COMPOSITIONS AND METHODS FOR TREATING MPSI

BACKGROUND OF THE INVENTION

The mucopolysaccharidoses are a group of inherited disorders caused by a lack of specific lysosomal enzymes involved in the degradation of glycosaminoglycans (GAG), also called mucopolysaccharides. The accumulation of partially-degraded GAG causes interference with cell, tissue, and organ function. Over time, the GAG accumulates within cells, blood, and connective tissue, resulting in increasing cellular and organ damage. The most serious of the mucopolysaccharidosis (MPS) disorders, MPS I, is caused by a deficiency of the enzyme α-L-iduronidase (IDUA). This leads to three clinical syndromes which in order of severity are Hurler, Hurler-Scheie and Scheie syndromes. Each is inherited in an autosomal recessive manner with the extent of enzyme deficiency being directly related to the severity of the clinical phenotype.

The *IDUA* gene has been reported to provide instructions for producing an enzyme called alpha-L-iduronidase, which is essential for the breakdown of large sugar molecules called glycosaminoglycans (GAGs). Specifically, alpha-L-iduronidase is reported to remove sulfate from a molecule known as sulfated alpha-L-iduronic acid, which is present in two GAGs called heparan sulfate and dermatan sulfate. Alpha-L-iduronidase is located in lysosomes, compartments within cells that digest and recycle different types of molecules. More than 100 mutations in the *IDUA* gene have been found to cause mucopolysaccharidosis type I (MPS I). Mutations that change one DNA building block (nucleotide) are the most common. Mutations that cause MPS I to reduce or completely eliminate the function of alpha-L-iduronidase.

With respect to the clinical syndromes, the current standard of care for Hurler syndrome is hematopoietic stem cell transplantation (HSCT) such as bone marrow transplantation (BMT) or umbilical cord blood transplantations (UCBT). The procedure is done as early as possible, and before the age of two, to impact on both somatic and CNS aspects of the disease. However, HSCT for MPS I remains associated with a significant amount of morbidity and a 20% mortality rate. If transplantation is not an option, then enzyme replacement therapy (ERT) may be started which requires a weekly infusion of enzyme for the life of the patient. ERT does not impact on the progression of CNS disease but does partially improve the somatic manifestations. Organomegaly is significantly

improved although aspects of the disease in the skeletal system, eye and heart are only partially improved. Patients may require surgery to stabilize the hip and knee and to treat carpal tunnel syndrome and finger contractions. Cardiac disease is treated medically although surgery may eventually be required.

ERT for MPS I provides exogenous enzyme for uptake into lysosomes and increased catabolism of GAG. Although the lysosomal enzymes function internally, cell-surface mannose-6-phosphate receptors are capable of binding, internalizing, and delivering these enzymes to the lysosomes. Recombinant IDUA (Aldurazyme®, BioMarin) is approved by FDA for patients with Hurler and Hurler-Scheie forms of MPS I and for patients with the Scheie form who have moderate to severe symptoms and was shown to improve pulmonary function and walking capacity. ERT has also been observed to reduce hepatomegaly in MPS I patients, as well as the levels of urinary GAG. However, because intravenous enzyme does not easily cross into the brain, ERT does not currently address the neurological symptoms experienced by some MPS I patients.

Complications of ERT revolve around immune response to the recombinant enzyme which can range from mild to full-blown anaphylaxis as well as complications of life-long peripheral access such as local and systemic infections. Up to 91% of patients receiving Aldurazyme develop antibodies to the enzyme, although it is not clear how much it affects efficacy. Furthermore, ERT requires weekly intravenous (i.v.) infusions, administered over a period of 3-8 hours in a hospital setting, which significantly impacts patient quality of life and, at a high expense, is a major strain on health care reimbursement systems.

In light of these limitations, a treatment that can more effectively correct the morbidity associated with MPS I remains an unmet medical need.

SUMMARY OF THE INVENTION

In one aspect, the invention provides an expression cassette comprising a human alpha-L-iduronidase (hIDUA) gene having the nucleotide sequence of SEQ ID NO: 1 or a sequence at least about 95% identical to SEQ ID NO: 1 which encodes a functional human alpha-L-iduronidase in human cells, wherein said expression cassette further comprises regulatory control sequences which direct expression of the human alpha-L-iduronidase in human cells, said regulatory control sequences comprising a liver-specific promoter.

In another aspect, the invention provides a vector containing the expression cassette. In one embodiment, the expression cassette is located on a cis plasmid. In another embodiment, the expression cassette is located on pENN.TBG.hIDUA.nRBG.

In yet another aspect, the invention provides a recombinant adeno-associated virus (rAAV) particle having an AAV capsid and having packaged therein a left inverted terminal repeat (ITR), a human alpha-L-iduronidase (hIDUA) gene under the control of regulatory sequences which control expression thereof, and an AAV right ITR, wherein said hIDUA gene has a sequence shown in SEQ ID NO: 1 (FIG 1) or a sequence at least about 95% identical thereto which encodes a functional human alpha-L-iduronidase. In one embodiment, the functional hIDUA gene is expressed under the control of a liver-specific promoter. Such a promoter may be a thyroxin binding globulin (TBG) promoter.

In a further aspect, the invention provides the recombinant adeno-associated viral particle AAV2/8.TBG.hIDUA.co.

In a yet another aspect, the invention provides a composition useful for treating mucopolysaccharidosis type I (MPS I) comprising the rAAV comprising the expression cassette described herein and a pharmaceutically acceptable carrier.

In still a further aspect, the invention provides a method for treating type I mucopolysaccharidosis comprising delivering an effective amount of a composition comprising a pharmaceutically acceptable carrier and a rAAV as described herein.

In yet another aspect, the invention provides a method for treating or ameliorating the symptoms of Hurler, Hurler-Scheie and/or Scheie syndromes.

Still other aspects and advantages of the invention will be apparent from the detailed description of the invention.

BRIEF DESCRIPTION OF THE FIGURES

FIGs.1A-1D provides the sequence of the pENN.AAV.TBG.PI.hIDUA.RGB plasmid [SEQ ID NO:3] described herein, which includes the nucleic acid sequence of the functional human IDUA gene. The gene of the functional IDUA located at position 1251-3213 of FIG1 and its encoded enzyme sequence are also provided in SEQ ID NO: 1 and 2. The sequence is further annotated to identify the sequences of the alpha mic/bik enhancers, the intron 1, the rabbit globulin poly A, the ITRs, the origin of replication.

FIG. 2 provides the circular map of pENN.AAV.TBG.PI.hIDUA.RGB.

DETAILED DESCRIPTION OF THE INVENTION

The compositions described herein provide an expression cassette carrying a human IDUA gene which expresses a therapeutically effective amount of functional human alpha-L-iduronidase enzyme in a human subject.

As used herein, a "therapeutically effective amount" refers to the amount of the composition which delivers and expresses in the target cells an amount of enzyme sufficient to ameliorate or treat the symptoms of Hurler, Hurler-Scheie and/or Scheie syndromes, and or MPS I. "Treatment" may include preventing the worsening of the symptoms of one of the syndromes (or MPS I) and possibly reversal of one or more of the symptoms thereof.

As used herein a "functional human alpha-L-iduronidase" refers to a human alpha-L-iduronidase enzyme which functions normally in humans without MPS1 or an associated syndrome such as Hurler, Hurler-Scheie and/or Scheie syndromes. Conversely, a human alpha-L-iduronidase enzyme variant which causes MPS1 or one of these syndromes is considered non-functional. In one embodiment, a functional human alpha-l-iduronidase has the amino acid sequence of a wild-type human alpha-L-iduronidase described by Bremer et al, Mol. Genet. Metab. 104 (3): 289-294 (2011), NCBI Reference Sequence NP_000194.2, reproduced in SEQ ID NO:2 (653 amino acids). However, several naturally occurring functional polymorphisms (variants) of this sequence have been described and may be encompassed within the scope of this invention. These variants include, with reference to SEQ ID NO: 2, a N-linked glycosylation at position 110 [Chen *et al*, J Proteome Res. , 8:651-661 (2009)], a change from H to Q at amino acid position 33 [SEQ ID NO: 7, VAR_003350; Scott, HS, *et al*, Proc Natl Acad. Sci, 88:9695-9699 (1991); Scott, HS, *et al*, Genomics, 12:1311-1313 (1992); Scott HS, *et al*, Hum Genet, 90:327-327 (1992); Bertola F., *et al*, Hum Mutat, 32: E2189-E2210 (2011)], an H to Q reduction at amino acid position 82 [SEQ ID NO: 8, VAR_020976; Scott, HS, Hum Genet, cited above], a change from R to Q at position 105 [SEQ ID NO: 9, VAR_003356; Scott, Hum Genet, cited above; Bertola *et al*, cited above], a change from G to R at position 116 [SEQ ID NO: 12, VAR_003367], a change from V to A at position 279 [SEQ ID NO: 11, VAR_003359], a change from L to R at position 346 [SEQ ID NO: 12, VAR_017436, Teng, YN, *et al*, Clin. Genet, 57: 131-136 (2000)], a change from A to T at position 361 [SEQ ID NO: 13, VAR_003364; Scott, HS, *et al*, Hum Mol Genet, 2: 1471-1473 (1993); Yogalingam *et al*, Hum Mutat, 24: 199-207

(2004); Bertola, et al, cited above], a change from H to N at position 449 [SEQ ID NO: 14, VAR_066228, Bertola *et al*, cited above], a change from V to I at position 454 [SEQ ID NO: 15, VAR_003372; Yogalingam *et al*, cited above; Bertola, *et al*, cited above], a change from A to T at position 591 [SEQ ID NO: 16, VAR_0066231, Bertola *et al*, cited above], and a change from A to T at position 622 [SEQ ID NO: 17, Scott *et al*, Genomics, cited above]. *See, e.g.,* UniProtKB/Swiss-Prot; www.uniprot.org/uniprot/P35475. In another embodiment, a functional human alpha-L-iduronidase may include a synthetic amino acid sequence in which all or a portion of the first 26 amino acids of SEQ ID NO:2, which correspond to the leader (signal) peptide, are replaced with a heterologous leader peptide. This leader peptide, which is responsible for transporting the enzyme out of the cell through its secretory pathway into the circulation, may be substituted with another suitable leader peptide, *e.g.*, such as the leader peptides from interleukin-2 (IL-2) or oncostatin. Suitable leader peptides are preferably, although not necessarily of human original. Suitable leader peptides may be chosen from http://proline.bic.nus.edu.sg/spdb/zhang270.htm , which is incorporated by reference herein, or may be determined using a variety of computational programs for determining the leader (signal) peptide in a selected protein. Although not limited, such sequences may be from about 15 to about 50 amino acids in length, or about 20 to about 28 amino acids in length, or may be larger or smaller as required. In addition, at least one *in vitro* assay has been described as being useful to assess the enzymatic activity of an IDUA enzyme [*see, e.g.,* Kakkis *et al*, Mol Genet Metabol, 2001 Mar; 72(3): 199-208].

Suitably, the composition and method described herein do not require long term, repeated weekly injections of a therapeutic dose. Without wishing to be bound by theory, the method described herein is believed to be useful for correcting the central nervous system phenotype in addition to somatic symptoms associated with MPSI disorders.

Expression Cassette

The expression cassette is composed of, at a minimum, a gene and its regulatory sequences. Where the cassette is designed to be expressed from a recombinant adeno-associated virus, the expression cassette further contains 5' and 3' AAV inverted terminal repeats (ITRs). These ITR's may be full-length, or one or both of the ITRs may be truncated. For example, a truncated 5' ITR containing a deletion of the D sequence and a terminal resolution site (trs) deletion may be used, e.g., for a self-complementary AAV. In

one embodiment, the rAAV is pseudotyed, *i.e.*, the AAV capsid is from a different source AAV than that the AAV which provides the ITRs. In one embodiment, the ITRs of AAV serotype 2 are used. However, ITRs from other suitable sources may be selected.

As described herein, patients suffering from one of the conditions described herein are delivered an expression cassette which carries a functional human alpha-L-iduronidase (hIDUA) gene under control of regulatory sequences which direct expression of a functional human alpha-L-iduronidase enzyme in the cells.

The expression cassette contains a hIDUA gene characterized by having the nucleotide sequence of SEQ ID NO: 1. This sequence, developed by the inventors, has an identity of about 83% with the published gene sequence of Genbank NP000194.2 encoding SEQ ID NO: 2. In another embodiment, the expression cassette contains a hIDUA gene characterized by having the nucleotide sequence at least about 80% identical to SEQ ID NO: 1 and encodes a functional human alpha-L-iduronidase. In another embodiment, the sequence is at least about 85% identity to SEQ ID NO: 1 or at least about 90% identical to SEQ ID NO:1 and encodes a functional human alpha-L-iduronidase. In one embodiment, the sequence is at least about 95% identical to SEQ ID NO:1, at least about 97% identical to SEQ ID NO:1, or at least about 99% identical to SEQ ID NO: 1 and encodes a functional human alpha-L-iduronidase. In one embodiment, this encompasses full-length hIDUA gene, including the leader peptide sequences of the human alpha-L-iduronidase (*i.e.*, encoding about amino acid 26, or about amino acid 27, to about amino acid 653 of SEQ ID NO:2), corresponding to about 1 to about 78 of SEQ ID NO:1. In another embodiment, the hIDUA gene encodes a functional synthetic human alpha-L-iduronidase enzyme which is synthetic peptide comprising a heterologous leader sequence fused to the secreted portion of a functional alpha-L-iduronidase enzyme, *i.e.*, about amino acids 27 to about 653 of SEQ ID NO: 2 or one of the functional variants thereof which are identified herein.

Identity or similarity with respect to a sequence is defined herein as the percentage of amino acid residues in the candidate sequence that are identical (*i.e.*, same residue) or similar (*i.e.*, amino acid residue from the same group based on common side-chain properties, see below) with the peptide and polypeptide regions provided herein, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Percent (%) identity is a measure of the relationship between two polynucleotides or two polypeptides, as determined by comparing their nucleotide or amino acid sequences,

respectively. In general, the two sequences to be compared are aligned to give a maximum correlation between the sequences. The alignment of the two sequences is examined and the number of positions giving an exact amino acid or nucleotide correspondence between the two sequences determined, divided by the total length of the alignment and multiplied by 100 to give a % identity figure. This % identity figure may be determined over the whole length of the sequences to be compared, which is particularly suitable for sequences of the same or very similar length and which are highly homologous, or over shorter defined lengths, which is more suitable for sequences of unequal length or which have a lower level of homology. There are a number of algorithms, and computer programs based thereon, which are available to be used the literature and/or publically or commercially available for performing alignments and percent identity. The selection of the algorithm or program is not a limitation of the present invention.

Examples of suitable alignment programs including, *e.g.,* the software CLUSTALW under Unix and then be imported into the Bioedit program (Hall, T. A. 1999, BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucl. Acids. Symp. Ser. 41:95-98); the Wisconsin Sequence Analysis Package, version 9.1 (Devereux J. et al., Nucleic Acids Res., 12:387-395, 1984, available from Genetics Computer Group, Madison, Wis., USA). The programs BESTFIT and GAP, may be used to determine the % identity between two polynucleotides and the % identity between two polypeptide sequences.

Other programs for determining identity and/or similarity between sequences include, *e.g.,* the BLAST family of programs available from the National Center for Biotechnology Information (NCB), Bethesda, Md., USA and accessible through the home page of the NCBI at www.ncbi.nlm.nih.gov), the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used; and FASTA (Pearson W. R. and Lipman D. J., Proc. Natl. Acad. Sci. USA, 85:2444-2448, 1988, available as part of the Wisconsin Sequence Analysis Package). SeqWeb Software (a web-based interface to the GCG Wisconsin Package: Gap program).

As used throughout this specification and the claims, the terms "comprising" and "including" are inclusive of other components, elements, integers, steps and the like.

Conversely, the term "consisting" and its variants are exclusive of other components, elements, integers, steps and the like. The term "about" encompasses a variation within and including ± 10%, unless otherwise specified.

In one embodiment, the expression cassette is designed for human liver-directed expression. Thus, a liver-specific promoter is particularly well suited for the expression cassette. In one embodiment, thyroxin binding globulin promoter is selected. In one embodiment, the TBG promoter has the sequence of nucleotides 442 to 901 of FIG. 1. Alternatively, another liver-specific promoter may be selected. Examples of promoters that are tissue-specific are well known for liver and other tissues (albumin, Miyatake *et al.*, (1997) *J. Virol.*, **71**:5124-32; hepatitis B virus core promoter, Sandig *et al.*, (1996) *Gene Ther.*, **3**:1002-9; alpha-fetoprotein (AFP), Arbuthnot *et al.*, (1996) *Hum. Gene Ther.*, **7**:1503-14), bone osteocalcin (Stein *et al.*, (1997) *Mol. Biol. Rep.*, **24**:185-96); bone sialoprotein (Chen *et al.*, (1996) *J. Bone Miner. Res.*, **11**:654-64), lymphocytes (CD2, Hansal *et al.*, (1998) *J. Immunol.*, **161**:1063-8; immunoglobulin heavy chain; T cell receptor chain), neuronal such as neuron-specific enolase (NSE) promoter (Andersen *et al.*, (1993) *Cell. Mol. Neurobiol.*, **13**:503-15), neurofilament light-chain gene (Piccioli *et al.*, (1991) *Proc. Natl. Acad. Sci. USA*, **88**:5611-5), and the neuron-specific vgf gene (Piccioli *et al.*, (1995) *Neuron*, **15**:373-84), among others. Other promoters (not liver-specific) may be selected, but expression cassettes containing same may not have all of the advantages of those with TBG or another liver-specific promoter. Alternatively, a regulatable promoter may be selected. See, e.g., WO 2011/126808B2, incorporated by reference herein.

In one embodiment, the expression cassette comprises one or more expression enhancers. In one embodiment, the expression cassette contains two or more expression enhancers. These enhancers may be the same or may from one another different. For example, an enhancer may include an Alpha mic/bik enhancer. This enhancer may be present in two copies which are located adjacent to one another. Alternatively, the dual copies of the enhancer may be separated by one or more sequences. In still another embodiment, the expression cassette further contains an intron, e.g, the Promega intron. Other suitable introns include those known in the art, e.g., such as are described in WO 2011/126808.

Further, an expression cassette of the invention is provided with a suitable polyadenylation signal. In one embodiment, the polyA sequence is a rabbit globulin poly A.

In one embodiment, the polyA sequence is characterized by that of nt 3261-3387 of FIG. 1. Alternatively, another polyA, *e.g.,* a human growth hormone (hGH) polyadenylation sequence, an SV40 polyA, or a synthetic polyA. Still other conventional regulatory elements may be additional or optionally included in an expression cassette.

In one embodiment, the expression cassette is engineered onto a suitable vector, e.g., a plasmid vector using techniques known to those of skill in the art. Optionally, a composition of the invention may contain a first expression cassette comprising the modified human IDUA gene and a second expression cassette comprising a different gene. In still another embodiment, the functional human IDUA may be expressed from a more than one expression cassette, which may be located on a multiple vectors, *e.g.*, as described in WO 2011/126808.

In one embodiment, the expression cassette is carried by the pENN.TBG.hIDUA.nRBG, which plasmid is used to generate a recombinant adeno-associated virus carrying the expression cassette.

Production of AAV Viral Particles

In one embodiment, the invention provides a recombinant adeno-associated virus (rAAV) particle having an AAV capsid and having packaged therein a 5' inverted terminal repeat (ITR), a human alpha-L-iduronidase (hIDUA) gene under the control of regulatory sequences which control expression thereof, and an AAV 3' ITR, wherein said hIDUA gene has a sequence shown in SEQ ID NO: 1 (FIG 1) or a sequence at least about 95% identical thereto which encodes a functional human alpha-L-iduronidase. One particularly desirable rAAV is AAV2/8.TBG.hIDUA.co.

Methods of preparing AAV-based vectors are known. See, e.g., US Published Patent Application No. 2007/0036760 (February 15, 2007), which is incorporated by reference herein. The use of AAV capsids of AAV8 are particularly well suited for the compositions and methods described herein. The sequences of AAV8 and methods of generating vectors based on the AAV8 capsid are described in US Patent 7,282,199 B2, US 7,790,449, and US 8,318,480, which are incorporated herein by reference. Also well suited for use in the invention are AAV9 capsids. The sequences of AAV9 and methods of generating vectors based on the AAV9 capsid are described in US Patent 7,906,111, which is incorporated by reference herein. However, other AAV capsids may be selected or generated for use in the

invention. The sequences of a number of such AAV are provided in the above-cited US Patent 7,282,199 B2, US 7,790,449, US 8,318,480, and US Patent 7,906,111, and/or are available from GenBank. The sequences of any of the AAV capsids can be readily generated synthetically or using a variety of molecular biology and genetic engineering techniques. Suitable production techniques are well known to those of skill in the art. See, *e.g.*, Sambrook et al, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press (Cold Spring Harbor, NY). Alternatively, oligonucleotides encoding peptides (e.g., CDRs) or the peptides themselves can generated synthetically, *e.g.*, by the well-known solid phase peptide synthesis methods (Merrifield, (1962) *J. Am. Chem. Soc.*, **85**:2149; Stewart and Young, Solid Phase Peptide Synthesis (Freeman, San Francisco, 1969) pp. 27-62). See, also,, D M McCarty et al, "Self-complementary recombinant adeno-associated virus (scAAV) vectors promote efficient transduction independently of DNA synthesis", Gene Therapy, (August 2001), Vol 8, Number 16, Pages 1248-1254. Self-complementary AAVs are described in, e.g., U.S. Patent Nos. 6,596,535; 7,125,717; and 7,456,683, each of which is incorporated herein by reference in its entirety. These and other suitable production methods are within the knowledge of those of skill in the art and are not a limitation of the present invention.

The recombinant adeno-associated virus (AAV) described herein may be generated using techniques which are known. Such a method involves culturing a host cell which contains a nucleic acid sequence encoding an AAV capsid; a functional rep gene; a expression cassette composed of, at a minimum, AAV inverted terminal repeats (ITRs) and a transgene; and sufficient helper functions to permit packaging of the expression cassette into the AAV capsid protein.

The components required to be cultured in the host cell to package an AAV expression cassette in an AAV capsid may be provided to the host cell in *trans*. Alternatively, any one or more of the required components (*e.g.*, expression cassette, *rep* sequences, *cap* sequences, and/or helper functions) may be provided by a stable host cell which has been engineered to contain one or more of the required components using methods known to those of skill in the art. Most suitably, such a stable host cell will contain the required component(s) under the control of an inducible promoter. However, the required component(s) may be under the control of a constitutive promoter. Examples of suitable inducible and constitutive promoters are provided herein, in the discussion of regulatory elements suitable for use with the transgene. In still another alternative, a selected stable

host cell may contain selected component(s) under the control of a constitutive promoter and other selected component(s) under the control of one or more inducible promoters. For example, a stable host cell may be generated which is derived from 293 cells (which contain E1 helper functions under the control of a constitutive promoter), but which contains the rep and/or cap proteins under the control of inducible promoters. Still other stable host cells may be generated by one of skill in the art.

The expression cassette, *rep* sequences, *cap* sequences, and helper functions required for producing the rAAV of the invention may be delivered to the packaging host cell in the form of any genetic element which transfer the sequences carried thereon. The selected genetic element may be delivered by any suitable method, including those described herein. The methods used to construct any embodiment of this invention are known to those with skill in nucleic acid manipulation and include genetic engineering, recombinant engineering, and synthetic techniques. See, *e.g.*, Sambrook et al, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor, NY. Similarly, methods of generating rAAV virions are well known and the selection of a suitable method is not a limitation on the present invention. See, *e.g.*, K. Fisher *et al*, (1993) *J. Virol.*, **70**:520-532 and US Patent No. 5,478,745.

Unless otherwise specified, the AAV ITRs, and other selected AAV components described herein, may be readily selected from among any AAV. These ITRs or other AAV components may be readily isolated using techniques available to those of skill in the art from an AAV sequence. Such AAV may be isolated or obtained from academic, commercial, or public sources (*e.g.*, the American Type Culture Collection, Manassas, VA). Alternatively, the AAV sequences may be obtained through synthetic or other suitable means by reference to published sequences such as are available in the literature or in databases such as, *e.g.*, GenBank®, PubMed®, or the like.

A. The Expression cassette

The expression cassette is as defined herein. In addition, the expression cassette and/or a vector as described herein may contain additional transgene or regulatory sequences. The expression cassette that is packaged into a capsid protein and delivered to a selected host cell.

1. The transgene

The invention may include the use of multiple transgenes. Suitable transgenes may be readily selected by one of skill in the art. The selection of the transgene is not considered to be a limitation of this invention.

2. Regulatory Elements

In addition to the major elements identified above for the expression cassette, the vector also includes conventional control elements which are operably linked to the transgene in a manner which permits its transcription, translation and/or expression in a cell transfected with the plasmid vector or infected with the virus produced by the invention. As used herein, "operably linked" sequences include both expression control sequences that are contiguous with the gene of interest and expression control sequences that act in *trans* or at a distance to control the gene of interest. Expression control sequences include appropriate transcription initiation, termination, promoter and enhancer sequences; efficient RNA processing signals such as splicing and polyadenylation (polyA) signals; sequences that stabilize cytoplasmic mRNA; sequences that enhance translation efficiency (*i.e.*, Kozak consensus sequence); sequences that enhance protein stability; and when desired, sequences that enhance secretion of the encoded product. A great number of expression control sequences, including promoters which are native, constitutive, inducible and/or tissue-specific, are known in the art and may be utilized.

Examples of constitutive promoters include, without limitation, the retroviral Rous sarcoma virus (RSV) LTR promoter (optionally with the RSV enhancer), the cytomegalovirus (CMV) promoter (optionally with the CMV enhancer) [see, *e.g.*, Boshart *et al*, (1985) *Cell*, **41**:521-530], the SV40 promoter, the dihydrofolate reductase promoter, the β-actin promoter, the phosphoglycerol kinase (PGK) promoter, and the EF1 promoter [Invitrogen]. Inducible promoters allow regulation of gene expression and can be regulated by exogenously supplied compounds, environmental factors such as temperature, or the presence of a specific physiological state, *e.g.*, acute phase, a particular differentiation state of the cell, or in replicating cells only. Inducible promoters and inducible systems are available from a variety of commercial sources, including, without limitation, Invitrogen, Clontech and Ariad. Many other systems have been described and can be readily selected by one of skill in the art. Examples of inducible promoters regulated by exogenously supplied compounds, include, the zinc-inducible sheep metallothionine (MT) promoter, the dexamethasone (Dex)-inducible mouse mammary tumor virus (MMTV) promoter, the T7

polymerase promoter system [International Patent Publication No. WO 98/10088]; the ecdysone insect promoter [No *et al*, (1996) *Proc. Natl. Acad. Sci. USA*, **93**:3346-3351], the tetracycline-repressible system [Gossen *et al*, (1992) *Proc. Natl. Acad. Sci. USA*, **89**:5547-5551], the tetracycline-inducible system [Gossen *et al*, (1995) *Science*, **268**:1766-1769, see also Harvey *et al*, (1998) *Curr. Opin. Chem. Biol.*, **2**:512-518], the RU486-inducible system [Wang *et al*, (1997) *Nat. Biotech.*, **15**:239-243 and Wang *et al*, (1997) *Gene Ther.*, **4**:432-441] and the rapamycin-inducible system [Magari *et al*, (1997) *J. Clin. Invest.*, **100**:2865-2872], including, *e.g.,* the Argent™ system which is available from Ariad. Other types of inducible promoters which may be useful in this context are those which are regulated by a specific physiological state, *e.g.*, temperature, acute phase, a particular differentiation state of the cell, or in replicating cells only.

Another embodiment of the transgene includes a gene operably linked to a tissue-specific promoter. For instance, if expression in skeletal muscle is desired, a promoter active in muscle should be used. These include the promoters from genes encoding skeletal β-actin, myosin light chain 2A, dystrophin, desmin, MHC, muscle creatine kinase, as well as synthetic muscle promoters with activities higher than naturally-occurring promoters (see Li *et al.*, (1999) *Nat. Biotech.*, **17**:241-245). Examples of promoters that are tissue-specific are known for CNS/neuronal include, e.g., neuron-specific enolase (NSE) promoter (Andersen *et al.*, (1993) *Cell. Mol. Neurobiol.,* **13**:503-15), neurofilament light-chain gene (Piccioli *et al.*, (1991) *Proc. Natl. Acad. Sci. USA,* **88**:5611-5), and the neuron-specific vgf gene (Piccioli *et al.*, (1995) *Neuron,* **15**:373-84), among others. In another embodiment, the native promoter for the transgene will be used. The native promoter may be preferred when it is desired that expression of the transgene should mimic the native expression. The native promoter may be used when expression of the transgene must be regulated temporally or developmentally, or in a tissue-specific manner, or in response to specific transcriptional stimuli. In a further embodiment, other native expression control elements, such as enhancer elements, polyadenylation sites or Kozak consensus sequences may also be used to mimic the native expression.

The combination of the transgene, promoter/enhancer, and 5' and 3' AAV ITRs is referred to as an expression cassette for ease of reference herein. Provided with the teachings of this invention, the design of such an expression cassette can be made by resort to conventional techniques.

3. Delivery of the Expression Cassette to an AAV Packaging Host Cell

The expression cassette can be carried on any suitable vector, *e.g.*, a plasmid, which is delivered to a host cell. The plasmids useful in this invention may be engineered such that they are suitable for replication and, optionally, integration in prokaryotic cells, mammalian cells, or both. These plasmids (or other vectors carrying the expression cassette) contain sequences permitting replication of the expression cassette in eukaryotes and/or prokaryotes and selection markers for these systems. Selectable markers or reporter genes may include sequences encoding kanamycin, geneticin, hygromicin or purimycin resistance, among others. The plasmids may also contain certain selectable reporters or marker genes that can be used to signal the presence of the vector in bacterial cells, such as ampicillin resistance. Other components of the plasmid may include an origin of replication and an amplicon, such as the amplicon system employing the Epstein Barr virus nuclear antigen. This amplicon system, or other similar amplicon components permit high copy episomal replication in the cells. Preferably, the molecule carrying the expression cassette is transfected into the cell, where it may exist transiently. Alternatively, the expression cassette may be stably integrated into the genome of the host cell, either chromosomally or as an episome. In certain embodiments, the expression cassette may be present in multiple copies, optionally in head-to-head, head-to-tail, or tail-to-tail concatamers. Suitable transfection techniques are known and may readily be utilized to deliver the expression cassette to the host cell.

Generally, when delivering the vector comprising the expression cassette by transfection, the vector is delivered in an amount from about 5 μg to about 100 μg DNA, about 10 μg to about 50 μg DNA to about 1 x 10^4 cells to about 1 x 10^{13} cells, or about 1 x 10^5 cells. However, the relative amounts of vector DNA to host cells may be adjusted, taking into consideration such factors as the selected vector, the delivery method and the host cells selected.

B. Packaging Host Cells

In addition to the expression cassette, the host cell contains the sequences which drive expression of an AAV capsid protein of the invention in the host cell and rep sequences of the same source as the source of the AAV ITRs found in the expression cassette, or a cross-complementing source. The packaging host cell also requires helper

functions in order to package the rAAV of the invention. Such helper functions are well known in the art and will not be duplicated herein. Similarly, methods for producing suitable vectors having AAV capsids are known. [*See, e.g.*, US Published Patent Application No. US 2007/0036760].

The construct of a rAAV encoding an expression cassette described herein same can be suspended in a physiologically compatible carrier, may be administered to a subject. In one embodiment, the carrier is sterile saline alone or, optionally, with any of a number of buffering solutions (*e.g.*, phosphate buffered saline). Other exemplary carriers include lactose, sucrose, calcium phosphate, gelatin, dextran, agar, pectin, sesame oil, and water. The selection of the carrier is not a limitation of the present invention.

Optionally, the compositions of the invention may contain, in addition to the rAAV and carrier(s), other conventional pharmaceutical ingredients, such as preservatives, or chemical stabilizers. In one embodiment, delivery is via intravenous delivery. However, still other routes of administration may be selected. Alternatively or additionally, routes of administration may be combined, if desired.

In one embodiment, the invention includes a lyophilized composition which contains an rAAV as described herein, or a mixture of rAAV, in lyophilized form. Optionally, one or more stabilizers or preservatives is present in this composition. Suitably, for use, a lyophilized composition is reconstituted with a suitable diluent, e.g., sterile saline or a buffered saline.

Dosages of the viral vector will depend primarily on factors such as the condition being treated, the age, weight and health of the patient, and may thus vary among patients. For example, a therapeutically effective dosage of the viral vector is generally in the range of from about 0.1 mL to about 100 mL, or about 0.1 mL to about 10 mL, or about 0.1 mL to about 5 mL, or about 0.5 mL to about 1 mL, of solution containing concentrations of from about 3×10^9 to 3×10^{13} genomes viral vector (particles)/mL aqueous suspending agent. Another exemplary dosage is about 3×10^9 to 3×10^{13} AAV genomes per 1 kg. One suitable volume is about 1 mL. In another embodiment, a therapeutically effective dose of the rAAV construct is in the range of about 0.001 ng to about 1000 mg/70 kg animal, which may be delivered in a single dosage or over a series of two or more doses. Other suitable dosages may be determined. The dosage will be adjusted to balance the therapeutic benefit

against any side effects and such dosages may vary depending upon the therapeutic application for which the recombinant vector is employed.

METHODS OF TREATMENT

The compositions of the present invention avoid complications of enzyme replacement therapy related to immune response to the recombinant enzyme which can range from mild to full-blown anaphylaxis as well as complications of life-long peripheral access such as local and systemic infections. Further, in contrast to ERT, the composition of the invention does not require long term, repeated weekly injections. Without wishing to be bound by theory, the liver-directed therapeutic method described herein is believed to be useful for correcting the central nervous system phenotype associated with MPSI disorders by providing efficient, long-term gene transfer afforded by vectors with high transduction efficiency could provide continuous, elevated circulating IDUA levels, which provides therapeutic leverage across the blood brain barrier. In addition, AAV liver gene transfer may provide active tolerance and prevent antibody formation against the enzyme.

A method for treating type I mucopolysaccharidosis comprising delivering a therapeutically effective amount of a modified hIDUA expression cassette as described herein is provided. Also provided is a method for treating and/or ameliorating the symptoms of Hurler, Hurler-Scheie and Scheie syndromes.

In one embodiment, the rAAV is delivered intravenously.

In another embodiment, the rAAV is delivered in an amount of about 3×10^9 to about 3×10^{12} is delivered to the subject. While a single administration of the rAAV is anticipated to be effective, since the liver is a regenerative organ, administration by be repeated (e.g., quarterly, bi-annually, annually, or as otherwise needed. Optionally, an initial dose of a therapeutically effective amount may be delivered over split infusion sessions, taking into consideration the age and ability of the subject to tolerate infusions. However, repeated weekly injections of a full therapeutic dose are not required, providing an advantage to the patient in terms of both comfort and therapeutic outcome.

The following examples are illustrative only and are not a limitation on the invention described herein.

Example 1 - Transgene and vector production

A modified nucleotide sequence encoding a functional human alpha-L-iduronidase was synthesized. The resulting sequence is particularly well suited for human expression and has less than about 90% identical to the functional human IDUA gene (hIDUA; Genbank NP000194.2). The resultant transgene was then inserted into a plasmid containing *cis* elements necessary for packaging into an AAV vector available from UPenn Vector Core using engineered *MluI* and *SalI* sites. Gene expression was driven by the human thyroid binding globulin (TBG, Hayashi Y, Mori Y, Janssen OE, et al. Human thyroxine-binding globulin gene: complete sequence and transcriptional regulation. Mol Endocrinol 1993; 7: 1049–1060]. The resulting plasmid, shown in Figure 2, pENN.AAV.TBG.PI.hIDUA.RGB contains the modified hIDUA gene under the control of expression control sequences including the liver-specific TBG promoter. The plasmid further contains the AAV2 5' ITR, tandem repeats of the alpha mic/bic enhancers, the TBG promoter, a Promega intron sequence, the modified human IDUA gene of SEQ ID NO: 1, a rabbit globulin poly A, and an AAV2 – 3' ITR.

Large scale vector preparations were made essentially as described by Lock et al. [Rapid, simple, and versatile manufacturing of recombinant adeno-associated viral vectors at scale. Hum Gene Ther 21(10): 1259-1271. (2010)]. PEI-based transfections were performed in 10 layer cell stacks containing 75% confluent monolayers of HEK293 cells. 10L of feedstock culture medium from the cell stacks was clarified and then concentrated by tangential flow filtration. The concentrated clarified feedstock was purified over iodixanol (Optiprep; Sigma Chemical Co., St Louis, MO) gradients. All fractions directly below a visible contaminating protein band were collected and pooled. Pooled fractions were diafiltered against of PBS/35mM NaCl and concentrated using Amicon Ultra 15 spin concentrators (Millipore). Glycerol was added to the diafiltered, concentrated product to 5% final and the preparation was aliquoted and stored at -80 °C. The resulting vectors are termed herein AAV8.TBG.hIDUA or AAV2/8.TBG.hIDUA. In certain locations, the recombinant AAV particles are referred to as AAV8.TBG.hIDUAco or AAV2/8.TBG.hIDUAco. The plasmid further contains the AAV2 5' ITR, tandem repeats of the alpha mic/bic enhancers, the TBG promoter, a Promega intron sequence, the modified human IDUA gene of SEQ ID NO: 1, a rabbit globulin poly A, and an AAV2 – 3' ITR.

Example 2 –

A. Cell based assays

HEK 293 cells were maintained in growth medium containing Dulbecco's Modified Eagle Medium (DMEM; Gibco®, Life Technologies™) with 5% fetal bovine serum (FBS; XXX), 1% penicillin/streptomycin (p/s; Life Technologies ™). Plasmid DNA transfections were carried out using Lipofectamine™ 2000 (Invitrogen™, Life Technologies™) according to the manufacturer's recommendations. Briefly, cells were plated at a density of 5x10^5 cells/well in 6-well tissue culture dishes in transfection medium (DMEM + 5%FBS, no p/s) and allowed to adhere overnight at 37° in 5%CO_2. On the next day, cells were checked for 90-95% confluency and the media was refreshed. Plasmid DNA and Lipofectamine™ 2000 were diluted with Opti-MEM I ® Reduced Serum Medium (without serum) for a final ratio of 1:2.5 (DNA: Lipofectamine™ 2000). The Lipofectamine™ 2000 transfection solution was incubated for five minutes at 22°C before mixing with the DNA solution. This final transfection mixture containing the DNA: Lipofectamine™ 2000 solution was incubated further for 20 minutes (22°C) before addition to the wells containing cells and media. Mock cells received no plasmid DNA and a plasmid encoding for eGFP was used as a transfection control. Three wells were transfected for each construct tested. Cells were incubated at 37° in 5%CO_2; media was replaced with growth media four hours later. Contents of each well were harvested 72 hours later and collected at 4000rpm for 15 minutes at 4°C. Cells were resuspended in 100µls/well lysis buffer (0.2% Triton X-100, 0.9% NaCl, pH4.0) and freeze/thawed three times with vortexing. In addition, lysates were treated with Benzonase for 30 minutes at 37°C before the final freeze/thaw. Cell debris was pelleted at 10 000rpm (4°C) for 10 minutes and final clarified cell lysates were placed on ice and immediately assayed for enzyme activity.

B. Tissue lysis and protein extraction

Frozen tissues were semi-thawed in a box on a bed of dry ice and small pieces of wet tissue were cut (~20mgs, ~10 mgs of spleen) up in a small petri dish. The pre-processed tissues were then submerged in a 2-ml eppendorph with 1ml lysis buffer (0.2% Triton X-100, 0.9% NaCl, pH4.0) and a 5mm steel bead. Samples were homogenized on a tissue-lyzer at 30Hz for 2 minutes. Homogenized samples were briefly spun at 6000 rpm for

30 seconds and the 5mm steel beads were removed. Tissue lysates were further disrupted by sonication using a 1-1/16" diameter microhorn and frozen overnight at -80°C. Processed samples were thawed the next day at 22°C and clarified by centrifugation (10 000rpm/10 minutes/4°C). Floating lipid layers from brain, or other fatty tissues, were aspirated before assay. Samples were then stored on wet ice and assayed immediately for enzyme activity.

C. Protein estimation

Total protein was estimated using the Coomassie based Bradford assay (Thermo Scientific) following the manufacturer's protocol. Briefly, a standard curve was set up using bovine serum albumin (BSA) to generate a working range from 1-25µg/ml and a blank accounting for the protein dilution buffer with no BSA. Samples were diluted twofold from 1/300 -1/1200 and mixed at a 1:1 ratio of diluted protein: Bradford reagent in a 96-well flat-bottom dish. Samples were allowed to equilibrate at 22°C for 15 minutes and absorbance values were collected on a plate reader at the suggested wavelength of 595nm. Raw values were converted to µg/ml concentrations using the standard curve with blank correction. Microgram quantities were then converted and reported in milligrams.

D. Enzyme activity assays

IDUA enzyme activity was assayed using 4-Methylumbelliferyl alpha-L-Idopyranosiduronic Acid, Cyclohexylammonium Salt (4-MU-Ido; Toronto Research Chemicals, Inc.) as a substrate according to previously published methods [Kakkis et al, Mol Genet Metab, 2001 Mar; 72(3): 199-208]. Briefly, 5-15µls of lysates, or serum, were brought up to 100µls with double distilled water (ddH_2O) and 100µls of 100µM 4-MU-Ido substrate, diluted with reaction buffer (0.1M sodium acetate pH3.5, 0.15M NaCl, 0.05% Triton X-100) was combined in a methylacrylate cuvette (Thermo Scientific). Reactions were incubated for 1-3 hours in a 37°C water bath and ended with the addition of a 1x stop buffer (290mM glycine, 180mM sodium carbonate, pH 10.5). Products were read on a QuantiFluor™-ST (Promega) through the UV channel (Ex 365 nm, Em 440 - 470 nm). Raw fluorescence values were recorded and converted to nmol/ml/hr using a standard curve of known quantities of 4-Methylumbelliferone (M-5410; Biosynth®). Cell and tissue lysates were normalized to estimated protein values (nmol/mg/hr; see methods section entitled "protein estimation").

E. DNA extraction and genome copy analysis

Taqman PCR was used to determine the vector DNA load in diploid cells. For detection and quantification of vector genomes by real-time PCR, total cellular DNA was extracted from tissues using a QIAamp DNA Mini Kit (Qiagen, Valencia, CA, USA). Primer and probe sets were designed to target the nRBG polyA region of the vector, using the following sequences; forward: GCCAAAAATTATGGGGACAT, reverse: ATTCCAACACACTATTGCAATG, probe: 6FAM-ATGAAGCCCCTTGAGCATCTGACTTCT-TAMRA. Standard curves for vector genome quantification were established with the *cis* plasmids used for the production of the corresponding vector. The PCR was performed with a TaqMan Universal PCR Master Mix (Applied Biosystems, Foster City, CA, USA) with 200 ng total cellular DNA as template, 300 nM primers, and 200 nM probes each. Cycles were for 2 min at 50°C, 10 min at 95°C, 40 cycles of 15 s at 95°C, and 1 min at 60°C.

F. Immunoblotting

Immunoblotting was performed according to standard methods. In brief, the NuPAGE gel system (Life Technologies), 4-12% bis-tris gels was used. Transfer was following 30 minutes at 20V to a PVDF membrane. The block was 10% NFDM in T-PBS (overnight). The primary MAb was mouse anti-human IDUA 1:300 (1.5 hours); 1% NFDM in T-PBS. Secondary: HRP-linked rabbit anti-mouse 1:3000 (1hr); 1% NFDM in T-PBS Detection was by SuperSignal West Dura Chemiluminescent Substrate (Thermo Scientific), 30 second exposure on x-ray film.

Example 3 – In Vivo Studies in Mice and Dogs

IDUA deficiencies can be found in dogs, allowing for study of the disease and therapies in a large animal. MPS I dogs carry a recessive (null) mutation in the IDUA gene, in which a G>A mutation in the donor splice site of intron 1 creates a premature termination codon at the exon-intron junction [Menon, K.P., P.T. Tieu, and E.F. Neufeld, Architecture of the canine IDUA gene and mutation underlying canine mucopolysaccharidosis I. Genomics, 1992. 14(3): p. 763-8.]. The course of disease in the dog is analogous to Hurler-Scheie syndrome; disease manifestations include significant skeletal disease, including chest deformity.

Urine GAG analysis is a biochemical marker used to determine efficacy of treatments for MPS I in the clinical setting.

Accumulation of glycosaminoglycans (GAGs) were evaluated in major organs by Alcian Blue (pH1) stain of paraffin sections. The accumulation of unprocessed GAG within cells are particularly well visualized on 1 μm thin sections from plastic-embedded tissues stained with Toluidine Blue. Thin sections (1 μm) of epon-embedded tissues, stained with Toluidine Blue. This shows cells containing storage material ("foamy, sponge cells").

Immunohistochemistry was performed with antibody against ganglioside GM3 in brain. Shows abnormal storage of GM3 in neurons. The cortex was evaluated in dogs and cortex and hypothalamus in mice. Expression of human IDUA in liver was evaluated by immunofluorescence.

A. Mouse Studies

AAV8.TBG.modified hIDUA was prepared as described in Example 1. Mice (about 3 months) were injected intravenously at doses of about 1 x10^{11} GC, 3 x 10^{10} GC, 3 x 10^{9} GC, 1 x10^{9} GC and evaluated ~ 2 weeks post injection.

The results showed diminished or complete absence of GAG staining in the animals dosed at 1 x 10^{11}, 3 x 10^{10}, and 3 x 10^{9}. In these animals, diminished or complete absence of storage lesions was observed in thin sections.

In the animals dosed at 1 x 10^{9} GAG storage looks more or less as in untreated mice and storage lesions look more or less as in untreated mice

For GM3 storage, only the animals dosed at 1 x 10^{11} GC and 3 x 10^{10} GC have been evaluated, and a very weak improvement in GM3 storage in neurons was observed.

Strong expression (100% of hepatocytes) of IDUA was observed in animals dosed at 1 x 10^{11} GC. This drops off with lower doses, with only very few positive hepatocytes visible at 1 x 10^{9} GC.

B. Canine Studies

AAV8.TBG.modified hIDUA was prepared as described in Example 1. Dogs (about 8 months age) were injected intravenously at a dose of 1 x10^{11} GC and evaluated after four months post injection (i.e. 1 year old).

This study shows reversal of storage lesions. More particularly, virtually complete clearance of GAG storage in all major organs is seen by Alcian Blue stain. No storage lesions are observed in heart, kidney or liver thin sections. A reduction or complete clearance of GM3 accumulation is observed in neurons. Expression of IDUA in liver is observed by immunofluorescence in >95% of hepatocytes.

Example 4 – Treatment of Hurler-Scheie with AAV2/8.TBG.hIDUA

AAV8-mediated gene transfer of IDUA will be evaluated in Hurler-Scheie patients. The subjects would receive a single infusion of vector into a peripheral vein which based on pre-clinical data should lead to stable production of the enzyme at levels that are close to what is obtained in normal subjects. The trial may involve different doses of vector for example, $3x10^{11}$ GC/kg; $1x10^{12}$ GC/kg; $3x10^{12}$ GC/kg and please add dose range. The most non-invasive assessment of efficacy is the level of urine GAG which are elevated in the disease and partially corrected following ERT. Transgene engraftment and its level of expression will be determined by measuring serum IDUA. Urine GAG will also be measured before and after gene therapy.

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A sequence listing labelled "Z6622PCT_ST25.txt" is being filed herewith in electronic form; this sequence listing is hereby incorporated by reference. All publications, patents, and patent applications cited in this application, including priority application US Patent Application No. 61/788,724, filed March 15, 2013, are hereby incorporated by reference in their entireties as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications can be made thereto without departing from the spirit or scope of the appended claims.

SEQUENCE LISTING

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His Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg
        35                  40                  45

Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
    50                  55                  60

Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
65                  70                  75                  80

Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
                85                  90                  95

Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr
            100                 105                 110

His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro
        115                 120                 125

Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu
    130                 135                 140

Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala
145                 150                 155                 160

Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn
                165                 170                 175

Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser
            180                 185                 190

Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly
        195                 200                 205

Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
    210                 215                 220

Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His
225                 230                 235                 240

Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu
                245                 250                 255

Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile
            260                 265                 270

Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro
        275                 280                 285

Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val
    290                 295                 300
```

```
Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala
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Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn
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Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe
            340                 345                 350

Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg
        355                 360                 365

Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys
    370                 375                 380

Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln
385                 390                 395                 400

Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His
                405                 410                 415

Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp
            420                 425                 430

Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala
        435                 440                 445

His Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro
    450                 455                 460

Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu
465                 470                 475                 480

Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro
                485                 490                 495

Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala
            500                 505                 510

Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro
        515                 520                 525

Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro
    530                 535                 540

Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr
545                 550                 555                 560

Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys
                565                 570                 575
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Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr
            580                 585                 590

Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser
        595                 600                 605

Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp
    610                 615                 620

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu
625                 630                 635                 640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
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<222> (221)..(320)
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<223> f1\ori (located on complement)

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<222> (5566)..(6381)
<223> kanamycin resistance located on complementary strand

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aggggttcct tgtagttaat gattaacccg ccatgctact tatctaccag ggtaatgggg 180

atcctctaga actatagcta gaattcgccc ttaagctagc aggttaattt ttaaaaagca 240

gtcaaaagtc caagtggccc ttggcagcat ttactctctc tgtttgctct ggttaataat 300

ctcaggagca caaacattcc agatccaggt taatttttaa aaagcagtca aaagtccaag 360

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aatttataac taagagtgct ctagttttgc aatacaggac atgctataaa aatggaaaga 900

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tttgcctttc tctccacagg tgtccactcc cagttcaatt acagctctta aggctagagt 1200

acttaatacg actcactata ggctagcctc gagaattcac gcgtgccacc atg cgg 1256
Met Arg
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ccc ctg agg cct aga gct gct ctg ctg gca ctg ctg gcc agt ctg ctg 1304
Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser Leu Leu
5 10 15

gct gcc cct cct gtg gcc cct gcc gaa gcc cct cac ctg gtg cat gtg 1352
Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val His Val
20 25 30

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gat gcc gcc aga gcc ctg tgg cct ctg cgg aga ttc tgg cgg agc acc        1400
Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr
35                  40                  45                  50

ggc ttt tgc ccc cca ctg cct cac agc cag gcc gac cag tac gtg ctg        1448
Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr Val Leu
                55                  60                  65

agc tgg gac cag cag ctg aac ctg gcc tac gtg ggc gcc gtg ccc cac        1496
Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val Pro His
            70                  75                  80

aga ggc atc aaa cag gtg aga acc cac tgg ctg ctg gaa ctg gtg aca        1544
Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu Val Thr
        85                  90                  95

acc cgg ggc tcc acc ggc aga ggc ctg agc tac aac ttc acc cac ctg        1592
Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr His Leu
    100                 105                 110

gac ggc tac ctg gac ctg ctg aga gag aac cag ctg ctg ccc ggc ttc        1640
Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro Gly Phe
115                 120                 125                 130

gag ctg atg ggc agc gcc agc ggc cac ttc acc gac ttc gag gac aag        1688
Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu Asp Lys
                135                 140                 145

cag caa gtc ttt gag tgg aag gac ctg gtg tcc agc ctg gcc aga cgg        1736
Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala Arg Arg
            150                 155                 160

tac atc ggc aga tac gga ctg gcc cac gtg tcc aag tgg aac ttc gag        1784
Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn Phe Glu
        165                 170                 175

aca tgg aac gag ccc gac cac cac gac ttc gac aac gtg tca atg acc        1832
Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser Met Thr
    180                 185                 190

atg cag ggc ttt ctg aac tac tac gac gcc tgc tcc gag ggc ctg aga        1880
Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly Leu Arg
195                 200                 205                 210

gcc gcc agt cct gcc ctg aga ctg ggc gga ccc ggc gat agc ttc cac        1928
Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser Phe His
                215                 220                 225

acc ccc ccc aga agc ccc ctg agc tgg ggc ctg ctg aga cac tgc cac        1976
Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His Cys His
            230                 235                 240

gac ggc acc aat ttc ttc acc ggc gag gcc ggc gtg cgg ctg gac tac        2024
Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu Asp Tyr
        245                 250                 255

atc agc ctg cac cgg aag ggc gcc aga agc agc atc agc atc ctg gaa        2072
Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile Leu Glu
    260                 265                 270

cag gaa aag gtc gtc gcc cag cag atc cgg cag ctg ttc ccc aag ttc        2120
Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro Lys Phe
275                 280                 285                 290

gcc gac acc ccc atc tac aac gac gag gcc gac ccc ctg gtg gga tgg        2168
Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val Gly Trp
                295                 300                 305

tca ctg cct cag cct tgg aga gcc gac gtg acc tac gcc gct atg gtg        2216
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Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala Met Val
            310                 315                 320

gtg aaa gtg atc gcc cag cat cag aac ctg ctg ctg gcc aac acc acc       2264
Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn Thr Thr
        325                 330                 335

agc gcc ttc cct tac gcc ctg ctg agc aac gac aac gcc ttc ctg agc       2312
Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu Ser
    340                 345                 350

tac cac ccc cac ccc ttc gcc cag aga acc ctg acc gcc cgg ttc cag       2360
Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln
355                 360                 365                 370

gtg aac aac acc aga ccc ccc cac gtg cag ctg ctg aga aag ccc gtg       2408
Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys Pro Val
                375                 380                 385

ctg acc gct atg gga ctg ctg gct ctg ctg gac gag gaa cag ctg tgg       2456
Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln Leu Trp
            390                 395                 400

gcc gaa gtg tcc cag gcc ggc acc gtg ctg gac agc aat cat aca gtg       2504
Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His Thr Val
        405                 410                 415

ggc gtg ctg gcc tcc gcc cac aga cct cag gga ccc gcc gat gct tgg       2552
Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp Ala Trp
    420                 425                 430

cgg gct gcc gtg ctg atc tac gcc agc gac gat acc aga gcc cac ccc       2600
Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His Pro
435                 440                 445                 450

aac aga tcc gtg gcc gtg acc ctg cgg ctg aga ggc gtg cca cca ggc       2648
Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro Gly
                455                 460                 465

cct gga ctg gtg tac gtg acc aga tac ctg gac aac ggc ctg tgc agc       2696
Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys Ser
            470                 475                 480

ccc gac ggc gaa tgg cgc aga ctg ggc aga cct gtg ttc ccc acc gcc       2744
Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro Thr Ala
        485                 490                 495

gag cag ttc cgg cgg atg aga gcc gct gag gat cct gtg gct gct gcc       2792
Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala Ala Ala
    500                 505                 510

cct aga cct ctg cct gct ggc ggc aga ctg acc ctg agg ccc gct ctg       2840
Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro Ala Leu
515                 520                 525                 530

aga ctg cct agt ctg ctg ctg gtg cac gtg tgc gcc agg ccc gag aag       2888
Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro Glu Lys
                535                 540                 545

cct ccc ggc cag gtg aca aga ctg aga gcc ctg ccc ctg acc cag ggc       2936
Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln Gly
            550                 555                 560

cag ctg gtg ctg gtg tgg tcc gat gag cac gtg ggc agc aag tgc ctg       2984
Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu
        565                 570                 575

tgg acc tac gag atc cag ttc agc cag gac ggc aag gcc tac acc ccc       3032
Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr Pro
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    580                 585                 590

gtg tcc cgg aag ccc agc acc ttc aac ctg ttc gtg ttc agc ccc gat      3080
Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser Pro Asp
595                 600                 605                 610

aca ggc gcc gtg tcc ggc tct tat aga gtg cgg gcc ctg gac tac tgg      3128
Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp Tyr Trp
                615                 620                 625

gcc aga ccc ggc cct ttc agc gac ccc gtg ccc tac ctg gaa gtg ccc      3176
Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu Val Pro
            630                 635                 640

gtg cct aga ggc ccc cct agc ccc ggc aac cct tga gtcgacccgg           3222
Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
        645                 650

gcggcctcga ggacggggtg aactacgcct gaggatccga tctttttccc tctgccaaaa    3282

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tgaccatgat tacgccagat ttaattaagg ccttaattag g 6863

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<400> 4

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Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val
20 25 30

His Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg
35 40 45

Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
50 55 60

Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
65 70 75 80

Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
85 90 95

Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr
100 105 110

His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro
115 120 125

Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu
130 135 140

Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala
145 150 155 160

Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn
165 170 175

Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser
180 185 190

Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly
195 200 205

Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
210 215 220

Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His
225 230 235 240

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Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu
                245                 250                 255

Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile
            260                 265                 270

Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro
        275                 280                 285

Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val
    290                 295                 300

Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala
305                 310                 315                 320

Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn
                325                 330                 335

Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe
            340                 345                 350

Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg
        355                 360                 365

Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys
    370                 375                 380

Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln
385                 390                 395                 400

Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His
                405                 410                 415

Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp
            420                 425                 430

Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala
        435                 440                 445

His Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro
    450                 455                 460

Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu
465                 470                 475                 480

Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro
                485                 490                 495

Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala
            500                 505                 510
```

```
Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro
        515                 520                 525

Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro
    530                 535                 540

Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr
545                 550                 555                 560

Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys
                565                 570                 575

Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr
            580                 585                 590

Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser
        595                 600                 605

Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp
    610                 615                 620

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu
625                 630                 635                 640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
                645                 650
```

<210> 5
<211> 20
<212> DNA
<213> synthetic

<400> 5
gccaaaaatt atggggacat 20

<210> 6
<211> 27
<212> DNA
<213> probe for nRBG polyA region of vector

<400> 6
atgaagcccc ttgagcatct gacttct 27

<210> 7
<211> 653
<212> PRT
<213> hIDUA variant H to Q at aa pos 33 [VAR_003350]

<400> 7

```
Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser
1               5                   10                  15

Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val
            20                  25                  30
```

```
Gln Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg
        35                  40                  45

Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
    50                  55                  60

Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
65                  70                  75                  80

Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
                85                  90                  95

Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr
            100                 105                 110

His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro
        115                 120                 125

Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu
    130                 135                 140

Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala
145                 150                 155                 160

Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn
                165                 170                 175

Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser
            180                 185                 190

Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly
        195                 200                 205

Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
    210                 215                 220

Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His
225                 230                 235                 240

Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu
                245                 250                 255

Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile
            260                 265                 270

Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro
        275                 280                 285

Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val
    290                 295                 300

Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala
```

305 310 315 320

Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn
325 330 335

Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe
340 345 350

Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg
355 360 365

Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys
370 375 380

Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln
385 390 395 400

Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His
405 410 415

Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp
420 425 430

Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala
435 440 445

His Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro
450 455 460

Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu
465 470 475 480

Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro
485 490 495

Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala
500 505 510

Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro
515 520 525

Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro
530 535 540

Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr
545 550 555 560

Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys
565 570 575

Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr
580 585 590

```
Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser
        595                 600                 605

Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp
    610                 615                 620

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu
625                 630                 635                 640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
                645                 650
```

<210> 8
<211> 653
<212> PRT
<213> hIDUA variant

<400> 8

```
Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser
1               5                   10                  15

Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val
            20                  25                  30

His Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg
        35                  40                  45

Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
    50                  55                  60

Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
65                  70                  75                  80

Pro Gln Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
                85                  90                  95

Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr
            100                 105                 110

His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro
        115                 120                 125

Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu
    130                 135                 140

Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala
145                 150                 155                 160

Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn
                165                 170                 175
```

```
Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser
            180                 185                 190

Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly
        195                 200                 205

Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
    210                 215                 220

Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His
225                 230                 235                 240

Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu
                245                 250                 255

Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile
            260                 265                 270

Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro
        275                 280                 285

Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val
    290                 295                 300

Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala
305                 310                 315                 320

Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn
                325                 330                 335

Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe
            340                 345                 350

Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg
        355                 360                 365

Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys
    370                 375                 380

Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln
385                 390                 395                 400

Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His
                405                 410                 415

Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp
            420                 425                 430

Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala
        435                 440                 445

His Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro
```

```
     450                 455                 460

Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu
465                 470                 475                 480

Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro
                485                 490                 495

Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala
            500                 505                 510

Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro
        515                 520                 525

Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro
    530                 535                 540

Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr
545                 550                 555                 560

Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys
                565                 570                 575

Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr
            580                 585                 590

Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser
        595                 600                 605

Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp
    610                 615                 620

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu
625                 630                 635                 640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
                645                 650
```

<210> 9
<211> 653
<212> PRT
<213> hIDUA variant

<400> 9

```
Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser
1               5                   10                  15

Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val
            20                  25                  30

His Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg
        35                  40                  45
```

```
Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
    50                  55                  60

Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
65                  70                  75                  80

Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
                85                  90                  95

Val Thr Thr Arg Gly Ser Thr Gly Gln Gly Leu Ser Tyr Asn Phe Thr
            100                 105                 110

His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro
        115                 120                 125

Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu
    130                 135                 140

Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala
145                 150                 155                 160

Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn
                165                 170                 175

Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser
            180                 185                 190

Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly
        195                 200                 205

Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
    210                 215                 220

Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His
225                 230                 235                 240

Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu
                245                 250                 255

Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile
            260                 265                 270

Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro
        275                 280                 285

Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val
    290                 295                 300

Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala
305                 310                 315                 320
```

```
Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn
                325                 330                 335

Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe
            340                 345                 350

Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg
        355                 360                 365

Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys
    370                 375                 380

Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln
385                 390                 395                 400

Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His
                405                 410                 415

Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp
            420                 425                 430

Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala
        435                 440                 445

His Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro
    450                 455                 460

Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu
465                 470                 475                 480

Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro
                485                 490                 495

Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala
            500                 505                 510

Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro
        515                 520                 525

Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro
    530                 535                 540

Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr
545                 550                 555                 560

Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys
                565                 570                 575

Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr
            580                 585                 590

Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser
```

595 600 605

Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp
610 615 620

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu
625 630 635 640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
645 650

<210> 10
<211> 653
<212> PRT
<213> hIDUA variant

<400> 10

Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser
1 5 10 15

Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val
20 25 30

His Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg
35 40 45

Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
50 55 60

Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
65 70 75 80

Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
85 90 95

Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr
100 105 110

His Leu Asp Arg Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro
115 120 125

Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu
130 135 140

Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala
145 150 155 160

Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn
165 170 175

Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser
180 185 190

```
Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly
        195                 200                 205

Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
    210                 215                 220

Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His
225                 230                 235                 240

Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu
                245                 250                 255

Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile
            260                 265                 270

Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro
        275                 280                 285

Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val
    290                 295                 300

Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala
305                 310                 315                 320

Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn
                325                 330                 335

Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe
            340                 345                 350

Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg
        355                 360                 365

Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys
    370                 375                 380

Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln
385                 390                 395                 400

Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His
                405                 410                 415

Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp
            420                 425                 430

Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala
        435                 440                 445

His Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro
    450                 455                 460
```

```
Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu
465                 470                 475                 480

Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro
                485                 490                 495

Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala
            500                 505                 510

Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro
        515                 520                 525

Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro
    530                 535                 540

Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr
545                 550                 555                 560

Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys
                565                 570                 575

Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr
            580                 585                 590

Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser
        595                 600                 605

Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp
    610                 615                 620

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu
625                 630                 635                 640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
                645                 650
```

<210> 11
<211> 653
<212> PRT
<213> hIDUA variant

<400> 11

```
Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser
1               5                   10                  15

Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val
            20                  25                  30

His Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg
        35                  40                  45

Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
    50                  55                  60
```

```
Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
65                  70                  75                  80

Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
                85                  90                  95

Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr
            100                 105                 110

His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro
        115                 120                 125

Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu
    130                 135                 140

Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala
145                 150                 155                 160

Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn
                165                 170                 175

Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser
            180                 185                 190

Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly
        195                 200                 205

Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
    210                 215                 220

Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His
225                 230                 235                 240

Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu
                245                 250                 255

Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile
            260                 265                 270

Leu Glu Gln Glu Lys Val Ala Ala Gln Gln Ile Arg Gln Leu Phe Pro
        275                 280                 285

Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val
    290                 295                 300

Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala
305                 310                 315                 320

Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn
                325                 330                 335
```

```
Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe
            340                 345                 350

Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg
        355                 360                 365

Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys
    370                 375                 380

Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln
385                 390                 395                 400

Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His
                405                 410                 415

Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp
            420                 425                 430

Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala
        435                 440                 445

His Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro
    450                 455                 460

Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu
465                 470                 475                 480

Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro
                485                 490                 495

Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala
            500                 505                 510

Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro
        515                 520                 525

Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro
    530                 535                 540

Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr
545                 550                 555                 560

Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys
                565                 570                 575

Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr
            580                 585                 590

Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser
        595                 600                 605
```

```
Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp
    610                 615                 620

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu
625                 630                 635                 640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
                645                 650
```

<210> 12
<211> 653
<212> PRT
<213> hIDUA variant

<400> 12

```
Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser
1               5                   10                  15

Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val
            20                  25                  30

His Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg
        35                  40                  45

Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
    50                  55                  60

Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
65                  70                  75                  80

Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
                85                  90                  95

Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr
            100                 105                 110

His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro
        115                 120                 125

Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu
    130                 135                 140

Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala
145                 150                 155                 160

Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn
                165                 170                 175

Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser
            180                 185                 190

Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly
        195                 200                 205
```

Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
210 215 220

Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His
225 230 235 240

Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu
245 250 255

Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile
260 265 270

Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro
275 280 285

Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val
290 295 300

Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala
305 310 315 320

Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn
325 330 335

Thr Thr Ser Ala Phe Pro Tyr Ala Leu Arg Ser Asn Asp Asn Ala Phe
340 345 350

Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg
355 360 365

Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys
370 375 380

Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln
385 390 395 400

Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His
405 410 415

Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp
420 425 430

Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala
435 440 445

His Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro
450 455 460

Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu
465 470 475 480

```
Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro
                485                 490                 495

Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala
            500                 505                 510

Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro
        515                 520                 525

Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro
    530                 535                 540

Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr
545                 550                 555                 560

Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys
                565                 570                 575

Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr
            580                 585                 590

Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser
        595                 600                 605

Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp
    610                 615                 620

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu
625                 630                 635                 640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
                645                 650
```

<210> 13
<211> 653
<212> PRT
<213> hIDUA variant

<400> 13

```
Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser
1               5                   10                  15

Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val
            20                  25                  30

His Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg
        35                  40                  45

Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
    50                  55                  60

Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
```

65 70 75 80

Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
85 90 95

Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr
100 105 110

His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro
115 120 125

Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu
130 135 140

Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala
145 150 155 160

Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn
165 170 175

Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser
180 185 190

Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly
195 200 205

Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
210 215 220

Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His
225 230 235 240

Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu
245 250 255

Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile
260 265 270

Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro
275 280 285

Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val
290 295 300

Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala
305 310 315 320

Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn
325 330 335

Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe
340 345 350

```
Leu Ser Tyr His Pro His Pro Phe Thr Gln Arg Thr Leu Thr Ala Arg
        355                 360                 365

Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys
    370                 375                 380

Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln
385                 390                 395                 400

Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His
                405                 410                 415

Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp
            420                 425                 430

Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala
        435                 440                 445

His Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro
    450                 455                 460

Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu
465                 470                 475                 480

Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro
                485                 490                 495

Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala
            500                 505                 510

Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro
        515                 520                 525

Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro
    530                 535                 540

Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr
545                 550                 555                 560

Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys
                565                 570                 575

Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr
            580                 585                 590

Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser
        595                 600                 605

Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp
    610                 615                 620
```

```
Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu
625                 630                 635                 640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
                645                 650
```

<210> 14
<211> 653
<212> PRT
<213> hIDUA variant

<400> 14

```
Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser
1               5                   10                  15

Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val
            20                  25                  30

His Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg
        35                  40                  45

Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
    50                  55                  60

Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
65                  70                  75                  80

Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
                85                  90                  95

Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr
            100                 105                 110

His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro
        115                 120                 125

Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu
    130                 135                 140

Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala
145                 150                 155                 160

Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn
                165                 170                 175

Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser
            180                 185                 190

Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly
        195                 200                 205

Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
```

```
    210                 215                 220

Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His
225                 230                 235                 240

Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu
                245                 250                 255

Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile
            260                 265                 270

Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro
        275                 280                 285

Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val
    290                 295                 300

Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala
305                 310                 315                 320

Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn
                325                 330                 335

Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe
            340                 345                 350

Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg
        355                 360                 365

Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys
    370                 375                 380

Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln
385                 390                 395                 400

Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His
                405                 410                 415

Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp
            420                 425                 430

Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala
        435                 440                 445

Asn Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro
    450                 455                 460

Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu
465                 470                 475                 480

Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro
                485                 490                 495
```

```
Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala
            500                 505                 510

Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro
        515                 520                 525

Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro
    530                 535                 540

Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr
545                 550                 555                 560

Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys
                565                 570                 575

Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr
            580                 585                 590

Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser
        595                 600                 605

Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp
    610                 615                 620

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu
625                 630                 635                 640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
                645                 650
```

<210> 15
<211> 653
<212> PRT
<213> hIDUA variant

<400> 15

```
Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser
1               5                   10                  15

Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val
            20                  25                  30

His Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg
        35                  40                  45

Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
    50                  55                  60

Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
65                  70                  75                  80
```

```
Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
                85                  90                  95

Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr
            100                 105                 110

His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro
        115                 120                 125

Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu
    130                 135                 140

Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala
145                 150                 155                 160

Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn
                165                 170                 175

Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser
            180                 185                 190

Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly
        195                 200                 205

Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
    210                 215                 220

Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His
225                 230                 235                 240

Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu
                245                 250                 255

Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile
            260                 265                 270

Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro
        275                 280                 285

Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val
    290                 295                 300

Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala
305                 310                 315                 320

Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn
                325                 330                 335

Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe
            340                 345                 350

Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg
```

```
        355                 360                 365

Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys
    370                 375                 380

Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln
385                 390                 395                 400

Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His
                405                 410                 415

Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp
            420                 425                 430

Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala
        435                 440                 445

His Pro Asn Arg Ser Ile Ala Val Thr Leu Arg Leu Arg Gly Val Pro
    450                 455                 460

Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu
465                 470                 475                 480

Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro
                485                 490                 495

Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala
            500                 505                 510

Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro
        515                 520                 525

Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro
    530                 535                 540

Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr
545                 550                 555                 560

Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys
                565                 570                 575

Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr
            580                 585                 590

Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser
        595                 600                 605

Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp
    610                 615                 620

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu
625                 630                 635                 640
```

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
645 650

<210> 16
<211> 653
<212> PRT
<213> hIDUA variant

<400> 16

Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser
1 5 10 15

Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val
20 25 30

His Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg
35 40 45

Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
50 55 60

Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
65 70 75 80

Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
85 90 95

Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr
100 105 110

His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro
115 120 125

Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu
130 135 140

Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala
145 150 155 160

Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn
165 170 175

Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser
180 185 190

Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly
195 200 205

Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
210 215 220

```
Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His
225                 230                 235                 240

Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu
                245                 250                 255

Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile
            260                 265                 270

Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro
        275                 280                 285

Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val
    290                 295                 300

Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala
305                 310                 315                 320

Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn
                325                 330                 335

Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe
            340                 345                 350

Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg
        355                 360                 365

Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys
    370                 375                 380

Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln
385                 390                 395                 400

Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His
                405                 410                 415

Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp
            420                 425                 430

Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala
        435                 440                 445

His Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro
    450                 455                 460

Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu
465                 470                 475                 480

Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro
                485                 490                 495

Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala
```

```
            500                 505                 510

Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro
        515                 520                 525

Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro
    530                 535                 540

Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr
545                 550                 555                 560

Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys
                565                 570                 575

Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Thr Tyr
            580                 585                 590

Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser
        595                 600                 605

Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp
    610                 615                 620

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu
625                 630                 635                 640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
                645                 650
```

<210> 17
<211> 653
<212> PRT
<213> hIDUA variant

<400> 17

```
Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser
1               5                   10                  15

Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val
            20                  25                  30

His Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg
        35                  40                  45

Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
    50                  55                  60

Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
65                  70                  75                  80

Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
                85                  90                  95
```

```
Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr
            100                 105                 110

His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro
        115                 120                 125

Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu
    130                 135                 140

Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala
145                 150                 155                 160

Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn
                165                 170                 175

Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser
            180                 185                 190

Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly
        195                 200                 205

Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
    210                 215                 220

Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His
225                 230                 235                 240

Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu
                245                 250                 255

Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile
            260                 265                 270

Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro
        275                 280                 285

Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val
    290                 295                 300

Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala
305                 310                 315                 320

Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn
                325                 330                 335

Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe
            340                 345                 350

Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg
        355                 360                 365
```

```
Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys
    370                 375                 380

Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln
385                 390                 395                 400

Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His
                405                 410                 415

Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp
            420                 425                 430

Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala
        435                 440                 445

His Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro
    450                 455                 460

Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu
465                 470                 475                 480

Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro
                485                 490                 495

Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala
            500                 505                 510

Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro
        515                 520                 525

Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro
    530                 535                 540

Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr
545                 550                 555                 560

Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys
                565                 570                 575

Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr
            580                 585                 590

Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser
        595                 600                 605

Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Thr Leu Asp
    610                 615                 620

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu
625                 630                 635                 640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
```

645 650

CLAIMS:

1. A recombinant vector carrying an expression cassette comprising a human alpha-L-iduronidase (hIDUA) gene having the nucleotide sequence of SEQ ID NO: 1 or a sequence at least about 80% identical to SEQ ID NO: 1 which encodes a functional human alpha-L-iduronidase, wherein said expression cassette further comprises regulatory control sequences which direct expression of the human alpha-L-iduronidase, said regulatory control sequences comprising a liver-specific promoter.

2. The recombinant vector according to claim 1, wherein the modified hIDUA gene is at least about 85 % to about 90 % identical to SEQ ID NO: 1.

3. The recombinant vector according to claim 2, wherein the modified hIDUA gene is at least about 95% to about 99% identical to SEQ ID NO: 1.

4. The recombinant vector according to claim 1, wherein the functional human alpha-L-iduronidase is selected from the group consisting of:

(a) about amino acid 1 to about 653 of SEQ ID NO: 2;

(b) a synthetic human enzyme comprising a heterologous leader sequence fused to about acids 27 to about 653 of SEQ ID NO: 2; and

(c) a variant of amino acid sequence of SEQ ID NO:2 having one or more of the modifications comprising: an H to Q reduction at amino acid position 82 (SEQ ID NO: 8); a change from R to Q at position 105 (SEQ ID NO: 9); a change from G to R at position 116 (SEQ ID NO: 10); a change from V to A at position 279 (SEQ ID NO: 11); a change from L to R at position 346 (SEQ ID NO: 12); a change from A to T at position 361 (SEQ ID NO: 13); a change from H to N at position 449 (SEQ ID NO: 14); a change from V to I at position 454 (SEQ ID NO: 15); a change from A to T at position 591 (SEQ ID NO: 16); and a change from A to T at position 622 (SEQ ID NO: 17).

5. The recombinant vector according to claim 1, wherein the promoter is a TBG promoter.

6. The recombinant vector according to claim 1, wherein the vector further comprises one or more enhancers.

7. The recombinant vector according to claim 6, wherein the enhancers are the same or different.

8. The recombinant vector according to claim 6, wherein the enhancers are selected from the group consisting of an intron, a CMV enhancer, and an Alpha mic/bik enhancer.

9. The recombinant vector according to claim 6, wherein more than one copy of the selected enhancer is present in the vector.

10. The recombinant vector according to claim 9, wherein the more than one copy of the enhancer are located in tandem.

11. The recombinant vector according to claim 1, wherein the expression cassette further comprises a poly A selected from rabbit globulin poly A.

12. The recombinant vector according to claim 1 which is plasmid is pENN.TBG.hIDUA.nRBG.

13. A recombinant adeno-associated virus (rAAV) particle having an AAV capsid and having packaged therein a 5' inverted terminal repeat (ITR), a human alpha-L-iduronidase (hIDUA) gene under the control of regulatory sequences which control expression thereof, and an AAV 3' ITR, wherein said hIDUA gene has a sequence shown in SEQ ID NO: 1 (FIG 1) or a sequence at least about 95% identical thereto which encodes a functional human alpha-L-iduronidase.

14. The rAAV according to claim 13, wherein the modified hIDUA gene is expressed under the control of a liver-specific promoter.

15. The rAAV according to claim 14, wherein the promoter is a TBG promoter.

16. The rAAV according to claim 13, wherein the vector further comprises one or more enhancers.

17. The rAAV according to claim 16, wherein the enhancers are the same or different.

18. The rAAV according to claim 16, wherein the enhancers are selected from the group consisting of an intron, a CMV enhancer, and an Alpha mic/bik enhancer.

19. The rAAV according to claim 18, wherein more than one copy of a selected enhancer is present in the vector.

20. The rAAV according to claim 19, wherein the more than one copy of the enhancer are located in tandem.

21. The rAAV according to claim 13, wherein the rAAV particle comprises an AAV capsid selected from AAV8 and AAV9.

22. The rAAV according to claim 21, wherein the rAAV is pseudotyped.

23. The rAAV according to claim 22, wherein the ITRs are from an AAV2.

24. A recombinant adeno-associated viral particle AAV2/8.TBG.hIDUA.co.

25. A composition useful for treating mucopolysaccharidosis type I (MPS I) comprising the rAAV according to any of claims 13 to 24 and a pharmaceutically acceptable carrier.

26. A method for treating type I mucopolysaccharidosis comprising delivering an effective amount of a composition comprising a pharmaceutically acceptable carrier and a rAAV according to any of claims 13 to 24.

27. The method according to claim 25, wherein said rAAV is delivered intravenously.

28. The method according to claim 1, wherein about 3×10^9 to about 3×10^{12} genome copies of the rAAV is delivered to the subject.

29. Use of a composition comprising the rAAV according to any of claims 13 to 24 and a pharmaceutically acceptable carrier for use in treating mucopolysaccharidosis type I (MPS I).