COMPARATIVE AND INTEGRATIVE GENOMIC APPROACH TOWARD DISEASE GENE IDENTIFICATION: APPLICATION TO BARDET-BIEDL SYNDROME

by

Annie Pei-Fen Chiang

An Abstract

Of a thesis submitted in partial fulfillment
of the requirements for the Doctor of Philosophy
degree in Genetics (Computational Genetics)
in the Graduate College of
The University of Iowa

December 2006

Thesis Supervisors: Assistant Professor Terry A. Braun
Professor Thomas L. Casavant
Professor Val C. Sheffield

ABSTRACT

The identification of disease genes (genes that when mutated cause human diseases) is an important and challenging problem. Proper diagnosis, prevention, as well as care for patients require an understanding of disease pathophysiology, which is best understood when the underlying causative gene(s) or genetic element(s) are identified. While the availability of the sequenced human genome helped to lead to the discovery of more than 1,900 disease genes, the rate of disease gene discovery is still occurring at a slow pace. The use of genetic linkage methods have successfully led to the identification of numerous disease genes. However, linkage studies are ultimately restricted by available meioses (clinical samples) which result in numerous candidate disease genes. This thesis addresses candidate gene prioritizations in disease gene discovery as applied toward a genetically heterogeneous disease known as Bardet-Biedl Syndrome (BBS). Specifically, the integration of various functional information and the development of a novel comparative genomic approach (Computational Orthologous Prioritization – COP) that led to the identification of *BBS3* and *BBS11*. Functional data integration and application of the COP method may be helpful toward the identification of other disease genes.

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PH.D. THESIS

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To my parents

To get through the hardest journey we need take only one step at a time,
but we must keep on stepping

-- Chinese proverb

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ABSTRACT

The identification of disease genes (genes that when mutated cause human diseases) is an important and challenging problem. Proper diagnosis, prevention, as well as care for patients require an understanding of disease pathophysiology, which is best understood when the underlying causative gene(s) or genetic element(s) are identified. While the availability of the sequenced human genome helped to lead to the discovery of more than 1,900 disease genes, the rate of disease gene discovery is still occurring at a slow pace. The use of genetic linkage methods have successfully led to the identification of numerous disease genes. However, linkage studies are ultimately restricted by available meioses (clinical samples) which result in numerous candidate disease genes. This thesis addresses candidate gene prioritizations in disease gene discovery as applied toward a genetically heterogeneous disease known as Bardet-Biedl Syndrome (BBS). Specifically, the integration of various functional information and the development of a novel comparative genomic approach (Computational Orthologous Prioritization – COP) that led to the identification of *BBS3* and *BBS11*. Functional data integration and application of the COP method may be helpful toward the identification of other disease genes.

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CHAPTER 1

INTRODUCTION

1.1 Introduction

The field of human genetics, often synonymous with medical genetics, is concerned with the study of hereditability of genetic variations in humans, particularly as it relates to human diseases. It is a field that has gained considerable momentum since the pioneering work performed by Hersey and Chase to identify DNA (and not protein) as the hereditary material in bacteriophages, and ultimately all organisms (Hershey and Chase 1952). Together, many scientific discoveries and technological advances such as advances in protein biochemistry and x-ray crystallographic methods that led to the elucidation of the DNA structure (Watson and Crick 1953), and discoveries of restriction endonuclease enzymes (Arber and Dussoix 1962; Danna and Nathans 1971; Smith and Wilcox 1970), polymorphic genetic markers (Lander and Botstein 1986), polymerase chain reaction (PCR) (Mullis 1990), and DNA sequencing methods (Sanger and Coulson 1975; Maxam and Gilbert 1977) along with an international effort in sequencing the human genome - Human Genome Project (HGP), made it possible to study genetic origins of human diseases.

One of the major pillars of human genetics is the study of disease genes and how defects at the genetic level can lead to the observed disease phenotype. This requires the initial identification of the causative (disease) gene or genetic element, a process often referred to as disease gene discovery, or the identification of those genes or genetic elements, that if mutated, cause human diseases. Since the initial discovery that sickle-cell anemia resulted from a single amino acid substitution in 1957 (Ingram 1957), only 1,952 genes (OMIM, August 15, 2006) have been identified to cause or be associated with higher risk of developing human diseases.

Many factors contribute to the difficulty of the disease gene discovery process. The clinical phenotype(s) of a disease may overlap with that of another; the heterogeneity of clinical phenotypes of a single disease can mislead or confound genetic studies; the genetic contributions of a single gene or genetic element may not provide strong linkage signal(s) thus requiring the development of different methodologies; finally, lack of cost-effective high-throughput technologies for mutational screening all combine to serve as strong impediments in the disease gene discovery process.

Despite rapid advancement in the field of medicine over the last half century, much of patient care is directed at the intermediate phenotype or symptoms rather than the underlying cause of disorders. This is primarily because the lack of in-depth understanding of disease states and pathophysiologies. Though challenging, there are additional reasons for a focused effort on disease gene discovery. Different diseases can sometimes present similar phenotypes, potentially leading to misdiagnosis and/or improper care. The identification of a disease gene would allow for development of diagnostic tests that will either confirm or refute the initial diagnosis. Knowing the disease gene also allows for functional studies to better understand the disease state for disease prevention and may eventually lead to drug development. Thus, to effectively prevent, diagnose and treat disease, one must first identify the defective gene or genetic element present in diseased patients.

1.2 Goals

Traditional disease gene discovery efforts have relied primarily on cytogenetic studies or the use of large and/or multiple families for genetic linkage mapping studies to

map the disease phenotype to genetic loci or intervals. However, until relatively recently, the combined lack of human genome sequence, scarcity of large and/or multiple pedigrees to allow for further interval delineation, and lack of densely-spaced informative genetic markers have impeded the rate of disease gene discovery, leaving some 1,542 disease loci mapped but the causative gene or genetic element unidentified (OMIM, August 15, 2006).

The sequencing of the human genome (HGP), began in the late 1980's and completed fifteen years later, helped usher in the 'omics' era: an era founded on the ability to interrogate the activities of thousands of cellular components (e.g. RNA, proteins) from a single experiment, owing to technological advances such as microarray chips (Schena et al. 1995). These large-scale efforts undoubtly provide tremendous resources upon which additional studies can build, however, one of the major challenges at hand is to sort and integrate these large datasets so that interesting, meaningful information can be extracted and studied further.

Functional studies in model organisms ranging from the intestinal bacterium *Escherichia coli* to the chimpanzee *Pan troglodytes* are able to provide specific mechanistic information on human diseases primarily because basic biological features are conserved between the model organisms and humans. With the availability of various genomic sequences generated concomitantly along with the sequenced human genome, comparisons at the genomic level between model organisms and humans may yield additional insights. This process, also known as comparative genomics, has already been applied successfully toward genome assemblies (Kirkness et al. 2003; Pop et al. 2004) as well as identification of regulatory elements (Kellis et al. 2003; Bofffeli et al. 2003).

The primary goal of this thesis is to utilize the already abundant existing information from multiple sources, particularly the genome sequence of humans (HGP) as well as other organisms to help prioritize candidate genes for disease gene discovery. The combined use of comparative genomics and integration of other sources of functional information will be applied to a genetically heterogeneous disorder known as Bardet-Biedl Syndrome (BBS).

1.3 Organization

The rest of the thesis will be organized as follows. Chapter 2 will provide some background on candidate gene prioritization methods and BBS. A novel comparative genomics methodology, Computational Orthologous Prioritization (COP), developed for candidate gene prioritization will be outlined in Chapter 3. Chapter 4 will describe the identification of *BBS3*, including how the COP method played a pivotal role in *BBS3* discovery. Chapter 5 will describe the identification of *BBS11* with the integration of multiple sources of functional information. Chapter 6 will evaluate the phylogenetic profile of some heterogeneous disorders in an attempt to determine if the COP method could have contributed to the respective (disease) gene discovery. Finally, conclusions and future work will be presented in Chapter 7.

CHAPTER 2

CANDIDATE GENE PRIORITIZATION

2.1 Candidate gene prioritization approaches

The primary goal of disease gene discovery is to determine if a shared common genetic feature(s) exist among disease patients and are not found in healthy individuals (at statistically significant frequencies). Many methods are available to assist disease gene discovery efforts and can be categorized into two major groups: knowledge-dependent and knowledge-independent approaches.

2.1.1 Knowledge-dependent approach

Knowledge-dependent approaches are sometimes referred to as candidate gene approach. The knowledge-dependent approach requires the formation of specific hypotheses involved in disease pathogenesis. It is based on these hypotheses that certain genes or genetic elements are selected for mutation analysis. Successful applications of knowledge-based approaches included the identification of the gene coding for the enzyme phenylalanine hydroxylase (PAH), that when mutated, cause phenylketonuria. Phenylketonuria was long known to be caused by PAH deficiency, however, the *PAH* gene eluded discovery until the use of antibodies raised against normal rat PAH enzyme allowed successful isolation of human PAH enzyme (Robson et al. 1982). Similarly, the identification of *DNAI1*, that when mutated, cause primary ciliary dyskinesis (PCD), was facilitated by the observation of axonemal defects in the biflagellated green algae model organism *Chlamymonas reinhardtii* that was similar to those observed in PCD patients (Pennarun et al. 1999). The association of apolipoprotein E (*ApoE*) *E4* allele with higher

risk of developing late-onset Alzheimer's disease was discovered based on specific hypotheses observed in Alzheimer's patients (Corder et al. 1993). Interestingly, the *E2* allele of the same gene, *ApoE*, is associated with decreased risk for developing Alzheimer's disease (Talbot et al. 1994; Corder et al. 1994). In sum, the candidate gene approach can be powerful and cost effective if the hypothesis is correct.

2.1.2 Knowledge-independent approach

Knowledge-independent approach is often referred as positional cloning (Collins 1992). It is so named because this approach requires no prior knowledge of disease pathogenesis except linkage based on chromosomal location. Two popular approaches are linkage-based on cytogenetic methods and polymorphic genetic markers. The processes are outlined in Figure 1.

2.1.2.1 Linkage via cytogenetics

Human cytogenetics, a branch of genetics that really began with the determination by Tjio and Levan in 1956 that normal human cells have only 46 chromosomes (Tjio and Levan 1956), not 48, as was believed for the previous thirty years (Painter 1923). This simple observation that established the normal human karyotype helped pave the way for numerous discoveries that included the cause of Down's Syndrome due to trisomy of chrosome 21 (normal individuals have only two chrosome 21) by a French group in 1959 (Lejeune et al. 1959) and the shortened "Philadelphia" chromosome 22 found in chronic myeloid leukemia (CML) patients (Nowell and Hungerford 1960).

By collecting cells from disease patients and comparing them against those in normal, healthy individuals, one can survey for differences between the two groups. The resolution of cytogenetic methods increased substiantially when staining methods

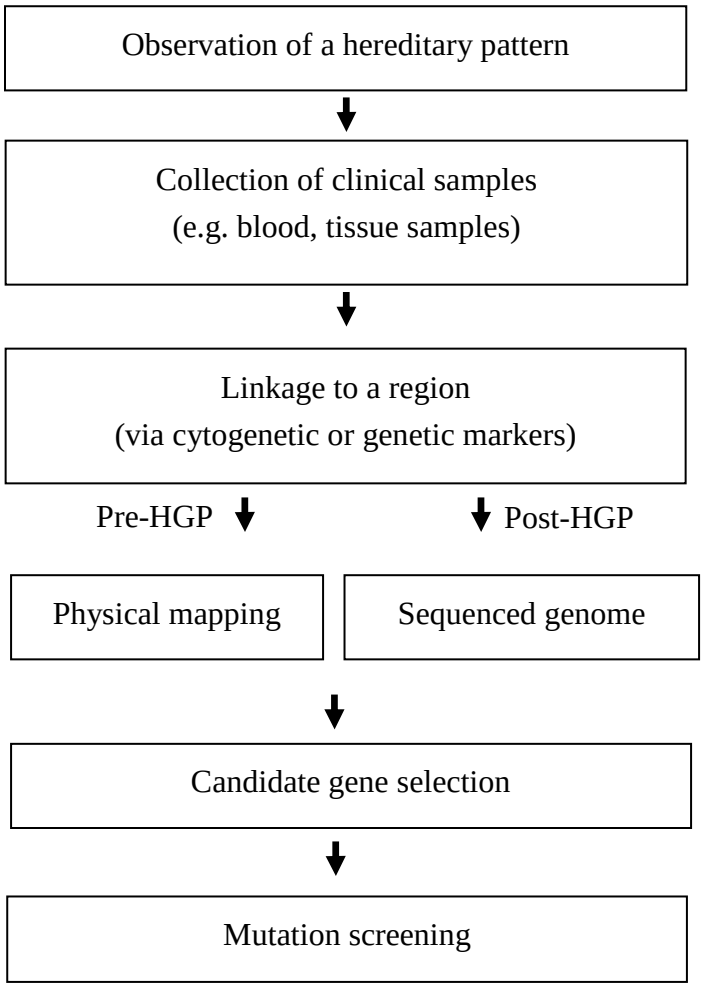


Figure 1. Schematic illustration of knowledge-independent approaches toward disease gene discovery.

developed by Torbjorn Caspersson and colleagues demonstrated the patterns of "light" and "dark" bands that serve as unique markers along chromosmes (Caspersson et al. 1968). From this, Janet Rowley determined that the "Philadelphia" chromosome was due to reciprocal translocation between chrosomes 9 and 22 (Rowley 1973). Even today, cytogenetics continue to play a pivotal role. Karyotypes from fetal cells extracted from amniotic fluid are routinely screened for chromosomal abnormalities. However, despite the development of additional methods such as somatic-cell hybrids (Harris and Watkins

1965; Ephrussi and Weiss 1965), fluorescence in situ hybridization (FISH) (Landegent et al. 1985), and continued increases in marker resolution, cytogenetic methods can only detect gross chromosomal abnormalities (e.g. macrodeletions), leaving defects affecting <1 kilobases (kb) of DNA virtually undetectable.

2.1.2.2 Linkage via genetic markers

Taking into account the characterization of the first sequence specific restriction endonucleases and how sequence length variations (polymorphisms) exist after cleavage by these restriction enzymes, Solomon and Bodmer (Solomon and Bodmer 1979) and Botsetein et al. (Botstein et al. 1980) suggested the use of these restriction fragment length polymorphisms (RFLP) as DNA (genetic) markers in family-based genetic linkage studies. By analyzing the patterns of certain polymorphisms in families with a (disease) trait, certain genetic markers can be linked to the disease.

Once again, a simple idea (observation) helped pave the way for disease mapping of family-based studies. Similar to cytogenetic studies, linkage-based disease mapping, otherwise known as positional cloning, begins not with polymorphic genetic markers but with something even more fundamental (Figure 1). The observation and/or characterization of a shared inherited clinical phenotype in a family is required before clinical samples (e.g. blood, tissue samples) are obtained from both the diseased (affected) members as well as normal (unaffected) members. Following the extraction of DNA from clinical samples, genome-wide polymorphic genetic markers (e.g. short tandem repeat polymorphism [STRP] markers) are applied to DNA from both affected and unaffected individuals. The resulting ordinal pattern (haplotype) of the sequence length polymorphisms in all affected individuals are compared against those in

unaffected individuals. Those regions or intervals that are found in common in affected individuals and not in unaffected individuals are evaluated further for statistical significance based on family structure. The goal is to identify chromosomal region(s) that are linked to the disease phenotype.

A hypothesis first proposed by C.A.B. Smith described the theoretical framework for homozygosity mapping (Smith 1953). Homozygosity mapping is a variation in theme from traditional linkage methods. It is designed for the mapping of (Mendelian) recessive traits in consanguineous families, particularly rare disorders where clinical samples are scarce. This method is based upon the premise that the region containing the disease locus in offspring(s) with recessive disorders of consanguineous marriage(s) are more likely to be in those regions that are homozygous by descent. The lack of complete genome-wide polymorphic genetic markers imposed an "impractical" obstacle (Smith 1953). Three and a half decades later, with the reality of genome-wide genetic polymorphic (RFLP) linkage maps more practical, Lander and Botstein revisited the idea of homozygosity mapping (Lander and Botstein 1987). This powerful strategy has led to the identification of many disease genes such as Friedreich ataxia (Ben Hamida et al. 1993) and Werner's Syndrome (Schellenberg et al. 1992).

Oftentimes, many studies are halted at this stage for a variety of reasons. The statistically significant intervals found in affected individuals are also found in unaffected individuals, thus ruling out these intervals. Sometimes, an individual may manifest the diseased phenyotype due to a non-genetic cause (i.e. environmental) in a phenomenon known as phenocopy that can confound the study. There may not be enough (affected) samples to achieve statistical significant power, effectively preventing further analysis

due to high costs associated with studying multiple weakly linked intervals. Typically, the use of evenly spaced lower-resolution genome-wide genetic markers (~10 centi Morgans [cM]) serve as a first pass for linkage analysis, however, there may be extraordinary cases due to recombination events, where the linkage is not easily detectable.

Each of the handful of linked intervals is refined further with additional higher-resolution markers to determine a single linked locus or critical candidate interval. Due to the density of these markers and/or the pedigree structure (e.g. number of samples/meioses, degree of consanguineity), the candidate interval mostly contains many candidate genes from which to select for mutational screening. The laborious and time-consuming task of physical mapping, the determination of the gene locations and their exon/intron boundaries, has to be performed before these genes can be analyzed for mutations. Prior to the HGP, this critical stage, the selection of candidate genes for mutation screening, was the major bottleneck of the entire process. Two of the early disease genes identified through positional cloning were *CFTR* and *HD*. Employing the physical mapping methods of chromosome walking and jumping, the cystic fibrosis gene *CFTR* was finally determined in 1989 (Riordan et al. 1989) after initial linkage to *D0CRI-917*, a DNA marker on chromosome 7, in 1985 (Tsui et al. 1985). After initial linkage (mapping) of Huntington's Disease (HD) to *G8* [D4S10], a DNA marker on chromosome 4, in 1983 (Gusella et al. 1983), it look another decade before HD was attributed to unusually long triplet CAG expansion in the *HD* gene (The Huntington's Disease Collaborative Research Group 1993). Since the HGP, with the exon/intron junctions of most genes defined, the bottleneck has shifted toward choosing which of the

many candidate genes for mutation screening. With the clinical samples serving as the ultimate limiting resource, candidate gene selection becomes a crucial step in disease gene discovery. It is this step of candidate gene selection and/or prioritization that this thesis will address, as it pertains to BBS.

2.2 Bardet-Biedl Syndrome (BBS)

BBS is a pleiotropic, autosomal recessive disorder with cardinal features of retinitis pigmentosa, central obesity, postaxial polydactyly, cognitive impairments, hypogonadism and kidney abnormalities (Bardet 1920; Biedl 1922; Green et al. 1989). In addition, BBS patients are also at higher risk of developing diabetes mellitus, hypertension and congenital heart diseases (Harnett et al. 1988; Green et al. 1989; Elbedour et al. 1994). Moreover, both intra- and inter- family expressivity of the cardinal features have been documented, a finding suggesting genetic complexity.

2.2.1 Phenotypic heterogeneity of BBS

The first description of the phenotypic manifestation of BBS was done by the French physician Georges Bardet in 1920. In his Ph.D. thesis, he described a case involving pigmentary retinopathy, obesity and polydactyly (Bardet 1920). Two years later, in a German medical journal, a report documented the observation by an Austrian physician, Arthur Biedl, that found these phenotypes as well as hypogonadism and mental deficits (Biedl 1922). These were later confirmed by Rabb in 1924 (Raab 1924). Since then, additional phenotypes have been ascribed in BBS patients, including diabetes mellitus, renal abnormalities, hearing impairments, asthma, dental abnormalities,

congenital heart diseases, and developmental delays (Harnett et al. 1988; Green et al. 1989; Elbedour et al. 1994; Beales et al. 1999).

Due to the wide spectrum of BBS phenotypes affecting multiple organ systems, the phenotypes of BBS patients often overlap with those of different disorders. To help with better diagnosis, Schachat and Maumenee proposed the criteria of having at least four of the five primary phenotypes (pigmentary retinopaty, mental retardation, obesity, polydactyly, hypogonadism) in order to be classified as BBS (Schachat and Maumenee 1982). This criteria was refined with the observation of high percentage of BBS patients with renal abnormalities by Green (Green et al. 1989) to include renal anomalies in the primary phenotype as well as secondary phenotypes such as diabetes, congenital heart defects and developmental delay (Elbedour et al. 1994; Beales et al. 1999).

Based on phenotypic similarities, BBS has been closely linked to Laurence-Moon Syndrome (LMS), Mukusick-Kaufmann Syndrome (MKS), Meckel-Gruber Syndrome (MGS), and Alstrom's Syndrome. BBS was initially considered as a variation of LMS and continues to be linked to LMS today. LMS was first characterized in the late 19th century with major symptoms of mental retardation, pigmentary retinopathy, obesity, hypogonadism as well as spastic paraparesis, distal muscle weakness and rare occurrences of polydactyly (Laurence and Moon 1866). MKS patients have primary features of hydrometrocolpos, congenital heart defects and postaxial polydactyly. The first BBS gene identified was a gene that also causes MKS (Katsanis et al. 2000; Slavotinek et al. 2000; Stone et al. 2000). MGS is a rare but lethal disorder with the characteristic triad of phenotypes: occipital encephalocele, polycystic kidneys, and postaxial polydactyly as well as hepatic fibrosis (Mecke and Passarge 1971). A recent

report identified mutations in BBS genes of MGS patients (Karmous-Benailly et al. 2005). Alstrom syndrome was first described by a Swedish physician in 1959 with primarily phenotypes of obesity, deafness, pigmentary retinopathy, diabetes mellitus and kidney abnormalities (Alstrom et al. 1959). Although Alstom syndrome is caused by *ALMS* (Collins et al. 2002), which to date has not been associated with BBS, the significant phenotypic overlap between the two disorders may indicate involvement of similar pathways.

2.2.2 Genetic heterogeneity of BBS

The complex landscape of phenotypic heterogeneity of BBS is complicated further by the genetic heterogeneity of BBS. The linkage mapping of the first BBS locus (*BBS2*) revealed a large, inbred Israeli Arab Bedouin family that was linked to chromosome 16 (16q21), however, a second, unrelated inbred Arab Bedouin family was excluded from the same region (Kwitek-Black et al. 1993). This finding was confirmed by additional reports showing linkage to other regions including *BBS1* to 11q13 (Leppert et al. 1994), *BBS3* to 3p12-13 (Sheffield et al. 1994), *BBS4* to 15q23 (Carmi et al. 1995), and *BBS5* to 2q31 (Young et al. 1999).

Even with the linkage mapping of five BBS loci, the first BBS gene cloned was at a sixth locus in 2000 that was facilitated by the cloning of *MKKS* on 20p12 causing MKS (Katsanis et al. 2000; Slavotinek et al. 2000; Stone et al. 2000). This is due to a combination of various factors: small number of patients, lack of sequenced human genome, and low resolution of genetic markers. With the exception of the mapping of the *BBS1* critical interval, strong linkage signal was achieved through homozygosity mapping in “large” inbred families. Although sufficient for a statistically significant

linkage signal, the 8-12 affected individuals were not sufficient to narrow the interval further. The lack of completed human genome (thus requiring physical mapping) coupled with low level of resolution provided by genetic markers prevented further candidate interval refinement without large expenditure of resources. The next year, two other BBS genes, *BBS2* and *BBS4*, were also identified by positional cloning approaches (Nishimura et al. 2001; Mykytyn et al. 2001). Subsequent identification of additional BBS genes, however, relied on sequence similarity to the three known BBS genes: *BBS1* and *BBS7* show weak sequence similarity to *BBS2* (Mykytyn et al. 2002; Badano et al. 2003), while *BBS8* shows sequence similarity to *BBS4* (Ansley et al. 2003). In a short span of three years, six genes were identified to cause BBS, however, two additional loci remained: the *BBS3* locus on 3p12-q13, mapped in 1994 (Sheffield et al. 1994) and the *BBS5* locus on 2q31, mapped in 1999 (Young et al. 1999). A summary of the eight mapped loci and six cloned genes (*BBS1*, *BBS2*, *BBS4*, *BBS6/MKKS*, *BBS7*, *BBS8*), as of 2003 is shown in Table 1. Although the six cloned genes all code for relatively large proteins, they do not share protein domain similarities, making additional BBS discovery (for *BBS3* and *BBS5*) based upon sequence similarity difficult. However, instead of relying only on sequence similarity of any BBS genes to one another, a methodology was developed that utilizes the collective sequence similarity of the BBS genes to prioritize the candidate genes in *BBS3* and *BBS5* loci. This method is called Computational Orthologous Prioritization (COP).

Table 1. Summary of the eight mapped loci of BBS as of 2003.

Gene name	Gene locus	Mapping reference	Exons	Protein length	Protein domain	Protein similarity	Cloning reference
BBS1	11q13	Leppert et al. 1994	17	593	CC	None	Mykytyn et al. 2002
BBS2	16q21	Kwitek-Black et al. 1993	17	721	CC	None	Nishimura et al. 2001
BBS3	3p12-q13	Sheffield et al. 1994					
BBS4	15q23	Carmi et al. 1994	16	519	8 TPR	O-linked GlcNAc transferase	Mykytyn et al. 2001
BBS5	2q31	Young et al. 1999					
BBS6 / MKKS	20p12	Katsanis et al. 2000; Slavotinek et al. 2000	4	570	Cpn60 _Tcp1	Chaperonin	Katsanis et al. 2000; Slavotinek et al. 2000
BBS7	4q27	Badano et al. 2003	19	715	CC	None	Badano et al. 2003
BBS8	14q32.1	Ansley et al. 2003	15	531	8 TPR	pilF	Ansley et al. 2003

Protein domain abbreviations: CC, coiled-coil; TPR, tetratricopeptide repeat, Cpn60_TCP1, chaperonin domain; pilF, pilus formation domain.

CHAPTER 3

COMPUTATIONAL ORTHOLOGOUS PRIORITIZATION

3.1 Overview of the Computational Orthologous Prioritization (COP) approach

The COP method is a computationally iterative ranking approach designed to prioritize candidate genes for mutation screening. This method does not preclude the use of other currently used prioritization methods but rather is meant to augment the existing prioritizations in the disease gene identification process. This process is depicted in Figure 2, and described below:

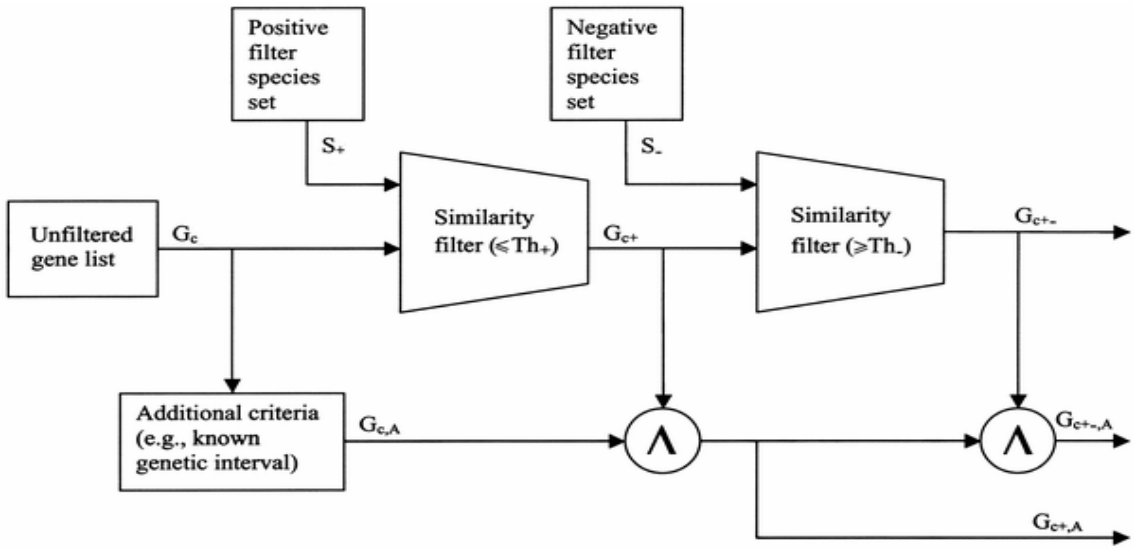


Figure 2. General outline of the candidate ranking process. A list of unfiltered genes (G_c) can be prioritized through a set of positive filter species (S_+) on the basis of a similarity filter threshold (Th_+), which yields a subset of genes (G_{c+}) found in all positive filter species (S_+). These can be further screened with similarity filter threshold (Th_-) in a set of negative filter species (S_-) to yield a more restrictive subset of genes (G_{c+-}). Further filtering continues by intersection (Λ) with additional criteria (A) to generate ($G_{c+,A}$). An even more refined set ($G_{c+-,A}$) can be obtained by intersecting $G_{c+,A}$ with G_{c+-}.

1. Initial determination of candidate gene set G_c.
2. Selection of positive and/or negative sets of species: S_+ and/or S_-, based on training gene set G_t.
3. Determination of thresholds for similarity filters: Th_+ and/or Th_-, based G_t.
    a. Similarity analysis of G_t relative to S_+, and selection of a similarity threshold Th_+, whereby a subset of the genes in G_t exceed Th_+. This subset is referred to as "G_{t+}".
    b. Similarity analysis of G_t relative to S_-, and selection of a similarity threshold Th_-, whereby a subset of the genes in G_t fall below Th_-. This subset is referred to as "G_{t-}".
4. Computational application of filters S_+ and S_- to candidate gene set G_c.
    a. Similarity analysis of G_c relative to S_+, and retention of candidates exceeding Th_+. This subset is referred to as "G_{c+}".
    b. Similarity analysis of G_c relative to S_-, and rejection of candidates falling below Th_-. This subset is referred to as "G_{c-}".
    c. Combination of similarity analyses of G_c relative to S_+ and S_-, and retention of candidates exceeding Th_+ as well as the rejection of candidates falling below Th_-. This subset is referred to as "G_{c+-}".
5. Application of additional criteria, A, for candidate gene ranking. Intersection of the subset of genes prioritized based additional criteria, A, to gene subsets G_c, G_{c+}, G_{c-}, and G_{c+-}. This subset is referred to as "$G_{c,A}$", "$G_{c+,A}$", "$G_{c-,A}$", and "$G_{c+-,A}$", respectively.
    a. Utilization of known or suspected linkage interval(s).

b. Utilization of available expression information.

c. Utilization of animal model(s) information.

d. Utilization of other annotations (e.g., Gene Ontology Consortium [GO] (Ashburner et al. 2000), protein domain similarities).

3.2 Initial determination of candidate gene set (G_c)

One key aspect of any disease gene discovery effort is the proper determination of the candidate gene set (G_c), namely, the set of genes most likely to contain those gene(s), that when mutated, can result in the disease phenotype. Initially, this is likely to include all genes annotated in the human genome, however, the observed disease phenotype may help narrow the starting set, such as in sex-linked diseases, to genes on sex chromosomes. Furthermore, additional prioritization criteria such as positional, expression or functional information can help reduce the number of genes in G_c.

3.3 Selection of positive (S_+) and/or negative sets (S_-) of species

The fundamental basis of the COP method is that species sharing conserved structural and/or functional traits, such as that of a circulatory system, tend to share genes that underlie the biological processes responsible for these features. Similarly, species that do not share these features are less likely to contain these genes. Additionally, those genes that are involved in the parallel structural and/or functional processes are more likely to be evolutionarily conserved and therefore orthologous to one another.

Thus, using the presence or absence of biological feature(s) as a criterion, one can readily identify two subsets of mutually exclusive species whose genomes/proteomes can

serve as positive and negative filters. These filters act as reference standards against which sequence similarities can be compared. The positive filter or species set (S_+) consists of those species that share one or more biological feature(s) whereas the negative filter or species set (S_-) contains those species that specifically lack these biological feature(s). One good source from which to select the structural and/or functional characteristic(s) is from those (physiological) feature(s) that are affected and/or defective in diseased patients.

The association of a disease with functional feature(s), however, is not a prerequisite for the selection of positive and/or negative filters. The existence of previously identified genes for the same or similar disease(s) can also serve as a partitioning factor. This is based on the notion that the set of defective gene(s) which lead to identical disease phenotype(s) are more likely to be involved in the same or similar (defective) pathway. In short, there are two different approaches on which to base the selection of positive and/or negative species sets: functional feature(s) and/or previously identified genes.

3.4 Determination of thresholds for similarity filters: Th_+ and Th_-, based on training gene set G_t.

To validate the inclusion of species in S_+ and/or S_- and set corresponding thresholds for similarity filters (Th_+ and Th_-), the utilization of a similarity analysis tool is necessary to compare genes in G_c against those in S_+ and/or S_-. Although genome sequencing projects are not expected to continue indefinitely, the current dynamic nature of both the number of genomes available and the constant improvements of genome

assemblies, dictate that the similarity analysis tool be both quick and sensitive. Two such tools are BLAST (Altschul et al. 1997) and BLAT (Kent 2002) for the evaluation of sequence similarities. As BLAT is a tool that is designed to identify highly similar sequences (>95%), it is more appropriate for the detection of orthologs in closely related species. For the general detection of orthologs in a wide range of organisms, BLAST is a more suitable tool. Many parameters, ranging from percentage identity, length of match, to e(xpect)-values, inherent to sequence similarity analysis tools can be selected on which to filter G_c. The parameter chosen depends largely on G_t, although generally e-values are reflective of most parameters.

To effectively prioritize candidate genes, appropriate thresholds need to be empirically determined, oftentimes in an iterative fashion to accommodate new information as it is generated. As genome assemblies get updated and/or known (related) disease genes increase in number, the thresholds for S_+ (Th_+) and/or S_- (Th_-) can change with each iteration. The establishment of proper thresholds relies on the appropriate selection of a separate set of genes, G_t, which consists of the training gene set, that is distinct from those in G_c. The set of previously known genes would ideally be included in G_t, however, in diseases where no genetic heterogeneity exists, the use of disease genes with similar phenotype and/or information from functional studies may provide some clues. For instance, the use of previously identified genes involved in the circulatory system may serve to identify additional genes involved in similar pathway(s). Alternatively, with proper selection for S_+ and/or S_- based on functional feature(s), one can generate a set of genes to establish thresholds for the evaluation of the likelihood of a set of genes to be involved in functional feature(s). For example, by setting organisms

with circulatory systems as S_+ and organisms without circulatory systems as S_-, one can apply the filters to generate a list of genes from which threshold values can be derived to determine if genes with unknown function are likely to be involved in circulatory pathways.

Once the G_t is initially chosen, the next step is to generate a phylogenetic profile of the genes in G_t using the similarity analysis tool to determine the species that make up S_+ and/or S_-. In other words, a phylogenetic profile is the profile summary from comparing the genes in G_t against the genes/proteins from various genomes/proteomes with a similarity analysis tool. Preferably, the use of a wide range of organisms from different branches of the tree of life would allow for the identification of the most optimal species to use, however, there may be cases where the study restricts the number of species analyzed. From a phylogenetic profile, the organisms that best distinguish (most or all of the) genes in G_t such that an inverse conservation profile exists (high conservation in some, low conservation in others) are then designated as S_+ and S_-, respectively. In the case where no inverse conservation profile exists, a subset or all of the organisms used can be selected for either as S_+ or S_-. The selection of multiple organisms from different branches of the tree of life, while not necessary, would help eliminate those genes that are specific to that that particular tree of branch. Furthermore, an organism's gene set (either predicted, verified, or a combination of both), should also be considered. Logically, the smaller the gene set, the more the enrichment for a certain type of genes.

After selecting species belonging to S_+ and/or S_-, the thresholds for S_+ (Th_+) and/or S_- (Th_-) can then be established. Setting the Th_+ and/or Th_- is in essence setting a

floor and/or ceiling against which sequences with certain level of conservation (similarity) will either be retained or eliminated. In general, the Th_+ serve as the floor, or the lowest allowed level of conservation such that sequences will be retained, while the Th_- is the ceiling, or the highest allowed level of conservation such that sequences will be eliminated. Thus, the subset of G_t that exceeds Th_+ is G_{t+} whereas the subset of G_t that falls below Th_- is G_{t-}. As the evolutionary relationship between the organisms will most likely be of disparate distance, there may be a need for establishing species-specific thresholds. Moreover, in those cases where e-value distribution/range G_t genes used to determine S_+ is relatively small and well-defined, for instance, between values of 1e-200 and 1e-100, then a more stringent Th_+ range can be set accordingly. However, a less stringent criterion of a value rather than a range, such as 1-e100 or even 1-80 (from the previous example) can allow for the detection of those genes that may be more distantly related. Thus, the stringency of the thresholds is largely dependent on the distribution/range of the phylogenetic profile of the G_t genes as well as the desired sensitivity/specificity tradeoffs. As such, threshold establishment may need to be performed iteratively.

By comparing the genes in G_t against various organisms, one can choose the proper species (S_+ and/or S_-) and thresholds (Th_+ and/or Th_-) that best capture the phylogenetic 'signature' of the genes in G_t so that it can be used in genome-wide searches. Additionally, functionally related genes and/or organisms can also be used to identify the thresholds (Th_+ and/or Th_-) and appropriate species (S_+ and/or S_-), respectively.

3.5 Computational application of filters S_+ and S_- to candidate gene set G_c.

Together, with the appropriate selection of species as filters (S_+ and/or S_-) and corresponding thresholds (Th_+ and/or Th_-), as well as the chosen sequence similarity search tool, three different computational applications of similarity analyses can be performed on the candidate gene set G_c. These similarity analyses are designed to prioritize candidate genes for further experimental analysis and validation, such as mutational screening. A less stringent criteria involves singular application of either filters (S_+ or S_-) to G_c; the similarity analysis of G_c relative to S_+, and retention of (high conservation) candidates exceeding Th_+ results in a subset referred to as G_{c+}. Likewise, the similarity analysis of G_c relative to S_-, and rejection of (high conservation) candidates falling below Th_- result in a subset referred as G_{c-}. The most stringent criteria combines the similarity analyses of G_c relative to S_+ and S_-, and retention of candidates exceeding Th_+ as well as the rejection of candidates falling below Th_- to yield a compact subset referred as G_{c+-}. Additional stringency can be achieved in those cases involving two or more species for either S_+ and/or S_-, such that the retention or rejection of candidates is only performed when similarity analyses exceeds or falls below for two or more species. On the other hand, depending on the completeness and quality of annotation of various genomes, particularly in those cases involving two or more species in either S_+ and/or S_-, a reduced stringency criteria can be made such that the candidate gene is kept (for S_+) or removed (for S_-) by passing the Th_+ and/or Th_- of only one of the two or more species in either S_+ and/or S_-. In addition, species-specific threshold may serve to increase sensitivity and specificity of the desired candidates. Although somewhat circuitous, the genes in G_t should be a subset of G_{c+}, G_{c-}, or G_{c+-}.

3.6 Application of additional criteria, *A*, for candidate gene ranking.

Historically, the identification of disease genes, is aided by knowledge-based hypotheses formed based on the incorporation of multiple sources of information to prioritize candidate genes. As a result, the application of additional criteria, *A*, is an essential step in the COP method. More specifically, the application of *A* to G_c, G_{c+}, G_{c-}, or G_{c+-} would result in more restrictive subsets $G_{c,A}$, $G_{c+,A}$, $G_{c-,A}$, or $G_{c+-,A}$, respectively. One primary resource, for example, is the use of known or suspected linkage intervals from cytogenetic or genetic linkage studies, however, additional resources such as those on gene expression (from ESTs, microarray experiments, SAGE, etc), proteomics data, animal model information, interaction data, and functional annotations (e.g. Gene Ontology Consortium [GO], protein domain similarities) all can combine to help prioritize candidate genes.

CHAPTER 4

IDENTIFICATION OF *ARL6* AS *BBS3*

4.1 BBS and cilia

The genetic landscape of BBS at the end of 2003 stands with eight mapped loci accounting for less than 50% of the BBS patient population (Katsanis 2004; Hichri et al. 2005; Nishimura et al. 2005). Within the eight mapped loci, six genes were cloned (*BBS1*, *BBS2*, *BBS4*, *BBS6/MKKS*, *BBS7*, *BBS8*), leaving two remaining mapped loci (*BB3* and *BBS5*) (Table 1). It seems to reason that the existence of six known BBS genes could potentially assist in the identification of *BBS3* and *BBS5*. However, there is no common shared sequence similarity among all six BBS genes. BBS6/MKKS shows weak sequence similarity to the α subunit of the *Thermoplasma acidophilum* thermosome (Stone et al. 2000), a prokaryotic chaperonin complex with similarity to a eukaryotic chaperonin called “tailless complex polypeptide ring complex” (TRiC) (Frydman et al. 1992). BBS4 and BBS8 contain multiple copies of tetratricopeptide repeat (TPR) domains, which are thought to be involved in protein-protein interactions. Additionally, BBS8 also shows sequence similarity to a prokaryotic pilF domain involved in pilus formation and twitching mobility (Ansley et al. 2004). Except for small regions of sequence similarity in the form of coiled-coil domains in BBS1, BBS2, and BBS7, the three proteins are considered novel proteins with unknown function.

Despite the lack of known protein function of the six known BBS proteins, there were three important clues linking the involvement of BBS proteins in cilia function. First, the initial characterization of BBS8 found BBS8 proteins localized to the basal

body, which is a centriole-like cylindrical structure that nucleate cilia and flagella, of ciliated cells (Ansley et al. 2003). Second, BBS4 was also found localized to the centriolar satellite of centrosomes and basal bodies of primary cilia (Kim et al. 2004). Finally, the first BBS mouse model of BBS, that of BBS4 knockout (ko) mice, exhibit general cilia formation except for spermatozoa flagellar formation (Mykytyn et al. 2004). Moreover, the absence of BBS4 protein did not disrupt initial formation of photoreceptor outer segments, including the connecting cilia; rather, photoreceptors underwent cell death due to apoptosis. Considering these cilia associations, it was not a surprise that the identification of *BBS5* involved cilia. Li et al. (2004) used comparative genomics (between ciliated and nonciliated organisms) to construct the flagellar apparatus-basal body (FABB) proteome containing 688 proteins. Only two of the 230 proteins that mapped to the *BBS5* critical interval were found in FABB: NM_024753 and NM_152384. Complete sequencing of the coding regions of NM_152384 detected mutations in BBS patients from four different families, thus identifying *BBS5*.

The cilia connection is even more striking in light of the phylogenetic profile of the first six BBS genes (as *BBS5* was identified during the course of the study). Table 2 shows the expect value (e-value) from BLAST analysis comparing the known BBS proteins against the proteomes from both predicted and verified genes, hereafter referred to as proteomes, of various genomes, ranging from the unicellular human parasites, trypanosomes (*Trypanosoma brucei* [TB], *Trypanosoma cruzi* [TC]) to the vertebrate rodent *Mus musculus* [MM]. BLAST is a sequence similarity analysis tool that takes a query sequence as input, which in this case is the protein sequence of one of the six BBS proteins, and compares it against the proteomes of the organisms listed.

The proteomes of *M. musculus* [MM] and *D. rerio* [DR] contain all six BBS orthologues with highly significant e-values (consisting of mostly 0's – the best possible value indicating the highest conservation), sequence percent identity (>63%), and similarity (>75%) to five known BBS proteins. Even the lower ciliated organisms (*T. brucei, T. cruzi, C. reinhardtii,* and *Ciona intestinalis*) showed significant e-values ($\leq e^{-40}$),

Table 2. Phylogenetic genetic profile of BBS protein sequence similarities across various genomes showing e-values obtained from BLAST analysis of human BBS proteins against predicted protein databases of a set of ciliated (MM, DR, CI, CE, CR, TC, TB, DM) and nonciliated (SC, SP, AN, AT) organisms.

	MM	DR	CI	CE	CR	TC	TB	DM	SC	SP	AN	AT
BBS1	0.0	2e-82	1e-138	7e-64	3e-75	2e-73	6e-64	5e-64	3.1	2.5	1.1	3.2
BBS2	0.0	0.0	0.0	1e-85	6e-55	4e-98	1e-87	0.24	0.024	0.13	3.0	1.1
BBS4	0.0	0.0	1e-134	8e-11	2e-9	2e-80	3e-72	3e-55	5e-9	2e-7	1e-6	3e-13
BBS6/ MKKS	0.0	1e-130	6e-26	4e-8	2e-7	5e-18	2e-11	2e-11	5e-13	3e-15	9e-13	2e-8
BBS7	0.0	0.0	0.0	1e-110	1e-115	3e-50	8e-41	2.0	0.16	0.62	1.3	1.8
BBS8	0.0	0.0	0.0	1e-109	1e-135	4e-92	1e-79	4e-53	2e-4	2e-5	4e-5	2e-7
Estimated genome size	2.5 GB	1.6 GB	160 MB	100 MB	100 MB	35 MB	35 MB	130 MB	12 MB	12 MB	31 MB	115 MB

Matches showing high conservation (low e-values) are highlighted in pink. Abbreviations: MM, *Mus musculus;* DR, *Danio rerio;* CI, *Ciona intestinalis;* CE, *C. elegans;* CR, *Chlamydomonas reinhardtii;* TC, *T. cruzi;* TB, *T. brucei;* DM, *D. melanogaster;* SC, *S. cerevisiae;* SP, *Schizoaccharomyces pombe;* AN, *Aspergillus nidulans;* AT, *A. thaliana*, MB, megabases (nucleotides); GB, gigabases.

percent identity (>20%), and similarity (>40%) to BBS1, BBS2, BBS4, BBS7, and BBS8.

So, instead of relying on sequence similarity of any BBS genes to one another, the COP methodology was developed and implemented to take advantage of the collective

sequence similarity of the BBS genes to prioritize the candidate genes in the *BBS3* and *BBS5* loci. This is further described in section 4.3.

4.2 Refinement of the *BBS3* critical interval

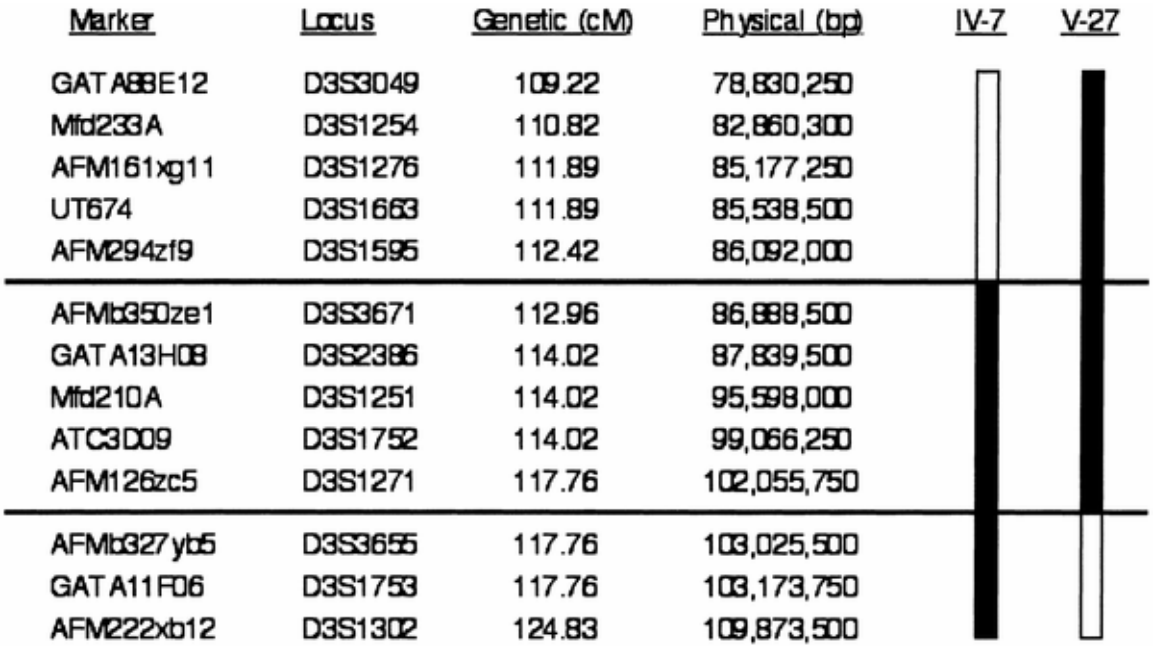
The *BBS3* locus was initially mapped to a ~11 cM region on chromosome 3 in a large, inbred Israeli Bedouin kindred in a study that showed the utility of using pooled DNA samples for genetic mapping of human disorders (Sheffield et al. 1994). The availability of higher resolution STRPs allowed refinement of the interval to a ~5.3 cM region in two affected individuals who were not homozygous for all markers in the original interval (Figure 3). This interval proved to be a region of below average recombination, in part because the 16.9 Mb region between the flanking markers (D3S1595 and D3S3655) crosses the centromere. Analysis of the human genome (UCSC Genome Browser) across the *BBS3* interval revealed a minimum of 67 UniGene clusters. Additional refinement of the locus has been restricted by lack of other BBS3 families.

4.3 Identification of *BBS3* and *BBS5* with the COP method

Here, each step of the COP method is described as it applies toward the identification of *BBS3* as well as the detection of *BBS5*.

1. *Initial determination of candidate gene set G_c.*

   To evaluate the genome-wide applicability of the COP method, the 21,184 predicted and verified human genes (as annotated by Ensembl build 22.34a) were chosen as the initial candidate gene set G_c.



Marker	Locus	Genetic (cM)	Physical (bp)	IV-7	V-27
GATA88E12	D3S3049	109.22	78,830,250		
Mfd233A	D3S1254	110.82	82,860,300		
AFM161xg11	D3S1276	111.89	85,177,250		
UT674	D3S1663	111.89	85,538,500		
AFM294zf9	D3S1595	112.42	86,092,000		
AFMb350ze1	D3S3671	112.96	86,888,500		
GATA13H08	D3S2386	114.02	87,839,500		
Mfd210A	D3S1251	114.02	95,598,000		
ATC3D09	D3S1752	114.02	99,066,250		
AFM126zc5	D3S1271	117.76	102,055,750		
AFMb327yb5	D3S3655	117.76	103,025,500		
GATA11F06	D3S1753	117.76	103,173,750		
AFM222xb12	D3S1302	124.83	109,873,500		

Figure 3. Refinement of genetic localization of the BBS3 candidate interval. The genetic map was obtained from the Marshfield Medical Clinic Web site, and the physical map distances were obtained from the UCSC Genome Browser on the basis of the July 2003 data release. Critical recombination events are also illustrated. The patient identification terminology is the same as was published previously (Sheffield et al. 1994).

2. *Selection of positive and/or negative sets of species: S_+ and/or S_-, based on training gene set G_t.*

Since there were already six known BBS genes, the six BBS proteins BBS1, BBS2, BBS4, BBS6, BBS7, BBS8 were selected as the training gene set G_t. The existence of orthologs of human BBS proteins in the distantly related invertebrate roundworm *Caenorhabditis elegans*, suggests BLAST as a better similarity analysis tool. Moreover, it also ruled out the use of the biological structure "backbone" as a partitioning factor. While many parameters can be utilized as a conservation metric, including singular or combinatory use of e-value, percentage identity (of match),

and/or match length, analyses using BBS genes as an example determined the use criteria other than e-value did not exhibit improvement in sequence conservation detection.

A phylogenetic profile of G_t genes generated from similarity analysis with BLAST in various organisms that are of different evolutionary distance is presented in Table 2. Of note, *BBS6* do not have any orthologs in invertebrate organisms. Interestingly, *Drosophila melanogaster* lacks orthologs (high conservation matches) to BBS2 and BBS7, perhaps implying the specific absence of ciliary related components found in other lower organisms (e.g. TB, CR). Ciliated structures are only found in sensory cilia and the sperm in DM, although in CE, whose proteome contains both BBS2 and BBS7 orthologs but lacks a BBS4 ortholog, cilia is only found in sensory neurons. Reasoning that the low conservation seen in similarity analysis of BBS4 against the *C. reinhardtii* proteome was likely due to incomplete annotation (the complete *C. elegans* genome was sequenced in 1998, compared with a sequenced *C. reinhardtii* genome in 2003 (Li et al. 2003), it was observed that an inverse conservation profile (high conservation of BBS proteins in ciliated organisms, little or no conservation in nonciliated organisms) in five of the six BBS proteins (BBS1, BBS2, BBS4, BBS7, BBS8).

This phylogenetic bifurcation based on the biological structure “cilia”, coupled with recent functional studies that found BBS4 and BBS8 localized to basal bodies (Ansley et al. 2003; Kim et al. 2004), prompted the selection of “cilia” as the partitioning factor. Remarkably, the high conservation (as indicated by low e-values) of BBS proteins in lower, ciliated organisms, particularly in unicellular organisms

such as *C. reinhardtii* [CR], *T. brucei* [TB], and *T. cruzi* [TC], suggests increased enrichment or sensitivity of cilia-related and/or BBS genes with the use of these genomes. Thus, the invertebrates *C. intestinalis* [CI], *C. reinhardtii* [CR], *T. brucei* [TB], and *T. cruzi* [TC] as S_+ and *Saccharomyces cerevisiae* [SC] and the land plant *Arabidopsis thalina* [AT] as S_- were selected. Multiple organisms were chosen for both S_+ and S_- to eliminate species-specific genes.

3. *Determination of thresholds for similarity filters: Th_+ and/or Th_-, based on G_t.*

Due to the high conservation (low e-values) even in unicellular organisms (e.g. conservation of BBS2 in TC with an e-value of 4e-98), a single general threshold for both S_+ and S_- was chosen.

   a. *Similarity analysis of G_t relative to S_+, and selection of a similarity threshold Th_+, whereby a subset of the genes in G_t exceed Th_+. This subset is referred to as "G_{t+}".*

An e-value of 9e-35 as Th_+ with a “less than” relationship was chosen, this is slightly higher than the highest e-value of 8e-41 (BBS7 to TB) to allow for inclusion of “borderline conservation” candidate genes that may have been otherwise eliminated. The gene subset G_{t+} that exceed Th_+ include *BBS1*, *BBS2*, *BBS4*, *BBS7*, and *BBS8*.

   b. *Similarity analysis of G_t relative to S_-, and selection of a similarity threshold Th_-, whereby a subset of the genes in G_t fall below Th_-. This subset is referred to as "G_{t-}".*

Similarly, a “greater than” Th_- e-value threshold of 1e-35 was chosen with a “greater than” relationship (lowest e-value of 5e-13 from BBS6

comparison to SC) to specifically filter out those genes with high conservation to retain borderline conservation candidate genes. The gene subset G_{t-} that fall below Th_- contains BBS1, BBS2, BBS4, BBS6, BBS7, and BBS8.

4. *Computational application of filters S_+ and S_- to candidate gene set G_c.*

Similarity analysis of G_c relative to S_+ and/or S_- to yield three subsets of genes G_{c+}, G_{c-}, G_{c+-}. Where appropriate, a high stringency criterion of having high conservation (e-value ≤ 9e-35) in all four organisms (CI, CR, TB, and TC) of S_+ and/or low conservation (e-value ≥ 1e-35) in both species of S_- (SC and AT) were selected.

a. *Similarity analysis of G_c relative to S_+, and retention of candidates exceeding Th_+. This subset is referred to as "G_{c+}".*

Of the five genes in G_t use for training Th_+, only four (*BBS1*, *BBS2*, *BBS7*, *BBS8*) remained in the 1,588 gene set that make up G_{c+} (Table 3). *BBS4* was eliminated by the incomplete annotation of the CR translated genome. The list of the 1,588 genes, hereafter referred to as the "cilia set". The cilia set of genes include those genes involved in axoneme, the core component of ciliary structures, such as dynein light chain (e.g. *DNALI1*), dynein intermediate chain (e.g. *DNAI2*), dynein heavy chain (e.g. *DNAH12*), intraflagellar transport genes (e.g. *IFT88*, *IFT74*) as well as genes found in eukaryotes such as those of kinases (e.g. *MAPK9*, *MAP3K1*), DNA repair (e.g. *RAD51*, *MLH1*) and molecular motors (e.g. *MYO7A*, *ACTB*, *TUBA2*).

Table 3. Ensembl genes from each stage of the comparative genomic approach.

	All Ensembl genes	S_+ filter only	S_+ and S_- filters
All chromosomes	21,184 (G_c)	1,588 (G_{c+})	114 (G_{c+-})
BBS3 interval	62 ($G_{c,A[BBS3\ interval]}$)	4 ($G_{c+,A[BBS3\ interval]}$)	0 ($G_{c+-,A[BBS3\ interval]}$)

b. Similarity analysis of G_c relative to S_-, and rejection of candidates falling below Th_-. This subset is referred to as "G_{c-}".

All six known BBS proteins (*BBS1*, *BBS2*, *BBS4*, *BBS6*, *BBS7*, *BBS8*) were included in the gene subset G_{c-} along with genes coding for IFT (e.g. *IFT122*).

c. Combination of similarity analyses of G_c relative to S_+ and S_-, and retention of candidates exceeding Th_+ as well as the rejection of candidates falling below Th_- This subset is referred to as "G_{c+-}".

The intersection of G_{c-} and G_{c+} results in the most stringent set G_{c+-} which is intended to enrich for genes involved in cilia, as the similarity analysis relative to S_- was designed to remove those essential and common genes to all eukaryotes. Some of the 114 members, hereafter referred to as “restricted cilia set”, include genes involved in IFT (e.g. *IFT88*, *IFT52*), axonemal components (e.g. *DNAH11*, *DNALI1*, *DNAI1*). Interestingly, members of the the tubulin tyrosine ligase-like (TTLL) family (e.g. *TTLL4, TTLL7*) and cAMP-specific 3',5'-cyclic phosphodiesterases (e.g. *PDE8A*, *PDE4D*) are highly enriched in this set.

Of note, two genes in G_{c+-} (the cilia set) mapped to the BBS5 critical interval: NM_024753 (ENSG00000123607) and NM_152384

(ENSG00000163093). Even though NM_152384 was identified as *BBS5* by a separate group during the course of our study, the ability to enrich (reduce) the candidate genes in the *BBS5* candidate interval in a genome-wide prioritization lends credence that the COP method may be used to prioritize candidate BBS genes. As none of the 114 genes in G_{c+-} mapped to the *BBS3* critical interval, additional criteria were employed to prioritize the candidate genes in the BBS3 critical interval.

5. *Application of additional criteria, A, for candidate gene ranking. Intersection of the subset of genes prioritized based additional criteria, A, to gene subsets* G_c, G_{c+}, G_{c-}, *and* G_{c+-}. *This subset is referred to as "*$G_{c,A}$*", "*$G_{c+,A}$*", "*$G_{c-,A}$*", and "*$G_{c+-,A}$*", respectively.*
   a. *Utilization of known or suspected linkage interval(s).*
   b. *Utilization of available expression information.*
   c. *Utilization of animal model(s) information.*
   d. *Utilization of other annotations (e.g., Gene Ontology Consortium [GO] (Ashburner et al. 2000), protein domain similarities).*

Armed with the additional criteria from linkage interval *A*[BBS3 interval] applied to G_c, only 62 genes remained that make up $G_{c,A[BBS3\ interval]}$. From the genome-wide G_c analysis, it was known that $G_{c+-,A[BBS3\ interval]}$ is an empty set. Further investigation determined that this was due to Th_- (i.e. $G_{c-,A[BBS3\ interval]}$ is also an empty set) and not Th_+. The candidancy of the four genes in $G_{c+,A[BBS3\ interval]}$ as putative BBS genes were evaluated based on additional functional information. The four genes (*ARL6*, *NIT2*, *WWP1*, and *PCNP*) are listed in Table 4 by their Ensembl gene

ID, gene symbol, gene description, protein domain and functional annotation. Based on internal laboratory experiments A[experiment] in which intracellular defects were observed in zebrafish BBS models (Yen et al. 2006) and annotation from Gene Ontology, A[GO], *ARL6* was selected as the best candidate gene (i.e. the set $G_{c+,A[BBS3\ interval],A[zebrafish\ BBS\ models],A[GO]}$ contains only one gene - *ARL6*).

Table 4. Four genes ($G_{c+,A[BBS3\ interval]}$) in the *BBS3* interval that are highly conserved in ciliated organisms.

Ensembl gene ID	Gene symbol	Gene description	Protein Domain	Functional annotation
ENSG00000113966	ARL6	ADP-ribosylation factor 6	ADP ribosylation factor (ARF)	Intracellular protein transport, small GTPase mediated signal transduction
ENSG00000114021	NIT2	Nitrilase protein 2	Nitrilase	Nitrogen compound metabolism
ENSG00000189290	WWP1	E3 ubiquitin ligase	WW domains and HECT	Ubiqutin ligase activity
ENSG00000081154	PCNP	PEST-containing nuclear protein	PCNP	Cell cycle

Abbreviations: WW, tryptophan-tryptophane domain; HECT, homologous to the E6-associated protein carboxyl terminus; PNCP, PEST-containing nuclear protein.

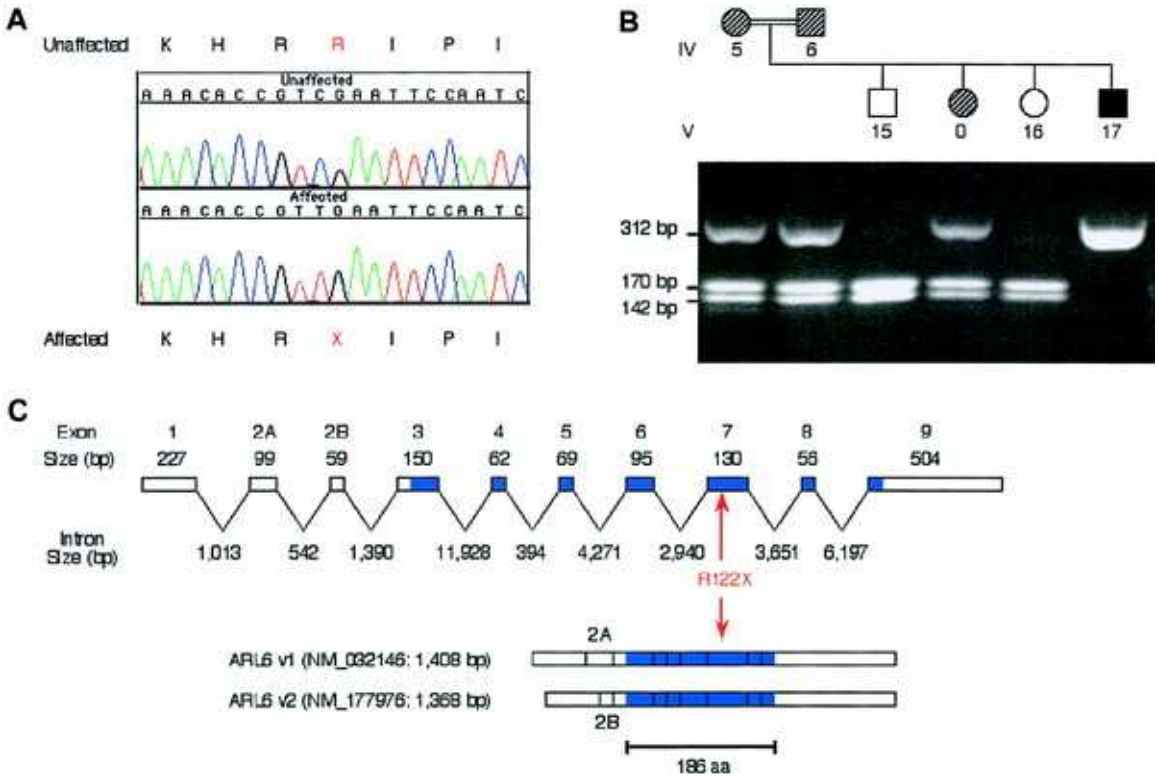


Figure 4. BBS3 mutation (R122X) detected in a large Bedouin kindred. ***A***, Sequence from an affected individual from the Bedouin family and a control sample, showing the homozygous C→T change that results in premature termination at codon 122. Data for the figure generated by A. Ferguson. ***B***, An example of the *Taq*I restriction enzyme digest that was used to confirm the R122X mutation. Data for the figure generated by C. Searby. The mutation results in the abolition of a *Taq*I site within exon 7. Following *Taq*I digestion of a PCR fragment containing exon 7, the wild-type allele is observed as two bands (142 bp and 170 bp), whereas the uncut mutant allele produces a 312-bp fragment. For the pedigree, the hatched symbols represent BBS carriers, as determined by genetic analysis; the filled symbol denotes an individual with BBS; and the open symbols are unaffected individuals. The patient-identification terminology is the same as was published previously (Sheffield et al. 1994), with the exception of the 0, which denotes a sample that was not previously available. ***C***, The genomic structure of the *ARL6* gene is shown, with the blue shading representing the translated region. The two *ARL6* isoforms that are produced by alternative splicing are shown below. The location of the R122X mutation within the *ARL6* gene is indicated in red.

4.4 Mutational analysis identifies *ARL6* as *BBS3*

Mutational screening in all 13 of the BBS3 patients (performed by Amanda Ferguson of the Sheffield laboratory) detected a nonsense mutation (C→ T) that results in

truncation of the last 65 amino acids (aa) of the normal (186 aa) ARL6 protein and confirms that *ARL6* is *BBS3* (Chiang et al. 2004). A representative chromatograph showing the R122X mutation in an affected individual, compared to a control sample is shown in Figure 4A (data generated by A. Ferguson). Figure 4B depicts a restriction enzyme assay (based on a TaqI site in exon 7) that was used to confirm the mutation (data generated by Charles Searby of the Sheffield laboratory). Although *ARL6* has two isoforms derived from alternative splicing of exon 2, the R122X mutation lies in exon 7 and affects both isoforms (Figure 4C).

4.5 Identification of additional BBS genes using similar comparative genomic approach

4.5.1 Identification of *BBS5*

The identification of *BBS5* was briefly described above (section 4.3, COP method 4C). Li et al. (2004) compared the human proteome to the proteomes of *C. reinhardtii* as S_+ and *A. thaliana* as S_- with both Th_+ and Th_- at 1e-10 to construct the flagellar apparatus-basal body (FABB) proteome containing 688 proteins. Only two of the 230 proteins that mapped to the BBS5 critical interval were found in FABB: NM_024753 and NM_152384. Complete sequencing of the coding regions of NM_152384 detected mutations in BBS patients from four different families, thus identifying NM_152384 as *BBS5*. Unlike the COP method, in which the Th_+ and Th_- were selected based on previously known BBS genes (training gene set), the chosen e-value thresholds (1e-10) of the

comparative genomic approach employed by Li et al. (Li et al. 2005) was not based upon a training gene set G_t.

4.5.2 Identification of *BBS9*

Nishimura et al. (Nishimura et al. 2005) chose ciliated organisms *T. cruzi* and *Leishmania major* as S_+, *Giardia lambia* [GL], a flagellated eukaryote without any of the know BBS orthologs (based on similarity analysis comparing the known BBS proteins against the predicted proteome of GL), and *S. cerevisiae* as S_-. 239 unique proteins were obtained from the use of an e-value of 1e-37 as both Th_+ and Th_- and a stringency criterion in which proteins were eliminated if similarity analysis fulfilled "greater than" Th_- in either GL or SC. By intersecting these proteins with data from homozygosity mapping (with high density [10K] SNP chips), as well as reduced gene expression in *Bbs4-/-* mouse models, they were able to identify the parathyroid hormone-responsive B1 (*PTHB1*) gene as *BBS9*.

4.5.3 Identification of *BBS5* using an alternative approach

Fan et al. (Fan et al. 2004) employed a different strategy to identify *ARL6* as *BBS3*. Reasoning that the existence of a DAF-19 RFX transcription factor binding site (X box) is found in the promoters of all *C. elegans* bbs genes, they detected 168 X box-containing genes that have human orthologs. Three of these mapped to the BBS3 critical interval and complete sequencing of all three genes detected different missense mutations in four separate families, thus identify *ARL6* as *BBS3*.

4.6 BBS and *ARL6*

ARL6 was not in $G_{c\text{-},A[BBS3\ interval]}$ due to Th_{-} of 1e-35. Similarity analysis of ARL6 to SC and AT resulted in e-values of 1e-36 and 4e-36, respectively. While a decrease in stringency of Th_{-} to 1e-37, for instance, would result in elimination of best BLAST hit matches of CAA98769 (in SC) and AB87634.1 (in AT), additional analysis determined that those two proteins are considered orthologs (i.e. the hits are reciprocal best hits) and is reflected in the multiple alignment of ARL6 and the top hit (from BLAST analysis) of various proteomes (Figure 5). Note that while the best BLAST hit to (human) ARL6 in SC (CAA98769), AT (AB87634.1), and AN (EAA66244) show high protein sequence identity and conservation, the arginine at residue 122 is not conserved in SC, AT, or AN.

Despite the fact it took more than a decade to clone *ARL6*, after an ~11 cM candidate interval was first defined in 1994 (Sheffield et al. 1994), the identification of *ARL6* as *BBS3* is considered a story of success. This is because for a rare, autosomal recessive disorder such as BBS, the number of clinical samples (in conjunction with densely-spaced genetic markers) is crucial. The lack of additional families combined with a reasonable number candidate genes (62) stalled the discovery effort. Only with additional prioritization was *ARL6* identified as *BBS3*. The use of comparative genomics can be applied to speed up the rate of disease gene discovery, particularly for BBS. This is illustrated by a novel application of comparative genomics in the identifications of *ARL6* as *BBS3* using COP, of *BBS5* and *BBS9* using similar comparative genomic methods. However, it is worthwhile to note that comparative genomics was only one of many components responsible for successful discoveries in each case. Using the *BBS3*

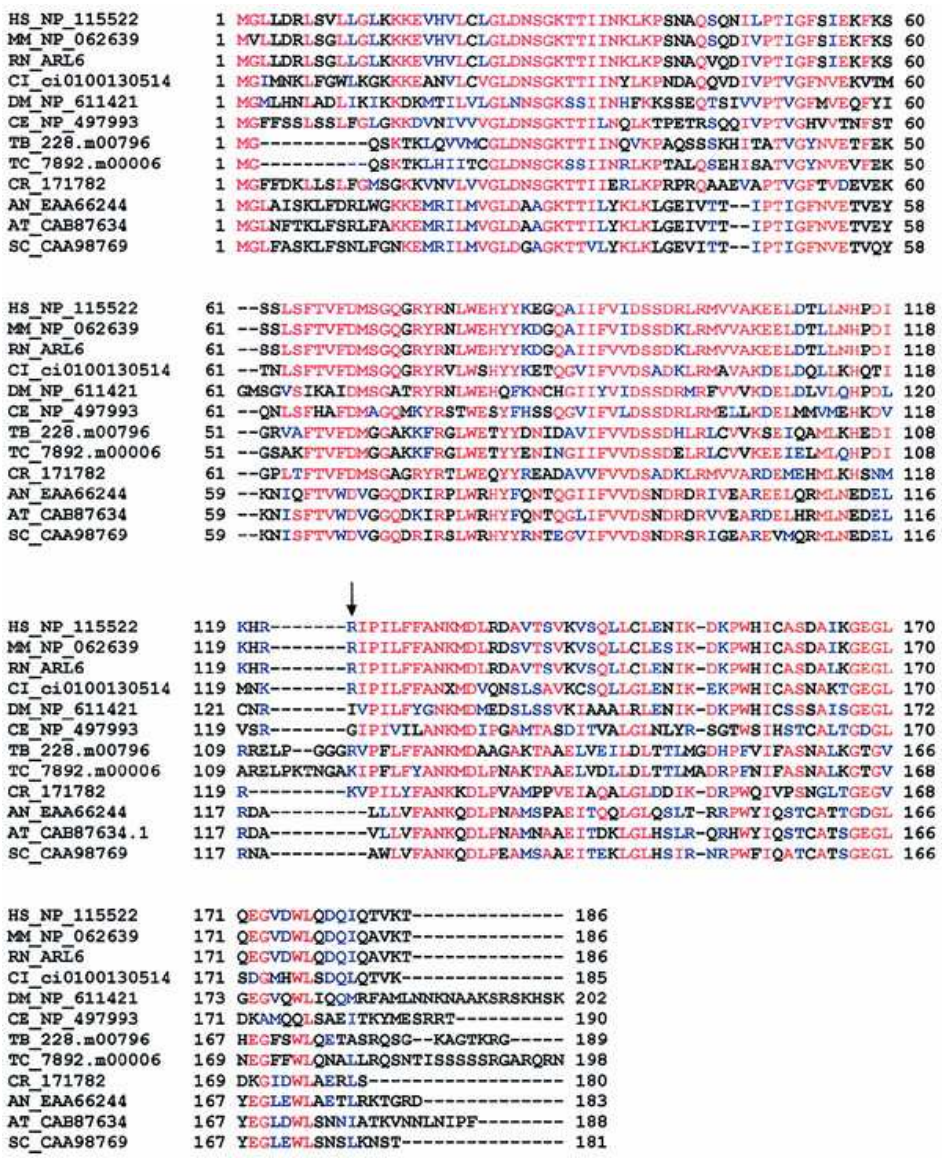


Figure 5. Multiple alignment of ARL6 (HS_NP_115522) and the corresponding best BLAST hit in 11 other model organisms. The mutation (R122X) is denoted by an arrow. Each sequence is denoted by the first letter of the genus-species name, followed by a GenBank accession number (whenever possible) or a unique identifier (e.g., "DM_NP_611421" refers to the protein represented by NP_611421 in the genome of *Drosophila melanogaster*). Consensus residues are shown in red; conserved residues are shown in blue. Numbers flanking sequences correspond to the position of the residue within each sequence (excluding gaps). Abbreviations are as follows: HS, *Homo sapiens*; MM, *Mus musculus*; RN, *Rattus norvegicus*; CI, *Ciona intestinalis*; DM, *Drosophila melanogaster*; CE, *Caenorhabditis elegans*; TB, *Trypanosoma brucei*; TC, *Trypanosoma cruzi*; CR, *Chlamydomonas reinhardtii*; AN, *Aspergillus nidulans*; AT, *Arabidopsis thaliana*; and SC, *Saccharomyces cerevisiae*.

discovery with COP as an example, the COP method was only successful when applied to a mapped interval. This reduced the 62 candidate genes to 4. Only with additional prioritization based on function annotation (GO – intracellular transport) and zebrafish BBS models did *ARL6* emerge as the best candidate gene. Thus, the discovery of *BBS3* was made possible by the integration of multiple sources of functional information.

While the specific function of ARL6 is unknown, ARL6 is the first BBS gene with significant functional information. ARL6 contains an ADP-ribosylation factor (ARF/SAR) domain, which is named after the best characterized members of the family ARF1, ARF6 and SAR1. Members of the ARF/SAR protein family have been implicated in the regulation of vesicle assembly and intracellular trafficking (D'Souza-Schorey and Chavrier 2006). There are at least 50 members of the ARF/SAR protein family in the human genome, thus ARL6 may perform a specialized function related to vesicle assembly and intracellular trafficking. The fact that ARL6 belongs to a protein family with a reasonable number of members is consistent with the seven identified BBS genes. BBS6 has a weak similarity to chaperonin domain, of which there are many members. BBS1, BBS3, and BBS7 contain coiled-coil domain, which is a very common protein domain. This is also true of TPR containing proteins, which include BBS4 and BBS8. Based on protein domain similarity, one general statement can be made. BBS proteins contain commonly found domains, perhaps reflecting the specificity and scope of phenotypes found in BBS patients. By building on existing studies of other ARF containing proteins, the study of ARL6 may provide quick insights into the pathophysiology of BBS.

CHAPTER 5

IDENTIFICATION OF *TRIM32* AS *BBS11*

5.1 BBS11 family and linkage mapping

At the end of 2004, there were no more BBS mapped critical intervals. Yet mutation screening of the eight known genes indicates that additional BBS genes and mutations have yet to be identified. This can partly be attributed to the limited number of meioses that do not provide strong linkage signals (at any single locus). However, clinical samples of a new BBS family, hereafter referred to as BBS11 family, was identified in late 2004, giving rise to the possibility of an additional BBS interval. The pedigree of this small family is shown in Figure 6. This Israeli Arab Bedouin family is highly consanguineous, as indicated by double horizontal bars.

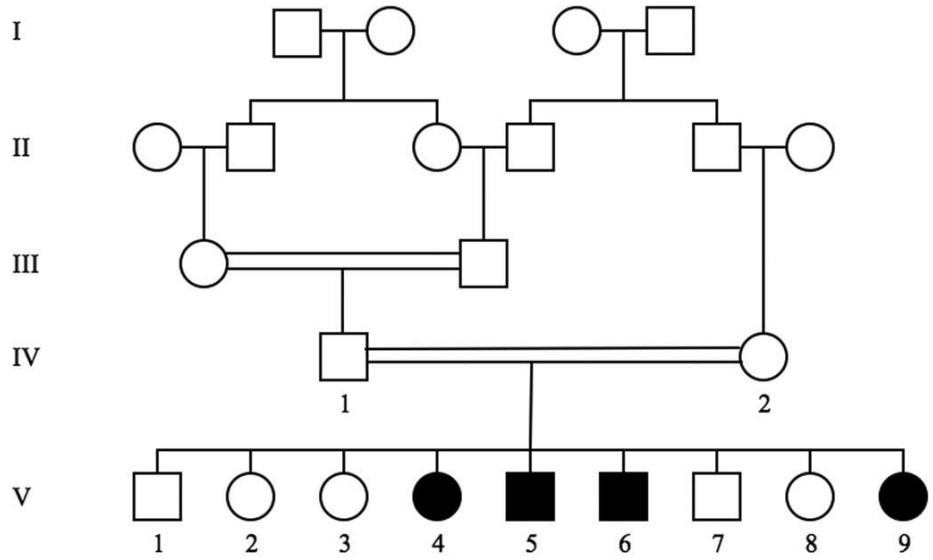


Figure 6. Pedigree of the BBS11 family. Males are represented by boxes and females are represented by circles. Affected individuals are shaded. Double horizontal bar indicate consanguineity, or inbredness.

5.1.1 Clinical features of BBS11 family

Table 5 lists the clinical phenotypes of the BBS11 family. The affected individuals have BBS hallmark phenotypes including obesity (high BMI), polydactyly, retinitis pigmentosa, mental retardation, and genital defects.

Table 5. Clinical phenotypes of BBS11 family.

Fam ID	BMI	HC (cm)	BW (g)	Polydactyly/ syndacyly	RP/ blindness	MR	Genital defects	Co-morbidity
V-6	24.88	52.5	4,500	Polydactyly right and left feet, syndactyly, wide and short forefeet	Night blindness, RP	MR	Micro-penis	s/p asthma
V-5	22.77	51.0	3,500	No polydactyly, wide short forefeet	Night and day blindness, RP, cong. ptosis, nistagmus, bilateral esotropia	MR		
V-4	26.78	51.5	4,000	Polydactyly: left hand (bifid 5th finger), right and left feet. Brachydactyly, wide and short forefeet		MR		
V-1	19.15	52.5	2,570					
V-7	16.58	51.0	3,250					
V-8	13.19	48.5	2,500					
V-2	19.63		2,750					
V-3	19.29	52.0	3,200					
V-9	13.87	50.0	3,250	No polydactyly	Night blindness, RP	MR		s/p craniosynostosis surgery
IV-1	27.70	51.0						
IV-2	32.74	56.0						

Abbreviations: Fam ID, family identifier; BMI, body mass index; HC, head circumference; BW, birth weight; RP, retinitis pigmentosa; MR, mental retardation.

5.1.2 Genome-wide linkage mapping

The high degree of consanguineity in the BBS11 family makes it a good candidate for mapping the disease locus by homozygosity mapping. STRP genotyping using 400 highly informative STRP markers was performed by John Beck of the Sheffield laboratory. However, no informative STRPs were homozygous in all four affected individuals.

Reasoning that the density provided by STRPs (average intermarker density of ~10 Mb) was insufficient, the use of high-density SNP (Single Nucleotide Polymorphism) microarrays for application toward linkage mapping was evaluated. While the informativity of SNPs on the (Affymetrix) microarrays (average heterozygosity of 0.3) as compared to those of genotyping STRPs (average heterozygosity of >0.7), is much lower, it is anticipated the the SNP arrays can overcome this deficiency by using large number of markers to achieve greater coverage at finer resolution. To identify homozygous regions consistent with linkage, the four affected members of the BBS family were genotyped with the Affymetrix GeneChip HindIII array (of the two-chip 100K set) containing 57,244 SNPs (average intermarker distance ~47 kb). The SNP genotyping was performed by John Beck of the Sheffield laboratory.

In order to identify regions of homozygosity across all four affected individuals, a simple "homozygosity allowing for NoCalls" (HANC) criteria was implemented. As the SNPs chosen for the SNP arrays are biallelic, there are three possible genotype states at every SNP: AA, AB, or BB. Both genotypes of AA and BB are considered homozygous, while an AB genotype is not. Additionally, as each genotype assignment ("call") is made based on the detected fluorescence of twenty probe pair sets for each allele, each

genotype call is assigned a confidence value (CV) between 0 and 1, with 0 being the highest confidence. Thus, for those SNPs, for which a clear SNP genotype (AA, AB, or BB) cannot be assigned, a fourth "NoCall" state is assigned (with high CVs) in its place. For this additional genotype state, the HANC criteria excludes any SNP genotypes assigned with "NoCall" from being considered. In other words, the NoCall genotypes are merely passive placeholders. Six examples illustrating the HANC criteria are shown in Table 6.

Table 6. Six hypothetical SNP genotyping examples (1-6) illustrating the HANC (homozygous allowing for NoCalls) criteria as applied to four individuals (V-4, V-5, V-6, and V-9).

Example / Individual	V-4	V-5	V-6	V-9	Homozygous?
1	AA	AA	BB	BB	No
2	AA	AB	AA	AA	No
3	BB	BB	BB	BB	Yes
4	NC	NC	NC	NC	Yes
5	AA	NC	NC	BB	No
6	NC	BB	NC	BB	Yes

SNPs fulfilling the HANC criteria are considered homozygous.

Briefly, SNP example 1 (second row) demonstrates that while the SNP genotypes across all four affected individuals (V-4, V-5, V-6, and V-9, the identifier correspond to those in Table 6) are homozygous, they do not share identical homozygous SNP genotypes (e.g. V-5 has AA compared with BB genotype of V-6) and therefore would not be classified as a homozygous SNP under the HANC criteria. Example 2 shows that individual V-5 is not homozygous (SNP genotype of AB) and thus the SNP would not be classified as homozygous. Examples 3 and 4 illustrate two instances in which the SNP

genotypes would be considered homozygous. Example 5 reinforces the idea behind example 1 (AA in V-4 is not equivalent to the BB genotype in V-9), as well as the "NoCall" (in individuals V-5 and V-6) exclusion criterion. This exclusion is also demonstrated by the sixth and final example whereby the SNP genotypes of V-4 and V-6 are ignored. Only the genotypes of V-5 and V-9 are evaluated for homozygosity in the final example and because both share identical genotype (BB), the SNP genotype is considered homozygous.

A "slice" of the homozygosity analysis based on the HANC criteria can be seen in Figure 7. First, each individual SNP is evaluated for homozygosity using the HANC criteria. SNPs that are considered homozygous are then highlighted in light yellow. Next, the number of consecutative homozygous SNP - CHS (based on the physical location of the SNPs) and the total physical distance (nucleotides) spanned by the CHS "blocks" are computed.

Table 7 shows that individually (when including those SNP genotype calls of NoCalls), each of the affected individuals is homozygous for >75% of the SNPs. On average, the SNP genotype call rate was >96%, and only 42 SNP genotypes (≈ 0.07%) were found in common across all four affected siblings. Not surprisingly, 32,631 (≈ 57%) SNP genotypes were homozygous in all four affected individuals, a finding reflecting the relative lack of informativity of SNP markers and the inbred nature of the pedigree. Moreover, the breakdown for the four SNP genotype states and their average CVs conform to the expectation that the three major genotype states (AA, AB, and BB) have lower average confidence values than those of NoCalls.

Row #	SNP ID	Chr	Physical Position	V-4	V-5	V-6	V-9	CHS	Distance
55894	SNP_A-1750306	9	116,488,409	BB	BB	BB	BB	76	
55895	SNP_A-1755333	9	116,509,648	AA	AA	AA	AA	77	
55896	SNP_A-1757186	9	116,516,683	BB	BB	BB	BB	78	
55897	SNP_A-1667709	9	116,588,086	AA	AA	AA	AA	79	
55898	SNP_A-1722169	9	116,696,339	AA	AA	AA	AA	80	
55899	SNP_A-1722367	9	116,697,042	AA	AA	AA	AA	81	
55900	SNP_A-1655002	9	116,775,274	AA	AA	AA	AA	82	
55901	SNP_A-1663697	9	116,826,402	BB	BB	BB	BB	83	
55902	SNP_A-1703674	9	116,839,267	AA	AB	AA	AA	0	2,417,023
55903	SNP_A-1703824	9	116,839,541	AA	AA	AA	AA	1	
55904	SNP_A-1705248	9	116,840,400	BB	BB	BB	BB	2	
55905	SNP_A-1707130	9	116,844,327	AA	AA	AA	AA	3	
55906	SNP_A-1716030	9	116,873,283	AA	AA	AA	AA	4	
55907	SNP_A-1648819	9	116,912,554	AA	AA	AA	AA	5	
55908	SNP_A-1650539	9	116,922,433	BB	BB	BB	BB	6	
55909	SNP_A-1650763	9	116,922,938	AA	AB	AA	AA	0	82,892
55910	SNP_A-1651055	9	116,923,032	BB	BB	BB	BB	1	
55911	SNP_A-1652677	9	116,926,080	AA	AB	AA	AA	0	0
55912	SNP_A-1706754	9	117,104,856	AA	AB	AA	AA	0	
55913	SNP_A-1686273	9	117,214,464	BB	BB	BB	BB	1	
55914	SNP_A-1686447	9	117,215,973	AA	AA	AA	AA	2	
55915	SNP_A-1686587	9	117,216,436	AA	AA	AA	AA	3	
55916	SNP_A-1688535	9	117,240,430	BB	BB	BB	BB	4	
55917	SNP_A-1693736	9	117,280,410	AA	AA	AA	AA	5	
55918	SNP_A-1742600	9	117,322,555	BB	BB	BB	BB	6	
55919	SNP_A-1749396	9	117,351,252	BB	BB	BB	BB	7	
55920	SNP_A-1749526	9	117,352,089	AA	AA	AA	AA	8	
55921	SNP_A-1756958	9	117,383,760	BB	BB	BB	BB	9	
55922	SNP_A-1647199	9	117,540,509	AA	AA	AA	AA	10	
55923	SNP_A-1706304	9	117,632,530	BB	BB	BB	BB	11	
55924	SNP_A-1706496	9	117,633,299	BB	AB	BB	BB	0	418,066
55925	SNP_A-1709944	9	117,640,621	BB	BB	BB	BB	1	
55926	SNP_A-1710040	9	117,640,758	AA	AA	AA	AA	2	
55927	SNP_A-1642730	9	117,669,953	AA	AA	AA	AA	3	

Figure 7. A sample result from the SNP analysis based on the HANC criteria. SNPs fulfilling the homozygosity criteria across all four affected siblings are highlighted in yellow. Each row represents a SNP by its unique identifiers (row number [#], SNP identifier [ID], chromosomal location [Chr], and physical position (in nucleotides) as well as the genotype calls from the four affected siblings (V-4, V-5, V-6, and V-9). Tabulation of the number of consecutative homozygous SNPs (CHS, highlighted in yellow) is stored the CHS column and the physical distance spanned between the CHS "blocks" is store in the Distance column.

Table 7. Distribution of the genotyping calls and their associated confidence values (CV) in the four affected siblings (V-4, V-5, V-6, and V-9).

Fam ID	Genotyping rate (%)	% of homozygosity	% of AA calls	Avg CV of AA calls	% of BB calls	Avg CV of BB calls	% of AB calls	Avg CV of AB calls	% of NC calls	Avg CV of NC calls
V-4	98	76	38	0.0072	36	0.0084	24	0.0210	2	0.3815
V-5	92	79	36	0.0150	35	0.0181	21	0.0358	8	0.4094
V-6	97	77	38	0.0092	36	0.0116	23	0.0251	3	0.3832
V-9	99	76	38	0.0135	37	0.0147	24	0.0146	1	0.0151

The consensus row refers to the average or shared percentage (%) across all four individuals. Abbreviations: %, percentage; Avg, average; NC, NoCall.

Table 8. Top autosomal homozygosity regions, as ordered by the number of consecutative homozygous SNP genotypes (CHS) in the four affected individuals (V-4, V-5, V-6, V-9, cut-off at 80 CHS) as well as the consensus homozygous regions in all four affecteds, cut-off at 25 CHS. The disease locus is shown in bold. Abbreviations: DIS, physical distance

	V-4			**V-5**			**V-6**			**V-9**			**Consensus**		
Top Regions	Chromosome band	CHS	DIS	Chromosome band	CHS	DIS	Chromosome band	CHS	DIS	Chromosome band	CHS	DIS	Chromosome band	CHS	DIS
1	15q21.3-q26.1	522	33.45	15q21.3-q23	335	15.75	15q21.3-q25.3	506	31.9	12p11.21-q13.13	406	22.36	**9q33.1**	**83**	**2.40**
2	8q21.13-q22.2	352	17.69	4q22.1-q23	283	10.70	**9q31.2-q33.2**	**306**	**17.0**	8q21.13-q22.2	387	18.89	16q16.3	50	0.96
3	**9q31.2-q33.2**	**306**	**17.07**	13q31.1-q31.2	241	9.88	10q22.2-q23.2	258	12.2	8q12.1-q13.1	274	11.66	10q23.1	42	0.90
4	12q23.2-q24.22	278	17.36	4q21.21-q22.1	216	7.57	9q22.2-q31.1	247	14.3	9q22.31-q31.1	262	14.13	2p22.1	34	1.20
5	4q22.1-q23	261	10.18	8q13.2-q21.11	190	6.18	6q21-q22.1	165	7.67	12q33.2-q24.21	237	13.92	8q13.3	34	0.69
6	8q21.11-q21.13	226	8.07	13q22.1-q31.1	175	5.65	6q22.31-q22.33	165	6.36	8q143.2-q21.11	222	7.01	3p26.3	32	0.53
7	8q13.2-q21.11	214	6.66	6q14.1-q14.3	172	6.11	6q22.1-q22.31	162	5.61	6q14.3-q16.1	216	7.89	2q21.1	30	2.96
8	6q14.1-q15	205	7.83	8p21.2-12	170	7.58	12q13.11-q13.3	126	11.1	6q16.1-q13.3	215	7.92	2q24.3	30	1.00
9	6p25.1-p24.2	199	6.51	8q21.11-q21.13	168	5.53	8p23.2	114	1.19	**9q32-q33.2**	**191**	**10.00**	4q21.22	30	0.67
10	15q21.3	90	3.18	6q16.1	161	5.28	1p36.32-p36.21	104	10.4	12p12.2-p11.23	191	6.84	9q31.1	29	0.95
11				13q21.1-q32.3	155	6.44	6p24.1-p22.3	103	4.29	8q21.11-q21.13	191	6.60	6q16.1	28	0.69
12				13q33.1-q33.2	153	2.84	12q14.1	93	3.76	10q22.3-q23.2	179	7.58	4p15.1	26	1.24
13				12q23.2-q23.3	152	7.04	15q21.3	90	3.18	6q14.1-q14.3	157	5.01	9q31.1	26	1.14
14				13q31.3	147	4.16				12p11.23-p11.21	130	3.72	7q11.2	25	1.25
15				3p14.1-913	133	4.86				6p24.1-p22.3	103	4.29			
16				6p24.2-p22.3	126	5.05				12q14.1	93	3.76			
17				10q23.1-q23.2	115	4.91									
18				10q23.31	109	3.08									
19				6q14.3-q15	98	4.18									
20				2q24.3	95	3.42									
21				7p13-p12.3	94	3.63									
22				**9q32-q33.1**	**93**	**3.41**									
23				15q24.1-q25.2	88	8.78									
24				9q31.2-q31.3	88	4.60									

Due to the uninformativity of the SNP markers and the high degree of consanguineity in the family, additional prioritization based on the number of consecutative homozygous SNPs (across all four affected individuals) was performed to yield consensus homozygous regions. Table 8 summarizes the homozygous regions of all four affected individuals as well as the consensus homozygous regions. Fourteen autosomal regions were consistent with linkage based on homozygosity of 25 CHS in the four affected siblings. The largest consensus homozygous region (as defined by the number of CHS) is a 2.4 Mb region in 9q33.1 that is spanned by 83 CHS across all four affected siblings. The next biggest consensus homozygous region is a much smaller region (0.96 Mb) that falls in 16q16.3 and is spanned by 50 CHS. Notably, three regions (15q21.3, 8q21.11, and 6q14.1) were highly homozygous in three of the four affected siblings but failed to be prioritized as a consensus region as a result of the fourth sibling not sharing the region of homozygosity.

Next, in order to reduce cost associated with the use of high-density SNP genotyping and to exclude homozygosity regions found in phenotypically normal individuals, genotyping was performed (by J. Beck) on the the four affected patients, their unaffected siblings, and their parents with STRP markers that mapped within the fourteen regions of apparent homozygosity identified by the SNP genotyping. Genotyping with informative STRPs excluded all but one region as being linked to the disease phenotype, a 2.4-Mb region containing 83 consecutive homozygous SNPs (CHS) on chromosome 9q33.1 (Figure 8). Of interest, this region contained no STRPs from the original 400 STRPs that were used for linkage analysis. Logarithm of the odds score analysis (performed by Val Sheffield) using completely informative markers within the

2.4-Mb region reveals highly significant linkage with a maximum logarithm of the odds score of 3.7 (Θ= 0).

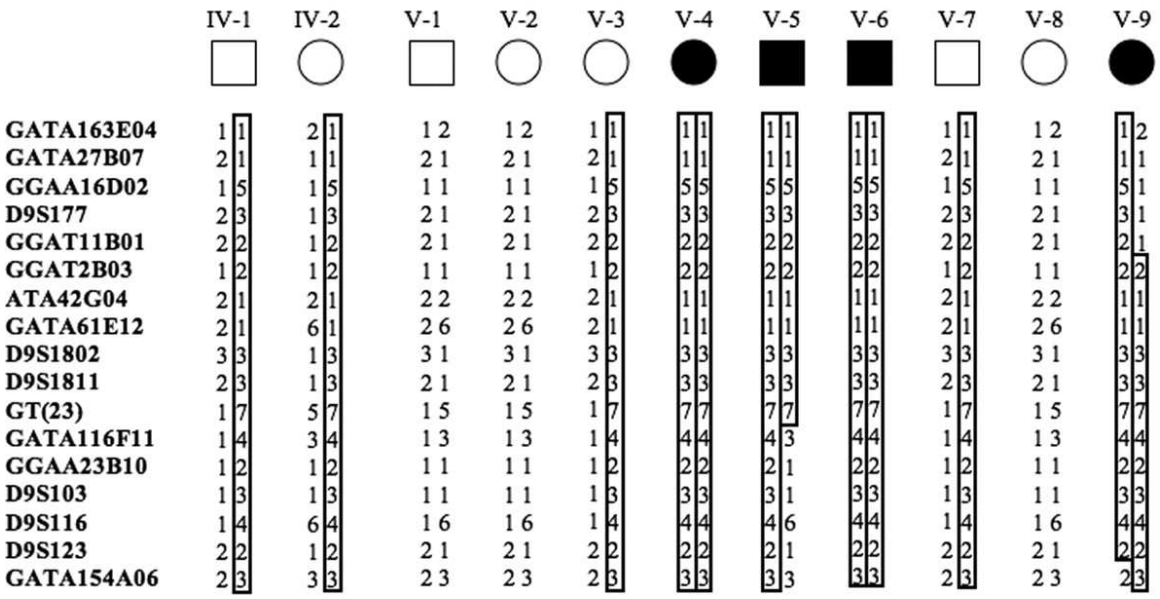


Figure 8. Haplotype of 9q33.1 in the nuclear BBS11 family. The haplotype segregating with the disease phenotype is boxed in affected individuals. Data for the figure generated by J. Beck.

5.1.3 9q33.1 Candidate genes and mutational analysis

Analysis of the 2.4-Mb homozygous region on chromosome 9 reveals four RefSeq genes [pregnancy-associated plasma protein-A (*PAPPA*, NM_002581), astrotactin 2 isoform a (*ASTN2*, NM_014010), tripartite motif (TRIM)-containing protein 32 (*TRIM32*, NM_012210), and Toll-like receptor 4 precursor (*TLR4*, NM_138554)] and two placental-specific genes (*DIPLA* and *DIPLAS*). No gene within the linked interval showed sequence similarity to the proteomes of microbial eukaryotes such as CR or TB.

Many lines of evidence suggest *TRIM32* as the best BBS candidate gene in the 2.4-Mb interval. First, the expression pattern of *TRIM32* is similar to the other known BBS genes (Reymond et al. 2001; Frosk et al. 2002; Horn et al. 2004). Second, there are three relevant knockout mouse models for genes within the linked interval (no mouse model exists for *Trim32*): *Pappa* (Conover et al. 2004), *Astn1* (a paralog of *Astn2*) (Adams et al. 2002), and *Tlr4* (Hoshino et al. 1999). The phenotypes of the mouse models of the three genes are summarized in Table 9. Briefly, mice with *Pappa*$^{-/-}$ show developmental delays but are fertile, this is in constrast to the absence of flagella in the spermatozoa observed in mouse models of *BBS2*, *BBS4*, and *BBS6*. Similarly, mice with *Astn1*$^{-/-}$ exhibit primarily neuronal defects which have not been observed in the three BBS mouse models. Finally, there are three transgene and one knockout mouse models of *Tlr4*. These models display general immunological defects which are not found in mouse BBS models. In short, these three models do not have phenotypes that resemble BBS mouse models (Mykytyn et al. 2004; Nishimura et al. 2004; Fath et al. 2005). Third, functional characterization of other TRIM proteins indicates involvement with components of the cytoskeleton, a finding consistent with the function of other BBS proteins (Kim et al.

Table 9. Summary table outlining the phenotypes observed in mouse models of three of the four candidate genes in the *BBS11* candidate interval: Pappa, Astn1, and Tlr4.

Target gene	**Knockout/transgene model(s) phenotypes**
Pappa	Smaller embryo size , slow growth, fertile, delayed bone ossification
Astn1	Reduced cerebellum size, abnormal Purkinje cell morphology, reduced coordination performance on Rotarod
Tlr4	Hyporesponsive to bacterial liposaccharide

2004; Kulaga et al. 2004; Blacque et al. 2004). Fourth, in terms of being members of protein families, both PAPPA and ASTN2 have only one other paralog (PAPP2 and ASTN1, respectively) while TLR4 has ~14 paralogs. In contrast, TRIM32 belongs to a relatively large protein family consisting of ~70 members. TRIM32 membership in a relatively large protein family fits well with the recent identification of *ARL6* as *BBS3*, which itself belongs to the ~50-member ARF/SAR protein family. In protein families with many members, it is generally believed that each member performs functionally similar but somewhat specialized role. Examples of specializations are differences in spatial (e.g. different cellular localizations) and/or temporal expression (e.g. different developmental stages). Given the specific yet muti-organ system defects observed in BBS patients, some of whom live past their sixth decade, it seems to reason that genes that belonging to large protein families (with some functional redundancies) may be better candidates. Additionally, TRIM32 has been implicated in apoptosis (Horn et al. 2004) which has been observed in the three BBS mouse models in which photoreceptors degenerate as a result of apoptosis (Mykytyn et al. 2004; Nishimura et al. 2004; Fath et al. 2005). The observation of webbing of fingers and toes in BBS patients may also indicate incomplete apoptotic process that involved E3 ubiquitin ligases (which is a predicted function of TRIM32). While any single functional information described above may not be sufficient to prioritize the four candidate genes alone, however, based on the combination of various functional information, *TRIM32* was selected as the best candidate gene.

DNA sequencing of the entire coding sequence and consensus splice sites of the six genes within the 2.4-Mb interval (performed by A. Ferguson and J. Beck) revealed a

single potential disease-causing variant in the four affected siblings, a homozygous transition (C388T) resulting in a proline to serine substitution at codon 130 (P130S) in *TRIM32* (Figure 9). The parents were heterozygous for the P130S allele, and all five unaffected siblings were either heterozygous for P130S or homozygous for the normal allele. No P130S alleles were detected in 184 control individuals, including 94 Bedouin Arab control individuals and 90 ethnic diversity controls. The proline residue at position 130 was found in a conserved B-box domain of TRIM32 (Figure 10).

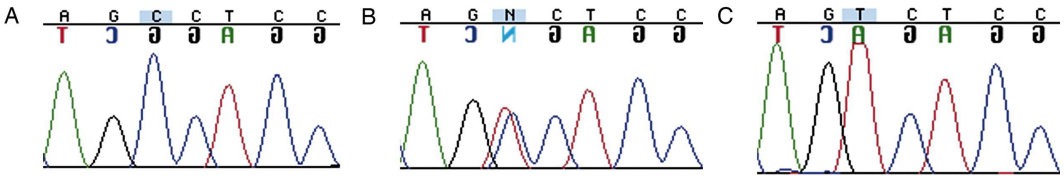


Figure 9. Representative *TRIM32* sequence. (*A*) Normal proline homozygote at position 130 (CCT). (*B*) Heterozygous sequence. (*C*) Mutant serine homozygote (TCT). Data for the figure generated by A. Ferguson and J. Beck.

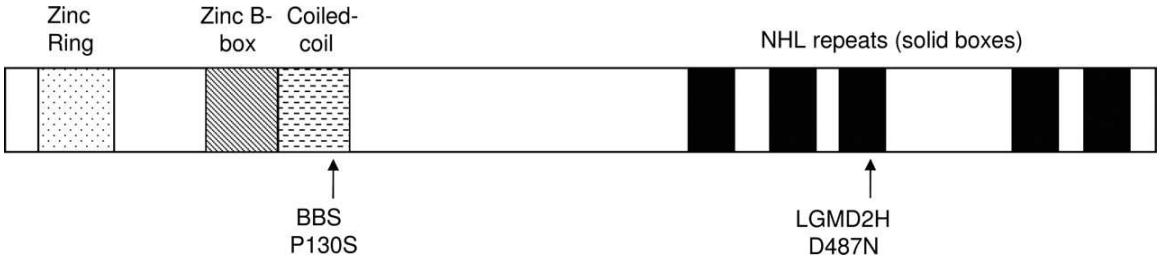


Figure 10. Schematic diagram of TRIM32 (653 residues). N-terminal tripartite motif (zinc RING finger, zinc B-box, and coiled-coil domains) and five NHL repeats (solid boxes) are shown.

Mutation screening using single-strand conformational polymorphism analysis of the coding sequence (of *TRIM32)* in a panel of 90 BBS probands (performed by J. Beck)

failed to detect any additional mutant alleles. Additional studies, described below, were performed to validate *TRIM32* as a BBS gene.

5.2 *TRIM32* expression is strongly correlated with expression of other BBS genes

The tissue expression pattern of *TRIM32* has been reported (Reymond et al. 2001; Frosk et al. 2002; Horn et al. 2004) and is similar to the pattern of expression of other BBS genes. Expression of *TRIM32* in the mammalian eye and hypothalamus has not been previously evaluated. Northern blot analysis on RNA isolated from multiple mouse tissues including whole eye and hypothalamus with a 3' UTR *Trim32* probe was performed by Ruth Swiderski of the Sheffield laboratory. The northern blot results confirm an expression pattern similar to other BBS genes, including expression in the eye and hypothalamus.

Recent studies in humans and animal models have used microarray expression data from thousands of genes in combination with genome-wide polymorphism data to search for loci controlling variation in gene expression (Brem et al. 2002; Schadt et al. 2003; Morley et al. 2004). This approach, known as expression quantitative trait loci (eQTL) mapping, demonstrates the correlation of expression of specific genes with specific genetic loci. A large-scale eQTL mapping study was performed by other members of the Sheffield and Stone laboratory with a cross of 120 F_2 rats genotyped with 400 STRPs across the rat genome to identify loci involved in regulation of thousands of genes expressed in the eye. In addition to eQTL mapping analysis, pairwise gene expression correlation analysis of the microarray expression data was performed by Todd Scheetz and Kwan-Youn Kim of the Sheffield laboratory to identify genes whose

expression levels are highly correlated among the 120 F_2 animals. The pairwise correlation analysis was performed to explore the hypothesis that the genetic permutations created by the mapping cross would allow the detection of functional relationships among genes because the regulatory mechanisms shared by related genes would likely cause their expression to respond to biological variations in a coordinated fashion.

The Affymetrix rat 230.20 chip containing ≈ 31,000 probe sets was used for the experiments, and ≈ 19,000 probe sets, including the nine known BBS genes and *Trim32*, were shown to be expressed in the eye and exhibit enough expression variation among the 120 F_2 animals to allow for detection of significantly correlated expression. Evaluation of pairwise gene expression correlations in the eyes from the 120 F_2 rats revealed that the expression levels of the nine known BBS genes were positively correlated with one another. Specifically, of the 36 possible pairwise comparisons of expression correlations among the nine BBS genes, all displayed positive correlation and 21 of the 36 comparisons were individually statistically significant (Table 10). The correlation among the nine known BBS genes was determined by comparing the mean multiple correlation coefficient of each gene individually to the other eight, and the significance of this value was assessed by comparing it to 10,000 randomly selected sets of nine genes. The result is highly significant ($P = 0.0027$). This finding leads to the hypothesis that expression of novel BBS genes should be positively correlated with the known BBS genes and suggests an approach for prioritizing candidate BBS genes. The pairwise gene expression variation correlation of each gene in the 2.4-Mb 9q33.1 candidate interval with the nine known BBS genes was examined. The only gene demonstrating significant positive

correlation with multiple BBS genes was *Trim32* (Table 10). The significance of the correlation of *Trim32* was determined to be $P < 0.0001$ based on a multiple correlation coefficient of 0.72 between *Trim32* and the nine known BBS genes and after correcting for assessment of the multiple genes in the interval.

Table 10. Pairwise (Pearson's) correlation expression values (among the 120 F2 rats analyzed with Affymetrix expression arrays) between the nine known BBS genes and four genes in the 9q33.1 candidate interval.

Gene Name	*BBS1*	*BBS2*	*BBS3*	*BBS4*	*BBS5*	*BBS6*	*BBS7*	*BBS8*	*BBS9*	*TRIM32*	*PAPPA*	*ASTN2*	*TLR4*
BBS1	1	0.59	0.44	0.41	0.47	0.43	0.53	0.40	0.47	0.40	-0.36	-0.29	0.22
BBS2		1	0.71	0.41	0.69	0.55	0.73	0.72	0.68	0.58	-0.30	-0.38	0.35
BBS3			1	0.31	0.82	0.34	0.78	0.77	0.57	0.60	-0.17	-0.18	0.28
BBS4				1	0.54	0.25	0.62	0.23	0.31	0.23	-0.08	-0.25	0.23
BBS5					1	0.34	0.79	0.65	0.52	0.63	-0.22	-0.28	0.30
BBS6						1	0.46	0.35	0.30	0.40	-0.24	-0.35	0.52
BBS7							1	0.65	0.57	0.53	-0.16	-0.32	0.38
BBS8								1	0.58	0.62	-0.25	-0.15	0.24
BBS9									1	0.49	-0.37	-0.30	0.10
TRIM32										1	-0.44	-0.34	0.43
PAPPA											1	0.27	-0.29
ASTN2												1	-0.50
TLR4													1

Empirically, correlation values >0.48 are significant at $P < 0.05$, and correlation values >0.64 are significant at $P < 0.01$. Data for the table generated by T. Scheetz and K. Kim.

5.3 Knockdown of TRIM32 in zebrafish reveals BBS phenotypes

Recently, zebrafish BBS models have been developed using antisense morpholino oligonucleotides (MOs) to knock down the expression of BBS genes in developing zebrafish embryos (Yen et al. 2006). Two specific phenotypes were observed in common with individual knockdown of known BBS zebrafish orthologs (bbs1–bbs8): (*i*) disruption of Kupffer's vesicle (KV), a transient ciliated organ involved in left–right

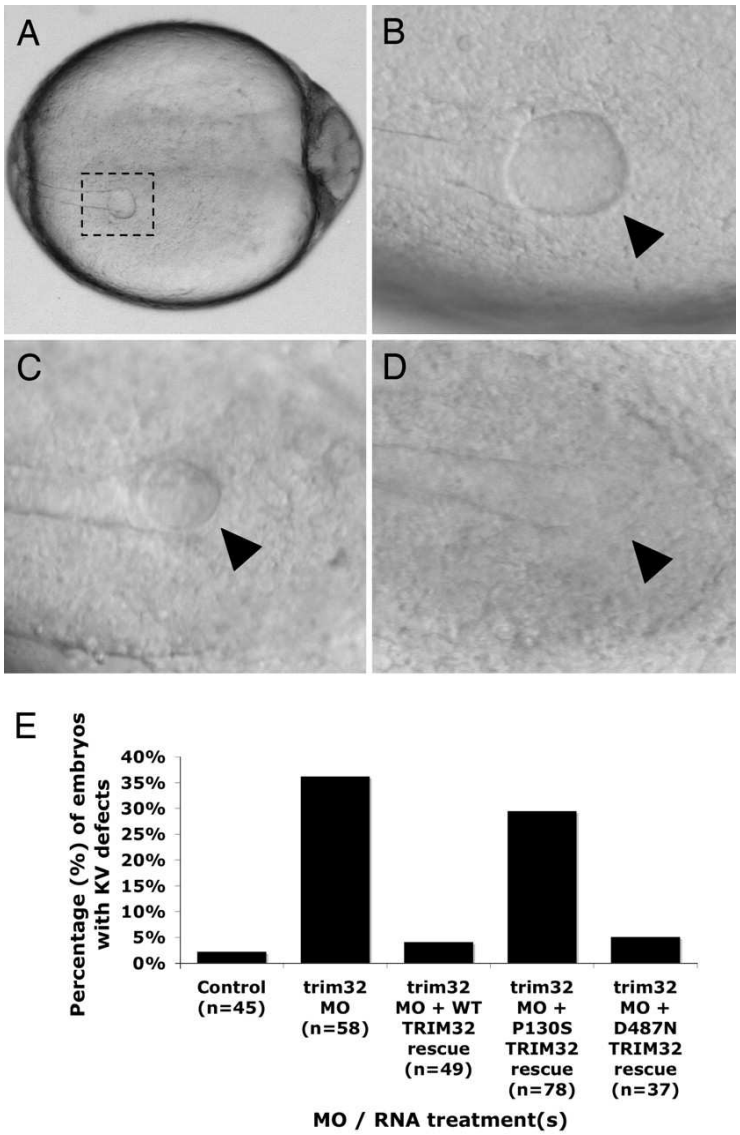


Figure 11. Representative KV phenotypes and summary of zebrafish *trim32* knockdown. (*A–D*) Photographs of live zebrafish embryos at the 10- to 13-somite stage. (*A*) KV (dashed box) located in the posterior tailbud in a representative control-injected embryo. (*B*) Control KV (arrowhead). (*C*) *trim32* MO-injected embryo with a reduced KV (arrowhead). (*D*) *trim32* MO-injected embryo with no morphologically visible KV (arrowhead). (Magnifications: *A*, x5; *B–D*, x10.) (*E*) Percentage of zebrafish with altered KV (reduced or absent). MO refers to zebrafish *trim32* antisense MO-injected embryos. In rescue experiments, WT, P130S, or D487N containing full-length *trim32* mRNA was coinjected with the *trim32* MO. Controls were injected with an MO containing mismatched bases to the *trim32* sequence. Thirty-six percent of *trim32* MO-injected embryos displayed KV defects, whereas only 2% of control-injected embryos exhibited KV defects ($P < 0.0001$). Both WT human *TRIM32* (4%) and the D487N allele (11%) rescued the KV phenotype (not significantly different from controls); however, the P130S allele (30%) failed to rescue the KV phenotype ($P < 0.0001$ compared with controls). Data for the figures generated by J. Beck, Hsan-Jen Yen, and Marwan Tayeh.

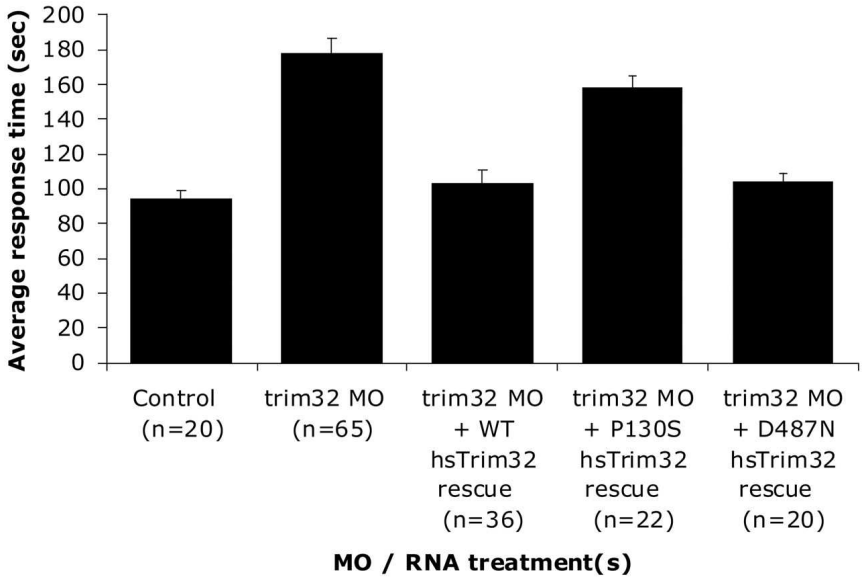


Figure 12. Summary of the melanosome transport assay in 5-day zebrafish embryos injected with *trim32* MO with and without mRNA rescue. Control MO- and *trim32* MO-injected embryos were observed for melanosome transport response time after epinephrine treatment. Embryos treated with *trim32* MO alone showed an average response time of 178 s compared with an average 94-s response time for embryos treated with the control MO ($P < 0.0001$). Both WT human *TRIM32* (103 s) and the D487N allele mRNA (103 s) rescued the melanosome transport defect (not significantly different from controls). The P130S allele (158 s) failed to rescue the transport defect ($P < 0.0001$ compared with controls). Data for the figure generated by J. Beck.

patterning, and (*ii*) delay of intracellular transport as determined by measuring the intracellular rate of retrograde melanosome transport (Yen et al. 2006). To determine whether knockdown of zebrafish *trim32* results in similar defects, the zebrafish trim32 sequence was first identified by BLAST analysis using human TRIM32 as the query sequence and subsequently sequenced by J. Beck. The zebrafish trim32 is 62% identical and 75% similar to the human protein. Knockdown of zebrafish *trim32* with an antisense MO flanking the initiator methionine resulted in 36% of fish having abnormal KV as defined by a reduced KV diameter compared with control-injected embryos ($P < 0.0001$)

(Figure 11). This finding is consistent with those observed with knockdown of other zebrafish BBS orthologues (range 25–40%) (Yen et al. 2006). In addition, similar to knockdown of other BBS genes, *trim32*-MO injected fish showed a delay in melanosome transport compared with controls ($P < 0.0001$) (Figure 12). Both the KV and melanosome transport phenotypes were rescued when MOs were coinjected with normal human *TRIM32* mRNA ($P < 0.0001$) (Figures 11 and 12).

Of interest, a single *TRIM32* missense variant (D487N) has been reported to cause limb-girdle muscular dystrophy type 2H (LGMD2H) (Figure 10) (Frosk et al. 2002). To evaluate the known human *TRIM32* variants as BBS-causing mutations, expression constructs individually containing the BBS P130S allele and the LGMD2H D487N allele were individually generated by C. Searby (Figure 10). Coinjection of the variant human mRNAs with the *trim32* MO was performed by J. Beck to determine whether mutant variants could functionally rescue both the KV defects and the melanosome transport delay. Human *TRIM32* mRNA containing the P130S variant failed to rescue both the KV defect and melanosome transport, indicating that the P130S variant results in an abnormal protein. Human *TRIM32* mRNA containing the D487N variant successfully rescued both phenotypes (Figures 11 and 12). In short, two functional analyses (pairwise correlation in the eye eQTL study and zebrafish knockdown and rescue experiments) further support that *TRIM32* is a BBS gene.

5.4 TRIM32 and BBS

TRIM32 was first characterized in a yeast two-hybrid study screening for proteins that bind to the Tat protein, a protein that activates the transcription of lentiviruses

(Fridell et al. 1995). As a member of the TRIM protein family (of which there ~70 members in the human genome), TRIM32 contains the shared N-terminal domain structure composed of a zinc RING finger, a zinc B-box, and a coiled-coil domain found in all TRIM proteins. The C-terminal of TRIM32 consists five C-terminal NHL repeats and is only found in one other TRIM protein, TRIM2, which also contains a filamin protein domain. The BBS mutation (P130S) in TRIM32 affects the N-terminal B-box domain. The B-box domain is composed of ~40 aa and spanned by eight ligands of cysteines and histidines in the highly conserved C-x_2-[CH]-x_{7-12}-C-x_2-[CH]-x_4-C-x_2-C-x_{3-6}-H-x_{2-4}-H motif. The proline mutated in the BBS11 family is the 2nd (of 4) residue between the final two ligands. With their non-polar, hydrophobic ring-based structure (no free amino group), prolines are known for introducing a 'bend' in α-helices. Thus, it seems likely that a substitution by a polar, hydrophilic serine residue (in place of proline) may cause a change in the conformation of TRIM32 to alter its activity. Members of the TRIM protein family participates in a variety of cellular processes, including apoptosis, cell growth, differentiation, transcriptional regulation, and ubiquitination. Recent studies show that TRIM32 has E3 ubiquitin ligase activity and binds to the head and neck region of myosin and ubiquitinates actin (Kudryashova et al. 2005), implicating TRIM32 in regulating components of the cytoskeleton, a function that fits well with the observed zebrafish knockdown phenotypes (Yen et al. 2006).

Of note is a previous report that a single TRIM32 missense variant (D487N) is associated with autosomal recessive LGMD (Frosk et al. 2002). There are many examples where different mutations in the same gene can result in different disorders (Bonne et al. 1999; Cao and Hegele 2000; Muchir et al. 2000; Speckman et al. 2000;

Eriksson et al. 2003). The TRIM32 LGMD2H mutation lies in a different domain (C-terminal NHL domain) than the BBS mutation (N-terminal B-box domain). A study of 37 members of the TRIM protein family has shown that ablation or disruption of N-terminal domains have differential subcellular localization effects than those observed with disruption of C-terminal domains (Reymond et al. 2001). A recent study determined that the LGMD2H allele D487N did not affect the E3 ubiquitin ligase activity, whereas disruption of TRIM32 coiled-coil domain reduced the binding affinity to myosin (Kudryashova et al. 2005). The hypothesis that different domains of TRIM32 may be involved in different processes is supported by our study of the two different mutations in the zebrafish model system. Although the LGMD2H D487N mRNA is able to rescue the zebrafish *trim32* knockdown phenotypes, the P130S mRNA does not rescue the zebrafish knockdown phenotypes, indicating that the P130S mutation disrupts aspects of the protein function that are not affected by the D487N variant.

Similar to the identification of *BBS3*, the discovery of *TRIM32* as *BBS11* resulted from the integration of multiple sources of functional information. The combined use of the linkage interval (9q33.1) from the high-density SNP genotyping, the elimination of candidate genes based on animal models and expression profile of all the genes in the BBS11 candidate interval, as well as existing functional information on *TRIM32* helped to prioritize *TRIM32* as the best candidate gene in the interval.

TRIM32 is the first BBS gene identified to be involved in the ubiquitin/proteasome system. This system of protein degradation is a multistep cascade that relies on a series of enzymes to tag substrates with multiubiquitin for degradation (Ciechanover 2005a; Ciechanover 2005b; Hershko 2005; Rose 2005). The third enzyme

in this series, an E3 ubiquitin-protein ligase, of which there are many in the human genome, is involved in the recognition and transfer of ubiquitin to the protein substrate. Determination of substrate specificity provided by TRIM32 may help to explain the highly specialized and multiorgan system defects observed in BBS patients. Additional BBS genes may be either direct or downstream targets of TRIM32.

CHAPTER 6

PHYLOGENETIC PROFILES OF SOME DISEASE PROTEINS

6.1 Introduction

The development of a novel application of comparative genomic approach (COP) toward candidate gene prioritization has been outlined in Chapter 3. This comparative genomic approach has been shown to be powerful for the identification of BBS genes (Chapter 4; Chiang et al. 2004; Li et al. 2004; Nishimura et al. 2005). This chapter explores the possibility of utilizing the COP method for more general disorders. That is, perhaps disease genes (proteins) causing diseases other than BBS have similar (though not identical) phylogenetic profiles. To explore the answer to this question, the phylogenetic profiles of several genetically heterogeneous diseases that involve ciliated and nonciliated structures were chosen. In order to construct the phylogenetic profile of those disease proteins, the proteomes of 28 organisms that were available were selected. These 28 organisms are listed in Table 11. In essence, the primary goal is to determine if

Table 11. The list of 28 organisms along with two-letter abbreviations used for phylogenetic profile construction.

Pan troglodytes (PT)	*Danio rerio* (DR)	*Caenorhabditis elegans* (CE)	*Trypanosoma cruzi* (TC)
Bos Taurus (BT)	*Takifugu rubripes* (FR)	*Arabidopsis thaliana* (AT)	*Tetrahymena thermophila* (TT)
Canis familiaris (CF)	*Tetraodon nigroviridis* (TN)	*Aspergillus nidulans* (AN)	*Chlamydomonas reinhardtii* (CR)
Mus musculus (MM)	*Ciona intestinalis* (CI)	*Neurospora crassa* (NC)	*Entamoeba histolytica* (EH)
Rattus norvegicus (RN)	*Drosophila melanogaster* (DM)	*Saccharomyces cerevisiae* (SC)	*Dictyostelium discoideum* (DD)
Gallus gallus (GG)	*Anopheles gambiae* (AG)	*Leishmania major* (LM)	*Phytophthora ramorum* (PR)
Xenopus tropicalis (XT)	*Apis mellifera* (AM)	*Trypanosoma brucei* (TB)	*Girardia lambia* (GL)

there exist conservation pattern(s) that can be detected through the phylogenetic profiles of cilia related proteins. By extension, if such a pattern exists, then to assess if the COP method could have contributed toward the discovery of the disesase proteins (genes) examined.

6.2 Cilial diseases

As the connection between BBS and cilia is somewhat indirect (and unclear), an obvious question to ask is whether those disease genes encoding proteins (hereafter referred to as disease proteins) that play a role in ciliated structures in humans have similar phylogenetic profiles as BBS proteins. The motile cilia from primary ciliary dyskinesia (PCD) patients have been observed with abnormal dynein arms (required for normal motile functions) and irregular cilia beat frequencies (Eley et al. 2005). Defects in three proteins (DNAH11, DNAH5, and DNAI1) have been identified to cause PCD. Moreover, defects in additional proteins cause the most common hereditary kidney diseases. The proteins causing nephronophthisis (NPHP1, NPHP2, NPHP3, NPHP4, NPHP5) and polycystic kidneys (PKD1, PKD2) have been found to localize to the renal primary cilium (Menezes et al. 2004; Otto et al. 2003; Wang et al. 2004; Yoder et al. 2002; Zhang et al. 2004). It is believed that each cilium that is generated by the principal cell of the nephron extends into the tubule lumen to perform chemo- or mechano-sensor functions. These principal cells play an important role and are responsible for water and salt absorption. Thus, one would expect that those proteins that cause PCD, NPHP, and PKD to be highly conserved in ciliated organisms and not in nonciliated organisms. However, this is not the case, as seen from Figure 13. The phylogenetic profiles of the three proteins that cause PCD are somewhat unexpected. These three proteins show overall high conservation (e-val $\leq$ 9e-35, shown in pink in Figure 13) to all 28 proteomes, even nonciliated organisms (e.g. NC and SC). Notably, none of the three proteins are

	pt_eVal	bt_eVal	cf_eVal	mm_eVal	rn_eVal	gg_eVal	xt_eVal	dr_eVal	fr_eVal	tn_eVal
DNAH11	0	0	0	0	0	0	0	0	0	0
DNAH5	0	0	0	0	0	0	0	0	0	0
DNAI1	0	0	0	0	0	0	2.00E-43	1.00E-143	0	6.00E-42
NPHP1	0	0	0	0	0	0	2.00E-152	1.00E-155	1.00E-116	2.00E-113
NPHP2	0	0	0	0	0	0	0	0	0	0
NPHP3	0	0	0	0	0	0	0	0	0	0
NPHP4	3.00E-29	2.00E-34	0	0	0	8.00E-149	0	5.00E-122	0	0
NPHP5	0	0	0	0	0	5.00E-163	3.00E-138	5.00E-74	0.02	0.009
PKD1	0	0	0	0	0	0	0	3.00E-86	0	0
PKD2	0	0	0	0	0	0	0	0	0	0

	ci_eVal	cr_eVal	dm_eVal	ag_eVal	am_eVal	ce_eVal	at_eVal	an_eVal	nc_eVal	sc_eVal
DNAH11	0	0	0	0	0	0.02	0	0	0	0
DNAH5	0	0	0	0	0	0.058	0	0	0	2.00E-112
DNAI1	0	1.00E-151	2.00E-154	3.00E-133	7.00E-17	2.00E-06	3.00E-17	2.00E-20	3.00E-19	8.00E-06
NPHP1	6.00E-08	3.00E-06	1.00E-05	2.00E-05	3.00E-19	0.042	1.00E-04	1.00E-04	5.00E-05	1.00E-04
NPHP2	1.00E-142	1.00E-52	5.00E-52	1.00E-44	1.00E-47	1.00E-20	2.00E-47	1.00E-51	3.00E-23	3.00E-16
NPHP3	1.00E-36	4.00E-35	8.00E-35	2.00E-35	1.00E-36	9.00E-17	4.00E-25	1.00E-49	2.00E-12	2.00E-04
NPHP4	0	6.1	2.5	0.002	1.00E-36	2.8	1	1.3	0.54	NOHIT!!
NPHP5	9.00E-56	0.005	0.008	0.18	0.059	0.007	2.00E-04	0.52	0.012	2
PKD1	2.00E-18	9.00E-13	2.00E-10	2.00E-10	2.00E-13	0.011	2.00E-04	0.002	0.15	1.3
PKD2	0	2.00E-65	0.43	0.007	1.00E-87	0.13	3.00E-22	5.5	1.4	0.02

	lm_eVal	tb_eVal	tc_eVal	tt_eVal	eh_eVal	dd_eVal	pr_eVal	gl_eVal
DNAH11	0.003	0	0	0	0	0	0	0
DNAH5	7.00E-05	0	0	0	0	0	0	0
DNAI1	4.00E-06	3.00E-164	2.00E-120	8.00E-153	9.00E-120	8.00E-122	1.00E-117	8.00E-62
NPHP1	4.00E-08	0.078	8.00E-08	8.00E-05	0.063	2.00E-04	3.00E-04	0.29
NPHP2	1.00E-24	2.00E-40	2.00E-19	8.00E-36	1.00E-19	5.00E-20	9.00E-21	2.00E-36
NPHP3	0.001	1.00E-16	1.00E-36	2.00E-23	3.00E-18	1.00E-18	1.00E-15	1.00E-07
NPHP4	7.5	5.00E-43	2.00E-33	1.00E-80	8.00E-04	9.00E-06	2.00E-05	0.58
NPHP5	0.48	0.029	1.3	0.003	0.091	9.00E-05	0.013	1.6
PKD1	0.002	9.00E-08	0.18	3.00E-11	0.003	0.029	0.06	0.12
PKD2	1.7	2.00E-32	2.00E-07	5.00E-08	0.25	0.44	0.063	0.1

Figure 13. Phylogenetic profiles of 10 proteins the cause cilial disorders, including PCD, NPHP and PKD, against 28 proteomes that are from different branches of the tree of life. Each protein is represented by a row and each proteome is presented by a column. The conservation match between the human protein and the corresponding proteome is measured by BLAST e-val (e.g. tb_eVal shows the e-val comparison result to proteome of TB). High conservation matches with e-val ≤ 9e-35 is shown in pink.

conserved in proteomes of CE or LM. This may be partially attributed to incomplete proteome annotation. In addition, DNAI1 orthologs are not found in the proteomes of AM, AT, AN, NC, and SC. This suggests that the function of DNAI1 is more cilia related, as DNAI1 is not found in nonciliated organisms. Similarly, the high conservation

(e-val of 0) of DNAH11 and DNAH5 in nonciliated organisms AT, AN, NC, and SC indicate that the proteins may either be multifunctional, that is, these proteins likely perform non-cilia related functions in nonciliated organisms, or that these proteins are not tightly linked to cilia function.

The phylogenetic profiles of the seven known proteins that cause common hereditary kidney diseases are somewhat random. All seven proteins are found in vertebrate proteomes (the lack of detectable orthologs, e.g. NPHP4 in proteomes of PT and BT are likely due to incomplete annotation). Based on the phylogenetic profiles of the five proteins that cause NPHP, at least two groups or clusters can be made. NPHP1 is not found in the proteomes of invertebrates or protozoans, indicating that the protein is not an essential eukaryotic protein. The remaining four proteins exhibit intermittent conservation to the proteomes of invertebrates and protozoans. Thus, there is no conserved pattern among the phylogenetic profile of these four proteins. A similar non-conservation pattern is also observed in the two proteins causing PKD. Like NPHP1, PKD1 orthologs are only found in the proteomes of vertebrates while PKD2 show only partial conservation to proteomes of some invertebrates.

In light of the phylogenetic profiles of ten proteins involved in cilial diseases evaluated above, the conservation patterns of BBS proteins seem even more remarkable. Overall, the three proteins involved in PCD exhibit strong conservation to the proteomes of the 28 organisms surveyed. This is in contrast to the conservation pattern observed for those proteins involved in NPHP and PKD, which only have intermittent conservation to the proteomes of invertebrates and protozoans.

6.3 Retinal diseases

Retinis pigmentosa (RP) is caused by progressive degeneration of photoreceptors. Photoreceptor cells are photosensitive neurons that transduce light signals into electrical signals so that these signals can be transmitted to the brain. Each

photoreceptor cell is composed of four major components: an outer segment that is responsible for light absorption and electrical signal generation; an inner segment that produces energy and synthesizes proteins; a cell body (soma); and an axon for transmitting electrical signals. Within the inner segment lies a connecting cilium that connects to the outer segment. It is through this narrow cilium that all the proteins (e.g. visual pigments such as rhodopsins) needed by the outer segment are transported.

It is estimated that the outer segment, which itself is a modified cilium, experiences a high rate (10%) of protein turnover. Thus, given the importance of cilia to photoreceptors, phylogenetic profiles of disease proteins causing retinal disease were constructed. The retinal phylogenetic profiles were constructed based on disease proteins annotated in the Retinal Information Network against the proteomes of the 28 organisms listed in Table 11. The Retinal Information Network (RetNet, http://www.sph.uth.tmc.edu/Retnet/) is a comprehensive resource that assembles all disease genes (proteins) causing inherited retinal disorders. Figure 14 shows the phylogenetic profiles of 114 unique retinal proteins ordered by their degree of conservation with the highest conserved proteins on top. High conservation matches (sequence alignments at an e-val $\leq$ 9e-35) are highlighted in pink.

Overall, some proteins (e.g. ABCC6, PEX1) seem to be essential for all eukaryotes while other proteins are only found in the proteomes of vertebrates (e.g. RBP4, RP1). Clearly, no distinct conservation pattern was observed in the phylogenetic profiles of the 114 proteins. However, thinking that these retinal phylogenetic profiles are made up of many separate disorders, a closer analysis of the phylogenetic profiles of Usher Syndrome and Leber congenital amaurosis (LCA) were performed. Usher Syndrome is the most common inherited disorder that results in combined deafness and RP. Individuals diagnosed with LCA suffer from severe vision loss at birth. The phylogenetic profiles Usher Syndrome and LCA proteins are shown in Figures 15 and 16. For Usher Syndrome disease proteins, all are conserved in vertebrate proteomes (low

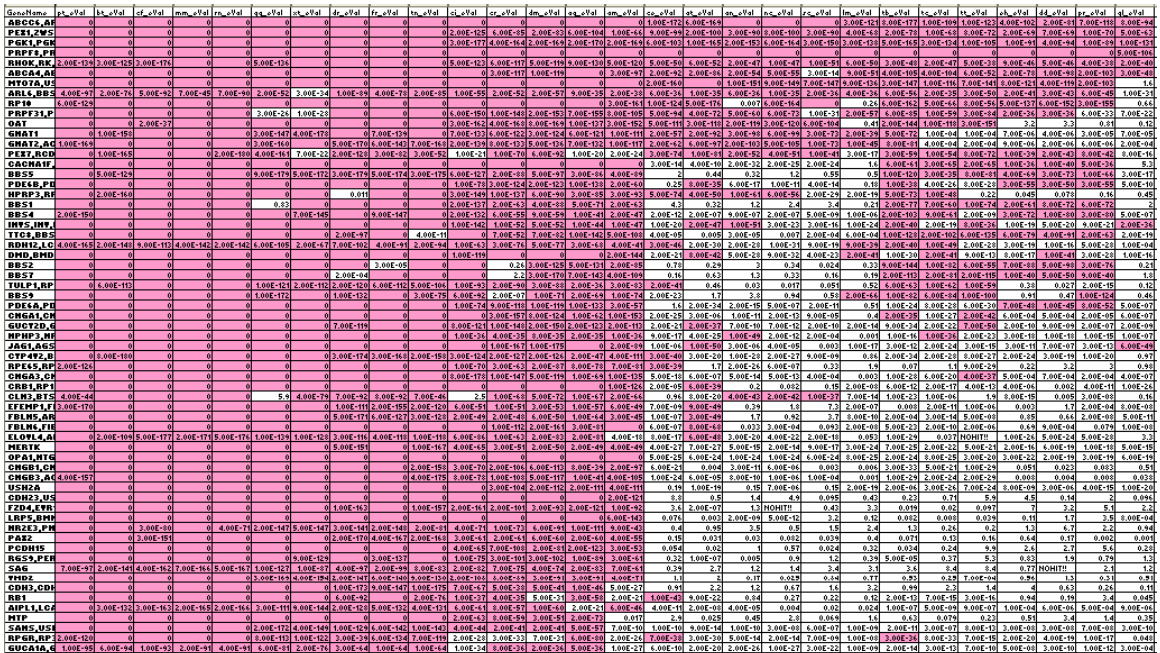


Figure 14. Phylogenetic profiles of 114 proteins that cause retinal disorders, including RP, Usher Syndrome, and Leber congenital amaurosis, against 28 proteomes that are from different branches of the tree of life. Each protein is represented by a row and each proteome is presented by a column. The conservation match between the human protein and the corresponding proteome is measured by BLAST e-val (e.g. tb_eVal shows the e-val comparison result to proteome of TB). High conservation matches with e-val ≤ 9e-35 is shown in pink.

conservation matches of USH3A to RN and TN are likely due to incomplete proteome annotation. Most are conserved in invertebrate proteomes and only myosin 7 is conserved in all 28 proteomes. The LCA disease proteins are conserved in all vertebrate

and most invertebrate proteomes. Intermittent conservation is observed in the proteomes of microbial eukaryotes. In sum, no disease-specific phylogenetic conservation patterns were detected in these diseases. Additional rearrangement of the phylogenetic profiles based on disease classification (e.g. Usher Syndrome) or mode of inheritance (e.g. recessive) did not yield any conservation pattern as observed for BBS proteins. Thus, similar to the phylogenetic profiles of proteins involved in PCD, PKD, and NPH, the retinal phylogenetic profiles failed to yield "unique" conservation pattern(s) based on either disease or mode of inheritance classifications.

	pt_eVal	bt_eVal	cf_eVal	mm_eVal	rn_eVal	gg_eVal	xt_eVal	dr_eVal	fr_eVal	tn_eVal
USH1B	0	0	0	0	0	0	0	0	0	0
USH1C	0	0	0	0	0	0	3.00E-81	3.00E-35	0	1.00E-121
USH1D	0	0	0	0	0	0	0	0	0	0
USH1F	0	0	0	0	0	0	0	0	0	0
USH1G	0	0	0	0	0	2.00E-172	4.00E-149	1.00E-129	6.00E-142	1.00E-143
USH2A	0	0	0	0	0	0	0	0	0	0
USH2C	0	0	0	0	0	0	0	0	0	0
USH3A	9.00E-123	5.00E-115	2.00E-114	2.00E-112	5.00E-34	9.00E-93	8.00E-87	4.00E-77	1.00E-67	9.00E-16

	ci_eVal	cr_eVal	dm_eVal	ag_eVal	am_eVal	ce_eVal	at_eVal	an_eVal	nc_eVal	sc_eVal
USH1B	0	0	0	0	0	2.00E-160	0	1.00E-151	9.00E-149	7.00E-147
USH1C	1.00E-14	1.00E-36	3.00E-30	3.00E-21	1.00E-15	0.001	0.019	0.12	0.023	1.3
USH1D	0	0	0	0	2.00E-121	8.8	0.5	1.4	4.9	0.095
USH1F	4.00E-65	7.00E-108	2.00E-81	2.00E-123	3.00E-53	0.054	0.02	1	0.57	0.024
USH1G	4.00E-44	2.00E-41	2.00E-41	5.00E-57	7.00E-10	1.00E-10	9.00E-14	1.00E-10	3.00E-08	6.00E-07
USH2A	0	3.00E-104	2.00E-112	2.00E-111	4.00E-111	0.19	1.00E-19	0.15	7.00E-06	0.15
USH2C	1.00E-18	2.00E-11	9.00E-10	3.00E-11	8.00E-12	3.3	6.00E-09	0.53	4.2	0.23
USH3A	0.79	1.1	6.9	3.5	3.2	2	3.6	2.7	3.3	4.6

	lm_eVal	tb_eVal	tc_eVal	tt_eVal	eh_eVal	dd_eVal	pr_eVal
USH1B	9.00E-136	3.00E-147	1.00E-116	7.00E-141	8.00E-121	4.00E-119	2.00E-103
USH1C	0.92	7.00E-06	1.1	0.06	0.51	0.53	0.64
USH1D	0.43	0.23	0.71	5.9	4.5	0.14	2
USH1F	0.32	0.034	0.24	9.9	2.6	2.7	5.6
USH1G	1.00E-09	2.00E-11	3.00E-07	8.00E-13	3.00E-08	3.00E-08	7.00E-08
USH2A	2.00E-19	2.00E-06	3.00E-26	7.00E-24	8.00E-09	3.00E-06	4.00E-15
USH2C	1.4	0.086	0.071	2.00E-13	0.27	1.8	4.8
USH3A	1.5	1.7	4.9	NOHIT!!	0.073	0.61	2.9

Figure 15. Phylogenetic profiles of 8 proteins that cause Usher Syndrome against 28 proteomes that are from different branches of the tree of life. Each protein is represented by a row and each proteome is presented by a column. The conservation match between the human protein and the corresponding proteome is measured by BLAST e-val (e.g. tb_eVal shows the e-val comparison result to proteome of TB). High conservation matches with e-val $\leq$ 9e-35 is shown in pink.

If nothing else, the retinal phylogenetic profiles highlight the effectiveness of BBS candidate gene prioritization. Of the ten proteins that are highly conserved in protozoans (e.g. TB, CR) and are not conserved in fungi (e.g. AN, NC) or the land plant AT, six of them are BBS proteins (BBS1, BBS2, BBS4, BBS5, BBS7, BBS8). Notably BBS3 is considered highly conserved in nonciliated organisms, based on e-val threshold of 9e-35, and thus was not included in this group. Likewise, this group excluded BBS6, BBS10, and BBS11 as these proteins appear to be vertebrate-specific.

	pt_eVal	bt_eVal	cf_eVal	mm_eVal	rn_eVal	gg_eVal	xt_eVal	dr_eVal	fr_eVal	tn_eVal
RP10	6.00E-129	0	0	0	0	0	0	0	0	0
RDH12,LCA	4.00E-165	2.00E-148	9.00E-113	4.00E-142	2.00E-142	6.00E-105	2.00E-67	7.00E-102	4.00E-91	2.00E-94
TULP1,RP1	0	6.00E-113	0	0	0	1.00E-121	2.00E-112	2.00E-120	6.00E-112	5.00E-106
GUCY2D,GU	0	0	0	0	0	0	0	7.00E-119	0	0
CRB1,RP12	0	0	0	0	0	0	0	0	0	0
RPE65,RP2	2.00E-126	0	0	0	0	0	0	0	0	0
AIPL1,LCA4	0	3.00E-132	3.00E-163	2.00E-165	2.00E-166	3.00E-111	9.00E-144	2.00E-128	5.00E-132	4.00E-131
RPGRIP1,L	0	0	0	0	0	3.00E-90	4.00E-122	2.00E-06	5.00E-89	1.00E-114
CRX,CORD	7.00E-68	6.00E-98	4.00E-113	3.00E-94	3.00E-113	5.00E-17	8.00E-57	5.00E-56	2.00E-49	1.00E-46
LRAT	1.00E-121	2.00E-102	3.00E-106	1.00E-91	5.00E-91	6.00E-76	4.00E-11	1.00E-66	5.00E-67	2.00E-67

	ci_eVal	cr_eVal	dm_eVal	ag_eVal	am_eVal	ce_eVal	at_eVal	an_eVal	nc_eVal	sc_eVal
RP10	0	0	0	0	3.00E-161	1.00E-124	5.00E-176	0.007	6.00E-164	0
RDH12,LCA	1.00E-63	3.00E-76	5.00E-77	3.00E-68	4.00E-41	3.00E-46	2.00E-30	2.00E-28	1.00E-31	9.00E-19
TULP1,RP1	1.00E-93	2.00E-90	3.00E-88	2.00E-36	3.00E-83	2.00E-41	0.46	0.03	0.017	0.051
GUCY2D,GU	8.00E-121	1.00E-148	2.00E-150	2.00E-123	2.00E-113	2.00E-21	2.00E-37	7.00E-10	7.00E-12	2.00E-10
CRB1,RP12	0	0	0	0	1.00E-126	2.00E-05	6.00E-39	0.2	0.082	0.15
RPE65,RP2	1.00E-70	3.00E-63	2.00E-87	8.00E-78	7.00E-81	3.00E-39	1.7	2.00E-26	6.00E-07	0.33
AIPL1,LCA4	6.00E-61	8.00E-57	1.00E-60	2.00E-21	6.00E-46	4.00E-11	2.00E-08	4.00E-05	0.004	0.02
RPGRIP1,L	1.00E-114	5.00E-06	5.00E-07	2.00E-08	8.00E-15	8.00E-07	5.00E-08	2.00E-04	6.00E-10	7.00E-08
CRX,CORD	6.00E-27	8.00E-24	3.00E-19	8.00E-27	3.00E-20	8.00E-06	3.00E-07	0.001	4.00E-07	1.00E-04
LRAT	5.1	0.076	4	5.9	0.17	8.00E-04	0.19	3.5	0.86	1.6

	lm_eVal	tb_eVal	tc_eVal	tt_eVal	eh_eVal	dd_eVal	pr_eVal	gl_eVal
RP10	0.26	6.00E-162	5.00E-66	8.00E-56	5.00E-137	6.00E-152	3.00E-155	0.66
RDH12,LCA	9.00E-39	2.00E-40	1.00E-49	2.00E-28	3.00E-19	1.00E-16	5.00E-28	1.00E-04
TULP1,RP1	0.52	6.00E-63	1.00E-62	1.00E-59	0.38	0.027	2.00E-15	0.12
GUCY2D,GU	2.00E-14	9.00E-34	2.00E-22	7.00E-50	2.00E-10	9.00E-09	2.00E-07	2.00E-09
CRB1,RP12	2.00E-08	6.00E-12	2.00E-17	4.00E-13	4.00E-06	0.002	4.00E-11	1.00E-26
RPE65,RP2	1.9	0.07	1.1	9.00E-29	0.22	3.2	3	0.98
AIPL1,LCA4	0.024	1.00E-07	5.00E-09	9.00E-07	1.00E-04	6.00E-06	5.00E-04	9.00E-06
RPGRIP1,L	7.00E-08	1.00E-05	4.00E-18	0.006	2.00E-06	3.00E-09	4.00E-06	8.00E-05
CRX,CORD	1.2	0.13	9.5	0.23	5.7	7.5	5.4	2.4
LRAT	0.85	9.00E-07	0.57	6.4	0.61	0.79	8.2	0.43

Figure 16. Phylogenetic profiles of 10 proteins that cause Leber congenital amaurosis against 28 proteomes that are from different branches of the tree of life. Each protein is represented by a row and each proteome is presented by a column. The conservation match between the human protein and the corresponding proteome is measured by BLAST e-val (e.g. tb_eVal shows the e-val comparison result to proteome of TB). High conservation matches with e-val $\leq$ 9e-35 is shown in pink.

6.4 Charcot-Marie Tooth Disease

The evaluation of phylogenetic profiles of cilia-related disease proteins (sections 6.2 and 6.3) failed to identify any conservation pattern(s) based on disease, disease subtype, and mode of inheritance. Thinking that perhaps ciliated structures are evolutionarily highly conserved, an evaluation of the phylogenetic profiles of disease proteins affecting non-ciliated structure was performed. Charcot-Marie Tooth (CMT) is the most commonly inherited neurological disorder. CMT is characterized by progressive deterioriation of muscles in the limbs. This is due to lack of (electrical) signal (conduction) preservation in the axons of neurons as a result of loss of myelin shealth (insulation) or components of axon. The phylogenetic profiles of CMT proteins arranged by the disease subtype is shown in Figure 17. Most CMT proteins are conserved in vertebrate proteomes. Two proteins, kinesin family member 1B (CMT2A) and Glycyl-tRNA synthetase (CMT2D), are conserved in all 28 organisms. Interestingly, Ras-associated protein RAB7 (CMT2B) is only found in humans. Thus, similar to the phylogenetic profiles of the cilia-related proteins examined in Sections 6.2 and 6.3, the phylogenetic profiles of CMT proteins do not share conservation pattern(s) based on disease, disease subtype or mode of inheritance.

6.5 Conclusions

By examining the phylogenetic profiles of 124 proteins (including BBS proteins) involved in cilia function, only a subset of BBS proteins (BBS1, BBS2, BBS4, BBS5, BBs7, BBS8) exhibit a ‘specialized’ conservation pattern. This pattern of conservation in ciliated organisms, particularly those of microbial eukaryotes (e.g. CR, TB), and non-conservation in nonciliated organisms was not observed in other disease proteins evaluated. This can be attributed to several factors. First, the number of genes (proteins) that cause any particular disease may not be sufficient for conservation pattern

	pt_eVal	bt_eVal	gg_eVal	cf_eVal	mm_eVal	rn_eVal	xt_eVal	dr_eVal	fr_eVal	tn_eVal	ci_eVal
CMT1A	7.00E-69	1.00E-62	9.00E-49	9.00E-65	1.00E-60	7.00E-61	1.00E-47	4.00E-35	1.00E-29	2.00E-35	0.037
CMT1B	1.00E-106	3.00E-99	3.00E-25	3.00E-90	7.00E-101	3.00E-100	9.00E-66	8.00E-39	2.00E-17	1.00E-39	0.72
CMT1C	5.00E-47	5.00E-40	5.00E-21	3.00E-57	8.00E-40	1.00E-40	4.2	6.00E-08	0.27	0.056	3.8
CMT1D	0	0	1.00E-56	0	0	0	5.00E-130	3.00E-124	8.00E-83	4.00E-83	7.00E-34
CMT1E	7.00E-69	1.00E-62	9.00E-49	9.00E-65	1.00E-60	7.00E-61	1.00E-47	4.00E-35	1.00E-29	2.00E-35	0.037
CMT1F	0	0	8.00E-167	1.00E-174	0	0	3.00E-131	2.00E-109	2.00E-98	1.00E-94	2.00E-59
CMT2A	0	0	0	0	0	0	0	0	0	0	0
CMT2A	0	1.00E-175	0	0	0	0	0	0	0	0	0
CMT2B	4.4	NOHIT!!	NOHIT!!	8.8	3.5	7.4	NOHIT!!	0.92	0.8	7	3
CMT2B1	8.00E-141	0	3.00E-129	0	0	0	0	1.00E-130	5.00E-158	1.00E-156	7.00E-49
CMT2D	3.00E-109	0	0	0	0	0	0	0.007	0	0	0
CMT2E	0	0	8.00E-167	1.00E-174	0	0	3.00E-131	2.00E-109	2.00E-98	1.00E-94	2.00E-59
CMT2F	2.00E-59	5.00E-51	1.00E-73	2.00E-98	1.00E-93	1.00E-90	3.00E-77	2.00E-66	2.00E-62	4.00E-60	3.00E-32
CMT2I	1.00E-106	3.00E-99	3.00E-25	3.00E-90	7.00E-101	3.00E-100	9.00E-66	8.00E-39	2.00E-17	1.00E-39	0.72
CMT2J	1.00E-106	3.00E-99	3.00E-25	3.00E-90	7.00E-101	3.00E-100	9.00E-66	8.00E-39	2.00E-17	1.00E-39	0.72
CMT2K	0	5.00E-126	1.00E-161	0	0	0	4.00E-159	1.00E-141	2.00E-96	5.00E-130	6.00E-04
CMT2L	2.00E-105	2.00E-100	1.00E-69	3.00E-67	4.00E-99	4.00E-100	2.00E-21	3.00E-50	3.00E-46	4.00E-48	4.00E-20
CMT4A	0	5.00E-126	1.00E-161	0	0	0	4.00E-159	1.00E-141	2.00E-96	5.00E-130	6.00E-04
CMT4B1	0	0	0	0	0	0	0	0	0	0	0
CMT4B2	0	0	0	0	0	0	0	0	0	0	0
CMT4D	2.00E-117	0	0	0	0	0	9.00E-165	1.00E-130	1.00E-146	2.00E-138	8.00E-67
CMT4E	0	0	1.00E-56	0	0	0	5.00E-130	3.00E-124	8.00E-83	4.00E-83	7.00E-34
CMT4F	3.00E-57	0	2.00E-43	0	0	0	5.00E-54	8.00E-59	2.00E-32	9.00E-41	7.00E-16
CMTX	4.00E-159	2.00E-144	3.00E-101	5.00E-157	5.00E-157	5.00E-157	2.00E-68	2.00E-96	5.00E-101	1.00E-101	3.00E-40

	ci_eVal	dm_eVal	ag_eVal	am_eVal	ce_eVal	at_eVal	eh_eVal	dd_eVal	an_eVal	nc_eVal	sc_eVal
CMT1A	0.037	4.9	0.43	0.82	1.3	5	2.3	1.5	7.1	NOHIT!!	7.4
CMT1B	0.72	0.45	0.086	0.076	0.011	4	2.9	2.5	2.4	3.9	5.4
CMT1C	3.8	0.13	0.004	NOHIT!!	0.29	3.3	2.00E-04	0.008	0.69	2.5	2.6
CMT1D	7.00E-34	1.00E-52	7.00E-53	1.00E-51	7.00E-45	1.00E-09	2.00E-16	3.00E-19	2.00E-16	1.00E-17	9.00E-19
CMT1E	0.037	4.9	0.43	0.82	1.3	5	2.3	1.5	7.1	NOHIT!!	7.4
CMT1F	2.00E-59	9.00E-28	1.00E-21	1.00E-22	2.00E-31	4.00E-06	2.00E-06	3.00E-04	7.00E-05	2.00E-04	4.00E-04
CMT2A	0	0	0	0	0	1.00E-65	1.00E-54	3.00E-162	3.00E-129	2.00E-126	2.00E-55
CMT2A	0	0	0	0	2.00E-113	6.00E-05	5.00E-05	0.006	0.012	0.001	0.009
CMT2B	3	1.1	3.1	NOHIT!!	3.2	9.7	7.2	NOHIT!!	NOHIT!!	3.3	4.6
CMT2B1	7.00E-49	1.00E-76	5.00E-63	5.00E-47	3.00E-44	4.00E-06	3.00E-08	2.00E-07	9.00E-08	2.00E-07	1.00E-06
CMT2D	0	0	0	1.00E-80	0	0	1.00E-156	0	0	0	2.00E-171
CMT2E	2.00E-59	9.00E-28	1.00E-21	1.00E-22	2.00E-31	4.00E-06	2.00E-06	3.00E-04	7.00E-05	2.00E-04	4.00E-04
CMT2F	3.00E-32	5.00E-24	1.00E-26	1.00E-23	6.00E-14	0.017	0.037	0.35	0.12	0.42	0.092
CMT2I	0.72	0.45	0.086	0.076	0.011	4	2.9	2.5	2.4	3.9	5.4
CMT2J	0.72	0.45	0.086	0.076	0.011	4	2.9	2.5	2.4	3.9	5.4
CMT2K	6.00E-04	3.00E-28	1.00E-24	0.002	3.00E-04	1.00E-16	0.006	0.011	4.00E-04	0.065	4.00E-04
CMT2L	4.00E-20	1.00E-17	5.00E-14	2.00E-13	1.00E-08	0.18	0.51	0.19	0.7	0.1	4.7
CMT4A	6.00E-04	3.00E-28	1.00E-24	0.002	3.00E-04	1.00E-16	0.006	0.011	4.00E-04	0.065	4.00E-04
CMT4B1	0	0	0	0	2.00E-135	5.00E-84	6.00E-80	1.00E-112	1.3	1.5	2.00E-69
CMT4B2	0	0	0	0	8.00E-119	6.00E-25	2.00E-32	2.00E-36	5.00E-13	3.00E-13	5.00E-15
CMT4D	8.00E-67	8.00E-62	1.00E-58	2.00E-63	1.00E-42	7.00E-32	0.16	6.00E-42	0.003	0.074	0.005
CMT4E	7.00E-34	1.00E-52	7.00E-53	1.00E-51	7.00E-45	1.00E-09	2.00E-16	3.00E-19	2.00E-16	1.00E-17	9.00E-19
CMT4F	7.00E-16	9.00E-18	1.00E-16	2.00E-25	1.00E-23	1.00E-57	4.00E-08	5.00E-06	7.00E-07	8.00E-24	9.00E-10
CMTX	3.00E-40	NOHIT!!	2.4	0.96	1.2	0.14	1.1	1.7	1.2	0.89	1.2

	eh_eVal	dd_eVal	pr_eVal	lm_eVal	tb_eVal	tc_eVal	tt_eVal	cr_eVal	gl_eVal
CMT1A	2.3	1.5	0.51	1.5	1.2	7.8	0.64	0.89	3.4
CMT1B	2.9	2.5	0.13	NOHIT!!	4.6	8	7.6	5.9	5.7
CMT1C	2.00E-04	0.008	4.7	4.7	1	NOHIT!!	0.03	0.57	NOHIT!!
CMT1D	2.00E-16	3.00E-19	6.00E-16	0.25	0.004	0.16	1.00E-18	0.002	7.00E-04
CMT1E	2.3	1.5	0.51	1.5	1.2	7.8	0.64	0.89	3.4
CMT1F	2.00E-06	3.00E-04	1.00E-04	3.00E-04	1.00E-07	8.00E-07	5.00E-06	3.00E-06	4.00E-05
CMT2A	1.00E-54	3.00E-162	1.00E-95	3.00E-89	2.00E-82	2.00E-79	1.00E-86	1.00E-77	5.00E-90
CMT2A	5.00E-05	0.006	0.25	0.023	0.04	0.2	0.024	0.031	0.048
CMT2B	7.2	NOHIT!!	NOHIT!!	1.3	NOHIT!!	5.1	1.7	4.9	NOHIT!!
CMT2B1	3.00E-08	2.00E-07	5.00E-06	1.00E-08	6.00E-08	2.00E-06	7.00E-09	4.00E-08	4.00E-06
CMT2D	1.00E-156	0	7.00E-176	2.00E-143	6.00E-144	7.00E-145	1.00E-167	9.00E-76	8.00E-143
CMT2E	2.00E-06	3.00E-04	1.00E-04	3.00E-04	1.00E-07	8.00E-07	5.00E-06	3.00E-06	4.00E-05
CMT2F	0.037	0.35	0.27	0.62	1.5	0.059	1	0.005	0.47
CMT2I	2.9	2.5	0.13	NOHIT!!	4.6	8	7.6	5.9	5.7
CMT2J	2.9	2.5	0.13	NOHIT!!	4.6	8	7.6	5.9	5.7
CMT2K	0.006	0.011	0.007	0.019	0.009	0.021	4.00E-05	0.076	0.47
CMT2L	0.51	0.19	0.03	0.44	0.072	0.042	2.1	0.006	0.98
CMT4A	0.006	0.011	0.007	0.019	0.009	0.021	4.00E-05	0.076	0.47
CMT4B1	6.00E-80	1.00E-112	1.00E-106	3.00E-47	3.00E-46	4.00E-54	7.00E-93	2.4	6.00E-49
CMT4B2	2.00E-32	2.00E-36	1.00E-36	8.00E-28	3.00E-24	1.00E-27	7.00E-35	1.00E-12	2.00E-26
CMT4D	0.16	6.00E-42	0.028	1.00E-04	0.023	0.2	0.039	3.00E-05	0.4
CMT4E	2.00E-16	3.00E-19	6.00E-16	0.25	0.004	0.16	1.00E-18	0.002	7.00E-04
CMT4F	4.00E-08	5.00E-06	2.00E-12	0.002	4.00E-25	7.00E-27	6.00E-07	1.00E-06	8.00E-06
CMTX	1.1	1.7	5	0.27	3.1	1.4	1.3	8.8	2.2

Figure 17. Phylogenetic profiles of the proteins that cause Charcot-Marie Tooth disease against 28 proteomes that are from different branches of the tree of life. Each protein is represented by a row and each proteome is presented by a column. The conservation match between the human protein and the corresponding proteome is measured by BLAST e-val (e.g. tb_eVal shows the e-val comparison result to proteome of TB). High conservation matches with e-val $\leq$ 9e-35 is shown in pink.

evaluation. The comparative genomic approach of BBS candidate gene prioritizations relied on at least six pre-existing BBS genes (protein). Diseases such as PCD and PKD have less than four genes identified to date. Additional disease gene discoveries may allow for better conservation pattern detection. Second, the exact functions of BBS proteins remain poorly understood. Thus, the phylogenetic profile of BBS proteins may reflect a property (e.g. clinical, mechanistic) that has not yet been uncovered. A better understanding of why a subset of BBS proteins gives such striking conservation pattern may also aid the analysis of phylogenetic profiles of other disease proteins. Third, the phylogenetic profiles were constructed based on 28 organisms that were available at the start of the study. The incorporation of additional proteomes that have since been completed (updated) may provide additional insights into other disease proteins. Finally, the phylogenetic profiles constructed here provide only a partial glimpse of the disease proteins. Specifically, it relied on primary sequence conservation. It is well-known that the sequence conservation among members of the globin protein family member can be rather low but that the globins share similar three dimensional structural conformations. So, the lack of conservation patterns for the other disease proteins (based on phylogenetic profiles) does not demonstrate that the COP method is not generalizable. It simply requires additional investigations into why this particular approach worked so well for BBS before it can be applied toward other diseases.

CHAPTER 7
CONCLUSIONS AND FUTURE WORK

7.1 Conclusions

In the last half century, many scientific discoveries and technological advances have helped to pave the way toward greater understanding of the genetic components of human diseases. One of the first steps toward this is the identification of those genes or genetic elements, that cause human disorders. This process is also known as disease gene discovery. There are two major strategies toward genetic dissection of human disorders: (1) knowledge-dependent candidate gene approach, and (2) knowledge-independent positional cloning approach.

This thesis addressed disease gene discovery as it pertains to a genetically heterogeneous disorder known as Bardet-Biedl syndrome (BBS). Utilizing (1) positional cloning, (2) a new comparative genomic methodology, Computational Orthologous Prioritization (COP), developed to prioritize candidate genes, and (3) functional annotation, only one gene was prioritized in the *BBS3* critical interval. Mutational analysis determined that this candidate gene, *ARL6*, was mutated in all BBS3 patients. Similarly, the identification of *BBS11* was the result of the integration of multiple sources of functional information. Based on (1) genetic linkage mapping from high-density SNP arrays, (2) known animal models of candidate genes in the the critical interval, (3) gene expression profile of the candidate genes, (4) functional studies indicating BBS involvement in apoptosis, and (5) additional sources of functional information to together determined *TRIM32* as the best candidate gene. Indeed, a missense mutation in *TRIM32*

was detected in all BBS11 patients. This BBS mutation fell in the N-terminal B-box domain of the TRIM32 protein, which is different from the missense mutation in the C-terminal NHL domain that has been shown to cause LGMD2H. Together, the identification of *BBS3* and *BBS11* described here emphasizes the importance of integration of multiple sources of functional informations toward disease gene discovery.

While the identification of *BBS3* and *BBS11* have occurred only in the last two years, of the eleven BBS genes identified to date (as *BBS10* was identified during the publication of *BBS11* [Stoetzel et al. 2006]), *ARL6* and *TRIM32* are considered to be more functionally well-characterized than the other nine. This can be attributed to the fact that both *ARL6* and *TRIM32* belong to moderate-size protein families. Thus, existing knowledge about the ARF/SAR protein family and the TRIM protein family can be quickly extrapolated to aid the functional dissection of the pathophysiology of BBS. Furthermore, the existence of common protein domains (e.g. coiled-coil, tetratricopeptide repeats, and chaperonin doamins) in the eleven known BBS genes may also provide additional clues as to other BBS genes, as there are still 30% of BBS patients, of which no genetic defects have been determined.

The phylogenetic profile of the eleven BBS genes presents an intriguing piece of the puzzle toward understanding BBS pathophysiology. Eight BBS proteins (BBS1, BBS2, BBS3, BBS4, BBS5, BBS7, BBS8, and BBS9) are highly conserved in the proteomes of microbial eukaryotic organisms, all except GL, while the other three BBS proteomes (BBS6, BBS10, and BBS11) are only conserved in the proteomes of vertebrate organisms. One hypothesis can be proposed to explain the uniqueness of the phylogenetic profiles of all eleven BBS proteins. This hypothesis takes advantage of the

fact that BBS patients exhibit a very specialized and progressive set of phenotypes. Thus, the phylogenetic profiles may indicate that BBS proteins play very specialized roles. To date, ARL6 represents an interesting outlier, as it is conserved both in ciliated and nonciliated organisms. It is likely that this protein plays a broader or more multifunctional role than the other BBS proteins, given the high conservation in nonciliated organisms. This role is somewhat fitting considering that other ARF/SAR protein family members have been implicated in the regulation of vesicle assembly and intracellular trafficking. The six BBS proteins that show high conservation in microbial ciliated eukaryotes and not in nonciliated organisms suggest that their functions are tightly linked to ciliated structures but not absolutely essential for ciliogenesis. This idea is supported by several BBS mouse models. Normal global ciliogenesis was observed in all mouse models, the lone exception being the loss of the flagellum found in the spermatozoa. Finally, the three vertebrate-specific proteins indicate that these proteins are newly-evolved proteins that likely function in regulatory roles, perhaps in vertebrate ciliation. This is supported by protein sequence similarity of BBS6 and BBS10 to chaperonin domains and BBS11 to E3 ubiqutin ligases. Over a short span of sixteen years, eleven genes have been discovered to cause the same disease – BBS. The phylogenetic profiles of the BBS proteins provide only one viewpoint of BBS. It is anticipated that additional functional studies over the next sixteen years (and beyond) will provide a clearer picture of the true pathophysiology of BBS.

7.2 Future work

The development of a novel application of comparative genomic approach (Computational Orthologous Prioritization – COP) toward candidate gene prioritization has been outlined in this thesis and shown to be powerful for the identification of BBS genes. The examination of phylogenetic profiles of 100+ proteins involved in cilia related diseases such as PCD and RP and a non-ciliated disorder (CMT) failed to detect any conserved phylogenetic pattern. Thus, the conservation of the six BBS proteins to the proteomes of microbial ciliated eukaryotes and not to the proteomes of nonciliated eukaryotes seem to be a specialized feature not detected in the phylogenetic profiles of the other cilia related disease proteins. Additionally, it is worthwhile to note that the COP approach was unable to prioritize the recent discovery efforts of *BBS10* and *BBS11* as both genes are only found in vertebrate organisms.

The lack of a conservation pattern in the other cilia related proteins does not suggest that the COP method is not generalizable. What it does highlight is that without the incorporation of multiple sources of (disease-specific) functional information, disease gene discovery can be very challenging. The power of the COP approach toward the identification of *BBS3* relied primarily on three major sources of functional information: 1) the phylogenetic profiles of previously identified genes; 2) the functional connection to cilia; and 3) additional information from functional sources such as phenotypes of animal models. The pathophysiologies of different disorders varies from disease to disease, therefore, it is plausible that disease gene discovery of other diseases may not rely on conserved phylogenetic profiles.

There are several ways that can perhaps fine-tune the COP method to explore other biological questions and even to extend the applicability of the method toward other diseases. First, the parameters used for the COP method should be evaluated for its usefulness and importance. These include altering the thresholds, establishing species-specific thresholds, or doing away with thresholds and instead focus on a rank order. By analyzing the different (sub-) sets of genes obtained from the various parameters and correlating these genes with functional information, specialized properties may be uncovered. Additionally, the COP method currently implement a one-way BLAST as its measure of conservation, this may lead to false positives as paralogs may give the false impression that a true ortholog exists. One way to address this deficiency is to implement reciprocal BLAST analysis. Second, one unique property of the COP method is the utilization of either a training gene set (e.g. previously known genes) and/or a functional feature (e.g. cilia) from which to select the positive and/or negative filter set(s) as well as to establish similarity analysis thresholds. Perhaps the exploration of different training gene sets and/or functional features may reveal previously undetectable pattern. Third, the COP method stresses the inclusion of multiple organisms in the selection of positive and/or negative filter set(s) to increase the sensitivity of the approach. By examining the inclusion and/or exclusion of genes based on different combinations of species, one can achieve additional enrichment. For instance, the candidate gene prioritization of the *BBS3* interval relied on the use of two trypanosome proteomes (TB and TC). The evolutionary distance between these two organisms is less than 100 million years apart. One would expect that the use of just one organism would be sufficient, yet additional enrichment is obtained with the use of both. This may be partly explained by the

incomplete proteome annotation during the course of the study, as the genome sequence of the trypanosomes were still unpublished then. Another explanation is that the proteomes of the two species were sufficiently different to attain enrichment. Thus, additional analysis of the gene set(s) that result from the inclusion of closely related species may aid future use of the COP method. Finally, the success of the COP method for the prioritization of candidate BBS genes relied on sequence comparisons at the protein level. However, as protein-coding genes/elements account for only ~2% of the entire human genome, the expansion of the COP method toward the detection of non-protein-coding genetic elements may augment the power of the COP method. This may require more efforts as sequence conservations at the nucleotide level are required. The primary difference lies in the the alphabet size between nucleotides (4) and amino acids (20). A larger alphabet may be more sensitive as it allows for some degeneracy (e.g. substitution of one polar amino acid for another). One potential approach would be to use closely related organisms, such as those of the trypanosomes (TB and TC) in combination with a more stringent sequence similarity tool (e.g. BLAT) in order to identify high conservation regions at the nucleotide level.

APPENDIX A

GENOMEWIDE CILIA SET

Appendix A lists the "cilia" set of genes (G_{c+}, 1,588), including the Ensembl gene identifier (ID), gene symbol, and gene description, that is highly conserved in all four ciliated organisms CI, TB, TC, and CI. Those 114 genes (G_{c+-}), "restricted cilia set", that are highly conserved in all four ciliated organisms (CI, TB, TC, and CI) and not conserved in two nonciliated organisms SC and AT are listed in bold.

Ensembl GeneID	Gene Symbol	Gene Description
ENSG0000 0001626	CFTR	Cystic fibrosis transmembrane conductance regulator (CFTR) (cAMP- dependent chloride channel). [Source:Uniprot/SWISSPROT;Acc:P13569]
ENSG0000 0002079	MYH16	"myosin, heavy polypeptide 16 (MYH16) on chromosome 7 [Source:RefSeq_dna;Acc:NR_002147]"
ENSG0000 0002746	HECW1	NEDD4-like ubiquitin-protein ligase 1 [Source:RefSeq_peptide;Acc:NP_055867]
ENSG0000 0003989	SLC7A2	Low-affinity cationic amino acid transporter-2 (CAT-2) (CAT2). [Source:Uniprot/SWISSPROT;Acc:P52569]
ENSG0000 0004059	ARF5	ADP-ribosylation factor 5. [Source:Uniprot/SWISSPROT;Acc:P84085]
ENSG0000 0004272		
ENSG0000 0004660	CAMK K1	Calcium/calmodulin-dependent protein kinase kinase 1 (EC 2.7.1.37) (Calcium/calmodulin-dependent protein kinase kinase alpha) (CaM-kinase kinase alpha) (CaM-KK alpha) (CaMKK alpha) (CaMKK 1) (CaM-kinase IV kinase). [Source:Uniprot/SWISSPROT;Acc:Q8N5S9]
ENSG0000 0004700	RECQL	ATP-dependent DNA helicase Q1 (DNA-dependent ATPase Q1). [Source:Uniprot/SWISSPROT;Acc:P46063]
ENSG0000 0004846	ABCB5	"ATP-binding cassette, sub-family B, member 5 [Source:RefSeq_peptide;Acc:NP_848654]"
ENSG0000 0005007	RENT1	Regulator of nonsense transcripts 1 (EC 3.6.1.-) (ATP-dependent helicase RENT1) (Nonsense mRNA reducing factor 1) (NORF1) (Up- frameshift suppressor 1 homolog) (hUpf1). [Source:Uniprot/SWISSPROT;Acc:Q92900]
ENSG0000 0005022	SLC25A 5	"ADP/ATP translocase 2 (Adenine nucleotide translocator 2) (ANT 2) (ADP,ATP carrier protein 2) (Solute carrier family 25 member 5) (ADP,ATP carrier protein, fibroblast isoform). [Source:Uniprot/SWISSPROT;Acc:P05141]"
ENSG0000 0005100	DHX33	Putative ATP-dependent RNA helicase DHX33 (EC 3.6.1.-) (DEAH box protein 33). [Source:Uniprot/SWISSPROT;Acc:Q9H6R0]
ENSG0000 0005156	LIG3	DNA ligase III (EC 6.5.1.1) (Polydeoxyribonucleotide synthase [ATP]). [Source:Uniprot/SWISSPROT;Acc:P49916]
ENSG0000 0005187	ACSM3	SA hypertension-associated homolog isoform 1 [Source:RefSeq_peptide;Acc:NP_005613]
ENSG0000 0005471	ABCB4	Multidrug resistance protein 3 (P-glycoprotein 3). [Source:Uniprot/SWISSPROT;Acc:P21439]
ENSG0000 0006071	ABCC8	Sulfonylurea receptor 1. [Source:Uniprot/SWISSPROT;Acc:Q09428]
ENSG0000 0006717	UBA52	Ubiquitin. [Source:Uniprot/SWISSPROT;Acc:P62988]
ENSG0000 0006788	MYH13	"Myosin-13 (Myosin heavy chain, skeletal muscle, extraocular) (MyHC- eo). [Source:Uniprot/SWISSPROT;Acc:Q9UKX3]"
ENSG0000 0006831	ADIPO R2	Adiponectin receptor protein 2 (Progestin and adipoQ receptor family member II). [Source:Uniprot/SWISSPROT;Acc:Q86V24]
ENSG0000 0006837	CDKL3	Cyclin-dependent kinase-like 3 (EC 2.7.1.37) (Serine/threonine protein kinase NKIAMRE). [Source:Uniprot/SWISSPROT;Acc:Q8IVW4]
ENSG0000 0007047	MARK4	MAP/microtubule affinity-regulating kinase 4 (EC 2.7.1.37) (MAP/microtubule affinity-regulating kinase-like 1). [Source:Uniprot/SWISSPROT;Acc:Q96L34]
ENSG0000 0007168	PAFAH 1B1	Platelet-activating factor acetylhydrolase IB alpha subunit (PAF acetylhydrolase 45 kDa subunit) (PAF-AH 45 kDa subunit) (PAF-AH alpha) (PAFAH alpha) (Lissencephaly-1 protein) (LIS-1). [Source:Uniprot/SWISSPROT;Acc:P43034]
ENSG0000 0007171	NOS2A	"Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS type II) (Inducible NO synthase) (Inducible NOS) (iNOS) (Hepatocyte NOS) (HEP- NOS). [Source:Uniprot/SWISSPROT;Acc:P35228]"
ENSG0000	DNAH9	Ciliary dynein heavy chain 9 (Axonemal beta dynein heavy chain 9). [Source:Uniprot/SWISSPROT;Acc:Q9NYC9]

0007174		
ENSG0000 0007314	**SCN4A**	**"Sodium channel protein type IV alpha subunit (Voltage-gated sodium channel alpha subunit Nav1.4) (Sodium channel protein, skeletal muscle alpha-subunit) (SkM1). [Source:Uniprot/SWISSPROT;Acc:P35499]"**
ENSG0000 0007816	WDR46	WD-repeat protein 46 (WD-repeat protein BING4). [Source:Uniprot/SWISSPROT;Acc:O15213]
ENSG0000 0007869		
ENSG0000 0008086	CDKL5	Cyclin-dependent kinase-like 5 (EC 2.7.1.37) (Serine/threonine-protein kinase 9). [Source:Uniprot/SWISSPROT;Acc:O76039]
ENSG0000 0008118	CAMK1G	Calcium/calmodulin-dependent protein kinase type 1G (EC 2.7.1.123) (CaM kinase IG) (CaM kinase I gamma) (CaMKI gamma) (CaMKI-gamma) (CaM- KI gamma) (CaMKIG) (CaMK-like CREB kinase III) (CLICK III). [Source:Uniprot/SWISSPROT;Acc:Q96NX5]
ENSG0000 0008128	CDC2L2	PITSLRE serine/threonine-protein kinase CDC2L2 (EC 2.7.1.37) (Galactosyltransferase-associated protein kinase p58/GTA) (Cell division cycle 2-like protein kinase 2) (CDK11). [Source:Uniprot/SWISSPROT;Acc:Q9UQ88]
ENSG0000 0008177		
ENSG0000 0008364		
ENSG0000 0009335	UBE3C	Ubiquitin-protein ligase E3C (EC 6.3.2.-). [Source:Uniprot/SWISSPROT;Acc:Q15386]
ENSG0000 0009413	REV3L	DNA polymerase zeta catalytic subunit (EC 2.7.7.7) (hREV3). [Source:Uniprot/SWISSPROT;Acc:O60673]
ENSG0000 0010219	DYRK4	Dual specificity tyrosine-phosphorylation regulated kinase 4 (EC 2.7.1.-). [Source:Uniprot/SWISSPROT;Acc:Q9NR20]
ENSG0000 0010256	UQCRC1	"Ubiquinol-cytochrome-c reductase complex core protein I, mitochondrial precursor (EC 1.10.2.2). [Source:Uniprot/SWISSPROT;Acc:P31930]"
ENSG0000 0011021	CLCN6	Chloride channel protein 6 (ClC-6). [Source:Uniprot/SWISSPROT;Acc:P51797]
ENSG0000 0011052	NME1	Nucleoside diphosphate kinase A (EC 2.7.4.6) (NDK A) (NDP kinase A) (Tumor metastatic process-associated protein) (Metastasis inhibition factor nm23) (nm23-H1) (Granzyme A-activated DNase) (GAAD). [Source:Uniprot/SWISSPROT;Acc:P15531]
ENSG0000 0011485	PPP5C	Serine/threonine protein phosphatase 5 (EC 3.1.3.16) (PP5) (Protein phosphatase T) (PP-T) (PPT). [Source:Uniprot/SWISSPROT;Acc:P53041]
ENSG0000 0011566	MAP4K3	Mitogen-activated protein kinase kinase kinase kinase 3 (EC 2.7.1.37) (MAPK/ERK kinase kinase kinase 3) (MEK kinase kinase 3) (MEKKK 3) (Germinal center kinase-related protein kinase) (GLK). [Source:Uniprot/SWISSPROT;Acc:Q8IVH8]
ENSG0000 0012983	MAP4K5	Mitogen-activated protein kinase kinase kinase kinase 5 (EC 2.7.1.37) (MAPK/ERK kinase kinase kinase 5) (MEK kinase kinase 5) (MEKKK 5) (Kinase homologous to SPS1/STE20) (KHS). [Source:Uniprot/SWISSPROT;Acc:Q9Y4K4]
ENSG0000 0013275	PSMC4	26S protease regulatory subunit 6B (MIP224) (MB67-interacting protein) (TAT-binding protein 7) (TBP-7). [Source:Uniprot/SWISSPROT;Acc:P43686]
ENSG0000 0013293	SLC7A14	"solute carrier family 7 (cationic amino acid transporter, y+ system), member 14 [Source:RefSeq_peptide;Acc:NP_066000]"
ENSG0000 0013375	PGM3	Phosphoacetylglucosamine mutase (EC 5.4.2.3) (PAGM) (Acetylglucosamine phosphomutase) (N-acetylglucosamine-phosphate mutase) (Phosphoglucomutase 3). [Source:Uniprot/SWISSPROT;Acc:O95394]
ENSG0000 0013441	CLK1	Dual specificity protein kinase CLK1 (EC 2.7.1.37) (EC 2.7.1.112) (CDC-like kinase 1). [Source:Uniprot/SWISSPROT;Acc:P49759]
ENSG0000 0013503	POLR3B	DNA-directed RNA polymerase III subunit 127.6 kDa polypeptide (EC 2.7.7.6) (RNA polymerase III subunit 2) (RPC2). [Source:Uniprot/SWISSPROT;Acc:Q9NW08]
ENSG0000 0014641	MDH1	"Malate dehydrogenase, cytoplasmic (EC 1.1.1.37). [Source:Uniprot/SWISSPROT;Acc:P40925]"
ENSG0000 0014919	COX15	Cytochrome c oxidase assembly protein COX15 homolog. [Source:Uniprot/SWISSPROT;Acc:Q7KZN9]
ENSG0000 0017260	ATP2C1	Calcium-transporting ATPase type 2C member 1 (EC 3.6.3.8) (ATPase 2C1) (ATP-dependent Ca(2+) pump PMR1). [Source:Uniprot/SWISSPROT;Acc:P98194]
ENSG0000 0018625	ATP1A2	Sodium/potassium-transporting ATPase alpha-2 chain precursor (EC 3.6.3.9) (Sodium pump 2) (Na+/K+ ATPase 2). [Source:Uniprot/SWISSPROT;Acc:P50993]
ENSG0000 0020922	MRE11A	Double-strand break repair protein MRE11A (MRE11 homolog 1) (MRE11 meiotic recombination 11 homolog A). [Source:Uniprot/SWISSPROT;Acc:P49959]
ENSG0000 0021374		
ENSG0000 0021574	SPAST	Spastin. [Source:Uniprot/SWISSPROT;Acc:Q9UBP0]
ENSG0000 0021826	CPS1	"Carbamoyl-phosphate synthase [ammonia], mitochondrial precursor (EC 6.3.4.16) (Carbamoyl-phosphate synthetase I) (CPSase I). [Source:Uniprot/SWISSPROT;Acc:P31327]"
ENSG0000 0023228	NDUFS1	"NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-75Kd) (CI-75Kd). [Source:Uniprot/SWISSPROT;Acc:P28331]"
ENSG0000 0023734	STRAP	Serine-threonine kinase receptor-associated protein (UNR-interacting protein) (WD-40 repeat protein PT-WD) (MAP activator with WD repeats). [Source:Uniprot/SWISSPROT;Acc:Q9Y3F4]
ENSG0000 0023839	ABCC2	Canalicular multispecific organic anion transporter 1 (ATP-binding cassette sub-family C member 2) (Multidrug resistance-associated protein 2) (Canalicular multidrug resistance protein). [Source:Uniprot/SWISSPROT;Acc:Q92887]
ENSG0000 0023957		
ENSG0000 0025800	KPNA6	Importin alpha-7 subunit (Karyopherin alpha-6). [Source:Uniprot/SWISSPROT;Acc:O60684]
ENSG0000 0026036	RTEL1	Tumor necrosis factor receptor superfamily member 6B precursor (Decoy receptor for Fas ligand) (Decoy receptor 3) (DcR3) (M68). [Source:Uniprot/SWISSPROT;Acc:O95407]
ENSG0000 0027001	MIPEP	"Mitochondrial intermediate peptidase, mitochondrial precursor (EC 3.4.24.59) (MIP). [Source:Uniprot/SWISSPROT;Acc:Q99797]"

ENSG0000 0027075	PRKCH	"Protein kinase C, eta type (EC 2.7.1.-) (nPKC-eta) (PKC-L). [Source:Uniprot/SWISSPROT;Acc:P24723]"
ENSG0000 0029514		
ENSG0000 0031698	SARS	Seryl-tRNA synthetase (EC 6.1.1.11) (Serine--tRNA ligase) (SerRS). [Source:Uniprot/SWISSPROT;Acc:P49591]
ENSG0000 0032514	ERCC6	DNA excision repair protein ERCC-6 (EC 3.6.1.-) (ATP-dependent helicase ERCC6) (Cockayne syndrome protein CSB). [Source:Uniprot/SWISSPROT;Acc:Q03468]
ENSG0000 0032742	**IFT88**	**Intraflagellar transport 88 homolog (Tetratricopeptide repeat protein 10) (TPR repeat protein 10) (Recessive polycystic kidney disease protein Tg737 homolog). [Source:Uniprot/SWISSPROT;Acc:Q13099]**
ENSG0000 0033050	ABCF2	ATP-binding cassette sub-family F member 2 (Iron-inhibited ABC transporter 2). [Source:Uniprot/SWISSPROT;Acc:Q9UG63]
ENSG0000 0033178	NP_060 697.3	
ENSG0000 0033627	ATP6V 0A1	Vacuolar proton translocating ATPase 116 kDa subunit a isoform 1 (V- ATPase 116-kDa isoform a1) (Clathrin-coated vesicle/synaptic vesicle proton pump 116 kDa subunit) (Vacuolar proton pump subunit 1) (Vacuolar adenosine triphosphatase subunit Ac116). [Source:Uniprot/SWISSPROT;Acc:Q93050]
ENSG0000 0034827		
ENSG0000 0035664	DAPK2	Death-associated protein kinase 2 (EC 2.7.1.37) (DAP kinase 2) (DAP- kinase-related protein 1) (DRP-1). [Source:Uniprot/SWISSPROT;Acc:Q9UIK4]
ENSG0000 0035681	NSMAF	Protein FAN (Factor associated with N-SMase activation) (Factor associated with neutral sphingomyelinase activation). [Source:Uniprot/SWISSPROT;Acc:Q92636]
ENSG0000 0035928	RFC1	Activator 1 140 kDa subunit (Replication factor C large subunit) (A1 140 kDa subunit) (RF-C 140 kDa subunit) (Activator 1 large subunit) (DNA-binding protein PO-GA). [Source:Uniprot/SWISSPROT;Acc:P35251]
ENSG0000 0036257	CUL3	Cullin-3 (CUL-3). [Source:Uniprot/SWISSPROT;Acc:Q13618]
ENSG0000 0036672	USP2	Ubiquitin carboxyl-terminal hydrolase 2 (EC 3.1.2.15) (Ubiquitin thiolesterase 2) (Ubiquitin-specific processing protease 2) (Deubiquitinating enzyme 2) (41 kDa ubiquitin-specific protease). [Source:Uniprot/SWISSPROT;Acc:O75604]
ENSG0000 0037042	TUBG2	Tubulin gamma-2 chain (Gamma-2 tubulin). [Source:Uniprot/SWISSPROT;Acc:Q9NRH3]
ENSG0000 0037897	METTL 1	tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA(m7G46)- methyltransferase) (Methyltransferase-like protein 1). [Source:Uniprot/SWISSPROT;Acc:Q9UBP6]
ENSG0000 0039123	SKIV2L 2	Superkiller viralicidic activity 2-like 2 (EC 3.6.1.-) (ATP-dependent helicase SKIV2L2). [Source:Uniprot/SWISSPROT;Acc:P42285]
ENSG0000 0039139	DNAH5	Ciliary dynein heavy chain 5 (Axonemal beta dynein heavy chain 5) (HL1). [Source:Uniprot/SWISSPROT;Acc:Q8TE73]
ENSG0000 0041353	RAB27 B	Ras-related protein Rab-27B (C25KG). [Source:Uniprot/SWISSPROT;Acc:O00194]
ENSG0000 0041357	PSMA4	Proteasome subunit alpha type 4 (EC 3.4.25.1) (Proteasome component C9) (Macropain subunit C9) (Multicatalytic endopeptidase complex subunit C9) (Proteasome subunit L). [Source:Uniprot/SWISSPROT;Acc:P25789]
ENSG0000 0041515	NP_055 826.1	myosin heavy chain Myr 8 [Source:RefSeq_peptide;Acc:NP_055826]
ENSG0000 0041802	LSG1	
ENSG0000 0042753	AP2S1	Clathrin coat assembly protein AP17 (Clathrin coat-associated protein AP17) (Plasma membrane adaptor AP-2 17 kDa protein) (HA2 17 kDa subunit) (Clathrin assembly protein 2 small chain). [Source:Uniprot/SWISSPROT;Acc:P53680]
ENSG0000 0044574	HSPA5	78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain binding protein) (BiP) (Endoplasmic reticulum lumenal Ca(2+) binding protein grp78). [Source:Uniprot/SWISSPROT;Acc:P11021]
ENSG0000 0047188	YTHDC 2	YTH domain containing 2 [Source:RefSeq_peptide;Acc:NP_073739]
ENSG0000 0047230	CTPS2	cytidine triphosphate synthase II [Source:RefSeq_peptide;Acc:NP_062831]
ENSG0000 0047249	ATP6V 1H	Vacuolar ATP synthase subunit H (EC 3.6.3.14) (V-ATPase H subunit) (Vacuolar proton pump H subunit) (V-ATPase 50/57 kDa subunits) (Vacuolar proton pump subunit SFD) (VMA13) (Nef binding protein 1) (NBP1). [Source:Uniprot/SWISSPROT;Acc:Q9UI12]
ENSG0000 0047315	POLR2 B	DNA-directed RNA polymerase II 140 kDa polypeptide (EC 2.7.7.6) (RNA polymerase II subunit 2) (RPB2). [Source:Uniprot/SWISSPROT;Acc:P30876]
ENSG0000 0047343		
ENSG0000 0048152		
ENSG0000 0049496		
ENSG0000 0049541	RFC2	Activator 1 40 kDa subunit (Replication factor C 40 kDa subunit) (A1 40 kDa subunit) (RF-C 40 kDa subunit) (RFC40). [Source:Uniprot/SWISSPROT;Acc:P35250]
ENSG0000 0049656	NP_110 409.2	cisplatin resistance related protein CRR9p [Source:RefSeq_peptide;Acc:NP_110409]
ENSG0000 0049759	NEDD4 L	E3 ubiquitin-protein ligase NEDD4-like protein (EC 6.3.2.-) (Nedd4-2) (NEDD4.2). [Source:Uniprot/SWISSPROT;Acc:Q96PU5]
ENSG0000 0050748	MAPK9	Mitogen-activated protein kinase 9 (EC 2.7.1.37) (Stress-activated protein kinase JNK2) (c-Jun N-terminal kinase 2) (JNK-55). [Source:Uniprot/SWISSPROT;Acc:P45984]
ENSG0000 0051180	RAD51	DNA repair protein RAD51 homolog 1 (hRAD51) (HsRAD51). [Source:Uniprot/SWISSPROT;Acc:Q06609]
ENSG0000 0051341	POLQ	DNA polymerase theta (EC 2.7.7.7) (DNA polymerase eta). [Source:Uniprot/SWISSPROT;Acc:O75417]
ENSG0000 0053059		

ENSG0000 0053372	MRT4_ HUMA N	mRNA turnover protein 4 homolog. [Source:Uniprot/SWISSPROT;Acc:Q9UKD2]
ENSG0000 0054523	KIF1B	Kinesin-like protein KIF1B (Klp). [Source:Uniprot/SWISSPROT;Acc:O60333]
ENSG0000 0054793	ATP9A	Probable phospholipid-transporting ATPase IIA (EC 3.6.3.1) (ATPase class II type 9A) (ATPase IIA). [Source:Uniprot/SWISSPROT;Acc:O75110]
ENSG0000 0055044	NOP5_ HUMA N	Nucleolar protein NOP5 (Nucleolar protein 5) (NOP58). [Source:Uniprot/SWISSPROT;Acc:Q9Y2X3]
ENSG0000 0055130	CUL1	Cullin-1 (CUL-1). [Source:Uniprot/SWISSPROT;Acc:Q13616]
ENSG0000 0055468		
ENSG0000 0055917	PUM2	Pumilio homolog 2 (Pumilio-2). [Source:Uniprot/SWISSPROT;Acc:Q8TB72]
ENSG0000 0056678	KIFC1	Kinesin-like protein KIFC1 (Kinesin-like protein 2) (Kinesin-related protein HSET). [Source:Uniprot/SWISSPROT;Acc:Q9BW19]
ENSG0000 0057608	GDI2	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2). [Source:Uniprot/SWISSPROT;Acc:P50395]
ENSG0000 0058056	USP13	Ubiquitin carboxyl-terminal hydrolase 13 (EC 3.1.2.15) (Ubiquitin thiolesterase 13) (Ubiquitin-specific processing protease 13) (Deubiquitinating enzyme 13) (Isopeptidase T-3) (ISOT-3). [Source:Uniprot/SWISSPROT;Acc:Q92995]
ENSG0000 0058063	ATP11B	Probable phospholipid-transporting ATPase IF (EC 3.6.3.1) (ATPase class I type 11B) (ATPase IR). [Source:Uniprot/SWISSPROT;Acc:Q9Y2G3]
ENSG0000 0058091	PFTK1	Serine/threonine-protein kinase PFTAIRE-1 (EC 2.7.1.37). [Source:Uniprot/SWISSPROT;Acc:O94921]
ENSG0000 0058262	SEC61A 1	Protein transport protein Sec61 alpha subunit isoform 1 (Sec61 alpha- 1). [Source:Uniprot/SWISSPROT;Acc:P61619]
ENSG0000 0058404	CAMK2 B	Calcium/calmodulin-dependent protein kinase type II beta chain (EC 2.7.1.123) (CaM-kinase II beta chain) (CaM kinase II beta subunit) (CaMK-II beta subunit). [Source:Uniprot/SWISSPROT;Acc:Q13554]
ENSG0000 0058668	ATP2B4	Plasma membrane calcium-transporting ATPase 4 (EC 3.6.3.8) (PMCA4) (Plasma membrane calcium pump isoform 4) (Plasma membrane calcium ATPase isoform 4). [Source:Uniprot/SWISSPROT;Acc:P23634]
ENSG0000 0059133		
ENSG0000 0059758	PCTK2	Serine/threonine-protein kinase PCTAIRE-2 (EC 2.7.1.37) (PCTAIRE-motif protein kinase 2). [Source:Uniprot/SWISSPROT;Acc:Q00537]
ENSG0000 0062282	DGAT2	diacylglycerol O-acyltransferase homolog 2 [Source:RefSeq_peptide;Acc:NP_115953]
ENSG0000 0062822	POLD1	DNA polymerase delta catalytic subunit (EC 2.7.7.7) (DNA polymerase delta subunit p125). [Source:Uniprot/SWISSPROT;Acc:P28340]
ENSG0000 0063177	RPL18	60S ribosomal protein L18. [Source:Uniprot/SWISSPROT;Acc:Q07020]
ENSG0000 0063761	ADCK1	aarF domain containing kinase 1 [Source:RefSeq_peptide;Acc:NP_065154]
ENSG0000 0064270	AT2C2_ HUMA N	Probable calcium-transporting ATPase KIAA0703 (EC 3.6.3.8). [Source:Uniprot/SWISSPROT;Acc:O75185]
ENSG0000 0064393	HIPK2	Homeodomain-interacting protein kinase 2 (EC 2.7.1.37) (hHIPk2). [Source:Uniprot/SWISSPROT;Acc:Q9H2X6]
ENSG0000 0064601	PPGB	Lysosomal protective protein precursor (EC 3.4.16.5) (Cathepsin A) (Carboxypeptidase C) (Protective protein for beta-galactosidase) [Contains: Lysosomal protective protein 32 kDa chain; Lysosomal protective protein 20 kDa chain]. [Source:Uniprot/SWISSPROT;Acc:P10619]
ENSG0000 0064687	ABCA7	"ATP-binding cassette, sub-family A, member 7 isoform a [Source:RefSeq_peptide;Acc:NP_061985]"
ENSG0000 0064703	DDX20	Probable ATP-dependent RNA helicase DDX20 (EC 3.6.1.-) (DEAD box protein 20) (DEAD box protein DP 103) (Component of gems 3) (Gemin-3). [Source:Uniprot/SWISSPROT;Acc:Q9UHI6]
ENSG0000 0065183	WDR3	WD-repeat protein 3. [Source:Uniprot/SWISSPROT;Acc:Q9UNX4]
ENSG0000 0065243	PKN2	Protein kinase N2 (EC 2.7.1.37) (Protein kinase C-like 2) (Protein- kinase C-related kinase 2). [Source:Uniprot/SWISSPROT;Acc:Q16513]
ENSG0000 0065427	KARS	Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS). [Source:Uniprot/SWISSPROT;Acc:Q15046]
ENSG0000 0065613	SLK	serine/threonine kinase 2 [Source:RefSeq_peptide;Acc:NP_055535]
ENSG0000 0065665	SEC61A 2	Protein transport protein Sec61 alpha subunit isoform 2 (Sec61 alpha- 2). [Source:Uniprot/SWISSPROT;Acc:Q9H9S3]
ENSG0000 0065675	PRKCQ	"Protein kinase C, theta type (EC 2.7.1.-) (nPKC-theta). [Source:Uniprot/SWISSPROT;Acc:Q04759]"
ENSG0000 0065883	CDC2L 5	Cell division cycle 2-like protein kinase 5 (EC 2.7.1.37) (CDC2- related protein kinase 5) (Cholinesterase-related cell division controller). [Source:Uniprot/SWISSPROT;Acc:Q14004]
ENSG0000 0065911	MTHFD 2	"Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial precursor [Includes: NAD-dependent methylenetetrahydrofolate dehydrogenase (EC 1.5.1.15); Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9)]. [Source:Uniprot/SWISSPROT;Acc:P13995]"
ENSG0000 0065989	**PDE4A**	**"cAMP-specific 3',5'-cyclic phosphodiesterase 4A (EC 3.1.4.17) (DPDE2) (PDE46). [Source:Uniprot/SWISSPROT;Acc:P27815]"**
ENSG0000 0066933	MYO9A	myosin IXA [Source:RefSeq_peptide;Acc:NP_008832]
ENSG0000	DDX3Y	"ATP-dependent RNA helicase DDX3Y (EC 3.6.1.-) (DEAD box protein 3, Y- chromosomal).

0067048		[Source:Uniprot/SWISSPROT;Acc:O15523]"
ENSG0000 0067225	PKM2	"Pyruvate kinase, isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase muscle isozyme) (Cytosolic thyroid hormone-binding protein) (CTHBP) (THBP1). [Source:Uniprot/SWISSPROT;Acc:P14618]"
ENSG0000 0067248	DHX29	DEAH (Asp-Glu-Ala-His) box polypeptide 29 [Source:RefSeq_peptide;Acc:NP_061903]
ENSG0000 0067596	DHX8	ATP-dependent RNA helicase DHX8 (EC 3.6.1.-) (DEAH box protein 8) (RNA helicase HRH1). [Source:Uniprot/SWISSPROT;Acc:Q14562]
ENSG0000 0067606	PRKCZ	"Protein kinase C, zeta type (EC 2.7.1.37) (nPKC-zeta). [Source:Uniprot/SWISSPROT;Acc:Q05513]"
ENSG0000 0067704	IARS2	mitochondrial isoleucine tRNA synthetase [Source:RefSeq_peptide;Acc:NP_060530]
ENSG0000 0067842	ATP2B3	Plasma membrane calcium-transporting ATPase 3 (EC 3.6.3.8) (PMCA3) (Plasma membrane calcium pump isoform 3) (Plasma membrane calcium ATPase isoform 3). [Source:Uniprot/SWISSPROT;Acc:Q16720]
ENSG0000 0067900	ROCK1	"Rho-associated protein kinase 1 (EC 2.7.1.37) (Rho-associated, coiled- coil containing protein kinase 1) (p160 ROCK-1) (p160ROCK). [Source:Uniprot/SWISSPROT;Acc:Q13464]"
ENSG0000 0068366	ACSL4	Long-chain-fatty-acid--CoA ligase 4 (EC 6.2.1.3) (Long-chain acyl-CoA synthetase 4) (LACS 4). [Source:Uniprot/SWISSPROT;Acc:O60488]
ENSG0000 0068438	FTSJ1	Putative ribosomal RNA methyltransferase 1 (EC 2.1.1.-) (rRNA (uridine-2'-O-)-methyltransferase). [Source:Uniprot/SWISSPROT;Acc:Q9UET6]
ENSG0000 0068650	ATP11 A	Probable phospholipid-transporting ATPase IH (EC 3.6.3.1) (ATPase class I type 11A) (ATPase IS). [Source:Uniprot/SWISSPROT;Acc:P98196]
ENSG0000 0068654	POLR1 A	DNA-directed RNA polymerase I largest subunit (EC 2.7.7.6) (RNA polymerase I 194 kDa subunit) (RPA194). [Source:Uniprot/SWISSPROT;Acc:O95602]
ENSG0000 0068796	KIF2	Kinesin-like protein KIF2 (Kinesin-2) (HK2). [Source:Uniprot/SWISSPROT;Acc:O00139]
ENSG0000 0068885	**IFT80**	**Intraflagellar transport 80 homolog (WD-repeat protein 56). [Source:Uniprot/SWISSPROT;Acc:Q9P2H3]**
ENSG0000 0069020	MAST4	
ENSG0000 0069345	DNAJA 2	DnaJ homolog subfamily A member 2 (HIRA-interacting protein 4) (Cell cycle progression restoration gene 3 protein) (Dnj3). [Source:Uniprot/SWISSPROT;Acc:O60884]
ENSG0000 0069431	ABCC9	Sulfonylurea receptor 2. [Source:Uniprot/SWISSPROT;Acc:O60706]
ENSG0000 0069869	NEDD4	E3 ubiquitin-protein ligase NEDD4 (EC 6.3.2.-). [Source:Uniprot/SWISSPROT;Acc:P46934]
ENSG0000 0069956	MAPK6	Mitogen-activated protein kinase 6 (EC 2.7.1.37) (Extracellular signal-regulated kinase 3) (ERK-3) (MAP kinase isoform p97) (p97- MAPK). [Source:Uniprot/SWISSPROT;Acc:Q16659]
ENSG0000 0069998	CECR5	Cat eye syndrome critical region protein 5 precursor. [Source:Uniprot/SWISSPROT;Acc:Q9BXW7]
ENSG0000 0070371	CLTCL 1	Clathrin heavy chain 2 (CLH-22). [Source:Uniprot/SWISSPROT;Acc:P53675]
ENSG0000 0070490	TUBA8	Tubulin alpha-8 chain (Alpha-tubulin 8). [Source:Uniprot/SWISSPROT;Acc:Q9NY65]
ENSG0000 0070718	AP3M2	Adapter-related protein complex 3 mu 2 subunit (Clathrin coat assembly protein AP47 homolog 2) (Clathrin coat-associated protein AP47 homolog 2) (Golgi adaptor AP-1 47 kDa protein homolog 2) (HA1 47 kDa subunit homolog 2) (Clathrin assembly protein assemb [Source:Uniprot/SWISSPROT;Acc:P53677]
ENSG0000 0070756	PABPC 1	Polyadenylate-binding protein 1 (Poly(A)-binding protein 1) (PABP 1). [Source:Uniprot/SWISSPROT;Acc:P11940]
ENSG0000 0070761	NP_037 374.1	transcription factor IIB [Source:RefSeq_peptide;Acc:NP_037374]
ENSG0000 0070770	CSNK2 A2	"Casein kinase II, alpha' chain (CK II) (EC 2.7.1.37). [Source:Uniprot/SWISSPROT;Acc:P19784]"
ENSG0000 0070808	CAMK2 A	Calcium/calmodulin-dependent protein kinase type II alpha chain (EC 2.7.1.123) (CaM-kinase II alpha chain) (CaM kinase II alpha subunit) (CaMK-II alpha subunit). [Source:Uniprot/SWISSPROT;Acc:Q9UQM7]
ENSG0000 0070961	ATP2B1	Plasma membrane calcium-transporting ATPase 1 (EC 3.6.3.8) (PMCA1) (Plasma membrane calcium pump isoform 1) (Plasma membrane calcium ATPase isoform 1). [Source:Uniprot/SWISSPROT;Acc:P20020]
ENSG0000 0071054	MAP4K 4	Mitogen-activated protein kinase kinase kinase kinase 4 (EC 2.7.1.37) (MAPK/ERK kinase kinase kinase 4) (MEK kinase kinase 4) (MEKKK 4) (HPK/GCK-like kinase HGK) (Nck interacting kinase). [Source:Uniprot/SWISSPROT;Acc:O95819]
ENSG0000 0071242	RPS6K A2	Ribosomal protein S6 kinase alpha 2 (EC 2.7.1.37) (S6K-alpha 2) (90 kDa ribosomal protein S6 kinase 2) (p90-RSK 2) (Ribosomal S6 kinase 3) (RSK-3) (pp90RSK3). [Source:Uniprot/SWISSPROT;Acc:Q15349]
ENSG0000 0071539	TRIP13	Thyroid receptor-interacting protein 13 (Thyroid hormone receptor interactor 13) (Trip-13) (Human papillomavirus type 16 E1 protein- binding protein) (HPV16 E1 protein-binding protein) (16E1-BP). [Source:Uniprot/SWISSPROT;Acc:Q15645]
ENSG0000 0071909	MYO3B	Myosin IIIB (EC 2.7.1.37). [Source:Uniprot/SWISSPROT;Acc:Q8WXR4]
ENSG0000 0072062	PRKAC A	"cAMP-dependent protein kinase, alpha-catalytic subunit (EC 2.7.1.37) (PKA C-alpha). [Source:Uniprot/SWISSPROT;Acc:P17612]"
ENSG0000 0072133	RPS6K A6	Ribosomal protein S6 kinase alpha 6 (EC 2.7.1.37) (S6K-alpha 6) (90 kDa ribosomal protein S6 kinase 6) (p90-RSK 6) (Ribosomal S6 kinase 4) (RSK-4) (pp90RSK4). [Source:Uniprot/SWISSPROT;Acc:Q9UK32]
ENSG0000 0072401	UBE2D 1	Ubiquitin-conjugating enzyme E2 D1 (EC 6.3.2.19) (Ubiquitin-protein ligase D1) (Ubiquitin carrier protein D1) (UbcH5) (Ubiquitin- conjugating enzyme E2-17 kDa 1) (E2(17)KB 1). [Source:Uniprot/SWISSPROT;Acc:P51668]
ENSG0000 0072501	SMC1L 1	Structural maintenance of chromosome 1-like 1 protein (SMC1alpha protein) (DXS423E protein) (Sb1.8). [Source:Uniprot/SWISSPROT;Acc:Q14683]
ENSG0000 0072518	MARK2	Serine/threonine-protein kinase MARK2 (EC 2.7.1.37) (MAP/microtubule affinity-regulating kinase 2) (ELKL motif kinase) (EMK1) (PAR1 homolog). [Source:Uniprot/SWISSPROT;Acc:Q7KZI7]
ENSG0000 0072786	STK10	Serine/threonine-protein kinase 10 (EC 2.7.1.37) (Lymphocyte-oriented kinase). [Source:Uniprot/SWISSPROT;Acc:O94804]

ENSG0000 0072958	AP1M1	"Adaptor-related protein complex 1, mu 1 subunit (Mu-adaptin 1) (Adaptor protein complex AP-1 mu-1 subunit) (Golgi adaptor HA1/AP1 adaptin mu-1 subunit) (Clathrin assembly protein assembly protein complex 1 medium chain 1) (Clathrin coat assembly protein A [Source:Uniprot/SWISSPROT;Acc:Q9BXS5]"
ENSG0000 0073111	MCM2	DNA replication licensing factor MCM2 (Minichromosome maintenance protein 2 homolog) (Nuclear protein BM28). [Source:Uniprot/SWISSPROT;Acc:P49736]
ENSG0000 0073417	**PDE8A**	**"High-affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8A (EC 3.1.4.17). [Source:Uniprot/SWISSPROT;Acc:O60658]"**
ENSG0000 0073536	NLE1	Notchless homolog 1. [Source:Uniprot/SWISSPROT;Acc:Q9NVX2]
ENSG0000 0073578	SDHA	"Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor (EC 1.3.5.1) (Fp) (Flavoprotein subunit of complex II). [Source:Uniprot/SWISSPROT;Acc:P31040]"
ENSG0000 0073711	PPP2R3 A	"Serine/threonine protein phosphatase 2A, 72/130 kDa regulatory subunit B (PP2A, subunit B, B"-PR72/PR130) (PP2A, subunit B, B72/B130 isoforms) (PP2A, subunit B, PR72/PR130 isoforms) (PP2A, subunit B, R3 isoform). [Source:Uniprot/SWISSPROT;Acc:Q06190]"
ENSG0000 0073734	ABCB1 1	Bile salt export pump (ATP-binding cassette sub-family B member 11). [Source:Uniprot/SWISSPROT;Acc:O95342]
ENSG0000 0073969	NSF	Vesicle-fusing ATPase (EC 3.6.4.6) (Vesicular-fusion protein NSF) (N- ethylmaleimide sensitive fusion protein) (NEM-sensitive fusion protein). [Source:Uniprot/SWISSPROT;Acc:P46459]
ENSG0000 0074370	ATP2A 3	Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 (EC 3.6.3.8) (Calcium pump 3) (SERCA3) (SR Ca(2+)-ATPase 3). [Source:Uniprot/SWISSPROT;Acc:Q93084]
ENSG0000 0074590	NUAK1	"NUAK family, SNF1-like kinase 1 (EC 2.7.1.37) (AMPK-related protein kinase 5). [Source:Uniprot/SWISSPROT;Acc:O60285]"
ENSG0000 0074800	ENO1	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non- neural enolase) (NNE) (Enolase 1) (Phosphopyruvate hydratase) (C-myc promoter-binding protein) (MBP-1) (MPB-1) (Plasminogen-binding protein). [Source:Uniprot/SWISSPROT;Acc:P06733]
ENSG0000 0074935	TUBE1	Tubulin epsilon chain (Epsilon tubulin). [Source:Uniprot/SWISSPROT;Acc:Q9UJT0]
ENSG0000 0075413	MARK3	MAP/microtubule affinity-regulating kinase 3 (EC 2.7.1.37) (Cdc25C- associated protein kinase 1) (cTAK1) (C-TAK1) (Serine/threonine protein kinase p78) (Ser/Thr protein kinase PAR-1) (Protein kinase STK10). [Source:Uniprot/SWISSPROT;Acc:P27448]
ENSG0000 0075415	SLC25A 3	"Phosphate carrier protein, mitochondrial precursor (PTP). [Source:Uniprot/SWISSPROT;Acc:Q00325]"
ENSG0000 0075624	ACTB	"Actin, cytoplasmic 1 (Beta-actin). [Source:Uniprot/SWISSPROT;Acc:P60709]"
ENSG0000 0075673	ATP12 A	Potassium-transporting ATPase alpha chain 2 (EC 3.6.3.10) (Proton pump) (Non-gastric H(+)/K(+) ATPase alpha subunit). [Source:Uniprot/SWISSPROT;Acc:P54707]
ENSG0000 0075785	RAB7	Ras-related protein Rab-7. [Source:Uniprot/SWISSPROT;Acc:P51149]
ENSG0000 0075886	TUBA2	Tubulin alpha-2 chain (Alpha-tubulin 2). [Source:Uniprot/SWISSPROT;Acc:Q13748]
ENSG0000 0076003	MCM6	DNA replication licensing factor MCM6 (P105MCM). [Source:Uniprot/SWISSPROT;Acc:Q14566]
ENSG0000 0076242	MLH1	DNA mismatch repair protein Mlh1 (MutL protein homolog 1). [Source:Uniprot/SWISSPROT;Acc:P40692]
ENSG0000 0077080	ACTL6 B	Actin-like protein 6B (53 kDa BRG1-associated factor B) (Actin-related protein Baf53b) (ArpNalpha). [Source:Uniprot/SWISSPROT;Acc:O94805]
ENSG0000 0077097	TOP2B	"DNA topoisomerase 2-beta (EC 5.99.1.3) (DNA topoisomerase II, beta isozyme). [Source:Uniprot/SWISSPROT;Acc:Q02880]"
ENSG0000 0077147	TM9S3_ HUMA N	Transmembrane 9 superfamily protein member 3 precursor (SM-11044 binding protein) (EP70-P-iso). [Source:Uniprot/SWISSPROT;Acc:Q9HD45]
ENSG0000 0077264	PAK3	Serine/threonine-protein kinase PAK 3 (EC 2.7.1.37) (p21-activated kinase 3) (PAK-3) (Beta-PAK) (Oligophrenin-3). [Source:Uniprot/SWISSPROT;Acc:O75914]
ENSG0000 0077327	**SPAG6**	**Sperm-associated antigen 6 (PF16 protein homolog) (Sperm flagellar protein) (Repro-SA-1). [Source:Uniprot/SWISSPROT;Acc:O75602]**
ENSG0000 0077721	UBE2A	Ubiquitin-conjugating enzyme E2 A (EC 6.3.2.19) (Ubiquitin-protein ligase A) (Ubiquitin carrier protein A) (HR6A) (hHR6A). [Source:Uniprot/SWISSPROT;Acc:P49459]
ENSG0000 0077935	SMC1L 2	Structural maintenance of chromosome 1-like 2 protein (SMC1beta protein). [Source:Uniprot/SWISSPROT;Acc:Q8NDV3]
ENSG0000 0078747	ITCH	Itchy homolog E3 ubiquitin protein ligase (EC 6.3.2.-) (Itch) (Atrophin-1-interacting protein 4) (AIP4) (NFE2-associated polypeptide 1) (NAPP1). [Source:Uniprot/SWISSPROT;Acc:Q96J02]
ENSG0000 0078814	MYH7B	"myosin, heavy polypeptide 7B, cardiac muscle, beta [Source:RefSeq_peptide;Acc:NP_065935]"
ENSG0000 0078872	NFS1	"Cysteine desulfurase, mitochondrial precursor (EC 2.8.1.7). [Source:Uniprot/SWISSPROT;Acc:Q9Y697]"
ENSG0000 0078967	UBE2D 4	ubiquitin-conjugating enzyme E2D 4 (putative) [Source:RefSeq_peptide;Acc:NP_057067]
ENSG0000 0079332	SAR1A	GTP-binding protein SAR1a (COPII-associated small GTPase). [Source:Uniprot/SWISSPROT;Acc:Q9NR31]
ENSG0000 0079335	CDC14 A	Dual specificity protein phosphatase CDC14A (EC 3.1.3.48) (EC 3.1.3.16) (CDC14 cell division cycle 14 homolog A). [Source:Uniprot/SWISSPROT;Acc:Q9UNH5]
ENSG0000 0079616	KIF22	Kinesin-like protein KIF22 (Kinesin-like DNA-binding protein) (Kinesin-like protein 4). [Source:Uniprot/SWISSPROT;Acc:Q14807]
ENSG0000 0079722		
ENSG0000 0079805	DNM2	Dynamin-2 (EC 3.6.5.5). [Source:Uniprot/SWISSPROT;Acc:P50570]
ENSG0000	**RABL2**	**Rab-like protein 2B. [Source:Uniprot/SWISSPROT;Acc:Q9UNT1]**

0079974	**B**	
ENSG0000 0080007	DDX43	Probable ATP-dependent RNA helicase DDX43 (EC 3.6.1.-) (DEAD box protein 43) (DEAD box protein HAGE) (Helical antigen). [Source:Uniprot/SWISSPROT;Acc:Q9NXZ2]
ENSG0000 0080220		
ENSG0000 0080371	RAB21	Ras-related protein Rab-21. [Source:Uniprot/SWISSPROT;Acc:Q9UL25]
ENSG0000 0080469	TAP2	Antigen peptide transporter 2 (APT2) (Peptide transporter TAP2) (Peptide transporter PSF2) (Peptide supply factor 2) (PSF-2) (Peptide transporter involved in antigen processing 2). [Source:Uniprot/SWISSPROT;Acc:Q03519]
ENSG0000 0080503	SMARC A2	Possible global transcription activator SNF2L2 (EC 3.6.1.-) (ATP- dependent helicase SMARCA2) (SNF2-alpha) (SWI/SNF-related matrix associated actin dependent regulator of chromatin subfamily A member 2) (hBRM). [Source:Uniprot/SWISSPROT;Acc:P51531]
ENSG0000 0080603	NP_006 653.1	Snf2-related CBP activator protein [Source:RefSeq_peptide;Acc:NP_006653]
ENSG0000 0080823	RAGE	MAPK/MAK/MRK overlapping kinase (EC 2.7.1.37) (MOK protein kinase) (Renal tumor antigen 1) (RAGE-1). [Source:Uniprot/SWISSPROT;Acc:Q9UQ07]
ENSG0000 0080824	HSPCA	Heat shock protein HSP 90-alpha (HSP 86). [Source:Uniprot/SWISSPROT;Acc:P07900]
ENSG0000 0081014	AP4E1	Adapter-related protein complex 4 epsilon 1 subunit (Epsilon subunit of AP-4) (AP-4 adapter complex epsilon subunit). [Source:Uniprot/SWISSPROT;Acc:Q9UPM8]
ENSG0000 0081248	**CACN A1S**	**"Voltage-dependent L-type calcium channel alpha-1S subunit (Voltage- gated calcium channel alpha subunit Cav1.1) (Calcium channel, L type, alpha-1 polypeptide, isoform 3, skeletal muscle). [Source:Uniprot/SWISSPROT;Acc:Q13698]"**
ENSG0000 0081377	CDC14 B	Dual specificity protein phosphatase CDC14B (EC 3.1.3.48) (EC 3.1.3.16) (CDC14 cell division cycle 14 homolog B). [Source:Uniprot/SWISSPROT;Acc:O60729]
ENSG0000 0081923	ATP8B1	Probable phospholipid-transporting ATPase IC (EC 3.6.3.1) (Familial intrahepatic cholestasis type 1) (ATPase class I type 8B member 1). [Source:Uniprot/SWISSPROT;Acc:O43520]
ENSG0000 0082701	GSK3B	Glycogen synthase kinase-3 beta (EC 2.7.1.37) (GSK-3 beta). [Source:Uniprot/SWISSPROT;Acc:P49841]
ENSG0000 0082898	XPO1	Exportin-1 (Chromosome region maintenance 1 protein homolog). [Source:Uniprot/SWISSPROT;Acc:O14980]
ENSG0000 0083123	BCKDH B	"2-oxoisovalerate dehydrogenase beta subunit, mitochondrial precursor (EC 1.2.4.4) (Branched-chain alpha-keto acid dehydrogenase E1 component beta chain) (BCKDH E1-beta). [Source:Uniprot/SWISSPROT;Acc:P21953]"
ENSG0000 0083168	MYST3	"Histone acetyltransferase MYST3 (EC 2.3.1.48) (EC 2.3.1.-) (MYST protein 3) (MOZ, YBF2/SAS3, SAS2 and TIP60 protein 3) (Runt-related transcription factor binding protein 2) (Monocytic leukemia zinc finger protein) (Zinc finger protein 220). [Source:Uniprot/SWISSPROT;Acc:Q92794]"
ENSG0000 0083312	TNPO1	Transportin-1 (Importin beta-)2 (Karyopherin beta-2) (M9 region interaction protein) (MIP). [Source:Uniprot/SWISSPROT;Acc:Q92973]
ENSG0000 0083520	KIAA10 08	Exosome complex exonuclease RRP44 (EC 3.1.13.-) (Ribosomal RNA processing protein 44) (DIS3 protein homolog). [Source:Uniprot/SWISSPROT;Acc:Q9Y2L1]
ENSG0000 0083845	RPS5	40S ribosomal protein S5. [Source:Uniprot/SWISSPROT;Acc:P46782]
ENSG0000 0084072	PPIE	Peptidyl-prolyl cis-trans isomerase E (EC 5.2.1.8) (PPIase E) (Rotamase E) (Cyclophilin E) (Cyclophilin 33). [Source:Uniprot/SWISSPROT;Acc:Q9UNP9]
ENSG0000 0084623	EIF3S2	Eukaryotic translation initiation factor 3 subunit 2 (eIF-3 beta) (eIF3 p36) (eIF3i) (TGF-beta receptor-interacting protein 1) (TRIP-1). [Source:Uniprot/SWISSPROT;Acc:Q13347]
ENSG0000 0084731	KIF3C	Kinesin-like protein KIF3C. [Source:Uniprot/SWISSPROT;Acc:O14782]
ENSG0000 0084733	RAB10	Ras-related protein Rab-10. [Source:Uniprot/SWISSPROT;Acc:P61026]
ENSG0000 0084774	CAD	CAD protein [Includes: Glutamine-dependent carbamoyl-phosphate synthase (EC 6.3.5.5); Aspartate carbamoyltransferase (EC 2.1.3.2); Dihydroorotase (EC 3.5.2.3)]. [Source:Uniprot/SWISSPROT;Acc:P27708]
ENSG0000 0085224	ATRX	Transcriptional regulator ATRX (EC 3.6.1.-) (ATP-dependent helicase ATRX) (X-linked helicase II) (X-linked nuclear protein) (XNP) (Znf- HX). [Source:Uniprot/SWISSPROT;Acc:P46100]
ENSG0000 0085377	PREP	Prolyl endopeptidase (EC 3.4.21.26) (Post-proline cleaving enzyme) (PE). [Source:Uniprot/SWISSPROT;Acc:P48147]
ENSG0000 0085382	HACE1	"HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 [Source:RefSeq_peptide;Acc:NP_065822]"
ENSG0000 0085511	MAP3K 4	Mitogen-activated protein kinase kinase kinase 4 (EC 2.7.1.37) (MAPK/ERK kinase kinase 4) (MEK kinase 4) (MEKK 4) (MAP three kinase 1). [Source:Uniprot/SWISSPROT;Acc:Q9Y6R4]
ENSG0000 0085545		
ENSG0000 0085563	ABCB1	Multidrug resistance protein 1 (P-glycoprotein 1) (CD243 antigen). [Source:Uniprot/SWISSPROT;Acc:P08183]
ENSG0000 0085662	AKR1B 1	Aldose reductase (EC 1.1.1.21) (AR) (Aldehyde reductase). [Source:Uniprot/SWISSPROT;Acc:P15121]
ENSG0000 0085999	RAD54 L	DNA repair and recombination protein RAD54-like (EC 3.6.1.-) (RAD54 homolog) (hRAD54) (hHR54). [Source:Uniprot/SWISSPROT;Acc:Q92698]
ENSG0000 0086015	MAST2	Microtubule-associated serine/threonine-protein kinase 2 (EC 2.7.1.37). [Source:Uniprot/SWISSPROT;Acc:Q6P0Q8]
ENSG0000 0086061	DNAJA 1	DnaJ homolog subfamily A member 1 (Heat shock 40 kDa protein 4) (DnaJ protein homolog 2) (HSJ-2) (HSDJ). [Source:Uniprot/SWISSPROT;Acc:P31689]
ENSG0000 0086102	NFX1	"Transcriptional repressor NF-X1 (EC 6.3.2.-) (Nuclear transcription factor, X box-binding, 1). [Source:Uniprot/SWISSPROT;Acc:Q12986]"
ENSG0000 0086117		
ENSG0000 0086189	DIMH_ HUMA	"Probable dimethyladenosine transferase (EC 2.1.1.-) (S- adenosylmethionine-6-N',N'-adenosyl(rRNA) dimethyltransferase) (18S rRNA dimethylase). [Source:Uniprot/SWISSPROT;Acc:Q9UNQ2]"

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ENSG0000 0086717	PPEF1	Serine/threonine protein phosphatase with EF-hands-1 (EC 3.1.3.16) (PPEF-1) (Protein phosphatase with EF calcium-binding domain) (PPEF) (Serine/threonine protein phosphatase 7) (PP7). [Source:Uniprot/SWISSPROT;Acc:O14829]
ENSG0000 0086758	HUWE1	"HECT, UBA and WWE domain containing protein 1 (EC 6.3.2.-) (E3 ubiquitin protein ligase URE-B1) (Mcl-1 ubiquitin ligase E3) (Mule) (ARF-binding protein 1) (ARF-BP1). [Source:Uniprot/SWISSPROT;Acc:Q7Z6Z7]"
ENSG0000 0087095	NLK	Serine/threonine kinase NLK (EC 2.7.1.37) (Nemo-like kinase) (LAK1 protein). [Source:Uniprot/SWISSPROT;Acc:Q9UBE8]
ENSG0000 0087187		
ENSG0000 0087191	PSMC5	26S protease regulatory subunit 8 (Proteasome subunit p45) (p45/SUG) (Proteasome 26S subunit ATPase 5) (Thyroid hormone receptor interacting protein 1) (TRIP1). [Source:Uniprot/SWISSPROT;Acc:P62195]
ENSG0000 0087255		
ENSG0000 0087470	DNM1L	Dynamin-1-like protein (EC 3.6.5.5) (Dynamin-like protein) (Dnm1p/Vps1p-like protein) (DVLP) (Dynamin family member proline-rich carboxyl-terminal domain less) (Dymple) (Dynamin-related protein 1) (Dynamin-like protein 4) (Dynamin-like protein IV) (HdynIV [Source:Uniprot/SWISSPROT;Acc:O00429]
ENSG0000 0087586	STK6	Serine/threonine-protein kinase 6 (EC 2.7.1.37) (Serine/threonine kinase 15) (Aurora/IPL1-related kinase 1) (Aurora-related kinase 1) (hARK1) (Aurora-A) (Breast-tumor-amplified kinase). [Source:Uniprot/SWISSPROT;Acc:O14965]
ENSG0000 0087997		
ENSG0000 0088168		
ENSG0000 0088205	DDX18	ATP-dependent RNA helicase DDX18 (EC 3.6.1.-) (DEAD box protein 18) (Myc-regulated DEAD box protein) (MrDb). [Source:Uniprot/SWISSPROT;Acc:Q9NVP1]
ENSG0000 0088298	CT031_ HUMA N	Putative alpha-mannosidase C20orf31 precursor (EC 3.2.1.-). [Source:Uniprot/SWISSPROT;Acc:Q9BV94]
ENSG0000 0088481		
ENSG0000 0088727	KIF9	Kinesin-like protein KIF9. [Source:Uniprot/SWISSPROT;Acc:Q9HAQ2]
ENSG0000 0088930	XRN2	5'-3' exoribonuclease 2 (EC 3.1.11.-) (DHM1-like protein) (DHP protein). [Source:Uniprot/SWISSPROT;Acc:Q9H0D6]
ENSG0000 0089101	**CT026_ HUMA N**	
ENSG0000 0089154	GCN1L 1	GCN1-like protein 1 (HsGCN1). [Source:Uniprot/SWISSPROT;Acc:Q92616]
ENSG0000 0089177	SNX23_ HUMA N	Kinesin-like motor protein C20orf23 (Sorting nexin 23). [Source:Uniprot/SWISSPROT;Acc:Q96L93]
ENSG0000 0089250	NOS1	"Nitric-oxide synthase, brain (EC 1.14.13.39) (NOS type I) (Neuronal NOS) (N-NOS) (nNOS) (Constitutive NOS) (NC-NOS) (bNOS). [Source:Uniprot/SWISSPROT;Acc:P29475]"
ENSG0000 0089597	GANAB	Neutral alpha-glucosidase AB precursor (EC 3.2.1.84) (Glucosidase II alpha subunit). [Source:Uniprot/SWISSPROT;Acc:Q14697]
ENSG0000 0089737	DDX24	ATP-dependent RNA helicase DDX24 (EC 3.6.1.-) (DEAD box protein 24). [Source:Uniprot/SWISSPROT;Acc:Q9GZR7]
ENSG0000 0089876	DHX32	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 32 [Source:RefSeq_peptide;Acc:NP_060650]
ENSG0000 0090054	SPTLC1	Serine palmitoyltransferase 1 (EC 2.3.1.50) (Long chain base biosynthesis protein 1) (LCB 1) (Serine-palmitoyl-CoA transferase 1) (SPT 1) (SPT1). [Source:Uniprot/SWISSPROT;Acc:O15269]
ENSG0000 0090060	PAPOL A	Poly(A) polymerase alpha (EC 2.7.7.19) (PAP) (Polynucleotide adenylyltransferase alpha). [Source:Uniprot/SWISSPROT;Acc:P51003]
ENSG0000 0090273	NUDC	Nuclear migration protein nudC (Nuclear distribution protein C homolog). [Source:Uniprot/SWISSPROT;Acc:Q9Y266]
ENSG0000 0090520	DNAJB 11	DnaJ homolog subfamily B member 11 precursor (ER-associated dnaJ protein 3) (ErJ3) (ER-associated Hsp40 co-chaperone) (hDj9) (PWP1- interacting protein 4). [Source:Uniprot/SWISSPROT;Acc:Q9UBS4]
ENSG0000 0090621	PABPC 4	Polyadenylate-binding protein 4 (Poly(A)-binding protein 4) (PABP 4) (Inducible poly(A)-binding protein) (iPABP) (Activated-platelet protein 1) (APP-1). [Source:Uniprot/SWISSPROT;Acc:Q13310]
ENSG0000 0090861	AARS	Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS). [Source:Uniprot/SWISSPROT;Acc:P49588]
ENSG0000 0090889	KIF4A	Chromosome-associated kinesin KIF4A (Chromokinesin). [Source:Uniprot/SWISSPROT;Acc:O95239]
ENSG0000 0091140	DLD	"Dihydrolipoyl dehydrogenase, mitochondrial precursor (EC 1.8.1.4) (Dihydrolipoamide dehydrogenase) (Glycine cleavage system L protein). [Source:Uniprot/SWISSPROT;Acc:P09622]"
ENSG0000 0091262	ABCC6	Multidrug resistance-associated protein 6 (ATP-binding cassette sub- family C member 6) (Anthracycline resistance-associated protein) (Multi-specific organic anion tranporter-E) (MOAT-E). [Source:Uniprot/SWISSPROT;Acc:O95255]
ENSG0000 0091536	MYO15 A	Myosin-15 (Myosin XV) (Unconventional myosin-15). [Source:Uniprot/SWISSPROT;Acc:Q9UKN7]
ENSG0000 0092054	MYH7	"Myosin heavy chain, cardiac muscle beta isoform (MyHC-beta). [Source:Uniprot/SWISSPROT;Acc:P12883]"
ENSG0000 0092108	SCFD1	Sec1 family domain containing protein 1 (Syntaxin-binding protein 1- like 2) (Sly1p). [Source:Uniprot/SWISSPROT;Acc:Q8WVM8]
ENSG0000 0092201	SUPT16 H	chromatin-specific transcription elongation factor large subunit [Source:RefSeq_peptide;Acc:NP_009123]
ENSG0000 0092529	CAPN3	Calpain-3 (EC 3.4.22.-) (Calpain L3) (Calpain p94) (Calcium-activated neutral proteinase 3) (CANP 3) (Muscle-specific calcium-activated neutral protease 3) (nCL-1). [Source:Uniprot/SWISSPROT;Acc:P20807]
ENSG0000	**ULK4**	**ULK4 protein. [Source:Uniprot/SPTREMBL;Acc:Q96C45]**

0093222		
ENSG0000 0094841	NP_659 489.1	
ENSG0000 0094880	CDC23	Cell division cycle protein 23 homolog (Anaphase promoting complex subunit 8) (APC8) (Cyclosome subunit 8). [Source:Uniprot/SWISSPROT;Acc:Q9UJX2]
ENSG0000 0095015	MAP3K 1	Mitogen-activated protein kinase kinase kinase 1 (EC 2.7.1.37) (MAPK/ERK kinase kinase 1) (MEK kinase 1) (MEKK 1) (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q13233]
ENSG0000 0095059	DHPS	Deoxyhypusine synthase (EC 2.5.1.46) (DHS). [Source:Uniprot/SWISSPROT;Acc:P49366]
ENSG0000 0095139	ARCN1	Coatomer delta subunit (Delta-coat protein) (Delta-COP) (Archain). [Source:Uniprot/SWISSPROT;Acc:P48444]
ENSG0000 0095492		
ENSG0000 0095564	BTAF1	TATA-binding-protein-associated factor 172 (EC 3.6.1.-) (ATP-dependent helicase BTAF1) (TBP-associated factor 172) (TAF-172) (TAF(II)170) (B- TFIID transcription factor-associated 170 kDa subunit). [Source:Uniprot/SWISSPROT;Acc:O14981]
ENSG0000 0095777	MYO3A	Myosin IIIA (EC 2.7.1.37). [Source:Uniprot/SWISSPROT;Acc:Q8NEV4]
ENSG0000 0095906	NUBP2	Nucleotide binding protein 2 (NBP 2). [Source:Uniprot/SWISSPROT;Acc:Q9Y5Y2]
ENSG0000 0096063	SRPK1	Serine/threonine-protein kinase SRPK1 (EC 2.7.1.37) (Serine/arginine- rich protein-specific kinase 1) (SR-protein-specific kinase 1) (SFRS protein kinase 1). [Source:Uniprot/SWISSPROT;Acc:Q96SB4]
ENSG0000 0096093	**EFHC1**	**EF-hand domain-containing protein 1. [Source:Uniprot/SWISSPROT;Acc:Q5JVL4]**
ENSG0000 0096150	RPS18	40S ribosomal protein S18 (Ke-3) (Ke3). [Source:Uniprot/SWISSPROT;Acc:P62269]
ENSG0000 0096171	VARS	Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (ValRS) (G7a protein). [Source:Uniprot/SWISSPROT;Acc:P26640]
ENSG0000 0096384	HSPCB	Heat shock protein HSP 90-beta (HSP 84) (HSP 90). [Source:Uniprot/SWISSPROT;Acc:P08238]
ENSG0000 0096469		
ENSG0000 0096872	**IFT74**	**Intraflagellar transport 74 homolog (Coiled-coil domain-containing protein 2) (Capillary morphogenesis protein 1) (CMG-1). [Source:Uniprot/SWISSPROT;Acc:Q96LB3]**
ENSG0000 0097054		
ENSG0000 0099246	RAB18	Ras-related protein Rab-18. [Source:Uniprot/SWISSPROT;Acc:Q9NP72]
ENSG0000 0099308	MAST3	Microtubule-associated serine/threonine-protein kinase 3 (EC 2.7.1.37). [Source:Uniprot/SWISSPROT;Acc:O60307]
ENSG0000 0099331	MYO9B	Myosin-9B (Myosin IXb) (Unconventional myosin-9b). [Source:Uniprot/SWISSPROT;Acc:Q13459]
ENSG0000 0099725	PRKY	Serine/threonine-protein kinase PRKY (EC 2.7.1.37). [Source:Uniprot/SWISSPROT;Acc:O43930]
ENSG0000 0100029	PES1	Pescadillo homolog 1. [Source:Uniprot/SWISSPROT;Acc:O00541]
ENSG0000 0100030	MAPK1	Mitogen-activated protein kinase 1 (EC 2.7.1.37) (Extracellular signal-regulated kinase 2) (ERK-2) (Mitogen-activated protein kinase 2) (MAP kinase 2) (MAPK 2) (p42-MAPK) (ERT1). [Source:Uniprot/SWISSPROT;Acc:P28482]
ENSG0000 0100033	PRODH	"Proline oxidase, mitochondrial precursor (EC 1.5.3.-) (Proline dehydrogenase). [Source:Uniprot/SWISSPROT;Acc:O43272]"
ENSG0000 0100038	TOP3B	DNA topoisomerase III beta-1 (EC 5.99.1.2). [Source:Uniprot/SWISSPROT;Acc:O95985]
ENSG0000 0100077	ADRBK 2	Beta-adrenergic receptor kinase 2 (EC 2.7.1.126) (Beta-ARK-2) (G- protein coupled receptor kinase 3). [Source:Uniprot/SWISSPROT;Acc:P35626]
ENSG0000 0100171		
ENSG0000 0100181	CSNK1 E	"Casein kinase I, epsilon isoform (EC 2.7.1.-) (CKI-epsilon) (CKIe). [Source:Uniprot/SWISSPROT;Acc:P49674]"
ENSG0000 0100196	KDELR 3	ER lumen protein retaining receptor 3 (KDEL receptor 3) (KDEL endoplasmic reticulum protein retention receptor 3). [Source:Uniprot/SWISSPROT;Acc:O43731]
ENSG0000 0100201	DDX17	Probable ATP-dependent RNA helicase DDX17 (EC 3.6.1.-) (DEAD box protein 17) (RNA-dependent helicase p72) (DEAD box protein p72). [Source:Uniprot/SWISSPROT;Acc:Q92841]
ENSG0000 0100206	DMC1	Meiotic recombination protein DMC1/LIM15 homolog. [Source:Uniprot/SWISSPROT;Acc:Q14565]
ENSG0000 0100243	CYB5R 3	NADH-cytochrome b5 reductase (EC 1.6.2.2) (B5R) (Diaphorase-1) (Cytochrome b5 reductase 3) [Contains: NADH-cytochrome b5 reductase membrane-bound form; NADH-cytochrome b5 reductase soluble form]. [Source:Uniprot/SWISSPROT;Acc:P00387]
ENSG0000 0100271	**TTLL1**	**Tubulin tyrosine ligase-like protein 1. [Source:Uniprot/SWISSPROT;Acc:O95922]**
ENSG0000 0100297	MCM5	DNA replication licensing factor MCM5 (CDC46 homolog) (P1-CDC46). [Source:Uniprot/SWISSPROT;Acc:P33992]
ENSG0000 0100345	MYH9	"Myosin-9 (Myosin heavy chain, nonmuscle IIa) (Nonmuscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA) (Cellular myosin heavy chain, type A) (Nonmuscle myosin heavy chain-A) (NMMHC-A). [Source:Uniprot/SWISSPROT;Acc:P35579]"
ENSG0000 0100346	**CACN A1I**	**Voltage-dependent T-type calcium channel alpha-1I subunit (Voltage- gated calcium channel alpha subunit Cav3.3) (Ca(v)3.3). [Source:Uniprot/SWISSPROT;Acc:Q9P0X4]**
ENSG0000 0100412	ACO2	"Aconitate hydratase, mitochondrial precursor (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase). [Source:Uniprot/SWISSPROT;Acc:Q99798]"

ENSG0000 0100490	CDKL1	Cyclin-dependent kinase-like 1 (EC 2.7.1.37) (Serine/threonine-protein kinase KKIALRE) (Protein kinase p42 KKIALRE). [Source:Uniprot/SWISSPROT;Acc:Q00532]
ENSG0000 0100519	PSMC6	26S protease regulatory subunit S10B (Proteasome subunit p42) (Proteasome 26S subunit ATPase 6). [Source:Uniprot/SWISSPROT;Acc:P62333]
ENSG0000 0100554	ATP6V 1D	Vacuolar ATP synthase subunit D (EC 3.6.3.14) (V-ATPase D subunit) (Vacuolar proton pump D subunit) (V-ATPase 28 kDa accessory protein). [Source:Uniprot/SWISSPROT;Acc:Q9Y5K8]
ENSG0000 0100567	PSMA3	Proteasome subunit alpha type 3 (EC 3.4.25.1) (Proteasome component C8) (Macropain subunit C8) (Multicatalytic endopeptidase complex subunit C8). [Source:Uniprot/SWISSPROT;Acc:P25788]
ENSG0000 0100591	AHSA1	Activator of 90 kDa heat shock protein ATPase homolog 1 (AHA1) (p38). [Source:Uniprot/SWISSPROT;Acc:O95433]
ENSG0000 0100596	SPTLC2	Serine palmitoyltransferase 2 (EC 2.3.1.50) (Long chain base biosynthesis protein 2) (LCB 2) (Serine-palmitoyl-CoA transferase 2) (SPT 2). [Source:Uniprot/SWISSPROT;Acc:O15270]
ENSG0000 0100614	PPM1A	Protein phosphatase 2C isoform alpha (EC 3.1.3.16) (PP2C-alpha) (IA) (Protein phosphatase 1A). [Source:Uniprot/SWISSPROT;Acc:P35813]
ENSG0000 0100654		
ENSG0000 0100714	MTHFD 1	"C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) [Includes: Methylenetetrahydrofolate dehydrogenase (EC 1.5.1.5); Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9); Formyltetrahydrofolate synthetase (EC 6.3.4.3)]. [Source:Uniprot/SWISSPROT;Acc:P11586]"
ENSG0000 0100764	PSMC1	26S protease regulatory subunit 4 (P26s4) (Proteasome 26S subunit ATPase 1). [Source:Uniprot/SWISSPROT;Acc:P62191]
ENSG0000 0100784	RPS6K A5	Ribosomal protein S6 kinase alpha 5 (EC 2.7.1.37) (Nuclear mitogen-and stress-activated protein kinase 1) (90 kDa ribosomal protein S6 kinase 5) (RSK-like protein kinase) (RLSK). [Source:Uniprot/SWISSPROT;Acc:O75582]
ENSG0000 0100804	PSMB5	Proteasome subunit beta type 5 precursor (EC 3.4.25.1) (Proteasome epsilon chain) (Macropain epsilon chain) (Multicatalytic endopeptidase complex epsilon chain) (Proteasome subunit X) (Proteasome chain 6) (Proteasome subunit MB1). [Source:Uniprot/SWISSPROT;Acc:P28074]
ENSG0000 0100839		
ENSG0000 0100883	SRP54	Signal recognition particle 54 kDa protein (SRP54). [Source:Uniprot/SWISSPROT;Acc:P61011]
ENSG0000 0100888	CHD8	Chromodomain-helicase-DNA-binding protein 8 (EC 3.6.1.-) (ATP- dependent helicase CHD8) (CHD-8) (Helicase with SNF2 domain 1). [Source:Uniprot/SWISSPROT;Acc:Q9HCK8]
ENSG0000 0100926	TM9SF 1	Transmembrane 9 superfamily protein member 1 precursor (hMP70). [Source:Uniprot/SWISSPROT;Acc:O15321]
ENSG0000 0100934	SEC23A	Protein transport protein Sec23A (SEC23-related protein A). [Source:Uniprot/SWISSPROT;Acc:Q15436]
ENSG0000 0100983	GSS	Glutathione synthetase (EC 6.3.2.3) (Glutathione synthase) (GSH synthetase) (GSH-S). [Source:Uniprot/SWISSPROT;Acc:P48637]
ENSG0000 0101049	SGK2	Serine/threonine-protein kinase Sgk2 (EC 2.7.1.37) (Serum/glucocorticoid regulated kinase 2). [Source:Uniprot/SWISSPROT;Acc:Q9HBY8]
ENSG0000 0101052	**IFT52**	**Intraflagellar transport 52 homolog (Protein NGD5 homolog). [Source:Uniprot/SWISSPROT;Acc:Q9Y366]**
ENSG0000 0101109	STK4	Serine/threonine-protein kinase 4 (EC 2.7.1.37) (STE20-like kinase MST1) (MST-1) (Mammalian STE20-like protein kinase 1) (Serine/threonine-protein kinase Krs-2). [Source:Uniprot/SWISSPROT;Acc:Q13043]
ENSG0000 0101156		
ENSG0000 0101162	TUBB1	Tubulin beta-1 chain. [Source:Uniprot/SWISSPROT;Acc:Q9H4B7]
ENSG0000 0101181	GTPBP 5	Putative GTP-binding protein 5. [Source:Uniprot/SWISSPROT;Acc:Q9H4K7]
ENSG0000 0101182	PSMA7	Proteasome subunit alpha type 7 (EC 3.4.25.1) (Proteasome subunit RC6- 1) (Proteasome subunit XAPC7). [Source:Uniprot/SWISSPROT;Acc:O14818]
ENSG0000 0101210	EEF1A2	Elongation factor 1-alpha 2 (EF-1-alpha-2) (Elongation factor 1 A-2) (eEF1A-2) (Statin S1). [Source:Uniprot/SWISSPROT;Acc:Q05639]
ENSG0000 0101229	SPTLC2 L	"CDNA FLJ90790 fis, clone THYRO1001529, moderately similar to Serine palmitoyltransferase 2 (EC 2.3.1.50). [Source:Uniprot/SPTREMBL;Acc:Q8N2H1]"
ENSG0000 0101247	NP_077 025.2	
ENSG0000 0101266	CSNK2 A1	"Casein kinase II, alpha chain (EC 2.7.1.37) (CK II). [Source:Uniprot/SWISSPROT;Acc:P68400]"
ENSG0000 0101290	CDS2	Phosphatidate cytidylyltransferase 2 (EC 2.7.7.41) (CDP-diglyceride synthetase 2) (CDP-diglyceride pyrophosphorylase 2) (CDP- diacylglycerol synthase 2) (CDS 2) (CTP:phosphatidate cytidylyltransferase 2) (CDP-DAG synthase 2) (CDP-DG synthetase 2). [Source:Uniprot/SWISSPROT;Acc:O95674]
ENSG0000 0101294	HM13	Minor histocompatibility antigen H13 (EC 3.4.99.-) (Signal peptide peptidase) (Presenilin-like protein 3) (hIMP1 protein). [Source:Uniprot/SWISSPROT;Acc:Q8TCT9]
ENSG0000 0101310	SEC23B	Protein transport protein Sec23B (SEC23-related protein B). [Source:Uniprot/SWISSPROT;Acc:Q15437]
ENSG0000 0101337	TM9SF 4	Transmembrane 9 superfamily protein member 4. [Source:Uniprot/SWISSPROT;Acc:Q92544]
ENSG0000 0101343	CRNKL 1	Crooked neck-like protein 1 (Crooked neck homolog) (hCrn). [Source:Uniprot/SWISSPROT;Acc:Q9BZJ0]
ENSG0000 0101347	SAMH D1	SAM domain and HD domain-containing protein 1 (Dendritic cell-derived IFNG-induced protein) (DCIP) (Monocyte protein 5) (MOP-5). [Source:Uniprot/SWISSPROT;Acc:Q9Y3Z3]
ENSG0000 0101349	PAK7	Serine/threonine-protein kinase PAK 7 (EC 2.7.1.37) (p21-activated kinase 7) (PAK-7) (PAK-5). [Source:Uniprot/SWISSPROT;Acc:Q9P286]
ENSG0000 0101350	KIF3B	Kinesin-like protein KIF3B (Microtubule plus end-directed kinesin motor 3B) (HH0048). [Source:Uniprot/SWISSPROT;Acc:O15066]
ENSG0000	NOL5A	Nucleolar protein Nop56 (Nucleolar protein 5A). [Source:Uniprot/SWISSPROT;Acc:O00567]

0101361		
ENSG0000 0101444	AHCY	Adenosylhomocysteinase (EC 3.3.1.1) (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase). [Source:Uniprot/SWISSPROT;Acc:P23526]
ENSG0000 0101452	DHX35	Probable ATP-dependent RNA helicase DHX35 (EC 3.6.1.-) (DEAH box protein 35). [Source:Uniprot/SWISSPROT;Acc:Q9H5Z1]
ENSG0000 0101557	USP14	Ubiquitin carboxyl-terminal hydrolase 14 (EC 3.1.2.15) (Ubiquitin thiolesterase 14) (Ubiquitin-specific processing protease 14) (Deubiquitinating enzyme 14). [Source:Uniprot/SWISSPROT;Acc:P54578]
ENSG0000 0101577	LPIN2	Lipin-2. [Source:Uniprot/SWISSPROT;Acc:Q92539]
ENSG0000 0101868	POLA	DNA polymerase alpha catalytic subunit (EC 2.7.7.7). [Source:Uniprot/SWISSPROT;Acc:P09884]
ENSG0000 0101911	PRPS2	Ribose-phosphate pyrophosphokinase II (EC 2.7.6.1) (Phosphoribosyl pyrophosphate synthetase II) (PRS-II) (PPRibP). [Source:Uniprot/SWISSPROT;Acc:P11908]
ENSG0000 0101974	ATP11C	Probable phospholipid-transporting ATPase IG (EC 3.6.3.1) (ATPase class I type 11C) (ATPase IG) (ATPase IQ) (ATPase class VI type 11C). [Source:Uniprot/SWISSPROT;Acc:Q8NB49]
ENSG0000 0102001	**CACN A1F**	**Voltage-dependent L-type calcium channel alpha-1F subunit (Voltage- gated calcium channel alpha subunit Cav1.4). [Source:Uniprot/SWISSPROT;Acc:O60840]**
ENSG0000 0102038	SMARC A1	Possible global transcription activator SNF2L1 (EC 3.6.1.-) (ATP- dependent helicase SMARCA1) (SWI/SNF-related matrix associated actin dependent regulator of chromatin subfamily A member 1). [Source:Uniprot/SWISSPROT;Acc:P28370]
ENSG0000 0102069	UBE2N L	
ENSG0000 0102129		
ENSG0000 0102144	PGK1	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Primer recognition protein 2) (PRP 2). [Source:Uniprot/SWISSPROT;Acc:P00558]
ENSG0000 0102225	PCTK1	Serine/threonine-protein kinase PCTAIRE-1 (EC 2.7.1.37) (PCTAIRE-motif protein kinase 1). [Source:Uniprot/SWISSPROT;Acc:Q00536]
ENSG0000 0102314		
ENSG0000 0102572	STK24	Serine/threonine-protein kinase 24 (EC 2.7.1.37) (STE20-like kinase MST3) (MST-3) (Mammalian STE20-like protein kinase 3). [Source:Uniprot/SWISSPROT;Acc:Q9Y6E0]
ENSG0000 0102753	KPNA3	Importin alpha-3 subunit (Karyopherin alpha-3 subunit) (SRP1-gamma). [Source:Uniprot/SWISSPROT;Acc:O00505]
ENSG0000 0102781	KATNA L1	Katanin p60 ATPase-containing subunit A-like 1 (EC 3.6.4.3) (Katanin p60 subunit A-like 1) (p60 katanin-like 1). [Source:Uniprot/SWISSPROT;Acc:Q9BW62]
ENSG0000 0102882	MAPK3	Mitogen-activated protein kinase 3 (EC 2.7.1.37) (Extracellular signal-regulated kinase 1) (ERK-1) (Insulin-stimulated MAP2 kinase) (MAP kinase 1) (MAPK 1) (p44-ERK1) (ERT2) (p44-MAPK) (Microtubule- associated protein 2 kinase). [Source:Uniprot/SWISSPROT;Acc:P27361]
ENSG0000 0103024	NME3	Nucleoside diphosphate kinase 3 (EC 2.7.4.6) (NDK 3) (NDP kinase 3) (Nucleoside diphosphate kinase C) (NDPKC) (nm23-H3) (DR-nm23). [Source:Uniprot/SWISSPROT;Acc:Q13232]
ENSG0000 0103200	NME4	"Nucleoside diphosphate kinase, mitochondrial precursor (EC 2.7.4.6) (NDP kinase, mitochondrial) (NDK) (nm23-H4) (Nucleoside diphosphate kinase D) (NDPKD). [Source:Uniprot/SWISSPROT;Acc:O00746]"
ENSG0000 0103222	ABCC1	Multidrug resistance-associated protein 1 (ATP-binding cassette sub- family C member 1). [Source:Uniprot/SWISSPROT;Acc:P33527]
ENSG0000 0103245	NARFL	nuclear prelamin A recognition factor-like [Source:RefSeq_peptide;Acc:NP_071938]
ENSG0000 0103249	CLCN7	Chloride channel protein 7 (ClC-7). [Source:Uniprot/SWISSPROT;Acc:P51798]
ENSG0000 0103274	NUBP1	Nucleotide-binding protein 1 (NBP 1). [Source:Uniprot/SWISSPROT;Acc:P53384]
ENSG0000 0103275	UBE2I	Ubiquitin-conjugating enzyme E2 I (EC 6.3.2.19) (Ubiquitin-protein ligase I) (Ubiquitin carrier protein I) (SUMO-1-protein ligase) (SUMO- 1-conjugating enzyme) (Ubiquitin carrier protein 9) (p18). [Source:Uniprot/SWISSPROT;Acc:P63279]
ENSG0000 0103342	GSPT1	G1 to S phase transition protein 1 homolog (GTP-binding protein GST1- HS). [Source:Uniprot/SWISSPROT;Acc:P15170]
ENSG0000 0103351	**CLUAP 1**	**clusterin associated protein 1 isoform 2 [Source:RefSeq_peptide;Acc:NP_079069]**
ENSG0000 0103510	MYST1	"Probable histone acetyltransferase MYST1 (EC 2.3.1.48) (MYST protein 1) (MOZ, YBF2/SAS3, SAS2 and TIP60 protein 1) (hMOF). [Source:Uniprot/SWISSPROT;Acc:Q9H7Z6]"
ENSG0000 0103769	RAB11 A	Ras-related protein Rab-11A (Rab-11) (YL8). [Source:Uniprot/SWISSPROT;Acc:P62491]
ENSG0000 0103811	CTSH	Cathepsin H precursor (EC 3.4.22.16) [Contains: Cathepsin H mini chain; Cathepsin H heavy chain; Cathepsin H light chain]. [Source:Uniprot/SWISSPROT;Acc:P09668]
ENSG0000 0104043	ATP8B4	Probable phospholipid-transporting ATPase IM (EC 3.6.3.1) (ATPase class I type 8B member 4). [Source:Uniprot/SWISSPROT;Acc:Q8TF62]
ENSG0000 0104205	SGK3	Serine/threonine-protein kinase Sgk3 (EC 2.7.1.37) (Serum/glucocorticoid regulated kinase 3) (Serum/glucocorticoid regulated kinase-like). [Source:Uniprot/SWISSPROT;Acc:Q96BR1]
ENSG0000 0104375	STK3	Serine/threonine-protein kinase 3 (EC 2.7.1.37) (STE20-like kinase MST2) (MST-2) (Mammalian STE20-like protein kinase 2) (Serine/threonine-protein kinase Krs-1). [Source:Uniprot/SWISSPROT;Acc:Q13188]
ENSG0000 0104388	RAB2	Ras-related protein Rab-2A. [Source:Uniprot/SWISSPROT;Acc:P61019]
ENSG0000 0104687	GSR	"Glutathione reductase, mitochondrial precursor (EC 1.8.1.7) (GR) (GRase). [Source:Uniprot/SWISSPROT;Acc:P00390]"
ENSG0000 0104695	PPP2CB	"Serine/threonine protein phosphatase 2A, catalytic subunit, beta isoform (EC 3.1.3.16) (PP2A-beta). [Source:Uniprot/SWISSPROT;Acc:P62714]"
ENSG0000 0104731	KLHDC 4	kelch domain containing 4 [Source:RefSeq_peptide;Acc:NP_060036]

ENSG00000104732		
ENSG00000104738	MCM4	DNA replication licensing factor MCM4 (CDC21 homolog) (P1-CDC21). [Source:Uniprot/SWISSPROT;Acc:P33991]
ENSG00000104814	MAP4K1	Mitogen-activated protein kinase kinase kinase kinase 1 (EC 2.7.1.37) (MAPK/ERK kinase kinase kinase 1) (MEK kinase kinase 1) (MEKKK 1) (Hematopoietic progenitor kinase). [Source:Uniprot/SWISSPROT;Acc:Q92918]
ENSG00000104833	TUBB4	Tubulin beta-4 chain (Tubulin 5 beta). [Source:Uniprot/SWISSPROT;Acc:P04350]
ENSG00000104853	CLPTM1	cleft lip and palate associated transmembrane protein 1 [Source:RefSeq_peptide;Acc:NP_001285]
ENSG00000104884	ERCC2	TFIIH basal transcription factor complex helicase subunit (EC 3.6.1.-) (DNA-repair protein complementing XP-D cells) (Xeroderma pigmentosum group D complementing protein) (CXPD) (DNA excision repair protein ERCC-2). [Source:Uniprot/SWISSPROT;Acc:P18074]
ENSG00000104889	RNASEH2A	Ribonuclease HI large subunit (EC 3.1.26.4) (RNase HI large subunit) (Ribonuclease H2) (RNase H2) (RNase H(35)). [Source:Uniprot/SWISSPROT;Acc:O75792]
ENSG00000104936	DMPK	Myotonin-protein kinase (EC 2.7.1.37) (Myotonic dystrophy protein kinase) (MDPK) (DM-kinase) (DMK) (DMPK) (MT-PK). [Source:Uniprot/SWISSPROT;Acc:Q09013]
ENSG00000104946	TBC1D17	TBC1 domain family member 17. [Source:Uniprot/SWISSPROT;Acc:Q9HA65]
ENSG00000105146	AURKC	Serine/threonine-protein kinase 13 (EC 2.7.1.37) (Aurora/Ipl1/Eg2 protein 2) (Aurora/Ipl1-related kinase 3) (Aurora-C). [Source:Uniprot/SWISSPROT;Acc:Q9UQB9]
ENSG00000105202	FBL	Fibrillarin (34 kDa nucleolar scleroderma antigen). [Source:Uniprot/SWISSPROT;Acc:P22087]
ENSG00000105204	DYRK1B	Dual specificity tyrosine-phosphorylation regulated kinase 1B (EC 2.7.1.37) (EC 2.7.1.112) (Mirk protein kinase) (Minibrain-related kinase). [Source:Uniprot/SWISSPROT;Acc:Q9Y463]
ENSG00000105221	AKT2	"RAC-beta serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-beta) (Protein kinase Akt-2) (Protein kinase B, beta) (PKB beta). [Source:Uniprot/SWISSPROT;Acc:P31751]"
ENSG00000105287	PRKD2	"Protein kinase C, D2 type (EC 2.7.1.-) (nPKC-D2) (Protein kinase D2). [Source:Uniprot/SWISSPROT;Acc:Q9BZL6]"
ENSG00000105357	MYH14	"Myosin-14 (Myosin heavy chain, nonmuscle IIc) (Nonmuscle myosin heavy chain IIc) (NMHC II-C). [Source:Uniprot/SWISSPROT;Acc:Q7Z406]"
ENSG00000105379	ETFB	Electron transfer flavoprotein beta-subunit (Beta-ETF). [Source:Uniprot/SWISSPROT;Acc:P38117]
ENSG00000105409	ATP1A3	Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) (Sodium pump 3) (Na+/K+ ATPase 3) (Alpha(III)). [Source:Uniprot/SWISSPROT;Acc:P13637]
ENSG00000105438	KDELR1	ER lumen protein retaining receptor 1 (KDEL receptor 1) (KDEL endoplasmic reticulum protein retention receptor 1). [Source:Uniprot/SWISSPROT;Acc:P24390]
ENSG00000105447	GRWD1	Glutamate-rich WD repeat-containing protein 1. [Source:Uniprot/SWISSPROT;Acc:Q9BQ67]
ENSG00000105486	LIG1	DNA ligase I (EC 6.5.1.1) (Polydeoxyribonucleotide synthase [ATP]). [Source:Uniprot/SWISSPROT;Acc:P18858]
ENSG00000105514	RAB3D	Ras-related protein Rab-3D. [Source:Uniprot/SWISSPROT;Acc:O95716]
ENSG00000105576	TNPO2	Transportin-2 (Karyopherin beta-2b). [Source:Uniprot/SWISSPROT;Acc:O14787]
ENSG00000105613	MAST1	Microtubule-associated serine/threonine-protein kinase 1 (EC 2.7.1.37) (Syntrophin-associated serine/threonine-protein kinase). [Source:Uniprot/SWISSPROT;Acc:Q9Y2H9]
ENSG00000105649	RAB3A	Ras-related protein Rab-3A. [Source:Uniprot/SWISSPROT;Acc:P20336]
ENSG00000105650	**PDE4C**	**"cAMP-specific 3',5'-cyclic phosphodiesterase 4C (EC 3.1.4.17) (DPDE1) (PDE21). [Source:Uniprot/SWISSPROT;Acc:Q08493]"**
ENSG00000105671	DDX49	Probable ATP-dependent RNA helicase DDX49 (EC 3.6.1.-) (DEAD box protein 49). [Source:Uniprot/SWISSPROT;Acc:Q9Y6V7]
ENSG00000105675	ATP4A	Potassium-transporting ATPase alpha chain 1 (EC 3.6.3.10) (Proton pump) (Gastric H+/K+ ATPase alpha subunit). [Source:Uniprot/SWISSPROT;Acc:P20648]
ENSG00000105679	GAPDHS	"Glyceraldehyde-3-phosphate dehydrogenase, testis-specific (EC 1.2.1.12) (Spermatogenic cell-specific glyceraldehyde 3-phosphate dehydrogenase 2) (GAPDH-2). [Source:Uniprot/SWISSPROT;Acc:O14556]"
ENSG00000105723	GSK3A	Glycogen synthase kinase-3 alpha (EC 2.7.1.37) (GSK-3 alpha). [Source:Uniprot/SWISSPROT;Acc:P49840]
ENSG00000105726	Q8TEG5_HUMAN	
ENSG00000105810	CDK6	Cell division protein kinase 6 (EC 2.7.1.37) (Serine/threonine-protein kinase PLSTIRE). [Source:Uniprot/SWISSPROT;Acc:Q00534]
ENSG00000105819	PMPCB	"Mitochondrial processing peptidase beta subunit, mitochondrial precursor (EC 3.4.24.64) (Beta-MPP) (P-52). [Source:Uniprot/SWISSPROT;Acc:O75439]"
ENSG00000105865	DUS4L	dihydrouridine synthase 4-like [Source:RefSeq_peptide;Acc:NP_853559]
ENSG00000105877	**DNAH11**	**Ciliary dynein heavy chain 11 (Axonemal beta dynein heavy chain 11). [Source:Uniprot/SWISSPROT;Acc:Q96DT5]**
ENSG00000105929	ATP6V0A4	Vacuolar proton translocating ATPase 116 kDa subunit a isoform 4 (V- ATPase 116-kDa isoform a4) (Vacuolar proton translocating ATPase 116 kDa subunit a kidney isoform). [Source:Uniprot/SWISSPROT;Acc:Q9HBG4]
ENSG00000105948	**NP_079202.1**	
ENSG00000105953	OGDH	"2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor (EC 1.2.4.2) (Alpha-ketoglutarate dehydrogenase). [Source:Uniprot/SWISSPROT;Acc:Q02218]"
ENSG00000106066	CPVL	"Probable serine carboxypeptidase CPVL precursor (EC 3.4.16.-) (Carboxypeptidase, vitellogenic-like) (Vitellogenic carboxypeptidase- like protein) (VCP-like protein). [Source:Uniprot/SWISSPROT;Acc:Q9H3G5]"

ENSG0000 0106105	GARS	Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS). [Source:Uniprot/SWISSPROT;Acc:P41250]
ENSG0000 0106348	IMPDH 1	Inosine-5'-monophosphate dehydrogenase 1 (EC 1.1.1.205) (IMP dehydrogenase 1) (IMPDH-I) (IMPD 1). [Source:Uniprot/SWISSPROT;Acc:P20839]
ENSG0000 0106384	NP_835 470.1	monoacylglycerol O-acyltransferase 3 [Source:RefSeq_peptide;Acc:NP_835470]
ENSG0000 0106580		
ENSG0000 0106588	PSMA2	Proteasome subunit alpha type 2 (EC 3.4.25.1) (Proteasome component C3) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3). [Source:Uniprot/SWISSPROT;Acc:P25787]
ENSG0000 0106976	DNM1	Dynamin-1 (EC 3.6.5.5). [Source:Uniprot/SWISSPROT;Acc:Q05193]
ENSG0000 0107290	SETX	Probable helicase senataxin (EC 3.6.1.-) (SEN1 homolog). [Source:Uniprot/SWISSPROT;Acc:Q7Z333]
ENSG0000 0107331	ABCA2	ATP-binding cassette sub-family A member 2 (ATP-binding cassette transporter 2) (ATP-binding cassette 2). [Source:Uniprot/SWISSPROT;Acc:Q9BZC7]
ENSG0000 0107625	DDX50	ATP-dependent RNA helicase DDX50 (EC 3.6.1.-) (DEAD box protein 50) (Nucleolar protein Gu2) (Gu-beta). [Source:Uniprot/SWISSPROT;Acc:Q9BQ39]
ENSG0000 0107643	MAPK8	Mitogen-activated protein kinase 8 (EC 2.7.1.37) (Stress-activated protein kinase JNK1) (c-Jun N-terminal kinase 1) (JNK-46). [Source:Uniprot/SWISSPROT;Acc:P45983]
ENSG0000 0107671		
ENSG0000 0107758	PPP3CB	"Serine/threonine protein phosphatase 2B catalytic subunit, beta isoform (EC 3.1.3.16) (Calmodulin-dependent calcineurin A subunit, beta isoform) (CAM-PRP catalytic subunit). [Source:Uniprot/SWISSPROT;Acc:P16298]"
ENSG0000 0107796	ACTA2	"Actin, aortic smooth muscle (Alpha-actin-2). [Source:Uniprot/SWISSPROT;Acc:P62736]"
ENSG0000 0107937	GTPBP 4	Nucleolar GTP-binding protein 1 (Chronic renal failure gene protein) (GTP-binding protein NGB). [Source:Uniprot/SWISSPROT;Acc:Q9BZE4]
ENSG0000 0107987		
ENSG0000 0108055	CSPG6	Structural maintenance of chromosome 3 (Chondroitin sulfate proteoglycan 6) (Chromosome-associated polypeptide) (hCAP) (Bamacan) (Basement membrane-associated chondroitin proteoglycan). [Source:Uniprot/SWISSPROT;Acc:Q9UQE7]
ENSG0000 0108094	CUL2	Cullin-2 (CUL-2). [Source:Uniprot/SWISSPROT;Acc:Q13617]
ENSG0000 0108106	UBE2S	Ubiquitin-conjugating enzyme E2S (EC 6.3.2.19) (Ubiquitin-conjugating enzyme E2-24 kDa) (Ubiquitin-protein ligase) (Ubiquitin carrier protein) (E2-EPF5). [Source:Uniprot/SWISSPROT;Acc:Q16763]
ENSG0000 0108179	PPIF	"Peptidyl-prolyl cis-trans isomerase, mitochondrial precursor (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin F). [Source:Uniprot/SWISSPROT;Acc:P30405]"
ENSG0000 0108298	RPL19	60S ribosomal protein L19. [Source:Uniprot/SWISSPROT;Acc:P84098]
ENSG0000 0108344	PSMD3	26S proteasome non-ATPase regulatory subunit 3 (26S proteasome regulatory subunit S3) (Proteasome subunit p58). [Source:Uniprot/SWISSPROT;Acc:O43242]
ENSG0000 0108406	DHX40	DEAH (Asp-Glu-Ala-His) box polypeptide 40 [Source:RefSeq_peptide;Acc:NP_078888]
ENSG0000 0108423	TUBD1	Tubulin delta chain (Delta tubulin). [Source:Uniprot/SWISSPROT;Acc:Q9UJT1]
ENSG0000 0108424	KPNB1	Importin beta-1 subunit (Karyopherin beta-1 subunit) (Nuclear factor P97) (Importin 90). [Source:Uniprot/SWISSPROT;Acc:Q14974]
ENSG0000 0108443	RPS6K B1	Ribosomal protein S6 kinase 1 (EC 2.7.1.37) (S6K) (S6K1) (70 kDa ribosomal protein S6 kinase 1) (p70 S6 kinase alpha) (p70(S6K)-alpha) (p70-S6K) (p70-alpha). [Source:Uniprot/SWISSPROT;Acc:P23443]
ENSG0000 0108469	RECQL 5	ATP-dependent DNA helicase Q5 (EC 3.6.1.-) (RecQ protein-like 5) (RecQ5). [Source:Uniprot/SWISSPROT;Acc:O94762]
ENSG0000 0108504	CDK3	Cell division protein kinase 3 (EC 2.7.1.37). [Source:Uniprot/SWISSPROT;Acc:Q00526]
ENSG0000 0108515	ENO3	Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase) (Enolase 3). [Source:Uniprot/SWISSPROT;Acc:P13929]
ENSG0000 0108591	DRG2	Developmentally regulated GTP-binding protein 2 (DRG 2). [Source:Uniprot/SWISSPROT;Acc:P55039]
ENSG0000 0108654	DDX5	Probable ATP-dependent RNA helicase DDX5 (EC 3.6.1.-) (DEAD box protein 5) (RNA helicase p68). [Source:Uniprot/SWISSPROT;Acc:P17844]
ENSG0000 0108671	PSMD1 1	26S proteasome non-ATPase regulatory subunit 11 (26S proteasome regulatory subunit S9) (26S proteasome regulatory subunit p44.5). [Source:Uniprot/SWISSPROT;Acc:O00231]
ENSG0000 0108774	RAB5C	Ras-related protein Rab-5C (RAB5L) (L1880). [Source:Uniprot/SWISSPROT;Acc:P51148]
ENSG0000 0108846	ABCC3	Canalicular multispecific organic anion transporter 2 (Multidrug resistance-associated protein 3) (Multi-specific organic anion tranporter-D) (MOAT-D). [Source:Uniprot/SWISSPROT;Acc:O15438]
ENSG0000 0108854	SMURF 2	Smad ubiquitination regulatory factor 2 (EC 6.3.2.-) (Ubiquitin-- protein ligase SMURF2) (Smad-specific E3 ubiquitin ligase 2) (hSMURF2). [Source:Uniprot/SWISSPROT;Acc:Q9HAU4]
ENSG0000 0108883	EFTUD 2	"116 kDa U5 small nuclear ribonucleoprotein component (U5 snRNP- specific protein, 116 kDa) (U5-116 kDa) (Elongation factor Tu GTP binding domain protein 2). [Source:Uniprot/SWISSPROT;Acc:Q15029]"
ENSG0000 0108946	PRKAR 1A	cAMP-dependent protein kinase type I-alpha regulatory subunit (Tissue- specific extinguisher 1) (TSE1). [Source:Uniprot/SWISSPROT;Acc:P10644]
ENSG0000 0108953	YWHA E	14-3-3 protein epsilon (14-3-3E). [Source:Uniprot/SWISSPROT;Acc:P62258]
ENSG0000 0109061	MYH1	"Myosin-1 (Myosin heavy chain, skeletal muscle, adult 1) (Myosin heavy chain IIx/d) (MyHC-IIx/d). [Source:Uniprot/SWISSPROT;Acc:P12882]"
ENSG0000	MYH3	"Myosin heavy chain, fast skeletal muscle, embryonic (Muscle embryonic myosin heavy chain) (SMHCE).

0109063		[Source:Uniprot/SWISSPROT;Acc:P11055]"
ENSG0000 0109103	**UNC11 9**	**Unc-119 protein homolog (Retinal protein 4) (HRG4). [Source:Uniprot/SWISSPROT;Acc:Q13432]**
ENSG0000 0109107	ALDOC	Fructose-bisphosphate aldolase C (EC 4.1.2.13) (Brain-type aldolase). [Source:Uniprot/SWISSPROT;Acc:P09972]
ENSG0000 0109332	UBE2D 3	Ubiquitin-conjugating enzyme E2 D3 (EC 6.3.2.19) (Ubiquitin-protein ligase D3) (Ubiquitin carrier protein D3) (Ubiquitin-conjugating enzyme E2-17 kDa 3) (E2(17)KB 3). [Source:Uniprot/SWISSPROT;Acc:P61077]
ENSG0000 0109339	MAPK1 0	Mitogen-activated protein kinase 10 (EC 2.7.1.37) (Stress-activated protein kinase JNK3) (c-Jun N-terminal kinase 3) (MAP kinase p49 3F12). [Source:Uniprot/SWISSPROT;Acc:P53779]
ENSG0000 0109606	DHX15	Putative pre-mRNA splicing factor ATP-dependent RNA helicase DHX15 (EC 3.6.1.-) (DEAH box protein 15) (ATP-dependent RNA helicase #46). [Source:Uniprot/SWISSPROT;Acc:O43143]
ENSG0000 0109670	FBXW7	F-box/WD-repeat protein 7 (F-box and WD-40 domain protein 7) (F-box protein FBX30) (hCdc4) (Archipelago homolog) (hAgo) (SEL-10). [Source:Uniprot/SWISSPROT;Acc:Q969H0]
ENSG0000 0109775	NP_060 829.1	
ENSG0000 0109832	DDX25	ATP-dependent RNA helicase DDX25 (EC 3.6.1.-) (DEAD box protein 25) (Gonadotropin-regulated testicular RNA helicase). [Source:Uniprot/SWISSPROT;Acc:Q9UHL0]
ENSG0000 0109971	HSPA8	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8). [Source:Uniprot/SWISSPROT;Acc:P11142]
ENSG0000 0110025	SNX15	Sorting nexin-15. [Source:Uniprot/SWISSPROT;Acc:Q9NRS6]
ENSG0000 0110060	PUS3	tRNA pseudouridine synthase 3 (EC 5.4.99.-) (tRNA-uridine isomerase 3) (tRNA pseudouridylate synthase 3). [Source:Uniprot/SWISSPROT;Acc:Q9BZE2]
ENSG0000 0110367	DDX6	Probable ATP-dependent RNA helicase DDX6 (EC 3.6.1.-) (DEAD box protein 6) (ATP-dependent RNA helicase p54) (Oncogene RCK). [Source:Uniprot/SWISSPROT;Acc:P26196]
ENSG0000 0110422	HIPK3	Homeodomain-interacting protein kinase 3 (EC 2.7.1.37) (Homolog of protein kinase YAK1) (Fas-interacting serine/threonine-protein kinase) (FIST) (Androgen receptor-interacting nuclear protein kinase) (ANPK). [Source:Uniprot/SWISSPROT;Acc:Q9H422]
ENSG0000 0110435	PDHX	"Pyruvate dehydrogenase protein X component, mitochondrial precursor (Dihydrolipoamide dehydrogenase-binding protein of pyruvate dehydrogenase complex) (Lipoyl-containing pyruvate dehydrogenase complex component X) (E3-binding protein) (E3BP) (proX). [Source:Uniprot/SWISSPROT;Acc:O00330]"
ENSG0000 0110619	CARS	Cysteinyl-tRNA synthetase (EC 6.1.1.16) (Cysteine--tRNA ligase) (CysRS). [Source:Uniprot/SWISSPROT;Acc:P49589]
ENSG0000 0110719	TCIRG1	Vacuolar proton translocating ATPase 116 kDa subunit a isoform 3 (V- ATPase 116-kDa isoform a3) (Osteoclastic proton pump 116 kDa subunit) (OC-116 kDa) (OC116) (T-cell immune regulator 1) (T cell immune response cDNA7 protein) (TIRC7). [Source:Uniprot/SWISSPROT;Acc:Q13488]
ENSG0000 0110871	NP_115 690.2	
ENSG0000 0110931	CAMK K2	Calcium/calmodulin-dependent protein kinase kinase 2 (EC 2.7.1.37) (Calcium/calmodulin-dependent protein kinase kinase beta) (CaM-kinase kinase beta) (CaM-KK beta) (CaMKK beta). [Source:Uniprot/SWISSPROT;Acc:Q96RR4]
ENSG0000 0110955	ATP5B	"ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14). [Source:Uniprot/SWISSPROT;Acc:P06576]"
ENSG0000 0111058	NP_078 836.1	
ENSG0000 0111142	METAP 2	Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2) (Peptidase M 2) (Initiation factor 2-associated 67 kDa glycoprotein) (p67) (p67eIF2). [Source:Uniprot/SWISSPROT;Acc:P50579]
ENSG0000 0111196	MGN2_ HUMA N	Mago nashi protein homolog 2. [Source:Uniprot/SWISSPROT;Acc:Q96A72]
ENSG0000 0111218	HRMT1 L4	Protein arginine N-methyltransferase 4 (EC 2.1.1.-) (Heterogeneous nuclear ribonucleoprotein methyltransferase-like protein 4). [Source:Uniprot/SWISSPROT;Acc:Q9NR22]
ENSG0000 0111231	ATPBD 1C	"ATP binding domain 1 family, member C [Source:RefSeq_peptide;Acc:NP_057385]"
ENSG0000 0111237	VPS29	Vacuolar protein sorting 29 (Vesicle protein sorting 29) (hVPS29) (PEP11). [Source:Uniprot/SWISSPROT;Acc:Q9UBQ0]
ENSG0000 0111275	ALDH2	"Aldehyde dehydrogenase, mitochondrial precursor (EC 1.2.1.3) (ALDH class 2) (ALDHI) (ALDH-E2). [Source:Uniprot/SWISSPROT;Acc:P05091]"
ENSG0000 0111278		
ENSG0000 0111364	DDX55	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55 [Source:RefSeq_peptide;Acc:NP_065987]
ENSG0000 0111445	RFC5	Activator 1 36 kDa subunit (Replication factor C 36 kDa subunit) (A1 36 kDa subunit) (RF-C 36 kDa subunit) (RFC36) (Replication factor C subunit 5). [Source:Uniprot/SWISSPROT;Acc:P40937]
ENSG0000 0111540	RAB5B	Ras-related protein Rab-5B. [Source:Uniprot/SWISSPROT;Acc:P61020]
ENSG0000 0111615	HRB2	HIV-1 Rev-binding protein 2 (Rev-interacting protein 1) (Rip-1). [Source:Uniprot/SWISSPROT;Acc:Q13601]
ENSG0000 0111640	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH). [Source:Uniprot/SWISSPROT;Acc:P04406]
ENSG0000 0111641	NOL1	Proliferating-cell nucleolar antigen p120 (Proliferation-associated nucleolar protein p120). [Source:Uniprot/SWISSPROT;Acc:P46087]
ENSG0000 0111642	CHD4	Chromodomain helicase-DNA-binding protein 4 (EC 3.6.1.-) (ATP- dependent helicase CHD4) (CHD-4) (Mi-2 autoantigen 218 kDa protein) (Mi2-beta). [Source:Uniprot/SWISSPROT;Acc:Q14839]
ENSG0000 0111667	USP5	Ubiquitin carboxyl-terminal hydrolase 5 (EC 3.1.2.15) (Ubiquitin thiolesterase 5) (Ubiquitin-specific processing protease 5) (Deubiquitinating enzyme 5) (Isopeptidase T). [Source:Uniprot/SWISSPROT;Acc:P45974]
ENSG0000 0111669	TPI1	Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase). [Source:Uniprot/SWISSPROT;Acc:P60174]
ENSG0000	ENO2	Gamma-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (Neuron-specific enolase) (NSE)

0111674		(Enolase 2). [Source:Uniprot/SWISSPROT;Acc:P09104]
ENSG0000 0111737	RAB35	Ras-related protein Rab-35 (Rab-1C) (GTP-binding protein RAY). [Source:Uniprot/SWISSPROT;Acc:Q15286]
ENSG0000 0111837	MAK	Serine/threonine-protein kinase MAK (EC 2.7.1.37) (Male germ cell- associated kinase). [Source:Uniprot/SWISSPROT;Acc:P20794]
ENSG0000 0111838		
ENSG0000 0111877	MCMD C1	minichromosome maintenance protein domain containing 1 [Source:RefSeq_peptide;Acc:NP_694987]
ENSG0000 0111885	MAN1A 1	"Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA (EC 3.2.1.113) (Processing alpha-1,2-mannosidase IA) (Alpha-1,2-mannosidase IA) (Mannosidase alpha class 1A member 1) (Man(9)-alpha-mannosidase) (Man9-mannosidase). [Source:Uniprot/SWISSPROT;Acc:P33908]"
ENSG0000 0111968	CSNK2 B	Casein kinase II beta subunit (CK II beta) (Phosvitin) (G5a). [Source:Uniprot/SWISSPROT;Acc:P67870]
ENSG0000 0112031	MTRF1 L	mitochondrial translational release factor 1-like [Source:RefSeq_peptide;Acc:NP_061914]
ENSG0000 0112062	MAPK1 4	Mitogen-activated protein kinase 14 (EC 2.7.1.37) (Mitogen-activated protein kinase p38 alpha) (MAP kinase p38 alpha) (Cytokine suppressive anti-inflammatory drug binding protein) (CSAID-binding protein) (CSBP) (MAX-interacting protein 2) (MAP kinase MXI2 [Source:Uniprot/SWISSPROT;Acc:Q16539]
ENSG0000 0112079	STK38	Serine/threonine-protein kinase 38 (EC 2.7.1.37) (NDR1 protein kinase) (Nuclear Dbf2-related kinase 1). [Source:Uniprot/SWISSPROT;Acc:Q15208]
ENSG0000 0112082	PSMB9	Proteasome subunit beta type 9 precursor (EC 3.4.25.1) (Proteasome chain 7) (Macropain chain 7) (Multicatalytic endopeptidase complex chain 7) (RING12 protein) (Low molecular mass protein 2). [Source:Uniprot/SWISSPROT;Acc:P28065]
ENSG0000 0112096	SOD2	"Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1). [Source:Uniprot/SWISSPROT;Acc:P04179]"
ENSG0000 0112118	MCM3	DNA replication licensing factor MCM3 (DNA polymerase alpha holoenzyme-associated protein P1) (RLF beta subunit) (P102 protein) (P1-MCM3). [Source:Uniprot/SWISSPROT;Acc:P25205]
ENSG0000 0112144	ICK	Serine/threonine-protein kinase ICK (EC 2.7.1.37) (Intestinal cell kinase) (hICK) (MAK-related kinase) (MRK) (Laryngeal cancer kinase 2) (LCK2). [Source:Uniprot/SWISSPROT;Acc:Q9UPZ9]
ENSG0000 0112159	MDN1	Midasin (MIDAS-containing protein). [Source:Uniprot/SWISSPROT;Acc:Q9NU22]
ENSG0000 0112249	ASCC3	"Activating signal cointegrator 1 complex subunit 3 (EC 3.6.1.-) (ASC-1 complex subunit p200) (Trip4 complex subunit p200) (Helicase, ATP binding 1). [Source:Uniprot/SWISSPROT;Acc:Q8N3C0]"
ENSG0000 0112294	ALDH5 A1	"Succinate semialdehyde dehydrogenase, mitochondrial precursor (EC 1.2.1.24) (NAD(+)-dependent succinic semialdehyde dehydrogenase). [Source:Uniprot/SWISSPROT;Acc:P51649]"
ENSG0000 0112339	HBS1L	HBS1-like protein (ERFS). [Source:Uniprot/SWISSPROT;Acc:Q9Y450]
ENSG0000 0112357	PEX7	Peroxisomal targeting signal 2 receptor (PTS2 receptor) (Peroxin-7). [Source:Uniprot/SWISSPROT;Acc:O00628]
ENSG0000 0112578	BYSL	Bystin. [Source:Uniprot/SWISSPROT;Acc:Q13895]
ENSG0000 0112698		
ENSG0000 0112739	PRPF4B	Serine/threonine-protein kinase PRP4 homolog (EC 2.7.1.37) (PRP4 pre- mRNA processing factor 4 homolog) (PRP4 kinase). [Source:Uniprot/SWISSPROT;Acc:Q13523]
ENSG0000 0112941	POLS	DNA polymerase sigma (EC 2.7.7.7) (Topoisomerase-related function protein 4-1) (TRF4-1) (LAK-1) (DNA polymerase kappa). [Source:Uniprot/SWISSPROT;Acc:Q5XG87]
ENSG0000 0113013	HSPA9 B	"Stress-70 protein, mitochondrial precursor (75 kDa glucose regulated protein) (GRP 75) (Peptide-binding protein 74) (PBP74) (Mortalin) (MOT). [Source:Uniprot/SWISSPROT;Acc:P38646]"
ENSG0000 0113231	**PDE8B**	**"High-affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8B (EC 3.1.4.17) (HSPDE8B). [Source:Uniprot/SWISSPROT;Acc:O95263]"**
ENSG0000 0113240	CLK4	Dual specificity protein kinase CLK4 (EC 2.7.1.37) (EC 2.7.1.112) (CDC-like kinase 4). [Source:Uniprot/SWISSPROT;Acc:Q9HAZ1]
ENSG0000 0113407	TARS	"Threonyl-tRNA synthetase, cytoplasmic (EC 6.1.1.3) (Threonine--tRNA ligase) (ThrRS). [Source:Uniprot/SWISSPROT;Acc:P26639]"
ENSG0000 0113448	**PDE4D**	**"cAMP-specific 3',5'-cyclic phosphodiesterase 4D (EC 3.1.4.17) (DPDE3) (PDE43). [Source:Uniprot/SWISSPROT;Acc:Q08499]"**
ENSG0000 0113460	BXDC2	Brix domain containing protein 2 (Ribosome biogenesis protein Brix). [Source:Uniprot/SWISSPROT;Acc:Q8TDN6]
ENSG0000 0113575	PPP2CA	"Serine/threonine protein phosphatase 2A, catalytic subunit, alpha isoform (EC 3.1.3.16) (PP2A-alpha) (Replication protein C) (RP-C). [Source:Uniprot/SWISSPROT;Acc:P67775]"
ENSG0000 0113595	TRIM23	GTP-binding protein ARD-1 (ADP-ribosylation factor domain protein 1) (Tripartite motif protein 23) (RING finger protein 46). [Source:Uniprot/SWISSPROT;Acc:P36406]
ENSG0000 0113615	SEC24A	Protein transport protein Sec24A (SEC24-related protein A) (Fragment). [Source:Uniprot/SWISSPROT;Acc:O95486]
ENSG0000 0113643	RARS	Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS). [Source:Uniprot/SWISSPROT;Acc:P54136]
ENSG0000 0113712	CSNK1 A1	"Casein kinase I, alpha isoform (EC 2.7.1.-) (CKI-alpha) (CK1). [Source:Uniprot/SWISSPROT;Acc:P48729]"
ENSG0000 0113810	SMC4L 1	Structural maintenance of chromosomes 4-like 1 protein (Chromosome- associated polypeptide C) (hCAP-C) (XCAP-C homolog). [Source:Uniprot/SWISSPROT;Acc:Q9NTJ3]
ENSG0000 0113966	ARL6	ADP-ribosylation factor-like protein 6. [Source:Uniprot/SWISSPROT;Acc:Q9H0F7]
ENSG0000 0114021	NIT2	"nitrilase family, member 2 [Source:RefSeq_peptide;Acc:NP_064587]"
ENSG0000 0114030	KPNA1	Importin alpha-1 subunit (Karyopherin alpha-1 subunit) (SRP1-beta) (RAG cohort protein 2) (Nucleoprotein interactor 1) (NPI-1). [Source:Uniprot/SWISSPROT;Acc:P52294]

ENSG0000 0114054	PCCB	"Propionyl-CoA carboxylase beta chain, mitochondrial precursor (EC 6.4.1.3) (PCCase beta subunit) (Propanoyl-CoA:carbon dioxide ligase beta subunit). [Source:Uniprot/SWISSPROT;Acc:P05166]"
ENSG0000 0114062	UBE3A	Ubiquitin-protein ligase E3A (EC 6.3.2.-) (E6AP ubiquitin-protein ligase) (Oncogenic protein-associated protein E6-AP) (Human papillomavirus E6-associated protein). [Source:Uniprot/SWISSPROT;Acc:Q05086]
ENSG0000 0114064		
ENSG0000 0114127	XRN1	5'-3' exoribonuclease 1 (EC 3.1.11.-) (Strand-exchange protein 1 homolog). [Source:Uniprot/SWISSPROT;Acc:Q8IZH2]
ENSG0000 0114268	PFKFB4	"6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 (6PF-2-K/Fru- 2,6-P2ASE testis-type isozyme) [Includes: 6-phosphofructo-2-kinase (EC 2.7.1.105); Fructose-2,6-bisphosphatase (EC 3.1.3.46)]. [Source:Uniprot/SWISSPROT;Acc:Q16877]"
ENSG0000 0114446	**IFT57**	**estrogen-related receptor beta like 1 [Source:RefSeq_peptide;Acc:NP_060480]**
ENSG0000 0114573	ATP6V 1A	"Vacuolar ATP synthase catalytic subunit A, ubiquitous isoform (EC 3.6.3.14) (V-ATPase A subunit 1) (Vacuolar proton pump alpha subunit 1) (V-ATPase 69 kDa subunit 1) (Isoform VA68). [Source:Uniprot/SWISSPROT;Acc:P38606]"
ENSG0000 0114670	NEK11	Serine/threonine-protein kinase Nek11 (EC 2.7.1.37) (NimA-related protein kinase 11) (Never in mitosis A-related kinase 11). [Source:Uniprot/SWISSPROT;Acc:Q8NG66]
ENSG0000 0114770	ABCC5	Multidrug resistance-associated protein 5 (Multi-specific organic anion tranporter-C) (MOAT-C) (pABC11) (SMRP). [Source:Uniprot/SWISSPROT;Acc:O15440]
ENSG0000 0114841	DNAH1	"dynein, axonemal, heavy polypeptide 1 [Source:RefSeq_peptide;Acc:NP_056327]"
ENSG0000 0114904	NEK4	Serine/threonine-protein kinase Nek4 (EC 2.7.1.37) (NimA-related protein kinase 4) (Serine/threonine-protein kinase 2) (Serine/threonine-protein kinase NRK2). [Source:Uniprot/SWISSPROT;Acc:P51957]
ENSG0000 0114978	MOBK1 B	Mps one binder kinase activator-like 1B (Mob1 homolog 1B) (Mob1 alpha) (Mob1A) (Protein Mob4B). [Source:Uniprot/SWISSPROT;Acc:Q9H8S9]
ENSG0000 0115073	ACTR1 B	Beta-centractin (Actin-related protein 1B) (ARP1B). [Source:Uniprot/SWISSPROT;Acc:P42025]
ENSG0000 0115091	ACTR3	Actin-like protein 3 (Actin-related protein 3). [Source:Uniprot/SWISSPROT;Acc:P61158]
ENSG0000 0115137	**NP_057 628.1**	**Ras-associated protein Rap1 [Source:RefSeq_peptide;Acc:NP_057628]**
ENSG0000 0115233	PSMD1 4	26S proteasome non-ATPase regulatory subunit 14 (26S proteasome regulatory subunit rpn11) (26S proteasome-associated PAD1 homolog 1). [Source:Uniprot/SWISSPROT;Acc:O00487]
ENSG0000 0115252	**PDE1A**	**"Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1A (EC 3.1.4.17) (Cam-PDE 1A) (61 kDa Cam-PDE) (hCam-1). [Source:Uniprot/SWISSPROT;Acc:P54750]"**
ENSG0000 0115254	XAB1	XPA-binding protein 1. [Source:Uniprot/SWISSPROT;Acc:Q9HCN4]
ENSG0000 0115373		
ENSG0000 0115404		
ENSG0000 0115421	PAPOL G	Poly(A) polymerase gamma (EC 2.7.7.19) (PAP gamma) (Polynucleotide adenylyltransferase gamma) (SRP RNA 3' adenylating enzyme). [Source:Uniprot/SWISSPROT;Acc:Q9BWT3]
ENSG0000 0115423	Q9H5E1 _HUMA N	
ENSG0000 0115484	CCT4	"T-complex protein 1, delta subunit (TCP-1-delta) (CCT-delta) (Stimulator of TAR RNA binding). [Source:Uniprot/SWISSPROT;Acc:P50991]"
ENSG0000 0115524	SF3B1	Splicing factor 3B subunit 1 (Spliceosome associated protein 155) (SAP 155) (SF3b155) (Pre-mRNA splicing factor SF3b 155 kDa subunit). [Source:Uniprot/SWISSPROT;Acc:O75533]
ENSG0000 0115657	ABCB6	"ATP-binding cassette sub-family B member 6, mitochondrial precursor (Mitochondrial ABC transporter 3) (Mt-ABC transporter 3) (ABC transporter umat). [Source:Uniprot/SWISSPROT;Acc:Q9NP58]"
ENSG0000 0115694	STK25	Serine/threonine-protein kinase 25 (EC 2.7.1.37) (Sterile 20/oxidant stress-response kinase 1) (Ste20/oxidant stress response kinase 1) (SOK-1) (Ste20-like kinase). [Source:Uniprot/SWISSPROT;Acc:O00506]
ENSG0000 0115761	NOL10	Nucleolar protein 10. [Source:Uniprot/SWISSPROT;Acc:Q9BSC4]
ENSG0000 0115816	CEBPZ	CCAAT/enhancer binding protein zeta (CCAAT-box-binding transcription factor) (CCAAT-binding factor) (CBF). [Source:Uniprot/SWISSPROT;Acc:Q03701]
ENSG0000 0115825	PRKD3	"Protein kinase C, nu type (EC 2.7.1.-) (nPKC-nu) (Protein kinase EPK2). [Source:Uniprot/SWISSPROT;Acc:O94806]"
ENSG0000 0115866	DARS	Aspartyl-tRNA synthetase (EC 6.1.1.12) (Aspartate--tRNA ligase) (AspRS). [Source:Uniprot/SWISSPROT;Acc:P14868]
ENSG0000 0115896	PLCL1	phospholipase C-like 1 [Source:RefSeq_peptide;Acc:NP_006217]
ENSG0000 0115946	NP_064 528.1	putatative 28 kDa protein [Source:RefSeq_peptide;Acc:NP_064528]
ENSG0000 0116039	ATP6V 1B1	"Vacuolar ATP synthase subunit B, kidney isoform (EC 3.6.3.14) (V- ATPase B1 subunit) (Vacuolar proton pump B isoform 1) (Endomembrane proton pump 58 kDa subunit). [Source:Uniprot/SWISSPROT;Acc:P15313]"
ENSG0000 0116062	MSH6	DNA mismatch repair protein MSH6 (MutS-alpha 160 kDa subunit) (G/T mismatch binding protein) (GTBP) (GTMBP) (p160). [Source:Uniprot/SWISSPROT;Acc:P52701]
ENSG0000 0116141	MARK1	Serine/threonine-protein kinase MARK1 (EC 2.7.1.37) (MAP/microtubule affinity-regulating kinase 1). [Source:Uniprot/SWISSPROT;Acc:Q9P0L2]
ENSG0000 0116198	**K0562_ HUMA N**	
ENSG0000 0116254	CHD5	Chromodomain helicase-DNA-binding protein 5 (EC 3.6.1.-) (ATP- dependent helicase CHD5) (CHD-5). [Source:Uniprot/SWISSPROT;Acc:Q8TDI0]
ENSG0000	AMPD2	AMP deaminase 2 (EC 3.5.4.6) (AMP deaminase isoform L). [Source:Uniprot/SWISSPROT;Acc:Q01433]

0116337		
ENSG0000 0116406	CA022_ HUMA N	Putative alpha-mannosidase C1orf22 (EC 3.2.1.-). [Source:Uniprot/SWISSPROT;Acc:Q9BZQ6]
ENSG0000 0116478	HDAC1	Histone deacetylase 1 (HD1). [Source:Uniprot/SWISSPROT;Acc:Q13547]
ENSG0000 0116649	SRM	Spermidine synthase (EC 2.5.1.16) (Putrescine aminopropyltransferase) (SPDSY). [Source:Uniprot/SWISSPROT;Acc:P19623]
ENSG0000 0116748	AMPD1	AMP deaminase 1 (EC 3.5.4.6) (Myoadenylate deaminase) (AMP deaminase isoform M). [Source:Uniprot/SWISSPROT;Acc:P23109]
ENSG0000 0116761	CTH	Cystathionine gamma-lyase (EC 4.4.1.1) (Gamma-cystathionase). [Source:Uniprot/SWISSPROT;Acc:P32929]
ENSG0000 0117020	AKT3	"RAC-gamma serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-gamma) (Protein kinase Akt-3) (Protein kinase B, gamma) (PKB gamma) (STK-2). [Source:Uniprot/SWISSPROT;Acc:Q9Y243]"
ENSG0000 0117133	BXDC5	Ribosome production factor 1 (Ribosome biogenesis protein RPF1) (Brix domain containing protein 5). [Source:Uniprot/SWISSPROT;Acc:Q9H9Y2]
ENSG0000 0117143	UAP1	UDP-N-acetylhexosamine pyrophosphorylase (Antigen X) (AGX) (Sperm- associated antigen 2) [Includes: UDP-N-acetylgalactosamine pyrophosphorylase (EC 2.7.7.-) (AGX-1); UDP-N-acetylglucosamine pyrophosphorylase (EC 2.7.7.23) (AGX-2)]. [Source:Uniprot/SWISSPROT;Acc:Q16222]
ENSG0000 0117148	ACTL8	actin like protein [Source:RefSeq_peptide;Acc:NP_110439]
ENSG0000 0117238		
ENSG0000 0117266	NP_997 668.1	PCTAIRE protein kinase 3 isoform a [Source:RefSeq_peptide;Acc:NP_997668]
ENSG0000 0117308	GALE	UDP-glucose 4-epimerase (EC 5.1.3.2) (Galactowaldenase) (UDP-galactose 4-epimerase). [Source:Uniprot/SWISSPROT;Acc:Q14376]
ENSG0000 0117410	ATP6V 0B	Vacuolar ATP synthase 21 kDa proteolipid subunit (EC 3.6.3.14) (HATPL). [Source:Uniprot/SWISSPROT;Acc:Q99437]
ENSG0000 0117448	AKR1A 1	Alcohol dehydrogenase [NADP+] (EC 1.1.1.2) (Aldehyde reductase) (Aldo- keto reductase family 1 member A1). [Source:Uniprot/SWISSPROT;Acc:P14550]
ENSG0000 0117450	PRDX1	Peroxiredoxin 1 (EC 1.11.1.15) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2) (Proliferation-associated protein PAG) (Natural killer cell-enhancing factor A) (NKEF-A). [Source:Uniprot/SWISSPROT;Acc:Q06830]
ENSG0000 0117643	MAN1C 1	"Mannosyl-oligosaccharide 1,2-alpha-mannosidase IC (EC 3.2.1.113) (Processing alpha-1,2-mannosidase IC) (Alpha-1,2-mannosidase IC) (Mannosidase alpha class 1C member 1) (HMIC). [Source:Uniprot/SWISSPROT;Acc:Q9NR34]"
ENSG0000 0117650	NEK2	Serine/threonine-protein kinase Nek2 (EC 2.7.1.37) (NimA-related protein kinase 2) (NimA-like protein kinase 1) (HSPK 21). [Source:Uniprot/SWISSPROT;Acc:P51955]
ENSG0000 0117676	RPS6K A1	Ribosomal protein S6 kinase alpha 1 (EC 2.7.1.37) (S6K-alpha 1) (90 kDa ribosomal protein S6 kinase 1) (p90-RSK 1) (Ribosomal S6 kinase 1) (RSK-1) (pp90RSK1). [Source:Uniprot/SWISSPROT;Acc:Q15418]
ENSG0000 0118096	**NP_064 538.2**	
ENSG0000 0118193	KIF14	Kinesin-like protein KIF14. [Source:Uniprot/SWISSPROT;Acc:Q15058]
ENSG0000 0118197	DDX59	DEAD (Asp-Glu-Ala-Asp) box polypeptide 59 isoform 2 [Source:RefSeq_peptide;Acc:NP_112596]
ENSG0000 0118226		
ENSG0000 0118322	ATP10B	Probable phospholipid-transporting ATPase VB (EC 3.6.3.1). [Source:Uniprot/SWISSPROT;Acc:O94823]
ENSG0000 0118514	ALDH8 A1	aldehyde dehydrogenase 8A1 isoform 1 [Source:RefSeq_peptide;Acc:NP_072090]
ENSG0000 0118515	SGK	Serine/threonine-protein kinase Sgk1 (EC 2.7.1.37) (Serum/glucocorticoid-regulated kinase 1). [Source:Uniprot/SWISSPROT;Acc:O00141]
ENSG0000 0118777	ABCG2	ATP-binding cassette sub-family G member 2 (Placenta-specific ATP- binding cassette transporter) (Breast cancer resistance protein) (Mitoxantrone resistance-associated protein) (CDw338 antigen). [Source:Uniprot/SWISSPROT;Acc:Q9UNQ0]
ENSG0000 0118965	**WDR35**	**WD-repeat protein 35. [Source:Uniprot/SWISSPROT;Acc:Q9P2L0]**
ENSG0000 0118997	DNAH7	axonemal dynein heavy chain 7 [Source:RefSeq_peptide;Acc:NP_061720]
ENSG0000 0119048	UBE2B	Ubiquitin-conjugating enzyme E2 B (EC 6.3.2.19) (Ubiquitin-protein ligase B) (Ubiquitin carrier protein B) (HR6B) (hHR6B) (E2-17 kDa). [Source:Uniprot/SWISSPROT;Acc:P63146]
ENSG0000 0119203	CPSF3	"Cleavage and polyadenylation specificity factor, 73 kDa subunit (CPSF 73 kDa subunit). [Source:Uniprot/SWISSPROT;Acc:Q9UKF6]"
ENSG0000 0119396	RAB14	Ras-related protein Rab-14. [Source:Uniprot/SWISSPROT;Acc:P61106]
ENSG0000 0119408	NEK6	Serine/threonine-protein kinase Nek6 (EC 2.7.1.37) (NimA-related protein kinase 6) (Protein kinase SID6-1512). [Source:Uniprot/SWISSPROT;Acc:Q9HC98]
ENSG0000 0119414	PPP6C	Serine/threonine protein phosphatase 6 (EC 3.1.3.16) (PP6). [Source:Uniprot/SWISSPROT;Acc:O00743]
ENSG0000 0119523	ALG2	"Alpha-1,3-mannosyltransferase ALG2 (EC 2.4.1.-) (GDP- Man:Man(1)GlcNAc(2)-PP-dolichol mannosyltransferase). [Source:Uniprot/SWISSPROT;Acc:Q9H553]"
ENSG0000 0119541	VPS4B	Vacuolar sorting protein 4b (SKD1 protein). [Source:Uniprot/SWISSPROT;Acc:O75351]
ENSG0000 0119616	CN111_ HUMA N	
ENSG0000	NEK9	Serine/threonine-protein kinase Nek9 (EC 2.7.1.37) (NimA-related protein kinase 9) (Nercc1 kinase) (NIMA-related

0119638		kinase 8) (Nek8). [Source:Uniprot/SWISSPROT;Acc:Q8TD19]
ENSG0000 0119682	KIAA03 17	
ENSG0000 0119685	**TTLL5**	**"tubulin tyrosine ligase-like family, member 5 [Source:RefSeq_peptide;Acc:NP_055887]"**
ENSG0000 0119689	DLST	"Dihydrolipoyllysine-residue succinyltransferase component of 2- oxoglutarate dehydrogenase complex, mitochondrial precursor (EC 2.3.1.61) (Dihydrolipoamide succinyltransferase component of 2- oxoglutarate dehydrogenase complex) (E2) (E2K). [Source:Uniprot/SWISSPROT;Acc:P36957]"
ENSG0000 0119711	ALDH6 A1	"Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial precursor (EC 1.2.1.27) (MMSDH) (Malonate-semialdehyde dehydrogenase [acylating]) (EC 1.2.1.18). [Source:Uniprot/SWISSPROT;Acc:Q02252]"
ENSG0000 0119912	IDE	Insulin-degrading enzyme (EC 3.4.24.56) (Insulysin) (Insulinase) (Insulin protease). [Source:Uniprot/SWISSPROT;Acc:P14735]
ENSG0000 0119969	NP_060 533.2	"helicase, lymphoid-specific [Source:RefSeq_peptide;Acc:NP_060533]"
ENSG0000 0120051	**NP_001 008723. 1**	
ENSG0000 0120053	GOT1	"Aspartate aminotransferase, cytoplasmic (EC 2.6.1.1) (Transaminase A) (Glutamate oxaloacetate transaminase 1). [Source:Uniprot/SWISSPROT;Acc:P17174]"
ENSG0000 0120158	RCL1	RNA 3'-terminal phosphate cyclase-like protein. [Source:Uniprot/SWISSPROT;Acc:Q9Y2P8]
ENSG0000 0120162	MOBK L2B	Mps one binder kinase activator-like 2B (Mob1 homolog 2b) (Protein Mob3B). [Source:Uniprot/SWISSPROT;Acc:Q86TA1]
ENSG0000 0120438	TCP1	"T-complex protein 1, alpha subunit (TCP-1-alpha) (CCT-alpha). [Source:Uniprot/SWISSPROT;Acc:P17987]"
ENSG0000 0120440	**TTLL2**	**Tubulin tyrosine ligase-like protein 2 (Testis-specific protein NYD- TSPG). [Source:Uniprot/SWISSPROT;Acc:Q9BWV7]**
ENSG0000 0120694	HSPH1	Heat-shock protein 105 kDa (Heat shock 110 kDa protein) (Antigen NY- CO-25). [Source:Uniprot/SWISSPROT;Acc:Q92598]
ENSG0000 0120705	ETF1	Eukaryotic peptide chain release factor subunit 1 (eRF1) (Eukaryotic release factor 1) (TB3-1) (Cl1 protein). [Source:Uniprot/SWISSPROT;Acc:P62495]
ENSG0000 0120805	ARL1	ADP-ribosylation factor-like protein 1. [Source:Uniprot/SWISSPROT;Acc:P40616]
ENSG0000 0120910	PPP3CC	"Serine/threonine protein phosphatase 2B catalytic subunit, gamma isoform (EC 3.1.3.16) (Calmodulin-dependent calcineurin A subunit, gamma isoform) (Calcineurin, testis-specific catalytic subunit) (CAM- PRP catalytic subunit). [Source:Uniprot/SWISSPROT;Acc:P48454]"
ENSG0000 0121054	NME2	Nucleoside diphosphate kinase B (EC 2.7.4.6) (NDK B) (NDP kinase B) (nm23-H2) (C-myc purine-binding transcription factor PUF). [Source:Uniprot/SWISSPROT;Acc:P22392]
ENSG0000 0121270	ABCC1 1	"ATP-binding cassette, sub-family C, member 11 isoform a [Source:RefSeq_peptide;Acc:NP_115972]"
ENSG0000 0121316	**NP_079 105.3**	
ENSG0000 0121495		
ENSG0000 0121621	KIF18A	Kinesin family member 18A. [Source:Uniprot/SWISSPROT;Acc:Q8NI77]
ENSG0000 0121722	AP4M1	Adapter-related protein complex 4 mu 1 subunit (Mu subunit of AP-4) (AP-4 adapter complex mu subunit) (Mu-adaptin-related protein 2) (mu- ARP2) (mu4). [Source:Uniprot/SWISSPROT;Acc:O00189]
ENSG0000 0121749	TBC1D 15	TBC1 domain family member 15. [Source:Uniprot/SWISSPROT;Acc:Q8TC07]
ENSG0000 0122218	COPA	Coatomer alpha subunit (Alpha-coat protein) (Alpha-COP) (HEPCOP) (HEP- COP) [Contains: Xenin (Xenopsin-related peptide); Proxenin]. [Source:Uniprot/SWISSPROT;Acc:P53621]
ENSG0000 0122406	RPL5	60S ribosomal protein L5. [Source:Uniprot/SWISSPROT;Acc:P46777]
ENSG0000 0122729	ACO1	Iron-responsive element binding protein 1 (IRE-BP 1) (Iron regulatory protein 1) (IRP1) (Ferritin repressor protein) (Aconitate hydratase) (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase). [Source:Uniprot/SWISSPROT;Acc:P21399]
ENSG0000 0122735	**DNAI1**	**"Dynein intermediate chain 1, axonemal (Axonemal dynein intermediate chain 1). [Source:Uniprot/SWISSPROT;Acc:Q9UI46]"**
ENSG0000 0122787	AKR1D 1	3-oxo-5-beta-steroid 4-dehydrogenase (EC 1.3.99.6) (Delta(4)-3- ketosteroid 5-beta-reductase) (Aldo-keto reductase family 1 member D1). [Source:Uniprot/SWISSPROT;Acc:P51857]
ENSG0000 0122958	VPS26A	Vacuolar protein sorting 26 (Vesicle protein sorting 26) (hVPS26). [Source:Uniprot/SWISSPROT;Acc:O75436]
ENSG0000 0122965	RBM19	Probable RNA-binding protein 19 (RNA-binding motif protein 19). [Source:Uniprot/SWISSPROT;Acc:Q9Y4C8]
ENSG0000 0122966	CIT	"Citron Rho-interacting kinase (EC 2.7.1.37) (CRIK) (Rho-interacting, serine/threonine-protein kinase 21). [Source:Uniprot/SWISSPROT;Acc:O14578]"
ENSG0000 0122970	**IFT81**	**Intraflagellar transport 81 (Carnitine deficiency-associated protein expressed in ventricle 1) (CDV-1 protein). [Source:Uniprot/SWISSPROT;Acc:Q8WYA0]**
ENSG0000 0123009	NME2P 1	Putative nucleoside diphosphate kinase (EC 2.7.4.6) (NDK) (NDP kinase). [Source:Uniprot/SWISSPROT;Acc:O60361]
ENSG0000 0123064	DDX54	ATP-dependent RNA helicase DDX54 (EC 3.6.1.-) (DEAD box protein 54) (ATP-dependent RNA helicase DP97). [Source:Uniprot/SWISSPROT;Acc:Q8TDD1]
ENSG0000 0123124	WWP1	NEDD4-like E3 ubiquitin-protein ligase WWP1 (EC 6.3.2.-) (WW domain- containing protein 1) (Atropin-1 interacting protein 5) (AIP5). [Source:Uniprot/SWISSPROT;Acc:Q9H0M0]
ENSG0000 0123131	PRDX4	Peroxiredoxin 4 (EC 1.11.1.15) (Prx-IV) (Thioredoxin peroxidase AO372) (Thioredoxin-dependent peroxide reductase A0372) (Antioxidant enzyme AOE372) (AOE37-2). [Source:Uniprot/SWISSPROT;Acc:Q13162]
ENSG0000 0123136	DDX39	ATP-dependent RNA helicase DDX39 (EC 3.6.1.-) (DEAD box protein 39) (Nuclear RNA helicase URH49). [Source:Uniprot/SWISSPROT;Acc:O00148]

ENSG0000 0123143	PKN1	Protein kinase N1 (EC 2.7.1.37) (Protein kinase C-like 1) (Protein- kinase C-related kinase 1) (Protein kinase C-like PKN) (Serine- threonine protein kinase N) (Protein kinase PKN-alpha). [Source:Uniprot/SWISSPROT;Acc:Q16512]
ENSG0000 0123165	ACTRT 1	actin-related protein T1 [Source:RefSeq_peptide;Acc:NP_612146]
ENSG0000 0123191	ATP7B	Copper-transporting ATPase 2 (EC 3.6.3.4) (Copper pump 2) (Wilson disease-associated protein). [Source:Uniprot/SWISSPROT;Acc:P35670]
ENSG0000 0123213	NLN	"Neurolysin, mitochondrial precursor (EC 3.4.24.16) (Neurotensin endopeptidase) (Mitochondrial oligopeptidase M) (Microsomal endopeptidase) (MEP). [Source:Uniprot/SWISSPROT;Acc:Q9BYT8]"
ENSG0000 0123360	**PDE1B**	**"Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1B (EC 3.1.4.17) (Cam-PDE 1B) (63 kDa Cam-PDE). [Source:Uniprot/SWISSPROT;Acc:Q01064]"**
ENSG0000 0123374	CDK2	Cell division protein kinase 2 (EC 2.7.1.37) (p33 protein kinase). [Source:Uniprot/SWISSPROT;Acc:P24941]
ENSG0000 0123416	TBAK_ HUMA N	Tubulin alpha-ubiquitous chain (Alpha-tubulin ubiquitous) (Tubulin K- alpha-1). [Source:Uniprot/SWISSPROT;Acc:P68363]
ENSG0000 0123510		
ENSG0000 0123570	RAB9B	Ras-related protein Rab-9B (Rab-9L) (RAB9-like protein). [Source:Uniprot/SWISSPROT;Acc:Q9NP90]
ENSG0000 0123572	NRK	Nik related kinase [Source:RefSeq_peptide;Acc:NP_940867]
ENSG0000 0123595	RAB9A	Ras-related protein Rab-9A (Rab-9). [Source:Uniprot/SWISSPROT;Acc:P51151]
ENSG0000 0123607	**TTC21 B**	**tetratricopeptide repeat domain 21B [Source:RefSeq_peptide;Acc:NP_079029] ** one of two genes that mapped to *BBS5* critical interval ****
ENSG0000 0123815	ADCK4	aarF domain containing kinase 4 [Source:RefSeq_peptide;Acc:NP_079152]
ENSG0000 0123836	PFKFB2	"6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 (6PF-2-K/Fru- 2,6-P2ASE heart-type isozyme) (PFK-2/FBPase-2) [Includes: 6- phosphofructo-2-kinase (EC 2.7.1.105); Fructose-2,6-bisphosphatase (EC 3.1.3.46)]. [Source:Uniprot/SWISSPROT;Acc:O60825]"
ENSG0000 0123977	WDR69	
ENSG0000 0123983	ACSL3	Long-chain-fatty-acid--CoA ligase 3 (EC 6.2.1.3) (Long-chain acyl-CoA synthetase 3) (LACS 3). [Source:Uniprot/SWISSPROT;Acc:O95573]
ENSG0000 0123992	DNPEP	Aspartyl aminopeptidase (EC 3.4.11.21). [Source:Uniprot/SWISSPROT;Acc:Q9ULA0]
ENSG0000 0124003	MOGA T1	monoacylglycerol O-acyltransferase 1 [Source:RefSeq_peptide;Acc:NP_477513]
ENSG0000 0124177	CHD6	Chromodomain-helicase-DNA-binding protein 6 (EC 3.6.1.-) (ATP- dependent helicase CHD6) (CHD-6) (Radiation-induced gene B protein). [Source:Uniprot/SWISSPROT;Acc:Q8TD26]
ENSG0000 0124183		
ENSG0000 0124201		
ENSG0000 0124209	RAB22 A	Ras-related protein Rab-22A (Rab-22). [Source:Uniprot/SWISSPROT;Acc:Q9UL26]
ENSG0000 0124228	DDX27	Probable ATP-dependent RNA helicase DDX27 (EC 3.6.1.-) (DEAD box protein 27). [Source:Uniprot/SWISSPROT;Acc:Q96GQ7]
ENSG0000 0124255		
ENSG0000 0124275	MTRR	"Methionine synthase reductase, mitochondrial precursor (EC 1.16.1.8) (MSR). [Source:Uniprot/SWISSPROT;Acc:Q9UBK8]"
ENSG0000 0124406	ATP8A 1	Probable phospholipid-transporting ATPase IA (EC 3.6.3.1) (Chromaffin granule ATPase II) (ATPase class I type 8A member 1). [Source:Uniprot/SWISSPROT;Acc:Q9Y2Q0]
ENSG0000 0124487	DDX3X	"ATP-dependent RNA helicase DDX3X (EC 3.6.1.-) (DEAD box protein 3, X- chromosomal) (Helicase-like protein 2) (HLP2) (DEAD box, X isoform). [Source:Uniprot/SWISSPROT;Acc:O00571]"
ENSG0000 0124567		
ENSG0000 0124574	ABCC1 0	"ATP-binding cassette, sub-family C, member 10 [Source:RefSeq_peptide;Acc:NP_258261]"
ENSG0000 0124587	PEX6	Peroxisome assembly factor 2 (PAF-2) (Peroxisomal-type ATPase 1) (Peroxin-6) (Peroxisomal biogenesis factor 6). [Source:Uniprot/SWISSPROT;Acc:Q13608]
ENSG0000 0124608	AARSL	alanyl-tRNA synthetase like [Source:RefSeq_peptide;Acc:NP_065796]
ENSG0000 0124670		
ENSG0000 0124721	DNAH8	"dynein, axonemal, heavy polypeptide 8 [Source:RefSeq_peptide;Acc:NP_001362]"
ENSG0000 0125107	CNOT1	"CCR4-NOT transcription complex, subunit 1 isoform a [Source:RefSeq_peptide;Acc:NP_057368]"
ENSG0000 0125124	**BBS2**	**Bardet-Biedl syndrome 2 protein. [Source:Uniprot/SWISSPROT;Acc:Q9BXC9]**
ENSG0000 0125166	GOT2	"Aspartate aminotransferase, mitochondrial precursor (EC 2.6.1.1) (Transaminase A) (Glutamate oxaloacetate transaminase 2). [Source:Uniprot/SWISSPROT;Acc:P00505]"
ENSG0000 0125257	ABCC4	Multidrug resistance-associated protein 4 (MRP/cMOAT-related ABC transporter) (Multi-specific organic anion tranporter-B) (MOAT-B). [Source:Uniprot/SWISSPROT;Acc:O15439]
ENSG0000 0125304	TM9SF 2	Transmembrane 9 superfamily protein member 2 precursor (p76). [Source:Uniprot/SWISSPROT;Acc:Q99805]

ENSG0000 0125414	MYH2	"Myosin heavy chain, skeletal muscle, adult 2 (Myosin heavy chain IIa) (MyHC-IIa). [Source:Uniprot/SWISSPROT;Acc:Q9UKX2]"
ENSG0000 0125485	DDX31	Probable ATP-dependent RNA helicase DDX31 (EC 3.6.1.-) (DEAD box protein 31) (Helicain). [Source:Uniprot/SWISSPROT;Acc:Q9H8H2]
ENSG0000 0125630	POLR1 B	DNA-directed RNA polymerase I 135 kDa polypeptide (EC 2.7.7.6) (RNA polymerase I subunit 2) (RPA135). [Source:Uniprot/SWISSPROT;Acc:Q9H9Y6]
ENSG0000 0125822		
ENSG0000 0125885	MCM8	DNA replication licensing factor MCM8 (Minichromosome maintenance 8). [Source:Uniprot/SWISSPROT;Acc:Q9UJA3]
ENSG0000 0126005	ITGB4B P	Eukaryotic translation initiation factor 6 (eIF-6) (B4 integrin interactor) (CAB) (p27(BBP)) (B(2)GCN homolog). [Source:Uniprot/SWISSPROT;Acc:P56537]
ENSG0000 0126216	TUBGC P3	Gamma-tubulin complex component 3 (GCP-3) (Spindle pole body protein Spc98 homolog) (hSpc98) (hGCP3) (h104p). [Source:Uniprot/SWISSPROT;Acc:Q96CW5]
ENSG0000 0126457	HRMT1 L2	Protein arginine N-methyltransferase 1 (EC 2.1.1.-) (Interferon receptor 1-bound protein 4). [Source:Uniprot/SWISSPROT;Acc:Q99873]
ENSG0000 0126524	SBDS	Shwachman-Bodian-Diamond syndrome protein. [Source:Uniprot/SWISSPROT;Acc:Q9Y3A5]
ENSG0000 0126583	PRKCG	"Protein kinase C, gamma type (EC 2.7.1.37) (PKC-gamma). [Source:Uniprot/SWISSPROT;Acc:P05129]"
ENSG0000 0126602	TRAP1	"Heat shock protein 75 kDa, mitochondrial precursor (HSP 75) (Tumor necrosis factor type 1 receptor associated protein) (TRAP-1) (TNFR- associated protein 1). [Source:Uniprot/SWISSPROT;Acc:Q12931]"
ENSG0000 0126740		
ENSG0000 0126803	HSPA2	Heat shock-related 70 kDa protein 2 (Heat shock 70 kDa protein 2). [Source:Uniprot/SWISSPROT;Acc:P54652]
ENSG0000 0126814	TRMT5	tRNA-(N1G37) methyltransferase [Source:RefSeq_peptide;Acc:NP_065861]
ENSG0000 0126934	MAP2K 2	Dual specificity mitogen-activated protein kinase kinase 2 (EC 2.7.1.-) (MAP kinase kinase 2) (MAPKK 2) (ERK activator kinase 2) (MAPK/ERK kinase 2) (MEK2). [Source:Uniprot/SWISSPROT;Acc:P36507]
ENSG0000 0127022	CANX	Calnexin precursor (Major histocompatibility complex class I antigen- binding protein p88) (p90) (IP90). [Source:Uniprot/SWISSPROT;Acc:P27824]
ENSG0000 0127054	CPSF3L	related to CPSF subunits 68 kDa isoform 1 [Source:RefSeq_peptide;Acc:NP_060341]
ENSG0000 0127249	ATP13 A4	ATPase type 13A4 [Source:RefSeq_peptide;Acc:NP_115655]
ENSG0000 0127334	DYRK2	Dual specificity tyrosine-phosphorylation regulated kinase 2 (EC 2.7.1.112) (EC 2.7.1.37). [Source:Uniprot/SWISSPROT;Acc:Q92630]
ENSG0000 0127589	TUBB4 Q	Tubulin beta-4q chain. [Source:Uniprot/SWISSPROT;Acc:Q99867]
ENSG0000 0127616	SMARC A4	Possible global transcription activator SNF2L4 (EC 3.6.1.-) (ATP- dependent helicase SMARCA4) (SNF2-beta) (BRG-1 protein) (Mitotic growth and transcription activator) (Brahma protein homolog 1) (SWI/SNF-related matrix associated actin dependent regulator [Source:Uniprot/SWISSPROT;Acc:P51532]
ENSG0000 0127824	TUBA1	Tubulin alpha-1 chain (Alpha-tubulin 1) (Testis-specific alpha- tubulin) (Tubulin H2-alpha). [Source:Uniprot/SWISSPROT;Acc:P68366]
ENSG0000 0127884	**ECHS1**	**"Enoyl-CoA hydratase, mitochondrial precursor (EC 4.2.1.17) (Short chain enoyl-CoA hydratase) (SCEH) (Enoyl-CoA hydratase 1). [Source:Uniprot/SWISSPROT;Acc:P30084]"**
ENSG0000 0127917	ARF1P1	DJ133P16.1 (ADP-ribosylation factor 1). [Source:Uniprot/SPTREMBL;Acc:Q9H516]
ENSG0000 0127948	POR	NADPH--cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R). [Source:Uniprot/SWISSPROT;Acc:P16435]
ENSG0000 0127980	PEX1	Peroxisome biogenesis factor 1 (Peroxin-1) (Peroxisome biogenesis disorder protein 1). [Source:Uniprot/SWISSPROT;Acc:O43933]
ENSG0000 0128245	YWHA H	14-3-3 protein eta (Protein AS1). [Source:Uniprot/SWISSPROT;Acc:Q04917]
ENSG0000 0128833	MYO5C	Myosin-5C (Myosin Vc). [Source:Uniprot/SWISSPROT;Acc:Q9NQX4]
ENSG0000 0128881	TTBK2	tau tubulin kinase 2 [Source:RefSeq_peptide;Acc:NP_775771]
ENSG0000 0128908	INOC1	yeast INO80-like protein [Source:RefSeq_peptide;Acc:NP_060023]
ENSG0000 0128918	ALDH1 A2	Retinal dehydrogenase 2 (EC 1.2.1.36) (RalDH2) (RALDH 2) (RALDH(II)) (Retinaldehyde-specific dehydrogenase type 2) (Aldehyde dehydrogenase family 1 member A2). [Source:Uniprot/SWISSPROT;Acc:O94788]
ENSG0000 0129083	COPB	Coatomer beta subunit (Beta-coat protein) (Beta-COP). [Source:Uniprot/SWISSPROT;Acc:P53618]
ENSG0000 0129084	PSMA1	Proteasome subunit alpha type 1 (EC 3.4.25.1) (Proteasome component C2) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit C2) (Proteasome nu chain) (30 kDa prosomal protein) (PROS-30). [Source:Uniprot/SWISSPROT;Acc:P25786]
ENSG0000 0129250	KIF1C	Kinesin-like protein KIF1C. [Source:Uniprot/SWISSPROT;Acc:O43896]
ENSG0000 0129295	**LRRC6**	**Leucine-rich repeat-containing protein 6 (Leucine-rich testis-specific protein) (Testis-specific leucine-rich repeat protein). [Source:Uniprot/SWISSPROT;Acc:Q86X45]**
ENSG0000 0129348	**QTRT1**	**Queuine tRNA-ribosyltransferase (EC 2.4.2.29) (tRNA-guanine transglycosylase) (Guanine insertion enzyme). [Source:Uniprot/SWISSPROT;Acc:Q9BXR0]**
ENSG0000 0129354	AP1M2	"Adaptor-related protein complex 1, mu 2 subunit (Mu-adaptin 2) (Adaptor protein complex AP-1 mu-2 subunit) (Golgi adaptor HA1/AP1 adaptin mu-2 subunit) (Clathrin assembly protein assembly protein complex 1 medium chain 2) (AP-mu chain family member mu1B). [Source:Uniprot/SWISSPROT;Acc:Q9Y6Q5]"
ENSG0000	RAB2B	Ras-related protein Rab-2B. [Source:Uniprot/SWISSPROT;Acc:Q8WUD1]

0129472		
ENSG0000 0129543		
ENSG0000 0129824	RPS4Y1	"40S ribosomal protein S4, Y isoform 1. [Source:Uniprot/SWISSPROT;Acc:P22090]"
ENSG0000 0129932	HLRC1	HEAT-like (PBS lyase) repeat containing 1 [Source:RefSeq_peptide;Acc:NP_112594]
ENSG0000 0130119	GNL3L	guanine nucleotide binding protein-like 3 (nucleolar)-like [Source:RefSeq_peptide;Acc:NP_061940]
ENSG0000 0130270	ATP8B3	Probable phospholipid-transporting ATPase IK (EC 3.6.3.1) (ATPase class I type 8B member 3). [Source:Uniprot/SWISSPROT;Acc:O60423]
ENSG0000 0130294	KIF1A	Kinesin-like protein KIF1A (Axonal transporter of synaptic vesicles). [Source:Uniprot/SWISSPROT;Acc:Q12756]
ENSG0000 0130363	**RSHL2**	**radial spokehead-like 2 [Source:RefSeq_peptide;Acc:NP_114130]**
ENSG0000 0130413	STK33	serine/threonine kinase 33 [Source:RefSeq_peptide;Acc:NP_112168]
ENSG0000 0130589	PR285_ HUMA N	Peroxisomal proliferator-activated receptor A interacting complex 285 kDa protein (EC 3.6.1.-) (ATP-dependent helicase PRIC285) (PPAR-alpha interacting complex protein 285). [Source:Uniprot/SWISSPROT;Acc:Q9BYK8]
ENSG0000 0130669	PAK4	Serine/threonine-protein kinase PAK 4 (EC 2.7.1.37) (p21-activated kinase 4) (PAK-4). [Source:Uniprot/SWISSPROT;Acc:O96013]
ENSG0000 0130724	CHMP2 A	Charged multivesicular body protein 2a (Chromatin modifying protein 2a) (CHMP2a) (Vacuolar protein sorting 2-1) (Vps2-1) (hVps2-1) (Putative breast adenocarcinoma marker BC-2). [Source:Uniprot/SWISSPROT;Acc:O43633]
ENSG0000 0130741	EIF2S3	Eukaryotic translation initiation factor 2 subunit 3 (Eukaryotic translation initiation factor 2 gamma subunit) (eIF-2-gamma). [Source:Uniprot/SWISSPROT;Acc:P41091]
ENSG0000 0130826	DKC1	H/ACA ribonucleoprotein complex subunit 4 (EC 5.4.99.-) (Dyskerin) (Nucleolar protein family A member 4) (snoRNP protein DKC1) (Nopp140- associated protein of 57 kDa) (Nucleolar protein NAP57) (CBF5 homolog). [Source:Uniprot/SWISSPROT;Acc:O60832]
ENSG0000 0130957	FBP2	"Fructose-1,6-bisphosphatase isozyme 2 (EC 3.1.3.11) (D-fructose-1,6- bisphosphate 1-phosphohydrolase 2) (FBPase 2). [Source:Uniprot/SWISSPROT;Acc:O00757]"
ENSG0000 0130985	UBE1	Ubiquitin-activating enzyme E1 (A1S9 protein). [Source:Uniprot/SWISSPROT;Acc:P22314]
ENSG0000 0130997	POLN	polymerase (DNA directed) nu [Source:RefSeq_peptide;Acc:NP_861524]
ENSG0000 0131023	LATS1	Serine/threonine-protein kinase LATS1 (EC 2.7.1.37) (Large tumor suppressor homolog 1) (WARTS protein kinase) (h-warts). [Source:Uniprot/SWISSPROT;Acc:O95835]
ENSG0000 0131044	**Q5VX4 8_HUM AN**	**OTTHUMP00000030566 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q9BR18]**
ENSG0000 0131069	ACSS2	"Acetyl-coenzyme A synthetase, cytoplasmic (EC 6.2.1.1) (Acetate--CoA ligase) (Acyl-activating enzyme) (Acetyl-CoA synthetase) (ACS) (AceCS) (Acyl-CoA synthetase short-chain family member 2). [Source:Uniprot/SWISSPROT;Acc:Q9NR19]"
ENSG0000 0131269	ABCB7	"ATP-binding cassette sub-family B member 7, mitochondrial precursor (ATP-binding cassette transporter 7) (ABC transporter 7 protein). [Source:Uniprot/SWISSPROT;Acc:O75027]"
ENSG0000 0131437	KIF3A	Kinesin-like protein KIF3A (Microtubule plus end-directed kinesin motor 3A). [Source:Uniprot/SWISSPROT;Acc:Q9Y496]
ENSG0000 0131459	GFPT2	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 2 (EC 2.6.1.16) (Hexosephosphate aminotransferase 2) (D-fructose-6- phosphate amidotransferase 2) (GFAT 2) (GFAT2). [Source:Uniprot/SWISSPROT;Acc:O94808]
ENSG0000 0131462	TUBG1	Tubulin gamma-1 chain (Gamma-1 tubulin) (Gamma-tubulin complex component 1) (GCP-1). [Source:Uniprot/SWISSPROT;Acc:P23258]
ENSG0000 0131508	UBE2D 2	Ubiquitin-conjugating enzyme E2 D2 (EC 6.3.2.19) (Ubiquitin-protein ligase D2) (Ubiquitin carrier protein D2) (Ubiquitin-conjugating enzyme E2-17 kDa 2) (E2(17)KB 2). [Source:Uniprot/SWISSPROT;Acc:P62837]
ENSG0000 0131747	Q71UQ 5_HUM AN	Topoisomerase II alpha (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q71UQ5]
ENSG0000 0131778	CHD1L	chromodomain helicase DNA binding protein 1-like [Source:RefSeq_peptide;Acc:NP_004275]
ENSG0000 0131844	MCCC2	"Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial precursor (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 2) (MCCase beta subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase beta subunit) (3- Methylcrotonyl-CoA carboxylase non-biotin-containing [Source:Uniprot/SWISSPROT;Acc:Q9HCC0]"
ENSG0000 0132002	DNAJB 1	DnaJ homolog subfamily B member 1 (Heat shock 40 kDa protein 1) (Heat shock protein 40) (HSP40) (DnaJ protein homolog 1) (HDJ-1). [Source:Uniprot/SWISSPROT;Acc:P25685]
ENSG0000 0132141	CCT6B	"T-complex protein 1, zeta-2 subunit (TCP-1-zeta-2) (CCT-zeta-2) (TCP- 1-zeta-like) (CCT-zeta-like) (Testis-specific Tcp20) (Testis-specific protein TSA303). [Source:Uniprot/SWISSPROT;Acc:Q92526]"
ENSG0000 0132153	DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30 isoform 1 [Source:RefSeq_peptide;Acc:NP_619520]
ENSG0000 0132183		
ENSG0000 0132330	SCLY	selenocysteine lyase [Source:RefSeq_peptide;Acc:NP_057594]
ENSG0000 0132341	RAN	GTP-binding nuclear protein Ran (GTPase Ran) (Ras-like protein TC4) (Androgen receptor-associated protein 24). [Source:Uniprot/SWISSPROT;Acc:P62826]
ENSG0000 0132356	PRKAA 1	"5'-AMP-activated protein kinase, catalytic alpha-1 chain (EC 2.7.1.-) (AMPK alpha-1 chain). [Source:Uniprot/SWISSPROT;Acc:Q13131]"
ENSG0000 0132383	RPA1	Replication protein A 70 kDa DNA-binding subunit (RP-A) (RF-A) (Replication factor-A protein 1) (Single-stranded DNA-binding protein). [Source:Uniprot/SWISSPROT;Acc:P27694]
ENSG0000	FIGNL1	fidgetin-like 1 [Source:RefSeq_peptide;Acc:NP_071399]

0132436		
ENSG0000 0132603	NIP7	60S ribosome subunit biogenesis protein NIP7 homolog (KD93). [Source:Uniprot/SWISSPROT;Acc:Q9Y221]
ENSG0000 0132612	VPS4A	Vacuolar sorting protein 4a (SKD2 protein) (hVPS4) (VPS4-1). [Source:Uniprot/SWISSPROT;Acc:Q9UN37]
ENSG0000 0132646	PCNA	Proliferating cell nuclear antigen (PCNA) (Cyclin). [Source:Uniprot/SWISSPROT;Acc:P12004]
ENSG0000 0132681	ATP1A 4	Sodium/potassium-transporting ATPase alpha-4 chain (EC 3.6.3.9) (Sodium pump 4) (Na+/K+ ATPase 4). [Source:Uniprot/SWISSPROT;Acc:Q13733]
ENSG0000 0132698	RAB25	Ras-related protein Rab-25 (CATX-8). [Source:Uniprot/SWISSPROT;Acc:P57735]
ENSG0000 0132781	MUTY H	A/G-specific adenine DNA glycosylase (EC 3.2.2.-) (MutY homolog) (hMYH). [Source:Uniprot/SWISSPROT;Acc:Q9UIF7]
ENSG0000 0132786	Q4VXU 1_HUM AN	Chromsome 20 open reading frame 119. [Source:Uniprot/SPTREMBL;Acc:Q4VXU1]
ENSG0000 0132793		
ENSG0000 0132826		
ENSG0000 0132932	ATP8A 2	Probable phospholipid-transporting ATPase IB (EC 3.6.3.1) (ATPase class I type 8A member 2) (ML-1). [Source:Uniprot/SWISSPROT;Acc:Q9NTI2]
ENSG0000 0132964	CDK8	Cell division protein kinase 8 (EC 2.7.1.37) (Protein kinase K35). [Source:Uniprot/SWISSPROT;Acc:P49336]
ENSG0000 0133020	MYH8	"Myosin-8 (Myosin heavy chain, skeletal muscle, perinatal) (MyHC- perinatal). [Source:Uniprot/SWISSPROT;Acc:P13535]"
ENSG0000 0133026	MYH10	"Myosin-10 (Myosin heavy chain, nonmuscle IIb) (Nonmuscle myosin heavy chain IIb) (NMMHC II-b) (NMMHC-IIB) (Cellular myosin heavy chain, type B) (Nonmuscle myosin heavy chain-B) (NMMHC-B). [Source:Uniprot/SWISSPROT;Acc:P35580]"
ENSG0000 0133083	DCAM KL1	Serine/threonine-protein kinase DCAMKL1 (EC 2.7.1.37) (Doublecortin- like and CAM kinase-like 1). [Source:Uniprot/SWISSPROT;Acc:O15075]
ENSG0000 0133119	RFC3	Activator 1 38 kDa subunit (Replication factor C 38 kDa subunit) (A1 38 kDa subunit) (RF-C 38 kDa subunit) (RFC38) (Replication factor C subunit 3). [Source:Uniprot/SWISSPROT;Acc:P40938]
ENSG0000 0133275	CSNK1 G2	"Casein kinase I, gamma 2 isoform (EC 2.7.1.-) (CKI-gamma 2). [Source:Uniprot/SWISSPROT;Acc:P78368]"
ENSG0000 0133392	MYH11	"Myosin-11 (Myosin heavy chain, smooth muscle isoform) (SMMHC). [Source:Uniprot/SWISSPROT;Acc:P35749]"
ENSG0000 0133511	PIK4CA	Phosphatidylinositol 4-kinase alpha (EC 2.7.1.67) (PI4-kinase) (PtdIns-4-kinase) (PI4K-alpha). [Source:Uniprot/SWISSPROT;Acc:P42356]
ENSG0000 0133627	ACTR3 B	actin-related protein 3-beta [Source:RefSeq_peptide;Acc:NP_065178]
ENSG0000 0133657	ATP13 A3	Probable cation-transporting ATPase 13A3 (EC 3.6.3.-) (ATPase family homolog up-regulated in senescence cells 1). [Source:Uniprot/SWISSPROT;Acc:Q9H7F0]
ENSG0000 0133805	AMPD3	AMP deaminase 3 (EC 3.5.4.6) (AMP deaminase isoform E) (Erythrocyte AMP deaminase). [Source:Uniprot/SWISSPROT;Acc:Q01432]
ENSG0000 0133879		
ENSG0000 0134001	EIF2S1	Eukaryotic translation initiation factor 2 subunit 1 (Eukaryotic translation initiation factor 2 alpha subunit) (eIF-2-alpha) (EIF- 2alpha) (EIF-2A). [Source:Uniprot/SWISSPROT;Acc:P05198]
ENSG0000 0134058	CDK7	Cell division protein kinase 7 (EC 2.7.1.37) (CDK-activating kinase) (CAK) (TFIIH basal transcription factor complex kinase subunit) (39 kDa protein kinase) (P39 Mo15) (STK1) (CAK1). [Source:Uniprot/SWISSPROT;Acc:P50613]
ENSG0000 0134072	CAMK1	Calcium/calmodulin-dependent protein kinase type 1 (EC 2.7.1.123) (CaM kinase I) (CaM-KI) (CaM kinase I alpha) (CaMKI-alpha). [Source:Uniprot/SWISSPROT;Acc:Q14012]
ENSG0000 0134109	EDEM1	ER degradation-enhancing alpha-mannosidase-like. [Source:Uniprot/SWISSPROT;Acc:Q92611]
ENSG0000 0134257		
ENSG0000 0134287	ARF3	ADP-ribosylation factor 3. [Source:Uniprot/SWISSPROT;Acc:P61204]
ENSG0000 0134308	YWHA Q	14-3-3 protein theta (14-3-3 protein tau) (14-3-3 protein T-cell) (HS1 protein). [Source:Uniprot/SWISSPROT;Acc:P27348]
ENSG0000 0134318	ROCK2	"Rho-associated protein kinase 2 (EC 2.7.1.37) (Rho-associated, coiled- coil containing protein kinase 2) (p164 ROCK-2) (Rho kinase 2). [Source:Uniprot/SWISSPROT;Acc:O75116]"
ENSG0000 0134324	LPIN1	Lipin-1. [Source:Uniprot/SWISSPROT;Acc:Q14693]
ENSG0000 0134419	RPS15A	40S ribosomal protein S15a. [Source:Uniprot/SWISSPROT;Acc:P62244]
ENSG0000 0134594	RAB33 A	Ras-related protein Rab-33A (Small GTP-binding protein S10). [Source:Uniprot/SWISSPROT;Acc:Q14088]
ENSG0000 0134602	MST4_ HUMA N	Serine/threonine-protein kinase MST4 (EC 2.7.1.37) (STE20-like kinase MST4) (MST-4) (Mammalian STE20-like protein kinase 4) (Serine/threonine-protein kinase MASK) (Mst3 and SOK1-related kinase). [Source:Uniprot/SWISSPROT;Acc:Q9P289]
ENSG0000 0134644	PUM1	Pumilio homolog 1 (Pumilio-1) (HsPUM). [Source:Uniprot/SWISSPROT;Acc:Q14671]
ENSG0000 0134697	GNL2	Nucleolar GTP-binding protein 2 (Autoantigen NGP-1). [Source:Uniprot/SWISSPROT;Acc:Q13823]
ENSG0000 0134815	DHX34	Probable ATP-dependent RNA helicase DHX34 (EC 3.6.1.-) (DEAH box protein 34). [Source:Uniprot/SWISSPROT;Acc:Q14147]

ENSG0000 0134905	NP_078 813.1	
ENSG0000 0134910	ITM1	Oligosaccharyl transferase STT3 subunit homolog (B5) (Integral membrane protein 1) (TMC). [Source:Uniprot/SWISSPROT;Acc:P46977]
ENSG0000 0135047	CTSL	Cathepsin L precursor (EC 3.4.22.15) (Major excreted protein) (MEP) [Contains: Cathepsin L heavy chain; Cathepsin L light chain]. [Source:Uniprot/SWISSPROT;Acc:P07711]
ENSG0000 0135049	**AGTPB P1**	**ATP/GTP binding protein 1 [Source:RefSeq_peptide;Acc:NP_056054]**
ENSG0000 0135090	TAOK3	Serine/threonine-protein kinase TAO3 (EC 2.7.1.37) (Thousand and one amino acid protein 3) (Jun kinase-inhibitory kinase) (JNK/SAPK- inhibitory kinase) (Dendritic-cell derived protein kinase) (Cutaneous T-cell lymphoma tumor antigen HD-CL-09) (CTCL tumor [Source:Uniprot/SWISSPROT;Acc:Q9H2K8]
ENSG0000 0135205	**NP_065 930.1**	
ENSG0000 0135250	SRPK2	Serine/threonine-protein kinase SRPK2 (EC 2.7.1.37) (Serine/arginine- rich protein-specific kinase 2) (SR-protein-specific kinase 2) (SFRS protein kinase 2). [Source:Uniprot/SWISSPROT;Acc:P78362]
ENSG0000 0135372	ALP_H UMAN	N-acetyltransferase-like protein (EC 2.3.1.-). [Source:Uniprot/SWISSPROT;Acc:Q9H0A0]
ENSG0000 0135446	CDK4	Cell division protein kinase 4 (EC 2.7.1.37) (Cyclin-dependent kinase 4) (PSK-J3). [Source:Uniprot/SWISSPROT;Acc:P11802]
ENSG0000 0135624	CCT7	"T-complex protein 1, eta subunit (TCP-1-eta) (CCT-eta) (HIV-1 Nef interacting protein). [Source:Uniprot/SWISSPROT;Acc:Q99832]"
ENSG0000 0135776	ABCB1 0	"ATP-binding cassette sub-family B member 10, mitochondrial precursor (ATP-binding cassette transporter 10) (ABC transporter 10 protein) (Mitochondrial ATP-binding cassette 2) (M-ABC2). [Source:Uniprot/SWISSPROT;Acc:Q9NRK6]"
ENSG0000 0135821	GLUL	Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS). [Source:Uniprot/SWISSPROT;Acc:P15104]
ENSG0000 0135829	DHX9	ATP-dependent RNA helicase A (EC 3.6.1.-) (Nuclear DNA helicase II) (NDH II) (DEAH box protein 9). [Source:Uniprot/SWISSPROT;Acc:Q08211]
ENSG0000 0135912	**TTLL4**	**Tubulin tyrosine ligase-like protein 4. [Source:Uniprot/SWISSPROT;Acc:Q14679]**
ENSG0000 0136003	NIFUN	"NifU-like N-terminal domain containing protein, mitochondrial precursor (NifU-like protein) (Iron-sulfur cluster assembly enzyme ISCU). [Source:Uniprot/SWISSPROT;Acc:Q9H1K1]"
ENSG0000 0136010	ALDH1 L2	"aldehyde dehydrogenase 1 family, member L2 [Source:RefSeq_peptide;Acc:NP_001029345]"
ENSG0000 0136013		
ENSG0000 0136045	PWP1	Periodic tryptophan protein 1 homolog (Keratinocyte protein IEF SSP 9502). [Source:Uniprot/SWISSPROT;Acc:Q13610]
ENSG0000 0136098	NEK3	Serine/threonine-protein kinase Nek3 (EC 2.7.1.37) (NimA-related protein kinase 3) (HSPK 36). [Source:Uniprot/SWISSPROT;Acc:P51956]
ENSG0000 0136143	SUCLA 2	"Succinyl-CoA ligase [ADP-forming] beta-chain, mitochondrial precursor (EC 6.2.1.5) (Succinyl-CoA synthetase, betaA chain) (SCS-betaA) (ATP- specific succinyl-CoA synthetase beta subunit). [Source:Uniprot/SWISSPROT;Acc:Q9P2R7]"
ENSG0000 0136240	KDELR 2	ER lumen protein retaining receptor 2 (KDEL receptor 2) (KDEL endoplasmic reticulum protein retention receptor 2) (ERD2-like protein 1) (ELP-1). [Source:Uniprot/SWISSPROT;Acc:P33947]
ENSG0000 0136271	DDX56	Probable ATP-dependent RNA helicase DDX56 (EC 3.6.1.-) (DEAD box protein 56) (ATP-dependent 61 kDa nucleolar RNA helicase) (DEAD-box protein 21). [Source:Uniprot/SWISSPROT;Acc:Q9NY93]
ENSG0000 0136286	NM_03 3054.1	"myosin IG (MYO1G), mRNA [Source:RefSeq_dna;Acc:NM_033054]"
ENSG0000 0136381	IREB2	Iron-responsive element binding protein 2 (IRE-BP 2) (Iron regulatory protein 2) (IRP2). [Source:Uniprot/SWISSPROT;Acc:P48200]
ENSG0000 0136448	NMT1	Glycylpeptide N-tetradecanoyltransferase 1 (EC 2.3.1.97) (Peptide N- myristoyltransferase 1) (Myristoyl-CoA:protein N-myristoyltransferase 1) (NMT 1) (Type I N-myristoyltransferase). [Source:Uniprot/SWISSPROT;Acc:P30419]
ENSG0000 0136492	BRIP1	Fanconi anemia group J protein (EC 3.6.1.-) (ATP-dependent RNA helicase BRIP1) (Protein FACJ) (BRCA1-interacting protein C-terminal helicase 1) (BRCA1-interacting protein 1) (BRCA1-associated C-terminal helicase 1). [Source:Uniprot/SWISSPROT;Acc:Q9BX63]
ENSG0000 0136504	MYST2	"Histone acetyltransferase MYST2 (EC 2.3.1.48) (MYST protein 2) (MOZ, YBF2/SAS3, SAS2 and TIP60 protein 2) (Histone acetyltransferase binding to hORC1). [Source:Uniprot/SWISSPROT;Acc:O95251]"
ENSG0000 0136518	ACTL6 A	Actin-like protein 6A (53 kDa BRG1-associated factor A) (Actin-related protein Baf53a) (ArpNbeta). [Source:Uniprot/SWISSPROT;Acc:O96019]
ENSG0000 0136531	**SCN2A 2**	**"Sodium channel protein type II alpha subunit (Voltage-gated sodium channel alpha subunit Nav1.2) (Sodium channel protein, brain II alpha subunit) (HBSC II). [Source:Uniprot/SWISSPROT;Acc:Q99250]"**
ENSG0000 0136546	**SCN7A**	**"Sodium channel protein type VII alpha subunit (Putative voltage-gated sodium channel alpha subunit Nax) (Sodium channel protein, cardiac and skeletal muscle alpha-subunit). [Source:Uniprot/SWISSPROT;Acc:Q01118]"**
ENSG0000 0136628	EPRS	Bifunctional aminoacyl-tRNA synthetase [Includes: Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase); Prolyl-tRNA synthetase (EC 6.1.1.15) (Proline--tRNA ligase)]. [Source:Uniprot/SWISSPROT;Acc:P07814]
ENSG0000 0136631	VPS45A	Vacuolar protein sorting-associated protein 45 (h-VPS45) (hlVps45). [Source:Uniprot/SWISSPROT;Acc:Q9NRW7]
ENSG0000 0136709	WDR33	WD-repeat protein 33 (WD-repeat protein WDC146). [Source:Uniprot/SWISSPROT;Acc:Q9C0J8]
ENSG0000 0136718	IMP4	U3 small nucleolar ribonucleoprotein protein IMP4 (U3 snoRNP protein IMP4). [Source:Uniprot/SWISSPROT;Acc:Q96G21]
ENSG0000 0136758	YME1L 1	ATP-dependent metalloprotease YME1L1 (EC 3.4.24.-) (YME1-like protein 1) (ATP-dependent metalloprotease FtsH1) (Meg-4) (Presenilin- associated metalloprotease) (PAMP). [Source:Uniprot/SWISSPROT;Acc:Q96TA2]
ENSG0000 0136807	CDK9	Cell division protein kinase 9 (EC 2.7.1.37) (Cyclin-dependent kinase 9) (Serine/threonine-protein kinase PITALRE) (C-2K) (Cell division cycle 2-like protein kinase 4). [Source:Uniprot/SWISSPROT;Acc:P50750]
ENSG0000 0136824	SMC2L 1	Structural maintenance of chromosome 2-like 1 protein (Chromosome- associated protein E) (hCAP-E) (XCAP-E homolog). [Source:Uniprot/SWISSPROT;Acc:O95347]

ENSG0000 0136872	ALDOB	Fructose-bisphosphate aldolase B (EC 4.1.2.13) (Liver-type aldolase). [Source:Uniprot/SWISSPROT;Acc:P05062]
ENSG0000 0136883	KIF12	Kinesin-like protein KIF12. [Source:Uniprot/SWISSPROT;Acc:Q96FN5]
ENSG0000 0136930	PSMB7	Proteasome subunit beta type 7 precursor (EC 3.4.25.1) (Proteasome subunit Z) (Macropain chain Z) (Multicatalytic endopeptidase complex chain Z). [Source:Uniprot/SWISSPROT;Acc:Q99436]
ENSG0000 0136943	CTSL2	Cathepsin L2 precursor (EC 3.4.22.43) (Cathepsin V) (Cathepsin U). [Source:Uniprot/SWISSPROT;Acc:O60911]
ENSG0000 0137055	PLAA	Phospholipase A-2-activating protein (PLAP) (PLA2P). [Source:Uniprot/SWISSPROT;Acc:Q9Y263]
ENSG0000 0137094	DNAJB 5	DnaJ homolog subfamily B member 5 (Heat shock protein Hsp40-3) (Heat shock protein cognate 40) (Hsc40) (Hsp40-2). [Source:Uniprot/SWISSPROT;Acc:O75953]
ENSG0000 0137124	ALDH1 B1	"Aldehyde dehydrogenase X, mitochondrial precursor (EC 1.2.1.3) (ALDH class 2). [Source:Uniprot/SWISSPROT;Acc:P30837]"
ENSG0000 0137177	KIF13A	Kinesin-like protein KIF13A (Kinesin-like protein RBKIN). [Source:Uniprot/SWISSPROT;Acc:Q9H1H9]
ENSG0000 0137267	TUBB2 A	"tubulin, beta 2 [Source:RefSeq_peptide;Acc:NP_001060]"
ENSG0000 0137285	TUBB2 B	"tubulin, beta polypeptide paralog [Source:RefSeq_peptide;Acc:NP_821080]"
ENSG0000 0137328		
ENSG0000 0137333	DHX16	Putative pre-mRNA splicing factor ATP-dependent RNA helicase DHX16 (EC 3.6.1.-) (DEAH-box protein 16) (ATP-dependent RNA helicase #3). [Source:Uniprot/SWISSPROT;Acc:O60231]
ENSG0000 0137335	ABCF1	ATP-binding cassette sub-family F member 1 (ATP-binding cassette 50) (TNF-alpha-stimulated ABC protein). [Source:Uniprot/SWISSPROT;Acc:Q8NE71]
ENSG0000 0137379	TUBB	Tubulin beta-2 chain. [Source:Uniprot/SWISSPROT;Acc:P07437]
ENSG0000 0137411	VARSL	valyl-tRNA synthetase 2-like [Source:RefSeq_peptide;Acc:NP_065175]
ENSG0000 0137474	MYO7A	Myosin-7A (Myosin VIIa). [Source:Uniprot/SWISSPROT;Acc:Q13402]
ENSG0000 0137502	RAB30	Ras-related protein Rab-30. [Source:Uniprot/SWISSPROT;Acc:Q15771]
ENSG0000 0137601	NEK1	Serine/threonine-protein kinase Nek1 (EC 2.7.1.37) (NimA-related protein kinase 1) (NY-REN-55 antigen). [Source:Uniprot/SWISSPROT;Acc:Q96PY6]
ENSG0000 0137764	MAP2K 5	Dual specificity mitogen-activated protein kinase kinase 5 (EC 2.7.1.37) (MAP kinase kinase 5) (MAPKK 5) (MAPK/ERK kinase 5). [Source:Uniprot/SWISSPROT;Acc:Q13163]
ENSG0000 0137807	KIF23	Kinesin-like protein KIF23 (Mitotic kinesin-like protein 1) (Kinesin- like protein 5). [Source:Uniprot/SWISSPROT;Acc:Q02241]
ENSG0000 0137843	PAK6	Serine/threonine-protein kinase PAK 6 (EC 2.7.1.37) (p21-activated kinase 6) (PAK-6) (PAK-5). [Source:Uniprot/SWISSPROT;Acc:Q9NQU5]
ENSG0000 0137941	**TTLL7**	**Tubulin tyrosine ligase-like protein 7 (Protein NYD-SP30). [Source:Uniprot/SWISSPROT;Acc:Q6ZT98]**
ENSG0000 0137955	RABGG TB	Geranylgeranyl transferase type II beta subunit (EC 2.5.1.60) (Rab geranylgeranyltransferase beta subunit) (Rab geranyl-geranyltransferase beta subunit) (Rab GG transferase beta) (Rab GGTase beta). [Source:Uniprot/SWISSPROT;Acc:P53611]
ENSG0000 0138002	**IFT172**	**selective LIM binding factor homolog [Source:RefSeq_peptide;Acc:NP_056477]**
ENSG0000 0138032	PPM1B	Protein phosphatase 2C isoform beta (EC 3.1.3.16) (PP2C-beta). [Source:Uniprot/SWISSPROT;Acc:O75688]
ENSG0000 0138069	RAB1A	Ras-related protein Rab-1A (YPT1-related protein). [Source:Uniprot/SWISSPROT;Acc:P62820]
ENSG0000 0138071	ACTR2	Actin-like protein 2 (Actin-related protein 2). [Source:Uniprot/SWISSPROT;Acc:P61160]
ENSG0000 0138075	ABCG5	ATP-binding cassette sub-family G member 5 (Sterolin-1). [Source:Uniprot/SWISSPROT;Acc:Q9H222]
ENSG0000 0138107	ACTR1 A	Alpha-centractin (Centractin) (Centrosome-associated actin homolog) (Actin-RPV) (ARP1). [Source:Uniprot/SWISSPROT;Acc:P61163]
ENSG0000 0138138	ATAD1	ATPase family AAA domain containing protein 1. [Source:Uniprot/SWISSPROT;Acc:Q8NBU5]
ENSG0000 0138160	KIF11	Kinesin-like protein KIF11 (Kinesin-related motor protein Eg5) (Kinesin-like spindle protein HKSP) (Thyroid receptor interacting protein 5) (TRIP5) (Kinesin-like protein 1). [Source:Uniprot/SWISSPROT;Acc:P52732]
ENSG0000 0138175	ARL3	ADP-ribosylation factor-like protein 3. [Source:Uniprot/SWISSPROT;Acc:P36405]
ENSG0000 0138346	DNA2L	DNA2-like homolog (EC 3.6.1.-) (DNA replication ATP-dependent helicase-like homolog) (Fragment). [Source:Uniprot/SWISSPROT;Acc:P51530]
ENSG0000 0138395	ALS2C R7	Serine/threonine-protein kinase ALS2CR7 (EC 2.7.1.37) (Amyotrophic lateral sclerosis 2 chromosomal region candidate gene 7 protein). [Source:Uniprot/SWISSPROT;Acc:Q96Q40]
ENSG0000 0138398	PPIG	Peptidyl-prolyl cis-trans isomerase G (EC 5.2.1.8) (Peptidyl-prolyl isomerase G) (PPIase G) (Rotamase G) (Cyclophilin G) (Clk-associating RS-cyclophilin) (CARS-cyclophilin) (CARS-Cyp) (SR-cyclophilin) (SRcyp) (SR-cyp) (CASP10). [Source:Uniprot/SWISSPROT;Acc:Q13427]
ENSG0000 0138411	HECW2	"HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2 [Source:RefSeq_peptide;Acc:NP_065811]"
ENSG0000 0138413	IDH1	Isocitrate dehydrogenase [NADP] cytoplasmic (EC 1.1.1.42) (Oxalosuccinate decarboxylase) (IDH) (NADP(+)-specific ICDH) (IDP). [Source:Uniprot/SWISSPROT;Acc:O75874]
ENSG0000 0138430	PTD4_ HUMA	Putative GTP-binding protein PTD004. [Source:Uniprot/SWISSPROT;Acc:Q9NTK5]

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ENSG0000 0138592	USP8	Ubiquitin carboxyl-terminal hydrolase 8 (EC 3.1.2.15) (Ubiquitin thiolesterase 8) (Ubiquitin-specific processing protease 8) (Deubiquitinating enzyme 8) (hUBPy). [Source:Uniprot/SWISSPROT;Acc:P40818]
ENSG0000 0138669	PRKG2	cGMP-dependent protein kinase 2 (EC 2.7.1.37) (CGK 2) (cGKII) (Type II cGMP-dependent protein kinase). [Source:Uniprot/SWISSPROT;Acc:Q13237]
ENSG0000 0138686	**BBS7**	**Bardet-Biedl syndrome 7 protein (BBS2-like protein 1). [Source:Uniprot/SWISSPROT;Acc:Q8IWZ6]**
ENSG0000 0138769	CDKL2	Cyclin-dependent kinase-like 2 (EC 2.7.1.37) (Serine/threonine-protein kinase KKIAMRE) (Protein kinase p56 KKIAMRE). [Source:Uniprot/SWISSPROT;Acc:Q92772]
ENSG0000 0138778	CENPE	Centromeric protein E (CENP-E protein). [Source:Uniprot/SWISSPROT;Acc:Q02224]
ENSG0000 0138802	SEC24B	Protein transport protein Sec24B (SEC24-related protein B). [Source:Uniprot/SWISSPROT;Acc:O95487]
ENSG0000 0138814	PPP3CA	"Serine/threonine protein phosphatase 2B catalytic subunit, alpha isoform (EC 3.1.3.16) (Calmodulin-dependent calcineurin A subunit, alpha isoform) (CAM-PRP catalytic subunit). [Source:Uniprot/SWISSPROT;Acc:Q08209]"
ENSG0000 0139116	KIF21A	Kinesin family member 21A (Kinesin-like protein KIF2) (NY-REN-62 antigen). [Source:Uniprot/SWISSPROT;Acc:Q7Z4S6]
ENSG0000 0139151	PLCZ1	"phospholipase C, zeta 1 [Source:RefSeq_peptide;Acc:NP_149114]"
ENSG0000 0139197	PEX5	Peroxisomal targeting signal 1 receptor (Peroxismore receptor 1) (Peroxisomal C-terminal targeting signal import receptor) (PTS1-BP) (Peroxin-5) (PTS1 receptor). [Source:Uniprot/SWISSPROT;Acc:P50542]
ENSG0000 0139323	**WDR51 B**	**WD repeat domain 51B [Source:RefSeq_peptide;Acc:NP_758440]**
ENSG0000 0139514	SLC7A1	High-affinity cationic amino acid transporter-1 (CAT-1) (CAT1) (System Y+ basic amino acid transporter) (Ecotropic retroviral leukemia receptor homolog) (ERR) (Ecotropic retrovirus receptor homolog). [Source:Uniprot/SWISSPROT;Acc:P30825]
ENSG0000 0139637	MYG1_ HUMA N	MYG1 protein. [Source:Uniprot/SWISSPROT;Acc:Q9HB07]
ENSG0000 0139719	VPS33A	Vacuolar protein sorting 33A (hVPS33A). [Source:Uniprot/SWISSPROT;Acc:Q96AX1]
ENSG0000 0139842	CUL4A	Cullin-4A (CUL-4A). [Source:Uniprot/SWISSPROT;Acc:Q13619]
ENSG0000 0140105	WARS	Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase) (TrpRS) (IFP53) (hWRS). [Source:Uniprot/SWISSPROT;Acc:P23381]
ENSG0000 0140403	DNAJA 4	DnaJ homolog subfamily A member 4. [Source:Uniprot/SWISSPROT;Acc:Q8WW22]
ENSG0000 0140598	EFTUD 1	elongation factor Tu GTP binding domain containing 1 [Source:RefSeq_peptide;Acc:NP_078856]
ENSG0000 0140798	ABCC1 2	"ATP-binding cassette, sub-family C, member 12 isoform b [Source:RefSeq_peptide;Acc:NP_660189]"
ENSG0000 0140829	DHX38	Pre-mRNA splicing factor ATP-dependent RNA helicase PRP16 (EC 3.6.1.-) (ATP-dependent RNA helicase DHX38) (DEAH box protein 38). [Source:Uniprot/SWISSPROT;Acc:Q92620]
ENSG0000 0140854	KATNB 1	Katanin p80 WD40-containing subunit B1 (Katanin p80 subunit B1) (p80 katanin). [Source:Uniprot/SWISSPROT;Acc:Q9BVA0]
ENSG0000 0140859	KIFC3	Kinesin-like protein KIFC3. [Source:Uniprot/SWISSPROT;Acc:Q9BVG8]
ENSG0000 0140986	RPL3L	60S ribosomal protein L3-like. [Source:Uniprot/SWISSPROT;Acc:Q92901]
ENSG0000 0140992	PDPK1	3-phosphoinositide dependent protein kinase 1 (EC 2.7.1.37) (hPDK1). [Source:Uniprot/SWISSPROT;Acc:O15530]
ENSG0000 0141013	**GAS8**	**Growth-arrest-specific protein 8 (Growth arrest-specific 11). [Source:Uniprot/SWISSPROT;Acc:O95995]**
ENSG0000 0141018	Q6ZSU 8_HUM AN	
ENSG0000 0141037		
ENSG0000 0141048	MYH4	"Myosin-4 (Myosin heavy chain, skeletal muscle, fetal) (Myosin heavy chain IIb) (MyHC-IIb). [Source:Uniprot/SWISSPROT;Acc:Q9Y623]"
ENSG0000 0141140	MYOH D1	myosin head domain containing 1 isoform 1 [Source:RefSeq_peptide;Acc:NP_079385]
ENSG0000 0141141	DDX52	Probable ATP-dependent RNA helicase DDX52 (EC 3.6.1.-) (DEAD box protein 52) (ATP-dependent RNA helicase ROK1-like). [Source:Uniprot/SWISSPROT;Acc:Q9Y2R4]
ENSG0000 0141200	KIF2B	kinesin protein [Source:RefSeq_peptide;Acc:NP_115948]
ENSG0000 0141338	ABCA8	"ATP-binding cassette, sub-family A member 8 [Source:RefSeq_peptide;Acc:NP_009099]"
ENSG0000 0141367	CLTC	Clathrin heavy chain 1 (CLH-17). [Source:Uniprot/SWISSPROT;Acc:Q00610]
ENSG0000 0141385	AFG3L 2	AFG3-like protein 2 (EC 3.4.24.-) (Paraplegin-like protein). [Source:Uniprot/SWISSPROT;Acc:Q9Y4W6]
ENSG0000 0141401	IMPA2	Inositol monophosphatase 2 (EC 3.1.3.25) (IMPase 2) (IMP 2) (Inositol- 1(or 4)-monophosphatase 2) (Myo-inositol monophosphatase A2). [Source:Uniprot/SWISSPROT;Acc:O14732]
ENSG0000 0141503	MINK1	Misshapen-like kinase 1 (EC 2.7.1.37) (Mitogen-activated protein kinase kinase kinase kinase 6) (MAPK/ERK kinase kinase kinase 6) (MEK kinase kinase 6) (MEKKK 6) (Misshapen/NIK-related kinase) (GCK family kinase MiNK). [Source:Uniprot/SWISSPROT;Acc:Q8N4C8]
ENSG0000	DDX48	Probable ATP-dependent RNA helicase DDX48 (EC 3.6.1.-) (DEAD box protein 48) (Eukaryotic initiation factor 4A-like

0141543		NUK-34) (Nuclear matrix protein 265) (hNMP 265) (Eukaryotic translation initiation factor 4A isoform 3). [Source:Uniprot/SWISSPROT;Acc:P38919]
ENSG0000 0141551	CSNK1 D	"Casein kinase I, delta isoform (EC 2.7.1.-) (CKI-delta) (CKId). [Source:Uniprot/SWISSPROT;Acc:P48730]"
ENSG0000 0141639	MAPK4	Mitogen-activated protein kinase 4 (EC 2.7.1.37) (Extracellular signal-regulated kinase 4) (ERK-4) (MAP kinase isoform p63) (p63- MAPK). [Source:Uniprot/SWISSPROT;Acc:P31152]
ENSG0000 0141748		
ENSG0000 0141837	**CACN A1A**	**"Voltage-dependent P/Q-type calcium channel alpha-1A subunit (Voltage- gated calcium channel alpha subunit Cav2.1) (Calcium channel, L type, alpha-1 polypeptide isoform 4) (Brain calcium channel I) (BI). [Source:Uniprot/SWISSPROT;Acc:O00555]"**
ENSG0000 0141979	CALR3	Calreticulin-3 precursor (Calreticulin-2). [Source:Uniprot/SWISSPROT;Acc:Q96L12]
ENSG0000 0142149	HUNK	Hormonally up-regulated neu tumor-associated kinase (EC 2.7.1.37) (Serine/threonine-protein kinase MAK-V) (B19). [Source:Uniprot/SWISSPROT;Acc:P57058]
ENSG0000 0142178	SNF1L K	Serine/threonine-protein kinase SNF1-like kinase 1 (EC 2.7.1.37) (Serine/threonine-protein kinase SNF1LK). [Source:Uniprot/SWISSPROT;Acc:P57059]
ENSG0000 0142186	SCYL1	SCYL1 protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q96G50]
ENSG0000 0142208	AKT1	RAC-alpha serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-alpha) (Protein kinase B) (PKB) (C-AKT). [Source:Uniprot/SWISSPROT;Acc:P31749]
ENSG0000 0142347	MYO1F	Myosin If (Myosin-IE). [Source:Uniprot/SWISSPROT;Acc:O00160]
ENSG0000 0142507	PSMB6	Proteasome subunit beta type 6 precursor (EC 3.4.25.1) (Proteasome delta chain) (Macropain delta chain) (Multicatalytic endopeptidase complex delta chain) (Proteasome subunit Y). [Source:Uniprot/SWISSPROT;Acc:P28072]
ENSG0000 0142534	RPS11	40S ribosomal protein S11. [Source:Uniprot/SWISSPROT;Acc:P62280]
ENSG0000 0142541	RPL13A	60S ribosomal protein L13a (23 kDa highly basic protein). [Source:Uniprot/SWISSPROT;Acc:P40429]
ENSG0000 0142544	ATPBD 3	ATP binding domain 3 [Source:RefSeq_peptide;Acc:NP_660275]
ENSG0000 0142657	PGD	"6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44). [Source:Uniprot/SWISSPROT;Acc:P52209]"
ENSG0000 0142676	RPL11	60S ribosomal protein L11 (CLL-associated antigen KW-12). [Source:Uniprot/SWISSPROT;Acc:P62913]
ENSG0000 0142731	PLK4	Serine/threonine-protein kinase PLK4 (EC 2.7.1.37) (Polo-like kinase 4) (PLK-4) (Serine/threonine-protein kinase Sak) (Serine/threonine- protein kinase 18). [Source:Uniprot/SWISSPROT;Acc:O00444]
ENSG0000 0142733	MAP3K 6	Mitogen-activated protein kinase kinase kinase 6 (EC 2.7.1.37). [Source:Uniprot/SWISSPROT;Acc:O95382]
ENSG0000 0142875	PRKAC B	"cAMP-dependent protein kinase, beta-catalytic subunit (EC 2.7.1.37) (PKA C-beta). [Source:Uniprot/SWISSPROT;Acc:P22694]"
ENSG0000 0142892	PIGK	"GPI-anchor transamidase precursor (EC 3.-.-.-) (GPI transamidase) (Phosphatidylinositol-glycan biosynthesis, class K protein) (PIG-K) (hGPI8). [Source:Uniprot/SWISSPROT;Acc:Q92643]"
ENSG0000 0142937	RPS8	40S ribosomal protein S8. [Source:Uniprot/SWISSPROT;Acc:P62241]
ENSG0000 0142945	KIF2C	Kinesin-like protein KIF2C (Mitotic centromere-associated kinesin) (MCAK) (Kinesin-like protein 6). [Source:Uniprot/SWISSPROT;Acc:Q99661]
ENSG0000 0142961	MOBK L2C	Mps one binder kinase activator-like 2C (Mob1 homolog 3C) (Protein Mob3C). [Source:Uniprot/SWISSPROT;Acc:Q70IA8]
ENSG0000 0143106	PSMA5	Proteasome subunit alpha type 5 (EC 3.4.25.1) (Proteasome zeta chain) (Macropain zeta chain) (Multicatalytic endopeptidase complex zeta chain). [Source:Uniprot/SWISSPROT;Acc:P28066]
ENSG0000 0143149	ALDH9 A1	4-trimethylaminobutyraldehyde dehydrogenase (EC 1.2.1.47) (TMABADH) (Aldehyde dehydrogenase 9A1) (EC 1.2.1.3) (Aldehyde dehydrogenase E3 isozyme) (Gamma-aminobutyraldehyde dehydrogenase) (EC 1.2.1.19) (R-aminobutyraldehyde dehydrogenase). [Source:Uniprot/SWISSPROT;Acc:P49189]
ENSG0000 0143156	**NME7**	**Nucleoside diphosphate kinase 7 (EC 2.7.4.6) (NDK 7) (NDP kinase 7) (nm23-H7). [Source:Uniprot/SWISSPROT;Acc:Q9Y5B8]**
ENSG0000 0143222	UFC1	Ufm1-conjugating enzyme 1 (Ubiquitin-fold modifier-conjugating enzyme 1). [Source:Uniprot/SWISSPROT;Acc:Q9Y3C8]
ENSG0000 0143258	USP21	Ubiquitin carboxyl-terminal hydrolase 21 (EC 3.1.2.15) (Ubiquitin thiolesterase 21) (Ubiquitin-specific processing protease 21) (Deubiquitinating enzyme 21) (NEDD8-specific protease). [Source:Uniprot/SWISSPROT;Acc:Q9UK80]
ENSG0000 0143374	TARSL 1	threonyl-tRNA synthetase-like 1 [Source:RefSeq_peptide;Acc:NP_079426]
ENSG0000 0143387	CTSK	Cathepsin K precursor (EC 3.4.22.38) (Cathepsin O) (Cathepsin X) (Cathepsin O2). [Source:Uniprot/SWISSPROT;Acc:P43235]
ENSG0000 0143393	PIK4CB	Phosphatidylinositol 4-kinase beta (EC 2.7.1.67) (PtdIns 4-kinase) (PI4Kbeta) (PI4K-beta) (NPIK) (PI4K92). [Source:Uniprot/SWISSPROT;Acc:Q9UBF8]
ENSG0000 0143479	DYRK3	Dual specificity tyrosine-phosphorylation regulated kinase 3 (EC 2.7.1.-). [Source:Uniprot/SWISSPROT;Acc:O43781]
ENSG0000 0143515	ATP8B2	Probable phospholipid-transporting ATPase ID (EC 3.6.3.1) (ATPase class I type 8B member 2). [Source:Uniprot/SWISSPROT;Acc:P98198]
ENSG0000 0143545	RAB13	Ras-related protein Rab-13. [Source:Uniprot/SWISSPROT;Acc:P51153]
ENSG0000 0143627	PKLR	"Pyruvate kinase, isozymes R/L (EC 2.7.1.40) (R-type/L-type pyruvate kinase) (Red cell/liver pyruvate kinase). [Source:Uniprot/SWISSPROT;Acc:P30613]"
ENSG0000 0143632	ACTA1	"Actin, alpha skeletal muscle (Alpha-actin-1). [Source:Uniprot/SWISSPROT;Acc:P68133]"
ENSG0000 0143700		

ENSG0000 0143748	NVL	Nuclear valosin-containing protein-like (Nuclear VCP-like protein) (NVLp). [Source:Uniprot/SWISSPROT;Acc:O15381]
ENSG0000 0143761	ARF1	ADP-ribosylation factor 1. [Source:Uniprot/SWISSPROT;Acc:P84077]
ENSG0000 0143763		
ENSG0000 0143776	CDC42 BPA	Serine/threonine-protein kinase MRCK alpha (EC 2.7.1.37) (CDC42- binding protein kinase alpha) (Myotonic dystrophy kinase-related CDC42-binding kinase alpha) (Myotonic dystrophy protein kinase-like alpha) (MRCK alpha) (DMPK-like alpha). [Source:Uniprot/SWISSPROT;Acc:Q5VT25]
ENSG0000 0143815	LBR	Lamin-B receptor (Integral nuclear envelope inner membrane protein) (LMN2R). [Source:Uniprot/SWISSPROT;Acc:Q14739]
ENSG0000 0143882	ATP6V 1C2	"ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C isoform 2 [Source:RefSeq_peptide;Acc:NP_653184]"
ENSG0000 0143921	ABCG8	ATP-binding cassette sub-family G member 8 (Sterolin-2). [Source:Uniprot/SWISSPROT;Acc:Q9H221]
ENSG0000 0143933	CALM1	Calmodulin (CaM). [Source:Uniprot/SWISSPROT;Acc:P62158]
ENSG0000 0143942	**CHAC2**	
ENSG0000 0144028	ASCC3 L1	U5 small nuclear ribonucleoprotein 200 kDa helicase (EC 3.6.1.-) (U5 snRNP-specific 200 kDa protein) (U5-200KD) (Activating signal cointegrator 1 complex subunit 3-like 1). [Source:Uniprot/SWISSPROT;Acc:O75643]
ENSG0000 0144045	DQX1	DEAQ box polypeptide 1 (RNA-dependent ATPase) [Source:RefSeq_peptide;Acc:NP_598376]
ENSG0000 0144134	**RABL2 A**	**Rab-like protein 2A. [Source:Uniprot/SWISSPROT;Acc:Q9UBK7]**
ENSG0000 0144136	SLC20A 1	Sodium-dependent phosphate transporter 1 (Solute carrier family 20 member 1) (Phosphate transporter 1) (PiT-1) (Gibbon ape leukemia virus receptor 1) (GLVR-1) (Leukemia virus receptor 1 homolog). [Source:Uniprot/SWISSPROT;Acc:Q8WUM9]
ENSG0000 0144285	**SCN1A**	**"Sodium channel protein type I alpha subunit (Voltage-gated sodium channel alpha subunit Nav1.1) (Sodium channel protein, brain I alpha subunit). [Source:Uniprot/SWISSPROT;Acc:P35498]"**
ENSG0000 0144381	HSPD1	"60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 kDa chaperonin) (CPN60) (Heat shock protein 60) (HSP-60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein) (HuCHA60). [Source:Uniprot/SWISSPROT;Acc:P10809]"
ENSG0000 0144440		
ENSG0000 0144452	ABCA12	ATP-binding cassette sub-family A member 12 (ATP-binding cassette transporter 12) (ATP-binding cassette 12). [Source:Uniprot/SWISSPROT;Acc:Q86UK0]
ENSG0000 0144535	NP_689 596.3	
ENSG0000 0144566	RAB5A	Ras-related protein Rab-5A. [Source:Uniprot/SWISSPROT;Acc:P20339]
ENSG0000 0144579	CTDSP 1	Carboxy-terminal domain RNA polymerase II polypeptide A small phosphatase 1 (EC 3.1.3.16) (Nuclear LIM interactor-interacting factor 3) (NLI-interacting factor 3) (NLI-IF). [Source:Uniprot/SWISSPROT;Acc:Q9GZU7]
ENSG0000 0144580	RQCD1	RCD1 required for cell differentiation1 homolog [Source:RefSeq_peptide;Acc:NP_005435]
ENSG0000 0144591	GMPPA	GDP-mannose pyrophosphorylase A [Source:RefSeq_peptide;Acc:NP_995319]
ENSG0000 0144677	CTDSP L	CTD small phosphatase-like protein (CTDSP-like) (Small C-terminal domain phosphatase 3) (Small CTD phosphatase 3) (SCP3) (Nuclear LIM interactor-interacting factor 1) (NLI-interacting factor 1) (NIF-like protein) (RBSP3) (YA22 protein) (HYA22). [Source:Uniprot/SWISSPROT;Acc:O15194]
ENSG0000 0144744	UBE1C	NEDD8-activating enzyme E1 catalytic subunit (EC 6.3.2.-) (Ubiquitin- activating enzyme 3) (NEDD8-activating enzyme E1C) (Ubiquitin- activating enzyme E1C). [Source:Uniprot/SWISSPROT;Acc:Q8TBC4]
ENSG0000 0144821	MYH15	
ENSG0000 0144848	ATG3	Autophagy protein 3-like (APG3-like) (hApg3) (PC3-96 protein). [Source:Uniprot/SWISSPROT;Acc:Q9NT62]
ENSG0000 0144908	ALDH1 L1	10-formyltetrahydrofolate dehydrogenase (EC 1.5.1.6) (10-FTHFDH) (Aldehyde dehydrogenase 1 family member L1). [Source:Uniprot/SWISSPROT;Acc:O75891]
ENSG0000 0144975		
ENSG0000 0145017		
ENSG0000 0145020	AMT	"Aminomethyltransferase, mitochondrial precursor (EC 2.1.2.10) (Glycine cleavage system T protein) (GCVT). [Source:Uniprot/SWISSPROT;Acc:P48728]"
ENSG0000 0145075	**CCDC3 9**	
ENSG0000 0145234		
ENSG0000 0145246	ATP10 D	Probable phospholipid-transporting ATPase VD (EC 3.6.3.1) (ATPVD). [Source:Uniprot/SWISSPROT;Acc:Q9P241]
ENSG0000 0145268		
ENSG0000 0145349	CAMK2 D	Calcium/calmodulin-dependent protein kinase type II delta chain (EC 2.7.1.123) (CaM-kinase II delta chain) (CaM kinase II delta subunit) (CaMK-II delta subunit). [Source:Uniprot/SWISSPROT;Acc:Q13557]
ENSG0000 0145375	SPATA 5	spermatogenesis associated factor SPAF [Source:RefSeq_peptide;Acc:NP_660208]
ENSG0000 0145632	PLK2	Serine/threonine-protein kinase PLK2 (EC 2.7.1.37) (Polo-like kinase 1) (PLK-2) (Serine/threonine-protein kinase SNK) (Serum inducible kinase). [Source:Uniprot/SWISSPROT;Acc:Q9NYY3]

ENSG0000 0145654		
ENSG0000 0145833	DDX46	Probable ATP-dependent RNA helicase DDX46 (EC 3.6.1.-) (DEAD box protein 46) (PRP5 homolog). [Source:Uniprot/SWISSPROT;Acc:Q7L014]
ENSG0000 0145987		
ENSG0000 0145996	CDKAL 1	CDK5 regulatory subunit associated protein 1-like 1 [Source:RefSeq_peptide;Acc:NP_060244]
ENSG0000 0146092		
ENSG0000 0146305		
ENSG0000 0146372		
ENSG0000 0146679		
ENSG0000 0146695		
ENSG0000 0146701	MDH2	"Malate dehydrogenase, mitochondrial precursor (EC 1.1.1.37). [Source:Uniprot/SWISSPROT;Acc:P40926]"
ENSG0000 0146731	CCT6A	"T-complex protein 1, zeta subunit (TCP-1-zeta) (CCT-zeta) (CCT-zeta-1) (Tcp20) (HTR3) (Acute morphine dependence related protein 2). [Source:Uniprot/SWISSPROT;Acc:P40227]"
ENSG0000 0146856	**AGBL3**	**ATP/GTP binding protein-like 3 [Source:RefSeq_peptide;Acc:NP_848658]**
ENSG0000 0146955	NP_001 008749. 1	GTP-binding protein RAB19B [Source:RefSeq_peptide;Acc:NP_001008749]
ENSG0000 0147044	CASK	Peripheral plasma membrane protein CASK (EC 2.7.1.-) (hCASK) (Calcium/calmodulin-dependent serine protein kinase) (Lin-2 homolog). [Source:Uniprot/SWISSPROT;Acc:O14936]
ENSG0000 0147127	RAB41	"RAB41, member RAS homolog family [Source:RefSeq_peptide;Acc:NP_001027898]"
ENSG0000 0147160	DGAT2 L4	diacylglycerol O-acyltransferase 2-like 4 [Source:RefSeq_peptide;Acc:NP_001002254]
ENSG0000 0147224	PRPS1	Ribose-phosphate pyrophosphokinase I (EC 2.7.6.1) (Phosphoribosyl pyrophosphate synthetase I) (PRS-I) (PPRibP). [Source:Uniprot/SWISSPROT;Acc:P60891]
ENSG0000 0147400	CETN2	Centrin-2 (Caltractin isoform 1). [Source:Uniprot/SWISSPROT;Acc:P41208]
ENSG0000 0147403	RPL10	60S ribosomal protein L10 (QM protein) (Tumor suppressor QM) (Laminin receptor homolog). [Source:Uniprot/SWISSPROT;Acc:P27635]
ENSG0000 0147416	ATP6V 1B2	"Vacuolar ATP synthase subunit B, brain isoform (EC 3.6.3.14) (V-ATPase B2 subunit) (Vacuolar proton pump B isoform 2) (Endomembrane proton pump 58 kDa subunit) (HO57). [Source:Uniprot/SWISSPROT;Acc:P21281]"
ENSG0000 0147419	CCDC2 5	coiled-coil domain containing 25 isoform 2 [Source:RefSeq_peptide;Acc:NP_060716]
ENSG0000 0147613	PSKH2	Serine/threonine-protein kinase H2 (EC 2.7.1.37) (PSK-H2). [Source:Uniprot/SWISSPROT;Acc:Q96QS6]
ENSG0000 0147614	ATP6V 0D2	"ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d isoform 2 [Source:RefSeq_peptide;Acc:NP_689778]"
ENSG0000 0147687	TATDN 1	TatD DNase domain containing 1 [Source:RefSeq_peptide;Acc:NP_114415]
ENSG0000 0148075		
ENSG0000 0148090	AUH	"Methylglutaconyl-CoA hydratase, mitochondrial precursor (EC 4.2.1.18) (AU-specific RNA-binding enoyl-CoA hydratase) (AU-binding protein/enoyl-CoA hydratase). [Source:Uniprot/SWISSPROT;Acc:Q13825]"
ENSG0000 0148156	ACTL7 B	Actin-like protein 7B (Actin-like-7-beta) (Actin-like 7B). [Source:Uniprot/SWISSPROT;Acc:Q9Y614]
ENSG0000 0148408	CACNA 1B	"Voltage-dependent N-type calcium channel alpha-1B subunit (Voltage- gated calcium channel alpha subunit Cav2.2) (Calcium channel, L type, alpha-1 polypeptide isoform 5) (Brain calcium channel III) (BIII). [Source:Uniprot/SWISSPROT;Acc:Q00975]"
ENSG0000 0148459	TPRT	trans-prenyltransferase [Source:RefSeq_peptide;Acc:NP_055132]
ENSG0000 0148571		
ENSG0000 0148606	POLR3 A	DNA-directed RNA polymerase III largest subunit (EC 2.7.7.6) (RPC155) (RPC1). [Source:Uniprot/SWISSPROT;Acc:O14802]
ENSG0000 0148634	HERC4	hect domain and RLD 4 isoform b [Source:RefSeq_peptide;Acc:NP_056416]
ENSG0000 0148660	CAMK2 G	Calcium/calmodulin-dependent protein kinase type II gamma chain (EC 2.7.1.123) (CaM-kinase II gamma chain) (CaM kinase II gamma subunit) (CaMK-II gamma subunit). [Source:Uniprot/SWISSPROT;Acc:Q13555]
ENSG0000 0148760		
ENSG0000 0148843	PDCD1 1	RRP5 protein homolog (Programmed cell death protein 11). [Source:Uniprot/SWISSPROT;Acc:Q14690]
ENSG0000 0149269	PAK1	Serine/threonine-protein kinase PAK 1 (EC 2.7.1.37) (p21-activated kinase 1) (PAK-1) (P65-PAK) (Alpha-PAK). [Source:Uniprot/SWISSPROT;Acc:Q13153]
ENSG0000 0149273	RPS3	40S ribosomal protein S3. [Source:Uniprot/SWISSPROT;Acc:P23396]
ENSG0000 0149345	Q9NTT 1_HUM	OTTHUMP00000030191. [Source:Uniprot/SPTREMBL;Acc:Q9NTT1]

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ENSG0000 0149428	HYOU1	150 kDa oxygen-regulated protein precursor (Orp150) (Hypoxia up- regulated 1). [Source:Uniprot/SWISSPROT;Acc:Q9Y4L1]
ENSG0000 0149554	CHEK1	Serine/threonine-protein kinase Chk1 (EC 2.7.1.37). [Source:Uniprot/SWISSPROT;Acc:O14757]
ENSG0000 0149809	TM7SF 2	Delta(14)-sterol reductase (EC 1.3.1.70) (C-14 sterol reductase) (Sterol C14-reductase) (Delta14-SR) (Transmembrane 7 superfamily member 2) (Another new gene 1 protein) (Putative sterol reductase SR- 1). [Source:Uniprot/SWISSPROT;Acc:O76062]
ENSG0000 0149923	PPP4C	Serine/threonine protein phosphatase 4 catalytic subunit (EC 3.1.3.16) (PP4C) (Pp4) (Protein phosphatase X) (PP-X). [Source:Uniprot/SWISSPROT;Acc:P60510]
ENSG0000 0149925	ALDOA	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase) (Lung cancer antigen NY-LU-1). [Source:Uniprot/SWISSPROT;Acc:P04075]
ENSG0000 0149930	TAOK2	Serine/threonine-protein kinase TAO2 (EC 2.7.1.37) (Thousand and one amino acid protein 2) (Prostate-derived STE20-like kinase 1) (PSK-1) (Kinase from chicken homolog C) (hKFC-C). [Source:Uniprot/SWISSPROT;Acc:Q9UL54]
ENSG0000 0150276		
ENSG0000 0150457	LATS2	Serine/threonine-protein kinase LATS2 (EC 2.7.1.37) (Large tumor suppressor homolog 2) (Serine/threonine-protein kinase kpm) (Kinase phosphorylated during mitosis protein) (Warts-like kinase). [Source:Uniprot/SWISSPROT;Acc:Q9NRM7]
ENSG0000 0150627	**WDR17**	**WD-repeat protein 17. [Source:Uniprot/SWISSPROT;Acc:Q8IZU2]**
ENSG0000 0150753	CCT5	"T-complex protein 1, epsilon subunit (TCP-1-epsilon) (CCT-epsilon). [Source:Uniprot/SWISSPROT;Acc:P48643]"
ENSG0000 0150768	DLAT	"Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial precursor (EC 2.3.1.12) (Pyruvate dehydrogenase complex E2 subunit) (PDCE2) (E2) (Dihydrolipoamide S- acetyltransferase component of pyruvate dehydrog [Source:Uniprot/SWISSPROT;Acc:P10515]"
ENSG0000 0150961	SEC24D	Protein transport protein Sec24D (SEC24-related protein D). [Source:Uniprot/SWISSPROT;Acc:O94855]
ENSG0000 0150967	ABCB9	ATP-binding cassette sub-family B member 9 precursor (ATP-binding cassette transporter 9) (ABC transporter 9 protein) (TAP-like protein) (TAPL) (hABCB9). [Source:Uniprot/SWISSPROT;Acc:Q9NP78]
ENSG0000 0150980	**O95495 _HUM AN**	**"Axonemal dynein, heavy chain (Fragment). [Source:Uniprot/SPTREMBL;Acc:O95495]"**
ENSG0000 0150990	DHX37	Probable ATP-dependent RNA helicase DHX37 (EC 3.6.1.-) (DEAH box protein 37). [Source:Uniprot/SWISSPROT;Acc:Q8IY37]
ENSG0000 0150991	UBC	Ubiquitin. [Source:Uniprot/SWISSPROT;Acc:P62988]
ENSG0000 0151093	OXSM	"3-oxoacyl-ACP synthase, mitochondrial [Source:RefSeq_peptide;Acc:NP_060367]"
ENSG0000 0151148	UBE3B	ubiquitin protein ligase E3B isoform b [Source:RefSeq_peptide;Acc:NP_904323]
ENSG0000 0151176	**NP_775 813.1**	
ENSG0000 0151224	MAT1A	S-adenosylmethionine synthetase alpha and beta forms (EC 2.5.1.6) (Methionine adenosyltransferase) (AdoMet synthetase) (MAT-I/III). [Source:Uniprot/SWISSPROT;Acc:Q00266]
ENSG0000 0151292	CSNK1 G3	"Casein kinase I, gamma 3 isoform (EC 2.7.1.-) (CKI-gamma 3). [Source:Uniprot/SWISSPROT;Acc:Q9Y6M4]"
ENSG0000 0151413	NUBPL	
ENSG0000 0151414	NEK7	Serine/threonine-protein kinase Nek7 (EC 2.7.1.37) (NimA-related protein kinase 7). [Source:Uniprot/SWISSPROT;Acc:Q8TDX7]
ENSG0000 0151475	SLC25A 31	"solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31 [Source:RefSeq_peptide;Acc:NP_112581]"
ENSG0000 0151502	VPS26B	
ENSG0000 0151632	AKR1C 2	"Aldo-keto reductase family 1 member C2 (EC 1.-.-.-) (Trans-1,2- dihydrobenzene-1,2-diol dehydrogenase) (EC 1.3.1.20) (Type III 3- alpha-hydroxysteroid dehydrogenase) (EC 1.1.1.213) (3-alpha-HSD3) (Chlordecone reductase homolog HAKRD) (Dihydrodiol dehydrog [Source:Uniprot/SWISSPROT;Acc:P52895]"
ENSG0000 0151726	ACSL1	Long-chain-fatty-acid--CoA ligase 1 (EC 6.2.1.3) (Long-chain acyl-CoA synthetase 1) (LACS 1) (Palmitoyl-CoA ligase 1) (Long-chain fatty acid CoA ligase 2) (Long-chain acyl-CoA synthetase 2) (LACS 2) (Acyl-CoA synthetase 1) (ACS1) (Palmitoyl-CoA ligase 2). [Source:Uniprot/SWISSPROT;Acc:P33121]
ENSG0000 0151729	SLC25A 4	"ADP/ATP translocase 1 (Adenine nucleotide translocator 1) (ANT 1) (ADP,ATP carrier protein 1) (Solute carrier family 25 member 4) (ADP,ATP carrier protein, heart/skeletal muscle isoform T1). [Source:Uniprot/SWISSPROT;Acc:P12235]"
ENSG0000 0151806	NP_068 746.1	
ENSG0000 0151846	PABPC 3	Polyadenylate-binding protein 3 (Poly(A)-binding protein 3) (PABP 3) (Testis-specific poly(A)-binding protein). [Source:Uniprot/SWISSPROT;Acc:Q9H361]
ENSG0000 0152086	NP_997 195.1	
ENSG0000 0152270	**PDE3B**	**"cGMP-inhibited 3',5'-cyclic phosphodiesterase B (EC 3.1.4.17) (Cyclic GMP-inhibited phosphodiesterase B) (CGI-PDE B) (CGIPDE1) (CGIP1). [Source:Uniprot/SWISSPROT;Acc:Q13370]"**
ENSG0000 0152465	NMT2	Glycylpeptide N-tetradecanoyltransferase 2 (EC 2.3.1.97) (Peptide N- myristoyltransferase 2) (Myristoyl-CoA:protein N-myristoyltransferase 2) (NMT 2) (Type II N-myristoyltransferase). [Source:Uniprot/SWISSPROT;Acc:O60551]
ENSG0000 0152495	CAMK4	Calcium/calmodulin-dependent protein kinase type IV (EC 2.7.1.123) (CAM kinase-GR) (CaMK IV). [Source:Uniprot/SWISSPROT;Acc:Q16566]
ENSG0000 0152670	DDX4	Probable ATP-dependent RNA helicase DDX4 (EC 3.6.1.-) (DEAD box protein 4) (VASA homolog). [Source:Uniprot/SWISSPROT;Acc:Q9NQI0]
ENSG0000	SAR1B	GTP-binding protein SAR1b (GTBPB). [Source:Uniprot/SWISSPROT;Acc:Q9Y6B6]

0152700		
ENSG0000 0152763	**WDR78**	**WD repeat domain 78 isoform 1 [Source:RefSeq_peptide;Acc:NP_079039]**
ENSG0000 0152932	RAB3C	Ras-related protein Rab-3C. [Source:Uniprot/SWISSPROT;Acc:Q96E17]
ENSG0000 0152945	STK38L	Serine/threonine-protein kinase 38-like (EC 2.7.1.37) (NDR2 protein kinase) (Nuclear Dbf2-related kinase 2). [Source:Uniprot/SWISSPROT;Acc:Q9Y2H1]
ENSG0000 0153132	CLGN	Calmegin precursor. [Source:Uniprot/SWISSPROT;Acc:O14967]
ENSG0000 0153147	SMARC A5	SWI/SNF-related matrix associated actin dependent regulator of chromatin subfamily A member 5 (EC 3.6.1.-) (SWI/SNF-related matrix- associated actin-dependent regulator of chromatin A5) (Sucrose nonfermenting protein 2 homolog) (hSNF2H). [Source:Uniprot/SWISSPROT;Acc:O60264]
ENSG0000 0153253	**SCN3A**	**"Sodium channel protein type III alpha subunit (Voltage-gated sodium channel alpha subunit Nav1.3) (Sodium channel protein, brain III alpha subunit) (Voltage-gated sodium channel subtype III). [Source:Uniprot/SWISSPROT;Acc:Q9NY46]"**
ENSG0000 0153287	PRPS1L 1	Ribose-phosphate pyrophosphokinase III (EC 2.7.6.1) (Phosphoribosyl pyrophosphate synthetase III) (PRS-III) (Phosphoribosyl pyrophosphate synthetase 1-like 1). [Source:Uniprot/SWISSPROT;Acc:P21108]
ENSG0000 0153827	TRIP12	Thyroid receptor interacting protein 12 (TRIP12). [Source:Uniprot/SWISSPROT;Acc:Q14669]
ENSG0000 0153922	CHD1	Chromodomain-helicase-DNA-binding protein 1 (EC 3.6.1.-) (ATP- dependent helicase CHD1) (CHD-1). [Source:Uniprot/SWISSPROT;Acc:O14646]
ENSG0000 0154099	**LRRC5 0**	**leucine rich repeat containing 50 [Source:RefSeq_peptide;Acc:NP_848547]**
ENSG0000 0154229	PRKCA	"Protein kinase C, alpha type (EC 2.7.1.37) (PKC-alpha) (PKC-A). [Source:Uniprot/SWISSPROT;Acc:P17252]"
ENSG0000 0154258	ABCA9	"ATP-binding cassette, sub-family A, member 9 isoform a [Source:RefSeq_peptide;Acc:NP_525022]"
ENSG0000 0154262	ABCA6	"ATP-binding cassette, sub-family A, member 6 isoform a [Source:RefSeq_peptide;Acc:NP_525023]"
ENSG0000 0154263	ABCA1 0	"ATP-binding cassette, sub-family A, member 10 [Source:RefSeq_peptide;Acc:NP_525021]"
ENSG0000 0154265	ABCA5	"ATP-binding cassette, sub-family A , member 5 [Source:RefSeq_peptide;Acc:NP_758424]"
ENSG0000 0154310	TNIK	TRAF2 and NCK-interacting kinase (EC 2.7.1.37). [Source:Uniprot/SWISSPROT;Acc:Q9UKE5]
ENSG0000 0154427		
ENSG0000 0154611	PSMA8	Proteasome subunit alpha type 7-like (EC 3.4.25.1). [Source:Uniprot/SWISSPROT;Acc:Q8TAA3]
ENSG0000 0154650		
ENSG0000 0154678	**PDE1C**	**"Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1C (EC 3.1.4.17) (Cam-PDE 1C) (hCam-3). [Source:Uniprot/SWISSPROT;Acc:Q14123]"**
ENSG0000 0154822	PLCL2	phospholipase C-like 2 [Source:RefSeq_peptide;Acc:NP_055999]
ENSG0000 0154917	RAB6B	Ras-related protein Rab-6B. [Source:Uniprot/SWISSPROT;Acc:Q9NRW1]
ENSG0000 0154930	ACSS1	"Acetyl-coenzyme A synthetase 2-like, mitochondrial precursor (EC 6.2.1.1) (Acetate--CoA ligase 2) (Acetyl-CoA synthetase 2) (Acyl- CoA synthetase short-chain family member 1). [Source:Uniprot/SWISSPROT;Acc:Q9NUB1]"
ENSG0000 0155026	**Q86ST9 _HUM AN**	
ENSG0000 0155097	ATP6V 1C1	Vacuolar ATP synthase subunit C (EC 3.6.3.14) (V-ATPase C subunit) (Vacuolar proton pump C subunit). [Source:Uniprot/SWISSPROT;Acc:P21283]
ENSG0000 0155111	CDC2L 6	Cell division cycle 2-like protein kinase 6 (EC 2.7.1.37) (CDC2- related protein kinase 6) (Death-preventing kinase) (Cyclin-dependent kinase 11). [Source:Uniprot/SWISSPROT;Acc:Q9BWU1]
ENSG0000 0155288	ABCC1 3	Putative ATP-binding cassette transporter C13. [Source:Uniprot/SWISSPROT;Acc:Q9NSE7]
ENSG0000 0155304	STCH	Stress 70 protein chaperone microsome-associated 60 kDa protein precursor (Microsomal stress 70 protein ATPase core). [Source:Uniprot/SWISSPROT;Acc:P48723]
ENSG0000 0155508	CNOT8	CCR4-NOT transcription complex subunit 8 (CCR4-associated factor 8) (CAF1-like protein) (CALIFp) (CAF2). [Source:Uniprot/SWISSPROT;Acc:Q9UFF9]
ENSG0000 0155624		
ENSG0000 0155660	PDIA4	Protein disulfide-isomerase A4 precursor (EC 5.3.4.1) (Protein ERp-72) (ERp72). [Source:Uniprot/SWISSPROT;Acc:P13667]
ENSG0000 0155961	RAB39 B	Ras-related protein Rab-39B. [Source:Uniprot/SWISSPROT;Acc:Q96DA2]
ENSG0000 0155980	KIF5A	Neuronal kinesin heavy chain (NKHC) (Kinesin heavy chain isoform 5A) (Kinesin heavy chain neuron-specific 1). [Source:Uniprot/SWISSPROT;Acc:Q12840]
ENSG0000 0156017	CI041_ HUMA N	
ENSG0000 0156194	PPEF2	Serine/threonine protein phosphatase with EF-hands-2 (EC 3.1.3.16) (PPEF-2). [Source:Uniprot/SWISSPROT;Acc:O14830]
ENSG0000 0156261	CCT8	"T-complex protein 1, theta subunit (TCP-1-theta) (CCT-theta). [Source:Uniprot/SWISSPROT;Acc:P50990]"
ENSG0000	CCRK	Cell cycle-related kinase (EC 2.7.1.37) (Cyclin-kinase activating kinase p42) (CDK-activating kinase p42) (CAK-kinase

0156345		p42). [Source:Uniprot/SWISSPROT;Acc:Q8IZL9]
ENSG0000 0156367		
ENSG0000 0156414	TDRD9	tudor domain containing 9 [Source:RefSeq_peptide;Acc:NP_694591]
ENSG0000 0156508	EEF1A1	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor 1 A-1) (eEF1A-1) (Elongation factor Tu) (EF-Tu). [Source:Uniprot/SWISSPROT;Acc:P68104]
ENSG0000 0156582		
ENSG0000 0156650	MYST4	"Histone acetyltransferase MYST4 (EC 2.3.1.48) (EC 2.3.1.-) (MYST protein 4) (MOZ, YBF2/SAS3, SAS2 and TIP60 protein 4) (Histone acetyltransferase MOZ2) (Monocytic leukemia zinc finger protein- related factor) (Histone acetyltransferase MORF). [Source:Uniprot/SWISSPROT;Acc:Q8WYB5]"
ENSG0000 0156711	MAPK1 3	Mitogen-activated protein kinase 13 (EC 2.7.1.37) (Stress-activated protein kinase 4) (Mitogen-activated protein kinase p38 delta) (MAP kinase p38 delta). [Source:Uniprot/SWISSPROT;Acc:O15264]
ENSG0000 0156802	ATAD2	ATPase family AAA domain containing protein 2. [Source:Uniprot/SWISSPROT;Acc:Q6PL18]
ENSG0000 0156873	PHKG2	"Phosphorylase b kinase gamma catalytic chain, testis/liver isoform (EC 2.7.1.38) (PHK-gamma-T) (Phosphorylase kinase gamma subunit 2) (PSK-C3). [Source:Uniprot/SWISSPROT;Acc:P15735]"
ENSG0000 0156976	EIF4A2	Eukaryotic initiation factor 4A-II (EC 3.6.1.-) (ATP-dependent RNA helicase eIF4A-2) (eIF4A-II) (eIF-4A-II). [Source:Uniprot/SWISSPROT;Acc:Q14240]
ENSG0000 0157020	SEC13L 1	SEC13-related protein (SEC13-like protein 1). [Source:Uniprot/SWISSPROT;Acc:P55735]
ENSG0000 0157087	ATP2B2	Plasma membrane calcium-transporting ATPase 2 (EC 3.6.3.8) (PMCA2) (Plasma membrane calcium pump isoform 2) (Plasma membrane calcium ATPase isoform 2). [Source:Uniprot/SWISSPROT;Acc:Q01814]
ENSG0000 0157106	NP_055 907.3	PI-3-kinase-related kinase SMG-1 [Source:RefSeq_peptide;Acc:NP_055907]
ENSG0000 0157349	DDX19 B	ATP-dependent RNA helicase DDX19B (EC 3.6.1.-) (DEAD box protein 19B) (DEAD box RNA helicase DEAD5). [Source:Uniprot/SWISSPROT;Acc:Q9UMR2]
ENSG0000 0157388	**CACN A1D**	**"Voltage-dependent L-type calcium channel alpha-1D subunit (Voltage- gated calcium channel alpha subunit Cav1.3) (Calcium channel, L type, alpha-1 polypeptide, isoform 2). [Source:Uniprot/SWISSPROT;Acc:Q01668]"**
ENSG0000 0157423	**NP_060 028.2**	**hydrocephalus inducing [Source:RefSeq_peptide;Acc:NP_060028]**
ENSG0000 0157483	MYO1E	Myosin Ie (Myosin Ic). [Source:Uniprot/SWISSPROT;Acc:Q12965]
ENSG0000 0157540	DYRK1 A	Dual specificity tyrosine-phosphorylation regulated kinase 1A (EC 2.7.1.-) (Protein kinase minibrain homolog) (MNBH) (HP86) (Dual specificity YAK1-related kinase). [Source:Uniprot/SWISSPROT;Acc:Q13627]
ENSG0000 0157601	MX1	Interferon-induced GTP-binding protein Mx1 (Interferon-regulated resistance GTP-binding protein MxA) (Interferon-induced protein p78) (IFI-78K). [Source:Uniprot/SWISSPROT;Acc:P20591]
ENSG0000 0157796	**WDR19**	**WD repeat domain 19 [Source:RefSeq_peptide;Acc:NP_079408]**
ENSG0000 0157828	RPS4Y2 P	"40S ribosomal protein S4, Y isoform 2. [Source:Uniprot/SWISSPROT;Acc:Q8TD47]"
ENSG0000 0158023	**WDR66**	**WD repeat domain 66 [Source:RefSeq_peptide;Acc:NP_653269]**
ENSG0000 0158066		
ENSG0000 0158290	CUL4B	Cullin-4B (CUL-4B). [Source:Uniprot/SWISSPROT;Acc:Q13620]
ENSG0000 0158417	EIF5B	Eukaryotic translation initiation factor 5B (eIF-5B) (Translation initiation factor IF-2). [Source:Uniprot/SWISSPROT;Acc:O60841]
ENSG0000 0158467	SAHH3 _HUMA N	Putative adenosylhomocysteinase 3 (EC 3.3.1.1) (S-adenosyl-L- homocysteine hydrolase) (AdoHcyase). [Source:Uniprot/SWISSPROT;Acc:Q96HN2]
ENSG0000 0158486	DNAH3	"dynein, axonemal, heavy polypeptide 3 [Source:RefSeq_peptide;Acc:NP_060009]"
ENSG0000 0158571	PFKFB1	"6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1 (6PF-2-K/Fru- 2,6-P2ASE liver isozyme) [Includes: 6-phosphofructo-2-kinase (EC 2.7.1.105); Fructose-2,6-bisphosphatase (EC 3.1.3.46)]. [Source:Uniprot/SWISSPROT;Acc:P16118]"
ENSG0000 0159247		
ENSG0000 0159251	ACTC	"Actin, alpha cardiac (Alpha-cardiac actin). [Source:Uniprot/SWISSPROT;Acc:P68032]"
ENSG0000 0159348	CYB5R 1	"NAD(P)H:quinone oxidoreductase type 3, polypeptide A2 [Source:RefSeq_peptide;Acc:NP_057327]"
ENSG0000 0159352	PSMD4	26S proteasome non-ATPase regulatory subunit 4 (26S proteasome regulatory subunit S5A) (Rpn10) (Multiubiquitin chain binding protein) (Antisecretory factor 1) (AF) (ASF). [Source:Uniprot/SWISSPROT;Acc:P55036]
ENSG0000 0159363	ATP13 A2	Probable cation-transporting ATPase 13A2 (EC 3.6.3.-). [Source:Uniprot/SWISSPROT;Acc:Q9NQ11]
ENSG0000 0159377	PSMB4	Proteasome subunit beta type 4 precursor (EC 3.4.25.1) (Proteasome beta chain) (Macropain beta chain) (Multicatalytic endopeptidase complex beta chain) (Proteasome chain 3) (HSN3) (HsBPROS26). [Source:Uniprot/SWISSPROT;Acc:P28070]
ENSG0000 0159720	ATP6V 0D1	Vacuolar ATP synthase subunit d (EC 3.6.3.14) (V-ATPase d subunit) (Vacuolar proton pump d subunit) (V-ATPase AC39 subunit) (V-ATPase 40 kDa accessory protein) (P39) (32 kDa accessory protein). [Source:Uniprot/SWISSPROT;Acc:P61421]
ENSG0000 0159792	PSKH1	Serine/threonine-protein kinase H1 (EC 2.7.1.37) (PSK-H1). [Source:Uniprot/SWISSPROT;Acc:P11801]
ENSG0000 0160087	UBE2J2	Ubiquitin-conjugating enzyme E2 J2 (EC 6.3.2.19) (Non-canonical ubiquitin-conjugating enzyme 2) (NCUBE2). [Source:Uniprot/SWISSPROT;Acc:Q8N2K1]

ENSG0000 0160179	ABCG1	ATP-binding cassette sub-family G member 1 (White protein homolog) (ATP-binding cassette transporter 8). [Source:Uniprot/SWISSPROT;Acc:P45844]
ENSG0000 0160191	**PDE9A**	**"High-affinity cGMP-specific 3',5'-cyclic phosphodiesterase 9A (EC 3.1.4.35). [Source:Uniprot/SWISSPROT;Acc:O76083]"**
ENSG0000 0160200	CBS	Cystathionine beta-synthase (EC 4.2.1.22) (Serine sulfhydrase) (Beta- thionase). [Source:Uniprot/SWISSPROT;Acc:P35520]
ENSG0000 0160220	PWP2H	Periodic tryptophan protein 2 homolog. [Source:Uniprot/SWISSPROT;Acc:Q15269]
ENSG0000 0160310	HRMT1 L1	Protein arginine N-methyltransferase 2 (EC 2.1.1.-). [Source:Uniprot/SWISSPROT;Acc:P55345]
ENSG0000 0160396	HIPK4	homeodomain interacting protein kinase 4 [Source:RefSeq_peptide;Acc:NP_653286]
ENSG0000 0160447	PKN3	Protein kinase N3 (EC 2.7.1.37) (Protein kinase PKN-beta) (Protein- kinase C-related kinase 3). [Source:Uniprot/SWISSPROT;Acc:Q6P5Z2]
ENSG0000 0160469	BRSK1	BR serine/threonine-protein kinase 1 (EC 2.7.1.37) (SAD1 kinase) (SAD1A). [Source:Uniprot/SWISSPROT;Acc:Q8TDC3]
ENSG0000 0160551	TAOK1	Serine/threonine-protein kinase TAO1 (EC 2.7.1.37) (Thousand and one amino acid protein 1) (STE20-like kinase PSK2) (Kinase from chicken homolog B) (hKFC-B). [Source:Uniprot/SWISSPROT;Acc:Q7L7X3]
ENSG0000 0160584	NP_079 440.2	
ENSG0000 0160602	NEK8	Serine/threonine-protein kinase Nek8 (EC 2.7.1.37) (NimA-related protein kinase 8) (NIMA-related kinase 12a). [Source:Uniprot/SWISSPROT;Acc:Q86SG6]
ENSG0000 0160752	FDPS	Farnesyl pyrophosphate synthetase (FPP synthetase) (FPS) (Farnesyl diphosphate synthetase) [Includes: Dimethylallyltranstransferase (EC 2.5.1.1); Geranyltranstransferase (EC 2.5.1.10)]. [Source:Uniprot/SWISSPROT;Acc:P14324]
ENSG0000 0161016	RPL8	60S ribosomal protein L8. [Source:Uniprot/SWISSPROT;Acc:P62917]
ENSG0000 0161057	PSMC2	26S protease regulatory subunit 7 (MSS1 protein). [Source:Uniprot/SWISSPROT;Acc:P35998]
ENSG0000 0161149	NP_659 479.2	
ENSG0000 0161203	AP2M1	Clathrin coat assembly protein AP50 (Clathrin coat-associated protein AP50) (Plasma membrane adaptor AP-2 50 kDa protein) (HA2 50 kDa subunit) (Clathrin assembly protein complex 2 medium chain) (AP-2 mu 2 chain). [Source:Uniprot/SWISSPROT;Acc:Q96CW1]
ENSG0000 0161204	ABCF3	"ATP-binding cassette, sub-family F (GCN20), member 3 [Source:RefSeq_peptide;Acc:NP_060828]"
ENSG0000 0161513	FDXR	"NADPH:adrenodoxin oxidoreductase, mitochondrial precursor (EC 1.18.1.2) (Adrenodoxin reductase) (AR) (Ferredoxin--NADP(+) reductase). [Source:Uniprot/SWISSPROT;Acc:P22570]"
ENSG0000 0161960	EIF4A1	Eukaryotic initiation factor 4A-I (EC 3.6.1.-) (ATP-dependent RNA helicase eIF4A-1) (eIF4A-I) (eIF-4A-I). [Source:Uniprot/SWISSPROT;Acc:P60842]
ENSG0000 0162129	CLPB	Suppressor of potassium transport defect 3 (SKD3 protein). [Source:Uniprot/SWISSPROT;Acc:Q9H078]
ENSG0000 0162302	RPS6K A4	Ribosomal protein S6 kinase alpha 4 (EC 2.7.1.37) (Nuclear mitogen-and stress-activated protein kinase 2) (90 kDa ribosomal protein S6 kinase 4) (Ribosomal protein kinase B) (RSKB). [Source:Uniprot/SWISSPROT;Acc:O75676]
ENSG0000 0162385	MAGO H	Mago nashi protein homolog. [Source:Uniprot/SWISSPROT;Acc:P61326]
ENSG0000 0162409	PRKAA 2	"5'-AMP-activated protein kinase, catalytic alpha-2 chain (EC 2.7.1.-) (AMPK alpha-2 chain). [Source:Uniprot/SWISSPROT;Acc:P54646]"
ENSG0000 0162526	TSSK3	Testis-specific serine/threonine-protein kinase 3 (EC 2.7.1.37) (TSSK- 3) (Testis-specific kinase 3) (TSK-3) (Serine/threonine-protein kinase 22C). [Source:Uniprot/SWISSPROT;Acc:Q96PN8]
ENSG0000 0162616	DNAJB 4	DnaJ homolog subfamily B member 4 (Heat shock 40 kDa protein 1 homolog) (Heat shock protein 40 homolog) (HSP40 homolog). [Source:Uniprot/SWISSPROT;Acc:Q9UDY4]
ENSG0000 0162643	**WDR63**	**testis development protein NYD-SP29 [Source:RefSeq_peptide;Acc:NP_660155]**
ENSG0000 0162980	ARL5A	ADP-ribosylation factor-like protein 5A. [Source:Uniprot/SWISSPROT;Acc:Q9Y689]
ENSG0000 0163004		
ENSG0000 0163017	ACTG2	"Actin, gamma-enteric smooth muscle (Smooth muscle gamma actin) (Alpha- actin-3). [Source:Uniprot/SWISSPROT;Acc:P63267]"
ENSG0000 0163019	Q8N9E7 _HUMA N	
ENSG0000 0163050	CABC1	"Chaperone-activity of bc1 complex-like, mitochondrial precursor (Chaperone-ABC1-like). [Source:Uniprot/SWISSPROT;Acc:Q8NI60]"
ENSG0000 0163093	**BBS5**	**Bardet-Biedl syndrome 5 [Source:RefSeq_peptide;Acc:NP_689597] ** one of the two genes that mapped to *BBS5* critical interval ****
ENSG0000 0163104	SMARC AD1	"SWI/SNF-related, matrix associated, actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1 (EC 3.6.1.-) (ATP- dependent helicase 1) (hHEL1). [Source:Uniprot/SWISSPROT;Acc:Q9H4L7]"
ENSG0000 0163131	CTSS	Cathepsin S precursor (EC 3.4.22.27). [Source:Uniprot/SWISSPROT;Acc:P25774]
ENSG0000 0163214	DHX57	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57 isoform 1 [Source:RefSeq_peptide;Acc:NP_945314]
ENSG0000 0163312	NP_598 375.1	DNA helicase HEL308 [Source:RefSeq_peptide;Acc:NP_598375]
ENSG0000 0163399	ATP1A 1	Sodium/potassium-transporting ATPase alpha-1 chain precursor (EC 3.6.3.9) (Sodium pump 1) (Na+/K+ ATPase 1). [Source:Uniprot/SWISSPROT;Acc:P05023]
ENSG0000	CCT3	"T-complex protein 1, gamma subunit (TCP-1-gamma) (CCT-gamma) (hTRiC5).

0163468		[Source:Uniprot/SWISSPROT;Acc:P49368]"
ENSG0000 0163482	STK36	"serine/threonine kinase 36 (fused homolog, Drosophila) [Source:RefSeq_peptide;Acc:NP_056505]"
ENSG0000 0163510	NP_065 994.1	
ENSG0000 0163526	TUBA4	"tubulin, alpha 4 [Source:RefSeq_peptide;Acc:NP_079295]"
ENSG0000 0163527	NP_849 193.1	source of immunodominant MHC-associated peptides [Source:RefSeq_peptide;Acc:NP_849193]
ENSG0000 0163541	SUCLG 1	"Succinyl-CoA ligase [GDP-forming] alpha-chain, mitochondrial precursor (EC 6.2.1.4) (Succinyl-CoA synthetase, alpha chain) (SCS-alpha). [Source:Uniprot/SWISSPROT;Acc:P53597]"
ENSG0000 0163544	Q96BL6 _HUMA N	
ENSG0000 0163545	NUAK2	"NUAK family, SNF1-like kinase, 2 [Source:RefSeq_peptide;Acc:NP_112214]"
ENSG0000 0163558	PRKCI	"Protein kinase C, iota type (EC 2.7.1.37) (nPKC-iota) (Atypical protein kinase C-lambda/iota) (aPKC-lambda/iota) (PRKC-lambda/iota). [Source:Uniprot/SWISSPROT;Acc:P41743]"
ENSG0000 0163624	CDS1	Phosphatidate cytidylyltransferase 1 (EC 2.7.7.41) (CDP-diglyceride synthetase 1) (CDP-diglyceride pyrophosphorylase 1) (CDP- diacylglycerol synthase 1) (CDS 1) (CTP:phosphatidate cytidylyltransferase 1) (CDP-DAG synthase 1) (CDP-DG synthetase 1). [Source:Uniprot/SWISSPROT;Acc:Q92903]
ENSG0000 0163636	PSMD6	26S proteasome non-ATPase regulatory subunit 6 (26S proteasome regulatory subunit S10) (p42A) (Proteasome regulatory particle subunit p44S10) (Phosphonoformate immuno-associated protein 4) (Breast cancer associated protein SGA-113M). [Source:Uniprot/SWISSPROT;Acc:Q15008]
ENSG0000 0163655	GMPS	GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (Glutamine amidotransferase) (GMP synthetase). [Source:Uniprot/SWISSPROT;Acc:P49915]
ENSG0000 0163669	**DNHD2**	
ENSG0000 0163673	DCAM KL3	
ENSG0000 0163788	SNRK	SNF related kinase [Source:RefSeq_peptide;Acc:NP_060189]
ENSG0000 0163806	PPP1CB	Serine/threonine protein phosphatase PP1-beta catalytic subunit (EC 3.1.3.16) (PP-1B). [Source:Uniprot/SWISSPROT;Acc:P62140]
ENSG0000 0163808	KIF15	kinesin family member 15 [Source:RefSeq_peptide;Acc:NP_064627]
ENSG0000 0163879	**DNALI 1**	**"Axonemal dynein light intermediate polypeptide 1 (Inner dynein arm light chain, axonemal) (hp28). [Source:Uniprot/SWISSPROT;Acc:O14645]"**
ENSG0000 0163913	**IFT122**	**Intraflagellar transport 122 homolog (WD-repeat protein 10). [Source:Uniprot/SWISSPROT;Acc:Q9HBG6]**
ENSG0000 0163918	RFC4	Activator 1 37 kDa subunit (Replication factor C 37 kDa subunit) (A1 37 kDa subunit) (RF-C 37 kDa subunit) (RFC37). [Source:Uniprot/SWISSPROT;Acc:P35249]
ENSG0000 0163932	PRKCD	"Protein kinase C, delta type (EC 2.7.1.-) (nPKC-delta). [Source:Uniprot/SWISSPROT;Acc:Q05655]"
ENSG0000 0164012	**WDR65**	
ENSG0000 0164024	METAP 1	Methionine aminopeptidase 1 (EC 3.4.11.18) (MetAP 1) (MAP 1) (Peptidase M 1). [Source:Uniprot/SWISSPROT;Acc:P53582]
ENSG0000 0164070	HSPA4 L	Heat shock 70 kDa protein 4L (Osmotic stress protein 94) (Heat shock 70-related protein APG-1). [Source:Uniprot/SWISSPROT;Acc:O95757]
ENSG0000 0164080	NP_055 921.1	
ENSG0000 0164087	**WDR51 A**	**WD repeat domain 51A [Source:RefSeq_peptide;Acc:NP_056241]**
ENSG0000 0164163	ABCE1	ATP-binding cassette sub-family E member 1 (RNase L inhibitor) (Ribonuclease 4 inhibitor) (RNS4I) (2'-5' oligoadenylate-binding protein) (HuHP68). [Source:Uniprot/SWISSPROT;Acc:P61221]
ENSG0000 0164346	TIP1_H UMAN	TGF beta-inducible nuclear protein 1 (Hairy cell leukemia protein 1). [Source:Uniprot/SWISSPROT;Acc:O95478]
ENSG0000 0164347	GFM2	"Elongation factor G 2, mitochondrial precursor (mEF-G 2) (Elongation factor G2). [Source:Uniprot/SWISSPROT;Acc:Q969S9]"
ENSG0000 0164543	STK17 A	Serine/threonine-protein kinase 17A (EC 2.7.1.37) (DAP kinase-related apoptosis-inducing protein kinase 1). [Source:Uniprot/SWISSPROT;Acc:Q9UEE5]
ENSG0000 0164587	RPS14	40S ribosomal protein S14. [Source:Uniprot/SWISSPROT;Acc:P62263]
ENSG0000 0164776	PHKG1	"Phosphorylase b kinase gamma catalytic chain, skeletal muscle isoform (EC 2.7.1.38) (Phosphorylase kinase gamma subunit 1). [Source:Uniprot/SWISSPROT;Acc:Q16816]"
ENSG0000 0164867	NOS3	"Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS type III) (NOSIII) (Endothelial NOS) (eNOS) (Constitutive NOS) (cNOS). [Source:Uniprot/SWISSPROT;Acc:P29474]"
ENSG0000 0164873		
ENSG0000 0164885	CDK5	Cell division protein kinase 5 (EC 2.7.1.37) (Tau protein kinase II catalytic subunit) (TPKII catalytic subunit) (Serine/threonine-protein kinase PSSALRE). [Source:Uniprot/SWISSPROT;Acc:Q00535]
ENSG0000 0164924	YWHA Z	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1). [Source:Uniprot/SWISSPROT;Acc:P63104]
ENSG0000 0164947		
ENSG0000 0165029	ABCA1	ATP-binding cassette sub-family A member 1 (ATP-binding cassette transporter 1) (ATP-binding cassette 1) (ABC-1) (Cholesterol efflux regulatory protein). [Source:Uniprot/SWISSPROT;Acc:O95477]

ENSG0000 0165059	PRKAC G	"cAMP-dependent protein kinase, gamma-catalytic subunit (EC 2.7.1.37) (PKA C-gamma). [Source:Uniprot/SWISSPROT;Acc:P22612]"
ENSG0000 0165092	ALDH1 A1	"Retinal dehydrogenase 1 (EC 1.2.1.36) (RalDH1) (RALDH 1) (Aldehyde dehydrogenase family 1 member A1) (Aldehyde dehydrogenase, cytosolic) (ALHDII) (ALDH-E1). [Source:Uniprot/SWISSPROT;Acc:P00352]"
ENSG0000 0165115	KIF27	kinesin family member 27 [Source:RefSeq_peptide;Acc:NP_060046]
ENSG0000 0165140	FBP1	"Fructose-1,6-bisphosphatase 1 (EC 3.1.3.11) (D-fructose-1,6- bisphosphate 1-phosphohydrolase 1) (FBPase 1). [Source:Uniprot/SWISSPROT;Acc:P09467]"
ENSG0000 0165240	ATP7A	Copper-transporting ATPase 1 (EC 3.6.3.4) (Copper pump 1) (Menkes disease-associated protein). [Source:Uniprot/SWISSPROT;Acc:Q04656]
ENSG0000 0165280	VCP	Transitional endoplasmic reticulum ATPase (TER ATPase) (15S Mg(2+)- ATPase p97 subunit) (Valosin-containing protein) (VCP). [Source:Uniprot/SWISSPROT;Acc:P55072]
ENSG0000 0165304	MELK	Maternal embryonic leucine zipper kinase (EC 2.7.1.37) (hMELK) (Protein kinase PK38) (hPK38). [Source:Uniprot/SWISSPROT;Acc:Q14680]
ENSG0000 0165324		
ENSG0000 0165338	HECTD 2	HECT domain containing 2 isoform a [Source:RefSeq_peptide;Acc:NP_877497]
ENSG0000 0165349	SLC7A3	Cationic amino acid transporter 3 (CAT-3) (Solute carrier family 7 member 3) (Cationic amino acid transporter y+). [Source:Uniprot/SWISSPROT;Acc:Q8WY07]
ENSG0000 0165392	WRN	Werner syndrome ATP-dependent helicase (EC 3.6.1.-). [Source:Uniprot/SWISSPROT;Acc:Q14191]
ENSG0000 0165496	RPL10L	60S ribosomal protein L10-like. [Source:Uniprot/SWISSPROT;Acc:Q96L21]
ENSG0000 0165527	ARF6	ADP-ribosylation factor 6. [Source:Uniprot/SWISSPROT;Acc:P62330]
ENSG0000 0165533	**TTC8**	**Tetratricopeptide repeat protein 8 (TPR repeat protein 8) (Bardet- Biedl syndrome 8 protein). [Source:Uniprot/SWISSPROT;Acc:Q8TAM2]**
ENSG0000 0165672	PRDX3	"Thioredoxin-dependent peroxide reductase, mitochondrial precursor (EC 1.11.1.15) (Peroxiredoxin 3) (Antioxidant protein 1) (AOP-1) (MER5 protein homolog) (HBC189) (PRX III). [Source:Uniprot/SWISSPROT;Acc:P30048]"
ENSG0000 0165732	DDX21	Nucleolar RNA helicase 2 (EC 3.6.1.-) (Nucleolar RNA helicase II) (Nucleolar RNA helicase Gu) (RH II/Gu) (Gu-alpha) (DEAD box protein 21). [Source:Uniprot/SWISSPROT;Acc:Q9NR30]
ENSG0000 0165733	BMS1L	Ribosome biogenesis protein BMS1 homolog. [Source:Uniprot/SWISSPROT;Acc:Q14692]
ENSG0000 0165752	STK32C	serine/threonine kinase 32C [Source:RefSeq_peptide;Acc:NP_775846]
ENSG0000 0165916	PSMC3	26S protease regulatory subunit 6A (TAT-binding protein 1) (TBP-1) (Proteasome subunit P50). [Source:Uniprot/SWISSPROT;Acc:P17980]
ENSG0000 0165923	**AGBL2**	**ATP/GTP binding protein-like 2 [Source:RefSeq_peptide;Acc:NP_079059]**
ENSG0000 0165997	ARL5B	ADP-ribosylation factor-like protein 5B (ADP-ribosylation factor-like protein 8). [Source:Uniprot/SWISSPROT;Acc:Q96KC2]
ENSG0000 0166094		
ENSG0000 0166123	GPT2	alanine aminotransferase 2 [Source:RefSeq_peptide;Acc:NP_597700]
ENSG0000 0166128	RAB8B	Ras-related protein Rab-8B. [Source:Uniprot/SWISSPROT;Acc:Q92930]
ENSG0000 0166166	NP_689 520.1	
ENSG0000 0166200	COPS2	COP9 signalosome complex subunit 2 (Signalosome subunit 2) (SGN2) (JAB1-containing signalosome subunit 2) (Thyroid receptor interacting protein 15) (Alien homolog). [Source:Uniprot/SWISSPROT;Acc:P61201]
ENSG0000 0166226	CCT2	"T-complex protein 1, beta subunit (TCP-1-beta) (CCT-beta). [Source:Uniprot/SWISSPROT;Acc:P78371]"
ENSG0000 0166233	ARIH1	Ariadne-1 protein homolog (ARI-1) (Ubiquitin-conjugating enzyme E2- binding protein 1) (UbcH7-binding protein) (UbcM4-interacting protein) (HHARI) (H7-AP2) (MOP-6). [Source:Uniprot/SWISSPROT;Acc:Q9Y4X5]
ENSG0000 0166291		
ENSG0000 0166377	ATP9B	Probable phospholipid-transporting ATPase IIB (EC 3.6.3.1). [Source:Uniprot/SWISSPROT;Acc:O43861]
ENSG0000 0166391	MOGA T2	monoacylglycerol O-acyltransferase 2 [Source:RefSeq_peptide;Acc:NP_079374]
ENSG0000 0166394	CYB5R 2	cytochrome b5 reductase b5R.2 isoform 1 [Source:RefSeq_peptide;Acc:NP_057313]
ENSG0000 0166484	MAPK7	Mitogen-activated protein kinase 7 (EC 2.7.1.37) (Extracellular signal-regulated kinase 5) (ERK-5) (ERK4) (BMK1 kinase). [Source:Uniprot/SWISSPROT;Acc:Q13164]
ENSG0000 0166501	PRKCB 1	"Protein kinase C, beta type (EC 2.7.1.37) (PKC-beta) (PKC-B). [Source:Uniprot/SWISSPROT;Acc:P05771]"
ENSG0000 0166508	MCM7	DNA replication licensing factor MCM7 (CDC47 homolog) (P1.1-MCM3). [Source:Uniprot/SWISSPROT;Acc:P33993]
ENSG0000 0166595	FAM96 B	Protein FAM96B. [Source:Uniprot/SWISSPROT;Acc:Q9Y3D0]
ENSG0000 0166596	**WDR16**	**WD40-repeat protein upregulated in HCC isoform b [Source:RefSeq_peptide;Acc:NP_001032383]**
ENSG0000 0166598	TRA1	Endoplasmin precursor (94 kDa glucose-regulated protein) (GRP94) (gp96 homolog) (Tumor rejection antigen 1). [Source:Uniprot/SWISSPROT;Acc:P14625]
ENSG0000 0166648	O00432 _HUMA	Cytoplasmic dynein heavy chain (Fragment). [Source:Uniprot/SPTREMBL;Acc:O00432]

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ENSG0000 0166747	AP1G1	Adapter-related protein complex 1 gamma 1 subunit (Gamma-adaptin) (Adaptor protein complex AP-1 gamma-1 subunit) (Golgi adaptor HA1/AP1 adaptin gamma-1 subunit) (Clathrin assembly protein complex 1 gamma-1 large chain). [Source:Uniprot/SWISSPROT;Acc:O43747]
ENSG0000 0166794	PPIB	Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin B) (S-cyclophilin) (SCYLP) (CYP-S1). [Source:Uniprot/SWISSPROT;Acc:P23284]
ENSG0000 0166866	MYO1A	Myosin Ia (Brush border myosin I) (BBM-I) (BBMI) (Myosin I heavy chain) (MIHC). [Source:Uniprot/SWISSPROT;Acc:Q9UBC5]
ENSG0000 0166913	YWHA B	14-3-3 protein beta/alpha (Protein kinase C inhibitor protein 1) (KCIP-1) (Protein 1054). [Source:Uniprot/SWISSPROT;Acc:P31946]
ENSG0000 0166938	NP_588 616.1	
ENSG0000 0167004	PDIA3	Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide isomerase ER-60) (ERp60) (58 kDa microsomal protein) (p58) (ERp57) (58 kDa glucose regulated protein). [Source:Uniprot/SWISSPROT;Acc:P30101]
ENSG0000 0167085	PHB	Prohibitin. [Source:Uniprot/SWISSPROT;Acc:P35232]
ENSG0000 0167216	KATNA L2	
ENSG0000 0167258	CRKRS	"Cell division cycle 2-related protein kinase 7 (EC 2.7.1.37) (CDC2- related protein kinase 7) (Cdc2-related kinase, arginine/serine-rich) (CrkRS). [Source:Uniprot/SWISSPROT;Acc:Q9NYV4]"
ENSG0000 0167325	RRM1	Ribonucleoside-diphosphate reductase large subunit (EC 1.17.4.1) (Ribonucleoside-diphosphate reductase M1 subunit) (Ribonucleotide reductase large chain). [Source:Uniprot/SWISSPROT;Acc:P23921]
ENSG0000 0167393	PPP2R3 B	"Serine/threonine protein phosphatase 2A, 48 kDa regulatory subunit B (PP2A, subunit B, PR48 isoform). [Source:Uniprot/SWISSPROT;Acc:Q9Y5P8]"
ENSG0000 0167461	RAB8A	Ras-related protein Rab-8A (Oncogene c-mel). [Source:Uniprot/SWISSPROT;Acc:P61006]
ENSG0000 0167552	TBA3_ HUMA N	Tubulin alpha-3 chain (Alpha-tubulin 3) (Tubulin B-alpha-1). [Source:Uniprot/SWISSPROT;Acc:Q71U36]
ENSG0000 0167553	TUBA6	Tubulin alpha-6 chain (Alpha-tubulin 6). [Source:Uniprot/SWISSPROT;Acc:Q9BQE3]
ENSG0000 0167578	RAB4B	Ras-related protein Rab-4B. [Source:Uniprot/SWISSPROT;Acc:P61018]
ENSG0000 0167657	DAPK3	Death-associated protein kinase 3 (EC 2.7.1.37) (DAP kinase 3) (DAP- like kinase) (Dlk) (ZIP-kinase). [Source:Uniprot/SWISSPROT;Acc:O43293]
ENSG0000 0167658	EEF2	Elongation factor 2 (EF-2). [Source:Uniprot/SWISSPROT;Acc:P13639]
ENSG0000 0167701	GPT	Alanine aminotransferase (EC 2.6.1.2) (Glutamic--pyruvic transaminase) (GPT) (Glutamic--alanine transaminase). [Source:Uniprot/SWISSPROT;Acc:P24298]
ENSG0000 0167702	KIFC2	Kinesin-like protein KIFC2. [Source:Uniprot/SWISSPROT;Acc:Q96AC6]
ENSG0000 0167721	TSR1	
ENSG0000 0167792	NDUFV 1	"NADH-ubiquinone oxidoreductase 51 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-51KD) (CI-51KD) (NADH dehydrogenase flavoprotein 1). [Source:Uniprot/SWISSPROT;Acc:P49821]"
ENSG0000 0167815	PRDX2	Peroxiredoxin 2 (EC 1.11.1.15) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1) (Thiol-specific antioxidant protein) (TSA) (PRP) (Natural killer cell-enhancing factor B) (NKEF-B). [Source:Uniprot/SWISSPROT;Acc:P32119]
ENSG0000 0167964	RAB26	Ras-related protein Rab-26. [Source:Uniprot/SWISSPROT;Acc:Q9ULW5]
ENSG0000 0167972	ABCA3	ATP-binding cassette sub-family A member 3 (ATP-binding cassette transporter 3) (ATP-binding cassette 3) (ABC-C transporter). [Source:Uniprot/SWISSPROT;Acc:Q99758]
ENSG0000 0168026	**TTC21 A**	**tetratricopeptide repeat domain 21A [Source:RefSeq_peptide;Acc:NP_665698]**
ENSG0000 0168067	MAP4K 2	Mitogen-activated protein kinase kinase kinase kinase 2 (EC 2.7.1.37) (MAPK/ERK kinase kinase kinase 2) (MEK kinase kinase 2) (MEKKK 2) (Germinal center kinase) (GC kinase) (Rab8 interacting protein) (B lymphocyte serine/threonine-protein kinase). [Source:Uniprot/SWISSPROT;Acc:Q12851]
ENSG0000 0168069		
ENSG0000 0168259	DNAJC 7	DnaJ homolog subfamily C member 7 (Tetratricopeptide repeat protein 2) (TPR repeat protein 2). [Source:Uniprot/SWISSPROT;Acc:Q99615]
ENSG0000 0168280	Q57YV 5_HUM AN	
ENSG0000 0168291	PDHB	"Pyruvate dehydrogenase E1 component beta subunit, mitochondrial precursor (EC 1.2.4.1) (PDHE1-B). [Source:Uniprot/SWISSPROT;Acc:P11177]"
ENSG0000 0168356	**SCN11 A**	**Sodium channel protein type XI alpha subunit (Voltage-gated sodium channel alpha subunit Nav1.9) (Sensory neuron sodium channel 2) (Peripheral nerve sodium channel 5) (hNaN). [Source:Uniprot/SWISSPROT;Acc:Q9UI33]**
ENSG0000 0168374	ARF4	ADP-ribosylation factor 4. [Source:Uniprot/SWISSPROT;Acc:P18085]
ENSG0000 0168394	TAP1	Antigen peptide transporter 1 (APT1) (Peptide transporter TAP1) (ATP- binding cassette sub-family B member 2) (Peptide transporter PSF1) (Peptide supply factor 1) (PSF-1) (Peptide transporter involved in antigen processing 1). [Source:Uniprot/SWISSPROT;Acc:Q03518]
ENSG0000 0168396	PSMB8	Proteasome subunit beta type 8 precursor (EC 3.4.25.1) (Proteasome component C13) (Macropain subunit C13) (Multicatalytic endopeptidase complex subunit C13). [Source:Uniprot/SWISSPROT;Acc:P28062]
ENSG0000 0168439	STIP1	Stress-induced-phosphoprotein 1 (STI1) (Hsc70/Hsp90-organizing protein) (Hop) (Transformation-sensitive protein IEF SSP 3521). [Source:Uniprot/SWISSPROT;Acc:P31948]

ENSG0000 0168496	FEN1	Flap endonuclease-1 (EC 3.-.-.-) (Maturation factor 1) (MF1). [Source:Uniprot/SWISSPROT;Acc:P39748]
ENSG0000 0168547		
ENSG0000 0168625	**Q9NTI0 _HUM AN**	
ENSG0000 0168710	AHCYL 1	Putative adenosylhomocysteinase 2 (EC 3.3.1.1) (S-adenosyl-L- homocysteine hydrolase) (AdoHcyase). [Source:Uniprot/SWISSPROT;Acc:O43865]
ENSG0000 0168777		
ENSG0000 0168806	LCMT2	Leucine carboxyl methyltransferase 2 (EC 2.1.1.-) (p21WAF1/CIP1 promoter-interacting protein). [Source:Uniprot/SWISSPROT;Acc:O60294]
ENSG0000 0168810		
ENSG0000 0168827	GFM1	"Elongation factor G 1, mitochondrial precursor (mEF-G 1) (Elongation factor G1). [Source:Uniprot/SWISSPROT;Acc:Q96RP9]"
ENSG0000 0168872	DDX19 A	ATP-dependent RNA helicase DDX19A (EC 3.6.1.-) (DEAD box protein 19A) (DDX19-like protein). [Source:Uniprot/SWISSPROT;Acc:Q9NUU7]
ENSG0000 0168906	MAT2A	S-adenosylmethionine synthetase gamma form (EC 2.5.1.6) (Methionine adenosyltransferase) (AdoMet synthetase) (MAT-II). [Source:Uniprot/SWISSPROT;Acc:P31153]
ENSG0000 0168938	PPIC	Peptidyl-prolyl cis-trans isomerase C (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin C). [Source:Uniprot/SWISSPROT;Acc:P45877]
ENSG0000 0169032	MAP2K 1	Dual specificity mitogen-activated protein kinase kinase 1 (EC 2.7.1.-) (MAP kinase kinase 1) (MAPKK 1) (ERK activator kinase 1) (MAPK/ERK kinase 1) (MEK1). [Source:Uniprot/SWISSPROT;Acc:Q02750]
ENSG0000 0169067	NP_001 017992. 1	
ENSG0000 0169100	SLC25A 6	"ADP/ATP translocase 3 (Adenine nucleotide translocator 2) (ANT 3) (ADP,ATP carrier protein 3) (Solute carrier family 25 member 6) (ADP,ATP carrier protein, isoform T2). [Source:Uniprot/SWISSPROT;Acc:P12236]"
ENSG0000 0169118	CSNK1 G1	"Casein kinase I, gamma 1 isoform (EC 2.7.1.-) (CKI-gamma 1). [Source:Uniprot/SWISSPROT;Acc:Q9HCP0]"
ENSG0000 0169154	GOT1L 1	
ENSG0000 0169213	RAB3B	Ras-related protein Rab-3B. [Source:Uniprot/SWISSPROT;Acc:P20337]
ENSG0000 0169402	**NP_775 836.2**	
ENSG0000 0169432	**NP_002 968.1**	**"sodium channel, voltage-gated, type IX, alpha [Source:RefSeq_peptide;Acc:NP_002968]"**
ENSG0000 0169596		
ENSG0000 0169606	NP_001 017421. 1	actin-like protein [Source:RefSeq_peptide;Acc:NP_001017421]
ENSG0000 0169653	RPL9	60S ribosomal protein L9. [Source:Uniprot/SWISSPROT;Acc:P32969]
ENSG0000 0169717	ACTRT 2	Actin-related protein M2 (Actin-related protein T2) (ARP-T2). [Source:Uniprot/SWISSPROT;Acc:Q8TDY3]
ENSG0000 0169718	DUS1L	PP3111 protein [Source:RefSeq_peptide;Acc:NP_071439]
ENSG0000 0169764	UGP2	UTP--glucose-1-phosphate uridylyltransferase 2 (EC 2.7.7.9) (UDP- glucose pyrophosphorylase 2) (UDPGP 2) (UGPase 2). [Source:Uniprot/SWISSPROT;Acc:Q16851]
ENSG0000 0169967	MAP3K 2	Mitogen-activated protein kinase kinase kinase 2 (EC 2.7.1.37) (MAPK/ERK kinase kinase 2) (MEK kinase 2) (MEKK 2). [Source:Uniprot/SWISSPROT;Acc:Q9Y2U5]
ENSG0000 0170004	CHD3	Chromodomain helicase-DNA-binding protein 3 (EC 3.6.1.-) (ATP- dependent helicase CHD3) (CHD-3) (Mi-2 autoantigen 240 kDa protein) (Mi2-alpha). [Source:Uniprot/SWISSPROT;Acc:Q12873]
ENSG0000 0170027	YWHA G	14-3-3 protein gamma (Protein kinase C inhibitor protein 1) (KCIP-1). [Source:Uniprot/SWISSPROT;Acc:P61981]
ENSG0000 0170035	UBE2E 3	Ubiquitin-conjugating enzyme E2 E3 (EC 6.3.2.19) (Ubiquitin-protein ligase E3) (Ubiquitin carrier protein E3) (Ubiquitin-conjugating enzyme E2-23 kDa) (UbcH9) (UbcM2). [Source:Uniprot/SWISSPROT;Acc:Q969T4]
ENSG0000 0170142	UBE2E 1	Ubiquitin-conjugating enzyme E2 E1 (EC 6.3.2.19) (Ubiquitin-protein ligase E1) (Ubiquitin carrier protein E1) (UbcH6). [Source:Uniprot/SWISSPROT;Acc:P51965]
ENSG0000 0170145	SNF1L K2	Serine/threonine-protein kinase SNF1-like kinase 2 (EC 2.7.1.37) (Qin- induced kinase). [Source:Uniprot/SWISSPROT;Acc:Q9H0K1]
ENSG0000 0170226		
ENSG0000 0170312	CDC2	Cell division control protein 2 homolog (EC 2.7.1.37) (p34 protein kinase) (Cyclin-dependent kinase 1) (CDK1). [Source:Uniprot/SWISSPROT;Acc:P06493]
ENSG0000 0170315	UBB	Ubiquitin. [Source:Uniprot/SWISSPROT;Acc:P62988]
ENSG0000 0170390	DCAM KL2	Serine/threonine-protein kinase DCAMKL2 (EC 2.7.1.37) (Doublecortin- like and CAM kinase-like 2). [Source:Uniprot/SWISSPROT;Acc:Q8N568]
ENSG0000 0170448	NP_694 540.2	"nuclear transcription factor, X-box binding-like 1 [Source:RefSeq_peptide;Acc:NP_694540]"
ENSG0000 0170515	PA2G4	Proliferation-associated protein 2G4 (Cell cycle protein p38-2G4 homolog) (hG4-1). [Source:Uniprot/SWISSPROT;Acc:Q9UQ80]
ENSG0000	PFKFB3	"6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (6PF-2-K/Fru- 2,6-P2ASE brain/placenta-type isozyme) (iPFK-2)

0170525		[Includes: 6- phosphofructo-2-kinase (EC 2.7.1.105); Fructose-2,6-bisphosphatase (EC 3.1.3.46)]. [Source:Uniprot/SWISSPROT;Acc:Q16875]"
ENSG0000 0170606	HSPA4	Heat shock 70 kDa protein 4 (Heat shock 70-related protein APG-2) (HSP70RY). [Source:Uniprot/SWISSPROT;Acc:P34932]
ENSG0000 0170703	**NP_775 894.1**	
ENSG0000 0170759	KIF5B	Kinesin heavy chain (Ubiquitous kinesin heavy chain) (UKHC). [Source:Uniprot/SWISSPROT;Acc:P33176]
ENSG0000 0170889	RPS9	40S ribosomal protein S9. [Source:Uniprot/SWISSPROT;Acc:P46781]
ENSG0000 0170950	PGK2	"Phosphoglycerate kinase, testis specific (EC 2.7.2.3). [Source:Uniprot/SWISSPROT;Acc:P07205]"
ENSG0000 0171132	PRKCE	"Protein kinase C, epsilon type (EC 2.7.1.-) (nPKC-epsilon). [Source:Uniprot/SWISSPROT;Acc:Q02156]"
ENSG0000 0171316	CHD7	Chromodomain-helicase-DNA-binding protein 7 (EC 3.6.1.-) (ATP- dependent helicase CHD7) (CHD-7) (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q9P2D1]
ENSG0000 0171408	**PDE7B**	**"cAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17). [Source:Uniprot/SWISSPROT;Acc:Q9NP56]"**
ENSG0000 0171497	PPID	40 kDa peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin-40) (CYP-40) (Cyclophilin-related protein). [Source:Uniprot/SWISSPROT;Acc:Q08752]
ENSG0000 0171503	ETFDH	"Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial precursor (EC 1.5.5.1) (ETF-QO) (ETF-ubiquinone oxidoreductase) (ETF dehydrogenase) (Electron-transferring- flavoprotein dehydrogenase). [Source:Uniprot/SWISSPROT;Acc:Q16134]"
ENSG0000 0171595	**DNAI2**	**"Dynein intermediate chain 2, axonemal (Axonemal dynein intermediate chain 2). [Source:Uniprot/SWISSPROT;Acc:Q9GZS0]"**
ENSG0000 0171597		
ENSG0000 0171763	SPATA 5L1	spermatogenesis associated 5-like 1 [Source:RefSeq_peptide;Acc:NP_076968]
ENSG0000 0171960	PPIH	Peptidyl-prolyl cis-trans isomerase H (EC 5.2.1.8) (PPIase H) (Rotamase H) (U-snRNP-associated cyclophilin SnuCyp-20) (USA-CYP) (Small nuclear ribonucleoprotein particle-specific cyclophilin H) (CypH). [Source:Uniprot/SWISSPROT;Acc:O43447]
ENSG0000 0172009	THOP1	Thimet oligopeptidase (EC 3.4.24.15) (Endopeptidase 24.15) (MP78). [Source:Uniprot/SWISSPROT;Acc:P52888]
ENSG0000 0172053	QARS	Glutaminyl-tRNA synthetase (EC 6.1.1.18) (Glutamine--tRNA ligase) (GlnRS). [Source:Uniprot/SWISSPROT;Acc:P47897]
ENSG0000 0172081	MOBK L2A	Mps one binder kinase activator-like 2A (Mob1 homolog 2A) (MOB-LAK) (Protein Mob3A). [Source:Uniprot/SWISSPROT;Acc:Q96BX8]
ENSG0000 0172269	DPAGT 1	UDP-N-acetylglucosamine--dolichyl-phosphate N- acetylglucosaminephosphotransferase (EC 2.7.8.15) (GPT) (G1PT) (N- acetylglucosamine-1-phosphate transferase) (GlcNAc-1-P transferase). [Source:Uniprot/SWISSPROT;Acc:Q9H3H5]
ENSG0000 0172340	SUCLG 2	"Succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial precursor (EC 6.2.1.4) (Succinyl-CoA synthetase, betaG chain) (SCS-betaG) (GTP- specific succinyl-CoA synthetase beta subunit). [Source:Uniprot/SWISSPROT;Acc:Q96I99]"
ENSG0000 0172350	ABCG4	ATP-binding cassette sub-family G member 4. [Source:Uniprot/SWISSPROT;Acc:Q9H172]
ENSG0000 0172432	**GTPBP 2**	**GTP binding protein 2 [Source:RefSeq_peptide;Acc:NP_061969]**
ENSG0000 0172493	AFF1	AF4/FMR2 family member 1 (AF-4 protein) (Proto-oncogene AF4) (FEL protein). [Source:Uniprot/SWISSPROT;Acc:P51825]
ENSG0000 0172531	PPP1CA	Serine/threonine protein phosphatase PP1-alpha catalytic subunit (EC 3.1.3.16) (PP-1A). [Source:Uniprot/SWISSPROT;Acc:P62136]
ENSG0000 0172572	**PDE3A**	**"cGMP-inhibited 3',5'-cyclic phosphodiesterase A (EC 3.1.4.17) (Cyclic GMP-inhibited phosphodiesterase A) (CGI-PDE A). [Source:Uniprot/SWISSPROT;Acc:Q14432]"**
ENSG0000 0172669		
ENSG0000 0172704		
ENSG0000 0172780	RAB43	RAB43 protein [Source:RefSeq_peptide;Acc:NP_940892]
ENSG0000 0172794	RAB37	Ras-related protein Rab-37. [Source:Uniprot/SWISSPROT;Acc:Q96AX2]
ENSG0000 0172878	NP_954 697.1	methionine aminopeptidase 1D [Source:RefSeq_peptide;Acc:NP_954697]
ENSG0000 0172900		
ENSG0000 0172939	OXSR1	Serine/threonine-protein kinase OSR1 (EC 2.7.1.37) (Oxidative stress- responsive 1 protein). [Source:Uniprot/SWISSPROT;Acc:O95747]
ENSG0000 0172977	HTATIP	Histone acetyltransferase HTATIP (EC 2.3.1.48) (60 kDa Tat interactive protein) (Tip60) (HIV-1 Tat interactive protein) (cPLA(2) interacting protein). [Source:Uniprot/SWISSPROT;Acc:Q92993]
ENSG0000 0172981		
ENSG0000 0173020	ADRBK 1	Beta-adrenergic receptor kinase 1 (EC 2.7.1.126) (Beta-ARK-1) (G- protein coupled receptor kinase 2). [Source:Uniprot/SWISSPROT;Acc:P25098]
ENSG0000 0173085	COQ2	"para-hydroxybenzoate-polyprenyltransferase, mitochondrial [Source:RefSeq_peptide;Acc:NP_056512]"
ENSG0000 0173110	HSPA6	Heat shock 70 kDa protein 6 (Heat shock 70 kDa protein B'). [Source:Uniprot/SWISSPROT;Acc:P17066]
ENSG0000 0173137	ADCK5	aarF domain containing kinase 5 [Source:RefSeq_peptide;Acc:NP_777582]

ENSG0000 0173213		
ENSG0000 0173344		
ENSG0000 0173394		
ENSG0000 0173540	GMPPB	GDP-mannose pyrophosphorylase B isoform 1 [Source:RefSeq_peptide;Acc:NP_037466]
ENSG0000 0173542	MOBK L1A	Mps one binder kinase activator-like 1A (Mob1 homolog 1A) (Mob1A) (Mob1B) (Protein Mob4A). [Source:Uniprot/SWISSPROT;Acc:Q7L9L4]
ENSG0000 0173571		
ENSG0000 0173575	CHD2	Chromodomain-helicase-DNA-binding protein 2 (EC 3.6.1.-) (ATP- dependent helicase CHD2) (CHD-2). [Source:Uniprot/SWISSPROT;Acc:O14647]
ENSG0000 0173576		
ENSG0000 0173580		
ENSG0000 0173692	PSMD1	26S proteasome non-ATPase regulatory subunit 1 (26S proteasome regulatory subunit RPN2) (26S proteasome regulatory subunit S1) (26S proteasome subunit p112). [Source:Uniprot/SWISSPROT;Acc:Q99460]
ENSG0000 0173810		
ENSG0000 0173846	PLK3	Serine/threonine-protein kinase PLK3 (EC 2.7.1.37) (Polo-like kinase 3) (PLK-3) (Cytokine-inducible serine/threonine-protein kinase) (FGF- inducible kinase) (Proliferation-related kinase). [Source:Uniprot/SWISSPROT;Acc:Q9H4B4]
ENSG0000 0173863		
ENSG0000 0173876	NP_817 124.1	"tubulin, beta 8 [Source:RefSeq_peptide;Acc:NP_817124]"
ENSG0000 0174080	CTSF	Cathepsin F precursor (EC 3.4.22.41) (CATSF). [Source:Uniprot/SWISSPROT;Acc:Q9UBX1]
ENSG0000 0174231	PRPF8	Pre-mRNA processing splicing factor 8 (Splicing factor Prp8) (PRP8 homolog) (220 kDa U5 snRNP-specific protein) (p220). [Source:Uniprot/SWISSPROT;Acc:Q6P2Q9]
ENSG0000 0174242		
ENSG0000 0174243	DDX23	Probable ATP-dependent RNA helicase DDX23 (EC 3.6.1.-) (DEAD box protein 23) (100 kDa U5 snRNP-specific protein) (U5-100kD) (PRP28 homolog). [Source:Uniprot/SWISSPROT;Acc:Q9BUQ8]
ENSG0000 0174371	EXO1	exonuclease 1 isoform b [Source:RefSeq_peptide;Acc:NP_569082]
ENSG0000 0174408		
ENSG0000 0174437	ATP2A 2	"Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 (EC 3.6.3.8) (Calcium pump 2) (SERCA2) (SR Ca(2+)-ATPase 2) (Calcium-transporting ATPase sarcoplasmic reticulum type, slow twitch skeletal muscle isoform) (Endoplasmic reticulum class 1/2 Ca(2+) ATPase). [Source:Uniprot/SWISSPROT;Acc:P16615]"
ENSG0000 0174444	RPL4	60S ribosomal protein L4 (L1). [Source:Uniprot/SWISSPROT;Acc:P36578]
ENSG0000 0174466		
ENSG0000 0174483	**BBS1**	**Bardet-Biedl syndrome 1 protein (BBS2-like protein 2). [Source:Uniprot/SWISSPROT;Acc:Q8NFJ9]**
ENSG0000 0174655		
ENSG0000 0174672	BRSK2	BR serine/threonine-protein kinase 2 (EC 2.7.1.37) (Serine/threonine- protein kinase 29) (SAD1B). [Source:Uniprot/SWISSPROT;Acc:Q8IWQ3]
ENSG0000 0174713		
ENSG0000 0174715		
ENSG0000 0174740	PABPC 5	Polyadenylate-binding protein 5 (Poly(A)-binding protein 5) (PABP 5). [Source:Uniprot/SWISSPROT;Acc:Q96DU9]
ENSG0000 0174748	RPL15	60S ribosomal protein L15. [Source:Uniprot/SWISSPROT;Acc:P61313]
ENSG0000 0174903	RAB1B	Ras-related protein Rab-1B. [Source:Uniprot/SWISSPROT;Acc:Q9H0U4]
ENSG0000 0174953	DHX36	DEAH (Asp-Glu-Ala-His) box polypeptide 36 [Source:RefSeq_peptide;Acc:NP_065916]
ENSG0000 0175054	ATR	Serine-protein kinase ATR (EC 2.7.1.37) (Ataxia telangiectasia and Rad3-related protein) (FRAP-related protein 1). [Source:Uniprot/SWISSPROT;Acc:Q13535]
ENSG0000 0175091	Q6NXQ 4_HUM AN	UBE2S protein. [Source:Uniprot/SPTREMBL;Acc:Q6NXQ4]
ENSG0000 0175215	CTDSP 2	Carboxy-terminal domain RNA polymerase II polypeptide A small phosphatase 2 (EC 3.1.3.16) (Small CTD phosphatase 2) (SCP2) (Nuclear LIM interactor-interacting factor 2) (NLI-interacting factor 2) (Protein OS-4). [Source:Uniprot/SWISSPROT;Acc:O14595]
ENSG0000 0175582	RAB6A	Ras-related protein Rab-6A (Rab-6). [Source:Uniprot/SWISSPROT;Acc:P20340]
ENSG0000 0175634	RPS6K B2	Ribosomal protein S6 kinase 2 (EC 2.7.1.37) (S6K2) (70 kDa ribosomal protein S6 kinase 2) (p70-S6KB) (p70 ribosomal S6 kinase beta) (p70 S6Kbeta) (p70 S6 kinase beta) (S6K-beta) (p70-beta) (S6 kinase-related kinase) (SRK) (Serine/threonine-protein kinase [Source:Uniprot/SWISSPROT;Acc:Q9UBS0]

ENSG00000175764	**TTLL11**	**Tubulin tyrosine ligase-like protein 11. [Source:Uniprot/SWISSPROT;Acc:Q8NHH1]**
ENSG00000175792	RUVBL1	RuvB-like 1 (EC 3.6.1.-) (49-kDa TATA box-binding protein-interacting protein) (49 kDa TBP-interacting protein) (TIP49a) (Pontin 52) (Nuclear matrix protein 238) (NMP 238) (54 kDa erythrocyte cytosolic protein) (ECP-54) (TIP60-associated protein 54-alpha) [Source:Uniprot/SWISSPROT;Acc:Q9Y265]
ENSG00000175793	SFN	14-3-3 protein sigma (Stratifin) (Epithelial cell marker protein 1). [Source:Uniprot/SWISSPROT;Acc:P31947]
ENSG00000175991		
ENSG00000176014	TUBB6	Tubulin beta-6 chain. [Source:Uniprot/SWISSPROT;Acc:Q9BUF5]
ENSG00000176047		
ENSG00000176444	CLK2	Dual specificity protein kinase CLK2 (EC 2.7.1.37) (EC 2.7.1.112) (CDC-like kinase 2). [Source:Uniprot/SWISSPROT;Acc:P49760]
ENSG00000176658	MYO1D	Myosin Id. [Source:Uniprot/SWISSPROT;Acc:O94832]
ENSG00000176668	HSPCAL3	Heat shock protein 86 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q14568]
ENSG00000176890	TYMS	Thymidylate synthase (EC 2.1.1.45) (TS) (TSase). [Source:Uniprot/SWISSPROT;Acc:P04818]
ENSG00000176992		
ENSG00000177084	POLE	"DNA polymerase epsilon, catalytic subunit A (EC 2.7.7.7) (DNA polymerase II subunit A). [Source:Uniprot/SWISSPROT;Acc:Q07864]"
ENSG00000177117		
ENSG00000177143	CETN1	Centrin-1 (Caltractin isoform 2). [Source:Uniprot/SWISSPROT;Acc:Q12798]
ENSG00000177156	TALDO1	Transaldolase (EC 2.2.1.2). [Source:Uniprot/SWISSPROT;Acc:P37837]
ENSG00000177189	RPS6KA3	Ribosomal protein S6 kinase alpha 3 (EC 2.7.1.37) (S6K-alpha 3) (90 kDa ribosomal protein S6 kinase 3) (p90-RSK 3) (Ribosomal S6 kinase 2) (RSK-2) (pp90RSK2) (Insulin-stimulated protein kinase 1) (ISPK-1). [Source:Uniprot/SWISSPROT;Acc:P51812]
ENSG00000177239	MAN1B1	"Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosidase (EC 3.2.1.113) (ER alpha-1,2-mannosidase) (Mannosidase alpha class 1B member 1) (Man9GlcNAc2-specific processing alpha-mannosidase). [Source:Uniprot/SWISSPROT;Acc:Q9UKM7]"
ENSG00000177302	TOP3A	DNA topoisomerase III alpha (EC 5.99.1.2). [Source:Uniprot/SWISSPROT;Acc:Q13472]
ENSG00000177453	NP_699192.1	
ENSG00000177479	ARIH2	Ariadne-2 protein homolog (ARI-2) (Triad1 protein). [Source:Uniprot/SWISSPROT;Acc:O95376]
ENSG00000177585		
ENSG00000177648		
ENSG00000177664	**DNAH12**	**Dynein heavy chain (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q92864]**
ENSG00000177889	UBE2N	Ubiquitin-conjugating enzyme E2 N (EC 6.3.2.19) (Ubiquitin-protein ligase N) (Ubiquitin carrier protein N) (Ubc13) (Bendless-like ubiquitin-conjugating enzyme). [Source:Uniprot/SWISSPROT;Acc:P61088]
ENSG00000177929		
ENSG00000178035	IMPDH2	Inosine-5'-monophosphate dehydrogenase 2 (EC 1.1.1.205) (IMP dehydrogenase 2) (IMPDH-II) (IMPD 2). [Source:Uniprot/SWISSPROT;Acc:P12268]
ENSG00000178093	TSSK6	serine/threonine protein kinase SSTK [Source:RefSeq_peptide;Acc:NP_114426]
ENSG00000178105	DDX10	Probable ATP-dependent RNA helicase DDX10 (EC 3.6.1.-) (DEAD box protein 10). [Source:Uniprot/SWISSPROT;Acc:Q13206]
ENSG00000178127	NDUFV2	"NADH-ubiquinone oxidoreductase 24 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3). [Source:Uniprot/SWISSPROT;Acc:P19404]"
ENSG00000178214	RANP1	TC4 protein (RAN). [Source:Uniprot/SPTREMBL;Acc:Q96QB7]
ENSG00000178363	CALML3	Calmodulin-like protein 3 (Calmodulin-related protein NB-1) (CaM-like protein) (CLP). [Source:Uniprot/SWISSPROT;Acc:P27482]
ENSG00000178462	TUBAL3	"tubulin, alpha-like 3 [Source:RefSeq_peptide;Acc:NP_079079]"
ENSG00000178655		
ENSG00000178802	MPI	Mannose-6-phosphate isomerase (EC 5.3.1.8) (Phosphomannose isomerase) (PMI) (Phosphohexomutase). [Source:Uniprot/SWISSPROT;Acc:P34949]
ENSG00000178834	CDC14C	CDC14C protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8NCT2]
ENSG00000178952	TUFM	"Elongation factor Tu, mitochondrial precursor (EF-Tu) (P43). [Source:Uniprot/SWISSPROT;Acc:P49411]"
ENSG00000178957		
ENSG00000	AURKB	Serine/threonine-protein kinase 12 (EC 2.7.1.37) (Aurora- and Ipl1- like midbody-associated protein 1) (AIM-1)

0178999		(Aurora/IPL1-related kinase 2) (Aurora-related kinase 2) (STK-1) (Aurora-B). [Source:Uniprot/SWISSPROT;Acc:Q96GD4]
ENSG0000 0179115	FARSL A	Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20) (Phenylalanine--tRNA ligase alpha chain) (PheRS) (CML33). [Source:Uniprot/SWISSPROT;Acc:Q9Y285]
ENSG0000 0179218	CALR	Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERp60) (grp60). [Source:Uniprot/SWISSPROT;Acc:P27797]
ENSG0000 0179331	RAB39	Ras-related protein Rab-39A (Rab-39). [Source:Uniprot/SWISSPROT;Acc:Q14964]
ENSG0000 0179335	CLK3	Dual specificity protein kinase CLK3 (EC 2.7.1.37) (EC 2.7.1.112) (CDC-like kinase 3). [Source:Uniprot/SWISSPROT;Acc:P49761]
ENSG0000 0179558		
ENSG0000 0179674	ARL14	ADP-ribosylation factor 7 [Source:RefSeq_peptide;Acc:NP_079323]
ENSG0000 0179843	Q53S08 _HUMA N	
ENSG0000 0179869	ABCA1 3	"ATP binding cassette, sub-family A (ABC1), member 13 [Source:RefSeq_peptide;Acc:NP_689914]"
ENSG0000 0180138	CSNK1 A1L	"Casein kinase I, alpha-like isoform (EC 2.7.1.-) (CKI-alpha-like) (CK1). [Source:Uniprot/SWISSPROT;Acc:Q8N752]"
ENSG0000 0180153		
ENSG0000 0180370	PAK2	Serine/threonine-protein kinase PAK 2 (EC 2.7.1.37) (p21-activated kinase 2) (PAK-2) (PAK65) (Gamma-PAK) (S6/H4 kinase). [Source:Uniprot/SWISSPROT;Acc:Q13177]
ENSG0000 0180501		
ENSG0000 0180574	Q2VIR3 _HUMA N	EIF-2gA protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q6KF84]
ENSG0000 0180815	NP_001 001671. 1	mitogen-activated protein kinase kinase kinase 15 [Source:RefSeq_peptide;Acc:NP_001001671]
ENSG0000 0180817	PPA1	Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho- hydrolase) (PPase). [Source:Uniprot/SWISSPROT;Acc:Q15181]
ENSG0000 0180874		
ENSG0000 0181085	MAPK1 5	mitogen-activated protein kinase 15 [Source:RefSeq_peptide;Acc:NP_620590]
ENSG0000 0181192	DHTKD 1	dehydrogenase E1 and transketolase domain containing protein 1 [Source:RefSeq_peptide;Acc:NP_061176]
ENSG0000 0181222	POLR2 A	DNA-directed RNA polymerase II largest subunit (EC 2.7.7.6) (RPB1). [Source:Uniprot/SWISSPROT;Acc:P24928]
ENSG0000 0181267		
ENSG0000 0181669		
ENSG0000 0181732		
ENSG0000 0181786	NP_848 620.1	
ENSG0000 0181789	COPG	Coatomer gamma subunit (Gamma-coat protein) (Gamma-COP). [Source:Uniprot/SWISSPROT;Acc:Q9Y678]
ENSG0000 0182054	IDH2	"Isocitrate dehydrogenase [NADP], mitochondrial precursor (EC 1.1.1.42) (Oxalosuccinate decarboxylase) (IDH) (NADP(+)-specific ICDH) (IDP) (ICD-M). [Source:Uniprot/SWISSPROT;Acc:P48735]"
ENSG0000 0182179	UBE1L	Ubiquitin-activating enzyme E1 homolog (D8). [Source:Uniprot/SWISSPROT;Acc:P41226]
ENSG0000 0182245		
ENSG0000 0182263	FIGN	fidgetin [Source:RefSeq_peptide;Acc:NP_060556]
ENSG0000 0182281		
ENSG0000 0182316		
ENSG0000 0182364	NM_19 9283.4	
ENSG0000 0182481	KPNA2	Importin alpha-2 subunit (Karyopherin alpha-2 subunit) (SRP1-alpha) (RAG cohort protein 1). [Source:Uniprot/SWISSPROT;Acc:P52292]
ENSG0000 0182490	TSSK2	Testis-specific serine/threonine-protein kinase 2 (EC 2.7.1.37) (TSSK- 2) (Testis-specific kinase 2) (TSK-2) (Serine/threonine-protein kinase 22B) (DiGeorge syndrome protein G). [Source:Uniprot/SWISSPROT;Acc:Q96PF2]
ENSG0000 0182584	NP_001 019846. 1	
ENSG0000 0182803		
ENSG0000 0182819		

ENSG0000 0182820		
ENSG0000 0183010	SIRT7	NAD-dependent deacetylase sirtuin-7 (EC 3.5.1.-) (SIR2-like protein 7). [Source:Uniprot/SWISSPROT;Acc:Q9NRC8]
ENSG0000 0183020	AP2A2	Adapter-related protein complex 2 alpha 2 subunit (Alpha-adaptin C) (Adaptor protein complex AP-2 alpha-2 subunit) (Clathrin assembly protein complex 2 alpha-C large chain) (100 kDa coated vesicle protein C) (Plasma membrane adaptor HA2/AP2 adaptin alpha [Source:Uniprot/SWISSPROT;Acc:O94973]
ENSG0000 0183125		
ENSG0000 0183199		
ENSG0000 0183207	RUVBL 2	RuvB-like 2 (EC 3.6.1.-) (48-kDa TATA box-binding protein-interacting protein) (48-kDa TBP-interacting protein) (TIP49b) (Repressing pontin 52) (Reptin 52) (51 kDa erythrocyte cytosolic protein) (ECP-51) (TIP60-associated protein 54-beta) (TAP54-beta). [Source:Uniprot/SWISSPROT;Acc:Q9Y230]
ENSG0000 0183227	Q96RI3 _HUMA N	Short heat shock protein 60 Hsp60s2. [Source:Uniprot/SPTREMBL;Acc:Q96RI3]
ENSG0000 0183229		
ENSG0000 0183258	DDX41	Probable ATP-dependent RNA helicase DDX41 (EC 3.6.1.-) (DEAD box protein 41) (DEAD box protein abstrakt homolog). [Source:Uniprot/SWISSPROT;Acc:Q9UJV9]
ENSG0000 0183298		
ENSG0000 0183299		
ENSG0000 0183300	Q14786 _HUMA N	Myosin (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q14786]
ENSG0000 0183486	MX2	Interferon-induced GTP-binding protein Mx2 (Interferon-regulated resistance GTP-binding protein MxB) (p78-related protein). [Source:Uniprot/SWISSPROT;Acc:P20592]
ENSG0000 0183495	NP_056 224.2	E1A binding protein p400 [Source:RefSeq_peptide;Acc:NP_056224]
ENSG0000 0183506	NP_954 977.2	
ENSG0000 0183524		
ENSG0000 0183533		
ENSG0000 0183585		
ENSG0000 0183690	**EFHC2**	**EF-hand domain (C-terminal) containing 2 [Source:RefSeq_peptide;Acc:NP_079460]**
ENSG0000 0183711		
ENSG0000 0183765	CHEK2	Serine/threonine-protein kinase Chk2 (EC 2.7.1.37) (Cds1). [Source:Uniprot/SWISSPROT;Acc:O96017]
ENSG0000 0183829		
ENSG0000 0183873	**SCN5A**	**"Sodium channel protein type V alpha subunit (Voltage-gated sodium channel alpha subunit Nav1.5) (Sodium channel protein, cardiac muscle alpha-subunit) (HH1). [Source:Uniprot/SWISSPROT;Acc:Q14524]"**
ENSG0000 0183914	DNHD3	protein similar to dynein [Source:RefSeq_peptide;Acc:NP_065928]
ENSG0000 0183920		
ENSG0000 0183943	PRKX	Serine/threonine-protein kinase PRKX (EC 2.7.1.37) (Protein kinase PKX1). [Source:Uniprot/SWISSPROT;Acc:P51817]
ENSG0000 0183982		
ENSG0000 0184009	ACTG1	"Actin, cytoplasmic 2 (Gamma-actin). [Source:Uniprot/SWISSPROT;Acc:P63261]"
ENSG0000 0184056	VPS33B	Vacuolar protein sorting 33B (hVPS33B). [Source:Uniprot/SWISSPROT;Acc:Q9H267]
ENSG0000 0184073	Q6ZN94 _HUMA N	
ENSG0000 0184078		
ENSG0000 0184086		
ENSG0000 0184254	ALDH1 A3	Aldehyde dehydrogenase 1A3 (EC 1.2.1.5) (Aldehyde dehydrogenase 6) (Retinaldehyde dehydrogenase 3) (RALDH-3). [Source:Uniprot/SWISSPROT;Acc:P47895]
ENSG0000 0184343	STK23	Serine/threonine-protein kinase 23 (EC 2.7.1.37) (Muscle-specific serine kinase 1) (MSSK-1). [Source:Uniprot/SWISSPROT;Acc:Q9UPE1]
ENSG0000 0184378	ARPM1 _HUMA N	Actin-related protein M1. [Source:Uniprot/SWISSPROT;Acc:Q9BYD9]
ENSG0000 0184428	TOP1M T	"DNA topoisomerase I, mitochondrial precursor (EC 5.99.1.2) (TOP1mt). [Source:Uniprot/SWISSPROT;Acc:Q969P6]"

ENSG0000 0184432	COPB2	Coatomer beta' subunit (Beta'-coat protein) (Beta'-COP) (p102). [Source:Uniprot/SWISSPROT;Acc:P35606]
ENSG0000 0184468		
ENSG0000 0184470	TXNRD 2	"Thioredoxin reductase 2, mitochondrial precursor (EC 1.8.1.9) (TR3) (TR-beta) (Selenoprotein Z) (SelZ). [Source:Uniprot/SWISSPROT;Acc:Q9NNW7]"
ENSG0000 0184475		
ENSG0000 0184572		
ENSG0000 0184588	**PDE4B**	**"cAMP-specific 3',5'-cyclic phosphodiesterase 4B (EC 3.1.4.17) (DPDE4) (PDE32). [Source:Uniprot/SWISSPROT;Acc:Q07343]"**
ENSG0000 0184591		
ENSG0000 0184627		
ENSG0000 0184732	Q2VIQ3 _HUMA N	KIF4B (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q2VIQ3]
ENSG0000 0184735	NM_18 2699.2	"DEAD (Asp-Glu-Ala-Asp) box polypeptide 53 (DDX53), mRNA [Source:RefSeq_dna;Acc:NM_182699]"
ENSG0000 0184758		
ENSG0000 0184843		
ENSG0000 0184847		
ENSG0000 0184885		
ENSG0000 0185003		
ENSG0000 0185009	AP3M1	Adapter-related protein complex 3 mu 1 subunit (Mu-adaptin 3A) (AP-3 adapter complex mu3A subunit). [Source:Uniprot/SWISSPROT;Acc:Q9Y2T2]
ENSG0000 0185023	RAB6C	Ras-related protein Rab-6C (Rab6-like protein WTH3). [Source:Uniprot/SWISSPROT;Acc:Q9H0N0]
ENSG0000 0185051		
ENSG0000 0185078	RPL9	60S ribosomal protein L9. [Source:Uniprot/SWISSPROT;Acc:P32969]
ENSG0000 0185163	DDX51	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51 [Source:RefSeq_peptide;Acc:NP_778236]
ENSG0000 0185211		
ENSG0000 0185233		
ENSG0000 0185236	RAB11 B	Ras-related protein Rab-11B (GTP-binding protein YPT3). [Source:Uniprot/SWISSPROT;Acc:Q15907]
ENSG0000 0185238	HRMT1 L3	Protein arginine N-methyltransferase 3 (EC 2.1.1.-) (Heterogeneous nuclear ribonucleoprotein methyltransferase-like protein 3). [Source:Uniprot/SWISSPROT;Acc:O60678]
ENSG0000 0185250	PPIL6	peptidylprolyl isomerase (cyclophilin)-like 6 [Source:RefSeq_peptide;Acc:NP_775943]
ENSG0000 0185313	**SCN10 A**	**Sodium channel protein type X alpha subunit (Voltage-gated sodium channel alpha subunit Nav1.8) (Peripheral nerve sodium channel 3) (hPN3). [Source:Uniprot/SWISSPROT;Acc:Q9Y5Y9]**
ENSG0000 0185324	CDK10	Cell division protein kinase 10 (EC 2.7.1.37) (Serine/threonine- protein kinase PISSLRE). [Source:Uniprot/SWISSPROT;Acc:Q15131]
ENSG0000 0185336		
ENSG0000 0185344	ATP6V 0A2	Vacuolar proton translocating ATPase 116 kDa subunit a isoform 2 (V- ATPase 116-kDa isoform a2) (TJ6). [Source:Uniprot/SWISSPROT;Acc:Q9Y487]
ENSG0000 0185360		
ENSG0000 0185386	MAPK1 1	Mitogen-activated protein kinase 11 (EC 2.7.1.37) (Mitogen-activated protein kinase p38 beta) (MAP kinase p38 beta) (p38b) (p38-2) (Stress- activated protein kinase 2). [Source:Uniprot/SWISSPROT;Acc:Q15759]
ENSG0000 0185410		
ENSG0000 0185418	TARSL 2	threonyl-tRNA synthetase-like 2 [Source:RefSeq_peptide;Acc:NP_689547]
ENSG0000 0185439		
ENSG0000 0185467		
ENSG0000 0185485		
ENSG0000 0185514		
ENSG0000 0185624	P4HB	Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) (Prolyl 4- hydroxylase beta subunit) (Cellular thyroid hormone binding protein) (p55). [Source:Uniprot/SWISSPROT;Acc:P07237]
ENSG0000	Q5VTE	Eukaryotic translation elongation factor 1 alpha 1 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q5JR01]

0185637	0_HUMAN	
ENSG00000185675		
ENSG00000185678		
ENSG00000185705		
ENSG00000185721	DRG1	Developmentally regulated GTP-binding protein 1 (DRG 1). [Source:Uniprot/SWISSPROT;Acc:Q9Y295]
ENSG00000185791		
ENSG00000185813	PCYT2	Ethanolamine-phosphate cytidylyltransferase (EC 2.7.7.14) (Phosphorylethanolamine transferase) (CTP:phosphoethanolamine cytidylyltransferase). [Source:Uniprot/SWISSPROT;Acc:Q99447]
ENSG00000185828		
ENSG00000185842	**DNAH14**	**Novel protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q5SUX3]**
ENSG00000185843		
ENSG00000185861		
ENSG00000185979		
ENSG00000186034		
ENSG00000186197	EDARADD	Ectodysplasin A receptor associated adapter protein (EDAR-associated death domain protein) (Crinkled homolog). [Source:Uniprot/SWISSPROT;Acc:Q8WWZ3]
ENSG00000186202		
ENSG00000186288	NP_001012995.1	
ENSG00000186298	PPP1CC	Serine/threonine protein phosphatase PP1-gamma catalytic subunit (EC 3.1.3.16) (PP-1G) (Protein phosphatase 1C catalytic subunit). [Source:Uniprot/SWISSPROT;Acc:P36873]
ENSG00000186331		
ENSG00000186468	RPS23	40S ribosomal protein S23. [Source:Uniprot/SWISSPROT;Acc:P62266]
ENSG00000186533		
ENSG00000186576		
ENSG00000186614		
ENSG00000186625	KATNA1	Katanin p60 ATPase-containing subunit A1 (EC 3.6.4.3) (Katanin p60 subunit A1) (p60 katanin). [Source:Uniprot/SWISSPROT;Acc:O75449]
ENSG00000186691		
ENSG00000186743		
ENSG00000186871	NP_001009954.1	
ENSG00000186961		
ENSG00000187003	ACTL7A	Actin-like protein 7A (Actin-like-7-alpha) (Actin-like 7A). [Source:Uniprot/SWISSPROT;Acc:Q9Y615]
ENSG00000187022		
ENSG00000187042	Q96RS2_HUMAN	Laminin receptor-like protein LAMRL5. [Source:Uniprot/SPTREMBL;Acc:Q96RS2]
ENSG00000187075		
ENSG00000187091	PLCD1	"1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta 1 (EC 3.1.4.11) (Phosphoinositide phospholipase C) (PLC-delta-1) (Phospholipase C-delta-1) (PLC-III). [Source:Uniprot/SWISSPROT;Acc:P51178]"
ENSG00000187097	ENTPD5	Ectonucleoside triphosphate diphosphohydrolase 5 precursor (EC 3.6.1.6) (NTPDase5) (Nucleoside diphosphatase) (CD39 antigen-like 4) (ER-UDPase). [Source:Uniprot/SWISSPROT;Acc:O75356]
ENSG00000187134	AKR1C1	"Aldo-keto reductase family 1 member C1 (EC 1.1.1.-) (20-alpha- hydroxysteroid dehydrogenase) (EC 1.1.1.149) (20-alpha-HSD) (Trans- 1,2-dihydrobenzene-1,2-diol dehydrogenase) (EC 1.3.1.20) (High- affinity hepatic bile acid-binding protein) (HBAB) (Chlordec [Source:Uniprot/SWISSPROT;Acc:Q04828]"
ENSG00000187162		
ENSG00000187165		
ENSG00000187230		

ENSG0000 0187240	**Q6ZU M6_HU MAN**	

APPENDIX B

GENES IN *BBS3* INTERVAL

Appendix B lists the set of genes ($G_{c,A[BBS3\ interval]}$, 62), including the Ensembl gene identifier (ID), gene symbol, and gene description in the *BBS3* interval. Only four genes ($G_{c[BBS3\ interval]+}$)are highly conserved in all four ciliated organisms CI, TB, TC, and CI. These four genes are listed in bold. No genes passed the *S*_ filter consisting of AT and SC.

Ensembl GeneID	Gene Symbol	Gene Description
ENSG0000 0036054	NP_0607 79.1	
ENSG0000 0044524	EPHA3	Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor ETK1) (HEK) (HEK4). [Source:Uniprot/SWISSPROT;Acc:P29320]
ENSG0000 0057019	DCBLD2	"Discoidin, CUB and LCCL domain containing protein 2 precursor (Endothelial and smooth muscle cell-derived neuropilin-like protein) (CUB, LCCL and coagulation factor V/VIII-homology domains protein 1). [Source:Uniprot/SWISSPROT;Acc:Q96PD2]"
ENSG0000 0064225	ST3GAL6	"Type 2 lactosamine alpha-2,3-sialyltransferase (EC 2.4.99.-) (CMP- NeuAc:beta-galactoside alpha-2,3-sialyltransferase VI) (ST3Gal VI) (Sialyltransferase 10). [Source:Uniprot/SWISSPROT;Acc:Q9Y274]"
ENSG0000 0064835	POU1F1	Pituitary-specific positive transcription factor 1 (Pit-1) (Growth hormone factor 1) (GHF-1). [Source:Uniprot/SWISSPROT;Acc:P28069]
ENSG0000 0066422	ZBTB11	Zinc finger and BTB domain-containing protein 11. [Source:Uniprot/SWISSPROT;Acc:O95625]
ENSG0000 0080200	Q8N262_ HUMAN	
ENSG0000 0080224	EPHA6	
ENSG0000 0080819	CPOX	"Coproporphyrinogen III oxidase, mitochondrial precursor (EC 1.3.3.3) (Coproporphyrinogenase) (Coprogen oxidase) (COX). [Source:Uniprot/SWISSPROT;Acc:P36551]"
ENSG0000 0080822	CLDND1	Protein C3orf4 (Membrane protein GENX-3745). [Source:Uniprot/SWISSPROT;Acc:Q9NY35]
ENSG0000 0081148	IMPG2	interphotoreceptor matrix proteoglycan 2 [Source:RefSeq_peptide;Acc:NP_057331]
ENSG0000 0081154	**PCNP_H UMAN**	**PEST-containing nuclear protein (PCNP). [Source:Uniprot/SWISSPROT;Acc:Q8WW12]**
ENSG0000 0083937	CHMP2B	Charged multivesicular body protein 2b (Chromatin modifying protein 2b) (CHMP2b) (CHMP2.5) (Vacuolar protein sorting 2-2) (Vps2-2) (hVps2- 2). [Source:Uniprot/SWISSPROT;Acc:Q9UQN3]
ENSG0000 0113966	**ARL6**	**ADP-ribosylation factor-like protein 6. [Source:Uniprot/SWISSPROT;Acc:Q9H0F7]**
ENSG0000 0114021	**NIT2**	**"nitrilase family, member 2 [Source:RefSeq_peptide;Acc:NP_064587]"**
ENSG0000 0114354	TFG	Protein TFG (TRK-fused gene protein). [Source:Uniprot/SWISSPROT;Acc:Q92734]
ENSG0000 0114391	RPL24	60S ribosomal protein L24 (Ribosomal protein L30). [Source:Uniprot/SWISSPROT;Acc:P83731]
ENSG0000 0138468	SENP7	Sentrin-specific protease 7 (EC 3.4.22.-) (Sentrin/SUMO-specific protease SENP7) (SUMO-1-specific protease 2). [Source:Uniprot/SWISSPROT;Acc:Q9BQF6]
ENSG0000 0144802	NFKBIZ	"nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta isoform a [Source:RefSeq_peptide;Acc:NP_113607]"
ENSG0000 0144805		
ENSG0000 0144808		
ENSG0000 0144810	COL8A1	Smooth muscle cell-expressed and macrophage conditioned medium-induced protein 64 (Smag-64). [Source:Uniprot/SWISSPROT;Acc:Q9NRT5]
ENSG0000 0144815	FAM55C	

ENSG00000144820	GPR128	Probable G-protein coupled receptor 128 precursor. [Source:Uniprot/SWISSPROT;Acc:Q96K78]
ENSG00000154165	GPR15	G-protein coupled receptor 15 (BOB). [Source:Uniprot/SWISSPROT;Acc:P49685]
ENSG00000154174	TOMM70A	Mitochondrial precursor proteins import receptor (Translocase of outer membrane TOM70). [Source:Uniprot/SWISSPROT;Acc:O94826]
ENSG00000154175	ABI3BP	Target of Nesh-SH3 precursor (Tarsh) (Nesh binding protein) (NeshBP) (ABI gene family member 3 binding protein). [Source:Uniprot/SWISSPROT;Acc:Q7Z7G0]
ENSG00000163320	NP_003654.3	CGG triplet repeat binding protein 1 [Source:RefSeq_peptide;Acc:NP_001008391]
ENSG00000168386	NP_055705.1	downregulated in ovarian cancer 1 isoform 1 [Source:RefSeq_peptide;Acc:NP_878913]
ENSG00000169379	ARL13B	ADP-ribosylation factor-like 2-like 1 isoform 2 [Source:RefSeq_peptide;Acc:NP_659433]
ENSG00000170854	MINA	MYC induced nuclear antigen isoform 2 [Source:RefSeq_peptide;Acc:NP_116167]
ENSG00000174166	Q9BTX9_HUMAN	
ENSG00000174173	RG9MTD1	RNA (guanine-9-) methyltransferase domain containing 1 [Source:RefSeq_peptide;Acc:NP_060289]
ENSG00000174314		
ENSG00000175105	ZNF654	zinc finger protein 654 [Source:RefSeq_peptide;Acc:NP_060763]
ENSG00000175841		
ENSG00000178660		
ENSG00000178694	NSUN3	"NOL1/NOP2/Sun domain family, member 3 [Source:RefSeq_peptide;Acc:NP_071355]"
ENSG00000178700	DHFRL1	Dihydrofolate reductase-like protein 1. [Source:Uniprot/SWISSPROT;Acc:Q86XF0]
ENSG00000178750	STX19	
ENSG00000179021	NP_776185.1	
ENSG00000179097	HTR1F	5-hydroxytryptamine 1F receptor (5-HT-1F) (Serotonin receptor 1F). [Source:Uniprot/SWISSPROT;Acc:P30939]
ENSG00000181458	TMEM45A	Transmembrane protein 45a (Dermal papilla derived protein 7) (DNA polymerase-transactivated protein 4). [Source:Uniprot/SWISSPROT;Acc:Q9NWC5]
ENSG00000181828	OR5K2	Olfactory receptor 5K2 (Olfactory receptor OR3-9). [Source:Uniprot/SWISSPROT;Acc:Q8NHB8]
ENSG00000181845		
ENSG00000182504	LRRIQ2	leucine-rich repeats and IQ motif containing 2 [Source:RefSeq_peptide;Acc:NP_078824]
ENSG00000182874		
ENSG00000183185	GABRR3	GABA-C receptor rho3 subunit (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q9UIV9]
ENSG00000184220	NP_115735.1	
ENSG00000184500	PROS1	Vitamin K-dependent protein S precursor. [Source:Uniprot/SWISSPROT;Acc:P07225]
ENSG00000185141	Q6UXN9_HUMAN	WD40 protein. [Source:Uniprot/SPTREMBL;Acc:Q6UXN9]
ENSG00000185408	NM_001004736.1	"olfactory receptor, family 5, subfamily K, member 1 (OR5K1), mRNA [Source:RefSeq_dna;Acc:NM_001004736]"
ENSG00000187093		
ENSG00000187557		
ENSG00000188106		
ENSG00000188767		
ENSG00000188974	Q6UWM0_HUMAN	EPA6. [Source:Uniprot/SPTREMBL;Acc:Q6UWM0]
ENSG00000189002		
ENSG00000189040		
ENSG00000189055		

ENSG0000 0189290	**NM_0070 13.3**	**"WW domain containing E3 ubiquitin protein ligase 1 (WWP1), mRNA [Source:RefSeq_dna;Acc:NM_007013]"**
ENSG0000 0189293		

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