTTTTAC	4161
2398	GAGUUAAC G CAGCCAGA	1329	TCTGGCTG GGCTAGCTACAACGA GTTAACTC	4162
2584	UCCCAAAU G CUCCCAUA	1337	TATGGGAG GGCTAGCTACAACGA ATTTGGGA	4163
2788	AUACUACU G CUCUCAUC	1348	GATGAGAG GGCTAGCTACAACGA AGTAGTAT	4164
2878	UUUUCAUU G CUAUUCAG	1351	CTGAATAG GGCTAGCTACAACGA AATGAAAA	4165
2929	CCAACAUU G CACGAGUA	1355	TACTCGTG GGCTAGCTACAACGA AATGTTGG	4166
2964	CAGACUCC G CCAGAGAC	1357	GTCTCTGG GGCTAGCTACAACGA GGAGTCTG	4167
2995	AAACGUCU G CUCCUUGU	1360	ACAAGGAG GGCTAGCTACAACGA AGACGTTT	4168
3078	GGAGAACU G CAGCUGUC	1361	GACAGCTG GGCTAGCTACAACGA AGTTCTCC	4169
3294	AAUAAAAU G CUAAACAA	1366	TTGTTTAG GGCTAGCTACAACGA ATTTTATT	4170
27	AAAUGGAU G UGGAAUAU	1367	ATATTCCA GGCTAGCTACAACGA ATCCATTT	4171
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75	GAAGAGGU G UUGAGGUU	1369	AACCTCAA GGCTAGCTACAACGA ACCTCTTC	4173
86	GAGGUUAU G UCAAGCAU	1370	ATGCTTGA GGCTAGCTACAACGA ATAACCTC	4174
155	AAGAUAUU G UUAUCAUU	1371	AATGATAA GGCTAGCTACAACGA AATATCTT	4175
221	AAAGACCU G UGAUAAAC	1372	GTTTATCA GGCTAGCTACAACGA AGGTCTTT	4176
253	GGAAACGU G UGUCUAUA	1373	TATAGACA GGCTAGCTACAACGA ACGTTTCC	4177
255	AAACGUGU G UCUAUAUU	1374	AATATAGA GGCTAGCTACAACGA ACACGTTT	4178
273	UCAUAUCU G UAUAUAUA	1375	TATATATA GGCTAGCTACAACGA AGATATGA	4179
344	AGGGAGAU G UACAGCAA	1376	TTGCTGTA GGCTAGCTACAACGA ATCTCCCT	4180
373	AGAGUUCU G UGUUCAUC	1377	GATGAACA GGCTAGCTACAACGA AGAACTCT	4181
375	AGUUCUGU G UUCAUCUU	1378	AAGATGAA GGCTAGCTACAACGA ACAGAACT	4182
457	AAGGCAUU G UCGUUGCA	1379	TGCAACGA GGCTAGCTACAACGA AATGCCTT	4183
478	ACCCCAAU G UGCCAGAA	1380	TTCTGGCA GGCTAGCTACAACGA ATTGGGGT	4184
537	GCAUCUCU G UAUCUGUU	1381	AACAGATA GGCTAGCTACAACGA AGAGATGC	4185
543	CUGUAUCU G UUUGAAGC	1382	GCTTCAAA GGCTAGCTACAACGA AGATACAG	4186
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625	CUGACUAU G UGAGACCA	1384	TGGTCTCA GGCTAGCTACAACGA ATAGTCAG	4188
661	AUGCUGAU G UUCUGGUU	1385	AACCAGAA GGCTAGCTACAACGA ATCAGCAT	4189
725	GGGCAACU G UGGAGAGA	1386	TCTCTCCA GGCTAGCTACAACGA AGTTGCCC	4190
814	AGGCAUUU G UCCAUGAG	1387	CTCATGGA GGCTAGCTACAACGA AAATGCCT	4191

911	AGUAAGAU G UUCAGCAG	1388	CTGCTGAA GGCTAGCTACAACGA ATCTTACT	4192
937	GUACAAAU G UAGUAAAG	1389	CTTTACTA GGCTAGCTACAACGA ATTTGTAC	4193
950	AAAGAAGU G UCAGGGAG	1390	CTCCCTGA GGCTAGCTACAACGA ACTTCTTT	4194
965	AGGCAGCU G UUACACCA	1391	TGGTGTAA GGCTAGCTACAACGA AGCTGCCT	4195
1019	AAAAGGAU G UGAGUUUG	1392	CAAACTCA GGCTAGCTACAACGA ATCCTTTT	4196
1027	GUGAGUUU G UUCUCCAA	1393	TTGGAGAA GGCTAGCTACAACGA AAACTCAC	4197
1065	UCUAUAAU G UUUGCACA	1394	TGTGCAAA GGCTAGCTACAACGA ATTATAGA	4198
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1272	AGAAUUGU G UGUUUAGU	1398	ACTAAACA GGCTAGCTACAACGA ACAATTCT	4202
1274	AAUUGUGU G UUUAGUCC	1399	GGACTAAA GGCTAGCTACAACGA ACACAATT	4203
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1573	CUGAAAUU G UGCUGCUG	1402	CAGCAGCA GGCTAGCTACAACGA AATTTCAG	4206
1695	GAGGAGCU G UCCAAAAU	1403	ATTTTGGA GGCTAGCTACAACGA AGCTCCTC	4207
1795	AUGGAGCU G UCUCUCAG	1404	CTGAGAGA GGCTAGCTACAACGA AGCTCCAT	4208
1902	GACACUUU G UUUCUUAU	1405	ATAAGAAA GGCTAGCTACAACGA AAAGTGTC	4209
1978	GUGGCUUU G UAGUGGAC	1406	GTCCACTA GGCTAGCTACAACGA AAAGCCAC	4210
2086	CCCUGACU G UCACGUCC	1407	GGACGTGA GGCTAGCTACAACGA AGTCAGGG	4211
2227	GGGCCAGU G UCACAGCC	1408	GGCTGTGA GGCTAGCTACAACGA ACTGGCCC	4212
2320	AUGACGGU G UCUACUCA	1409	TGAGTAGA GGCTAGCTACAACGA ACCGTCAT	4213
2368	GAUACAGU G UAAAAGUG	1410	CACTTTTA GGCTAGCTACAACGA ACTGTATC	4214
2439	GGAGCACU G UACAUACC	1411	GGTATGTA GGCTAGCTACAACGA AGTGCTCC	4215
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2529	AAGCAAGU G UGUUUCAG	1413	CTGAAACA GGCTAGCTACAACGA ACTTGCTT	4217
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2563	GCUCAUUU G UGGCUUCU	1415	AGAAGCCA GGCTAGCTACAACGA AAATGAGC	4219
2575	CUUCUGAU G UCCCAAAU	1416	ATTTGGGA GGCTAGCTACAACGA ATCAGAAG	4220
2829	GUCUUUUU G UUUAAACC	1417	GGTTTAAA GGCTAGCTACAACGA AAAAAGAC	4221
2890	UUCAGGCU G UUGAUAAG	1418	CTTATCAA GGCTAGCTACAACGA AGCCTGAA	4222
2943	GUAUCUUU G UUUAUUCC	1419	GGAATAAA GGCTAGCTACAACGA AAAGATAC	4223
3002	UGCUCCUU G UCCUAAUA	1420	TATTAGGA GGCTAGCTACAACGA AAGGAGCA	4224
3057	AAAAUUAU G UGGAAGUG	1421	CACTTCCA GGCTAGCTACAACGA ATAATTTT	4225
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3109	GAAUUUUU G UCAGAUAA	1423	TTATCTGA GGCTAGCTACAACGA AAAAATTC	4227
3166	UCUAAAAU G UAUUUUAG	1424	CTAAAATA GGCTAGCTACAACGA ATTTTAGA	4228
3182	GACUUCCU G UAGGGGGC	1425	GCCCCCTA GGCTAGCTACAACGA AGGAAGTC	4229
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3227	UACUAAAU G UAUUCCUG	1427	CAGGAATA GGCTAGCTACAACGA ATTTAGTA	4231
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63	UAAGGGGA G CAUGAAGA	1431	TCTTCATG GGCTAGCTACAACGA TCCCCTTA	4235
73	AUGAAGAG G UGUUGAGG	1432	CCTCAACA GGCTAGCTACAACGA CTCTTCAT	4236
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91	UAUGUCAA G CAUCUGGC	1434	GCCAGATG GGCTAGCTACAACGA TTGACATA	4238
98	AGCAUCUG G CACAGCUG	1435	CAGCTGTG GGCTAGCTACAACGA CAGATGCT	4239
103	CUGGCACA G CUGAAGGC	1436	GCCTTCAG GGCTAGCTACAACGA TGTGCCAG	4240
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188	GAGCAAUA G UAAAACAC	1440	GTGTTTTA GGCTAGCTACAACGA TATTGCTC	4244
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242	UCCGAUAA G UUGGAAAC	1443	GTTTCCAA GGCTAGCTACAACGA TTATCGGA	4247
251	UUGGAAAC G UGUGUCUA	1444	TAGACACA GGCTAGCTACAACGA GTTTCCAA	4248
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305	ACACCUUC G UAACCCGC	1446	GCGGGTTA GGCTAGCTACAACGA GAAGGTGT	4250
349	GAUGUACA G CAAUGGGG	1447	CCCCATTG GGCTAGCTACAACGA TGTACATC	4251
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368	AUUUAAGA G UUCUGUGU	1449	ACACAGAA GGCTAGCTACAACGA TCTTAAAT	4253
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780	GGAAAAAA G UUAGCUGA	1467	TCAGCTAA GGCTAGCTACAACGA TTTTTTCC	4271
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826	AUGAGUGG G CUCAUCUA	1472	TAGATGAG GGCTAGCTACAACGA CCACTCAT	4276
844	GAUGGGGA G UAUUUGAC	1473	GTCAAATA GGCTAGCTACAACGA TCCCCATC	4277
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916	GAUGUUCA G CAGGUAUU	1477	AATACCTG GGCTAGCTACAACGA TGAACATC	4281
920	UUCAGCAG G UAUUACUG	1478	CAGTAATA GGCTAGCTACAACGA CTGCTGAA	4282
929	UAUUACUG G UACAAAUG	1479	CATTTGTA GGCTAGCTACAACGA CAGTAATA	4283
940	CAAAUGUA G UAAAGAAG	1480	CTTCTTTA GGCTAGCTACAACGA TACATTTG	4284
948	GUAAAGAA G UGUCAGGG	1481	CCCTGACA GGCTAGCTACAACGA TTCTTTAC	4285
959	UCAGGGAG G CAGCUGUU	1482	AACAGCTG GGCTAGCTACAACGA CTCCCTGA	4286
962	GGGAGGCA G CUGUUACA	1483	TGTAACAG GGCTAGCTACAACGA TGCCTCCC	4287
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1054	CGGAGAAG G CUUCUAUA	1486	TATAGAAG GGCTAGCTACAACGA CTTCTCCG	4290
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1224	ACAACACA G CCACCAAA	1493	TTTGGTGG GGCTAGCTACAACGA TGTGTTGT	4297
1279	UGUGUUUA G UCCUUGAC	1494	GTCAAGGA GGCTAGCTACAACGA TAAACACA	4298
1298	AUCUGGAA G CAUGGCGA	1495	TCGCCATG GGCTAGCTACAACGA TTCCAGAT	4299
1303	GAAGCAUG G CGACUGGU	1496	ACCAGTCG GGCTAGCTACAACGA CATGCTTC	4300
1310	GGCGACUG G UAACCGCC	1497	GGCGGTTA GGCTAGCTACAACGA CAGTCGCC	4301
1336	UGAAUCAA G CAGGCCAG	1498	CTGGCCTG GGCTAGCTACAACGA TTGATTCA	4302

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1363	UGCAGACA G UUGAGCUG	1501	CAGCTCAA GGCTAGCTACAACGA TGTCTGCA	4305
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1442	GAUAAACA G UGGCAGUG	1508	CACTGCCA GGCTAGCTACAACGA TGTTTATC	4312
1445	AAACAGUG G CAGUGACA	1509	TGTCACTG GGCTAGCTACAACGA CACTGTTT	4313
1448	CAGUGGCA G UGACAGGG	1510	CCCTGTCA GGCTAGCTACAACGA TGCCACTG	4314
1483	UACCUGCA G CAGCUUCA	1511	TGAAGCTG GGCTAGCTACAACGA TGCAGGTA	4315
1486	CUGCAGCA G CUUCAGGA	1512	TCCTGAAG GGCTAGCTACAACGA TGCTGCAG	4316
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1511	CAUCUGCA G CGGGCUUC	1514	GAAGCCCG GGCTAGCTACAACGA TGCAGATG	4318
1515	UGCAGCGG G CUUCGAUC	1515	GATCGAAG GGCTAGCTACAACGA CCGCTGCA	4319
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1611	AUAAGUGG G UGCUUUAA	1518	TTAAAGCA GGCTAGCTACAACGA CCACTTAT	4322
1624	UUAACGAG G UCAAACAA	1519	TTGTTTGA GGCTAGCTACAACGA CTCGTTAA	4323
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1637	ACAAAGUG G UGCCAUCA	1521	TGATGGCA GGCTAGCTACAACGA CACTTTGT	4325
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1665	GCUUUGGG G CCCUCUGC	1523	GCAGAGGG GGCTAGCTACAACGA CCCAAAGC	4327
1675	CCUCUGCA G CUCAAGAA	1524	TTCTTGAG GGCTAGCTACAACGA TGCAGAGG	4328
1692	CUAGAGGA G CUGUCCAA	1525	TTGGACAG GGCTAGCTACAACGA TCCTCTAG	4329
1712	GACAGGAG G UUUACAGA	1526	TCTGTAAA GGCTAGCTACAACGA CTCCTGTC	4330
1738	CAGAUCAA G UUCAGAAC	1527	GTTCTGAA GGCTAGCTACAACGA TTGATCTG	4331
1751	GAACAAUG G CCUCAUUG	1528	CAATGAGG GGCTAGCTACAACGA CATTGTTC	4332
1771	CUUUUGGG G CCCUUUCA	1529	TGAAAGGG GGCTAGCTACAACGA CCCAAAAG	4333
1792	GAAAUGGA G CUGUCUCU	1530	AGAGACAG GGCTAGCTACAACGA TCCATTTC	4334
1803	GUCUCUCA G CGCUCCAU	1531	ATGGAGCG GGCTAGCTACAACGA TGAGAGAC	4335
1815	UCCAUCCA G CUUGAGAG	1532	CTCTCAAG GGCTAGCTACAACGA TGGATGGA	4336
1823	GCUUGAGA G UAAGGGAU	1533	ATCCCTTA GGCTAGCTACAACGA TCTCAAGC	4337
1847	CCAGAACA G CCAGUGGA	1534	TCCACTGG GGCTAGCTACAACGA TGTTCTGG	4338
1851	AACAGCCA G UGGAUGAA	1535	TTCATCCA GGCTAGCTACAACGA TGGCTGTT	4339
1862	GAUGAAUG G CACAGUGA	1536	TCACTGTG GGCTAGCTACAACGA CATTCATC	4340
1867	AUGGCACA G UGAUCGUG	1537	CACGATCA GGCTAGCTACAACGA TGTGCCAT	4341
1873	CAGUGAUC G UGGACAGC	1538	GCTGTCCA GGCTAGCTACAACGA GATCACTG	4342
1880	CGUGGACA G CACCGUGG	1539	CCACGGTG GGCTAGCTACAACGA TGTCCACG	4343
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1926	ACAACGCA G CCUCCCCA	1541	TGGGGAGG GGCTAGCTACAACGA TGCGTTGT	4345
1955	GGAUCCCA G UGGACAGA	1542	TCTGTCCA GGCTAGCTACAACGA TGGGATCC	4346
1965	GGACAGAA G CAAGGUGG	1543	CCACCTTG GGCTAGCTACAACGA TTCTGTCC	4347
1970	GAAGCAAG G UGGCUUUG	1544	CAAAGCCA GGCTAGCTACAACGA CTTGCTTC	4348
1973	GCAAGGUG G CUUUGUAG	1545	CTACAAAG GGCTAGCTACAACGA CACCTTGC	4349
1981	GCUUUGUA G UGGACAAA	1546	TTTGTCCA GGCTAGCTACAACGA TACAAAGC	4350
2002	CCAAAAUG G CCUACCUC	1547	GAGGTAGG GGCTAGCTACAACGA CATTTTGG	4351
2021	AAUCCCAG G CAUUGCUA	1548	TAGCAATG GGCTAGCTACAACGA CTGGGATT	4352
2032	UUGCUAAG G UUGGCACU	1549	AGTGCCAA GGCTAGCTACAACGA CTTAGCAA	4353
2036	UAAGGUUG G CACUUGGA	1550	TCCAAGTG GGCTAGCTACAACGA CAACCTTA	4354
2051	GAAAUACA G UCUGCAAG	1551	CTTGCAGA GGCTAGCTACAACGA TGTATTTC	4355
2059	GUCUGCAA G CAAGCUCA	1552	TGAGCTTG GGCTAGCTACAACGA TTGCAGAC	4356
2063	GCAAGCAA G CUCACAAA	1553	TTTGTGAG GGCTAGCTACAACGA TTGCTTGC	4357
2091	ACUGUCAC G UCCCGUGC	1554	GCACGGGA GGCTAGCTACAACGA GTGACAGT	4358

2096	CACGUCCC G UGCGUCCA	1555	TGGACGCA GGCTAGCTACAACGA GGGACGTG	4359
2100	UCCCGUGC G UCCAAUGC	1556	GCATTGGA GGCTAGCTACAACGA GCACGGGA	4360
2128	CAAUUACA G UGACUUCC	1557	GGAAGTCA GGCTAGCTACAACGA TGTAATTG	4361
2156	GGACACCA G CAAAUUCC	1558	GGAATTTG GGCTAGCTACAACGA TGGTGTCC	4362
2168	AUUCCCCA G CCCUCUGG	1559	CCAGAGGG GGCTAGCTACAACGA TGGGGAAT	4363
2176	GCCCUCUG G UAGUUUAU	1560	ATAAACTA GGCTAGCTACAACGA CAGAGGGC	4364
2179	CUCUGGUA G UUUAUGCA	1561	TGCATAAA GGCTAGCTACAACGA TACCAGAG	4365
2203	GCCAAGGA G CCUCCCCA	1562	TGGGGAGG GGCTAGCTACAACGA TCCTTGGC	4366
2221	UUCUCAGG G CCAGUGUC	1563	GACACTGG GGCTAGCTACAACGA CCTGAGAA	4367
2225	CAGGGCCA G UGUCACAG	1564	CTGTGACA GGCTAGCTACAACGA TGGCCCTG	4368
2233	GUGUCACA G CCCUGAUU	1565	AATCAGGG GGCTAGCTACAACGA TGTGACAC	4369
2248	UUGAAUCA G UGAAUGGA	1566	TCCATTCA GGCTAGCTACAACGA TGATTCAA	4370
2263	GAAAAACA G UUACCUUG	1567	CAAGGTAA GGCTAGCTACAACGA TGTTTTTC	4371
2290	AUAAUGGA G CAGGUGCU	1568	AGCACCTG GGCTAGCTACAACGA TCCATTAT	4372
2294	UGGAGCAG G UGCUGAUG	1569	CATCAGCA GGCTAGCTACAACGA CTGCTCCA	4373
2318	GGAUGACG G UGUCUACU	1570	AGTAGACA GGCTAGCTACAACGA CGTCATCC	4374
2331	UACUCAAG G UAUUUCAC	1571	GTGAAATA GGCTAGCTACAACGA CTTGAGTA	4375
2357	CACGAAUG G UAGAUACA	1572	TGTATCTA GGCTAGCTACAACGA CATTCGTG	4376
2366	UAGAUACA G UGUAAAAG	1573	CTTTTACA GGCTAGCTACAACGA TGTATCTA	4377
2374	GUGUAAAA G UGCGGGCU	1574	AGCCCGCA GGCTAGCTACAACGA TTTTACAC	4378
2380	AAGUGCGG G CUCUGGGA	1575	TCCCAGAG GGCTAGCTACAACGA CCGCACTT	4379
2392	UGGGAGGA G UUAACGCA	1576	TGCGTTAA GGCTAGCTACAACGA TCCTCCCA	4380
2401	UUAACGCA G CCAGACGG	1577	CCGTCTGG GGCTAGCTACAACGA TGCGTTAA	4381
2413	GACGGAGA G UGAUACCC	1578	GGGTATCA GGCTAGCTACAACGA TCTCCGTC	4382
2424	AUACCCCA G CAGAGUGG	1579	CCACTCTG GGCTAGCTACAACGA TGGGGTAT	4383
2429	CCAGCAGA G UGGAGCAC	1580	GTGCTCCA GGCTAGCTACAACGA TCTGCTGG	4384
2434	AGAGUGGA G CACUGUAC	1581	GTACAGTG GGCTAGCTACAACGA TCCACTCT	4385
2450	CAUACCUG G CUGGAUUG	1582	CAATCCAG GGCTAGCTACAACGA CAGGTATG	4386
2523	CAACACAA G CAAGUGUG	1583	CACACTTG GGCTAGCTACAACGA TTGTGTTG	4387
2527	ACAAGCAA G UGUGUUUC	1584	GAAACACA GGCTAGCTACAACGA TTGCTTGT	4388
2537	GUGUUUCA G CAGAACAU	1585	ATGTTCTG GGCTAGCTACAACGA TGAAACAC	4389
2555	CUCGGGAG G CUCAUUUG	1586	CAAATGAG GGCTAGCTACAACGA CTCCCGAG	4390
2566	CAUUUGUG G CUUCUGAU	1587	ATCAGAAG GGCTAGCTACAACGA CACAAATG	4391
2612	CCCACCUG G CCAAAUCA	1588	TGATTTGG GGCTAGCTACAACGA CAGGTGGG	4392
2632	ACCUGAAG G CGGAAAUU	1589	AATTTCCG GGCTAGCTACAACGA CTTCAGGT	4393
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2651	CGGGGGCA G UCUCAUUA	1591	TAATGAGA GGCTAGCTACAACGA TGCCCCCG	4395
2674	CUUGGACA G CUCCUGGG	1592	CCCAGGAG GGCTAGCTACAACGA TGTCCAAG	4396
2704	AUGGAACA G CUCACAAG	1593	CTTGTGAG GGCTAGCTACAACGA TGTTCCAT	4397
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2729	UCGAAUAA G UACAAGUA	1595	TACTTGTA GGCTAGCTACAACGA TTATTCGA	4399
2735	AAGUACAA G UAUUCUUG	1596	CAAGAATA GGCTAGCTACAACGA TTGTACTT	4400
2757	AGAGACAA G UUCAAUGA	1597	TCATTGAA GGCTAGCTACAACGA TTGTCTCT	4401
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2821	CUGAGGAA G UCUUUUUG	1600	CAAAAAGA GGCTAGCTACAACGA TTCCTCAG	4404
2861	UGAAAAUG G CACAGAUC	1601	GATCTGTG GGCTAGCTACAACGA CATTTTCA	4405
2887	CUAUUCAG G CUGUUGAU	1602	ATCAACAG GGCTAGCTACAACGA CTGAATAG	4406
2899	UUGAUAAG G UCGAUCUG	1603	CAGATCGA GGCTAGCTACAACGA CTTATCAA	4407
2935	UUGCACGA G UAUCUUUG	1604	CAAAGATA GGCTAGCTACAACGA TCGTGCAA	4408
2978	GACACCUA G UCCUGAUG	1605	CATCAGGA GGCTAGCTACAACGA TAGGTGTC	4409
2991	GAUGAAAC G UCUGCUCC	1606	GGAGCAGA GGCTAGCTACAACGA GTTTCATC	4410
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3035	CAUUCCUG G CAUUCACA	1608	TGTGAATG GGCTAGCTACAACGA CAGGAATG	4412
3063	AUGUGGAA G UGGAUAGG	1609	CCTATCCA GGCTAGCTACAACGA TTCCACAT	4413
3081	GAACUGCA G CUGUCAAU	1610	ATTGACAG GGCTAGCTACAACGA TGCAGTTC	4414

3091	UGUCAAUA G CCUAGGGC	1611	GCCCTAGG GGCTAGCTACAACGA TATTGACA	4415
3098	AGCCUAGG G CUGAAUUU	1612	AAATTCAG GGCTAGCTACAACGA CCTAGGCT	4416
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3242	UGUAGGGG G CGAUAUAC	1613	GTATATCG GGCTAGCTACAACGA CCCCTACA	4417
3210	UGUAUAUA G UACAUUUA	1614	TAAATGTA GGCTAGCTACAACGA TATATACA	4418
3279	UGUAGGGG G CGAUAAAA	1615	TTTTATCG GGCTAGCTACAACGA CCCCTACA	4419
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25	ACAAAUGG A UGUGGAAU	1617	ATTCCACA GGCTAGCTACAACGA CCATTTGT	4421
32	GAUGUGGA A UAUAAUUG	1618	CAATTATA GGCTAGCTACAACGA TCCACATC	4422
37	GGAAUAUA A UUGAAUAU	1619	ATATTCAA GGCTAGCTACAACGA TATATTCC	4423
42	AUAAUUGA A UAUUUUCU	1620	AGAAAATA GGCTAGCTACAACGA TCAATTAT	4424
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224	GACCUGUG A UAAACCAC	1630	GTGGTTTA GGCTAGCTACAACGA CACAGGTC	4434
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249	AGUUGGAA A CGUGUGUC	1633	GACACACG GGCTAGCTACAACGA TTCCAACT	4437
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636	AGACCAAA A CUUGAGAC	1661	GTCTCAAG GGCTAGCTACAACGA TTTGGTCT	4465
643	AACUUGAG A CCUACAAA	1662	TTTGTAGG GGCTAGCTACAACGA CTCAAGTT	4466
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2083	UGACCCUG A CUGUCACG	1771	CGTGACAG GGCTAGCTACAACGA CAGGGTCA	4575
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2150	GAACAAGG A CACCAGCA	1777	TGCTGGTG GGCTAGCTACAACGA CCTTGTTC	4581

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2160	ACCAGCAA A UUCCCCAG	1778	CTGGGGAA GGCTAGCTACAACGA TTGCTGGT	4582
2189	UUAUGCAA A UAUUCGCC	1779	GGCGAATA GGCTAGCTACAACGA TTGCATAA	4583
2212	CCUCCCCA A UUCUCAGG	1780	CCTGAGAA GGCTAGCTACAACGA TGGGGAGG	4584
2239	CAGCCCUG A UUGAAUCA	1781	TGATTCAA GGCTAGCTACAACGA CAGGGCTG	4585
2244	CUGAUUGA A UCAGUGAA	1782	TTCACTGA GGCTAGCTACAACGA TCAATCAG	4586
2252	AUCAGUGA A UGGAAAAA	1783	TTTTTCCA GGCTAGCTACAACGA TCACTGAT	4587
2260	AUGGAAAA A CAGUUACC	1784	GGTAACTG GGCTAGCTACAACGA TTTTCCAT	4588
2274	ACCUUGGA A CUACUGGA	1785	TCCAGTAG GGCTAGCTACAACGA TCCAAGGT	4589
2282	ACUACUGG A UAAUGGAG	1786	CTCCATTA GGCTAGCTACAACGA CCAGTAGT	4590
2285	ACUGGAUA A UGGAGCAG	1787	CTGCTCCA GGCTAGCTACAACGA TATCCAGT	4591
2300	AGGUGCUG A UGCUACUA	1788	TAGTAGCA GGCTAGCTACAACGA CAGCACCT	4592
2312	UACUAAGG A UGACGGUG	1789	CACCGTCA GGCTAGCTACAACGA CCTTAGTA	4593
2315	UAAGGAUG A CGGUGUCU	1790	AGACACCG GGCTAGCTACAACGA CATCCTTA	4594
2341	AUUUCACA A CUUAUGAC	1791	GTCATAAG GGCTAGCTACAACGA TGTGAAAT	4595
2348	AACUUAUG A CACGAAUG	1792	CATTCGTG GGCTAGCTACAACGA CATAAGTT	4596
2354	UGACACGA A UGGUAGAU	1793	ATCTACCA GGCTAGCTACAACGA TCGTGTCA	4597
2361	AAUGGUAG A UACAGUGU	1794	ACACTGTA GGCTAGCTACAACGA CTACCATT	4598
2396	AGGAGUUA A CGCAGCCA	1795	TGGCTGCG GGCTAGCTACAACGA TAACTCCT	4599
2406	GCAGCCAG A CGGAGAGU	1796	ACTCTCCG GGCTAGCTACAACGA CTGGCTGC	4600
2416	GGAGAGUG A UACCCCAG	1797	CTGGGGTA GGCTAGCTACAACGA CACTCTCC	4601
2455	CUGGCUGG A UUGAGAAU	1798	ATTCTCAA GGCTAGCTACAACGA CCAGCCAG	4602
2462	GAUUGAGA A UGAUGAAA	1799	TTTCATCA GGCTAGCTACAACGA TCTCAATC	4603
2465	UGAGAAUG A UGAAAUAC	1800	GTATTTCA GGCTAGCTACAACGA CATTCTCA	4604
2470	AUGAUGAA A UACAAUGG	1801	CCATTGTA GGCTAGCTACAACGA TTCATCAT	4605
2475	GAAAUACA A UGGAAUCC	1802	GGATTCCA GGCTAGCTACAACGA TGTATTTC	4606
2480	ACAAUGGA A UCCACCAA	1803	TTGGTGGA GGCTAGCTACAACGA TCCATTGT	4607
2490	CCACCAAG A CCUGAAAU	1804	ATTTCAGG GGCTAGCTACAACGA CTTGGTGG	4608
2497	GACCUGAA A UUAAUAAG	1805	CTTATTAA GGCTAGCTACAACGA TTCAGGTC	4609
2501	UGAAAUUA A UAAGGAUG	1806	CATCCTTA GGCTAGCTACAACGA TAATTTCA	4610
2507	UAAUAAGG A UGAUGUUC	1807	GAACATCA GGCTAGCTACAACGA CCTTATTA	4611
2510	UAAGGAUG A UGUUCAAC	1808	GTTGAACA GGCTAGCTACAACGA CATCCTTA	4612
2517	GAUGUUCA A CACAAGCA	1809	TGCTTGTG GGCTAGCTACAACGA TGAACATC	4613
2542	UCAGCAGA A CAUCCUCG	1810	CGAGGATG GGCTAGCTACAACGA TCTGCTGA	4614
2573	GGCUUCUG A UGUCCCAA	1811	TTGGGACA GGCTAGCTACAACGA CAGAAGCC	4615
2582	UGUCCCAA A UGCUCCCA	1812	TGGGAGCA GGCTAGCTACAACGA TTGGGACA	4616
2597	CAUACCUG A UCUCUUCC	1813	GGAAGAGA GGCTAGCTACAACGA CAGGTATG	4617
2617	CUGGCCAA A UCACCGAC	1814	GTCGGTGA GGCTAGCTACAACGA TTGGCCAG	4618
2624	AAUCACCG A CCUGAAGG	1815	CCTTCAGG GGCTAGCTACAACGA CGGTGATT	4619
2638	AGGCGGAA A UUCACGGG	1816	CCCGTGAA GGCTAGCTACAACGA TTCCGCCT	4620
2660	UCUCAUUA A UCUGACUU	1817	AAGTCAGA GGCTAGCTACAACGA TAATGAGA	4621
2665	UUAAUCUG A CUUGGACA	1818	TGTCCAAG GGCTAGCTACAACGA CAGATTAA	4622
2671	UGACUUGG A CAGCUCCU	1819	AGGAGCTG GGCTAGCTACAACGA CCAAGTCA	4623
2684	UCCUGGGG A UGAUUAUG	1820	CATAATCA GGCTAGCTACAACGA CCCCAGGA	4624
2687	UGGGGAUG A UUAUGACC	1821	GGTCATAA GGCTAGCTACAACGA CATCCCCA	4625
2693	UGAUUAUG A CCAUGGAA	1822	TTCCATGG GGCTAGCTACAACGA CATAATCA	4626
2701	ACCAUGGA A CAGCUCAC	1823	GTGAGCTG GGCTAGCTACAACGA TCCATGGT	4627
2725	UCAUUCGA A UAAGUACA	1824	TGTACTTA GGCTAGCTACAACGA TCGAATGA	4628
2744	UAUUCUUG A UCUCAGAG	1825	CTCTGAGA GGCTAGCTACAACGA CAAGAATA	4629
2753	UCUCAGAG A CAAGUUCA	1826	TGAACTTG GGCTAGCTACAACGA CTCTGAGA	4630
2762	CAAGUUCA A UGAAUCUC	1827	GAGATTCA GGCTAGCTACAACGA TGAACTTG	4631
2766	UUCAAUGA A UCUCUUCA	1828	TGAAGAGA GGCTAGCTACAACGA TCATTGAA	4632
2780	UCAAGUGA A UACUACUG	1829	CAGTAGTA GGCTAGCTACAACGA TCACTTGA	4633
2810	GGAAGCCA A CUCUGAGG	1830	CCTCAGAG GGCTAGCTACAACGA TGGCTTCC	4634
2835	UUGUUUAA A CCAGAAAA	1831	TTTTCTGG GGCTAGCTACAACGA TTAAACAA	4635
2843	ACCAGAAA A CAUUACUU	1832	AAGTAATG GGCTAGCTACAACGA TTTCTGGT	4636
2858	UUUUGAAA A UGGCACAG	1833	CTGTGCCA GGCTAGCTACAACGA TTTCAAAA	4637

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2867	UGGCACAG A UCUUUUCA	1834	TGAAAAGA GGCTAGCTACAACGA CTGTGCCA	4638
2894	GGCUGUUG A UAAGGUCG	1835	CGACCTTA GGCTAGCTACAACGA CAACAGCC	4639
2903	UAAGGUCG A UCUGAAAU	1836	ATTTCAGA GGCTAGCTACAACGA CGACCTTA	4640
2910	GAUCUGAA A UCAGAAAU	1837	ATTTCTGA GGCTAGCTACAACGA TTCAGATC	4641
2917	AAUCAGAA A UAUCCAAC	1838	GTTGGATA GGCTAGCTACAACGA TTCTGATT	4642
2924	AAUAUCCA A CAUUGCAC	1839	GTGCAATG GGCTAGCTACAACGA TGGATATT	4643
2959	CUCCACAG A CUCCGCCA	1840	TGGCGGAG GGCTAGCTACAACGA CTGTGGAG	4644
2971	CGCCAGAG A CACCUAGU	1841	ACTAGGTG GGCTAGCTACAACGA CTCTGGCG	4645
2984	UAGUCCUG A UGAAACGU	1842	ACGTTTCA GGCTAGCTACAACGA CAGGACTA	4646
2989	CUGAUGAA A CGUCUGCU	1843	AGCAGACG GGCTAGCTACAACGA TTCATCAG	4647
3008	UUGUCCUA A UAUUCAUA	1844	TATGAATA GGCTAGCTACAACGA TAGGACAA	4648
3020	UCAUAUCA A CAGCACCA	1845	TGGTGCTG GGCTAGCTACAACGA TGATATGA	4649
3052	UUUUAAAA A UUAUGUGG	1846	CCACATAA GGCTAGCTACAACGA TTTTAAAA	4650
3067	GGAAGUGG A UAGGAGAA	1847	TTCTCCTA GGCTAGCTACAACGA CCACTTCC	4651
3075	AUAGGAGA A CUGCAGCU	1848	AGCTGCAG GGCTAGCTACAACGA TCTCCTAT	4652
3088	AGCUGUCA A UAGCCUAG	1849	CTAGGCTA GGCTAGCTACAACGA TGACAGCT	4653
3103	AGGGCUGA A UUUUUGUC	1850	GACAAAAA GGCTAGCTACAACGA TCAGCCCT	4654
3114	UUUGUCAG A UAAAUAAA	1851	TTTATTTA GGCTAGCTACAACGA CTGACAAA	4655
3118	UCAGAUAA A UAAAAUAA	1852	TTATTTTA GGCTAGCTACAACGA TTATCTGA	4656
3123	UAAAUAAA A UAAAUCAU	1853	ATGATTTA GGCTAGCTACAACGA TTTATTTA	4657
3127	UAAAAUAA A UCAUUCAU	1854	ATGAATGA GGCTAGCTACAACGA TTATTTTA	4658
3146	UUUUUUUG A UUAUAAAA	1855	TTTTATAA GGCTAGCTACAACGA CAAAAAAA	4659
3154	AUUAUAAA A UUUUCUAA	1856	TTAGAAAA GGCTAGCTACAACGA TTTATAAT	4660
3164	UUUCUAAA A UGUAUUUU	1857	AAAATACA GGCTAGCTACAACGA TTTAGAAA	4661
3175	UAUUUUAG A CUUCCUGU	1858	ACAGGAAG GGCTAGCTACAACGA CTAAAATA	4662
3265	UAUUUUAG A CUUCCUGU	1858	ACAGGAAG GGCTAGCTACAACGA CTAAAATA	4662
3192	AGGGGGCG A UAUACUAA	1859	TTAGTATA GGCTAGCTACAACGA CGCCCCCT	4663
3245	AGGGGGCG A UAUACUAA	1859	TTAGTATA GGCTAGCTACAACGA CGCCCCCT	4663
3201	UAUACUAA A UGUAUAUA	1860	TATATACA GGCTAGCTACAACGA TTAGTATA	4664
3225	UAUACUAA A UGUAUUCC	1861	GGAATACA GGCTAGCTACAACGA TTAGTATA	4665
3254	UAUACUAA A UGUAUUUU	1862	AAAATACA GGCTAGCTACAACGA TTAGTATA	4666
3282	AGGGGGCG A UAAAAUAA	1863	TTATTTTA GGCTAGCTACAACGA CGCCCCCT	4667
3287	GCGAUAAA A UAAAAUGC	1864	GCATTTTA GGCTAGCTACAACGA TTTATCGC	4668
3292	AAAAUAAA A UGCUAAAC	1865	GTTTAGCA GGCTAGCTACAACGA TTTATTTT	4669
3299	AAUGCUAA A CAACUGGG	1866	CCCAGTTG GGCTAGCTACAACGA TTAGCATT	4670
3302	GCUAAACA A CUGGGUAA	1867	TTACCCAG GGCTAGCTACAACGA TGTTTAGC	4671

Input Sequence = NM_001285. Cut Site = R/Y
Arm Length = 8. Core Sequence = GGCTAGCTACAACGA
NM_001285 (Homo sapiens chloride channel, calcium activated, 1 (CLCA1) mRNA, 3311 bp)

Table VIII: Human CLCA1 Amberzyme and Target Sequence

249.021

Pos	Substrate	Seq ID No.	Amberzyme	Rz Seq ID No.
40	AUAUAAUU G AAUAUUUU	1211	AAAAUAUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAUUAUAU	4672
67	GGGAGCAU G AAGAGGUG	1212	CACCUCUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUGCUCCC	4673
78	GAGGUGUU G AGGUUAUG	1213	CAUAACCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AACACCUC	4674
106	GCACAGCU G AAGGCAGA	1214	UCUGCCUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGCUGUGC	4675
134	ACAAGUAC G CAAUUUGA	1215	UCAAAUUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GUACUUGU	4676
141	CGCAAUUU G AGACUAAG	1216	CUUAGUCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAAUUGCG	4677
172	CUCCUAUU G AAGACAAG	1217	CUUGUCUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAUAGGAG	4678
223	AGACCUGU G AUAAACCA	1218	UGGUUUAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACAGGUCU	4679
237	CCACUUCC G AUAAGUUG	1219	CAACUUAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GGAAGUGG	4680
312	CGUAACCC G CAUUUUCC	1220	GGAAAAUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GGGUUACG	4681
384	UUCAUCUU G AUUCUUCA	1221	UGAAGAAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAGAUGAA	4682
411	GGGGCCCU G AGUAAUUC	1222	GAAUUACU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGGGCCCC	4683
432	AUUCAGCU G AACAACAA	1223	UUGUUGUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGCUGAAU	4684
448	AUGGCUAU G AAGGCAUU	1224	AAUGCCUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUAGCCAU	4685
463	UUGUCGUU G CAAUCGAC	1225	GUCGAUUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AACGACAA	4686
469	UUGCAAUC G ACCCCAAU	1226	AUUGGGGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GAUUGCAA	4687
480	CCCAAUGU G CCAGAAGA	1227	UCUUCUGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACAUUGGG	4688
490	CAGAAGAU G AAACACUC	1228	GAGUGUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCUUCUG	4689
522	GACAUGGU G ACCCAGGC	1229	GCCUGGGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACCAUGUC	4690
547	AUCUGUUU G AAGCUACA	1230	UGUAGCUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAACAGAU	4691
563	AGGAAAGC G AUUUUAUU	1231	AAUAAAAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GCUUUCCU	4692
583	AAAAUGUU G CCAUUUUG	1232	CAAAAUGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AACAUUUU	4693
591	GCCAUUUU G AUUCCUGA	1233	UCAGGAAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAAAUGGC	4694
598	UGAUUCCU G AAACAUGG	1234	CCAUGUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGGAAUCA	4695
619	CAAAGGCU G ACUAUGUG	1235	CACAUAGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGCCUUUG	4696
627	GACUAUGU G AGACCAAA	1236	UUUGGUCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACAUAGUC	4697
640	CAAAACUU G AGACCUAC	1237	GUAGGUCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAGUUUUG	4698
655	ACAAAAAU G CUGAUGUU	1238	AACAUCAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUUUUGU	4699

658	AAAAUGCU G AUGUUCUG	1239	CAGAACAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGCAUUUU	4700
670	UUCUGGUU G CUGAGUCU	1240	AGACUCAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AACCAGAA	4701
673	UGGUUGCU G AGUCUACU	1241	AGUAGACU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGCAACCA	4702
694	CAGGUAAU G AUGAACCC	1242	GGGUUCAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUACCUG	4703
697	GUAAUGAU G AACCCUAC	1243	GUAGGGUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCAUUAC	4704
709	CCUACACU G AGCAGAUG	1244	CAUCUGCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGUGUAGG	4705
739	AGAAGGGU G AAAGGAUC	1245	GAUCCUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACCCUUCU	4706
760	UCACUCCU G AUUUCAUU	1246	AAUGAAAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGGAGUGA	4707
769	AUUUCAUU G CAGGAAAA	1247	UUUUCCUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAUGAAAU	4708
787	AGUUAGCU G AAUAUGGA	1248	UCCAUAUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGCUAACU	4709
820	UUGUCCAU G AGUGGGCU	1249	AGCCCACU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUGGACAA	4710
836	UCAUCUAC G AUGGGGAG	1250	CUCCCCAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GUAGAUGA	4711
850	GAGUAUUU G ACGAGUAC	1251	GUACUCGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAAUACUC	4712
853	UAUUUGAC G AGUACAAU	1252	AUUGUACU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GUCAAAUA	4713
865	ACAAUAAU G AUGAGAAA	1253	UUUCUCAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUAUUGU	4714
868	AUAAUGAU G AGAAAUUC	1254	GAAUUUCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCAUUAU	4715
980	CAAAAGAU G CACAUUCA	1255	UGAAUGUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCUUUUG	4716
1009	GACUCUAU G AAAAAGGA	1256	UCCUUUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUAGAGUC	4717
1021	AAGGAUGU G AGUUUGUU	1257	AACAAACU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACAUCCUU	4718
1040	CCAAUCCC G CCAGACGG	1258	CCGUCUGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GGGAUUGG	4719
1069	UAAUGUUU G CACAACAU	1259	AUGUUGUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAACAUUA	4720
1081	AACAUGUU G AUUCUAUA	1260	UAUAGAAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AACAUGUU	4721
1093	CUAUAGUU G AAUUCUGU	1261	ACAGAAUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AACUAUAG	4722
1151	UCAAAAAU G CAAUCUCC	1262	GGAGAUUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUUUUGA	4723
1160	CAAUCUCC G AAGCACAU	1263	AUGUGCUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GGAGAUUG	4724
1176	UGGGAAGU G AUCCGUGA	1264	UCACGGAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACUUCCCA	4725
1183	UGAUCCGU G AUUCUGAG	1265	CUCAGAAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACGGAUCA	4726
1189	GUGAUUCU G AGGACUUU	1266	AAAGUCCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGAAUCAC	4727
1215	ACUCCUAU G ACAACACA	1267	UGUGUUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUAGGAGU	4728
1248	UUCUCAUU G CUGCAGAU	1268	AUCUGCAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAUGAGAA	4729
1251	UCAUUGCU G CAGAUUGG	1269	CCAAUCUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGCAAUGA	4730
1285	UAGUCCUU G ACAAAUCU	1270	AGAUUUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAGGACUA	4731
1305	AGCAUGGC G ACUGGUAA	1271	UUACCAGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GCCAUGCU	4732

1316	UGGUAACC G CCUCAAUC	1272	GAUUGAGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GGUUACCA	4733
1325	CCUCAAUC G ACUGAAUC	1273	GAUUCAGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GAUUGAGG	4734
1329	AAUCGACU G AAUCAAGC	1274	GCUUGAUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGUCGAUU	4735
1353	CUUUUCCU G CUGCAGAC	1275	GUCUGCAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGGAAAAG	4736
1356	UUCCUGCU G CAGACAGU	1276	ACUGUCUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGCAGGAA	4737
1366	AGACAGUU G AGCUGGGG	1277	CCCCAGCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AACUGUCU	4738
1392	GGGAUGGU G ACAUUUGA	1278	UCAAAUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACCAUCCC	4739
1399	UGACAUUU G ACAGUGCU	1279	AGCACUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAAUGUCA	4740
1405	UUGACAGU G CUGCCCAU	1280	AUGGGCAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACUGUCAA	4741
1408	ACAGUGCU G CCCAUGUA	1281	UACAUGGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGCACUGU	4742
1423	UACAAAGU G AACUCAUA	1282	UAUGAGUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACUUUGUA	4743
1450	GUGGCAGU G ACAGGGAC	1283	GUCCCUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACUGCCAC	4744
1465	ACACACUC G CCAAAAGA	1284	UCUUUUGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GAGUGUGU	4745
1480	GAUUACCU G CAGCAGCU	1285	AGCUGCUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGGUAAUC	4746
1508	GUCCAUCU G CAGCGGGC	1286	GCCCGCUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGAUGGAC	4747
1520	CGGGCUUC G AUCGGCAU	1287	AUGCCGAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GAAGCCCG	4748
1536	UUUACUGU G AUUAGGAA	1288	UUCCUAAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACAGUAAA	4749
1558	AUCCAACU G AUGGAUCU	1289	AGAUCCAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGUUGGAU	4750
1567	AUGGAUCU G AAAUUGUG	1290	CACAAUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGAUCCAU	4751
1575	GAAAUUGU G CUGCUGAC	1291	GUCAGCAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACAAUUUC	4752
1578	AUUGUGCU G CUGACGGA	1292	UCCGUCAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGCACAAU	4753
1581	GUGCUGCU G ACGGAUGG	1293	CCAUCCGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGCAGCAC	4754
1613	AAGUGGGU G CUUUAACG	1294	CGUUAAAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACCCACUU	4755
1621	GCUUUAAC G AGGUCAAA	1295	UUUGACCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GUUAAAGC	4756
1639	AAAGUGGU G CCAUCAUC	1296	GAUGAUGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACCACUUU	4757
1657	ACACAGUC G CUUUGGGG	1297	CCCCAAAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GACUGUGU	4758
1672	GGCCCUCU G CAGCUCAA	1298	UUGAGCUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGAGGGCC	4759
1704	UCCAAAAU G ACAGGAGG	1299	CCUCCUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUUUGGA	4760
1726	AGACAUAU G CUUCAGAU	1300	AUCUGAAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUAUGUCU	4761
1759	GCCUCAUU G AUGCUUUU	1301	AAAAGCAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAUGAGGC	4762
1762	UCAUUGAU G CUUUUGGG	1302	CCCAAAAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCAAUGA	4763
1805	CUCUCAGC G CUCCAUCC	1303	GGAUGGAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GCUGAGAG	4764
1819	UCCAGCUU G AGAGUAAG	1304	CUUACUCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAGCUGGA	4765

1857	CAGUGGAU G AAUGGCAC	1305	GUGCCAUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCCACUG	4766
1869	GGCACAGU G AUCGUGGA	1306	UCCACGAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACUGUGCC	4767
1923	UGGACAAC G CAGCCUCC	1307	GGAGGCUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GUUGUCCA	4768
2026	CAGGCAUU G CUAAGGUU	1308	AACCUUAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAUGCCUG	4769
2055	UACAGUCU G CAAGCAAG	1309	CUUGCUUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGACUGUA	4770
2076	CAAACCUU G ACCCUGAC	1310	GUCAGGGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAGGUUUG	4771
2082	UUGACCCU G ACUGUCAC	1311	GUGACAGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGGGUCAA	4772
2098	CGUCCCGU G CGUCCAAU	1312	AUUGGACG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACGGGACG	4773
2107	CGUCCAAU G CUACCCUG	1313	CAGGGUAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUGGACG	4774
2115	GCUACCCU G CCUCCAAU	1314	AUUGGAGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGGGUAGC	4775
2130	AUUACAGU G ACUUCCAA	1315	UUGGAAGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACUGUAAU	4776
2142	UCCAAAAC G AACAAGGA	1316	UCCUUGUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GUUUUGGA	4777
2185	UAGUUUAU G CAAAUAUU	1317	AAUAUUUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUAAACUA	4778
2195	AAAUAUUC G CCAAGGAG	1318	CUCCUUGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GAAUAUUU	4779
2238	ACAGCCCU G AUUGAAUC	1319	GAUUCAAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGGGCUGU	4780
2242	CCCUGAUU G AAUCAGUG	1320	CACUGAUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAUCAGGG	4781
2250	GAAUCAGU G AAUGGAAA	1321	UUUCCAUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACUGAUUC	4782
2296	GAGCAGGU G CUGAUGCU	1322	AGCAUCAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACCUGCUC	4783
2299	CAGGUGCU G AUGCUACU	1323	AGUAGCAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGCACCUG	4784
2302	GUGCUGAU G CUACUAAG	1324	CUUAGUAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCAGCAC	4785
2314	CUAAGGAU G ACGGUGUC	1325	GACACCGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCCUUAG	4786
2347	CAACUUAU G ACACGAAU	1326	AUUCGUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUAAGUUG	4787
2352	UAUGACAC G AAUGGUAG	1327	CUACCAUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GUGUCAUA	4788
2376	GUAAAAGU G CGGGCUCU	1328	AGAGCCCG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACUUUUAC	4789
2398	GAGUUAAC G CAGCCAGA	1329	UCUGGCUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GUUAACUC	4790
2415	CGGAGAGU G AUACCCCA	1330	UGGGGUAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACUCUCCG	4791
2458	GCUGGAUU G AGAAUGAU	1331	AUCAUUCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAUCCAGC	4792
2464	UUGAGAAU G AUGAAAUA	1332	UAUUUCAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUCUCAA	4793
2467	AGAAUGAU G AAAUACAA	1333	UUGUAUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCAUUCU	4794
2494	CAAGACCU G AAAUUAAU	1334	AUUAAUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGGUCUUG	4795
2509	AUAAGGAU G AUGUUCAA	1335	UUGAACAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCCUUAU	4796
2572	UGGCUUCU G AUGUCCCA	1336	UGGGACAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGAAGCCA	4797
2584	UCCCAAAU G CUCCCAUA	1337	UAUGGGAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUUGGGA	4798

2596	CCAUACCU G AUCUCUUC	1338	GAAGAGAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGGUAUGG	4799
2623	AAAUCACC G ACCUGAAG	1339	CUUCAGGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GGUGAUUU	4800
2628	ACCGACCU G AAGGCGGA	1340	UCCGCCUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGGUCGGU	4801
2664	AUUAAUCU G ACUUGGAC	1341	GUCCAAGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGAUUAAU	4802
2686	CUGGGGAU G AUUAUGAC	1342	GUCAUAAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCCCCAG	4803
2692	AUGAUUAU G ACCAUGGA	1343	UCCAUGGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUAAUCAU	4804
2723	UAUCAUUC G AAUAAGUA	1344	UACUUAUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GAAUGAUA	4805
2743	GUAUUCUU G AUCUCAGA	1345	UCUGAGAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAGAAUAC	4806
2764	AGUUCAAU G AAUCUCUU	1346	AAGAGAUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUGAACU	4807
2778	CUUCAAGU G AAUACUAC	1347	GUAGUAUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACUUGAAG	4808
2788	AUACUACU G CUCUCAUC	1348	GAUGAGAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGUAGUAU	4809
2815	CCAACUCU G AGGAAGUC	1349	GACUUCCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGAGUUGG	4810
2854	UUACUUUU G AAAAUGGC	1350	GCCAUUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAAAGUAA	4811
2878	UUUUCAUU G CUAUUCAG	1351	CUGAAUAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAUGAAAA	4812
2893	AGGCUGUU G AUAAGGUC	1352	GACCUUAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AACAGCCU	4813
2902	AUAAGGUC G AUCUGAAA	1353	UUUCAGAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GACCUUAU	4814
2907	GUCGAUCU G AAAUCAGA	1354	UCUGAUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGAUCGAC	4815
2929	CCAACAUU G CACGAGUA	1355	UACUCGUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAUGUUGG	4816
2933	CAUUGCAC G AGUAUCUU	1356	AAGAUACU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GUGCAAUG	4817
2964	CAGACUCC G CCAGAGAC	1357	GUCUCUGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GGAGUCUG	4818
2983	CUAGUCCU G AUGAAACG	1358	CGUUUCAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGGACUAG	4819
2986	GUCCUGAU G AAACGUCU	1359	AGACGUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCAGGAC	4820
2995	AAACGUCU G CUCCUUGU	1360	ACAAGGAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGACGUUU	4821
3078	GGAGAACU G CAGCUGUC	1361	GACAGCUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGUUCUCC	4822
3101	CUAGGGCU G AAUUUUUG	1362	CAAAAAUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGCCCUAG	4823
3145	CUUUUUUU G AUUAUAAA	1363	UUUAUAAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAAAAAAG	4824
3191	UAGGGGGC G AUAUACUA	1364	UAGUAUAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GCCCCCUA	4825
3244	UAGGGGGC G AUAUACUA	1364	UAGUAUAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GCCCCCUA	4825
3281	UAGGGGGC G AUAAAAUA	1365	UAUUUUAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GCCCCCUA	4826
3294	AAUAAAAU G CUAAACAA	1366	UUGUUUAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUUUAUU	4827
27	AAAUGGAU G UGGAAUAU	1367	AUAUUCCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCCAUUU	4828
52	AUUUUCUU G UUUAAGGG	1368	CCCUUAAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAGAAAAU	4829
75	GAAGAGGU G UUGAGGUU	1369	AACCUCAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACCUCUUC	4830

86	GAGGUUAU G UCAAGCAU	1370	AUGCUUGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUAACCUC	4831
155	AAGAUAUU G UUAUCAUU	1371	AAUGAUAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAUAUCUU	4832
221	AAAGACCU G UGAUAAAC	1372	GUUUAUCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGGUCUUU	4833
253	GGAAACGU G UGUCUAUA	1373	UAUAGACA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACGUUUCC	4834
255	AAACGUGU G UCUAUAUU	1374	AAUAUAGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACACGUUU	4835
273	UCAUAUCU G UAUAUAUA	1375	UAUAUAUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGAUAUGA	4836
344	AGGGAGAU G UACAGCAA	1376	UUGCUGUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCUCCCU	4837
373	AGAGUUCU G UGUUCAUC	1377	GAUGAACA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGAACUCU	4838
375	AGUUCUGU G UUCAUCUU	1378	AAGAUGAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACAGAACU	4839
457	AAGGCAUU G UCGUUGCA	1379	UGCAACGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAUGCCUU	4840
478	ACCCCAAU G UGCCAGAA	1380	UUCUGGCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUGGGGU	4841
537	GCAUCUCU G UAUCUGUU	1381	AACAGAUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGAGAUGC	4842
543	CUGUAUCU G UUUGAAGC	1382	GCUUCAAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGAUACAG	4843
580	UCAAAAAU G UUGCCAUU	1383	AAUGGCAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUUUUGA	4844
625	CUGACUAU G UGAGACCA	1384	UGGUCUCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUAGUCAG	4845
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725	GGGCAACU G UGGAGAGA	1386	UCUCUCCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGUUGCCC	4847
814	AGGCAUUU G UCCAUGAG	1387	CUCAUGGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAAUGCCU	4848
911	AGUAAGAU G UUCAGCAG	1388	CUGCUGAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCUUACU	4849
937	GUACAAAU G UAGUAAAG	1389	CUUUACUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUUGUAC	4850
950	AAAGAAGU G UCAGGGAG	1390	CUCCCUGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACUUCUUU	4851
965	AGGCAGCU G UUACACCA	1391	UGGUGUAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGCUGCCU	4852
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1027	GUGAGUUU G UUCUCCAA	1393	UUGGAGAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAACUCAC	4854
1065	UCUAUAAU G UUUGCACA	1394	UGUGCAAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUAUAGA	4855
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1100	UGAAUUCU G UACAGAAC	1396	GUUCUGUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGAAUUCA	4857
1270	AAAGAAUU G UGUGUUUA	1397	UAAACACA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAUUCUUU	4858
1272	AGAAUUGU G UGUUUAGU	1398	ACUAAACA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACAAUUCU	4859
1274	AAUUGUGU G UUUAGUCC	1399	GGACUAAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACACAAUU	4860
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1534	CAUUUACU G UGAUUAGG	1401	CCUAAUCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGUAAAUG	4862
1573	CUGAAAUU G UGCUGCUG	1402	CAGCAGCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAUUUCAG	4863

1695	GAGGAGCU G UCCAAAAU	1403	AUUUUGGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGCUCCUC	4864
1795	AUGGAGCU G UCUCUCAG	1404	CUGAGAGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGCUCCAU	4865
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1978	GUGGCUUU G UAGUGGAC	1406	GUCCACUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAAGCCAC	4867
2086	CCCUGACU G UCACGUCC	1407	GGACGUGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGUCAGGG	4868
2227	GGGCCAGU G UCACAGCC	1408	GGCUGUGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACUGGCCC	4869
2320	AUGACGGU G UCUACUCA	1409	UGAGUAGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACCGUCAU	4870
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2439	GGAGCACU G UACAUACC	1411	GGUAUGUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGUGCUCC	4872
2512	AGGAUGAU G UUCAACAC	1412	GUGUUGAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCAUCCU	4873
2529	AAGCAAGU G UGUUUCAG	1413	CUGAAACA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACUUGCUU	4874
2531	GCAAGUGU G UUUCAGCA	1414	UGCUGAAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACACUUGC	4875
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2575	CUUCUGAU G UCCCAAAU	1416	AUUUGGGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCAGAAG	4877
2829	GUCUUUUU G UUUAAACC	1417	GGUUUAAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAAAAGAC	4878
2890	UUCAGGCU G UUGAUAAG	1418	CUUAUCAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGCCUGAA	4879
2943	GUAUCUUU G UUUAUUCC	1419	GGAAUAAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAAGAUAC	4880
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3057	AAAAUUAU G UGGAAGUG	1421	CACUUCCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUAAUUUU	4882
3084	CUGCAGCU G UCAAUAGC	1422	GCUAUUGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGCUGCAG	4883
3109	GAAUUUUU G UCAGAUAA	1423	UUAUCUGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAAAAUUC	4884
3166	UCUAAAAU G UAUUUUAG	1424	CUAAAAUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUUUAGA	4885
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3272	GACUUCCU G UAGGGGGC	1425	GCCCCCUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGGAAGUC	4886
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3227	UACUAAAU G UAUUCCUG	1427	CAGGAAUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUUAGUA	4888
3235	GUAUUCCU G UAGGGGGC	1428	GCCCCCUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGGAAUAC	4889
3256	UACUAAAU G UAUUUUAG	1429	CUAAAAUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUUAGUA	4890
15	UGCUUUUG G UACAAAUG	1430	CAUUUGUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAAAAGCA	4891
63	UAAGGGGA G CAUGAAGA	1431	UCUUCAUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCCCCUUA	4892
73	AUGAAGAG G UGUUGAGG	1432	CCUCAACA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUCUUCAU	4893
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91	UAUGUCAA G CAUCUGGC	1434	GCCAGAUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUGACAUA	4895

98	AGCAUCUG G CACAGCUG	1435	CAGCUGUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAGAUGCU	4896
103	CUGGCACA G CUGAAGGC	1436	GCCUUCAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUGCCAG	4897
110	AGCUGAAG G CAGAUGGA	1437	UCCAUCUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUCAGCU	4898
130	AUUUACAA G UACGCAAU	1438	AUUGCGUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUGUAAAU	4899
182	AGACAAGA G CAAUAGUA	1439	UACUAUUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCUUGUCU	4900
188	GAGCAAUA G UAAAACAC	1440	GUGUUUUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UAUUGCUC	4901
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210	GUCAGGGG G UUAAAGAC	1442	GUCUUUAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCCCUGAC	4903
242	UCCGAUAA G UUGGAAAC	1443	GUUUCCAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUAUCGGA	4904
251	UUGGAAAC G UGUGUCUA	1444	UAGACACA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GUUUCCAA	4905
287	AUAUAAUG G UAAAGAAA	1445	UUUCUUUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUUAUAU	4906
305	ACACCUUC G UAACCCGC	1446	GCGGGUUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GAAGGUGU	4907
349	GAUGUACA G CAAUGGGG	1447	CCCCAUUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUACAUC	4908
357	GCAAUGGG G CCAUUUAA	1448	UUAAAUGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCCAUUGC	4909
368	AUUUAAGA G UUCUGUGU	1449	ACACAGAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCUUAAAU	4910
406	UAGAAGGG G CCCUGAGU	1450	ACUCAGGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCCUUCUA	4911
413	GGCCCUGA G UAAUUCAC	1451	GUGAAUUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCAGGGCC	4912
429	CUCAUUCA G CUGAACAA	1452	UUGUUCAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGAAUGAG	4913
443	CAACAAUG G CUAUGAAG	1453	CUUCAUAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUUGUUG	4914
452	CUAUGAAG G CAUUGUCG	1454	CGACAAUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUCAUAG	4915
460	GCAUUGUC G UUGCAAUC	1455	GAUUGCAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GACAAUGC	4916
520	AGGACAUG G UGACCCAG	1456	CUGGGUCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUGUCCU	4917
529	UGACCCAG G CAUCUCUG	1457	CAGAGAUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUGGGUCA	4918
550	UGUUUGAA G CUACAGGA	1458	UCCUGUAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCAAACA	4919
561	ACAGGAAA G CGAUUUUA	1459	UAAAAUCG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUUCCUGU	4920
616	AGACAAAG G CUGACUAU	1460	AUAGUCAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUUGUCU	4921
667	AUGUUCUG G UUGCUGAG	1461	CUCAGCAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAGAACAU	4922
675	GUUGCUGA G UCUACUCC	1462	GGAGUAGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCAGCAAC	4923
689	UCCUCCAG G UAAUGAUG	1463	CAUCAUUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUGGAGGA	4924
711	UACACUGA G CAGAUGGG	1464	CCCAUCUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCAGUGUA	4925
719	GCAGAUGG G CAACUGUG	1465	CACAGUUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCAUCUGC	4926
737	AGAGAAGG G UGAAAGGA	1466	UCCUUUCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCUUCUCU	4927
780	GGAAAAAA G UUAGCUGA	1467	UCAGCUAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUUUUUCC	4928

784	AAAAGUUA G CUGAAUAU	1468	AUAUUCAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UAACUUUU	4929
803	ACCACAAG G UAAGGCAU	1469	AUGCCUUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUGUGGU	4930
808	AAGGUAAG G CAUUUGUC	1470	GACAAAUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUACCUU	4931
822	GUCCAUGA G UGGGCUCA	1471	UGAGCCCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCAUGGAC	4932
826	AUGAGUGG G CUCAUCUA	1472	UAGAUGAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCACUCAU	4933
844	GAUGGGGA G UAUUUGAC	1473	GUCAAAUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCCCCAUC	4934
855	UUUGACGA G UACAAUAA	1474	UUAUUGUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCGUCAAA	4935
901	GAAUACAA G CAGUAAGA	1475	UCUUACUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUGUAUUC	4936
904	UACAAGCA G UAAGAUGU	1476	ACAUCUUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGCUUGUA	4937
916	GAUGUUCA G CAGGUAUU	1477	AAUACCUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGAACAUC	4938
920	UUCAGCAG G UAUUACUG	1478	CAGUAAUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUGCUGAA	4939
929	UAUUACUG G UACAAAUG	1479	CAUUUGUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAGUAAUA	4940
940	CAAAUGUA G UAAAGAAG	1480	CUUCUUUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UACAUUUG	4941
948	GUAAAGAA G UGUCAGGG	1481	CCCUGACA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCUUUAC	4942
959	UCAGGGAG G CAGCUGUU	1482	AACAGCUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUCCCUGA	4943
962	GGGAGGCA G CUGUUACA	1483	UGUAACAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGCCUCCC	4944
994	UCAAUAAA G UUACAGGA	1484	UCCUGUAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUUAUUGA	4945
1023	GGAUGUGA G UUUGUUCU	1485	AGAACAAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCACAUCC	4946
1054	CGGAGAAG G CUUCUAUA	1486	UAUAGAAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUCUCCG	4947
1090	AUUCUAUA G UUGAAUUC	1487	GAAUUCAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UAUAGAAU	4948
1126	ACAAAGAA G CUCCAAAC	1488	GUUUGGAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCUUUGU	4949
1137	CCAAACAA G CAAAAUCA	1489	UGAUUUUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUGUUUGG	4950
1163	UCUCCGAA G CACAUGGG	1490	CCCAUGUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCGGAGA	4951
1174	CAUGGGAA G UGAUCCGU	1491	ACGGAUCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCCCAUG	4952
1181	AGUGAUCC G UGAUUCUG	1492	CAGAAUCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GGAUCACU	4953
1224	ACAACACA G CCACCAAA	1493	UUUGGUGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUGUUGU	4954
1279	UGUGUUUA G UCCUUGAC	1494	GUCAAGGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UAAACACA	4955
1298	AUCUGGAA G CAUGGCGA	1495	UCGCCAUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCCAGAU	4956
1303	GAAGCAUG G CGACUGGU	1496	ACCAGUCG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUGCUUC	4957
1310	GGCGACUG G UAACCGCC	1497	GGCGGUUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAGUCGCC	4958
1336	UGAAUCAA G CAGGCCAG	1498	CUGGCCUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUGAUUCA	4959
1340	UCAAGCAG G CCAGCUUU	1499	AAAGCUGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUGCUUGA	4960
1344	GCAGGCCA G CUUUUCCU	1500	AGGAAAAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGGCCUGC	4961

1363	UGCAGACA G UUGAGCUG	1501	CAGCUCAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUCUGCA	4962
1368	ACAGUUGA G CUGGGGUC	1502	GACCCCAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCAACUGU	4963
1374	GAGCUGGG G UCCUGGGU	1503	ACCCAGGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCCAGCUC	4964
1381	GGUCCUGG G UUGGGAUG	1504	CAUCCCAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCAGGACC	4965
1390	UUGGGAUG G UGACAUUU	1505	AAAUGUCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUCCCAA	4966
1403	AUUUGACA G UGCUGCCC	1506	GGGCAGCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUCAAAU	4967
1421	UGUACAAA G UGAACUCA	1507	UGAGUUCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUUGUACA	4968
1442	GAUAAACA G UGGCAGUG	1508	CACUGCCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUUUAUC	4969
1445	AAACAGUG G CAGUGACA	1509	UGUCACUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CACUGUUU	4970
1448	CAGUGGCA G UGACAGGG	1510	CCCUGUCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGCCACUG	4971
1483	UACCUGCA G CAGCUUCA	1511	UGAAGCUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGCAGGUA	4972
1486	CUGCAGCA G CUUCAGGA	1512	UCCUGAAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGCUGCAG	4973
1500	GGAGGGAC G UCCAUCUG	1513	CAGAUGGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GUCCCUCC	4974
1511	CAUCUGCA G CGGGCUUC	1514	GAAGCCCG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGCAGAUG	4975
1515	UGCAGCGG G CUUCGAUC	1515	GAUCGAAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCGCUGCA	4976
1525	UUCGAUCG G CAUUUACU	1516	AGUAAAUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CGAUCGAA	4977
1607	CACUAUAA G UGGGUGCU	1517	AGCACCCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUAUAGUG	4978
1611	AUAAGUGG G UGCUUUAA	1518	UUAAAGCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCACUUAU	4979
1624	UUAACGAG G UCAAACAA	1519	UUGUUUGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUCGUUAA	4980
1634	CAAACAAA G UGGUGCCA	1520	UGGCACCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUUGUUUG	4981
1637	ACAAAGUG G UGCCAUCA	1521	UGAUGGCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CACUUUGU	4982
1654	UCCACACA G UCGCUUUG	1522	CAAAGCGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUGUGGA	4983
1665	GCUUUGGG G CCCUCUGC	1523	GCAGAGGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCCAAAGC	4984
1675	CCUCUGCA G CUCAAGAA	1524	UUCUUGAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGCAGAGG	4985
1692	CUAGAGGA G CUGUCCAA	1525	UUGGACAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCCUCUAG	4986
1712	GACAGGAG G UUUACAGA	1526	UCUGUAAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUCCUGUC	4987
1738	CAGAUCAA G UUCAGAAC	1527	GUUCUGAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUGAUCUG	4988
1751	GAACAAUG G CCUCAUUG	1528	CAAUGAGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUUGUUC	4989
1771	CUUUUGGG G CCCUUUCA	1529	UGAAAGGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCCAAAAG	4990
1792	GAAAUGGA G CUGUCUCU	1530	AGAGACAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCCAUUUC	4991
1803	GUCUCUCA G CGCUCCAU	1531	AUGGAGCG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGAGAGAC	4992
1815	UCCAUCCA G CUUGAGAG	1532	CUCUCAAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGGAUGGA	4993
1823	GCUUGAGA G UAAGGGAU	1533	AUCCCUUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCUCAAGC	4994

1847	CCAGAACA G CCAGUGGA	1534	UCCACUGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUUCUGG	4995
1851	AACAGCCA G UGGAUGAA	1535	UUCAUCCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGGCUGUU	4996
1862	GAUGAAUG G CACAGUGA	1536	UCACUGUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUUCAUC	4997
1867	AUGGCACA G UGAUCGUG	1537	CACGAUCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUGCCAU	4998
1873	CAGUGAUC G UGGACAGC	1538	GCUGUCCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GAUCACUG	4999
1880	CGUGGACA G CACCGUGG	1539	CCACGGUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUCCACG	5000
1885	ACAGCACC G UGGGAAAG	1540	CUUUCCCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GGUGCUGU	5001
1926	ACAACGCA G CCUCCCCA	1541	UGGGGAGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGCGUUGU	5002
1955	GGAUCCCA G UGGACAGA	1542	UCUGUCCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGGGAUCC	5003
1965	GGACAGAA G CAAGGUGG	1543	CCACCUUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCUGUCC	5004
1970	GAAGCAAG G UGGCUUUG	1544	CAAAGCCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUGCUUC	5005
1973	GCAAGGUG G CUUUGUAG	1545	CUACAAAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CACCUUGC	5006
1981	GCUUUGUA G UGGACAAA	1546	UUUGUCCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UACAAAGC	5007
2002	CCAAAAUG G CCUACCUC	1547	GAGGUAGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUUUUGG	5008
2021	AAUCCCAG G CAUUGCUA	1548	UAGCAAUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUGGGAUU	5009
2032	UUGCUAAG G UUGGCACU	1549	AGUGCCAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUAGCAA	5010
2036	UAAGGUUG G CACUUGGA	1550	UCCAAGUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAACCUUA	5011
2051	GAAAUACA G UCUGCAAG	1551	CUUGCAGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUAUUUC	5012
2059	GUCUGCAA G CAAGCUCA	1552	UGAGCUUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUGCAGAC	5013
2063	GCAAGCAA G CUCACAAA	1553	UUUGUGAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUGCUUGC	5014
2091	ACUGUCAC G UCCCGUGC	1554	GCACGGGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GUGACAGU	5015
2096	CACGUCCC G UGCGUCCA	1555	UGGACGCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GGGACGUG	5016
2100	UCCCGUGC G UCCAAUGC	1556	GCAUUGGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GCACGGGA	5017
2128	CAAUUACA G UGACUUCC	1557	GGAAGUCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUAAUUG	5018
2156	GGACACCA G CAAAUUCC	1558	GGAAUUUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGGUGUCC	5019
2168	AUUCCCCA G CCCUCUGG	1559	CCAGAGGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGGGGAAU	5020
2176	GCCCUCUG G UAGUUUAU	1560	AUAAACUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAGAGGGC	5021
2179	CUCUGGUA G UUUAUGCA	1561	UGCAUAAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UACCAGAG	5022
2203	GCCAAGGA G CCUCCCCA	1562	UGGGGAGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCCUUGGC	5023
2221	UUCUCAGG G CCAGUGUC	1563	GACACUGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCUGAGAA	5024
2225	CAGGGCCA G UGUCACAG	1564	CUGUGACA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGGCCCUG	5025
2233	GUGUCACA G CCCUGAUU	1565	AAUCAGGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUGACAC	5026
2248	UUGAAUCA G UGAAUGGA	1566	UCCAUUCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGAUUCAA	5027

2263	GAAAAACA G UUACCUUG	1567	CAAGGUAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUUUUUC	5028
2290	AUAAUGGA G CAGGUGCU	1568	AGCACCUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCCAUUAU	5029
2294	UGGAGCAG G UGCUGAUG	1569	CAUCAGCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUGCUCCA	5030
2318	GGAUGACG G UGUCUACU	1570	AGUAGACA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CGUCAUCC	5031
2331	UACUCAAG G UAUUUCAC	1571	GUGAAAUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUGAGUA	5032
2357	CACGAAUG G UAGAUACA	1572	UGUAUCUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUUCGUG	5033
2366	UAGAUACA G UGUAAAAG	1573	CUUUUACA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUAUCUA	5034
2374	GUGUAAAA G UGCGGGCU	1574	AGCCCGCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUUUACAC	5035
2380	AAGUGCGG G CUCUGGGA	1575	UCCCAGAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCGCACUU	5036
2392	UGGGAGGA G UUAACGCA	1576	UGCGUUAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCCUCCCA	5037
2401	UUAACGCA G CCAGACGG	1577	CCGUCUGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGCGUUAA	5038
2413	GACGGAGA G UGAUACCC	1578	GGGUAUCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCUCCGUC	5039
2424	AUACCCCA G CAGAGUGG	1579	CCACUCUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGGGGUAU	5040
2429	CCAGCAGA G UGGAGCAC	1580	GUGCUCCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCUGCUGG	5041
2434	AGAGUGGA G CACUGUAC	1581	GUACAGUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCCACUCU	5042
2450	CAUACCUG G CUGGAUUG	1582	CAAUCCAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAGGUAUG	5043
2523	CAACACAA G CAAGUGUG	1583	CACACUUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUGUGUUG	5044
2527	ACAAGCAA G UGUGUUUC	1584	GAAACACA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUGCUUGU	5045
2537	GUGUUUCA G CAGAACAU	1585	AUGUUCUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGAAACAC	5046
2555	CUCGGGAG G CUCAUUUG	1586	CAAAUGAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUCCCGAG	5047
2566	CAUUUGUG G CUUCUGAU	1587	AUCAGAAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CACAAAUG	5048
2612	CCCACCUG G CCAAAUCA	1588	UGAUUUGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAGGUGGG	5049
2632	ACCUGAAG G CGGAAAUU	1589	AAUUUCCG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUCAGGU	5050
2648	UCACGGGG G CAGUCUCA	1590	UGAGACUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCCCGUGA	5051
2651	CGGGGGCA G UCUCAUUA	1591	UAAUGAGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGCCCCCG	5052
2674	CUUGGACA G CUCCUGGG	1592	CCCAGGAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUCCAAG	5053
2704	AUGGAACA G CUCACAAG	1593	CUUGUGAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUUCCAU	5054
2712	GCUCACAA G UAUAUCAU	1594	AUGAUAUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUGUGAGC	5055
2729	UCGAAUAA G UACAAGUA	1595	UACUUGUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUAUUCGA	5056
2735	AAGUACAA G UAUUCUUG	1596	CAAGAAUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUGUACUU	5057
2757	AGAGACAA G UUCAAUGA	1597	UCAUUGAA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUGUCUCU	5058
2776	CUCUUCAA G UGAAUACU	1598	AGUAUUCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUGAAGAG	5059
2806	CAAAGGAA G CCAACUCU	1599	AGAGUUGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCCUUUG	5060

2821	CUGAGGAA G UCUUUUUG	1600	CAAAAAGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCCUCAG	5061
2861	UGAAAAUG G CACAGAUC	1601	GAUCUGUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUUUUCA	5062
2887	CUAUUCAG G CUGUUGAU	1602	AUCAACAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUGAAUAG	5063
2899	UUGAUAAG G UCGAUCUG	1603	CAGAUCGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUAUCAA	5064
2935	UUGCACGA G UAUCUUUG	1604	CAAAGAUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCGUGCAA	5065
2978	GACACCUA G UCCUGAUG	1605	CAUCAGGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UAGGUGUC	5066
2991	GAUGAAAC G UCUGCUCC	1606	GGAGCAGA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GUUUCAUC	5067
3023	UAUCAACA G CACCAUUC	1607	GAAUGGUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUUGAUA	5068
3035	CAUUCCUG G CAUUCACA	1608	UGUGAAUG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAGGAAUG	5069
3063	AUGUGGAA G UGGAUAGG	1609	CCUAUCCA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCCACAU	5070
3081	GAACUGCA G CUGUCAAU	1610	AUUGACAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGCAGUUC	5071
3091	UGUCAAUA G CCUAGGGC	1611	GCCCUAGG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UAUUGACA	5072
3098	AGCCUAGG G CUGAAUUU	1612	AAAUUCAG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCUAGGCU	5073
3189	UGUAGGGG G CGAUAUAC	1613	GUAUAUCG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCCCUACA	5074
3242	UGUAGGGG G CGAUAUAC	1613	GUAUAUCG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCCCUACA	5074
3210	UGUAUAUA G UACAUUUA	1614	UAAAUGUA GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UAUAUACA	5075
3279	UGUAGGGG G CGAUAAAA	1615	UUUUAUCG GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCCCUACA	5076
14	AUGCUUUU G GUACAAAU	1868	AUUUGUAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAAAGCAU	5077
23	GUACAAAU G GAUGUGGA	1869	UCCACAUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUUGUAC	5078
24	UACAAAUG G AUGUGGAA	1870	UUCCACAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUUUGUA	5079
29	AUGGAUGU G GAAUAUAA	1871	UUAUAUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACAUCCAU	5080
30	UGGAUGUG G AAUAUAAU	1872	AUUAUAUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CACAUCCA	5081
58	UUGUUUAA G GGGAGCAU	1873	AUGCUCCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUAAACAA	5082
59	UGUUUAAG G GGAGCAUG	1874	CAUGCUCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUAAACA	5083
60	GUUUAAGG G GAGCAUGA	1875	UCAUGCUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCUUAAAC	5084
61	UUUAAGGG G AGCAUGAA	1876	UUCAUGCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCCUUAAA	5085
70	AGCAUGAA G AGGUGUUG	1877	CAACACCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCAUGCU	5086
72	CAUGAAGA G GUGUUGAG	1878	CUCAACAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCUUCAUG	5087
80	GGUGUUGA G GUUAUGUC	1879	GACAUAAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCAACACC	5088
97	AAGCAUCU G GCACAGCU	1880	AGCUGUGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGAUGCUU	5089
109	CAGCUGAA G GCAGAUGG	1881	CCAUCUGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCAGCUG	5090
113	UGAAGGCA G AUGGAAAU	1882	AUUUCCAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGCCUUCA	5091
116	AGGCAGAU G GAAAUAUU	1883	AAUAUUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCUGCCU	5092

117	GGCAGAUG G AAAUAUUU	1884	AAAUAUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUCUGCC	5093
143	CAAUUUGA G ACUAAGAU	1885	AUCUUAGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCAAAUUG	5094
149	GAGACUAA G AUAUUGUU	1886	AACAAUAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUAGUCUC	5095
175	CUAUUGAA G ACAAGAGC	1887	GCUCUUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCAAUAG	5096
180	GAAGACAA G AGCAAUAG	1888	CUAUUGCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUGUCUUC	5097
201	ACACAUCA G GUCAGGGG	1889	CCCCUGAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGAUGUGU	5098
206	UCAGGUCA G GGGGUUAA	1890	UUAACCCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGACCUGA	5099
207	CAGGUCAG G GGGUUAAA	1891	UUUAACCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUGACCUG	5100
208	AGGUCAGG G GGUUAAAG	1892	CUUUAACC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCUGACCU	5101
209	GGUCAGGG G GUUAAAGA	1893	UCUUUAAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCCUGACC	5102
216	GGGUUAAA G ACCUGUGA	1894	UCACAGGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUUAACCC	5103
245	GAUAAGUU G GAAACGUG	1895	CACGUUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AACUUAUC	5104
246	AUAAGUUG G AAACGUGU	1896	ACACGUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAACUUAU	5105
286	UAUAUAAU G GUAAAGAA	1897	UUCUUUAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUAUAUA	5106
292	AUGGUAAA G AAAGACAC	1898	GUGUCUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUUACCAU	5107
296	UAAAGAAA G ACACCUUC	1899	GAAGGUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUUCUUUA	5108
324	UUUCCAAA G AGAGGAAU	1900	AUUCCUCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUUGGAAA	5109
326	UCCAAAGA G AGGAAUCA	1901	UGAUUCCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCUUUGGA	5110
328	CAAAGAGA G GAAUCACA	1902	UGUGAUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCUCUUUG	5111
329	AAAGAGAG G AAUCACAG	1903	CUGUGAUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUCUCUUU	5112
337	GAAUCACA G GGAGAUGU	1904	ACAUCUCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUGAUUC	5113
338	AAUCACAG G GAGAUGUA	1905	UACAUCUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUGUGAUU	5114
339	AUCACAGG G AGAUGUAC	1906	GUACAUCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCUGUGAU	5115
341	CACAGGGA G AUGUACAG	1907	CUGUACAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCCCUGUG	5116
354	ACAGCAAU G GGGCCAUU	1908	AAUGGCCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUGCUGU	5117
355	CAGCAAUG G GGCCAUUU	1909	AAAUGGCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUUGCUG	5118
356	AGCAAUGG G GCCAUUUA	1910	UAAAUGGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCAUUGCU	5119
366	CCAUUUAA G AGUUCUGU	1911	ACAGAACU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUAAAUGG	5120
400	ACCUUCUA G AAGGGGCC	1912	GGCCCCUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UAGAAGGU	5121
403	UUCUAGAA G GGGCCCUG	1913	CAGGGCCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCUAGAA	5122
404	UCUAGAAG G GGCCCUGA	1914	UCAGGGCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUCUAGA	5123
405	CUAGAAGG G GCCCUGAG	1915	CUCAGGGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCUUCUAG	5124
442	ACAACAAU G GCUAUGAA	1916	UUCAUAGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUGUUGU	5125

451	GCUAUGAA G GCAUUGUC	1917	GACAAUGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCAUAGC	5126
484	AUGUGCCA G AAGAUGAA	1918	UUCAUCUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGGCACAU	5127
487	UGCCAGAA G AUGAAACA	1919	UGUUUCAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCUGGCA	5128
513	CAAAUAAA G GACAUGGU	1920	ACCAUGUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUUAUUUG	5129
514	AAAUAAAG G ACAUGGUG	1921	CACCAUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUUAUUU	5130
519	AAGGACAU G GUGACCCA	1922	UGGGUCAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUGUCCUU	5131
528	GUGACCCA G GCAUCUCU	1923	AGAGAUGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGGGUCAC	5132
556	AAGCUACA G GAAAGCGA	1924	UCGCUUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUAGCUU	5133
557	AGCUACAG G AAAGCGAU	1925	AUCGCUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUGUAGCU	5134
605	UGAAACAU G GAAGACAA	1926	UUGUCUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUGUUUCA	5135
606	GAAACAUG G AAGACAAA	1927	UUUGUCUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUGUUUC	5136
609	ACAUGGAA G ACAAAGGC	1928	GCCUUUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCCAUGU	5137
615	AAGACAAA G GCUGACUA	1929	UAGUCAGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUUGUCUU	5138
629	CUAUGUGA G ACCAAAAC	1930	GUUUUGGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCACAUAG	5139
642	AAACUUGA G ACCUACAA	1931	UUGUAGGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCAAGUUU	5140
666	GAUGUUCU G GUUGCUGA	1932	UCAGCAAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGAACAUC	5141
688	CUCCUCCA G GUAAUGAU	1933	AUCAUUAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGGAGGAG	5142
714	ACUGAGCA G AUGGGCAA	1934	UUGCCCAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGCUCAGU	5143
717	GAGCAGAU G GGCAACUG	1935	CAGUUGCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCUGCUC	5144
718	AGCAGAUG G GCAACUGU	1936	ACAGUUGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUCUGCU	5145
727	GCAACUGU G GAGAGAAG	1937	CUUCUCUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACAGUUGC	5146
728	CAACUGUG G AGAGAAGG	1938	CCUUCUCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CACAGUUG	5147
730	ACUGUGGA G AGAAGGGU	1939	ACCCUUCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCCACAGU	5148
732	UGUGGAGA G AAGGGUGA	1940	UCACCCUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCUCCACA	5149
735	GGAGAGAA G GGUGAAAG	1941	CUUUCACC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCUCUCC	5150
736	GAGAGAAG G GUGAAAGG	1942	CCUUUCAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUCUCUC	5151
743	GGGUGAAA G GAUCCACC	1943	GGUGGAUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUUCACCC	5152
744	GGUGAAAG G AUCCACCU	1944	AGGUGGAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUUCACC	5153
772	UCAUUGCA G GAAAAAAG	1945	CUUUUUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGCAAUGA	5154
773	CAUUGCAG G AAAAAAGU	1946	ACUUUUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUGCAAUG	5155
793	CUGAAUAU G GACCACAA	1947	UUGUGGUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUAUUCAG	5156
794	UGAAUAUG G ACCACAAG	1948	CUUGUGGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUAUUCA	5157
802	GACCACAA G GUAAGGCA	1949	UGCCUUAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUGUGGUC	5158

807	CAAGGUAA G GCAUUUGU	1950	ACAAAUGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUACCUUG	5159
824	CCAUGAGU G GGCUCAUC	1951	GAUGAGCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACUCAUGG	5160
825	CAUGAGUG G GCUCAUCU	1952	AGAUGAGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CACUCAUG	5161
839	UCUACGAU G GGGAGUAU	1953	AUACUCCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCGUAGA	5162
840	CUACGAUG G GGAGUAUU	1954	AAUACUCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUCGUAG	5163
841	UACGAUGG G GAGUAUUU	1955	AAAUACUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCAUCGUA	5164
842	ACGAUGGG G AGUAUUUG	1956	CAAAUACU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCCAUCGU	5165
870	AAUGAUGA G AAAUUCUA	1957	UAGAAUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCAUCAUU	5166
889	UAUCCAAU G GAAGAAUA	1958	UAUUCUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUGGAUA	5167
890	AUCCAAUG G AAGAAUAC	1959	GUAUUCUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUUGGAU	5168
893	CAAUGGAA G AAUACAAG	1960	CUUGUAUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCCAUUG	5169
908	AGCAGUAA G AUGUUCAG	1961	CUGAACAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUACUGCU	5170
919	GUUCAGCA G GUAUUACU	1962	AGUAAUAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGCUGAAC	5171
928	GUAUUACU G GUACAAAU	1963	AUUUGUAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGUAAUAC	5172
945	GUAGUAAA G AAGUGUCA	1964	UGACACUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUUACUAC	5173
954	AAGUGUCA G GGAGGCAG	1965	CUGCCUCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGACACUU	5174
955	AGUGUCAG G GAGGCAGC	1966	GCUGCCUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUGACACU	5175
956	GUGUCAGG G AGGCAGCU	1967	AGCUGCCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCUGACAC	5176
958	GUCAGGGA G GCAGCUGU	1968	ACAGCUGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCCCUGAC	5177
977	CACCAAAA G AUGCACAU	1969	AUGUGCAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUUUGGUG	5178
1000	AAGUUACA G GACUCUAU	1970	AUAGAGUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUAACUU	5179
1001	AGUUACAG G ACUCUAUG	1971	CAUAGAGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUGUAACU	5180
1015	AUGAAAAA G GAUGUGAG	1972	CUCACAUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUUUUCAU	5181
1016	UGAAAAAG G AUGUGAGU	1973	ACUCACAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUUUUCA	5182
1044	UCCCGCCA G ACGGAGAA	1974	UUCUCCGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGGCGGGA	5183
1047	CGCCAGAC G GAGAAGGC	1975	GCCUUCUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GUCUGGCG	5184
1048	GCCAGACG G AGAAGGCU	1976	AGCCUUCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CGUCUGGC	5185
1050	CAGACGGA G AAGGCUUC	1977	GAAGCCUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCCGUCUG	5186
1053	ACGGAGAA G GCUUCUAU	1978	AUAGAAGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCUCCGU	5187
1105	UCUGUACA G AACAAAAC	1979	GUUUUGUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUACAGA	5188
1123	ACAACAAA G AAGCUCCA	1980	UGGAGCUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUUGUUGU	5189
1169	AAGCACAU G GGAAGUGA	1981	UCACUUCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUGUGCUU	5190
1170	AGCACAUG G GAAGUGAU	1982	AUCACUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUGUGCU	5191

1171	GCACAUGG G AAGUGAUC	1983	GAUCACUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCAUGUGC	5192
1191	GAUUCUGA G GACUUUAA	1984	UUAAAGUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCAGAAUC	5193
1192	AUUCUGAG G ACUUUAAG	1985	CUUAAAGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUCAGAAU	5194
1200	GACUUUAA G AAAACCAC	1986	GUGGUUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUAAAGUC	5195
1254	UUGCUGCA G AUUGGACA	1987	UGUCCAAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGCAGCAA	5196
1258	UGCAGAUU G GACAAAGA	1988	UCUUUGUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAUCUGCA	5197
1259	GCAGAUUG G ACAAAGAA	1989	UUCUUUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAAUCUGC	5198
1265	UGGACAAA G AAUUGUGU	1990	ACACAAUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUUGUCCA	5199
1294	ACAAAUCU G GAAGCAUG	1991	CAUGCUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGAUUUGU	5200
1295	CAAAUCUG G AAGCAUGG	1992	CCAUGCUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAGAUUUG	5201
1302	GGAAGCAU G GCGACUGG	1993	CCAGUCGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUGCUUCC	5202
1309	UGGCGACU G GUAACCGC	1994	GCGGUUAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGUCGCCA	5203
1339	AUCAAGCA G GCCAGCUU	1995	AAGCUGGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGCUUGAU	5204
1359	CUGCUGCA G ACAGUUGA	1996	UCAACUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGCAGCAG	5205
1371	GUUGAGCU G GGGUCCUG	1997	CAGGACCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGCUCAAC	5206
1372	UUGAGCUG G GGUCCUGG	1998	CCAGGACC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAGCUCAA	5207
1373	UGAGCUGG G GUCCUGGG	1999	CCCAGGAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCAGCUCA	5208
1379	GGGGUCCU G GGUUGGGA	2000	UCCCAACC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGGACCCC	5209
1380	GGGUCCUG G GUUGGGAU	2001	AUCCCAAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAGGACCC	5210
1384	CCUGGGUU G GGAUGGUG	2002	CACCAUCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AACCCAGG	5211
1385	CUGGGUUG G GAUGGUGA	2003	UCACCAUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAACCCAG	5212
1386	UGGGUUGG G AUGGUGAC	2004	GUCACCAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCAACCCA	5213
1389	GUUGGGAU G GUGACAUU	2005	AAUGUCAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCCCAAC	5214
1434	CUCAUACA G AUAAACAG	2006	CUGUUUAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUAUGAG	5215
1444	UAAACAGU G GCAGUGAC	2007	GUCACUGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACUGUUUA	5216
1454	CAGUGACA G GGACACAC	2008	GUGUGUCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUCACUG	5217
1455	AGUGACAG G GACACACU	2009	AGUGUGUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUGUCACU	5218
1456	GUGACAGG G ACACACUC	2010	GAGUGUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCUGUCAC	5219
1472	CGCCAAAA G AUUACCUG	2011	CAGGUAAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUUUGGCG	5220
1492	CAGCUUCA G GAGGGACG	2012	CGUCCCUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGAAGCUG	5221
1493	AGCUUCAG G AGGGACGU	2013	ACGUCCCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUGAAGCU	5222
1495	CUUCAGGA G GGACGUCC	2014	GGACGUCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCCUGAAG	5223
1496	UUCAGGAG G GACGUCCA	2015	UGGACGUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUCCUGAA	5224

1497	UCAGGAGG G ACGUCCAU	2016	AUGGACGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCUCCUGA	5225
1513	UCUGCAGC G GGCUUCGA	2017	UCGAAGCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GCUGCAGA	5226
1514	CUGCAGCG G GCUUCGAU	2018	AUCGAAGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CGCUGCAG	5227
1524	CUUCGAUC G GCAUUUAC	2019	GUAAAUGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GAUCGAAG	5228
1541	UGUGAUUA G GAAGAAAU	2020	AUUUCUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UAAUCACA	5229
1542	GUGAUUAG G AAGAAAUA	2021	UAUUUCUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUAAUCAC	5230
1545	AUUAGGAA G AAAUAUCC	2022	GGAUAUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCCUAAU	5231
1561	CAACUGAU G GAUCUGAA	2023	UUCAGAUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCAGUUG	5232
1562	AACUGAUG G AUCUGAAA	2024	UUUCAGAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUCAGUU	5233
1584	CUGCUGAC G GAUGGGGA	2025	UCCCCAUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GUCAGCAG	5234
1585	UGCUGACG G AUGGGGAA	2026	UUCCCCAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CGUCAGCA	5235
1588	UGACGGAU G GGGAAGAC	2027	GUCUUCCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUCCGUCA	5236
1589	GACGGAUG G GGAAGACA	2028	UGUCUUCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUCCGUC	5237
1590	ACGGAUGG G GAAGACAA	2029	UUGUCUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCAUCCGU	5238
1591	CGGAUGGG G AAGACAAC	2030	GUUGUCUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCCAUCCG	5239
1594	AUGGGGAA G ACAACACU	2031	AGUGUUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCCCCAU	5240
1609	CUAUAAGU G GGUGCUUU	2032	AAAGCACC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACUUAUAG	5241
1610	UAUAAGUG G GUGCUUUA	2033	UAAAGCAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CACUUAUA	5242
1623	UUUAACGA G GUCAAACA	2034	UGUUUGAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCGUUAAA	5243
1636	AACAAAGU G GUGCCAUC	2035	GAUGGCAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACUUUGUU	5244
1662	GUCGCUUU G GGGCCCUC	2036	GAGGGCCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAAGCGAC	5245
1663	UCGCUUUG G GGCCCUCU	2037	AGAGGGCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAAAGCGA	5246
1664	CGCUUUGG G GCCCUCUG	2038	CAGAGGGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCAAAGCG	5247
1681	CAGCUCAA G AACUAGAG	2039	CUCUAGUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUGAGCUG	5248
1687	AAGAACUA G AGGAGCUG	2040	CAGCUCCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UAGUUCUU	5249
1689	GAACUAGA G GAGCUGUC	2041	GACAGCUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCUAGUUC	5250
1690	AACUAGAG G AGCUGUCC	2042	GGACAGCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUCUAGUU	5251
1708	AAAUGACA G GAGGUUUA	2043	UAAACCUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUCAUUU	5252
1709	AAUGACAG G AGGUUUAC	2044	GUAAACCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUGUCAUU	5253
1711	UGACAGGA G GUUUACAG	2045	CUGUAAAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCCUGUCA	5254
1719	GGUUUACA G ACAUAUGC	2046	GCAUAUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUAAACC	5255
1732	AUGCUUCA G AUCAAGUU	2047	AACUUGAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGAAGCAU	5256
1743	CAAGUUCA G AACAAUGG	2048	CCAUUGUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGAACUUG	5257

1750	AGAACAAU G GCCUCAUU	2049	AAUGAGGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUGUUCU	5258
1768	AUGCUUUU G GGGCCCUU	2050	AAGGGCCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAAAGCAU	5259
1769	UGCUUUUG G GGCCCUUU	2051	AAAGGGCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAAAAGCA	5260
1770	GCUUUUGG G GCCCUUUC	2052	GAAAGGGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCAAAAGC	5261
1783	UUUCAUCA G GAAAUGGA	2053	UCCAUUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGAUGAAA	5262
1784	UUCAUCAG G AAAUGGAG	2054	CUCCAUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUGAUGAA	5263
1789	CAGGAAAU G GAGCUGUC	2055	GACAGCUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUUCCUG	5264
1790	AGGAAAUG G AGCUGUCU	2056	AGACAGCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUUUCCU	5265
1821	CAGCUUGA G AGUAAGGG	2057	CCCUUACU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCAAGCUG	5266
1827	GAGAGUAA G GGAUUAAC	2058	GUUAAUCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUACUCUC	5267
1828	AGAGUAAG G GAUUAACC	2059	GGUUAAUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUACUCU	5268
1829	GAGUAAGG G AUUAACCC	2060	GGGUUAAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCUUACUC	5269
1842	ACCCUCCA G AACAGCCA	2061	UGGCUGUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGGAGGGU	5270
1853	CAGCCAGU G GAUGAAUG	2062	CAUUCAUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACUGGCUG	5271
1854	AGCCAGUG G AUGAAUGG	2063	CCAUUCAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CACUGGCU	5272
1861	GGAUGAAU G GCACAGUG	2064	CACUGUGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUCAUCC	5273
1875	GUGAUCGU G GACAGCAC	2065	GUGCUGUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACGAUCAC	5274
1876	UGAUCGUG G ACAGCACC	2066	GGUGCUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CACGAUCA	5275
1887	AGCACCGU G GGAAAGGA	2067	UCCUUUCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACGGUGCU	5276
1888	GCACCGUG G GAAAGGAC	2068	GUCCUUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CACGGUGC	5277
1889	CACCGUGG G AAAGGACA	2069	UGUCCUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCACGGUG	5278
1893	GUGGGAAA G GACACUUU	2070	AAAGUGUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUUCCCAC	5279
1894	UGGGAAAG G ACACUUUG	2071	CAAAGUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUUCCCA	5280
1916	UAUCACCU G GACAACGC	2072	GCGUUGUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGGUGAUA	5281
1917	AUCACCUG G ACAACGCA	2073	UGCGUUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAGGUGAU	5282
1946	CCUUCUCU G GGAUCCCA	2074	UGGGAUCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGAGAAGG	5283
1947	CUUCUCUG G GAUCCCAG	2075	CUGGGAUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAGAGAAG	5284
1948	UUCUCUGG G AUCCCAGU	2076	ACUGGGAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCAGAGAA	5285
1957	AUCCCAGU G GACAGAAG	2077	CUUCUGUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACUGGGAU	5286
1958	UCCCAGUG G ACAGAAGC	2078	GCUUCUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CACUGGGA	5287
1962	AGUGGACA G AAGCAAGG	2079	CCUUGCUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUCCACU	5288
1969	AGAAGCAA G GUGGCUUU	2080	AAAGCCAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUGCUUCU	5289
1972	AGCAAGGU G GCUUUGUA	2081	UACAAAGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACCUUGCU	5290

1983	UUUGUAGU G GACAAAAA	2082	UUUUUGUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACUACAAA	5291
1984	UUGUAGUG G ACAAAAAC	2083	GUUUUUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CACUACAA	5292
2001	ACCAAAAU G GCCUACCU	2084	AGGUAGGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUUUGGU	5293
2020	AAAUCCCA G GCAUUGCU	2085	AGCAAUGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGGGAUUU	5294
2031	AUUGCUAA G GUUGGCAC	2086	GUGCCAAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUAGCAAU	5295
2035	CUAAGGUU G GCACUUGG	2087	CCAAGUGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AACCUUAG	5296
2042	UGGCACUU G GAAAUACA	2088	UGUAUUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAGUGCCA	5297
2043	GGCACUUG G AAAUACAG	2089	CUGUAUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAAGUGCC	5298
2148	ACGAACAA G GACACCAG	2090	CUGGUGUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUGUUCGU	5299
2149	CGAACAAG G ACACCAGC	2091	GCUGGUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUGUUCG	5300
2175	AGCCCUCU G GUAGUUUA	2092	UAAACUAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGAGGGCU	5301
2200	UUCGCCAA G GAGCCUCC	2093	GGAGGCUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUGGCGAA	5302
2201	UCGCCAAG G AGCCUCCC	2094	GGGAGGCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUGGCGA	5303
2219	AAUUCUCA G GGCCAGUG	2095	CACUGGCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGAGAAUU	5304
2220	AUUCUCAG G GCCAGUGU	2096	ACACUGGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUGAGAAU	5305
2254	CAGUGAAU G GAAAAACA	2097	UGUUUUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUCACUG	5306
2255	AGUGAAUG G AAAAACAG	2098	CUGUUUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUUCACU	5307
2271	GUUACCUU G GAACUACU	2099	AGUAGUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAGGUAAC	5308
2272	UUACCUUG G AACUACUG	2100	CAGUAGUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAAGGUAA	5309
2280	GAACUACU G GAUAAUGG	2101	CCAUUAUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGUAGUUC	5310
2281	AACUACUG G AUAAUGGA	2102	UCCAUUAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAGUAGUU	5311
2287	UGGAUAAU G GAGCAGGU	2103	ACCUGCUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUAUCCA	5312
2288	GGAUAAUG G AGCAGGUG	2104	CACCUGCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUUAUCC	5313
2293	AUGGAGCA G GUGCUGAU	2105	AUCAGCAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGCUCCAU	5314
2310	GCUACUAA G GAUGACGG	2106	CCGUCAUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUAGUAGC	5315
2311	CUACUAAG G AUGACGGU	2107	ACCGUCAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUAGUAG	5316
2317	AGGAUGAC G GUGUCUAC	2108	GUAGACAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GUCAUCCU	5317
2330	CUACUCAA G GUAUUUCA	2109	UGAAAUAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUGAGUAG	5318
2356	ACACGAAU G GUAGAUAC	2110	GUAUCUAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUCGUGU	5319
2360	GAAUGGUA G AUACAGUG	2111	CACUGUAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UACCAUUC	5320
2378	AAAAGUGC G GGCUCUGG	2112	CCAGAGCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GCACUUUU	5321
2379	AAAGUGCG G GCUCUGGG	2113	CCCAGAGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CGCACUUU	5322
2385	CGGGCUCU G GGAGGAGU	2114	ACUCCUCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGAGCCCG	5323

2386	GGGCUCUG G GAGGAGUU	2115	AACUCCUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAGAGCCC	5324
2387	GGCUCUGG G AGGAGUUA	2116	UAACUCCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCAGAGCC	5325
2389	CUCUGGGA G GAGUUAAC	2117	GUUAACUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCCCAGAG	5326
2390	UCUGGGAG G AGUUAACG	2118	CGUUAACU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUCCCAGA	5327
2405	CGCAGCCA G ACGGAGAG	2119	CUCUCCGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGGCUGCG	5328
2408	AGCCAGAC G GAGAGUGA	2120	UCACUCUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GUCUGGCU	5329
2409	GCCAGACG G AGAGUGAU	2121	AUCACUCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CGUCUGGC	5330
2411	CAGACGGA G AGUGAUAC	2122	GUAUCACU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCCGUCUG	5331
2427	CCCCAGCA G AGUGGAGC	2123	GCUCCACU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGCUGGGG	5332
2431	AGCAGAGU G GAGCACUG	2124	CAGUGCUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACUCUGCU	5333
2432	GCAGAGUG G AGCACUGU	2125	ACAGUGCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CACUCUGC	5334
2449	ACAUACCU G GCUGGAUU	2126	AAUCCAGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGGUAUGU	5335
2453	ACCUGGCU G GAUUGAGA	2127	UCUCAAUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGCCAGGU	5336
2454	CCUGGCUG G AUUGAGAA	2128	UUCUCAAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAGCCAGG	5337
2460	UGGAUUGA G AAUGAUGA	2129	UCAUCAUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCAAUCCA	5338
2477	AAUACAAU G GAAUCCAC	2130	GUGGAUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUGUAUU	5339
2478	AUACAAUG G AAUCCACC	2131	GGUGGAUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUUGUAU	5340
2489	UCCACCAA G ACCUGAAA	2132	UUUCAGGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUGGUGGA	5341
2505	AUUAAUAA G GAUGAUGU	2133	ACAUCAUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUAUUAAU	5342
2506	UUAAUAAG G AUGAUGUU	2134	AACAUCAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUAUUAA	5343
2540	UUUCAGCA G AACAUCCU	2135	AGGAUGUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGCUGAAA	5344
2550	ACAUCCUC G GGAGGCUC	2136	GAGCCUCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GAGGAUGU	5345
2551	CAUCCUCG G GAGGCUCA	2137	UGAGCCUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CGAGGAUG	5346
2552	AUCCUCGG G AGGCUCAU	2138	AUGAGCCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCGAGGAU	5347
2554	CCUCGGGA G GCUCAUUU	2139	AAAUGAGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCCCGAGG	5348
2565	UCAUUUGU G GCUUCUGA	2140	UCAGAAGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACAAAUGA	5349
2611	UCCCACCU G GCCAAAUC	2141	GAUUUGGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGGUGGGA	5350
2631	GACCUGAA G GCGGAAAU	2142	AUUUCCGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUCAGGUC	5351
2634	CUGAAGGC G GAAAUUCA	2143	UGAAUUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GCCUUCAG	5352
2635	UGAAGGCG G AAAUUCAC	2144	GUGAAUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CGCCUUCA	5353
2644	AAAUUCAC G GGGGCAGU	2145	ACUGCCCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG GUGAAUUU	5354
2645	AAUUCACG G GGGCAGUC	2146	GACUGCCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CGUGAAUU	5355
2646	AUUCACGG G GGCAGUCU	2147	AGACUGCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCGUGAAU	5356

2647	UUCACGGG G GCAGUCUC	2148	GAGACUGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCCGUGAA	5357
2669	UCUGACUU G GACAGCUC	2149	GAGCUGUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AAGUCAGA	5358
2670	CUGACUUG G ACAGCUCC	2150	GGAGCUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAAGUCAG	5359
2680	CAGCUCCU G GGGAUGAU	2151	AUCAUCCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGGAGCUG	5360
2681	AGCUCCUG G GGAUGAUU	2152	AAUCAUCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAGGAGCU	5361
2682	GCUCCUGG G GAUGAUUA	2153	UAAUCAUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCAGGAGC	5362
2683	CUCCUGGG G AUGAUUAU	2154	AUAAUCAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCCAGGAG	5363
2698	AUGACCAU G GAACAGCU	2155	AGCUGUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUGGUCAU	5364
2699	UGACCAUG G AACAGCUC	2156	GAGCUGUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CAUGGUCA	5365
2750	UGAUCUCA G AGACAAGU	2157	ACUUGUCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGAGAUCA	5366
2752	AUCUCAGA G ACAAGUUC	2158	GAACUUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCUGAGAU	5367
2802	AUCCCAAA G GAAGCCAA	2159	UUGGCUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUUGGGAU	5368
2803	UCCCAAAG G AAGCCAAC	2160	GUUGGCUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUUUGGGA	5369
2817	AACUCUGA G GAAGUCUU	2161	AAGACUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCAGAGUU	5370
2818	ACUCUGAG G AAGUCUUU	2162	AAAGACUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUCAGAGU	5371
2839	UUAAACCA G AAAACAUU	2163	AAUGUUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGGUUUAA	5372
2860	UUGAAAAU G GCACAGAU	2164	AUCUGUGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AUUUUCAA	5373
2866	AUGGCACA G AUCUUUUC	2165	GAAAAGAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUGCCAU	5374
2886	GCUAUUCA G GCUGUUGA	2166	UCAACAGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGAAUAGC	5375
2898	GUUGAUAA G GUCGAUCU	2167	AGAUCGAC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UUAUCAAC	5376
2914	UGAAAUCA G AAAUAUCC	2168	GGAUAUUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGAUUUCA	5377
2958	CCUCCACA G ACUCCGCC	2169	GGCGGAGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGUGGAGG	5378
2968	CUCCGCCA G AGACACCU	2170	AGGUGUCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGGCGGAG	5379
2970	CCGCCAGA G ACACCUAG	2171	CUAGGUGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCUGGCGG	5380
3034	CCAUUCCU G GCAUUCAC	2172	GUGAAUGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG AGGAAUGG	5381
3059	AAUUAUGU G GAAGUGGA	2173	UCCACUUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACAUAAUU	5382
3060	AUUAUGUG G AAGUGGAU	2174	AUCCACUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CACAUAAU	5383
3065	GUGGAAGU G GAUAGGAG	2175	CUCCUAUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG ACUUCCAC	5384
3066	UGGAAGUG G AUAGGAGA	2176	UCUCCUAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CACUUCCA	5385
3070	AGUGGAUA G GAGAACUG	2177	CAGUUCUC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UAUCCACU	5386
3071	GUGGAUAG G AGAACUGC	2178	GCAGUUCU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUAUCCAC	5387
3073	GGAUAGGA G AACUGCAG	2179	CUGCAGUU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UCCUAUCC	5388
3096	AUAGCCUA G GGCUGAAU	2180	AUUCAGCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UAGGCUAU	5389

3097	UAGCCUAG G GCUGAAUU	2181	AAUUCAGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUAGGCUA	5390
3113	UUUUGUCA G AUAAAUAA	2182	UUAUUUAU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UGACAAAA	5391
3174	GUAUUUUA G ACUUCCUG	2183	CAGGAAGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UAAAAUAC	5392
3264	GUAUUUUA G ACUUCCUG	2183	CAGGAAGU GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UAAAAUAC	5392
3185	UUCCUGUA G GGGGCGAU	2184	AUCGCCCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UACAGGAA	5393
3238	UUCCUGUA G GGGGCGAU	2184	AUCGCCCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UACAGGAA	5393
3275	UUCCUGUA G GGGGCGAU	2184	AUCGCCCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG UACAGGAA	5393
3186	UCCUGUAG G GGGCGAUA	2185	UAUCGCCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUACAGGA	5394
3239	UCCUGUAG G GGGCGAUA	2185	UAUCGCCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUACAGGA	5394
3276	UCCUGUAG G GGGCGAUA	2185	UAUCGCCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CUACAGGA	5394
3187	CCUGUAGG G GGCGAUAU	2186	AUAUCGCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCUACAGG	5395
3240	CCUGUAGG G GGCGAUAU	2186	AUAUCGCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCUACAGG	5395
3188	CUGUAGGG G GCGAUAUA	2187	UAUAUCGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCCUACAG	5396
3241	CUGUAGGG G GCGAUAUA	2187	UAUAUCGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCCUACAG	5396
3277	CCUGUAGG G GGCGAUAA	2188	UUAUCGCC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCUACAGG	5397
3278	CUGUAGGG G GCGAUAAA	2189	UUUAUCGC GGA GCCGUUAGGC UCCCUUCAAGGA GCCGUUAGGC UCCGGG CCCUACAG	5398

Input Sequence = NM_001285. Cut Site = G/.
Arm Length = 8. Core Sequence = GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG
Underlined region can be any X sequence or linker, as described herein.
NM_001285 (Homo sapiens chloride channel, calcium activated, 1 (CLCA1) mRNA, 3311 bp)

Table IX: Human CLCA1 GeneBloc and Target Sequence

249.021

Pos	Substrate	Substrate Seq ID No.	RPI#	Alias	GeneBloc	Rz Seq ID No.
821	CAAGGUAAGGCAUUUGUCCAUGA	5399	19843	hCLCA1:821L23 GB3.3	**B** ucauggaC$_s$A$_s$A$_s$A$_s$T$_s$G$_s$C$_s$C$_s$T$_s$uaccuug **B**	5417
1141	CAAAGAAGCUCCAAACAAGCAAA	5400	19837	hCLCA1:1141L23 GB3.3	**B** uuugcuuG$_s$T$_s$T$_s$T$_s$G$_s$G$_s$A$_s$G$_s$C$_s$uucuuug **B**	5418
1646	GUCAAACAAAGUGGUGCCAUCAU	5401	19841	hCLCA1:1646L23 GB3.3	**B** augauggC$_s$A$_s$C$_s$C$_s$A$_s$C$_s$T$_s$T$_s$T$_s$guuugac **B**	5419
2464	CAUACCUGGCUGGAUUGAGAAUG	5402	19836	hCLCA1:2464L23 GB3.3	**B** cauucucA$_s$A$_s$T$_s$C$_s$C$_s$A$_s$G$_s$C$_s$C$_s$agguaug **B**	5420
2542	CAAGCAAGUGUGUUUCAGCAGAA	5403	19839	hCLCA1:2542L23 GB3.3	**B** uucugcuG$_s$A$_s$A$_s$A$_s$C$_s$A$_s$C$_s$A$_s$C$_s$uugcuug **B**	5421
2577	GCUCAUUUGUGGCUUCUGAUGUC	5404	19840	hCLCA1:2577L23 GB3.3	**B** gacaucaG$_s$A$_s$A$_s$G$_s$C$_s$C$_s$A$_s$C$_s$A$_s$aaugagc **B**	5422
2711	UAUGACCAUGGAACAGCUCACAA	5405	19842	hCLCA1:2711L23 GB3.3	**B** uugugagC$_s$T$_s$G$_s$T$_s$T$_s$C$_s$C$_s$A$_s$T$_s$ggucaua **B**	5423
3087	GGAUAGGAGAACUGCAGCUGUCA	5406	19838	hCLCA1:3087L23 GB3.3	**B** ugacagcT$_s$G$_s$C$_s$A$_s$G$_s$T$_s$T$_s$C$_s$T$_s$ccuaucc **B**	5424
69	TCTTGATTCTTCACC	5407	20960	hCLCA1-69 Rz-7 allyl stable	g$_s$g$_s$u$_s$g$_s$aag c**UGA**u**G**aggccguuaggcc**G**aa **A**ucaaga **B**	5425
70	CTTGATTCTTCACCT	5408	20961	hCLCA1-70 Rz-7 allyl stable	a$_s$g$_s$g$_s$u$_s$gaa c**UGA**u**G**aggccguuaggcc**G**aa **A**aucaag **B**	5426
71	TTGATTCTTCACCTT	5409	20968	hCLCA1-71 CHz-7 allyl stable	a$_s$a$_s$g$_s$g$_s$uga c**UGA**u**G**aggccguuaggcc**G**aa Iaaucaa **B**	5427
72	TGATTCTTCACCTTC	5410	20962	hCLCA1-72 Rz-7 allyl stable	g$_s$a$_s$a$_s$g$_s$gug c**UGA**u**G**aggccguuaggcc**G**aa **A**gaauca **B**	5428
73	GATTCTTCACCTTCT	5411	20963	hCLCA1-73 Rz-7 allyl stable	a$_s$g$_s$a$_s$a$_s$ggu c**UGA**u**G**aggccguuaggcc**G**aa **A**agaauc **B**	5429
445	TCCTGATTTCATTGC	5412	20964	hCLCA1-445 Rz-7 allyl stable	g$_s$c$_s$a$_s$a$_s$uga c**UGA**u**G**aggccguuaggcc**G**aa **A**ucagga **B**	5430

446	CCTGATTTCATTGCA	5413	20965	hCLCA1-446 Rz-7 allyl stable	$u_sg_sc_sa_s$aug c**UGA**u***G***aggccguuaggcc***G***aa ***A***aucagg **B**	5431
447	CTGATTTCATTGCAG	5414	20966	hCLCA1-447 Rz-7 allyl stable	$c_su_sg_sc_s$aau c**UGA**u***G***aggccguuaggcc***G***aa ***A***aaucag **B**	5432
448	TGATTTCATTGCAGG	5415	20969	hCLCA1-448 CHz-7 allyl staBle	$c_sc_su_sg_s$caa c**UGA**u***G***aggccguuaggcc***G***aa Iaaauca **B**	5433
450	ATTTCATTGCAGGAA	5416	20967	hCLCA1-450 Rz-7 allyl stable	$u_su_sc_sc_s$ugc c**UGA**u***G***aggccguuaggcc***G***aa ***A***ugaaau **B**	5434

lower case = 2'OMe; *A* = ri**B**o A
Upper Case = Deoxyri**B**ose (DNA)
s = phosphorothioate linkages
B = inverted a**B**asic
U = 2'-C-allyl Uridine
G = ri**B**o G

Table X: PCR Primers **249.021**

PCR primer	Seq ID No
CGAAATCTCGAGCAGACTTGTGGGAGAAGCTC	5435
AGCACACTGCAGAGTTGCTGGCCAGCTTACCTCC	5436

CLAIMS

What is claimed is:

1. A nucleic acid molecule that down regulates expression of CLCA1 (Chloride Channel Calcium Activated) gene.

2. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule is used to treat conditions selected from the group consisting of Chronic Obstructive Pulmonary Disease (COPD), chronic bronchitis, asthma, cystic fibrosis, and obstructive bowel syndrome.

3. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule is an enzymatic nucleic acid molecule.

4. The nucleic acid molecule of claim 3, wherein a binding arm of said enzymatic nucleic acid molecule comprise sequences complementary to any of sequences having SEQ ID NOs:1-2189 and 5399-5416.

5. The nucleic acid molecule of claim 3, wherein said enzymatic nucleic acid molecule comprises any of sequences havingSEQ ID NOs:2190-5398 and 5425-5434.

6. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule is an antisense nucleic acid molecule.

7. The nucleic acid molecule of claim 6, wherein said antisense nucleic acid molecule comprises sequences complementary to any of sequences having SEQ ID NOs:1-2189 and 5399-5416.

8. The nucleic acid molecule of claim 6, wherein said antisense nucleic acid molecule comprise any of sequences having SEQ ID NOs:5417-5424.

9. The nucleic acid molecule of claim 3, wherein said enzymatic nucleic acid molecule is in a hammerhead (HH) motif.

10. The nucleic acid molecule of claim 3, wherein said enzymatic nucleic acid molecule is in a hairpin, hepatitis Delta virus, group I intron, VS nucleic acid, amberzyme, zinzyme or RNAse P nucleic acid motif.

11. The nucleic acid molecule of claim 3, wherein said enzymatic nucleic acid molecule is in an Inozyme motif.

12. The nucleic acid molecule of claim 3, wherein said enzymatic nucleic acid molecule is in a G-cleaver motif.

13. The nucleic acid molecule of claim 3, wherein said enzymatic nucleic acid molecule is a DNAzyme.

14. The nucleic acid molecule of claims 3 or 6, wherein said nucleic acid molecule comprises between 12 and 100 bases complementary to RNA of a CLCA1 gene.

15. The nucleic acid molecule of claims 3 or 6, wherein said nucleic acid molecule comprises between 14 and 24 bases complementary to RNA of a CLCA1 gene.

16. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule is chemically synthesized.

17. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule comprises at least one 2'-sugar modification.

18. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule comprises at least one nucleic acid base modification.

19. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule comprises at least one phosphate backbone modification.

20. A mammalian cell comprising the nucleic acid molecule of claim 1.

21. The mammalian cell of claim 20, wherein said mammalian cell is a human cell.

22. A method of reducing CLCA1 activity in a cell, comprising the step of contacting said cell with the nucleic acid molecule of claim 1, under conditions suitable for said reduction of CLCA1 activity.

23. A method of treatment of a patient having a condition associated with the level of CLCA1, comprising contacting cells of said patient with the nucleic acid molecule of claim 1, under conditions suitable for said treatment.

24. The method of claim 23 further comprising the use of one or more therapies under conditions suitable for said treatment.

25. A method of cleaving RNA of a CLCA1 gene, comprising contacting the nucleic acid molecule of claim 3 with said RNA under conditions suitable for the cleavage of said RNA.

26. The method of claim 25, wherein said cleavage is carried out in the presence of a divalent cation.

27. The method of claim 26, wherein said divalent cation is Mg^{2+}.

28. The nucleic acid molecule of claim 1, wherein said nucleic acid comprises a cap structure, wherein the cap structure is at the 5'-end or 3'-end or both the 5'-end and the 3'-end.

29. The enzymatic nucleic acid molecule of claim 9, wherein said hammerhead motif comprises sequences complementary to any of sequences having SEQ ID NOs:1-575.

30. The enzymatic nucleic acid molecule of claim 11, wherein said Inozyme motif comprises sequences complementary to any of sequences having SEQ ID NOs:576-1210.

31. The enzymatic nucleic acid molecule of claim 12, wherein said G-cleaver motif comprises sequences complementary to any of sequences having SEQ ID NOs:1211-1429.

32. The enzymatic nucleic acid molecule of claim 13, wherein said DNAzyme comprises sequences complementary to any sequence shown as substrate sequences in Table VII.

33. The enzymatic nucleic acid molecule of claim 10, wherein said zinzyme comprises sequences complementary to any sequence shown as substrate sequences in Table VI.

34. The enzymatic nucleic acid molecule of claim 10, wherein said amberzyme comprises sequences complementary to any sequence shown as substrate sequences in Table VIII.

35. An expression vector comprising at least one nucleic acid molecule of claim 1, in a manner that allows expression of the nucleic acid molecule.

36. A mammalian cell comprising an expression vector of claim 35.

37. The mammalian cell of claim 36, wherein said mammalian cell is a human cell.

38. The expression vector of claim 35, wherein said nucleic acid molecule is an enzymatic nucleic acid molecule.

39. The expression vector of claim 35, wherein said expression vector further comprises an antisense nucleic acid molecule complementary to RNA of a CLCA1 gene.

40. The expression vector of claim 35, wherein said expression vector comprises at least two said nucleic acid molecules.

41. The expression vector of claim 40, wherein the at least two nucleic acid molecules are the same.

42. The expression vector of claim 40, wherein the at least two nucleic acid molecules are different.

43. The expression vector of claim 40, wherein one said expression vector further comprises an antisense nucleic acid molecule complementary to RNA of a CLCA1 gene.

44. The expression vector of claim 40, wherein one said expression vector further comprises an enzymatic nucleic acid molecule complementary to RNA of a CLCA1 gene.

45. A method for treatment of chronic obstructive pulmonary disease comprising the step of administering to a patient the nucleic acid molecule of claim 1 under conditions suitable for said treatment.

46. A method for treatment of cystic fibrosis comprising the step of administering to a patient the nucleic acid molecule of claim 1 under conditions suitable for said treatment.

47. An enzymatic nucleic acid molecule that cleaves RNA derived from a CLCA1 gene.

48. The enzymatic nucleic acid molecule of claim 47, wherein said enzymatic nucleic acid molecule is selected from the group consisting of Hammerhead, Hairpin, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme.

49. The method of claims 45 or 46, wherein said method further comprises administering to said patient the nucleic acid molecule of claim 1 in conjunction with one or more other therapies.

50. The method of claim 49, wherein said other therapies are therapies selected from the group consisting of oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylcysteine, mucokinetic agents, and DNase (Pulmozyme) treatments.

51. The nucleic acid molecule of claim 9, wherein said nucleic acid molecule comprises at least five ribose residues, at least ten 2'-*O*-methyl modifications, and a 3'- end modification.

52. The nucleic acid molecule of claim 51, wherein said nucleic acid molecule further comprises a phosphorothioate core with both 3' and 5' -end modifications.

53. The nucleic acid molecule of claims 51 or 52, wherein said 3' and/or 5'- end modification is 3'-3' inverted abasic moiety.

54. The nucleic acid molecule of claim 3, wherein said nucleic acid molecule comprises at least five ribose residues; at least ten 2'-*O*-methyl modifications, and a 3'- end modification.

55. The nucleic acid molecule of claim 54, wherein said nucleic acid molecule further comprises phosphorothioate linkages on at least three of the 5' terminal nucleotides.

56. The nucleic acid molecule of claim 54, wherein said 3'- end modification is 3'-3' inverted abasic moiety.

57. The enzymatic nucleic acid molecule of claim 13, wherein said DNAzyme comprises at least ten 2'-*O*-methyl modifications.

58. The enzymatic nucleic acid molecule of claim 57, wherein said DNAzyme further comprises phosphorothioate linkages on at least three of the 5' terminal nucleotides.

59. The enzymatic nucleic acid molecule of claim 57, wherein said DNAzyme further comprises a 3'-end modification.

60. The enzymatic nucleic acid molecule of claim 59, wherein said 3'- end modification is 3'-3' inverted abasic moiety.

Figure 1: Examples of Nuclease Stable Ribozyme Motifs

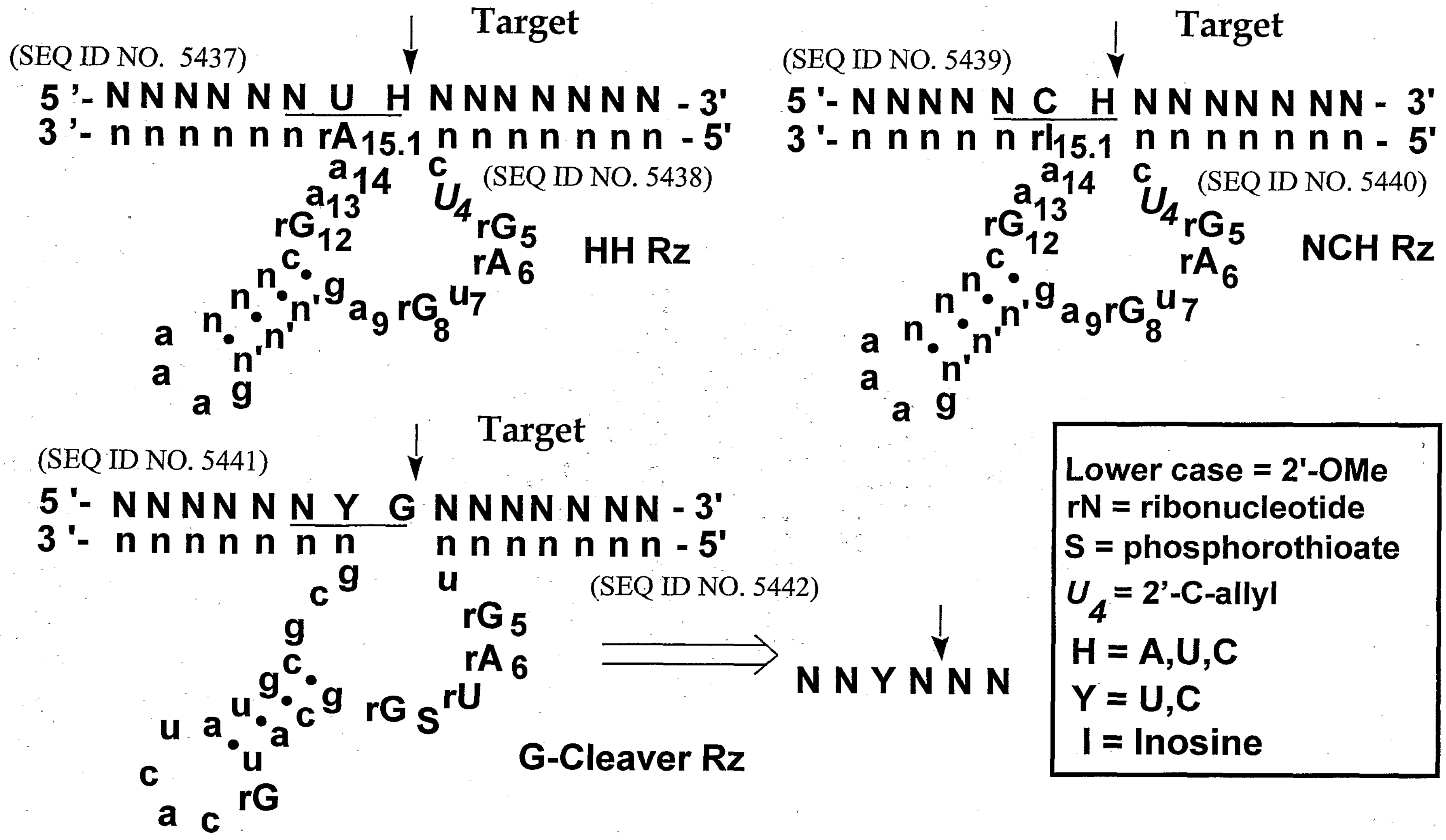


Figure 2: 2'-O-Me substituted Amberzyme Enzymatic Nucleic Acid Motif

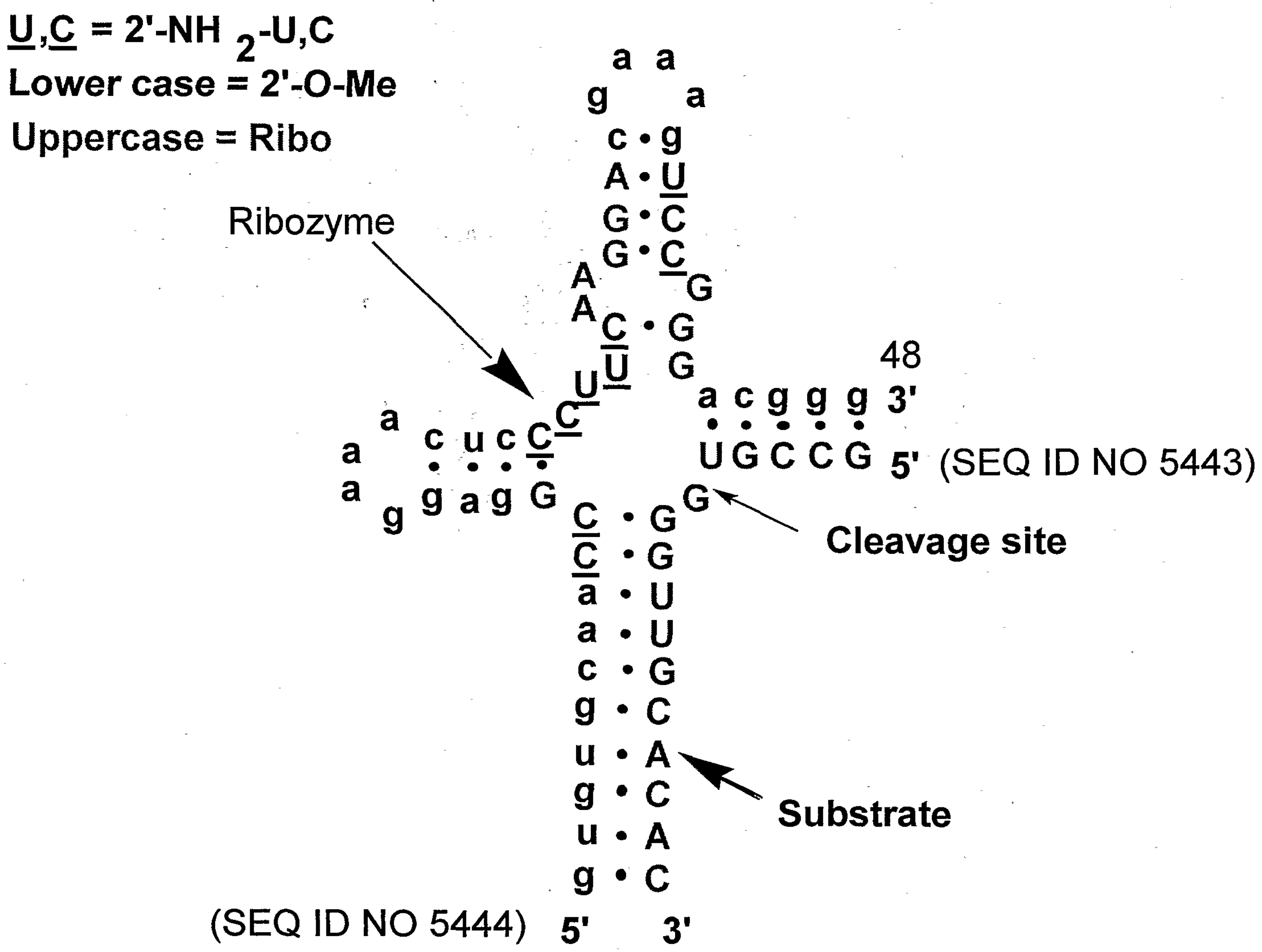
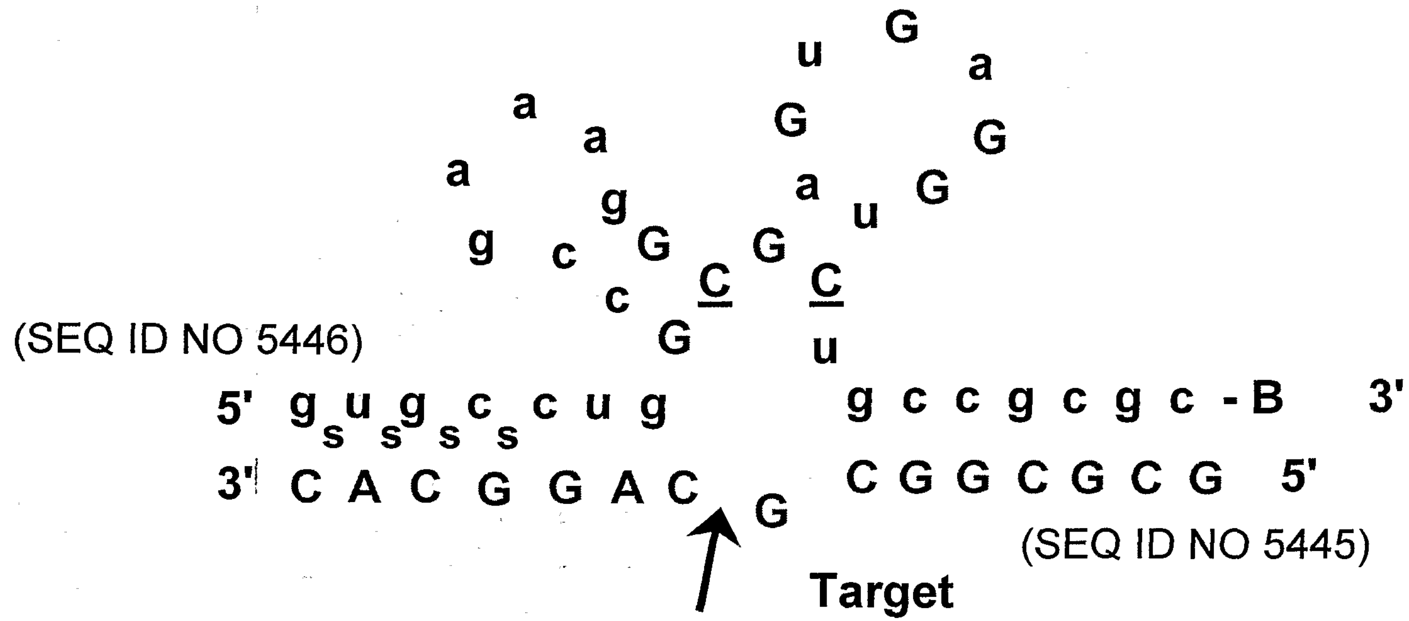


Figure 3: Stabilized Zinzyme Ribozyme Motif

Zinzyme A-motif RZ



Legend

Uppercase indicates natural ribo residues

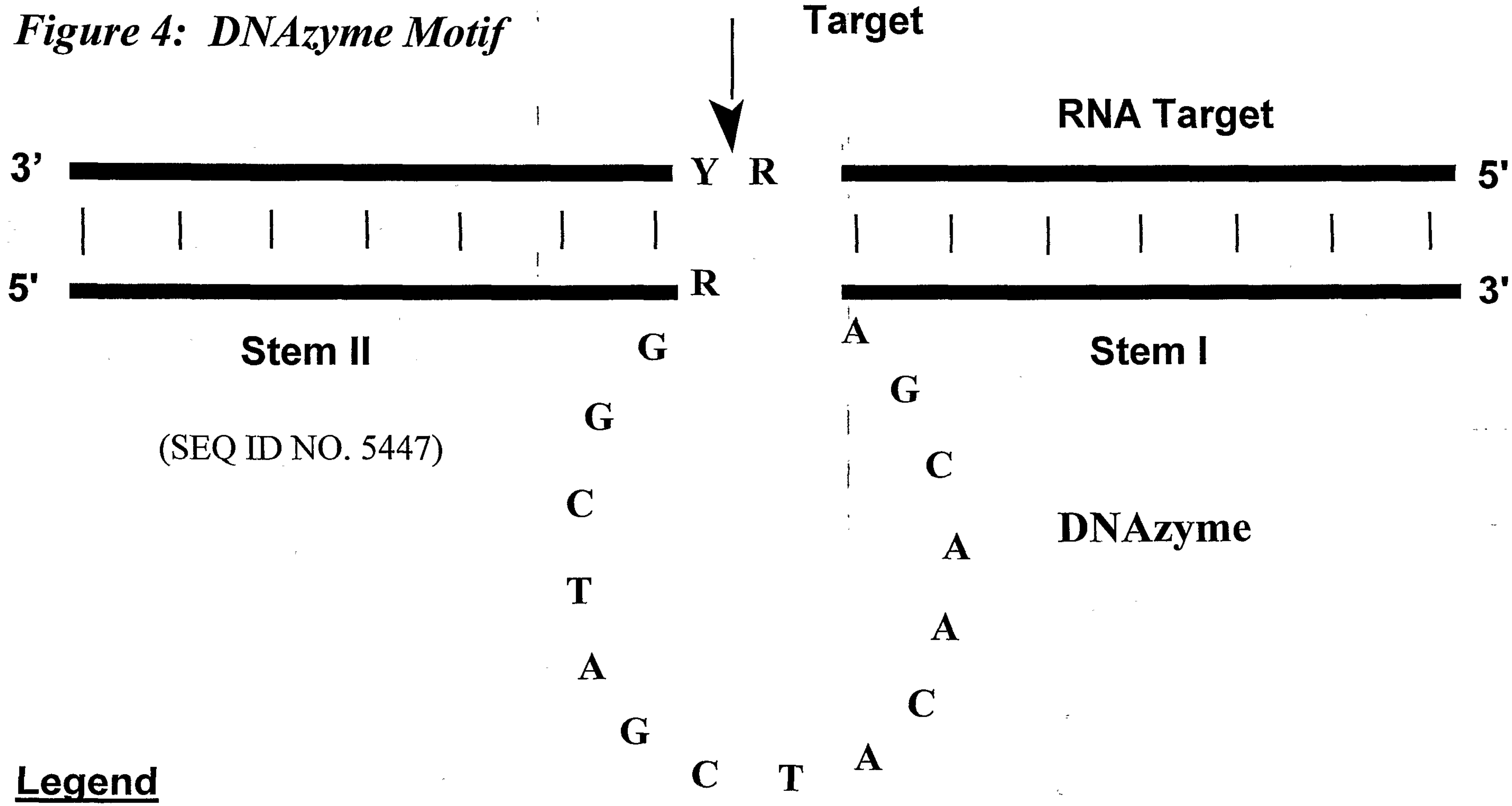
C indicates 2'- d-NH_2-C

Lowercase: 2'-O-Me

Subscript $_s$ indicates phosphothioate linkage

B: 3'- 3' abasic moiety

Figure 4: DNAzyme Motif



Legend
Y = U or C
R = A or G