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EXPRESSED DNA SEQUENCES INVOLVED IN MITOCHONDRIAL FUNCTIONS

BACKGROUND

Methods for constructing peptide and nucleotide libraries are well-known to the art, e.g. as described in U.S. Patents 6,156,511 and 6,130,092. Sequencing methods are also known to the art, e.g. as described in U.S. Patent 6,087,095. Arrays of nucleic acid probes on biological chips have been used for sequencing and for identifying exceptional alleles including disease-associated alleles. Nucleic acid arrays are described, e.g. in U.S. Patent 5,837,832, and PCT Publications WO 99/05324, 99/05591, WO 00/58516, US 5,807,522, US 6,110,426, WO9535505A1, JP10503841T2, GR3030430T3, ES2134481T3, EP913485A1, EP804731B1, EP804731A4, EP804731A1, DK804731T3, DE69509925T2, DE69509925C0, CA2192095AA, AU2862995A1, AU709276B2, and AT180570E, U.S. 6,110,426, 5,807,522, WO 99/42813, EP 1066506, AU 2780499, U.S. 6,007,987, WO 95/11995, U.S. 5,837,832. Such arrays can be incorporated into computerized methods for analyzing hybridization results when the arrays are contacted with label sample nucleotides, e.g. as described in PCT Publication WO 99/05574, and U.S. Patents 5,754,524, 6228,575, 5,593,839, and 5,856,101. Methods for screening for disease markers are also known to the art, e.g. as described in U.S. Patents 6,228,586, 6,160,104, 6,083,698, 6,268,398, 6,228,578, and 6,265,174. Mitochondrial DNA sequences have been associated with pathologies as described in U.S. 5,670,320, 5,296,349, 5,185,244, and 5,494,794. Publications on the subject of mitochondrial biology include: All publications referred to herein are incorporated by reference to the extent not inconsistent herewith.

Introduction

This invention provides human and mouse cDNA microarrays that encompass all known expressed DNA involved in mitochondrial biology, including bioenergetics and biogenesis, reactive oxygen species (ROS) biology and apoptosis. The Center for Molecular Medicine has demonstrated the importance of changes in mitochondrial functions in a variety of degenerative

diseases. These functions work in concert to determine the pathophysiology of many degenerative diseases. Such microarrays, which may be called "mitochips," may be used to provide expression profiles diagnostic for a wide variety of diseases.

Expression profiles from twelve Leigh's patients with Complex I defects have been analyzed using a mitochip of this invention as described herein to demonstrate the value of the mitochip for screening for diseases. Diagnosis of degenerative disease and cancer and monitoring of their progression and monitoring of treatment methods may be accomplished using mitochips of this invention. The mitochips of this invention may also be used to monitor the efficacy of new drug therapeutics for mitochondrial diseases.

Genes involved in mitochondrial biology occur both in the mitochondria and in the nucleus. It is estimated that there are approximately 1000 to 2000 mitochondrial genes encoded in the nucleus. Differential expression of such genes in mouse models are used to identify such genes.

Description

All sequences given herein are meant to encompass the complementary strand, as well as double-stranded polynucleotides comprising the given sequence.

This invention comprises a library of human polynucleotide molecules described in the attachment hereto titled "Human MitoChip." This invention also comprises a library of murine polynucleotide molecules described in the attachment hereto titled "Mouse MitoChip." Polynucleotides listed on these attachments were amplified from an I.M.A.G.E. clone, or if none was available, from a Research Genetics clone, or amplified from an in-house clone. Publicly available sequences of the named and numbered clones are indicated by Genbank accession numbers, or are available from the clone source, or from published sequences of the name of the clone listed under the "Description" column.

A library of polynucleotide molecules as used herein comprises a collection of such molecules, preferably stored under preserving conditions, as known to the art, e.g. as isolated molecules or in living cells. The library is preferably indexed by means of a database, spread sheet or the like so that desired sequences may be obtained from the library.

The invention further comprises a method of identifying expressed DNA sequences affecting human mitochondrial biology, i.e. bioenergetics, mitochondrial biogenesis, reactive oxygen species biology (ROS) and apoptosis. The method comprises: A method for determining a novel data set of murine expressed sequences participating in mitochondrial biology comprising:

providing a mutant mouse deficient in expressed genes governing functions involved in mitochondrial biology. For example, an ANT1 mouse may be used (Murdock et al. "Gene expression profile of an animal model of mitochondrial myopathy using cDNA microarrays"American Society for Human Genetics Conference, 2000, Program No. 55.) The polynucleotide molecules involved in mitochondrial biology identified using the ANT1 mouse are described in the attachment hereto entitled "ANT1 Sequences.";

providing a cDNA microarray chip comprising at least about 8000 mouse cDNAs known to the art, e.g. Mouse UniGene 1 as supplied by Incyte Genomics, Inc.;

providing two mouse tissue samples, the first from the mutant mouse and the second, a control, from at least one wild type mouse of the same strain;

isolating two RNA samples, one each from said tissue samples;

synthesizing cDNA samples from each of said RNA samples, and labeling said cDNA samples, preferably with different fluorescent labels;

hybridizing said chip with said labeled cDNA samples;

quantitating said hybridization from the mutant mouse labeled cDNA to create a first data set comprising a profile of gene expression in the mutant mouse;

quantitating said hybridization from the wild type control labeled cDNA to create a second data set comprising a profile of gene expression in the control mice;

comparing said first and second data sets to create a third data set comprising the statistically significant differences in the expression profile of mutant mouse; and

creating a fourth data set comprising the list of sequences of the cDNAs on the chip corresponding to the third data set, said sequences participating in mitochondrial biology.

This invention also comprises a data mining method for determining a data set of human or murine expressed DNA sequences participating in mitochondrial biology comprising comparing known and deduced expressed human or murine amino acid sequences with those of a large number, preferably all available, organisms, including prokaryotes, and comparing the resultant sequences with amino acid sequences of enzymes and other proteins known to participate in mitochondrial biology, to produce a data set of expressed human or murine sequences involved in mitochondrial biology. Proteins known to participate in mitochondrial biology are known to the art, e.g. Scheffler IE (1999) Mitochondria, Wiley-Liss, NY; Lestienne P Ed. (1999) Mitochondrial Diseases: Models and Methods, Springer-Verlag, Berlin; Methods in Enzymology (2000) 322:Section V Mitochondria and Apoptosis, Academic Press, CA; Mitochondria and Cell Death (1999) Princeton University Press, NJ; Papa S, Ferruciio G, and Tager J Eds. (1999) Frontiers of Cellular Bioenergetics: Molecular Biology, Biochemistry, and Physiopathology, Kluwer Academic / Plenum Publishers, NY; Lemasters J and Nieminen A (2001) Mitochondria in Pathogenesis, Kluwer Academic / Plenum Publishers, NY; MITOMAP, http://www.gen.emory.edu/cgi-gin/MITOMAP; Wallace DC (2001) "A mitochondrial paradigm for degenerative diseases and ageing" Novartis Foundation Symposium 235:247-266; Wallace DC

(1997) "Mitochondrial DNA in Aging and Disease" Scientific American August 277: 40-47; Wallace DC, Brown M, Melow S, Graham B, and Lott M (1998) "Mitochondrial biology, degenerative diseases and aging" BioFactors 7:187-190; Heddi A, Stepien G, Benke P and Wallace DC (1999) "Coordinate Induction of Energy Gene Expression in Tissues of Mitochondrial Disease Patients" JBC 274:22968-22976; Wallace DC (1999) "Mitochondrial Diseases in Man and Mouse" Science 283:1482-1488; Saraste M (1999) "Oxidative Phosphorylation at the *fin de siecle*" Science 283:1488-1493. These sequences may be in the mitochondria, or may be in the nuclear DNA. The method can also be applied to other organisms, including humans. The known human or murine amino acid sequences should include those identified using mutant mice as discussed above. As used herein, the term "data mining" refers to manipulation of data known to the art, such as data in Genbank or other sequence databases, with our without the addition of novel sequences not known to the art, in order to provide a data set containing useful information.

To be more specific, this method comprises:

providing a first data set comprising known human or murine expressed DNA sequences and their corresponding deduced or previously-determined polypeptide sequences;

providing a second data set comprising all known DNA sequences, their corresponding polypeptide sequences, and their putative or known, preferably known, functions;

providing a third data set comprising a large number, preferably all, DNA sequences previously known to be involved in mitochondrial biology, including sequences obtained by methods described herein, their corresponding polypeptide sequences, and their mitochondrial function;

combining said second data set with said third data set to create a fourth data set;

providing a fifth data set comprising the names of all proteins, including but not limited to enzymes, that participate in the biology, including but not limited to biochemistry, of the mitochondria, including biochemical pathways from any organism, including mitochondrial precursors, prokaryotes;

comparing said fourth data set with said first data set, by polypeptide sequence and then by DNA sequence, to create a sixth data set comprising human or murine expressed DNA sequences, associated with the DNA and polypeptide sequences with which they each have the greatest homology (e.g. about 70% amino acid sequence or about 50% nucleotide sequence, more preferably about 90% amino acid sequence or about 70% nucleotide sequence), and optionally also including their corresponding putative or known functions, and the percentages of homology;

comparing said fifth data set with said sixth data set to create a seventh data set comprising DNA expressed sequences that have greatest DNA or polypeptide homology with a protein that participates in the biology of the mitochondria associated with the putative or known functions, and optionally also including percents of homology. Said seventh data set comprises sequences selected from the group consisting of (as appropriate) the human or murine sequences of the polynucleotides described in the MitoChip attachments hereto.

Preferably the seventh data set includes all said human or murine sequences.

In comparing sequences in this invention, amino acid sequences may be compared (either deduced from known nucleotide sequences or from direct sequencing), or nucleotide sequences may be compared (either deduced from known amino acid sequences or from direct sequencing). Methods for deducing sequences are well known to the art.

The method may also be applied to identifying sequences from humans or other organisms which are involved in mitochondrial biology.

This invention also comprises a computer storage medium storing a data structure comprising said seventh data set. A computer program comprising code for implementing the above method steps is also included within this invention.

Microarrays (also referred to as "chips"), e.g. of the type described in US 5,807,522, US 6,110,426, WO9535505A1, JP10503841T2, GR3030430T3, ES2134481T3, EP913485A1, EP804731B1, EP804731A4, EP804731A1, DK804731T3, DE69509925T2, DE69509925C0, CA2192095AA, AU2862995A1, AU709276B2, and AT180570E are also provided herein. Such microarrays comprise nucleotide fragments of known sequence positioned, e.g. by covalent or noncovalent binding, at known positions on a substrate, such as a silicone chip or glass side, e.g. coated with polycationic polymer. Such microarrays also comprise appropriate positive and negative controls. The nucleotide fragments may have been purified or amplified as is known to the art. In one embodiment of this invention, fragments comprising at least one, and preferably all, sequences in said seventh data set are provided in such microarrays.

These chips can be used, for example, to determine the amount of expression of all murine expressed sequences participating in the biology of the mitochondria, in one cell type relative to a second cell type, said method comprising:

providing a microarray as described above, comprising sequences of said seventh data set, preferably all said sequences;

providing two murine cell samples, one of each type;

isolating RNA samples from said cell types;

synthesizing cDNA samples from each of said RNA samples, and labeling said cDNA samples, preferably with different fluorescent labels;

hybridizing said microarray with said labeled cDNA samples;

quantitating said hybridization from the first cell type to create a first data set and from the second cell type to create a second data set;

comparing said first and second data sets to create a third data set comprising the levels of expression of each murine expressed sequence participating in the biology of the mitochondria, in the first cell type relative to the second cell type.

The second cell type may be used as a standard. Cell samples may be taken from tissue culture or living organisms, and may be taken from the same or different organisms. Cells may be taken from the same tissue type, e.g. brain tissue, from two different organisms.

The method may also include a step of determining the range of normal variation, preferably as a standard deviation, in the expression of sequences participating in the biology of the mitochondria, said method comprising:

obtaining cell samples from the same tissue type from a number, N, of diverse, wild type mice, including a standard mouse;

performing the method described above in pairwise combinations where the first cell type is from one of the diverse mice and the second cell type is a standard;

creating the N third data sets comprising the levels of expression relative to the standard;

statistically analyzing said data sets to create a fourth data set comprising the normal range of variation, preferably expressed as standard deviations, in the expression of sequences participating in the biology of the mitochondria.

Computer programs comprising code to perform the above method steps, and computer storage media storing the fourth data set, which comprises an entry for expressed sequences participating in the biology of the mitochondria associated with an entry indicating the normal range of variation in expression of that sequence, are also provided.

Methods of this invention can also be used to screen an individual mouse for abnormalities in the expression of sequences participating in the biology of the mitochondria, the methods comprising:

comparing the levels of expression for each sequence participating in the biology of the mitochondria of the individual, to the normal range of variation for that sequence;

creating a data set comprising said differences in the levels of expression, preferably in units of standard deviation from average;

using said data set to determine the individual mouse's degree of abnormality. As used herein, the term "abnormality" means a profile of expression that is significantly outside the norm, as defined for each component of the profile for each experiment. The individual mouse may be a fetus or neonate as well as a juvenile or full-grown mouse. The method may also be used to determine changes in expression of sequences participating in the biology of the mitochondria in the same individual mouse over time due to the processes of aging.

The method can also be used to create a data set of a profile of abnormalities in expression levels associated with a mouse mutant cell line. A data set of this invention created by this method consists of at least one component of a profile or a profile comprising abnormalities

associated with a particular mutant cell line. Mutant cell lines useful in this method include the CAP^R mouse cell line and the ρ^0 mouse cell line (Levy et al "DNA microarrays as a method to monitor changes in mitochondria-related gene expression in mouse mutant cell lines" American Society of Human Genetics Conference 2000 Program No. 1501).

The method may also be used to create a data set of at least one of, or a profile of, abnormalities in expression levels associated with a mutant mouse strain, such as a mutant Sod2+/- knockout heteroyzgous mouse strain, as described in Kokoszka et al "Mitochondrial oxidative stress results in a decline of mitochondrial function and increased apoptosis with age in the Sod2+/- mouse," American Society of Human Genetics Conference 2000 Program No. 1618 and Kokoszka et al (2001) "Increased mitochondrial oxidative stress in the Sod2 (+/-) mouse results in the age-related decline of mitochondrial function culminating in increased apoptosis" PNAS 98:2278-2283.

The method may also be used to identify a mutation causing a pathological condition.

As discussed above, all methods herein may be used with other organisms besides mice, including humans. Mouse or human data derived from such methods may be used to diagnose an individual with the corresponding pathological condition by identifying expression patterns correlating with the pathological condition in a statistically significant sample to create a reference expression pattern, and comparing the expression pattern of the individual with that of the reference expression pattern. The reference expression pattern may include indicia of expression levels of anywhere from one critical expression product associated with a particular pathological condition, to expression patterns for all nucleotides associated with mitochondrial biology. The method may further include identifying and if necessary, sequencing the gene or genes identified as being implicated in the pathological condition. For example, expression patterns were identified by these methods which are implicated in Leigh's syndrome (Kerstann et al "Microarray Analysis of Human Mitochondrial Disease Patients" American Society of Human Genetics Conference 2000 Program No. 1484; Procaccio et al., "Alterations in Gene Expression in Leigh's

Patients with Complex 1 Defects Detected Using the Mitochip DNA Microarray," (copy of abstract attached). Once the faulty expression patterns are discovered, and the associated genes identified, therapies providing increased levels of under-expressed expression product, or means for reducing overexpressed expression product may be devised, or gene therapies undertaken as is known to the art.

Data sets derived by the above methods associating expression patterns with pathological conditions are included within the scope of this invention, as are computer storage media storing such data sets, and computer programs for generating and using such data sets.

Pathological conditions for which the above methods are useful include any pathological condition arising as a result of malexpression of genes involved in mitochondrial biology. Preferably the pathological condition is a human disease or models a human disease in another organism. Examples of pathological phenotypes exist in mouse mutants ANT1 (Murdock et al "Gene expression profile of an animal model of mitochondrial myopathy using cDNA microarrays" American Society of Human Genetics Conference 2000 Program No. 55), ^{CAR} (Sigh et al "Mouse models of mitochondrial disease" American Society of Human Genetics Conference 2000 Program No. 53), ρ0 (Levy et al "DNA microarrays as a method to monitor changes in mitochondria-related gene expression in mouse mutant cell lines" American Society of Human Genetics Conference 2000 Program No. 1501), Sod2 (Cowskin et al "Brain gene expression analysis using DNA microarrays of SOD2 knockout mice treated with the synthetic antioxidant MnTBAP" American Society of Human Genetics Conference 2000 Program No. 1616), Hsiang-fu K (2001) "The mouse model and human disease" Acta- Academiae Medicinae Sinicae 23:2-7, Hsiang-fu K (2001) "The mouse model and human disease (sequel)" Acta- Academiae Medicinae Sinicae 23:97-105, Hsiang-fu K (2001) "The mouse model and human disease (sequel): cancer" Acta- Academiae Medicinae Sinicae 23:205-209.

The method may also be used to screen therapeutic compounds. For example, the therapeutic compound MnTBAP was shown to affect mitochondrial biology expression profiles

when samples were obtained from Sod2 mutant murine tissues. (Kokoszka et al (2001) "Increased mitochondrial oxidative stress in the Sod2 (+/-) mouse results in the age-related decline of mitochondrial function culminating in increased apoptosis" PNAS 98:2278-2283 and Kokoszka et al., "Mitochondrial Oxidative Stress Results in a Decline of Mitochondrial Function and Increased Apoptosis with Age in the SOD2+/- Mouse," American Soc of Human Genetics Conference 2000, Program No. 1616).

The method may also be used to screen mutagenized mouse cell lines to ensure that they are producing the desired expression pattern for genes involved in mitochondrial biology. Mutagenized and transgenic mice, preferably transgenic mice modeling human disease, may also be screened in this way. The method can also be used to identify which genes to knock out to create a transgenic mouse modeling a human disease.

In addition to screening for and identifying therapeutic compounds useful to treat pathological conditions resulting from expression patterns of genes involved in mitochondrial biology, the method may also be used to monitor the effectiveness of a particular treatment such as administration of a pharmaceutical or gene therapy.

Again all methods of this invention may be automated by providing code to receive input of the appropriate data, perform the required calculations and create the data sets discussed above. Such data sets stored in computer-readable memory are also included in this invention. Computers and computer systems programmed with the appropriate code for carrying out the methods are also included in this invention.

All methods and materials specifically described as being derived from mice may also be derived from humans and/or other organisms.

In addition, this invention provides the sequences attached hereto, namely: Mouse ANT2, Genbank accession no. AF240003; Mouse ANT1, Genbank accession no. AF240002; Mouse

NADH dehydrogenase 1 Alpha subcomplex 2 (Ndufa2), Genbank accession no. NM010885; Mouse NADH dehydrogenase Fe-S Protein 4 (Ndufs4) Genbank accession no. NM010887; Mouse dynactin 6, Genbank accession no. NM011722; Mouse glycogen phosphorylase, Genbank accession no. NM 011224; Human mitochondrial DNA Genbank accession no. AB055387; Human ATP synthase beta subunit precursor, Genbank accession no. M27132; Human ATP synthase, H+ transporting mitochondrial F0 complex subunit F6, Genbank accession no. NM001685; Human solute carrier family 25 member 4, Genbank accession no. NM001151; Human translocase of intermitochondrial membrane 8 homolog A, Genbank accession no. NM004085.

As used herein, "I.M.A.G.E. clone no." refers to the clone number from the I.M.A.G.E. Consortium. Some I.M.A.G.E. clones represent only part of a Genbank accession no. sequence.

As used herein, "Research Genetics Clone No." refers to the clone number from Research Genetics, ResGen Invitrogen Corporation.

As used herein, "UG Cluster ID" and "Unigene Cluster ID" refer to the locus that Genbank has assigned one or more clones or sequences to. In the traditional terminology, a cluster is a "gene."

As used herein, "standard" refers to a labeled sample of cDNA, or cell type or organism from which it is derived, hybridized coincidently with an unknown sample. An unknown sample is hybridized and quantitated alongside a standard so that the resulting unknown data set is comparable with other data sets.

All sequences given herein are meant to encompass the complementary strand, as well as double-stranded polynucleotides comprising the given sequence.

As used herein, a "polymorphism" refers to the existence, of more than one allele at a given locus.

As used herein, "polymorphic locus" refers to a locus at which more than one allele is known to exist in corresponding sequences from different individuals. The allele could comprise a different nucleotide at that position, a deletion at that position, or an insertion at that position.

As used herein, a "nucleotide difference" refers to a polymorphism.

As used herein, a "polynucleotide" refers to a molecule consisting of more than one nucleotide, that may be obtained by purification, amplification, or chemical synthesis, by methods standard to the art.

As used herein, a "polypeptide fragment" refers to a molecule consisting of more than one peptide, that may be obtained by protein purification from cells, in vitro translation, or chemical synthesis, by methods standard to the art.

As used herein, "translation product" refers to the polypeptide fragment that would be produced if a polynucleotide were transcribed and translated in vitro or in vivo, or could be predicted to be produced using standard amino acid codon tables and synthesized, by methods standard to the art.

As used herein, "labeling" refers to covalently linking a reporter atom or molecule onto or within a polynucleotide fragment, preferentially using a fluorescein reporter molecule, but possibly using any reporter atom or molecule known to the art including, but not limited to ^{32}P, ^{35}S, and digoxygenin.

As used herein, "hybridize" refers to combining potentially complementary polynucleotide fragments, of such length, in such a solution, at such a temperature, for such a period of time,

such that these conditions provide adequate stringency minimizing background hybridization while allowing hybridization between homologs.

As used herein, "arrays" refer to oligonucleotides positioned in a known arrangement, on a solid support, such as glass or a silica chip.

As used herein, "quantitate" an amount of hybridization signal refers to a method of measuring the amount of hybridization signal, preferably scanning for fluorescence, from each component of a hybridized array, all components making together making a profile, independently or relative to a reference.

As used herein, "data set" refers to a collection of data including, but not limited to data comprising quantitation of hybridization signal from each component of a hybridized array, and data comprising expression levels at more than one locus comprising hybridization profiles.

As used herein, "determining a polynucleotide sequence" refers to sequencing a polynucleotide fragment by this invention or any method standard to the art, including deducing possible sequences from corresponding amino acid sequences. Similarly, "determining an amino acid sequence refers to sequencing a peptide or polypeptide or deducing an amino acid sequence from the corresponding polynucleotide sequence.

As used herein, "contacting said substrate" refers to combining all components that allow polynucleotide probes to hybridize to the bound polynucleotides on a solid support.

As used herein, "disease phenotype" or "pathological condition" refers to a description of the manifestation of a disease.

As used herein, "sample" of DNA refers to a purified or amplified amount of a portion of DNA from a given source that could include nuclear as well as mitochondrial DNA and may include all of the nuclear and mitochondrial DNA.

As used herein, "purify" refers to chemically isolating and concentrating one or a group of molecules away from other chemicals. Purifying RNA involves isolating RNA away from other cellular components.

As used herein, "mitochondrial biology" refers to all cellular functions involving, directly or indirectly, the mitochondria, including, but not limited to: mitochondrial bioenergetics, mitochondrial biogenesis, reactive oxygen species biology (ROS), and apoptosis.

As used herein, "data mining" refers to techniques used to explore and bring to the surface, complex relationships in very large data sets.

As used herein, "mitochondrial precursor" refers to prokaryotes that evolved into mitochondria via endosymbiosis with eukaryotic precursors.

As used herein, "amplify" refers to creating additional copies of a nucleotide fragment by the Polymerase Chain Reaction (PCR) method, as known to the art.

As used herein "haplotypes" refer to the various, genetically diverse, groups of inbred mice, that are known to the art.

As used herein, "abnormalities in expression" refers to a profile of expression that is significantly outside the norm, as defined for each experiment. For example, for pathology A, a profile 2 standard deviations (S.D.s) outside the norm might correlate with a manifestation of symptoms, but for pathology B, a profile at least 3 S.D.s outside the norm might be necessary for

manifestation of symptoms. Abnormality is a relative term defined in the context of each experiment.

As used herein, "corresponding polypeptide sequence" refers to the polypeptide fragment that would be produced if a polynucleotide were transcribed and translated in vitro or in vivo, or could be predicted to be produced using standard amino acid codon tables and synthesized, by methods standard to the art.

As used herein, "pairwise combinations" refers to, in a group of samples, identifying one sample as a standard, and pairing that standard, in experiments, with every other sample in that group.

As used herein "statistically analyzing" refers to analyzing a data set of expression profiles, so that for each component of the profile, an average and standard deviation is calculated.

As used herein, "statistically significant" refers to determining if a change in profile of expression is significantly different from the standard with methods standard to the art, i.e. Tusher et al (2001) "Significance analysis of microarrays applied to the ionizing radiation response" PNAS 98:5116-5121.

All references cited in the present application are incorporated by reference in their entirety herein to the extent that there is no inconsistency with the present disclosure. Copies of abstracts and articles published within the last year by inventor(s) hereof are attached hereto.

The following examples are provided for illustrative purposes, and are not intended to limit the scope of the invention as claimed herein. Any variations in the exemplified articles which occur to the skilled artisan are intended to fall within the scope of the present invention.

ANTI SEQUENCES

IMAGE Number	IMAGE Acc. Num.	GeneName
315773	W09924.1	IMAGE EST {IMAGE:315773}
536306	AA073604.1	Procollagen, type I, alpha 1 {IMAGE:536306}
890444	AA509565.1	Mus musculus GTP binding protein (GTP2) mRNA, complete cds {IMAGE:890444}
738252	AA271223.1	CCAAT/enhancer binding protein (C/EBP), alpha {IMAGE:738252}
331768	W08090.1	IMAGE EST {IMAGE:331768}
336085	AI322288.1	ESTs, Highly similar to CREATINE KINASE, SARCOMERIC MITOCHONDRIAL PRECURSOR [Rattus norvegicus] {IMAGE:336085}
331681	W14332.1	ESTs, Highly similar to PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE [Homo sapiens; Rattus norvegicus; Mus musculus] {IMAGE:331681}
872869	AA466432.1	Mus musculus calcium-binding protein S100A1 mRNA, complete cds {IMAGE:872869}
716941	AA266097.1	IMAGE EST {IMAGE:716941}
387449	W66757.1	ESTs, Highly similar to PUTATIVE REGULATORY PROTEIN TSC-22 [Mus musculus; Rattus norvegicus] {IMAGE:387449}
619501	AA175510.1	RAB1, member RAS oncogene family {IMAGE:619501}
596552	AA146442.1	Core binding factor beta {IMAGE:596552}
639212	AA200984.1	IMAGE EST {IMAGE:639212}
420322	W89883.1	Procollagen, type III, alpha 1 {IMAGE:420322}
831964	AA444490.1	Tissue inhibitor of metalloproteinase 2 {IMAGE:831964}
351420	W41309.1	IMAGE EST {IMAGE:351420}
660997	AA253853.1	ESTs {IMAGE:660997}
472860	AA038095.1	ESTs, Highly similar to CREATINE KINASE, SARCOMERIC MITOCHONDRIAL PRECURSOR [Rattus norvegicus] {IMAGE:472860}
735186	AA259674.1	ESTs, Weakly similar to vesicle membrane protein [M.musculus] {IMAGE:735186}
477066	AA047966.1	Mus musculus skeletal muscle LIM protein (FLH1) mRNA, complete cds {IMAGE:477066}
695695	AA222567.1	Mus musculus mRNA for sarco/endoplasmic reticulum Ca2+ -ATPase (SERCA2) {IMAGE:695695}
695279	AA220458.1	Surfeit gene 4 {IMAGE:695279}
737944	AA271505.1	Mus musculus pantophysin gene, complete cds {IMAGE:737944}
352450	W33786.1	Procollagen, type VI, alpha 1 {IMAGE:352450}
403728	W82212.1	House mouse; Musculus domesticus mRNA for LN1, complete cds {IMAGE:403728}
480896	AA064241.1	Mus musculus Stra13 mRNA, complete cds {IMAGE:480896}
330218	W13931.1	ESTs, Highly similar to DERMATOPONTIN [Bos taurus] {IMAGE:330218}
551003	AA098196.1	IG ALPHA CHAIN C REGION {IMAGE:551003}
536464	AI324436.1	Mus musculus PAF acetylhydrolase mRNA, complete cds {IMAGE:536464}
455401	AA020462.1	M.musculus mRNA for GTP-binding protein {IMAGE:455401}
902923	AA518165.1	Tissue inhibitor of metalloproteinase 2 {IMAGE:902923}
468817	AA035899.1	IMAGE EST {IMAGE:468817}

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717457	AA403432.1	Mus musculus FGF-binding protein (FGF-BP) mRNA, complete cds {IMAGE:717457}
318735	W34420.1	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1 {IMAGE:318735}
533314	AA104976.1	ESTs, Highly similar to MATERNAL EFFECT PROTEIN STAUFEN [Drosophila melanogaster] {IMAGE:533314}
748275	AA274576.1	Mus musculus mRNA for GM3 synthase, complete cds {IMAGE:748275}
374228	W63981.1	M.musculus mRNA for fibromodulin {IMAGE:374228}
572339	AA108475.1	ESTs, Highly similar to SUCCINATE DEHYDROGENASE [Homo sapiens] {IMAGE:572339}
777580	AA276835.1	Interleukin 1 receptor-associated kinase {IMAGE:777580}
748891	AA288040.1	ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUBUNIT [Bos taurus] {IMAGE:748891}
441176	AA009059.1	IMAGE EST {IMAGE:441176}
437523	AA003769.1	Microtubule-associated protein 4 {IMAGE:437523}
890932	AA511037.1	Calcium channel, voltage-dependent, L type, alpha 2 delta subunit {IMAGE:890932}
775464	AA388122.1	Maternal embryonic message 3 {IMAGE:775464}
418993	AA052179.1	Myostatin {IMAGE:418993}
479709	AA051664.1	IMAGE EST {IMAGE:479709}
420553	W89418.1	IMAGE EST {IMAGE:420553}
790449	AA289280.1	ESTs, Highly similar to PINCH PROTEIN [Homo sapiens] {IMAGE:790449}
920516	AA541842.1	Interferon gamma receptor {IMAGE:920516}
466551	AA030901.1	MAD homolog 4 (Drosophila) {IMAGE:466551}
693837	AA238435.1	GAMMA-ADAPTIN {IMAGE:693837}
945218	AA545607.1	Mus musculus metal response element DNA-binding protein M96 mRNA, complete cds {IMAGE:945218}
642467	AA190123.1	ESTs, Highly similar to (defline not available 4588044) [M.musculus] {IMAGE:642467}
833160	AA467585.1	ESTs, Weakly similar to (defline not available 3668141) [H.sapiens] {IMAGE:833160}
401958	W77711.1	Mus musculus rab6/rab5-associated protein (rab6) mRNA, partial cds {IMAGE:401958}
356181	W54234.1	DiGeorge syndrome chromosome region 6 {IMAGE:356181}
329863	W14142.1	ESTs {IMAGE:329863}
671212	AA222463.1	ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SGDH SUBUNIT PRECURSOR [Bos taurus] {IMAGE:671212}
846064	AA416246.1	Peripheral myelin protein, 22 kDa {IMAGE:846064}
465520	AA033138.1	Adenine nucleotide translocator 2, fibroblast {IMAGE:465520}
571789	AA109041.1	Calmodulin 3 {IMAGE:571789}
699236	AA245461.1	Mouse calcineurin catalytic subunit mRNA, complete cds {IMAGE:699236}
809016	AA466026.1	IMAGE EST {IMAGE:809016}
803416	AA473269.1	Mus musculus cytoplasmic protein Ndr1 (Ndr1) mRNA, complete cds {IMAGE:803416}
316427	W11161.1	Mus musculus Balb/c zinc finger protein PZF (Pzf) mRNA, complete cds {IMAGE:316427}

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466971	AA036546.1	Mus musculus hemin-sensitive initiation factor 2 alpha kinase mRNA, complete cds {IMAGE:466971}
575665	AA125367.1	MAP KINASE PHOSPHATASE-1 {IMAGE:575665}
932748	AA538419.1	ESTs, Weakly similar to survival motor neuron [M.musculus] {IMAGE:932748}
477535	AI323032.1	Suppressor of Ty 6 (S. cerevisiae) homolog {IMAGE:477535}
642977	AA184876.1	ESTs, Highly similar to putative ATP/GTP-binding protein [H.sapiens] {IMAGE:642977}
904900	AA519027.1	IMAGE EST {IMAGE:904900}
478865	AA048831.1	Mus musculus high mobility group protein homolog HMG4 (Hmg4) mRNA, complete cds {IMAGE:478865}
482952	AA060802.1	ESTs, Highly similar to NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT [Homo sapiens] {IMAGE:482952}
721970	AA268402.1	ESTs {IMAGE:721970}

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Mouse MitoChip

	Description	Genbank Acc. #	IMAGE Clone Acc. #	Unigene Cluster ID	Res. Gen.Clone ID
422	Protein Phosphatase inhibitor 2 (IPP2)	AA041826	AA041826	Mm.29617	475407
429	Mitochondrial LON protease	AA061310	AA061310	-------	514859
430	ATP synthase A Channel	AA106406	AA106406	Mm.5293	519329
343	H+-transporting ATP synthase chain delta **(EST)**	AA940343	AA896697	Mm.22514	***1279053***
350	~~Mouse Circadian output locomotor cycles kaput~~	AF000998	AI156715	Mm.3552	***1494023***
203	H+-transporting ATP synthase chain beta	AF030559	AI452208	Mm.17869	***576006***
318	transforming protein bcl-w (3' seq)	AF030769.1	AA563148		***975210***
332	transforming protein bcl-w (5'-seq)	AF030769.1	AA667328		***1139352***
134	Glutathione peroxidase-heart isoform (Gpx4)	AF045769.1	AI327053	Mm.2400	***420345***
325	14-3-3 protein beta	AF058797.1	AA624796	Mm.34454	***1039350***
152	14-3-3 protein gamma	AF058799		Mm.10802	464892
259	acatyl-CoA acetyltransferase 2	AF078751	AA239043		***694062***
99	2-amino-3ketobutyrate-coenzyme A ligase	AF093403	AI037094	Mm.18618	315143
322	Nuclear respiratory factor-1	AF098077	AI594316		***1006311***
347	~~Apoptosis-inducing factor~~	AF100927	AA866777		***1434491***
168	adenylate kinase isoenzyme 2 **(EST)**	AI155541	AA061587	Mm.29460	***483322***
285	probable aconitate hydratase, mitochondrial **(EST)**	AI385870	AA275929	Mm.30065	***775753***
501	Huntingtin	AI876894	AI876894	-------	1922060
107	Sim to α-ketoglutarate (hum)	D10523	W13320		***329728***
349	heat shock protein 70 precursor	D11089	AI132204	Mm.2849	***1481709***
191	coproporphyrinogen oxidase	D16333	AA108600		***570602***
271	coproporphyrinogen oxidase	D16333	AA259342		***734795***
118	coproporphyrinogen oxidase	D16333	W53951		***367358***
125	coproporphyrinogen III oxidase precursor	D16333	W71884	Mm.35820	***390487***
493	pyruvate kinase	D38379	AI035313	Mm.2635	1432851
396	Fructose 1-6 bis-phosphate	D42083	AI385602	Mm.2974	336727
177	Excitatory amino acid transporter 3	D43797	AA065502	Mm.24741	***524046***
244	25-hydroxyvitamin D3 24-hydroxylase precursor	D49438	AA240836	Mm.6575	***657172***
245	25-hydroxyvitamin D3 24-hydroxylase precursor	D49438	AI226268	Mm.6575	***658678***
337	ferredoxin--NADP+ reductase precursor	D49920	AA879949	Mm.4719	***1230740***
355	Pyruvate kinase	D63764	AI195164	Mm.8359	***1886895***
448	**HK-Phospholipase A2 (14-3-3 zeta/delta)**	D78647	AA1714341	Mm.3360	617315
247	14-3-3 protein epsilon	D87663.1	AA240827	Mm.678	***670982***
283	Sim to acetyl CoA acetyl transferase (hum)	D90228	AA272067		***761668***
360	**HK-Hypozanthine phosphoribosyl transferase**	J00423	AI256193	Mm.18675	***1890233***
116	**HK-A97Hypozanthine phosphoribosyl transferase**	J00423	W48168	Mm.18675	***355084***

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243	Glycogen Phosphorylase **(RAT)**	J03080	AA240684		***656882***
320	dihydrolipoamide dehydrogenase (E3) **(HUMAN)**	J03490	AA548170	Hs.74635	***994825***
110	Sim to glycogen phosphorylase (Hum)	J03544	W16286		***334236***
301	Phosphofructokinase 1	J03928, AF123533	AI480449	Mm.1166	***862787***
165	Sim to electron trans flavoprotein α sub (Hum)	J04058	AA060723		***481934***
147	methylenetetrahydrofolate dehydrogenase (NAD+)	J04627		Mm.443	440345
365	Mouse heatshock protein 86	J04633	AI649095		***1970053***
242	hexokinase I (5'-seq)	J05277	AA197916	Mm.5290	***654873***
267	hexokinase I (3'-seq)	J05277	AI661880	Mm.5290	***717383***
496	**HK-Myosin 1**	L00923	AI098184	Mm.3390	1481939
363	H+-transporting ATP synthase chain alpha	L01062	AI573940	Mm.4069	***1920315***
180	cyto C oxydase polypeptide VIa-liver precursor	L06465		Mm.19094	533628
112	Mouse mHox protein	L06502	W17990	Mm.3869	***335936***
410	Glucose-6-phosphate isomerase	L09104	AI327180	Mm.589	437357
358	pyruvate carboxylase	L09192	AI303529	Mm.1845	***1888741***
287	Sim to Fructose 1-6-bisphosphate (Hum)	L10320	AA276043		***776124***
344	Acyl-CoA dehyd, short-chain specific precursor	L11163	AI050239	Mm.18759	***1379035***
309	Pyruvate dehydrogenase E1 a subunit (human)	L13318	AA238899		***888842***
136	3-methyl-2-oxobutanoate dehydrogenase (lipoamide)	L16992		Mm.12819	422840
216	ATP synthase F0 component	L19737	AA139793		***580898***
310	ATP synth lipid-binding protein P1 precursor (subunit 9)	L19737	AI481739	Mm.258	***888863***
187	~~apoptosis regulator BAX, membrane isoform alpha~~	L22472	AI323521	Mm19904	***557643***
432	PMP 35	L27842	AI573377	Mm.16453	534171
300	adrenodoxin precursor	L29123	AA461849	Mm.1061	***851558***
340	transforming protein bcl-2-alpha	L31532	AA867214	Mm.5155	***1265430***
414	**HK-Ribosomal Protein S29**	L31609	AA032465	Mm.35816	465138
190	~~steroidogenic acute reg protein precursor, mito-~~	L36062	AA389406	Mm.3436	***569013***
222	~~NADH-ubiquinone oxidoreductase 13 kDa subunit~~	L38438	AA397301		***599804***
157	acatyl-CoA acetyltransferase 1	L42293		Mm.28099	472233
269	dihydrolipoamide transacylase precursor	L42996	AA254971	Mm.3636	***719973***
98	branched chain alpha-ketoacid dehyd chain E1-alpha	L47335		Mm.25848	314098
444	**HK-Murine ornithine decarboxylase**	M10624	AI325192	Mm.15259	608003
348	**HK-Actin- alpha (skeletal muscle)**	M12347	AI035279	Mm.4581	***1480709***
330	heat shock protein, 70K (hsp68) (fragment)	M12573	AA647374	Mm.6388	***1108306***
386	Glycerophosphate dehydrogenase	M13366	AI414023	Mm.10669	303389
286	Glucose Phospahate Isomerase I complex	M14220	AA276216		***776210***
113	Glucose Phospahate Isomerase I complex	M14220	W29397		***337413***

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240	Sim to enolase α subunit (Hum)	M14328	AA204262		***643854***
277	Surfeit locus protein 1	M14689	AA274488	Mm.6874	***748268***
231	5-aminolevulinate synthase precursor **(EST)**	M15268	AA189529	Mm.1217	***635215***
265	Malate dehydrogenase (mito)	M16229	AA266087		***717095***
341	transforming protein bcl-2-beta	M16506	AA867214		***1265430***
323	Lactate Dehydrogenase-A4	M17516	AI506641	Mm.26504	***1024774***
172	Lactate Dehydrogenase-sperm specific	M17587, L10389	AA110449	Mm.16563	***516582***
181	Heat shock protein, 84 kDa 1	M18186		Mm.2180	538585
182	Mouse breast heat shock 73 prot (hsc73)	M19141		Mm.2944	538418
258	Sim to 6-Phosphofructo-2-kinase (human)	M19938	AA397024		***693346***
173	cytochrome c oxidase chain VIc	M20153	AA062417		***516889***
351	mitochondrial uncoupling protein	M21247	AI131780	Mm.4177	***1498957***
97	**HK-Actin- gamma**	M21495	AI314957	Mm.29913	***192859***
335	**HK-A316Actin-gamma (smooth muscle)**	M26689	AA710883	Mm.16562	***1166855***
284	3-beta hydroxy-5-ene steroid dehydrogenase type I	M27137	AA274685		***766591***
342	Lactate Dehydrogenase-	M27554	AA880398		***1277670***
140	Antioxidant protein 1	M28723	W91307		***423832***
221	Antioxidant protein 1	M28723		Mm.29821	599017
198	Sim to succinate dehydrogenase	M32246	AA108475		***572339***
295	**HK-Glyceraldehyde phosphate dehydrogenase**	M32599	AA466618	Mm.5289	***817984***
232	ferrochelatase precursor	M59288		Mm.1070	635652
214	sterol carrier protein 2 precursor	M62361		Mm.1779	580813
274	Creatine kinase-complete	M74149	AA270310	Mm.16831	***736251***
362	3-beta hydroxy-5-ene steroid dehydrogenase type II	M75886	AI266804	Mm.30433	***1891212***
297	Pyruvate dehydrogenase	M76727	AA423301		***820409***
308	pyruvate dehydrogenase (lipoamide)	M76727	AA466268	Mm.34775	***888842***
171	pyruvate dehydrogenase (lipoamide)	M76728	AI323722	Mm.4223	***513684***
251	Glycerol 3-phosphate acyltransferase	M77003	AA209041		***676437***
252	3-beta hydroxy-5-ene steroid dehydrogenase type III	M77015	AA209060	Mm.335	***676577***
449	phosphoprotein phosphatase	M81475	AI449151	Mm.1567	619279
313	Sperm capsule seleno protein	M88463	AA497767		***917403***
331	cytochrome-b5 reductase **(HUMAN)**	NM_000398	AA816039		***1120651***
319	cytochrome c oxidase chain VIb **(HUMAN)**	NM_001863	AI503861		***991287***
127	Sim to ATP synthase F chain	PIR:A54211	W82194		***403660***
307	Sim to Translocase of inner mito. mem. (Tim 44) (Sac)	Q01852	AA498767		***888708***
314	sperm mitochondrial capsule selenoprotein	S49657, **M29603**	AI482284	Mm.554	***917537***
339	hydroxymethylglutaryl-CoA lyase	S65036	AA838929		***1261134***

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333	Friedreich ataxia	S75712	AA930748		***1150363***
302	monoamine oxidase A - mouse	S78615	AI643185		***864614***
211	Succinate dehydrogenase-Cyt B560	TR:G1019861	AA137762		***580040***
294	Sim to UTP-Gluc.-1-phosphate uridyltrans (Human)	TR:G881394	AA473123		***805218***
163	Sim to branched-chain α-ketoacid dehydrogenase kinase	TR:G924921	AA059497		***480575***
212	carnitine O-palmitoyltransferase II precursor	U01163		Mm.29499	580316
389	Perox. Proliferator receptor (PPAR) Gamma	U01841	W34083	Mm.3020	317536
141	2-oxoglutarate dehydrogenase E1 component	U02971	W98443		***424460***
326	Mouse heatshock protein 27	U03560.1	AA596241	Mm.13849	***1052188***
495	Transketolase (Tkt)	U05809	AI132421	Mm.9307	1481358
169	Mouse med. Chain acyl-CoA dehydrogenase	U07159	AA061679		***483333***
189	Acyl-CoA dehyd, med-chain specific precursor (MCAD)	U07159	AA104184	Mm.10530	***568149***
208	Aldehyde dehydrogenase	U07235	AA122975		***579570***
321	aldehyde dehydrogenase (NAD+) 2 precursor	U07235	AI503977	Mm.2621	***1001020***
299	cyto C oxydase polypeptide VIa-heart precursor	U08439	AA415934	Mm.21050	***846138***
135	chaperonin-10	U09659		Mm.12970	422572
224	Mouse Skd3 mRNA	U09874		Mm.3990	602340
162	Bcl-2 protein	U10102	AA051441		***478723***
178	peripheral-type benzodiazepine receptor 1	U12419	AA068577		***524463***
174	hydroxymethylglutaryl-CoA synthase, mitochondrial	U12790, **U12791**		Mm.10633	518481
122	adenylyl cyclase type VII	U12919	W65619		***387280***
438	Glutathione peroxidase-3 (plasma Gpx)	U13705	AA097557	Mm7156	552393
345	Glutathione peroxidase-plasma isoform	U13705.1	AI042912	Mm.7156	***1432410***
150	cytochrome C oxydase polypeptide VIII-H precursor	U15541	AI323348	Mm.3841	***463967***
201	Glutaryl-CoA dehydrogenase precursor (GCD)	U18992		Mm.2475	573351
233	Nuclear respiratory factor-2	U20532		Mm.1025	635541
268	Acyl-CoA dehydrog, long-chain spec. precursor (LCAD)	U21489	AA254905	Mm.2445	***719580***
255	voltage-dependent anion channel 1	U230840	AA244874		***680076***
166	protoporphyrinogen oxidase	U25114, D45185		Mm.4730	482868
334	ADP,ATP carrier protein, heart isoform T1	U27315	AA717872	Mm.16228	***1152250***
219	ADP,ATP carrier protein, fibroblast isoform 2 (ant2)	U27316		Mm.658	585992
315	voltage-dependent anion channel 2	U30838	AI507203	Mm.569	***931442***
327	voltage-dependent anion channel 3	U30839	AA616007	Mm.38513	***1066900***
175	Rnase P-complex (RS Williams work)	U31228	AI614577		***523232***
149	tetrahydrofolylpolyglutamate synthase precursor	U32197	AA030778	Mm.3830	***463571***
490	Glucose dependent insulinotropic polypeptide	U34295	AA871367	Mm.5115	1096156
282	Myeloid cell leukemia sequence 1	U35623, AF063886	AA387843	Mm.1639	***761106***

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385	Thiosulfate sulfurtransferase (mito) Tst1	U35741	AI195057	Mm.15312	188763
356	thiosulfate sulfurtransferase	U35741	AI196763	Mm.15312	***1887427***
126	cytochrome C-type heme lyase (CCHL)	U36778		Mm.3988	400735
491	Carbonic Anhydrase IV	U37091	AA71129	Mm.1614	1167078
164	cytochrome c oxidase chain VIII	U37721		Mm.14022	481408
253	Alpha-1 protease inhibitor	U38477	AA212578	Mm.16672	***676745***
401	ERV-1	U40494	AI413376	Mm.28124	367232
248	Acyl-CoA dehyd, very-long-chain specific precursor	U41497	AA250410	Mm.18630	***670916***
364	ATP-binding cassette transporter 7	U43892	AU019072	Mm.4739	***1920872***
238	H+-transporting ATP synthase chain gamma	U43893	AA210528		***640931***
499	**HK-calcium binding protein Cab45**	U45977	AI266799	Mm.30149	1891202
195	isocitrate dehydrogenase (NADP)	U51167		Mm.2966	571468
202	DNA polymerase gamma	U53584		Mm.3616	575332
117	uracil-DNA glycosylase	U55040	W48179		***355462***
188	14-3-3 protein eta	U57311	AI325059	Mm.3308	***558536***
293	14-3-3 protein theta (tau)	U57312	AA422980	Mm.14722	***803843***
183	mitochondrial transcription factor A - mouse	U57939		Mm.276	539693
352	H+-transporting ATP synthase chain e	U59283	AI115240		***1885128***
306	H+-transporting ATP synthase chain e	U59283	AI481625		***876416***
156	NADH-ubiquinone oxidoreductase 13 kDa subunit	U59509	AA035972		***468848***
324	14-3-3 protein zeta	U79231	AA671451	Mm.3360	***1039129***
81	mtDNA-12s rRNA	V00711	In House-Clone		
82	mtDNA-16s rRNA	V00711	In House-Clone		
83	mtDNA-COX 1	V00711	In House-Clone		
84	mtDNA-COX 2	V00711	In House-Clone		
85	mtDNA-COX 3	V00711	In House-Clone		
86	mtDNA-NADH 1	V00711	In House-Clone		
87	mtDNA-NADH 2	V00711	In House-Clone		
88	mtDNA-NADH 3	V00711	In House-Clone		
89	mtDNA-NADH 4	V00711	In House-Clone		
90	mtDNA-NADH 4L	V00711	In House-Clone		
91	mtDNA-NADH 5	V00711	In House-Clone		
92	mtDNA-NADH 6	V00711	In House-Clone		
93	mtDNA-Cyt b	V00711	In House-Clone		
94	mtDNA-ATPase 6	V00711	In House-Clone		
95	mtDNA-ATPase 8	V00711	In House-Clone		
447	α-amylase	V00719	AI325237	Mm.7074	608852

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436	**(-Glyceraldehyde 3-phosphate dehydrogenase (G3PD**	W14827	AA119563	Mm.5289	538210
483	Fructose bis-phosphate aldolase	W53351	AI553136	Mm.7729	902910
246	cytochrome C, somatic	X01756	AA221965	Mm.35389	***658678***
445	Creatine Kinase, muscle	X03233	AA166212	Mm.2375	608246
435	**HK–β-actin**	X03672	AA079937	Mm.297	536615
205	(2'-5')oligoadenylate synthetase 1	X04958, M33863	AI449562	Mm.14301	***577664***
227	glutamate oxaloacetaate transaminase-2	X06917, J02622		Mm.18916	617490
361	ornithine carbamoyltransferase precursor	X07092	AI266937	Mm.2611	***1891345***
132	malate dehydrogenase precursor, mitochondrial	X07295, M16229		Mm.21743	407143
101	carbonyl reductase (NADPH) - mouse	X07411, D26123	W11423	Mm.21454	***317572***
217	Sim to cytochrome c oxidase VI B (Hum)	X13923	AA139624		***581175***
290	Solute carrier family 2	X15684	AA275871		***776543***
353	cytochrome c oxidase chain Va precursor	X15963	AI131665	Mm.360	***1884978***
494	**HK-Ubiquitin**	X51703	AI181949	Mm.235	1451597
196	methylmalonyl-CoA mutase alpha chain precursor	X51941		Mm.4299	571282
359	carbonate dehydratase, hepatic	X51971	AI256540	Mm.35538	***1889415***
154	cytochrome c oxidase chain VIIc	X52940	AA031250	Mm.14831	***464966***
346	cytochrome c oxidase chain Vb precursor	X53157	AI035302	Mm.16769	***1432845***
275	cytochrome c oxidase chain IV precursor	X54691, M37829	AA260009	Mm.2136	***746546***
184	heat shock protein 60 precursor	X55023, X53584	AA154729	Mm.1777	***540881***
100	Sim to β–enolase (human)	X56832	W11965		***316967***
316	glutamate dehydrogenase (NAD(P)+) precursor	X57024	AA543797	Mm.10600	***949005***
338	cyt C oxydase polypeptide VIIa- liver/heart precursor	X58486	AA960158	Mm.2151	***1248366***
254	Aconitase (iron responsive element)	X61147	AA212704		***677092***
261	Aconitase (iron responsive element)	X61147	AA238899		***697949***
357	ornithine--oxo-acid transaminase precursor	X64837	AI196410	Mm.13694	***1887672***
120	Sim to Mito. 2-oxoglutarate/malate carrier (Human)	X66114	W54000		***367801***
262	Sim to ATP synthase lipid binding (Hum)	X69908	AA239148		***698109***
109	Sim to electron trans flavoprotein b sub (Hum)	X71129	W18161		***333641***
329	phospholipase A2, platelet, synovial fluid	X74266	AA871547	Mm.4675	***1096251***
161	Sim to cytochrome c oxidase VII	X80899	AA050684		***476180***
223	carnitine O-acetyltransferase (carnitine acetylase)	X85983	AI528757	Mm.20396	***602213***
311	Fructose Bisphosphate aldolase A	Y00516	AA518639		***903419***
225	Creatine kinase-mitochondrial	Z13968	AI528837	Mm.970	***607301***
336	creatine kinase	Z13968, Z13969	AA690010	Mm.970	***1167886***
354	3,2-trans-enoyl-CoA isom, mito precursor	Z14049	AI194961		***1886651***
292	superoxide dismutase (Mn) precursor	Z18857, L35525	AA415267	Mm.2597	***791140***

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215	NAD(P)+ transhydrogenase (B-specific) precursor	Z49204	AI323702	Mm.3842	***580717***
442	NADP transhydrogenase	Z49204	AI323702	Mm.3842	580717
142	**HK-40s Ribosomal protein S4**		AA000082		***425352***
143	Sim to hepatocyte gluc transporter		AA002666		***426758***
144	Branched-chain amino transferase I		AA003372		***426976***
411	Microtubule-associated protein 4		AA003769.1		437523
412	IMAGE EST		AA009059.1		441176
146	Sim to NADH-ubiquin. oxidoreduct.15 kd sub.		AA014507		***439668***
413	M.musculus mRNA for GTP-binding protein		AA020462.1		455401
14	IMAGE EST		AA028306		464099
416	MAD homolog 4 (Drosophila)		AA030901.1		466551
153	**HK-Alkaline Phosphatase**		AA032457		***465052***
151	defender against cell death 1		AA033006		***464622***
415	Adenine nucleotide translocator 2, fibroblast (Ant2)		AA033138.1		465520
155	**HK-40s Ribosomal protein S15**		AA033398		***466295***
417	Glutathione peroxidase-4 (phospholipid Gpx)		AA034666	Mm2400	466963
419	IMAGE EST		AA035899.1		468817
418	is hemin-sensitive initiation factor 2 alpha kinase mRNA, complete cds		AA036546.1		466971
420	ily similar to CREATINE KINASE, SARCOMERIC MITO. PRECUR.		AA038095.1		472860
421	Superoxide dismutase-1 (Cu/Zn Sod)		AA039044	Mm5274	474545
11	*Skel Mus LIM protein (FHL1) / RPB-assoc. mol. RAM14-1*		AA047966		477066
423	isculus skeletal muscle LIM protein (FLH1) mRNA, complete cds		AA047966.1		477066
425	bility group protein homolog HMG4 (Hmg4) mRNA, complete cds		AA048831.1		478865
159	Branched-chain α-ketoacid dehydrog. E1β		AA050586		***476163***
160	Cytochrome C oxidase sub VII		AA050684		***476180***
145	Sim to carbon catabolite repressor prot. (Sac)		AA051133		***438774***
426	IMAGE EST		AA051664.1		479709
407	Myostatin		AA052179.1		418993
428	ghly similar to NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT		AA060802.1		482952
167	Uncoupling protein 3		AA062091		***482847***
427	Mus musculus Stra13 mRNA, complete cds		AA064241.1		480896
176	Sim to UDP-glucose dehydrogenase		AA067191		***523796***
179	**HK-A16060s Ribosomal protein L15**		AA068842		***532770***
20	Procollagen Type 1		AA073604		536306
433	Procollagen, type I, alpha 1		AA073604.1		536306
170	Sim to ubiquinol-cty c reductase		AA087137		***493604***
186	Apoptosis inhibitor 3		AA097958		***550702***

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185	Caspase I	AA098139		***550766***
437	IG ALPHA CHAIN C REGION	AA098196.1		551003
431	, Highly similar to MATERNAL EFFECT PROTEIN STAUFEN	AA104976.1		533314
197	E1B 19k/Bcls-binding prot. Homolog (NIP3)	AA105295		***571367***
192	**HK-A17360s Ribosomal protein L3**	AA108363		***570533***
440	ESTs, Highly similar to SUCCINATE DEHYDROGENASE	AA108475.1		572339
199	Sim to ubiquinol-cty c reductase, core prot.	AA108590		***572127***
194	Sim to ATP synthase epsilon (Bov)	AA108733		***571214***
439	Calmodulin 3	AA109041.1		571789
193	Sim to acetyl Coenzyme A synthetase	AA109675		***570550***
200	Sim to NADH-ubiquin. oxidoreduct. 49 kd sub.	AA109715		***572585***
9	IMAGE EST	AA118290		574435
209	Glyceraldehyde 3-phosphate dehydrogenase	AA122891		***579715***
441	MAP KINASE PHOSPHATASE-1	AA125367.1		575665
220	Apoptosis inhibitor 2	AA144490		***597715***
443	Core binding factor beta	AA146442.1		596552
229	**HK-A21060s Ribosomal protein L1A**	AA170607		***619006***
450	RAB1, member RAS oncogene family	AA175510.1		619501
451	Nitric Oxide Synthase-3	AA177240	Mm12837	620940
235	**HK-A216RNA splicing protein**	AA183061		***636766***
234	Alcohol dehydrogenase 5	AA183192		***636207***
230	Mito matrix prot P1 precursor (hsp60)	AA184322		***633625***
239	ATP/GTP binding protein	AA184876		***642977***
454	ESTs, Highly similar to putative ATP/GTP-binding protein	AA184876.1		642977
453	ESTs, Highly similar to (defline not available 4588044)	AA190123.1		642467
236	Caspase 2	AA200808		***639403***
452	IMAGE EST	AA200984.1		639212
16	IMAGE EST	AA203878		640734
237	Sim to cytochrome b5 (outer mito mem)	AA203975		***640762***
250	Sim to serine hydroxymethyltransferase, mito. (Rab)	AA208877		***676311***
1	IMAGE EST	AA215024		652207
2	m to yeast ORF(Sim to rat synaptic glycoprotein) / SURF 4	AA220458		695279
460	Surfeit gene 4	AA220458.1		695279
260	Alcohol dehydrogenase I	AA221141		***695105***
17	~~IMAGE EST~~	AA221250		670393
249	Sim to NADH-ubiquin. oxidoreduct. sgdh sub.	AA222463		***671212***
456	similar to NADH-UBIQUINONE OXIDOREDUCTASE SGDH SUB PREC.	AA222463.1		671212

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461	IA for sarco/endoplasmic reticulum Ca2+ -ATPase (SERCA2)	AA222567.1		695695
458	GAMMA-ADAPTIN	AA238435.1		693837
457	Catalase	AA239490	Mm 4215	678773
241	Sim to quinone oxidoreductase	AA241313		***653324***
256	Sim to glucose dehydrogenase (Bac. Sub)	AA241896		***680935***
257	Thioredoxin	AA242573		***681159***
459	Antioxidant protein-2 (AO2)	AA243957	Mm6587	694088
263	Sim to carnitine/acylcarnitine carrier	AA245413		***699181***
462	Mouse calcineurin catalytic subunit mRNA, complete cds	AA245461.1		699236
264	Sim to mito. Elongation factor TS (Bov)	AA245481		***699237***
10	IMAGE EST	AA245545		699280
5	IMAGE EST	AA250652		697537
455	ESTs	AA253853.1		660997
6	Rat NRBF1	AA259674		735186
272	Sim to quinone oxidoreductase	AA259674		***735186***
467	ESTs, Weakly similar to vesicle membrane protein	AA259674.1		735186
276	Uncoupling Prot homology (UCPH)	AA260521		***748122***
466	Gluamate receptor, ionotropic, kainate 5 (gamma 2)	AA261334	Mm.2879	733368
463	IMAGE EST	AA266097.1		716941
102	Dynamin	AA266438		***317587***
270	Sim to NADH-ubiquin. oxidoreduct. mn11 sub.	AA267638		***723360***
465	ESTs	AA268402.1		721970
273	ATP synthase F0 component	AA269701		***735887***
15	IMAGE EST- CCAAT enhancer binding protein	AA271223		738252
469	CCAAT/enhancer binding protein (C/EBP), alpha	AA271223.1		738252
468	Mus musculus pantophysin gene, complete cds	AA271505.1		737944
470	Mus musculus mRNA for GM3 synthase, complete cds	AA274576.1		748275
23	*IMAGE EST*	AA275684		775722
288	ATPase-like vacule proton channel	AA276030		***776055***
473	Interleukin 1 receptor-associated kinase	AA276835.1		777580
289	CYTOSOLIC BRANCH CHAIN AMINOTRANSFERASE	AA286063		***776036***
279	Sim to NADH-ubiquin. oxidoreduct. 13 kd sub.	AA288040		***748891***
471	similar to NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUB	AA288040.1		748891
278	Dimethyl glycine dehydrogenase	AA288418		***748958***
474	ESTs, Highly similar to PINCH PROTEIN	AA289280.1		790449
158	Pyruvate decarboxylase	AA308254		***473778***
472	Maternal embryonic message 3	AA388122.1		775464

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280	Adenylosuccinate synthase	AA388461		***749837***
7	IMAGE EST	AA388512		790857
281	**HK-A262E2F transcription factor**	AA396123		***751755***
464	nusculus FGF-binding protein (FGF-BP) mRNA, complete cds	AA403432.1		717457
266	Sim to carbon catabolite repressor prot. (Sac)	AA404014		***717197***
291	**HK-A272Capping protein**	AA414612		***779754***
298	Sim to NADH-ubiquin. oxidoreduct. b22 sub.	AA415725		***846155***
479	Peripheral myelin protein, 22 kDa	AA416246.1		846064
296	Sim to NADH-ubiquin. oxidoreduct. b15 sub.	AA434897		***818906***
477	Tissue inhibitor of metalloproteinase 2	AA444490.1		831964
303	Sim to NADH-ubiquin. oxidoreduct. b14 sub.	AA462323		***871020***
476	IMAGE EST	AA466026.1		809016
24	EST highly similar to S-100 prot a-chain	AA466432		872869
480	nusculus calcium-binding protein S100A1 mRNA, complete cds	AA466432.1		872869
478	, Weakly similar to (defline not available 3668141) [H.sapiens]	AA467585.1		833160
305	Cellular apoptosis succep. Protein	AA471761		***874148***
475	nusculus cytoplasmic protein Ndr1 (Ndr1) mRNA, complete cds	AA473269.1		803416
3	IMAGE EST-yeast bile transporter	AA473289		803488
304	Pyruvate kinase	AA475121		***873690***
19	GTP-binding protein	AA509565		890444
481	musculus GTP binding protein (GTP2) mRNA, complete cds	AA509565.1		890444
482	ium channel, voltage-dependent, L type, alpha 2 delta subunit	AA511037.1		890932
487	Nitric Oxide Synthase-2	AA512708	Mm2893	922250
484	Tissue inhibitor of metalloproteinase 2	AA518165.1		902923
485	IMAGE EST	AA519027.1		904900
312	Sim to NADH-ubiquin. oxidoreduct. 9 kd sub.	AA521758		***903911***
317	Sim to acetyl Coenzyme A synthetase	AA537637		***949423***
488	STs, Weakly similar to survival motor neuron [M.musculus]	AA538419.1		932748
486	Interferon gamma receptor	AA541842.1		920516
489	esponse element DNA-binding protein M96 mRNA, complete cds	AA545607.1		945218
328	Fuzzy onion homolog (mouse)	AA674474		***1093002***
492	lusculus mRNA for glutamate receptor channel alpha 4 subunit	AI043222	Mm.42021	1431493
497	Gluamate receptor, ionotropic, NMDA2C epsilon 3)	AI256808	Mm.39090	1852361
500	Superoxide dismutase-3 (extracellular Sod)	AI314465	Mm2407	1907770
395	ily similar to CREATINE KINASE, SARCOMERIC MITO. PRECUR.	AI322288.1		336085
424	Suppressor of Ty 6 (S. cerevisiae) homolog	AI323032.1		477535
434	Mus musculus PAF acetylhydrolase mRNA, complete cds	AI324436.1		536464

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498	Thioredoxin Reductase	AI529082	Mm 25543	1887250
446	Sim to mito RNA pol (HUM)	AI892781	Mm.34645	608625
25	DD2a	In House-Clone		
26	DD4c	In House-Clone		
27	DD7a	In House-Clone		
28	DD10a	In House-Clone		
29	DD11b	In House-Clone		
30	DD14	In House-Clone		
31	DD15c	In House-Clone		
32	DD16c	In House-Clone		
33	DD17c	In House-Clone		
34	DD19a	In House-Clone		
35	DD23ba	In House-Clone		
36	DD24d	In House-Clone		
37	DD25c	In House-Clone		
38	DD26f	In House-Clone		
39	~~DD33a/pgf~~	In House-Clone		
40	38g cent.	In House-Clone		
41	~~41.2a cent.~~	In House-Clone		
42	~~44b cent.~~	In House-Clone		
43	45.2b cent.	In House-Clone		
44	55e cent.	In House-Clone		
45	p63a	In House-Clone		
46	65c cent.	In House-Clone		
47	~~66a cent.~~	In House-Clone		
48	~~67 cent.~~	In House-Clone		
49	CI 18K	In House-Clone		
50	GP4	In House-Clone		
51	SKD 3	In House-Clone		
52	mWS3	In House-Clone		
53	DD39	In House-Clone		
54	Kin 17	In House-Clone		
55	DD 43	In House-Clone		
56	CI B8	In House-Clone		
57	~~DD 47~~	In House-Clone		
58	DD 48	In House-Clone		
59	DD 53	In House-Clone		

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60	~~DD 64~~	In House-Clone
61	~~DD 68~~	In House-Clone
62	DD 69	In House-Clone
63	~~DD 73~~	In House-Clone
64	*DD 83*	In House-Clone
65	DD 84	In House-Clone
66	~~mDP 6~~	In House-Clone
67	C II 3	In House-Clone
68	GAPD	In House-Clone
69	ASC	In House-Clone
70	mTF 1	In House-Clone
71	MCK	In House-Clone
72	C IV is	In House-Clone
73	*Gpx*	In House-Clone
74	ER V	In House-Clone
75	**HK-HPRT**	In House-Clone
76	Ant 1	In House-Clone
77	**PL-A81Plant gene PG**	In House-Clone
78	**PL-Plant gene cLED6L16 GA oxidase**	In House-Clone
79	**PL-Tomato gene abscisic stress ripening prot 1**	In House-Clone
80	**PL-Tomato chlorophyl a/b binding protein gene cab-1B**	In House-Clone
96	***CN-Position Control***	In House-Clone
502	adapt	In House-Clone
503	GILZ	In House-Clone
504	TOAD	In House-Clone
505	TIMP2	In House-Clone
506	calm 1	In House-Clone
507	PACD	In House-Clone
508	sarc.	In House-Clone
509	col 3	In House-Clone
510	col 1	In House-Clone
511	~~GTP2~~	In House-Clone
512	SMOO	In House-Clone
513	~~SMCK~~	In House-Clone
514	RAB1	In House-Clone
515	S100	In House-Clone
516	PEBP2	In House-Clone

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517	CEBP	In House-Clone		
	~~BZP~~	In House-Clone		
	~~BZP~~	In House-Clone		
	~~BZP~~	In House-Clone		
12	-homolog of Unc33 (C.Elegans) / Collaspin reponse mediated prot. 2	W08090		331768
394	IMAGE EST	W08090.1		331768
13	IMAGE EST	W09924		315773
387	IMAGE EST	W09924.1		315773
388	isculus Balb/c zinc finger protein PZF (Pzf) mRNA, complete cds	W11161.1		316427
106	Hexokinase	W11571		***318642***
103	Sim to TIM17	W11644		***318134***
148	Dynamin 2	W13111		***457445***
105	Malate dehydrogenase (cyto)	W13686		***318346***
392	ESTs, Highly similar to DERMATOPONTIN [Bos taurus]	W13931.1		330218
391	ESTs	W14142.1		329863
108	Sim to citrate synthase (Por)	W14146		***329884***
393	ly similar to PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE	W14332.1		331681
8	IMAGE EST	W15031		330502
111	Pyruvate kinase-like protein	W17814		***334876***
4	~~IMAGE EST-sarcoplasmic creatine kinase~~	W18057		336085
114	Peroxisomal/Mitochondrial dienoyl-CoA isomerase	W29607		***338088***
398	Procollagen, type VI, alpha 1	W33786.1		352450
22	ATPase, Ca2+ transporting, heart	W34420		318735
390	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	W34420.1		318735
115	Sim to glycerol 3-phosphate dehydrogenase 1 (rat)	W41175		***351221***
21	IMAGE EST-Sim to gamma sarcoglycan	W41309		351420
397	IMAGE EST	W41309.1		351420
399	Gluamate receptor, ionotropic, NMDA1 (zeta 1)	W44130	Mm.3292	354244
121	Sim to NADH-ubiquin. oxidoreduct. B14.5 sub.	W54068		***367925***
400	DiGeorge syndrome chromosome region 6	W54234.1		356181
119	Sim to NADH-ubiquin. oxidoreduct. b17 sub.	W54448		***367651***
402	M.musculus mRNA for fibromodulin	W63981.1		374228
123	**HK-DNA ligase I**	W66626		***388245***
18	GE EST-Glucocorticoid-induced leucine zipper GILZ protein	W66757		387449
403	Highly similar to PUTATIVE REGULATORY PROTEIN TSC-22	W66757.1		387449
124	Hexokinase	W74835		***389177***
404	usculus rab6/rab5-associated protein (rab6) mRNA, partial cds	W77711.1		401958

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405	e mouse; Musculus domesticus mRNA for LN1, complete cds	W82212.1		403728
130	**HK-A111Acient ubiquinating protein**	W82989		***405768***
128	Sim to NADH-ubiquin. oxidoreduct. ashl.	W83085		***404593***
129	NADH dehydrogenase mwfe	W83104		***404499***
406	Type II Peroxiredoxin 1	W83228	Mm42948	405943
131	Sim to NADH-ubiquin. oxidoreduct. b9 sub.	W83574		***406509***
409	IMAGE EST	W89418.1		420553
133	Sim to putative mito. Ribosomal prot. S14	W89487		***419614***
408	Procollagen, type III, alpha 1	W89883.1		420322
137	Sim to NADH-ubiquin. oxidoreduct. Kfy1	W97248		***423071***
104	Sim to Glutathione-S-transferase (RAT)		Mm.27395	317849
138	Sim to Aldehyde dehydrogense (HUM)		Mm.24457	423605
139	Uncoupling Protein 2		Mm.12556	423616
204	Sim to arginyl-tRNA synthetase (Sac Cer)		Mm.22363	576572
206	Branched chain alpha ketoacid dehydrog. Kinase		Mm.8903	578018
207	Sim to sterol 26 hydroxylase		Mm.26793	578465
210	Thioredoxin		Mm.3533	579774
213	Carnitine palmitoyltransferase 2		Mm.29499	580316
218	Sim to Glutamate/Malate trans (BOV)		Mm.28466	582075
226	Unknown EST			608265
228	Glutamate oxaloacetate transaminase 2		Mm.18916	617490
366	***CN-Position Control Marker***			
367	***CN-Scan Control Marker***			
368	**PL-Tomato ethylene fruit ripening gene E8**			
369	**PL-Tomato pectinesterase**			
370	**PL-A371Tomato ERT ripening related mRNA**			
371	***CN-Scan Control Marker***			
372	***CN-Position Control Marker***			
373	**BLANK**			
374	**BLANK**			
375	**BLANK**			
376	**BLANK**			
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382	**BLANK**
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Human MitoChip

ResearchGenetics

Clone ID	Gene Name	Complete Gene Name	GenBank	UG_cluster_id	
1074487	SDHD	SDHD	AB006202		
1018253	AIF	AIF	AF100928, Z81364		
1556306	ANT3	ANT3	J03592		ox phos / apoptosis
1160934	UQCRC2	UBIQUINOL-CYTOCHROME C REDUCTASE CORE PROTEIN 2 PRECURSOR	J04973		
2301230	COX5B	COX5B	M19961, M59250		Complex IV
1318021	COX5A	COX5A	M22760		Complex IV
2250688	GT	GT	M31659		
197932	UQCRB	UQCRB	M35761, M26706, M26707	Hs.77385	
1114960	ETFDH	ESTs, Highly similar to HYPOTHETICAL 29.2 KD PROTEIN IN PHD1-PTM1 INTERGENIC REGION [Saccharomyces cerevisiae]	S69232	Hs.30661	
1911533	VDAC3	VDAC3	S75494		
1911533	VDAC4	VDAC4	S75651		
984496	NDUFB9	NDUFB9	S82655		Complex 1
2097122	COX6A1	COX6A1	X15341		Complex IV
2066585	LON-PEN	MITOCHONDRIAL LON PROTEASE HOMOLOG	X76040, X74215		
951683	PHC	PHC	X77337		
428215	ACTL6	actin-like 6	AA001745	Hs. 103180	
429222	EST	ESTs, Weakly similar to MSF1 PROTEIN [S.cerevisiae]	AA004210	Hs.3945	
428756	GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	AA005219	Hs.93201	energy metabolism
359723	EST	ESTs, Highly similar to ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]	AA011122	Hs.41066	

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360778	ATM	Ataxia telangiectasia mutated (includes complementation groups A, C and D)	AA016254	Hs.194382	
361565	GLUD1	glutamate dehydrogenase 1	AA018372	Hs.77508	
363086	CKMT1	Human mitochondrial creatine kinase (CKMT) gene, complete cds	AA019482	Hs.153998	nucleotide synthesis
363103	HMG2	High-mobility group (nonhistone chromosomal) protein 2	AA019511	Hs.80684	
365149	FECH	ferrochelatase (protoporphyria)	AA025142	Hs.26	
469412	FH	Fumarate hydratase	AA026917	Hs.75653	
470393	MMP7	matrix metalloproteinase 7 (matrilysin, uterine)	AA031513	Hs.2256	
375728	PRSM1	protease, metallo, 1, 33kD	AA033807	Hs.183138	
429942	EST	ESTs	AA034062	Hs.38750	
470861	NDUFB6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 (17kD, B17)	AA034268	Hs.109646	Complex 1
471498	GNS	glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)	AA035347	Hs.2703	
471597	API5L1	API5-like 1	AA035436	Hs.227913	
486221	VDAC1	Voltage-dependent anion channel 1	AA044059	Hs.149155	
487348	DYMPLE	Homo sapiens dynamin-like protein mRNA, complete cds	AA045529	Hs.180628	
488386	EST	ESTs, Highly similar to MITOCHONDRIAL RNA SPLICING PROTEIN MSR4 [Saccharomyces cerevisiae]	AA046639	Hs.34401	
487373	ATP5G1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	AA046701	Hs.80986	Complex V
377152	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase)	AA055101	Hs.10758	Complex 1
377152	NDUFS4	Homo sapiens NADH:ubiquinone oxidoreductase 18 kDa IP subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds	AA055101	Hs.10758	Complex 1
366132	SDHC	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD	AA062805	Hs.3577	

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366132	SDHC	Homo sapiens mRNA for cytochrome b large subunit of complex II, complete cds	AA062805	Hs.3577	
359982	BNIP3	Homo sapiens E1B 19K/Bcl-2-binding protein Nip3 mRNA, nuclear gene encoding mitochondrial protein, complete cds	AA063521	Hs.79428	apoptosis
511257	KIAA0719	ESTs, Weakly similar to MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR [Neurospora crassa]	AA088722	Hs.21198	
489519	TIMP3	tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)	AA099153	Hs.245188	
489626	PFKM	Phosphofructokinase, muscle	AA099169	Hs.75160	
489755	EST	EST	AA099554	Hs.246174	
489823	COX17	Homo sapiens COX17 mRNA, complete cds	AA099855	Hs.16297	Complex IV
490600	FOSL2	FOS-like antigen 2	AA101617	Hs.155210	signal transduction
490600	FOSL2	FOS-like antigen 2	AA101617	Hs.155210	signal transduction
530282	NDUFA1	H.sapiens mRNA for NADH dehydrogenase	AA111999	Hs.74823	Complex 1
530282	NDUFA1	H.sapiens mRNA for NADH dehydrogenase	AA111999	Hs.74823	Complex 1
563574	FRG1	Homo sapiens FRG1 mRNA, complete cds	AA113339	Hs.203772	
502141	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase)	AA127014	Hs.90443	Complex 1
501939	HHCMA56	putative oxidoreductase	AA128041	Hs.519	
504145	LSC2	SUCCINATE-COA LIGASE	AA132000		ox phos
490753	FLJ20420	ESTs, Weakly similar to head-elevated expression in 0.9 kb [D.melanogaster]	AA133166	Hs.6693	
490778	QP-C	Homo sapiens mRNA for low molecular mass ubiquinone-binding protein, complete cds	AA133191	Hs.3709	
586990	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	AA133656	Hs.57435	
587847	GPX2	Glutathione peroxidase 2, gastrointestinal	AA135289	Hs.2704	ROS
588911	OAS1	2',5'-oligoadenylate synthetase 1	AA146773	Hs.82396	
588911	OAS1	2',5'-oligoadenylate synthetase 1	AA146773	Hs.82396	
589276	AFG3L2	AFG3 (ATPase family gene 3, yeast)-like 2	AA147320	Hs.29385	

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504689	EST	ESTs, Moderately similar to 3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE II [Escherichia coli]	AA149172	Hs.55781	
491763	IL1B	Interleukin 1, beta	AA150507	Hs.126256	
504452	PPOX	protoporphyrinogen oxidase	AA151249	Hs.100016	
590727	RENT1	regulator of nonsense transcripts 1	AA156342	Hs.12719	
594079	TID1	tumorous imaginal discs (Drosophila) homolog	AA169872	Hs.6216	
624634	FDX1	ferredoxin 1	AA187349	Hs.744	
624627	RRM2	Ribonucleotide reductase M2 polypeptide	AA187351	Hs.75319	
626206	POLG	polymerase (DNA directed), gamma	AA188761	Hs.80961	
626206	POLG	DNA polymerase gamma	AA188761	Hs.80961	
628418	GPD1	glycerol-3-phosphate dehydrogenase 1 (soluble)	AA192547	Hs.255718	energy metabolism
628418	GPD1	glycerol-3-phosphate dehydrogenase 1 (soluble)	AA192547	Hs.255718	energy metabolism
628529	EST	uncoupling protein 3 (mitochondrial, proton carrier)	AA192553	Hs.76640	
628529	EST	Uncoupling protein 3 (mitochondrial, proton carrier)	AA192553	Hs.76640	
646657	SCO1	SCO1 (yeast homolog) cytochrome oxidase deficient 1	AA205413	Hs.14511	
562101	HERC1	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	AA211496	Hs.255561	
562409	NDUFS5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4 (15kD, B15)	AA214053	Hs.80595	Complex 1
562409	NDUFS5	Homo sapiens NADH:ubiquinone oxidoreductase 15 kDa IP subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds	AA214053	Hs.80595	Complex 1
629896	MAP1B	MICROTUBULE-ASSOCIATED PROTEIN 1B	AA219045	Hs.103042	
630013	MSH2	DNA repair protein MSH2	AA219060	Hs.78934	

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629916	TIM17B	ESTs, Highly similar to MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM17 [Saccharomyces cerevisiae]	AA219179	Hs.19105	
666425	PLCG1	DNA topoisomerase I	AA232856	Hs.317	
669471	23589 mRNA	Human clone 23589 mRNA sequence	AA234889	Hs.11506	
684582	WARS2	tryptophanyl tRNA synthetase 2 (mitochondrial)	AA251354	Hs.227274	
669419	FRDA	Friedreich ataxia	AA253413	Hs.95998	disease-related
669419	FRDA	Friedreich ataxia	AA253413	Hs.95998	disease-related
682528	SCA1	spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1)	AA256507	Hs.74520	
704299	TAZ	tafazzin (cardiomyopathy, dilated 3A (X-linked); endocardial fibroelastosis 2; Barth syndrome)	AA279440	Hs.79021	
712577	HCCS	HOLOCYTOCHROME C-TYPE SYNTHETASE	AA281548	Hs.88859	
171756	NDUFA8	NDUFA8	AA338496		Complex 1
758304	SLC25A14	solute carrier family 25 (mitochondrial carrier, brain), member 14	AA404241	Hs.194686	
772304	ANT2	Adenine nucleotide translocator 2 (fibroblast)	AA404486	Hs.79172	ox phos / apoptosis
753248	KIAA0381	Human mRNA for KIAA0381 gene, partial cds	AA406231	Hs.100113	
753775	GMPR	Glucose-6-phosphate dehydrogenase	AA406242	Hs.1435	energy metabolism
753457	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase)	AA406535	Hs.8248	Complex 1
753457	NDUFS1	NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR	AA406535	Hs.8248	Complex 1
753346	ALAS2	aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia)	AA410346	Hs.79103	
754490	SLC25A16	Human GT mitochondrial solute carrier protein homologue mRNA, complete cds	AA411554	Hs.180408	
754490	SLC25A16	ESTs, Weakly similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]	AA411554	Hs.180408	
730124	RPL7	Ribosomal protein L7	AA412470	Hs.153	

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731308	CS	ESTs, Highly similar to CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR [Sus scrofa]	AA416759	Hs.239760	
767441	HEXB	hexosaminidase B (beta polypeptide)	AA417946	Hs.51043	
767034	ILVBL	ilvB (bacterial acetolactate synthase)-like	AA424288	Hs.78880	
760148	UROD	Uroporphyrinogen decarboxylase	AA424441	Hs.78601	
773287	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8)	AA425211	Hs.163867	Complex 1
773266	MMP9	matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase)	AA425227	Hs.151738	
773399	DMD	dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272	AA425649	Hs.169470	
757265	EST	ESTs, Weakly similar to aralar1 [H.sapiens]	AA426113	Hs.183047	
770043	NDUFV1	Homo sapiens NADH:ubiquinone dehydrogenase 51 kDa subunit (NDUFV1) mRNA, nuclear gene encoding mitochondrial protein, complete cds	AA427570	Hs.7744	Complex 1
770835	BCKDHB	branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease)	AA427739	Hs.1265	energy metabolism
770835	BCKDHB	Branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease)	AA427739	Hs.1265	energy metabolism
771089	NDUFB7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 (18kD, B18)	AA428058	Hs.661	Complex 1
780947	POLD1	Polymerase (DNA directed), delta 1, catalytic subunit (125kD)	AA429661	Hs.99890	
782439	ATP5I	ESTs, Highly similar to ATP SYNTHASE E CHAIN, MITOCHONDRIAL [Cricetulus longicaudatus]	AA431433	Hs.85539	Complex V
756490	BCAT2	branched chain aminotransferase 2, mitochondrial	AA436410	Hs.101408	energy metabolism

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756490	BCAT2	Human branched chain aminotransferase precursor (BCATm) mRNA, nuclear gene encoding mitochondrial protein, complete cds	AA436410	Hs.101408	energy metabolism
774726	PPIF	peptidylprolyl isomerase F (cyclophilin F)	AA442081	Hs.173125	
784589	MMP15	Matrix metalloproteinase 2	AA443300	Hs.80343	
784589	MMP15	matrix metalloproteinase 15 (membrane-inserted)	AA443300	Hs.80343	
771173	23732 mRNA	Human clone 23732 mRNA, partial cds	AA443497	Hs.81281	
781017	EGR2	early growth response 2 (Krox-20 (Drosophila) homolog)	AA446027	Hs.1395	
781050	PFDN5	Human mRNA for c-myc binding protein, complete cds	AA446453	Hs.80686	
783696	OAT	ornithine aminotransferase (gyrate atrophy)	AA446819	Hs.75485	
783696	OAT	Ornithine aminotransferase (gyrate atrophy)	AA446819	Hs.75485	
783698	KIAA0188	Human mRNA for KIAA0188 gene, partial cds	AA446822	Hs.81412	
784214	EST	ESTs	AA446865	Hs.14018	
782635	NDUFAB1	Human Chromosome 16 BAC clone CIT987SK-A-735G6	AA447569	Hs.5556	Complex 1
813815	NR1I3	H.sapiens mRNA for orphan nuclear hormone receptor	AA447727	Hs.83623	
782800	UQCRFS1	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR	AA448184	Hs.3712	
782797	SMN1	survival of motor neuron 1, telomeric	AA448194	Hs.77306	
785845	TCF6L1	Transcription factor 6-like 1 (mitochondrial transcription factor 1-like)	AA449118	Hs.75133	
787938	SLC4A4	Homo sapiens sodium bicarbonate cotransporter (HNBC1) mRNA, complete cds	AA452278	Hs.5462	
788334	RPL23L	ribosomal protein L23-like	AA453015	Hs.3254	
789376	TXNRD1	Thioredoxin reductase	AA453335	Hs.13046	
789376	TXNRD1	thioredoxin reductase 1	AA453335	Hs.13046	

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813648	DLD	dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex)	AA453679	Hs.74635	
813651	ALAS1	aminolevulinate, delta-, synthase 1	AA453691	Hs.78712	
813678	SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	AA453823	Hs.75379	
813712	ATP5F1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	AA453849	Hs.181101	Complex V
809707	JUNB	jun B proto-oncogene	AA454711	Hs.198951	
814765	AKAP1	A kinase anchor protein, 149kD	AA454947	Hs.78921	
812246	HLCS	holocarboxylase synthetase (biotin-[proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] ligase)	AA455043	Hs.79375	
809876	ATP5G2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	AA455126	Hs.89399	Complex V
813444	BZRP	benzodiazapine receptor (peripheral)	AA455945	Hs.202	ox phos / apoptosis
812169	EST	ESTs, Weakly similar to PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S5 [S.cerevisiae]	AA456042	Hs.7807	
809578	RPS5	Ribosomal protein S5	AA456616	Hs.76194	
815564	DLST	Dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	AA456824	Hs.196416	
838568	COX6C	cytochrome c oxidase subunit VIc	AA456931	Hs.74649	Complex IV
810452	TOM34	Human putative outer mitochondrial membrane 34 kDa translocase hTOM34 mRNA, complete cds	AA457118	Hs.76927	
810452	TOM34	Human putative outer mitochondrial membrane 34 kDa translocase hTOM34 mRNA, complete cds	AA457118	Hs.76927	
838366	HMGCL	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)	AA458779	Hs.831	
814346	MTIF2	mitochondrial translational initiation factor 2	AA458825	Hs.149894	
814271	Est	ESTs, Highly similar to CGI-116 protein [H.sapiens]	AA459002	Hs.18885	

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814271	ESTs	ESTs, Highly similar to CGI-116 protein [H.sapiens]	AA459002	Hs.18885	
814444	CRSP9	33 kDa transcriptional co-activator	AA459244	Hs.7558	
814460	SURF5	H.sapiens SURF-5 mRNA	AA459247	Hs.78354	
814478	BCL2A1	Human Bcl-2 related (Bfl-1) mRNA, complete cds	AA459263	Hs.227817	apoptosis
810942	IDH3G	H.sapiens mRNA for NAD (H)-specific isocitrate dehydrogenase gamma subunit precursor	AA459380	Hs.75253	
810959	ARHGDIA	H.sapiens mRNA for rho GDP-dissociation Inhibitor 1	AA459400	Hs.159161	
795543	AOE372	Human antioxidant enzyme AOE37-2 mRNA, complete cds	AA459663	Hs.83383	
796646	ODC1	Ornithine decarboxylase 1	AA460115	Hs.75212	
796513	NDUFC1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1 (6kD, KFYI)	AA460251	Hs.84549	Complex 1
795729	BAD	Human Bcl-2 binding component 6 (bbc6) mRNA, complete cds	AA460291	Hs.76366	apoptosis
795965	CKMT2	Creatine kinase, mitochondrial 2 (sarcomeric)	AA460480	Hs.80691	nucleotide synthesis
796759	VDAC3	voltage-dependent anion channel 3	AA460728	Hs.7381	
796000	MPST	thiosulfate sulfurtransferase (rhodanese)	AA461065	Hs.74097	
796197	DMD	Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272	AA461118	Hs.169470	
796341	CLCN3	H. sapiens RNA for CLCN3	AA461332	Hs.174139	
811792	GSS	Glutathione synthetase	AA463458	Hs.82327	ROS
797016	SDHB	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	AA463565	Hs.64	
810325	IVD	isovaleryl Coenzyme A dehydrogenase	AA464149	Hs.77510	
810358	ACADVL	acyl-Coenzyme A dehydrogenase, very long chain	AA464163	Hs.82208	
810358	ACADVL	Acyl-Coenzyme A dehydrogenase, very long chain	AA464163	Hs.82208	
810316	KIAA0631	Homo sapiens mRNA for KIAA0631 protein, partial cds	AA464206	Hs.75154	

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810552	REA	Human B-cell receptor associated protein (hBAP) mRNA, partial cds	AA464669	Hs.7771	
814211	M6PR	Mannose-6-phosphate receptor (cation dependent)	AA465223	Hs.75709	
814899	BNIP3L	BCL2/adenovirus E1B 19kD-interacting protein 3-like	AA465697	Hs.132955	apoptosis
771327	NIFS	cysteine desulfurase	AA476245	Hs.194692	
740801	BCKDHA	branched chain keto acid dehydrogenase E1, alpha polypeptide (maple syrup urine disease)	AA477298	Hs.78950	energy metabolism
740801	BCKDHA	Branched chain keto acid dehydrogenase E1, alpha polypeptide (maple syrup urine disease)	AA477298	Hs.78950	energy metabolism
754106	TIMP3	tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)	AA479202	Hs.245188	
753602	EST	ESTs, Highly similar to MITOCHONDRIAL CARRIER PROTEIN RIM2 [Saccharomyces cerevisiae]	AA479944	Hs.42484	
814615	MTHFD2	NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase	AA480995	Hs.154672	
810787	HSPF1	DNAJ PROTEIN HOMOLOG 1	AA481758	Hs.82646	
840894	COX6A1	CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER PRECURSOR	AA482243	Hs.180714	Complex IV
611467	NDUFS6	ESTs, Highly similar to MITOCHONDRIAL TRIFUNCTONAL ENZYME ALPHA SUBUNIT PRECURSOR [Homo sapiens]	AA485132	Hs.49767	Complex 1
815683	WBSCR9	Williams-Beuren syndrome chromosome region 9	AA485132	Hs.194688	
840158	HK1	Hexokinase 1	AA485271	Hs.118625	
840158	HK1	Hexokinase 1	AA485272	Hs.118625	
810999	GPX1	glutathione peroxidase 1	AA485362	Hs.76686	ROS
810999	GPX1	Glutathione peroxidase 1	AA485362	Hs.76686	ROS
811062	LOC51629	ESTs, Highly similar to CGI-69 protein [H.sapiens]	AA485441	Hs.237924	
811108	TRIP6	Human zyxin related protein ZRP-1 mRNA, complete cds	AA485677	Hs.119498	

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811108	TRIP6	PRE-MRNA SPLICING FACTOR SF2, P32 SUBUNIT PRECURSOR	AA485677	Hs.119498	
843335	SUCLG1	ESTs, Highly similar to SUCCINYL-COA LIGASE [Rattus norvegicus]	AA485965	Hs.7043	
842846	TIMP2	tissue inhibitor of metalloproteinase 2	AA486280	Hs.246948	
842784	PHC	phosphate carrier, mitochondrial	AA486305	Hs.78713	
842818	KARS	Human mRNA for KIAA0070 gene, partial cds	AA486374	Hs.3100	
843134	PBP	Prostatic binding protein	AA486514	Hs.80423	
841008	GBP1	Guanylate binding protein 1, interferon-inducible, 67kD	AA486849	Hs.62661	
841334	STIP1	TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521	AA487635	Hs.75612	
841370	GOT2	Glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	AA487739	Hs.170197	
840708	SOD2	Superoxide dismutase 2, mitochondrial	AA488084	Hs.177781	
842989	MYL6	MYOSIN LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM	AA488346	Hs.77385	
843109	FARS1	phenylalanine-tRNA synthetase	AA488691	Hs.57969	
824911	EST	ESTs, Weakly similar to /prediction	AA489022	Hs.5080	
824911	ESTs	ESTs, Weakly similar to /prediction	AA489022	Hs.5080	
897448	C2ORF1	chromosome 2 open reading frame 1	AA489478	Hs.14454	
824568	KLK3	Prostate specific antigen	AA490981	Hs.171995	
768443	MGST1	microsomal glutathione S-transferase 1	AA495936	Hs.790	
755855	ANT3	adenine nucleotide translocator 3 (liver)	AA496376	Hs.164280	ox phos / apoptosis
755904	HSPA1A	HEAT SHOCK 70 KD PROTEIN 1	AA496544	Hs.8997	
755750	NME2	non-metastatic cells 2, protein (NM23B) expressed in	AA496628	Hs.255790	
897557	EST	ESTs, Weakly similar to myosin beta heavy chain, cardiac and skeletal muscle [H.sapiens]	AA497024	Hs.179817	
825229	LOC51017	ESTs, Highly similar to CGI-113 protein [H.sapiens]	AA504139	Hs.19077	
825170	ATP6A1	ATPase, H+ transporting, lysosomal (vacuolar proton pump), alpha polypeptide, 70kD, isoform 1	AA504160	Hs.255352	Complex V

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825386	ATP5JD	ESTs, Highly similar to ATP SYNTHASE D CHAIN, MITOCHONDRIAL [Bos taurus]	AA504246	Hs.64593	Complex V
825312	ATP5J	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6	AA504465	Hs.73851	Complex V
825312	ATP5J	ATP synthase, H+ transporting, mitochondrial	AA504465	Hs.73851	Complex V
827129	POLRMT	polymerase (RNA) mitochondrial (DNA directed)	AA521239	Hs.153880	
826077	PDHB	pyruvate dehydrogenase (lipoamide) beta	AA521401	Hs.979	
826077	PDHB	Pyruvate dehydrogenase (lipoamide) beta	AA521401	Hs.979	
826204	FLII	Human homolog of D. melanogaster flightless-I gene product mRNA, partial cds	AA521453	Hs.83849	
826211	PDCD2	Programmed cell death 2	AA521466	Hs.41639	
1057786	OAS2 (splice-varient)	2'-5'oligoadenylate synthetase 2	AA568217		
897774	APRT	Human APRT gene for adenine phosphoribosyltransferase	AA598510	Hs.28914	
898222	EST	ESTs	AA598602	Hs.13434	
897987	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 (39kD)	AA598884	Hs.75227	Complex 1
897987	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 (39kD)	AA598884	Hs.75227	Complex 1
950489	SOD1	Superoxide dismutase 1 (Cu/Zn)	AA599127	Hs.75428	
950578	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (13kD, B13)	AA608515	Hs.83916	Complex 1
950578	NDUFA5	Human NADH:ubiquinone oxidoreductase subunit B13 (B13) mRNA, complete cds	AA608515	Hs.83916	Complex 1
950700	PP	ESTs, Highly similar to INORGANIC PYROPHOSPHATASE [Bos taurus]	AA608572	Hs.184011	
950710	PCCA	propionyl Coenzyme A carboxylase, alpha polypeptide	AA608575	Hs.80741	
950710	PCCA	Propionyl-coA carboxylase alpha chain	AA608575	Hs.80741	
1030791	EST	ESTs, Highly similar to HYPOTHETICAL 44.9 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]	AA609009	Hs.63304	
1031185	MCSP	H.sapiens mRNA for mitochondrial capsule selenoprotein	AA609976	Hs.111850	

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1031185	MCSP	H.sapiens mRNA for mitochondrial capsule selenoprotein	AA609976	Hs.111850	
744417	CRAT	Carnitine acetyltransferase	AA621218	Hs.12068	
745314	HIRIP5	Homo sapiens mRNA for HIRA-interacting protein HIRIP5	AA625581	Hs.17368	
745503	ZNF9	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein)	AA625995	Hs.2110	
745542	ECHS1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	AA626255	Hs.76394	
745606	23759 mRNA	Human clone 23759 mRNA, partial cds	AA626336	Hs.118666	
745116	HMOX2	Heme oxygenase (decycling) 2	AA626370	Hs.83853	
884719	HSPA10	HEAT SHOCK COGNATE 71 KD PROTEIN	AA629567	Hs.180414	
884480	COX7C	cytochrome c oxidase subunit VIIc	AA629719	Hs.3462	Complex IV
884480	COX7C	Cytochrome c oxidase VIIc subunit	AA629719	Hs.3462	Complex IV
884644	LAMR1	Laminin receptor (2H5 epitope)	AA629897	Hs.181357	
884511	COX7B	cytochrome c oxidase subunit VIIb	AA629999	Hs.75752	Complex IV
884511	COX7B	Cytochrome c oxidase subunit VIIb	AA629999	Hs.75752	Complex IV
855890	cDNA	Homo sapiens mRNA; cDNA DKFZp586C0722 (from clone DKFZp586C0722)	AA630320	Hs.255914	
856167	TARS	threonyl-tRNA synthetase	AA630628	Hs.84131	
743811	NDUFS3	NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase)	AA634381	Hs.5273	Complex 1
845419	FANCA	Fanconi anemia, complementation group A	AA644129	Hs.86297	
845519	ATP5C1	ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR	AA644234	Hs.155433	Complex V
845441	KIAA0016	KIAA0016 gene product	AA644550	Hs.75187	
845630	SUCLA2	succinate-CoA ligase, ADP-forming, beta subunit	AA644577	Hs.182217	
853570	ANT3	Adenine nucleotide translocator 3 (liver)	AA663439	Hs.164280	ox phos / apoptosis
853506	23956 Mrna	Homo sapiens clone 23956 mRNA, partial cds	AA663549	Hs.8128	
855395	SCP2	sterol carrier protein 2	AA664009	Hs.75760	
855624	ALDH1	aldehyde dehydrogenase 1, soluble	AA664101	Hs.76392	
855523	GPX3	Glutathione peroxidase 3 (plasma)	AA664180	Hs.172153	ROS

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855843	UQCRB	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KD PROTEIN	AA664284	Hs.131255	
859228	IDH1	Homo sapiens NADP-dependent isocitrate dehydrogenase (IDH) mRNA, complete cds	AA666366	Hs.11223	
859627	KIAA0185	Human mRNA for KIAA0185 gene, partial cds	AA666405	Hs.255573	
856650	ATP5D	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	AA669314	Hs.89761	Complex V
878316	ESTs	ESTs, Highly similar to small zinc finger-like protein [H.sapiens]	AA670296	Hs.109571	
878413	SLC25A11	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	AA670357	Hs.184877	
896962	ACADS	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain	AA676663	Hs.127610	
455123	KIAA0429	Homo sapiens KIAA0430 mRNA, complete cds	AA676805	Hs.77694	
897107	SLC25A1	Homo sapiens mitochondrial citrate transport protein (CTP) mRNA, 3' end	AA676877	Hs.111024	
897107	SLC25A1	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	AA676877	Hs.111024	
455263	PET112L	PET112 (yeast homolog)-like	AA677572	Hs.11127	
430733	EST	ESTs, Highly similar to HYPOTHETICAL 16.5 KD PROTEIN IN PAS8-EGT2 INTERGENIC REGION [Saccharomyces cerevisiae]	AA677960	Hs.3585	
859858	STAR	steroidogenic acute regulatory protein	AA679454	Hs.3132	
869375	IDH2	Isocitrate dehydrogenase 2 (NADP+), mitochondrial	AA679907	Hs.252546	
869538	NDUFA4	ESTs	AA680322	Hs.108661	Complex 1
869538	NDUFA4	Human NADH:ubiquinone oxidoreductase MLRQ subunit mRNA, complete cds	AA680322	Hs.108661	Complex 1
433111	BAC clone CIT987SK-A-735G6	Human Chromosome 16 BAC clone CIT987SK-A-735G6	AA680407	Hs.47278	
970591	HMG1	High-mobility group (nonhistone chromosomal) protein 1	AA683085	Hs.189509	
432581	Novel Gene	Human BRCA2 region, mRNA sequence CG012	AA699390	Hs.184938	

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433553	CA5	Mitochondrial carbonic anhydrase	AA699469	Hs.177446	
433474	SURF1	Surfeit 1	AA699560	Hs.3196	
433481	TCF2	transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor	AA699573	Hs.169853	
433307	HNF6A	hepatocyte nuclear factor 6, alpha	AA699732	Hs.73168	
435314	EST	ESTs, Moderately similar to 5-AMINOLEVULINIC ACID SYNTHASE MITOCHONDRIAL PRECURSOR, ERYTHROID-SPECIFIC [H.sapiens]	AA699919	Hs.114018	
433350	SORD	Sorbitol dehydrogenase	AA700604	Hs.878	
434968	ATP5E	ESTs, Highly similar to ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL PRECURSOR [Bos taurus]	AA700688	Hs.177530	Complex V
436062	CPO	coproporphyrinogen oxidase (coproporphyria, harderoporphyria)	AA700808	Hs.89866	
384078	ATP6DV	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD	AA702541	Hs.106876	Complex V
447167	SFRS8	splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot, Drosophila homolog)	AA702973	Hs.84229	
450574	SCA7	Homo Sapiens mRNA for spinocerebellar ataxia 7	AA704255	Hs.108447	
461522	ABCB7	ESTs, Highly similar to MITOCHONDRIAL TRANSPORTER ATM1 PRECURSOR [Saccharomyces cerevisiae]	AA705237	Hs.125856	
461522	ABCB7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	AA705237	Hs.125856	
451706	POLA	Human mRNA for DNA polymerase alpha-subunit	AA707650	Hs.74090	
392622	ATP5B	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	AA708298	Hs.25	Complex V
392622	ATP5B	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	AA708298	Hs.25	Complex V
506032	TIM17	H.sapiens mRNA for TIM17 preprotein translocase	AA708446	Hs.20716	
1343732	SOD3	Superoxide dismutase 3, extracellular	AA725564	Hs.2420	

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399532	RPA40	Homo sapiens RNA polymerase I subunit hRPA39 mRNA, complete cds	AA733038	Hs.5409	
1308945	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE	AA748401		
395436	HUEL	Homo sapiens embryonic lung protein (HUEL) mRNA, complete cds	AA757427	Hs.44053	
970880	TPM4	tropomyosin 4	AA774983	Hs.102824	
868757	AK1	Adenylate kinase 1	AA775325	Hs.76240	
878676	XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kD)	AA775355	Hs.84981	
448619	GSR	Glutathione reductase	AA777289	Hs.121524	ROS
448491	mrp2	MITOCHONDRIAL RIBOSOMAL PROTEIN S14	AA777627		
449504	EST	EST, Weakly similar to predicted using Genefinder [C.elegans]	AA777928	Hs.121993	
896921	ME3	malic enzyme, NADP+-dependent, mitochondrial	AA779401	Hs.2838	
1354618	HSPF2	heat shock 40kD protein 2	AA830392	Hs.172847	
1390584	MIPEP	Human mitochondrial intermediate peptidase precursor (MIPEP) mRNA, mitochondrial gene encoding mitochondrial protein, complete cds	AA843592	Hs.68583	
1371793	OGDH	oxoglutarate dehydrogenase (lipoamide)	AA856769	Hs.168669	
1434908	VDAC2	ESTs, Weakly similar to similar to yeast adenylate cyclase [H.sapiens]	AA857093	Hs.78902	
1434908	VDAC2	Voltage-dependent anion channel 2	AA857093	Hs.78902	
1435103	ATP2A3	ATPase, Ca++ transporting, ubiquitous	AA857542	Hs.5541	Complex V
1469230	COX8	cytochrome c oxidase subunit VIII	AA862813	Hs.81097	Complex IV
1469230	COX8	CYTOCHROME C OXIDASE POLYPEPTIDE VIII-LIVER/HEART PRECURSOR	AA862813	Hs.81097	Complex IV
1455394	CYC1	cytochrome c-1	AA865265	Hs.697	
1455394	CYC1	CYTOCHROME C	AA865265	Hs.697	
1469138	FGA	Fibrinogen, A alpha polypeptide	AA865707	Hs.90765	
1475803	COX7A1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)	AA872125	Hs.114346	Complex IV

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1472754	COX6B	cytochrome c oxidase subunit VIb	AA872391	Hs.174031	Complex IV
1476157	PXR1	peroxisome receptor 1	AA873073	Hs.158084	
1472150	ATP5O	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)	AA873577	Hs.76572	Complex V
1472150	ATP5O	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)	AA873577	Hs.76572	Complex V
1256792	MAD4	Mad4 homolog	AA875977	Hs.102402	
1256737	SPG7	spastic paraplegia 7, paraplegin (pure and complicated autosomal recessive)	AA876165	Hs.78497	
1323203	ATP6B2	ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 2	AA877194	Hs.1697	Complex V
1323203	ATP6B2	ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 2	AA877194	Hs.1697	Complex V
1160732	NOS2A	Nitric oxide synthase 2A (inducible, hepatocytes)	AA877840	Hs.193788	
1417985	EST	heat shock 10kD protein 1 (chaperonin 10)	AA878786	Hs.203620	
1467799	KIAA0705	atrophin-1 interacting protein 1	AA883236	Hs.22599	
1467195	CYP11B1	cytochrome P450, subfamily XIB (steroid 11-beta-hydroxylase), polypeptide 1	AA884709	Hs.2610	
1468820	NOS3	nitric oxide synthase 3 (endothelial cell)	AA884967	Hs.166373	
1558965	CDC2L	cholinesterase-related cell division controller	AA917769	Hs.155266	
1474284	KAI1	kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))	AA922309	Hs.25409	
1486260	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD)	AA922326	Hs.51299	Complex 1
1486260	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD)	AA922326	Hs.51299	Complex 1
1568561	BCL2L1	BCL2-like 1	AA931820	Hs.180372	apoptosis
1574438	MMP11	matrix metalloproteinase 11 (stromelysin 3)	AA954935	Hs.155324	

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1569989	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	AA962407	Hs.182238	
1573778	C11ORF13	chromosome 11 open reading frame 13	AA970526	Hs.72925	
1573108	BCKDK	branched chain alpha-ketoacid dehydrogenase kinase	AA970731	Hs.20644	energy metabolism
1591788	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	AA976477	Hs.75103	
1591788	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	AA976477	Hs.75103	
1604342	HSPA9B	heat shock 70kD protein 9B (mortalin-2)	AA987644	Hs.3069	
1632011	NPR2	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)	AA994689	Hs.78518	
1606837	IMPDH2	IMP (inosine monophosphate) dehydrogenase 2	AA996028	Hs.75432	
1606894	HSF4	heat shock transcription factor 4	AA999776	Hs.75486	
1585499	NDUFS5	NDUFS5	AF020352		Complex 1
2297154	BCS1	BCS1	AF026849		ox phos
1902314	COX15.1	COX15.1	AF026850		Complex IV
2144562	PRAX-1	PRAX-1	AF039571		
2338136	COX11.1-11.2	COX11.1-11.2	AF044321		Complex IV
2170527	NDUFB10	NDUFB10	AF044954		Complex 1
929358	NDUFA3	NDUFA3	AF044955		Complex 1
2266937	NDUFB8	NDUFB8	AF044958		Complex 1
2103675	NDUFB3	NDUFB3	AF047183		Complex 1
1588691	NDUFA2	NDUFA2	AF047185		Complex 1
1270489	NDUFA7	NDUFA7	AF050637		Complex 1
1881693	NDUFB2	NDUFB2	AF050639		Complex 1
1019401	NDUFS2	NDUFS2	AF050640		Complex 1
998616	NDUFB1	NDUFB1	AF054181		Complex 1
2277817	NDUFC2	NDUFC2	AF087659		Complex 1
1473135	NDUFAB1	NDUFAB1	AF087660		Complex 1
994950	NDUFA10	NDUFA10	AF087661		Complex 1

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1636908	MDH2	malate dehydrogenase 2, NAD (mitochondrial)	AI000271	Hs.111076	
1637751	OXA1L	oxidase (cytochrome c) assembly 1-like	AI001180	Hs.151134	
1601947	COX7A2	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	AI002403	Hs.182684	Complex IV
1629264	hTIM44	Homo sapiens putative mitochondrial inner membrane protein import receptor (hTIM44) mRNA, nuclear gene encoding mitochondrial protein, complete cds	AI003393	Hs.123178	
1635681	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8)	AI017426	Hs.163867	Complex 1
1636741	ESTs	ESTs	AI017846	Hs.169539	
1645668	PDK1	pyruvate dehydrogenase kinase, isoenzyme 1	AI026814	Hs.159477	
1671299	HRK	harakiri, BCL2-interacting protein (contains only BH3 domain)	AI083676	Hs.87247	apoptosis
1566230	HYAL3	hyaluronoglucosaminidase 3	AI140794	Hs.129910	
1555659	GPX3	glutathione peroxidase 3 (plasma)	AI147534	Hs.172153	ROS
1734348	Go-alpha	Human guanine nucleotide-binding regulatory protein (Go-alpha) gene	AI188097	Hs.169647	
1870305	HSPB2	heat shock 27kD protein 2	AI245337	Hs.78846	
1880757	MAP3K5	mitogen-activated protein kinase kinase kinase 5	AI268273	Hs.151988	
1914863	DYSF	dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive)	AI310142	Hs.143897	disease-related
1917741	AOX1	aldehyde oxidase 1	AI343711	Hs.81047	
1916771	MTRF1	mitochondrial translational release factor 1	AI347695	Hs.80683	
1933324	MPZ	myelin protein zero (Charcot-Marie-Tooth neuropathy 1B)	AI351956	Hs.93883	disease-related
2010949	ME2	malic enzyme 2, mitochondrial	AI361039	Hs.75342	
2019469	CKMT1	creatine kinase, mitochondrial 1 (ubiquitous)	AI369378	Hs.153998	nucleotide synthesis
2043415	DAPK1	death-associated protein kinase 1	AI371096	Hs.153924	
2091860	MMPL1	matrix metalloproteinase-like 1	AI382081	Hs.198265	
2096376	S25665	DIHYDROLIPOAMIDE ACETYLTRANSFERASE COMPONENT	AI419467		
2098508	ATP2B2	ATP2B2	AI421603	Hs.89512	Complex V

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2029995	SLC12A7	solute carrier family 12 (potassium/chloride transporters), member 7	AI492956	Hs.172613	
2326129	BBC3	Human Bcl-2 binding component 3 (bbc3) mRNA, partial cds	AI688112	Hs.87246	apoptosis
2326019	COX5B	COX5B	AI688757	Hs.1342	Complex IV
1576254	2',5'-oligoadenylate synthetase 1	2',5'-oligoadenylate synthetase 1	BF898794	Hs.82396	
Control	DMSO	50% DMSO	Control	Control	control
2190112	A38234	2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT	D10523		
2367279	PN0673	PN0673	D16373		
964121	ATP5C1	ATP5C1	D16561, D16562		Complex V
2148505	JC4913	JC4913	D86061		
772304	ANT2	adenine nucleotide translocator 2 (fibroblast)	g2059228	Hs.79172	ox phos / apoptosis
149737	EST	Cytochrome P450, subfamily XIX (aromatization of androgens)	H00592	Hs.141142	
150466	EST	Nitric oxide synthase 3 (endothelial cell)	H01039	Hs.237163	
43884	PPIF	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, MITOCHONDRIAL PRECURSOR	H05580	Hs.173125	
43662	EST	ESTs, Weakly similar to similar to mitochrondrial carrier protein [C.elegans]	H05645	Hs.21262	
44255	RPML3	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3	H06113	Hs.79086	
45376	ACAA2	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	H07926	Hs.32500	
45632	GYS1	glycogen synthase 1 (muscle)	H08446	Hs.772	energy metabolism
45464	AK2	Human adenylate kinase 2 (adk2) mRNA, complete cds	H09730	Hs.171811	
47005	EST	ESTs	H09825	Hs.6818	
46248	ADPRT	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)	H09924	Hs.177766	
47853	ALDH4	aldehyde dehydrogenase 4 (glutamate gamma-semialdehyde dehydrogenase; pyrroline-5-carboxylate dehydrogenase)	H11346	Hs.77448	

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49464	UNG	uracil-DNA glycosylase	H15111	Hs.78853	
50754	MTIF2	INITIATION FACTOR IF-2, MITOCHONDRIAL PRECURSOR	H18070	Hs.149894	
51041	Est	protoporphyrinogen oxidase	H18633	Hs.123641	
160126	COX10	Cytochrome c oxidase subunit X (heme A: farnesyltransferase	H21868	Hs.77513	Complex IV
51702	GOT1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	H22856	Hs.597	
51826	NNT	ESTs, Highly similar to NAD(P) TRANSHYDROGENASE, MITOCHONDRIAL PRECURSOR [Bos taurus]	H22944	Hs.18136	
51826	NNT	nicotinamide nucleotide transhydrogenase	H22944	Hs.18136	
162775	DDX5	P68 PROTEIN	H27564	Hs.76053	
190732	SLC2A5	Solute carrier family 2 (facilitated glucose transporter), member 5	H38650	Hs.33084	
191826	EST	ESTs, Highly similar to MITOCHONDRIAL RNA SPLICING PROTEIN MRS3 [Saccharomyces cerevisiae]	H40449	Hs.34401	
193106	ATP5G3	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3	H47080	Hs.429	Complex V
179336	SDHA	ESTs, Highly similar to SUCCINATE DEHYDROGENASE [Homo sapiens]	H50345	Hs.469	
207808	NFATC3	nuclear factor of activated T-cells, cytoplasmic 3	H59048	Hs.172674	
205185	THBD	Thrombomodulin	H59861	Hs.2030	
236034	UCP2	uncoupling protein 2 (mitochondrial, proton carrier)	H61243	Hs.80658	
236034	UCP2	Human uncoupling protein homolog (UCPH) mRNA, complete cds	H61243	Hs.80658	
208531	EST	ESTs, Weakly similar to PUTATIVE MITOCHONDRIAL CARRIER YBR291C [Saccharomyces cerevisiae]	H61979	Hs.7994	
238907	D6S52E	ESTs, Moderately similar to ABC1 PROTEIN PRECURSOR [Saccharomyces cerevisiae]	H67876	Hs.243960	

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212198	TP53BP2	Human Bcl2, p53 binding protein Bbp/53BP2 (BBP/53BP2) mRNA, complete cds	H69153	Hs.44585	
214133	FSRG1	RING3 PROTEIN	H72520	Hs.75243	
213890	DECR1	2,4-dienoyl CoA reductase	H72937	Hs.81548	
233581	HIP2	Human huntingtin interacting protein (HIP2) mRNA, complete cds	H78483	Hs.155485	
241481	CASP10	Human apoptotic cysteine protease Mch4 (Mch4) mRNA, complete cds	H80712	Hs.5353	
253009	HSPCA	HEAT SHOCK PROTEIN HSP 90-ALPHA	H88540	Hs.180532	
243100	ACADSB	acyl-Coenzyme A dehydrogenase, short/branched chain	H96140	Hs.81934	
243100	ACADSB	Acyl-coA dehydrogenase	H96140	Hs.81934	
251047	MMP17	matrix metalloproteinase 17 (membrane-inserted)	H97792	Hs.159581	
261481	CUL3	Human Hs-cul-3 mRNA, partial cds	H98621	Hs.78946	
262932	ACO2	aconitase 2, mitochondrial	H99699	Hs.75900	
262932	ACO2	Aconitase 2, mitochondrial	H99699	Hs.75900	
2308263	A40487	A40487	J03826, M58509, M58508		
1744035	A31998	ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT	J04058		
1762200	VDAC1	VDAC1	L06132		
704360	LCFA_HUMAN	LCFA_HUMAN	L09229		
1587031	HSPA9	MITOCHONDRIAL STRESS-70 PROTEIN	L15189		
1632231	UQCRC1	P31930 UBIQUINOL-CYTOCHROME-C REDUCTASE COMPLEX CORE PROTEIN I PRECURSOR	L16842		
1675950	CRHU5	CARBONIC ANHYDRASE V PRECURSOR	L19297		
1520618	GABT_HUMAN	AMINOBUTYRATE AMINOTRANSFERASE	L32961		
2267229	S62767	ELONGATION FACTOR TU	L38995		
1724630	S14367	CYTOCHROME P450 XIA1	M14565		
1676983	RDHUB5	NADH-CYTOCHROME B5 REDUCTASE	M16462, M16461, M28705		
1704180	XNHUDM	ASPARTATE AMINOTRANSFERASE	M22632		

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2213770	CCHU	Matrix metalloproteinase 7 (matrilysin, uterine)	M22877		remodelling
1934125	B34181	steroid 11-beta-hydroxylase	M32864, X54741		
1175538	A39018	MITOCHONDRIAL CARNITINE PALMITOYLTRANSFERASE II PRECURSOR	M58581		
2091562	S40622	METHYLMALONYL-COA MUTASE PRECURSOR	M65131		
1338040	C46157	HEXOKINASE D, LIVER ISOZYMES	M69051		
2364396	DEHUH2	DEHUH2	M77144		
971851	COX7A1	COX7A1	M83186		Complex IV
986164	COX6A2	COX6A2	M83308		Complex IV
1542260	PDHA2	PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA	M86808		
2367249	B42665	B42665	M87434		
1338040	A46157	HEXOKINASE D, LIVER ISOZYMES	M90299		
1473506	MMSA_HUMAN	METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE	M93405		
266146	CYP24	cytochrome P450, subfamily XXIV (vitamin D 24-hydroxylase)	N21576	Hs.89663	
266146	CYP24	Human mitochondrial 1,25-dihydroxyvitamin D3 24-hydroxylase mRNA, complete cds	N21576	Hs.89663	
266106	YWHAE	Human 14-3-3 epsilon mRNA, complete cds	N21624	Hs.79474	
253725	EST	EST	N21972	Hs.43052	
254004	EST	ESTs	N22302	Hs.177861	
266312	ATP7B	ATPase, Cu++ transporting, beta polypeptide (Wilson disease)	N26536	Hs.84999	Complex V
261971	PRSM1	protease, metallo, 1, 33kD	N27227	Hs.183138	
259462	LOC54675	ESTs	N29545	Hs.3569	
259842	PMPCB	H.sapiens mRNA for M-phase phosphoprotein, mpp11	N29844	Hs.184211	
271006	DLAT	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	N29901	Hs.115285	

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271102	CCS	Homo sapiens copper chaperone for superoxide dismutase (CCS) mRNA, complete cds	N30404	Hs.5002	ROS
280507	HPRT1	Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	N47312	Hs.82314	control
280507	HPRT1	Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	N47312	Hs.82314	control
279665	PDX1	Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding protein	N48320	Hs.74642	
279691	CD2AP	CD2-associated protein	N48329	Hs.30490	
279790	FMR1	Fragile X mental retardation 1	N48355	Hs.89764	disease-related
283943	EST	ESTs, Highly similar to ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]	N50802	Hs.41066	
244146	APAF1	Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds	N51014	Hs.77579	apoptosis
280496	KIAA0123	Human mRNA for KIAA0123 gene, partial cds	N51632	Hs.75353	
247160	PPOX	protoporphyrinogen oxidase	N57891	Hs.100016	
246300	TIAL1	TIA1 cytotoxic granule-associated RNA-binding protein-like 1	N59426	Hs.182741	
248631	AMT	aminomethyltransferase (glycine cleavage system protein T)	N59532	Hs.102	
248669	EST	ESTs	N59553	Hs.8941	
287569	EST	EST	N62122	Hs.83313	
290111	HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	N62195	Hs.77910	
288796	BNIP2	Homo sapiens BCL2/adenovirus E1B 19kD-interacting protein 2 (BNIP2) mRNA, complete cds	N62514	Hs.155596	apoptosis
288888	EST	Homo sapiens clone 640 unknown mRNA, complete sequence	N62617	Hs.44563	
284620	EST	Cytochrome P450, subfamily XXI (steroid 21-hydroxylase, congenital adrenal hyperplasia)	N64794	Hs.124918	
278570	MITF	Microphthalmia-associated transcription factor	N66177	Hs.166017	

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295843	CYP27A1	cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1	N66957	Hs.82568	
290753	CS	ESTs, Highly similar to CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR [Sus scrofa]	N67639	Hs.239760	
290505	EST	ESTs	N67991	Hs.30487	
298155	ACADM	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	N70794	Hs.79158	
298155	ACADM	Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	N70794	Hs.79158	
298965	COX6B	Cytochrome c oxidase subunit VIb	N71160	Hs.174031	Complex IV
245920	GYS2	glycogen synthase 2 (liver)	N72934	Hs.82614	energy metabolism
248261	GLDC	glycine dehydrogenase (decarboxylating; glycine decarboxylase, glycine cleavage system protein P)	N78083	Hs.27	
300590	APACD	Homo sapiens mRNA for ATP binding protein, complete cds	N80741	Hs.153884	
293104	PHYH	Homo sapiens peroxisomal phytanoyl-CoA alpha-hydroxylase (PAHX) mRNA, complete cds	N91990	Hs.172887	
307873	ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	N93024	Hs.995	Complex V
307933	NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (16kD, SGDH)	N93053	Hs.19236	Complex 1
310519	F10	COAGULATION FACTOR X PRECURSOR	N98524	Hs.47913	
2118546	NDUFA6	NDUFA6	NM_002490		Complex 1
123474	SCD	Homo sapiens mRNA for stearoyl-CoA desaturase	R00707	Hs.119597	
124753	ABCD4	Homo sapiens peroxisomal membrane protein 69 (PMP69) mRNA, complete cds	R02189	Hs.94395	
125183	SSBP	single-stranded DNA-binding protein	R05693	Hs.923	
126229	EST	ESTs	R06313	Hs.77677	
126243	HMBS	Hydroxymethylbilane synthase	R06321	Hs.82609	
125722	DGUOK	deoxyguanosine kinase	R07560	Hs.77494	
127032	API2	apoptosis inhibitor 2	R07870	Hs.127799	apoptosis
127197	CXORF6	Human Xq28 mRNA, complete cds	R08270	Hs.20136	

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128875	SCA2	Spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant)	R10604	Hs.76253	
129146	COX7RP	Homo sapiens mRNA for COX7RP, complete cds	R10896	Hs.30888	Complex IV
129431	EST	BRCA2(?)	R11316	Hs.188591	
25499	UQCRH	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 11 KD PROTEIN PRECURSOR	R11698	Hs.73818	
25499	UQCRH	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 11 KD PROTEIN PRECURSOR	R11698	Hs.73818	
53385	EST	ESTs, Weakly similar to Similar to NAD(P) transhydrogenase, mitochondrial [C.elegans]	R16231	Hs.106620	
129606	EST	ESTs	R16545	Hs.70333	
129644	SSH3BP1	Homo sapiens eps8 binding protein e3B1 mRNA, complete cds	R16667	Hs.24752	
131653	RPMS12	Homo sapiens mRNA for mitochondrial ribosomal protein S12	R23752	Hs.9964	
131839	FOLR1	folate receptor 1 (adult)	R24635	Hs.73769	
133273	PMP22	peripheral myelin protein 22	R26960	Hs.103724	
134748	GCSH	glycine cleavage system protein H (aminomethyl carrier)	R28294	Hs.77631	
133565	CPT1A	carnitine palmitoyltransferase I, liver	R28631	Hs.29331	
134269	POLRMT	Human mitochondrial RNA polymerase mRNA, nuclear gene encoding mitochondrial protein, complete cds	R31115	Hs.153880	
32621	WARS2	tryptophanyl tRNA synthetase 2 (mitochondrial)	R43272	Hs.227274	
32621	WARS2	tryptophanyl tRNA synthetase 2 (mitochondrial)	R43272	Hs.227274	
41541	EST	Human mRNA for KIAA0017 gene, complete cds	R52789	Hs.253023	
138189	WFS1	Homo sapiens transmembrane protein (WFS1) mRNA, complete cds	R53910	Hs.26077	
40026	ANT1	ADP,ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1	R53942	Hs.2043	ox phos / apoptosis

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42558	GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	R61229	Hs.75335	
140131	ACADL	acyl-Coenzyme A dehydrogenase, long chain	R66006	Hs.1209	
140131	ACADL	Acyl-Coenzyme A dehydrogenase, long chain	R66006	Hs.1209	
141966	HSD3B1	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1	R68803	Hs.38586	
144777	HAX1	Human HS1 binding protein HAX-1 mRNA, nuclear gene encoding mitochondrial protein, complete cds	R76263	Hs.15318	
146605	FPRL1	formyl peptide receptor-like 1	R80041	Hs.99855	
194384	BTF3	Basic transcription factor 3	R83000	Hs.101025	transcription
180512	ENC1	ectodermal-neural cortex (with BTB-like domain)	R85090	Hs.104925	
165837	EST	ESTs	R86713	Hs.87595	
195712	CYP2C9	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 9	R89492	Hs.167529	
195712	CYP2C9	Human cytochrome P4502C9 (CYP2C9) mRNA, clone 65	R89492	Hs.167529	
194949	CYP3A7	Cytochrome P450 IIIA7 (P450-HFLa)	R91078	Hs.172323	
196189	CYB5	cytochrome b-5	R92281	Hs.83834	
196189	CYB5	Cytochrome b-5	R92281	Hs.83834	
196612	MMP12	matrix metalloproteinase 12 (macrophage elastase)	R92994	Hs.1695	
197657	ALDH5	ALDEHYDE DEHYDROGENASE, MITOCHONDRIAL X PRECURSOR	R93551	Hs.169517	
198312	KIAA0719	ESTs, Weakly similar to MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR [Neurospora crassa]	R94191	Hs.21198	
70201	EST	ESTs, Highly similar to MITOCHONDRIAL RNA SPLICING PROTEIN MSR4 [Saccharomyces cerevisiae]	T50082	Hs.34401	
81289	ACTG2	Gamma-actin, enteric smooth muscle form	T60048	Hs.77443	
81289	ACTG2	actin, gamma 2, smooth muscle, enteric	T60048	Hs.77443	
83605	CPS1	carbamoyl-phosphate synthetase 1, mitochondrial	T61078	Hs.50966	

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83605	CPS1	Carbamoyl-phosphate synthetase 1, mitochondrial	T61078	Hs.50966	
77915	PLA2G2A	phospholipase A2, group IIA (platelets, synovial fluid)	T61323	Hs.76422	
79655	EST	ESTs	T62655	Hs.11039	
79828	HD	Huntingtin (Huntington disease)	T64094	Hs.79391	disease-related
21738	HADHSC	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	T65482	Hs.7153	
80374	PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	T65833	Hs.1023	
80374	PDHA1	Pyruvate dehydrogenase (lipoamide) alpha 1	T65833	Hs.1023	
66534	GCKR	glucokinase (hexokinase 4) regulatory protein	T67007	Hs.89771	
66564	BDH	3-hydroxybutyrate dehydrogenase (heart, mitochondrial)	T67058	Hs.76893	
83279	TIM23	Homo sapiens inner mitochondrial membrane translocase Tim23 (TIM23) mRNA, nuclear gene encoding mitochondrial protein, complete cds	T68317	Hs.11866	
83279	TIM23	Homo sapiens inner mitochondrial membrane translocase Tim23 (TIM23) mRNA, nuclear gene encoding mitochondrial protein, complete cds	T68317	Hs.11866	
82874	EST	ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]	T69273	Hs.241336	
108208	HADHB	Human mRNA for mitochondrial 3-ketoacyl-CoA thiolase beta-subunit of trifunctional protein, complete cds	T69767	Hs.146812	energy metabolism
108208	HADHB	ESTs, Highly similar to MITOCHONDRIAL TRIFUNCTONAL ENZYME BETA SUBUNIT PRECURSOR [H.sapiens]	T69767	Hs.146812	
80924	HO3	histidyl-tRNA synthetase	T70104	Hs.77798	
85259	HMOX1	heme oxygenase (decycling) 1	T71757	Hs.202833	
85450	ACOX2	acyl-Coenzyme A oxidase 2, branched chain	T71782	Hs.9795	
85384	EST	ESTs, Weakly similar to anon2A5 [D.melanogaster]	T71965	Hs.10964	

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85561	CYP2A7	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7	T73031	Hs.252937	
84880	EST	ESTs, Weakly similar to VISC PROTEIN [Escherichia coli]	T74882	Hs.12239	
108378	PC	pyruvate carboxylase	T77729	Hs.89890	
113206	EST	ESTs, Highly similar to ARGINYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR [Saccharomyces cerevisiae]	T83996	Hs.15395	
111981	G1P3	interferon, alpha-inducible protein (clone IFI-6-16)	T84633	Hs.179972	
110744	SCO2	SCO (cytochrome oxidase deficient, yeast) homolog 2	T90560	Hs.180903	
control	Blank	50% DMSO	T90560	Hs.180903	control
110772	C14ORF2	chromosome 14 open reading frame 2	T90621	Hs.109052	
122636	G6PC	Glucose-6-phosphatase	T98886	Hs.242	energy metabolism
1870662	A54868	nuclear respiratory factor 1 (NRF1)	U18383		
2010933	KAD2_HUMAN	ADENYLATE KINASE ISOENZYME 2	U39945		
1571111	SCOT_HUMAN	Succinyl CoA:3-oxoacid CoA transferase	U62961		
2114841	U66035	translocase of inner mitochondrial membrane 8	U66035		
2338827	GCDH_HUMAN	GCDH_HUMAN	U69141		
control	Plant control rbcL	Arabidopsis ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	U91966		
302190	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog)	W16724	Hs.199160	
321354	EST	ESTs, Moderately similar to MSG1-related protein [H.sapiens]	W32403	Hs.18349	
322218	EST	ESTs, Highly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [Saccharomyces cerevisiae]	W37993	Hs.55609	
323500	CASP6	Human cysteine protease Mch2 isoform alpha (Mch2) mRNA, complete cds	W45688	Hs.3280	
324618	TSFM	MITOCHONDRIAL ELONGATION FACTOR TS PRECURSOR	W47015	Hs.3273	
324651	EST	ESTs, Weakly similar to MITOCHONDRIAL RESPIRATORY FUNCTION PROTEIN 1 [Saccharomyces cerevisiae]	W47099	Hs.19513	

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324885	C11ORF4	chromosome 11 open reading frame 4	W48701	Hs.75859	
321163	HSU79253	hypothetical protein	W53000	Hs.56155	
341328	TPM1	Tropomyosin alpha chain (skeletal muscle)	W58092	Hs.77899	
341246	CLPP	H.sapiens mRNA for CLPP	W58658	Hs.74362	
341901	EST	ESTs	W61374	Hs.11317	
342181	BCL2	B-cell CLL/lymphoma 2	W63749	Hs.79241	apoptosis
343555	EST	ESTs, Weakly similar to mitochondrial inner membrane protease 1 [S.cerevisiae]	W69379	Hs.62669	
346009	PFKL	Phosphofructokinase (liver type)	W72140	Hs.155455	
345621	CXX1	Homo sapiens mRNA for putatively prenylated protein	W72596	Hs.255532	
344825	LAS	Homo sapiens mRNA for putative lipoic acid synthetase, partial	W72965	Hs.53531	
344272	EMP3	epithelial membrane protein 3	W73810	Hs.9999	
346860	SOD2	superoxide dismutase 2, mitochondrial	W78148	Hs.177781	
347031	KIAA0195	Human mRNA for KIAA0195 gene, complete cds	W79511	Hs.80540	
415978	CPT1A	carnitine palmitoyltransferase I, liver	W85710	Hs.29331	
417385	Dihydroorotate dehydrogenase	Dihydroorotate dehydrogenase	W88472	Hs.125846	
417801	LOC51264	ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR [Saccharomyces cerevisiae]	W88752	Hs.7736	
417803	EST	ESTs, Highly similar to hypothetical protein [H.sapiens]	W88753	Hs.166406	
2277616	COX6B	COX6B	X13923		Complex IV
control	Plant control RUBISCO	Arabidopsis RUBISCO activase	X14212		
937944	COX7A2	COX7A2	X15822		Complex IV
2165301	DEHUMT	methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase	X16396		
control	Plant control CAB	Arabidopsis photosystem I chlorophyll a/b binding protein	X56062		
2138479	XNHUSP	SERINE--PYRUVATE AMINOTRANSFERASE	X56092		
1173869	ATP5A1	ATP5A1	X59066, X65460		Complex V

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1736058	ATP5F1	ATP5F1	X60221		Complex V
2241563	KIHUA3	KIHUA3	X60673		
control	Beta Actin	Human beta actin	X63432		control
1084029	A56650	MITOCHONDRIAL 2-OXOGLUTARATE/MALATE CARRIER PROTEIN	X66114		
2364633	A32422	A32422	X66785		
2168168	ETFB	isocitrate dehydrogenase 3 (NAD+) alpha (IDH3A),	X71129		
2274670	S32482	ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT	X71129		
1753047	ATP50	ATP50	X83218		Complex V
927606	ARAL-1	ARAL-1	Y14494		
824699	SUCA_HUMAN	SUCA_HUMAN	Z68204		
66686	No Data	QM PROTEIN			
133099	MMP1 Precursor	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR			
161476	COQ5	COQ5			
211780	No Data	Hexosaminidase B (beta polypeptide)			
233479	No Data	Oxoglutarate dehydrogenase (lipoamide)			
240766	Data unavailable	METALLOPROTEINASE INHIBITOR 1 PRECURSOR			
300237	No Data	H.sapiens DAP-3 mRNA			
366511	No Data	Actin, alpha 1, skeletal muscle			
609989	No Data	EST			
611027	dihydroorotate dehydrogenase	dihydroorotate dehydrogenase		Hs.94925	
645006	MRP4	MRP4			
814337	PCCB	propionyl Coenzyme A carboxylase, beta polypeptide		Hs.63788	
852273	AZF1	AZF1			
1060841	CIT1	CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR			ox phos
1472184	HUEL	Homo sapiens embryonic lung protein (HUEL) mRNA, complete cds		Hs.44053	
1502027	MGE1	GrpE-like protein cochaperone mRNA			
1709773	MCX1	ATP-DEPENDENT CLP PROTEASE			
1908746	MDH1	MALATE DEHYDROGENASE			

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1955460	MAS2	UCR1_HUMAN P31930 UBIQUINOL-CYTOCHROME-C REDUCTASE COMPLEX CORE PROTEIN I			
2095653	GLO4	HYDROXYACYLGLUTATHIONE HYDROLASE			
2114302	surfeit 1	surfeit 1		Hs.3196	
2119594	IDH1	ISOCITRATE DEHYDROGENASE			
2216141	IFM1	IFM1			
2240514	AAP1'	AAP1'			
2244621	MRF1	MRF1			
2266774	ABF2	ABF2			
control	Blank	50 % DMSO			control
control	Poly - A	Poly -A 40-60 oligonucleotide			
	mtDNA - 12S ribosome	Mitochondrial DNA 12S			mt DNA
	mtDNA - 16S ribosome	Mitochondrial DNA 16s			mt DNA
	mtDNA - ATP6	Mitochondrial DNA ATP6			mt DNA Complex V
	mtDNA - ATP8	Mitochondrial DNA ATP8			mt DNA Complex V
	mtDNA - COX1	Mitochondrial COX1			mt DNA Complex IV
	mtDNA - COX2	Mitochondrial DNA COX2			mt DNA Complex IV
	mtDNA - COX3	Mitochondrial DNA COX3			mt DNA Complex IV
	mtDNA - CYT B	Mitochondrial DNA CYTb			
	mtDNA - ND1	Mitochondrial DNA ND1			mt DNA Complex I
	mtDNA - ND2	Mitochondrial DNA ND2			mt DNA Complex I
	mtDNA - ND3	Mitochondrial DNA ND3			mt DNA Complex I
	mtDNA - ND4	Mitochondrial DNA ND4			mt DNA Complex I
	mtDNA - ND4L	Mitochondrial DNA ND4L			mt DNA Complex I
	mtDNA - ND5	Mitochondrial DNA ND5			mt DNA Complex I
	mtDNA - ND6	Mitochondrial DNA ND6			mt DNA Complex I
	PLANT #1	PLANT #1			
	PLANT #2	PLANT #2			

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