Comparative analysis of human and bovine protein kinases reveals unique relationship and functional diversity

Nuzhat N. Kabir¹ and Julhash U. Kazi¹ ²*

¹Laboratory of Computational Biochemistry, KN Biomedical Research Institute, Bagura Road, Barisal, Bangladesh.
²Quality Control Section, Opsonin Pharma Limited, Bagura Road, Barisal, Bangladesh.

Abstract

Reversible protein phosphorylation by protein kinases and phosphatases is a common event in various cellular processes. The eukaryotic protein kinase superfamily, which is one of the largest superfamilies of eukaryotic proteins, plays several roles in cell signaling and diseases. We identified 482 eukaryotic protein kinases and 39 atypical protein kinases in the bovine genome, by searching publicly accessible genetic-sequence databases. Bovines have 512 putative protein kinases, each orthologous to a human kinase. Whereas orthologous kinase pairs are, on an average, 90.6% identical, orthologous kinase catalytic domain pairs are, on an average, 95.9% identical at the amino acid level. This bioinformatic study of bovine protein kinases provides a suitable framework for further characterization of their functional and structural properties.

Key words: ePK, kinome, aPK, bovine.

Received: September 25, 2010; Accepted: June 1, 2011.

The protein kinase family is one of the largest families of proteins. Protein kinases play important roles in many intracellular or intercellular signaling pathways, resulting in cell proliferation, gene expression, metabolism, motility, membrane transport, apoptosis and differentiation. Furthermore, they modulate the activity of their substrate proteins by phosphorylating serine, threonine or tyrosine residues that mediate the activation, inhibition, translocation or degradation of substrate proteins (Brognard and Hunter, 2011).

Protein kinases are subdivided into two distinct superfamilies, referred to as eukaryotic protein kinases (ePKs) and atypical protein kinases (aPKs) (Hanks and Hunter, 1995). ePKs contain a conserved catalytic domain of approximately 250 amino acids. This domain is divided into 12 subdomains with highly conserved individual amino acids and motifs (Hanks et al., 1988). Within this domain, three motifs, ‘VAIK’, ‘HRD’ and ‘DFG’, are critical for the catalytic function, even though any residue from this region is fully conserved in all family members (Manning et al., 2002b). Conservation of these typical motifs is thought to be due to selection pressure for conserving important functions, such as the interaction with ATP, and the transfer of a phosphate group to the substrate. aPKs are functionally known to have kinase activity which lack significant sequence similarity to the ePK domain.

The sequencing of several vertebrate genomes has been completed. Initial estimates of the number of protein kinases in the human genome place this at around 1000 (Hunter, 1987), with later studies identifying 518 putative protein kinases (Manning et al., 2002b). The mouse and rat genomes contain 540 and 555 protein kinases, respectively, with 509 human orthologs (Caenepeel et al., 2004; Kazi et al., 2008), thereby implying possible functional conservation across species. In the present study, and by using sensitive bioinformatics approaches we identified the near complete set of bovine protein kinases. These were further classified into groups, families and subfamilies, based on the Hanks et al. (1988) and Manning et al. (2002b) classification scheme. This classification reveals many kinases that are conserved between bovine and human, thus reflecting functional constraints of these protein kinases in the core of signaling pathway. This study provides a suitable framework for further characterization of the functional and structural properties of these protein kinases.

A search was made of bovine proteome sequences available in GenBank (Benson et al., 2010) and Ensembl (Hubbard et al., 2009) for bovine protein kinases, using various tools. A preliminary search for protein kinases was performed using PSI-BLAST (Altschul et al., 1997), against the bovine proteome with an e-value threshold of 0.0001, and an h-value of 0.1 for five iterations. Previously published human (Manning et al., 2002b), mouse (Caenepeel et al., 2004) and rat (Kazi et al., 2008) eukaryotic protein kinases and kinase catalytic domains, as well as...
eukaryotic protein kinase catalytic domains from a variety of organisms available at the kinase.com database were used as query sequences. A further search for protein kinases was performed using HMMER (Eddy, 1998). A Hidden Markov profile was created and validated by means of known eukaryotic protein-kinase catalytic domains. A further search was made for atypical protein kinases, using human, mouse and rat atypical protein kinases by PSI-BLAST or HMMER. Hits identified by using the different methods were combined, and duplicate records removed. Where splice variants were encountered, the variant showing either the closest proximity to the human ortholog, or the longest protein encoding variant, was recorded. All protein kinases were then evaluated for the presence of a conserved eukaryotic protein kinase domain (Hanks et al., 1988; Manning et al., 2002b). Catalytic domains were defined using RPS-BLAST in the BLAST package (Altschul et al., 1997) against the Pfam database (Finn et al., 2010), and sequence alignments carried out with AliX implemented in the Vector-NTI package (Lu and Moriyama, 2004). Alignments were then manually edited, and all the kinases manually evaluated. Finally, 482 eukaryotic protein kinases and 39 atypical protein kinases were identified (Table S1). The primary names of the protein kinases were derived from their respective homologs in human (Manning et al., 2002b), mouse (Caenepeel et al., 2004) and rat (Kazi et al., 2008) protein kinases. On deriving a second name and synonyms from the Entrez Gene records (Maglott et al., 2005), the full protein names were retrieved thence. Representative records in Entrez Gene, corresponding to each bovine sequence, were identified, whereupon related information was included. Based upon the human protein kinases classification scheme (Manning et al., 2002b), these protein kinases were further classified into 10 groups, 129 families and 81 subfamilies (Table 1 and Table S1).

Previous studies have shown that almost all human protein-kinase orthologs are present in mouse and rat genomes (Caenepeel et al., 2004; Kazi et al., 2008). Thus, a search among bovine kinase sequences was conducted for the orthologous kinases using BLASTP (Altschul et al., 1997). The results were parsed, the symmetrically best hits being considered as orthologous kinases. The orthology relationships were further analyzed by CLUSTALW alignment (Thompson et al., 1997), followed by phylogenetic analysis. The latter was carried out by phylogenetic tree option incorporated into the CLUSTALW program. The NJ clustering algorithm was used for drawing bootstrap trees. As almost all bovine and human protein kinases exist as orthologous pairs (Figure S1), the similar functions in both organisms give to understand their evolutionary conservation. Human and bovine genomes contain 512 common protein kinase orthologs. Our search could not identify seven human protein kinase orthologs, likely due to the incomplete nature of bovine genome sequencing data (Table 2). In these seven human protein kinases, only TAF1L is absent in the chimpanzee genome. All are present in various higher eukaryotes, such as of orangutans and monkeys. Ten protein kinases were absent in the human genome, eight of which being bovine specific and the other two, PLK5 and TSSK5 found in other genomes (Table 2).

EphB1L might be a retrotransposed copy of the EphB1 gene, with 89.2% of amino acid sequence identity with the EphB1 protein.

Several proteins, such as ErbB3, SCYL1 and KSR1, have an inactive catalytic domain (Citri et al., 2003; Manning et al., 2002a). These inactive kinases, besides acting mainly as adaptor proteins, or dimerizing with active kinases, have also been shown to be involved in various cellular functions (Salerno et al., 2005; Schmidt et al., 2007; Sergina et al., 2007). Three conserved motifs, ‘VAIK’, ‘HRD’ and ‘DFG’, are important for catalytic activities. Inactive kinases lack at least one of these three conserved motifs. Fifty catalytic domains and 45 protein kinases in the human genome were predicted as cataclysmically inactive due to the lack of at least one of the three conserved residues (Manning et al., 2002b). The bovine complement of inactive kinases is equivalent to that of the human (Table S1).

All the human and bovine orthologous protein kinase pairs and orthologous catalytic domain pairs were analyzed for the percentage of identity by AlignX incorporated into Vector-NTI (Lu and Moriyama, 2004). In protein sequence alignments of orthologous kinase pairs we observed a wide variation in local sequence conservation (Figure 1A). These were, on an average, 90.6% identical (amino acid se-

| Table 1 | Protein-kinases and their distribution by groups in different genomes. |
|---------|---------------------------------------------------------------|
| Species | AGC | CAMK | CK1 | CMGC | Other | RGC | STE | TK | TKL | Atypical | Total |
| Human  | 63  | 74   | 12  | 61   | 83   | 5   | 47  | 90 | 43  | 40       | 518   |
| Bovine | 62  | 75   | 12  | 61   | 85   | 5   | 47  | 91 | 43  | 39       | 521   |
| Rat    | 60  | 112  | 11  | 61   | 84   | 7   | 46  | 91 | 43  | 40       | 555   |
| Mouse  | 60  | 97   | 11  | 60   | 84   | 7   | 47  | 90 | 43  | 39       | 538   |
| Drosophila melanogaster | 30  | 32   | 10  | 33   | 45   | 6   | 18  | 32 | 17  | 17       | 240   |
| Caenorhabditis elegans | 30  | 46   | 85  | 49   | 67   | 27  | 25  | 90 | 15  | 20       | 454   |
| Saccharomyces cerevisiae | 17  | 21   | 4   | 21   | 38   | 0   | 14  | 0  | 0   | 15       | 130   |
Comparative analysis of human and bovine protein kinases

**Table 2 - Lineage-specific protein kinases.**

| Found in | Gene Name | Introns | Paralog | Other orthologs |
|----------|-----------|---------|---------|-----------------|
| Human and bovine | 512 genes |         |         |                 |
| Human | CK1a2 | No | CK1a1 (91%) | Chimpanzee, Orangutan, Monkey |
| | TAF1L | No | TAF1 (94%) | Orangutan, Monkey |
| | PKA Cg | No | PKA C (83%) | Chimpanzee, Orangutan |
| | LTK | Yes | - | Chimpanzee, Orangutan, Rat, Mouse, Horse, Chicken |
| | ROS | Yes | - | - |
| | PSKH2 | Yes | - | Chimpanzee, Monkey, Dog, Orangutan, Rabbit, Horse |
| | PRKY | Yes | PRKX (92%) | Chimpanzee, Gorilla, Monkey |
| Bovine | AURL | Yes | AurB (61%) | - |
| | CK1b | Yes | CK1a (81%) | - |
| | EphB1L | No | EphB1 (89.2%) | - |
| | FERL | Yes | FER (82%) | - |
| | MARKL | Yes | - | - |
| | MASTL2 | Yes | - | - |
| | Par-1L | Yes | - | - |
| | PLK5 | Yes | - | Orangutan, Monkey, Mouse, Rat |
| | RYKL | Yes | - | - |
| | TSSK5 | Yes | - | Dog, Horse, Mouse, Rat |

In ‘Paralog’ parentheses show % of identity (amino acid) with respective paralog.

**Figure 1** - Conservation within orthologous kinases (A) and catalytic domains (B) is family-dependent. Triangles indicate mean identity within selected families, and bars indicate the range.
sequence), although some were as low as 47.7%, with four pairs presenting high levels of sequence identity throughout the protein (Table S1). Although most differences between orthologs are due to amino acid substitution, many proteins contained substantial insertions or deletions (indels) between orthologs, which may account for many of the functional differences between species. Several proteins contained insertions or deletions (indels), as shown by sequence alignment (Table S1). These comparisons are also informative within the conserved domains. Although orthologous catalytic domains were, on an average, 95.9% identical, some were as low as 63.8%. Sixty two pairs were identical across the full domain, whereas 48 differed by only one amino acid (Table S1), thus indicative of strong conservative pressure throughout the catalytic domain. Catalytic domain pairs showed clearly family-dependent variability (Figure 1B). For example, of the six casein kinase 1 (CK1) family domain pairs, three were identical, and the other three differed by two residues, an average difference of only 0.4%, thereby indicating that changes in almost any amino acid within the domain destroyed some function, and thus have been eliminated by evolution (Figure 2A). At the other extreme, PEK family catalytic domain pairs are 70-88% identical, thereby implying that the core functions of this family of kinases do not greatly constrain the domain sequence (Figure 2B).

Our study presents a bioinformatic overview and evolutionary insight into the kinases within the bovine genome. Comparison with the human kinome revealed the evolutionary conservation of the protein kinase function. The curated kinase dataset from the bovine genome, presented here, could serve as a framework for further investigation of this important gene family.

Acknowledgments

This work was supported by a KN Biomedical Research Grant. We are grateful to Nadid Ahnaf Kazi.

References

Altschul SF, Madden TL, Schaffer AA, Zhang J, Zhang Z, Miller W and Lipman DJ (1997) Gapped BLAST and PSI-BLAST: A new generation of protein database search programs. Nucleic Acids Res 25:3389-3402.

Benson DA, Karsch-Mizrachi I, Lipman DJ, Ostell J and Sayers EW (2010) GenBank. Nucleic Acids Res 38:D46-51.

Brognard J and Hunter T (2011) Protein kinase signaling networks in cancer. Curr Opin Genet Dev 21:4-11.

Caenepeel S, Charydczak G, Sudarsanam S, Hunter T and Manning G (2004) The mouse kinome: Discovery and comparative genomics of all mouse protein kinases. Proc Natl Acad Sci USA 101:11707-11712.

Citri A, Skaria KB and Yarden Y (2003) The deaf and the dumb: The biology of ErbB-2 and ErbB-3. Exp Cell Res 284:54-65.

Eddy SR (1998) Profile hidden Markov models. Bioinformatics 14:755-763.

Finn RD, Mistry J, Tate J, Coggill P, Heger A, Pollington JE, Gavin OL, Gunsalakanar P, Ceric G, Forslund K, et al. (2010) The Pfam protein families database. Nucleic Acids Res 38:D211-222.

Hanks SK and Hunter T (1995) Protein kinases 6. The eukaryotic protein kinase superfamly: Kinase (catalytic) domain structure and classification. FASEB J 9:576-596.

Hanks SK, Quinn AM and Hunter T (1988) The protein kinase family: Conserved features and deduced phylogeny of the catalytic domains. Science 241:42-52.

Hubbard TJ, Aken BL, Ayling S, Ballester B, Beal K, Bragin E, Brent S, Chen Y, Clapham P, Clarke L, et al. (2009) The Ensembl protein families database. Nucleic Acids Res 37:D211-222.

Hunter T (1987) A thousand and one protein kinases. Cell 50:823-829.

Kazi JU, Kabir NN and Soh JW (2008) Bioinformatic prediction and analysis of eukaryotic protein kinases in the rat genome. Gene 410:147-153.

Lu G and Moriyama EN (2004) Vector NTI, a balanced all-in-one sequence analysis suite. Brief Bioinform 5:378-388.

Maglott D, Ostell J, Pruitt KD and Tatusova T (2005) Entrez gene: Gene-centered information at NCBI. Nucleic Acids Res 33:D54-58.
Comparative analysis of human and bovine protein kinases

Manning G, Plowman GD, Hunter T and Sudarsanam S (2002a) Evolution of protein kinase signaling from yeast to man. Trends Biochem Sci 27:514-520.

Manning G, Whyte DB, Martinez R, Hunter T and Sudarsanam S (2002b) The protein kinase complement of the human genome. Science 298:1912-1934.

Salerno M, Palmieri D, Bouadis A, Halverson D and Steeg PS (2005) Nm23-H1 metastasis suppressor expression level influences the binding properties, stability, and function of the kinase suppressor of Ras I (KSR1) Erk scaffold in breast carcinoma cells. Mol Cell Biol 25:1379-1388.

Schmidt WM, Kraus C, Hoger H, Hochmeister S, Oberndorfer F, Branka M, Bingemann S, Lassmann H, Muller M, Macedo-Souza LI, et al. (2007) Mutation in the Scyl1 gene encoding amino-terminal kinase-like protein causes a recessive form of spinocerebellar neurodegeneration. EMBO Rep 8:691-697.

Sergina NV, Rausch M, Wang D, Blair J, Hann B, Shokat KM and Moasser MM (2007) Escape from HER-family tyrosine kinase inhibitor therapy by the kinase-inactive HER3. Nature 445:437-441.

Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F and Higgins DG (1997) The CLUSTAL_X windows interface: Flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Res 25:4876-4882.

Internet Resources

Kinase.com database, Genomics, evolution and function of protein kinases, http://kinase.com/kinbase/FastaFiles/.

Supplementary Material

The following online material is available for this article:

Table S1 - List of bovine kinases with sequences.
Figure S1 - Phylogenetic trees for human and bovine kinases.

This material is available as part of the online article from http://www.scielo.br/gmb.

Associate Editor: Alexandre Rodrigues Caetano

License information: This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.
Figure Legend

Figure S1.

Phylogenetic trees of bovine and human protein kinases. The phylogenetic trees were created by aligning the catalytic domain sequences of human and bovine protein kinases using the NJ method. Each empty node has a bootstrap value of 100. H, Human; B, Bovine.
Other
RGC
| Line # | Name   | Symbol | Group | Family | Subfamily | GeneID   |
|-------|--------|--------|-------|--------|-----------|----------|
| 1     | AKT1   | AKT1   | AGC   | AKT    |           | 280991   |
| 2     | AKT2   | AKT2   | AGC   | AKT    |           | 534923   |
| 3     | AKT3   | AKT3   | AGC   | AKT    |           | 100137872|
| 4     | DMPK1  | AGC    | DMPK  | GEK    |           | 518121   |
| 5     | DMPK2  | CDC42BPG | AGC   | DMPK  | GEK      | 538392   |
| 6     | MRCKa  | CDC42BPA | AGC   | DMPK  | GEK      | 785911   |
| 7     | MRCKb  | AGC    | DMPK  | GEK    |           | 282041   |
| 8     | ROCK1  | AGC    | DMPK  | ROCK   |           | 512489   |
| 9     | ROCK2  | AGC    | DMPK  | ROCK   |           | 281801   |
| 10    | CRIK   | AGC    | DMPK  |        |           | 282682   |
| 11    | BARK1  | ADRBK1 | AGC   | GRK    | BARK      | 534230   |
| 12    | BARK2  | ADRBK2 | AGC   | GRK    | BARK      | 534923   |
| 13    | GPRK4  | GRK4   | AGC   | GRK    | GRK       | 281801   |
| 14    | GPRK5  | GRK5   | AGC   | GRK    | GRK       | 281801   |
| 15    | GPRK6  | AGC    | GRK   | GRK    |           | 281801   |
| 16    | GPRK7  | GRK7   | AGC   | GRK    | GRK       | 281801   |
| 17    | RHOK   | GRK1   | AGC   | GRK    | GRK       | 281801   |
| 18    | MAST1  | MAST1  | AGC   | MAST   |           | 539825   |
| 19    | MAST2  | AGC    | MAST  |        |           | 534923   |
| 20    | MAST3  | MAST3  | AGC   | MAST   |           | 534923   |
| 21    | MAST4  | AGC    | MAST  |        |           | 534923   |
| 22    | MASTL  | MASTL  | AGC   | MASTL  |           | 534923   |
| 23    | MASTL2 | AGC    | MASTL |        |           | 534923   |
| 24    | LATS1  | LATS1  | AGC   | NDR    |           | 535935   |
| 25    | LATS2  | LATS2  | AGC   | NDR    |           | 508208   |
| 26    | NDR1   | STK38  | AGC   | NDR    |           | 536377   |
| 27    | NDR2   | STK38L | AGC   | NDR    |           | 514787   |
| 28    | PKACa  | PRKACA | AGC   | PKA    |           | 282322   |
| 29    | PKACb  | PRKACB | AGC   | PKA    |           | 282322   |
| 30    | PRKX   | PRKX   | AGC   | PKA    |           | 505773   |
| 31    | PDK1   | PDK1   | AGC   | PKB    |           | 100138102|
| 32    | PKCi   | PRKCI  | AGC   | PKC    | Atypical  | 528478   |
| 33    | PKCz   | PRKCZ  | AGC   | PKC    | Atypical  | 286877   |
| 34    | PKCa   | PRKCA  | AGC   | PKC    | Classical | 282001   |
| 35    | PKCb   | PRKCB1 | AGC   | PKC    | Classical | 282325   |
| 36    | PKCG   | PRKCG  | AGC   | PKC    | Classical | 282001   |
| 37    | PKCd   | PRKCD  | AGC   | PKC    | Nobel     | 505708   |
| 38    | PKCe   | PRKCE  | AGC   | PKC    | Nobel     | 507041   |
| 39    | PKCh   | PRKCH  | AGC   | PKC    | Nobel     | 518542   |
| 40    | PKCt   | PRKCQ  | AGC   | PKC    | Nobel     | 505901   |
| 41    | PKG1   | PRKGI  | AGC   | PKG    |           | 282004   |
| 42    | PKG2   | PRKG2  | AGC   | PKG    |           | 533330   |
| 43    | PKN1   | PKN1   | AGC   | PKN    |           | 509080   |
| 44    | PKN2   | PKN2   | AGC   | PKN    |           | 519754   |
| 45    | PKN3   | PKN3   | AGC   | PKN    |           | 505353   |
| 46    | MSK1   | RP56KAS | AGC   | RSK    | MSK       | 504408   |
| 47    | MSK2   | AGC    | RSK   | MSK    |           | 523746   |
| 48    | p70S6K | RP56KB1 | AGC   | RSK    | p70       | 404181   |
| 49    | p70S6Kb| RP56KB2 | AGC   | RSK    | p70       | 506083   |
|   | Gene Name | Description | Acronym | Gene Symbol | Reference |
|---|-----------|-------------|---------|-------------|-----------|
| 50 | RSK1      | AGC         | RSK     | RSK         | 517953    |
| 51 | RSK2      | AGC         | RSK     | RSK         | 511190    |
| 52 | RSK3      | AGC         | RSK     | RSK         | 533908    |
| 53 | RSK4      | AGC         | RSK     | RSK         | 526227    |
| 54 | RSKL1     | AGC         | RSKL    | RSKL        | 533192    |
| 55 | RSKL2     | AGC         | RSKL    | RSKL        | 530047    |
| 56 | SgK494    | AGC         | SgK     | SgK         | 527796    |
| 57 | SGK1      | AGC         | SGK     | SGK         | 515854    |
| 58 | SGK2      | AGC         | SGK     | SGK         | 517909    |
| 59 | SGK3      | AGC         | SGK     | SGK         | 504480    |
| 60 | YANK1     | AGC         | YANK    | YANK        | 100125774 |
| 61 | YANK2     | AGC         | YANK    | YANK        | 529134    |
| 62 | YANK3     | AGC         | YANK    | YANK        | 524218    |
| 63 | A6        | TWF1        | A6      | A6          | 506683    |
| 64 | A6r       | TWF2        | A6      | A6          | 282024    |
| 65 | ADCK3     | ABC1        | ABC1-A  | ABC1        | 536925    |
| 66 | ADCK4     | ABC1        | ABC1-A  | ABC1        | 514322    |
| 67 | ADCK1     | ABC1        | ABC1-B  | ABC1        | 533372    |
| 68 | ADCK5     | ABC1        | ABC1-B  | ABC1        | 522614    |
| 69 | ADCK2     | ABC1        | ABC1-C  | ABC1        | 539345    |
| 70 | ChaK1     | Alpha       | ChaK    | ChaK        | 514642    |
| 71 | ChaK2     | Alpha       | ChaK    | ChaK        | 527597    |
| 72 | eEF2K     | Alpha       | eEF2K   | eEF2K       | 521730    |
| 73 | AlphaK1   | ALPK3       | Alpha   | Alpha       | 524375    |
| 74 | AlphaK2   | ALPK2       | Alpha   | Alpha       | 510218    |
| 75 | AlphaK3   | ALPK1       | Alpha   | Alpha       | 524375    |
| 76 | BCR       | BCR         | BCR     | BCR         | 789892    |
| 77 | BRD2      | BRD2        | BRD     | BRD         | 505358    |
| 78 | BRD3      | BRD3        | BRD     | BRD         | 525051    |
| 79 | BRD4      | BRD4        | BRD     | BRD         | 614048    |
| 80 | BRDT      | BRDT        | BRD     | BRD         | 523971    |
| 81 | FASTK     | FASTK       | FAST    | FAST         | 509781   |
| 82 | G11       | STK19       | G11     | G11         | 508320    |
| 83 | H11       | HSPB8       | H11     | H11         | 539524    |
| 84 | BCKDK     | BCKDK       | PDHK    | PDHK         | 505005   |
| 85 | PDHK1     | PDK1        | PDHK    | PDHK         | 528655   |
| 86 | PDHK2     | PDK2        | PDHK    | PDHK         | 524075   |
| 87 | PDHK3     | PDK3        | PDHK    | PDHK         | 510841   |
| 88 | PDHK4     | PDK4        | PDHK    | PDHK         | 507367   |
| 89 | ATM       | ATM         | PIKK    | ATM          | 526824   |
| 90 | ATR       | ATR         | PIKK    | ATR          | 504869   |
| 91 | DNAPK     | PRKDC       | PIKK    | DNAPK        | 512740   |
| 92 | FRAP      | MTOR        | PIKK    | FRAP         | 100139219|
| 93 | SMG1      | SMG1        | PIKK    | SMG1         | 525143   |
| 94 | Trrap     | Trrap       | PIKK    | Trrap        | 507169   |
| 95 | RIOK1     | RIO1        | RIO     | RIO1         | 516289   |
| 96 | RIOK2     | RIO2        | RIO     | RIO2         | 540772   |
| 97 | RIOK3     | RIO3        | RIO     | RIO3         | 522917   |
| 98 | Taf1      | Taf1        | Taf1    | Taf1         | 504792   |
| 99 | Tif1a     | Trm33       | Tif1    | Tif1         | 533296   |
|   | TIF1b |   | Atypical  | TIF1 |
|---|-------|---|-----------|------|
| 100 | TIF1g | TRIM24 | Atypical  | TIF1 |
| 101 | CaMK1a | CAMK1 | CAMK | CAMK1 |
| 102 | CaMK1b | PNCK | CAMK | CAMK1 |
| 103 | CaMK1d | CAMK1D | CAMK | CAMK1 |
| 104 | CaMK1g | CAMK1G | CAMK | CAMK1 |
| 105 | CaMK2a | CAMK2A | CAMK | CAMK2 |
| 106 | CaMK2b | CAMK2B | CAMK | CAMK2 |
| 107 | CaMK2d | CAMK2D | CAMK | CAMK2 |
| 108 | CaMK2g | CAMK2G | CAMK | CAMK2 |
| 109 | CaMK4 | DC10033708 | CAMK | CAMK4 |
| 110 | AMPKa1 | PRKAA1 | CAMK | CAMKL |
| 111 | AMPKa2 | PRKAA2 | CAMK | CAMKL |
| 112 | BRSK1 | BRSK1 | CAMK | BRSK |
| 113 | BRSK2 | BRSK2 | CAMK | BRSK |
| 114 | CHK1 | CHEK1 | CAMK | CHK1 |
| 115 | HUNK | HUNK | CAMK | HUNK |
| 116 | LKB1 | STK11 | CAMK | LKB |
| 117 | MARK1 | MARK1 | CAMK | MARK |
| 118 | MARK2 | MARK2 | CAMK | MARK |
| 119 | MARK3 | MARK3 | CAMK | MARK |
| 120 | MARK4 | MARK4 | CAMK | MARK |
| 121 | MARKL | LOC618482 | CAMK | MARK |
| 122 | MELK | MELK | CAMK | MELK |
| 123 | NIM1 | LOC530210 | CAMK | NIM1 |
| 124 | NuaK1 | NUAK1 | CAMK | NuaK |
| 125 | NuaK2 | NUAK2 | CAMK | NuaK |
| 126 | PASK | PASK | CAMK | PASK |
| 127 | QIK | SNF1LK2 | CAMK | QIK |
| 128 | QSK | SIK3 | CAMK | QIK |
| 129 | SIK | SIK | CAMK | QIK |
| 130 | SNRK | SNRK | CAMK | SNRK |
| 131 | SgK495 | STK40 | CAMK | SgK |
| 132 | STK33 | STK33 | CAMK | STK33 |
| 133 | VACAMKL | CAMKV | CAMK | VACAMKL |
| 134 | CASK | CASK | CAMK | CASK |
| 135 | DAPK1 | DAPK1 | CAMK | DAPK |
| 136 | DAPK2 | DAPK2 | CAMK | DAPK |
| 137 | DAPK3 | DAPK3 | CAMK | DAPK |
| 138 | DRAK1 | STK17A | CAMK | DAPK |
| 139 | DRAK2 | STK17B | CAMK | DAPK |
| 140 | DCAMKL1 | CAMK | DCAMKL |
| 141 | DCAMKL2 | DCLK2 | CAMK | DCAMKL |
| 142 | DCAMKL3 | DCLK3 | CAMK | DCAMKL |
| 143 | MAPKAPK2 | MAPKAPK2 | CAMK | MAPKAPK |
| 144 | MAPKAPK3 | MAPKAPK3 | CAMK | MAPKAPK |
| 145 | MAPKAPK5 | MAPKAPK5 | CAMK | MAPKAPK |
| 146 | MNK1 | MNK1 | CAMK | MNK |
| 147 | MNK2 | MNK2 | CAMK | MNK |
| 148 | caMLCK | MYLK3 | CAMK | MLCK |
|   | Gene 1 | Gene 2 | Domain 1 | Domain 2 | Accession |
|---|--------|--------|----------|----------|-----------|
| 150 | SgK085 | MYLK4  | CAMK     | MLCK     | 518025    |
| 151 | skMLCK | MYLK2  | CAMK     | MLCK     | 533378    |
| 152 | smMLCK | MYLK   | CAMK     | MLCK     | 338037    |
| 153 | TTN    | TTN    | CAMK     | MLCK     | 540561    |
| 154 | PHKg1  | PHKG1  | CAMK     | PHK      | 540682    |
| 155 | PHKg2  | PHKG2  | CAMK     | PHK      | 512670    |
| 156 | PIM1   | PIM1   | CAMK     | PIM      | 281402    |
| 157 | PIM2   | PIM2   | CAMK     | PIM      | 508424    |
| 158 | PIM3   | PIM    | CAMK     | PIM      | 100336651 |
| 159 | PKD1   | PKRD1  | CAMK     | PKD      | 533270    |
| 160 | PKD2   | PKRD2  | CAMK     | PKD      | 782793    |
| 161 | PKD3   | PKRD3  | CAMK     | PKD      | 538447    |
| 162 | PSKH1  | PSKH1  | CAMK     | PSK      | 509656    |
| 163 | CHK2   | CHEK2  | CAMK     | RAD53    | 518897    |
| 164 | Trb1   | TRIB1  | CAMK     | Trbl     | 521857    |
| 165 | Trb2   | TRIB2  | CAMK     | Trbl     | 352960    |
| 166 | Trb3   | TRIB3  | CAMK     | Trbl     | 538465    |
| 167 | Obscn  | OBSCN  | CAMK     | Trio     | 508247    |
| 168 | SPEG   | SPEG   | CAMK     | Trio     | 523490    |
| 169 | Trad   | KALRN  | CAMK     | Trio     | 540675    |
| 170 | Trio   | TRIO   | CAMK     | Trio     | 538292    |
| 171 | SSTK   | TSSK6  | CAMK     | TSSK     | 539707    |
| 172 | TSSK1  | TSSK1B | CAMK     | TSSK     | 529193    |
| 173 | TSSK2  | TSSK2  | CAMK     | TSSK     | 538659    |
| 174 | TSSK3  | TSSK3  | CAMK     | TSSK     | 539477    |
| 175 | TSSK4  | TSSK4  | CAMK     | TSSK     | 523023    |
| 176 | TSSK5  | LOCS23023 | CAMK     | TSSK     | 523023    |
| 177 | CK1a   | CSNK1A1| CK1      | CK1      | 282684    |
| 178 | CK1b   | CSNK1B | CK1      | CK1      | 785423    |
| 179 | CK1d   | CSNK1D | CK1      | CK1      | 523542    |
| 180 | CK1e   | CSNK1E | CK1      | CK1      | 768234    |
| 181 | CK1g1  | CSNK1G1| CK1      | CK1      | 527889    |
| 182 | CK1g2  | CSNK1G2| CK1      | CK1      | 506060    |
| 183 | CK1g3  | CK1    | CK1      | CK1      |           |
| 184 | TTBK1  | CK1    | CK1      | TTBK     | 541215    |
| 185 | TTBK2  | TTBK2  | CK1      | TTBK     | 541215    |
| 186 | VRK1   | VRK1   | CK1      | VRK      | 618880    |
| 187 | VRK2   | VRK2   | CK1      | VRK      | 523902    |
| 188 | VRK3   | VRK3   | CK1      | VRK      | 520302    |
| 189 | CDC2   | CDC2   | CMGC     | CDK      | 281061    |
| 190 | CDK2   | CDK2   | CMGC     | CDK      | 519217    |
| 191 | CDK3   | CDK3   | CMGC     | CDK      | 618631    |
| 192 | CDK10  | CDK10  | CMGC     | CDK      | 615171    |
| 193 | CDK4   | CDK4   | CMGC     | CDK      | 510618    |
| 194 | CDK6   | CDK6   | CMGC     | CDK      | 511754    |
| 195 | CDK5   | CDK5   | CMGC     | CDK      | 281066    |
| 196 | CDK7   | CDK7   | CMGC     | CDK      | 515462    |
| 197 | CDK11  | CDC2L6 | CMGC     | CDK      | 511802    |
| 198 | CDK8   | CDK8   | CMGC     | CDK      | 507149    |
| 199 | CDK9   | CDK9   | CMGC     | CDK      | 520580    |
| 200 | CHED | CDC2L5 | CMGC | CDK | CRK7 | 511147 |
|-----|-------|--------|------|-----|------|--------|
| 201 | CRK7  | CRKRS  | CMGC | CDK | CRK7 | 511513 |
| 202 | PITSLE | CDC2L1 | CMGC | CDK | PITSLE | 493708 |
| 203 | PCTAIRE1 | PCTK1 | CMGC | CDK | TAIRE | 613810 |
| 204 | PCTAIRE2 | PCTK2 | CMGC | CDK | TAIRE | 539655 |
| 205 | PCTAIRE3 | PCTK3 | CMGC | CDK | TAIRE | 534048 |
| 206 | PFTAIRE1 | CDK14 | CMGC | CDK | TAIRE | 784403 |
| 207 | PFTAIRE2 | CDK15 | CMGC | CDK | TAIRE | 616118 |
| 208 | CCRK | CCRK | CMGC | CDK | 510920 |
| 209 | CDKL1 | CDKL1 | CMGC | CDKL | 523900 |
| 210 | CDKL2 | CDKL2 | CMGC | CDKL | 533114 |
| 211 | CDKL3 | CDKL3 | CMGC | CDKL | 541279 |
| 212 | CDKL4 | CDKL4 | CMGC | CDKL | 517478 |
| 213 | CDKL5 | CDKL5 | CMGC | CDKL | 538337 |
| 214 | CLK1 | CLK1 | CMGC | CLK | 613808 |
| 215 | CLK2 | CLK2 | CMGC | CLK | 512737 |
| 216 | CLK3 | CLK3 | CMGC | CLK | 505499 |
| 217 | CLK4 | CLK4 | CMGC | CLK | 529633 |
| 218 | DYRK1A | DYRK1A | CMGC | DYRK | Dyrk1 | 532989 |
| 219 | DYRK1B | DYRK1B | CMGC | DYRK | Dyrk1 | 507571 |
| 220 | DYRK2 | DYRK2 | CMGC | DYRK | Dyrk2 | 514916 |
| 221 | DYRK3 | DYRK3 | CMGC | DYRK | Dyrk2 | 505149 |
| 222 | DYRK4 | LOC531276 | CMGC | DYRK | Dyrk2 | 531276 |
| 223 | HIPK1 | HIPK1 | CMGC | DYRK | HIPK | 512233 |
| 224 | HIPK2 | HIPK2 | CMGC | DYRK | HIPK | 510158 |
| 225 | HIPK3 | HIPK3 | CMGC | DYRK | HIPK | 538866 |
| 226 | HIPK4 | HIPK4 | CMGC | DYRK | HIPK | 520157 |
| 227 | PRP4 | PRPF4B | CMGC | DYRK | PRP4 | 512236 |
| 228 | GSK3A | GSK3A | CMGC | GSK | 536561 |
| 229 | GSK3B | GSK3B | CMGC | GSK | 790875 |
| 230 | Erk1 | MAPK3 | CMGC | MAPK | ERK | 531391 |
| 231 | Erk2 | MAPK1 | CMGC | MAPK | ERK | 327672 |
| 232 | Erk3 | MAPK6 | CMGC | MAPK | ERK | 538094 |
| 233 | Erk4 | MAPK4 | CMGC | MAPK | ERK | 529183 |
| 234 | Erk5 | MAPK7 | CMGC | MAPK | ERK | 537703 |
| 235 | Erk7 | MAPK15 | CMGC | MAPK | Erk7 | 512125 |
| 236 | JNK1 | MAPK8 | CMGC | MAPK | JNK | 539941 |
| 237 | JNK2 | MAPK9 | CMGC | MAPK | JNK | 534125 |
| 238 | JNK3 | MAPK10 | CMGC | MAPK | JNK | 537631 |
| 239 | NLK | NLK | CMGC | MAPK | nmo | 507204 |
| 240 | p38a | MAPK14 | CMGC | MAPK | p38 | 534492 |
| 241 | p38b | MAPK11 | CMGC | MAPK | p38 | 618906 |
| 242 | p38d | MAPK13 | CMGC | MAPK | p38 | 535327 |
| 243 | p38g | MAPK12 | CMGC | MAPK | p38 | 512943 |
| 244 | ICK | ICK | CMGC | RCK | 506286 |
| 245 | MAK | MAK | CMGC | RCK | 536048 |
| 246 | MOK | RAGE | CMGC | RCK | 616277 |
| 247 | MSSK1 | SRPK3 | CMGC | SRPK | 508325 |
| 248 | SRPK1 | SRPK1 | CMGC | SRPK | 512631 |
| 249 | SRPK2 | SRPK2 | CMGC | SRPK | 505945 |
|   |   |   |   |   |   |
|---|---|---|---|---|---|
| 250 | AurA | AURKA | Other | AUR | 504437 |
| 251 | AurB | AURKB | Other | AUR | 360192 |
| 252 | AurC | AURKC | Other | AUR | 618599 |
| 253 | AurL | Other | AUR |   |   |
| 254 | BUB1 | BUB1 | Other | BUB | 514777 |
| 255 | BUBR1 | BUB1B | Other | BUB | 537027 |
| 256 | PRPK | TP53RK | Other | Bud32 | 619100 |
| 257 | CaMKK1 | CAMKK1 | Other | CAMKK | Meta | 510260 |
| 258 | CaMKK2 | CAMKK2 | Other | CAMKK | Meta | 509084 |
| 259 | CDC7 | CDC7 | Other | CDC7 |   | 516094 |
| 260 | CK2a1 | CSNK2A1 | Other | CK2 |   | 282419 |
| 261 | CK2a2 | CSNK2A2 | Other | CK2 |   | 282420 |
| 262 | Haspin | GSG2 | Other | Haspin |   | 767819 |
| 263 | IKKa | CHUK | Other | IKK |   | 281073 |
| 264 | IKKb | IKBKb | Other | IKK |   | 281854 |
| 265 | IKKe | IKBKE | Other | IKK |   | 533216 |
| 266 | TBK1 | TBK1 | Other | IKK |   | 533141 |
| 267 | IRE1 | IRE1 | Other | IRE |   |   |
| 268 | IRE2 | IRE2 | Other | IRE |   |   |
| 269 | MOS | MOS | Other | MOS |   | 444869 |
| 270 | AAK1 | AAK1 | Other | NAK |   | 532546 |
| 271 | BIKE | BIKE | Other | NAK |   | 505766 |
| 272 | GAK | GAK | Other | NAK |   | 511296 |
| 273 | MPSK1 | STK16 | Other | NAK |   | 521237 |
| 274 | NEK1 | Other | NEK |   | | |
| 275 | NEK10 | NEK10 | Other | NEK |   | 522335 |
| 276 | NEK11 | NEK11 | Other | NEK |   | 614924 |
| 277 | NEK2 | NEK2 | Other | NEK |   | 523998 |
| 278 | NEK3 | NEK3 | Other | NEK |   | 505876 |
| 279 | NEK4 | NEK4 | Other | NEK |   | 511455 |
| 280 | NEK5 | NEK5 | Other | NEK |   | 100138147 |
| 281 | NEK6 | NEK6 | Other | NEK |   | 515816 |
| 282 | NEK7 | NEK7 | Other | NEK |   | 781355 |
| 283 | NEK8 | NEK8 | Other | NEK |   | 532332 |
| 284 | NEK9 | NEK9 | Other | NEK |   | 534652 |
| 285 | SBK | LOC614815 | Other | NKF1 |   | 614815 |
| 286 | SgK069 | SBK2 | Other | NKF1 |   | 615123 |
| 287 | SgK110 | LOC789661 | Other | NKF1 |   | 789661 |
| 288 | PINK1 | PINK1 | Other | NKF2 |   | 510683 |
| 289 | SgK223 | SgK223 | Other | NKF3 |   |   |
| 290 | SgK269 | SgK269 | Other | NKF3 |   |   |
| 291 | CLIK1 | STK35 | Other | NKF4 |   | 540979 |
| 292 | CLIK1L | PD1K1L | Other | NKF4 |   | 510253 |
| 293 | SgK424 | LOC785881 | Other | NKF5 |   | 785881 |
| 294 | TEX14 | TEX14 | Other | NKF5 |   | 522810 |
| 295 | NRBp1 | NRBp1 | Other | NRBp |   | 532919 |
| 296 | NRBp2 | NRBp2 | Other | NRBp |   | 504664 |
| 297 | Kis | UHMK1 | Other | Other-Unique |   | 538770 |
| 298 | RNaseL | RNASEL | Other | Other-Unique |   | 100048947 |
| 299 | SgK071 | LOC614899 | Other | Other-Unique |   | 614899 |
|   |   |   |   |   |
|---|---|---|---|---|
| 300 | SgK196 | MGC151666 | Other | Other-Unique | 514490 |
| 301 | SgK396 | STK31 | Other | Other-Unique | 781749 |
| 302 | SgK493 | PKDCC | Other | Other-Unique | 539467 |
| 303 | SgK496 | RIPK5 | Other | Other-Unique | 534684 |
| 304 | GCN2 | GCN2 | Other | PEK | GCN2 |
| 305 | PEK | EIF2AK3 | Other | PEK | PEK | 535820 |
| 306 | HRI | EIF2AK1 | Other | PEK | 507689 |
| 307 | PKR | EIF2AK2 | Other | PEK | 347700 |
| 308 | PLK1 | PLK1 | Other | PLK | 538238 |
| 309 | PLK2 | PLK2 | Other | PLK | 539449 |
| 310 | PLK3 | PLK3 | Other | PLK | 504282 |
| 311 | PLK4 | PLK4 | Other | PLK | 514405 |
| 312 | PLK5 | LOC511891 | Other | PLK | 511891 |
| 313 | SCYL1 | SCYL1 | Other | SCY1 | 515247 |
| 314 | SCYL2 | SCYL2 | Other | SCY1 | 782059 |
| 315 | SCYL3 | SCYL3 | Other | SCY1 | 506600 |
| 316 | Slob | PKK | Other | Slob | 614093 |
| 317 | TBCK | TBCK | Other | TBCK | 528650 |
| 318 | TLK1 | TLK1 | Other | TLK | 537517 |
| 319 | TLK2 | TLK2 | Other | TLK | 534705 |
| 320 | PBK | PBK | Other | TOPK | 534781 |
| 321 | TTK | TTK | Other | TTK | 524925 |
| 322 | Fused | STK36 | Other | ULK | 508408 |
| 323 | ULK1 | ULK1 | Other | ULK | 526310 |
| 324 | ULK2 | ULK2 | Other | ULK | 618601 |
| 325 | ULK3 | ULK3 | Other | ULK | 506063 |
| 326 | ULK4 | ULK4 | Other | ULK | 531267 |
| 327 | PIK3R4 | PIK3R4 | Other | VPS15 | 507414 |
| 328 | MYT1 | PKMYT1 | Other | WEE | 522613 |
| 329 | Wee1 | WEE1 | Other | WEE | 540322 |
| 330 | Wee1B | WEE2 | Other | WEE | 520049 |
| 331 | Wnk1 | WNK1 | Other | Wnk | 506433 |
| 332 | Wnk2 | WNK2 | Other | Wnk | 506520 |
| 333 | Wnk3 | WNK3 | Other | Wnk | 533409 |
| 334 | Wnk4 | WNK4 | Other | Wnk | 533409 |
| 335 | ANPa | NPR1 | RGC | RGC | 533048 |
| 336 | ANPb | NPR2 | RGC | RGC | 281357 |
| 337 | CYGD | GUCY2D | RGC | RGC | 282245 |
| 338 | CYGF | GUCY2F | RGC | RGC | 282246 |
| 339 | HSER | GUCY2C | RGC | RGC | 282244 |
| 340 | MAP3K1 | MAP3K1 | STE | STE11 | 523962 |
| 341 | MAP3K2 | MAP3K2 | STE | STE11 | 504592 |
| 342 | MAP3K3 | MAP3K3 | STE | STE11 | 508943 |
| 343 | MAP3K4 | MAP3K4 | STE | STE11 | 511779 |
| 344 | MAP3K5 | MAP3K5 | STE | STE11 | 537380 |
| 345 | MAP3K6 | MAP3K6 | STE | STE11 | 614598 |
| 346 | MAP3K7 | MAP3K15 | STE | STE11 | 529335 |
| 347 | MAP3K8 | YSK4 | STE | STE11 | 538897 |
| 348 | OSR1 | OSR1 | STE | STE20 | FRAY |
| 349 | STLK3 | STK39 | STE | STE20 | FRAY | 522103 |
|   |   |   |   |   |   |
|---|---|---|---|---|---|
| 350 | GCK | MAP4K2 | STE | STE20 | KHS | 520058 |
| 351 | HPK1 | MAP4K1 | STE | STE20 | KHS | 522002 |
| 352 | KHS1 | MAP4K5 | STE | STE20 | KHS | 781335 |
| 353 | KHS2 | MAP4K3 | STE | STE20 | KHS | 507624 |
| 354 | ZC1 | ZC1 | STE | STE20 | MSN |   |
| 355 | ZC2 | TNIK | STE | STE20 | MSN | 539627 |
| 356 | ZC3 | MINK1 | STE | STE20 | MSN | 519558 |
| 357 | ZC4 | NRK | STE | STE20 | MST | 783774 |
| 358 | MST1 | STK4 | STE | STE20 | MST | 514886 |
| 359 | MST2 | STK3 | STE | STE20 | MST | 533815 |
| 360 | MYO3A | MYO3A | STE | STE20 | NinaC | 535824 |
| 361 | MYO3B | MYO3B | STE | STE20 | NinaC | 536123 |
| 362 | PAK1 | PAK1 | STE | STE20 | PAKA | 533729 |
| 363 | PAK2 | LOC513673 | STE | STE20 | PAKA | 513673 |
| 364 | PAK3 | PAK3 | STE | STE20 | PAKA | 534526 |
| 365 | PAK4 | PAK4 | STE | STE20 | PAKB | 539742 |
| 366 | PAK5 | PAK7 | STE | STE20 | PAKB | 513432 |
| 367 | PAK6 | PAK6 | STE | STE20 | PAKB | 539224 |
| 368 | LOK | STK10 | STE | STE20 | SLK | 526376 |
| 369 | SLK | SLK | STE | STE20 | SLK | 535342 |
| 370 | STLK5 | LYK5 | STE | STE20 | STLK | 515024 |
| 371 | STLK6 | STRADB | STE | STE20 | STLK | 506029 |
| 372 | TAO1 | TAOK1 | STE | STE20 | TAO | 536532 |
| 373 | TAO2 | TAOK2 | STE | STE20 | TAO | 533897 |
| 374 | TAO3 | TAOK3 | STE | STE20 | TAO | 534620 |
| 375 | MST3 | STK24-LIKE | STE | STE20 | YSK | 532455 |
| 376 | MST4 | MST4 | STE | STE20 | YSK | 539445 |
| 377 | YSK1 | STK25 | STE | STE20 | YSK | 373543 |
| 378 | MAP2K1 | MAP2K1 | STE | STE7 |   | 533199 |
| 379 | MAP2K2 | MAP2K2 | STE | STE7 |   | 510434 |
| 380 | MAP2K3 | MAP2K3 | STE | STE7 |   | 516039 |
| 381 | MAP2K4 | MAP2K4 | STE | STE7 |   | 526469 |
| 382 | MAP2K5 | MAP2K5 | STE | STE7 |   | 100295732 |
| 383 | MAP2K6 | MAP2K6 | STE | STE7 |   | 286883 |
| 384 | MAP2K7 | MAP2K7 | STE | STE7 |   | 787278 |
| 385 | COT | MAP3K8 | STE | STE-Unique |   | 535622 |
| 386 | NIK | MAP3K14 | STE | STE-Unique |   | 508367 |
| 387 | ABL | ABL1 | TK | Abl |   | 540876 |
| 388 | ARG | ABL2 | TK | Abl |   | 511845 |
| 389 | ACK | ACK1 | TK | Ack |   | 280710 |
| 390 | TNK1 | TNK1 | TK | Ack |   | 510356 |
| 391 | ALK | ALK | TK | Alk |   | 536642 |
| 392 | AXL | AXL | TK | Axl |   | 516598 |
| 393 | MER | MERTK | TK | Axl |   | 504429 |
| 394 | TYRO3 | TYRO3 | TK | Axl |   | 788224 |
| 395 | CCK4 | PTK7 | TK | CCK4 |   | 514819 |
| 396 | CSK | CSK | TK | Csk |   | 509246 |
| 397 | CTK | MATK | TK | Csk |   | 504668 |
| 398 | DDR1 | DDR1 | TK | DDR |   | 534092 |
| 399 | DDR2 | DDR2 | TK | DDR |   | 533523 |
|   |   |   |   |   |
|---|---|---|---|---|
| 400 | EGFR | EGFR | TK | EGFR |
| 401 | ErbB2 | ERBB2 | TK | EGFR |
| 402 | ErbB3 | ERBB3 | TK | EGFR |
| 403 | ErbB4 | ERBB4 | TK | EGFR |
| 404 | EphA1 | EPHA1 | TK | Eph |
| 405 | EphA10 | EPHA10 | TK | Eph |
| 406 | EphA2 | EPHA2 | TK | Eph |
| 407 | EphA3 | EPHA3 | TK | Eph |
| 408 | EphA4 | EPHA4 | TK | Eph |
| 409 | EphA5 | EPHA5 | TK | Eph |
| 410 | EphA6 | EPHA6 | TK | Eph |
| 411 | EphA7 | EPHA7 | TK | Eph |
| 412 | EphA8 | EPHA8 | TK | Eph |
| 413 | EphB1 | EPHB1 | TK | Eph |
| 414 | EphB1L | LOC618263 | TK | Eph |
| 415 | EphB2 | EPHB2 | TK | Eph |
| 416 | EphB3 | EPHB3 | TK | Eph |
| 417 | EphB4 | EPHB4 | TK | Eph |
| 418 | EphB6 | EPHB6 | TK | Eph |
| 419 | FAK | PTK2 | TK | Fak |
| 420 | PYK2 | PTK2B | TK | Fak |
| 421 | FER | FER | TK | Fer |
| 422 | FERL | TK | TK | Fer |
| 423 | FES | FES | TK | Fer |
| 424 | FGFR1 | FGFR1 | TK | FGFR |
| 425 | FGFR2 | FGFR2 | TK | FGFR |
| 426 | FGFR3 | FGFR3 | TK | FGFR |
| 427 | FGFR4 | FGFR4 | TK | FGFR |
| 428 | IGF1R | IGF1R | TK | InsR |
| 429 | INSR | INSR | TK | InsR |
| 430 | IRR | INSR | TK | InsR |
| 431 | JAK1 | JAK1 | TK | JakA |
| 432 | JAK2 | JAK2 | TK | JakA |
| 433 | JAK3 | JAK3 | TK | JakA |
| 434 | TYK2 | TYK2 | TK | JakA |
| 435 | LMR1 | AATK | TK | Lmr |
| 436 | LMR2 | LMTK2 | TK | Lmr |
| 437 | LMR3 | LMR3 | TK | Lmr |
| 438 | MET | MET | TK | Met |
| 439 | RON | MST1R | TK | Met |
| 440 | MUSK | MUSK | TK | Musk |
| 441 | FLT3 | FLT3 | TK | PDGFR |
| 442 | FMS | FMS | TK | PDGFR |
| 443 | KIT | KIT | TK | PDGFR |
| 444 | PDGFRa | PDGFRA | TK | PDGFR |
| 445 | PDGFRb | PDGFRB | TK | PDGFR |
| 446 | RET | RET | TK | Ret |
| 447 | ROR1 | ROR1 | TK | Ror |
| 448 | ROR2 | ROR2 | TK | Ror |
| 449 | RYK | RYK | TK | Ryk |
|   | RYKL | BLK  | TK  | Ryk  | Src  | 532587 |
|---|------|------|-----|------|------|--------|
| 451 | BLK  | PTK6 | TK  | Src  | Src  | 529814 |
| 452 | FGR  | FGR  | TK  | Src  | Src  | 516133 |
| 453 | FRK  | FRK  | TK  | Src  | Src  | 509227 |
| 454 | FYN  | FYN  | TK  | Src  | Src  | 527263 |
| 455 | HCK  | HCK  | TK  | Src  | Src  | 280814 |
| 456 | LCK  | LCK  | TK  | Src  | Src  | 508890 |
| 457 | SRC  | SRC  | TK  | Src  | Src  | 535742 |
| 458 | SRM  | SRMS | TK  | Src  | Src  | 521816 |
| 459 | YES  | YES1 | TK  | Src  | Src  | 507632 |
| 460 | SYK  | SYK  | TK  | Syk  | Syk  | 515515 |
| 461 | ZAP70| ZAP70| TK  | Syk  | Syk  | 504509 |
| 462 | BMX  | BMX  | TK  | Tec  | Tec  | 531514 |
| 463 | BTK  | BTK  | TK  | Tec  | Tec  | 533459 |
| 464 | ITK  | ITK  | TK  | Tec  | Tec  | 522311 |
| 465 | TEC  | TEC  | TK  | Tec  | Tec  | 504733 |
| 466 | TXK  | TXK  | TK  | Tec  | Tec  | 504782 |
| 467 | TIE1 | TIE1 | TK  | Tie  | Tie  | 280941 |
| 468 | TIE2 | TIE2 | TK  | Tie  | Tie  | 280939 |
| 469 | SuRTK106 | STYK1 | TK  | TK-Unique | 513920 |
| 470 | TRKA | NTRK1 | TK  | Trk  | 353111 |
| 471 | TRKB | TRKB | TK  | Trk  | 539126 |
| 472 | TRKC | NTRK3 | TK  | Trk  | 353111 |
| 473 | FLT1 | FLT1 | TK  | VEGFR | 503620 |
| 474 | FLT4 | FLT4 | TK  | VEGFR | 338031 |
| 475 | KDR  | KDR  | TK  | VEGFR | 407170 |
| 476 | IRAK1| IRAK1| TKL | IRAK | 539395 |
| 477 | IRAK2| IRAK2| TKL | IRAK | 515034 |
| 478 | IRAK3| IRAK3| TKL | IRAK | 510342 |
| 479 | IRAK4| IRAK4| TKL | IRAK | 533692 |
| 480 | IRAK5| IRAK5| TKL | IRAK | 533692 |
| 481 | LIMK1| LIMK1| TKL | LISK | 535225 |
| 482 | LIMK2| LIMK2| TKL | LISK | 513539 |
| 483 | LIMK3| LIMK3| TKL | LISK | 513539 |
| 484 | TESK1| TESK1| TKL | LISK | 527643 |
| 485 | TESK2| TESK2| TKL | LISK | 539979 |
| 486 | LRRK1| LRRK1| TKL | LRRK | 513994 |
| 487 | LRRK2| LRRK2| TKL | LRRK | 535652 |
| 488 | HH498| TNNI3K| TKL | MLK  | HH498 | 535940 |
| 489 | DLK  | DLK  | TKL | MLK  | LZK  | 505369 |
| 490 | LZK  | MAP3K13| TKL | MLK  | LZK  | 505369 |
| 491 | MLK1 | LOC538340| TKL | MLK  | MLK  | 538340 |
| 492 | MLK2 | MAP3K10| TKL | MLK  | MLK  | 781037 |
| 493 | MLK3 | MAP3K11| TKL | MLK  | MLK  | 514210 |
| 494 | MLK4 | LOC616014| TKL | MLK  | MLK  | 616014 |
| 495 | ZAK  | ZAK  | TKL | MLK  | MLK  | 519251 |
| 496 | TAK1 | MAP3K7 | TKL | MLK  | TAK1 | 529146 |
| 497 | BRAF | BRAF | TKL | RAF  | 540421 |
| 498 | KSR1 | KSR1 | TKL | RAF  | 536051 |
| 499 | KSR2 | KSR2 | TKL | RAF  | 100138565 |
|   |   |   |   |   |   |
|---|---|---|---|---|---|
| 500 | KSR2 | KSR2 | TKL | RAF | 617325 |
| 501 | RAF1 | RAF1 | TKL | RAF | 521196 |
| 502 | ANKRD3 | RIPK4 | TKL | RIPK | 508668 |
| 503 | RIPK1 | RIPK1 | TKL | RIPK | 504727 |
| 504 | RIPK2 | RIPK2 | TKL | RIPK | 534407 |
| 505 | RIPK3 | RIPK3 | TKL | RIPK | 507427 |
| 506 | SgK288 | SgK288 | TKL | RIPK | |
| 507 | ALK1 | ACVRL1 | TKL | STKR | Type1 | 534536 |
| 508 | ALK2 | ACVR1 | TKL | STKR | Type1 | 338068 |
| 509 | ALK4 | ACVR1B | TKL | STKR | Type1 | 539315 |
| 510 | ALK7 | ACVR1C | TKL | STKR | Type1 | 536380 |
| 511 | BMPR1A | BMPR1A | TKL | STKR | Type1 | 404101 |
| 512 | BMPR1B | BMPR1B | TKL | STKR | Type1 | 407128 |
| 513 | TGFbR1 | TGFBR1 | TKL | STKR | Type1 | 282382 |
| 514 | ACTR2 | ACVR2A | TKL | STKR | Type2 | 281598 |
| 515 | ACTR2B | ACVR2B | TKL | STKR | Type2 | 282131 |
| 516 | BMPR2 | BMPR2 | TKL | STKR | Type2 | 407127 |
| 517 | MISR2 | TKL | STKR | Type2 | |
| 518 | TGFbR2 | TGFBR2 | TKL | STKR | Type2 | 535376 |
| 519 | ILK | ILK | TKL | TKL-Unique | ILK | 540207 |
| 520 | MLKL | MLKL | TKL | TKL-Unique | | 790225 |
| 521 | Par-1L | TKL | TKL-Unique | | | |
| Protein Acc     | RNA acc         | Synonyms         |
|----------------|-----------------|------------------|
| NP_776411.1    | NM_173986.2     |                  |
| XP_870006.1    | XM_864913.2     |                  |
| NP_001178238.1 | NM_001191309.1  |                  |
| NP_001095972.1 | NM_001102502.1  | MGC155045        |
| XP_618596.3    | XM_618596.3     |                  |
| XP_001253770.1 | XM_001253769.1  |                  |
| NP_776877.1    | NM_174452.2     |                  |
| NP_777135.1    | NM_174710.2     | GRK2             |
| NP_776925.1    | NM_174500.2     |                  |
| XP_590012.3    | XM_590012.3     |                  |
| NP_776756.1    | NM_174331.2     | GPRK5            |
| NP_776757.1    | NM_174332.3     | GPRK7            |
| NP_776598.1    | NM_174173.2     | RHOK             |
| XP_002704808.1 | XM_002704762.1  |                  |
| XP_613922.3    | XM_613922.3     |                  |
| NP_001107237.1 | NM_001113765.1  |                  |
| XP_616050.3    | XM_616050.3     |                  |
| XP_584953.3    | XM_584953.3     |                  |
| NP_001075071.1 | NM_001081602.1  |                  |
| NP_001094562.1 | NM_001101092.1  |                  |
| NP_777009.1    | NM_174584.2     |                  |
| NP_777010.1    | NM_174585.2     |                  |
| XP_582115.3    | XM_582115.3     |                  |
| NP_001788715.1 | XM_001788663.2  |                  |
| XP_606901.3    | XM_606901.3     |                  |
| NP_001071301.1 | NM_001077833.1  |                  |
| NP_776860.1    | NM_174435.1     | PKRCA            |
| NP_777012.1    | NM_174587.1     |                  |
| XP_602125.3    | XM_602125.3     |                  |
| NP_001071323.1 | NM_001077855.1  |                  |
| NP_001104590.1 | NM_001111120.1  |                  |
| NP_001070331.1 | NM_001076863.1  |                  |
| XP_582266.3    | XM_582266.3     |                  |
| NP_776861.1    | NM_174436.2     | CGKI|cGKI-beta |
| XP_612707.3    | XM_612707.3     |                  |
| NP_001073715.1 | NM_001080246.1  |                  |
| XP_883499.2    | XM_878406.2     |                  |
| XP_581630.2    | XM_581630.3     |                  |
| XP_580522.3    | XM_580522.3     | MSK1             |
| NP_001178329.1 | NM_001191400.1  |                  |
| NP_991385.1    | NM_205816.1     |                  |
| XP_582478.3    | XM_582478.3     |                  |
| Code             | Name                  | Accession1 | Accession2 | Description   |
|------------------|-----------------------|------------|------------|---------------|
| XP_596135.3      | XM_596135.3           |            |            |               |
| NP_001092407.1   | NM_001098937.1        | MGC160087  |            |               |
| NP_001077191.1   | NM_001083722.1        | MGC139400  |            |               |
| XP_604590.3      | XM_604590.3           |            |            |               |
| XP_870724.1      | XM_865631.2           |            |            |               |
| NP_001032549.1   | NM_001037472.1        | MGC128730  |            |               |
| XP_606198.2      | XM_606198.3           |            |            |               |
| NP_001095503.1   | NM_001102033.1        | MGC166421  |            |               |
| NP_001069228.1   | NM_001075760.1        | MGC139463  |            |               |
| XP_870723.1      | XM_865630.2           |            |            |               |
| NP_001098517.1   | NM_001105047.1        | MGC148827  |            |               |
| XP_607574.3      | XM_607574.3           |            |            |               |
| XP_602539.3      | XM_602539.3           |            |            |               |
| NP_001020491.1   | NM_001025320.1        | MGC137976  |            |               |
| NP_001098794.1   | NM_001105324.1        | PTK9|MGC148415  |               |
| NP_001039884.1   | NM_001046419.1        | MGC137459  |            |               |
| XP_001790539.1   | XM_001790487.1        |            |            |               |
| NP_001070363.1   | NM_001076895.1        | MGC142877  |            |               |
| NP_001094580.1   | NM_001101110.1        |            |            |               |
| XP_586554.2      | XM_586554.3           |            |            |               |
| XP_870587.2      | XM_865494.3           |            |            |               |
| XP_605991.3      | XM_605991.3           |            |            |               |
| XP_599997.2      | XM_599997.3           |            |            |               |
| XP_587341.3      | XM_587341.4           |            |            |               |
| XP_602698.4      | XM_602698.4           |            |            |               |
| XP_001256514.1   | XM_001256513.1        |            |            |               |
| NP_001039331.1   | NM_001045866.1        |            |            |               |
| NP_001070341.1   | NM_001076873.1        | MGC142472  |            |               |
| XP_002704782.1   | XM_002704736.1        |            |            |               |
| NP_001069320.1   | NM_001075852.1        | MGC151933  |            |               |
| NP_001030249.2   | NM_001035077.2        |            |            |               |
| NP_001091466.1   | NM_001097997.1        |            |            |               |
| NP_001014955.1   | NM_001014955.1        | PTK9       |            |               |
| NP_001039371.1   | NM_001045906.1        | MGC127910  |            |               |
| XP_607085.4      | XM_607085.4           |            |            |               |
| NP_001069321.1   | NM_001075853.1        |            |            |               |
| NP_001095404.1   | NM_001101934.1        | MGC166016  |            |               |
| NP_001095353.1   | NM_001101883.1        | MGC166250  |            |               |
| XP_605200.3      | XM_605200.4           |            |            |               |
| XP_581054.3      | XM_581054.4           |            |            |               |
| XP_879315.2      | XM_874222.3           |            |            |               |
| XP_002694089.1   | XM_002694043.1        |            |            |               |
| XP_603490.3      | XM_603490.4           |            |            |               |
| XP_583735.3      | XM_583735.3           |            |            |               |
| XP_594442.2      | XM_594442.3           |            |            |               |
| NP_001178220.1   | NM_001191291.1        |            |            |               |
| NP_001069304.1   | NM_001075836.1        | MGC138071  |            |               |
| XP_580963.3      | XM_580963.3           |            |            |               |
| XP_001250500.1   | XM_001250499.2        |            |            |               |
| Accession   | Description | Accession   | Description |
|-------------|-------------|-------------|-------------|
| XP_596207.3 | XM_596207.3 | -           |             |
| NP_001077188.1 | NM_001083719.1 | MGC155182 |             |
| NP_788809.1 | NM_176636.2 | -           |             |
| XP_002703630.1 | XM_002703584.1 | -           |             |
| NP_001039951.1 | NM_001046486.1 | MGC137450 |             |
| NP_001039593.1 | NM_001046128.1 | MGC129049 |             |
| NP_776569.1 | NM_174144.2 | -           |             |
| XP_585196.3 | XM_585196.3 | -           |             |
| XP_002688056.1 | XM_002688010.1 | -           |             |
| XP_612625.3 | XM_612625.3 | -           |             |
| XP_001251452.1 | XM_001251451.1 | -           |             |
| XP_580387.3 | XM_580387.3 | -           |             |
| NP_001068881.1 | NM_001075413.1 | -           |             |
| NP_001029703.1 | NM_001034531.1 | -           |             |
| NP_001094575.1 | NM_001101105.1 | -           |             |
| NP_847887.2 | NM_178317.3 | TRB-2|TRB2 |             |
| NP_001069571.1 | NM_001076103.1 | MGC142660 |             |
| NP_585000.3 | XM_585000.3 | -           |             |
| XP_873585.2 | XM_868492.2 | -           |             |
| NP_001178293.1 | NM_001191364.1 | -           |             |
| NP_001095682.1 | NM_001102212.1 | MGC154976 |             |
| XP_588888.3 | XM_588888.3 | -           |             |
| NP_001077179.1 | NM_001083710.1 | TSSK2       |             |
| XP_581847.2 | XM_581847.3 | -           |             |
| XP_870097.1 | XM_865004.2 | -           |             |
| XP_601315.3 | XM_601315.3 | -           |             |
| NP_777136.1 | NM_174711.2 | MGC133860 |             |
| NP_001091628.1 | NM_001098159.1 | -           |             |
| NP_001095550.1 | NM_001102080.1 | MGC166392 |             |
| NP_001071577.1 | NM_001078109.1 | MGC143296 |             |
| NP_001033235.1 | NM_001038146.1 | MGC134312 |             |
| NP_001094526.1 | NM_001101056.1 | -           |             |
| XP_615092.2 | XM_615092.3 | -           |             |
| NP_001033313.1 | NM_001038224.1 | MGC128186 |             |
| NP_001069319.1 | NM_001075851.1 | -           |             |
| NP_001039716.1 | NM_001046251.1 | MGC133825 |             |
| NP_776441.1 | NM_174016.2 | MGC134454 |             |
| NP_001014934.1 | NM_001014934.1 | -           |             |
| NP_001092648.1 | NM_001099178.1 | MGC160000 |             |
| NP_001033666.1 | NM_001038577.2 | MGC134436 |             |
| NP_001032683.1 | NM_001037594.1 | MGC133903 |             |
| XP_589151.3 | XM_589151.3 | -           |             |
| NP_776442.1 | NM_174017.2 | MGC140720 |             |
| NP_001069183.1 | NM_001075715.1 | MGC140417 |             |
| XP_589209.3 | XM_589209.3 | -           |             |
| XP_583707.3 | XM_583707.3 | -           |             |
| NP_001014935.2 | NM_001014935.2 | MGC139578 |             |
| Accession     | Symbol      | Gene Symbol | Function  |
|--------------|-------------|-------------|-----------|
| XP_001251167.1 | XM_001251166.1 | -           |           |
| XP_588861.2   | XM_588861.3  | -           |           |
| NP_001007812.2| NM_001007811.2| -           |           |
| NP_001094696.1| NM_001101226.1| -           |           |
| XP_588580.3   | XM_588580.3  | -           |           |
| NP_001076942.1| NM_001083473.1| MGC155091   |           |
| XP_001789714.2| XM_001789662.2| PFTK1       |           |
| XP_873177.3   | XM_868084.3  | PFTK2       |           |
| NP_001092403.1| NM_001098933.1| MGC154961| MGC166397 |
| XP_001789714.2| XM_001789662.2| PFTK1       |           |
| NP_001094586.1| NM_001110116.1| -           |           |
| NP_001096744.1| NM_001103274.1| MGC142906   |           |
| NP_001179783.1| NM_001192854.1| -           |           |
| NP_001033218.1| NM_001038129.1| MGC133738   |           |
| XP_002700425.1| XM_002700379.1| -           |           |
| NP_001095741.1| NM_001102271.1| MGC148790   |           |
| XP_874270.2   | XM_869177.2  | -           |           |
| NP_001029420.1| NM_001034248.1| MGC128892   |           |
| XP_870005.1   | XM_864912.2  | -           |           |
| XP_612233.2   | XM_612233.3  | -           |           |
| NP_001074984.1| NM_001081515.1| DYRK1A|MGC155217 |
| XP_592833.3   | XM_592833.3  | -           |           |
| NP_001093768.1| NM_001100298.1| -           |           |
| XP_609767.3   | XM_609767.3  | -           |           |
| XP_001250674.1| XM_001250673.1| -           |           |
| NP_001095392.1| NM_001101922.1| MGC152387   |           |
| XP_870428.2   | XM_865335.2  | -           |           |
| NP_598392.3   | XM_598392.3  | -           |           |
| NP_001069025.1| NM_001075557.1| MGC139658   |           |
| NP_001095662.1| NM_001102192.1| MGC159759   |           |
| NP_001094780.1| NM_001101310.1| -           |           |
| NP_001103488.1| NM_001110018.1| ERK1        |           |
| NP_786987.1   | NM_175793.2  | ERK2        |           |
| XP_605323.3   | XM_605323.3  | -           |           |
| NP_001069388.1| NM_001075920.1| MGC152151   |           |
| NP_001092550.1| NM_001099080.1| MGC148520   |           |
| NP_001039575.1| NM_001046110.1| MGC138052   |           |
| XP_869760.1   | XM_864667.2  | JNK1        |           |
| NP_001039834.1| NM_001046369.1| MGC137545   |           |
| NP_001077197.1| NM_001083728.1| -           |           |
| XP_886284.2   | XM_881191.2  | -           |           |
| NP_001095644.1| NM_001102174.1| MGC142910   |           |
| NP_001073804.1| NM_001080335.1| MGC139500   |           |
| NP_001014947.1| NM_001014947.1| -           |           |
| NP_001092423.1| NM_001098953.1| MGC160082   |           |
| NP_001092357.1| NM_001098887.1| MGC157129   |           |
| NP_001039880.2| NM_001046415.2| -           |           |
| XP_873352.1   | XM_868259.2  | -           |           |
| NP_001076859.1| NM_001083390.1| MGC143354|MSSK1     |
| XP_590178.3   | XM_590178.3  | -           |           |
| XP_590213.3   | XM_590213.3  | -           |           |
| Accession   | Description | Accession   | Description |
|-------------|-------------|-------------|-------------|
| NP_001033117.1 | NM_001038028.1 | CDC7L1 | MGC134472 |
| NP_898907.2 | NM_183084.2 | STK12 | MGC142782 |
| XP_876025.1 | XM_870932.2 | - | - |
| NP_001095481.1 | NM_001102011.1 | STK12 | MGC148432 |
| XP_617181.3 | XM_617181.3 | - | - |
| NP_001092650.1 | NM_001099180.1 | STK12 | MGC159543 |
| XP_587386.3 | XM_587386.3 | - | - |
| NP_001068858.1 | NM_001075390.1 | - | - |
| NP_001032545.1 | NM_001037468.1 | CDC7L1 | MGC128732 |
| NP_777060.2 | NM_174635.2 | - | MGC137728 |
| NP_777061.1 | NM_174636.2 | - | - |
| NP_001070012.1 | NM_001076544.1 | - | MGC137325 |
| NP_776446.1 | NM_174021.2 | - | - |
| NP_776778.1 | NM_174353.2 | - | - |
| NP_00109810.1 | NM_001046345.1 | - | MGC137373 |
| XP_612449.3 | XM_612449.3 | - | - |
| XP_590874.2 | XM_590874.3 | C-MOS | - |
| XP_611658.3 | XM_611658.3 | - | - |
| NP_001039549.1 | NM_001046084.1 | - | MGC127293 |
| NP_001039720.1 | NM_001046255.1 | - | MGC137500 |
| XP_600615.3 | XM_600615.3 | - | - |
| XP_871668.2 | XM_866575.2 | - | - |
| NP_001039735.1 | NM_001046270.1 | - | MGC137163 |
| NP_001077112.1 | NM_001083643.1 | - | MGC143098 |
| NP_001095414.1 | NM_001101944.1 | - | MGC159441 |
| XM_001788409.1 | XP_001788461.1 | - | - |
| NP_001092458.1 | NM_001098988.1 | - | MGC149008 |
| XP_001249770.1 | XM_001249769.1 | - | - |
| XP_610844.3 | XM_610844.3 | - | - |
| XP_614489.3 | XM_614489.3 | - | - |
| XP_871544.2 | XM_866451.2 | - | - |
| XP_871937.2 | XM_866844.3 | - | - |
| XP_001256345.1 | XM_001256344.1 | - | - |
| NP_001093171.1 | NM_001099701.1 | - | - |
| NP_00107240.1 | NM_001113768.1 | - | - |
| XP_587377.2 | XM_587377.3 | - | - |
| NP_001092535.1 | NM_001098165.1 | - | - |
| NP_001091634.1 | NM_001098165.1 | - | - |
| XP_871637.2 | XM_866544.2 | - | - |
| Accession   | Description   | Accession   | Description   |
|-------------|---------------|-------------|---------------|
| NP_001091496.1 | NM_001098027.1 | -           |               |
| XP_001250240.1 | XM_001250239.1 | -           |               |
| XP_002700787.1 | XM_002700741.1 | -           |               |
| NP_001019995.1 | NM_001024824.1 | -           |               |
| NP_001091555.1 | NM_001098086.1 | -           |               |
| NP_001033142.1 | NM_001038053.1 | MGC134528   |               |
| NP_835210.2     | NM_178109.2    | PKR|PRKR       |               |
| NP_001033262.1 | NM_001038173.1 | MGC133927   |               |
| XP_587229.3     | XM_587229.3    | -           |               |
| NP_001068621.1 | NM_001075153.1 | MGC142543   |               |
| NP_001076896.1 | NM_001083427.1 | PLK-4       |               |
| XP_589317.3     | XM_589317.3    | -           |               |
| NP_001095491.1 | NM_001102021.1 | MGC165975   |               |
| NP_001095999.1 | NM_001102529.1 | MGC138084   |               |
| XP_001787951.1 | XM_001787899.1 | -           |               |
| NP_001092602.1 | NM_001099132.1 | MGC139332   |               |
| XP_607080.3     | XM_607080.3    | -           |               |
| XP_617685.3     | XM_617685.3    | -           |               |
| XP_614568.3     | XM_614568.3    | -           |               |
| NP_001095648.1 | NM_001102178.1 | MGC165897   |               |
| XP_603264.3     | XM_603264.3    | -           |               |
| XP_585177.3     | XM_585177.3    | -           |               |
| XP_604678.3     | XM_604678.3    | -           |               |
| NP_001095791.1 | NM_001102321.1 | -           |               |
| NP_001039399.2 | NM_001045934.2 | -           |               |
| XP_609757.3     | XM_609757.3    | -           |               |
| NP_001093784.1 | NM_001100314.1 | -           |               |
| XP_600897.2     | XM_600897.3    | -           |               |
| NP_001094675.1 | NM_001101205.1 | -           |               |
| XP_598279.3     | XM_598279.3    | -           |               |
| XP_582882.3     | XM_582882.3    | -           |               |
| XP_582977.3     | XM_582977.3    | -           |               |
| XP_612806.5     | XM_612806.3    | -           |               |
| XP_612318.2     | XM_612318.3    | -           |               |
| NP_776551.1     | NM_174126.2    | -           |               |
| NP_776973.1     | NM_174548.2    | -           |               |
| NP_776974.1     | NM_174549.2    | -           |               |
| NP_776972.1     | NM_174547.2    | -           |               |
| XP_602275.3     | XM_602275.3    | -           |               |
| XP_580739.2     | XM_580739.3    | -           |               |
| XP_886022.2     | XM_880929.2    | -           |               |
| XP_589178.3     | XM_589178.3    | -           |               |
| NP_001137553.1 | NM_001144081.1 | ASK1        |               |
| XP_882494.1     | XM_877401.2    | -           |               |
| XP_607781.3     | XM_607781.3    | -           |               |
| XP_583510.2     | XM_583510.2    | -           |               |
| NP_001069294.1 | NM_001075826.1 | -           |               |
| Accession | Description | HGK | MGC139676 | MGC138047 | MGC128993 | ABLL | MGC134398 | MGC140486 | MGC151903 | MGC140244 | MGC159463 | ACK | MGC137695 | MGC142896 | MGC140218 |
|-----------|-------------|-----|-----------|-----------|-----------|------|-----------|-----------|-----------|-----------|-----------|------|-----------|-----------|-----------|
| XP_874795.2 | XM_869702.2 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| NP_001069293.2 | NM_001075825.2 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_001249611.1 | XM_001249610.1 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_584270.3 | XM_584270.3 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_588438.3 | XM_588438.3 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| NP_001092846.1 | NM_001099376.1 | MINK | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_001251137.1 | XM_001251136.1 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| NP_001015602.1 | NM_001015602.1 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_001250083.1 | XM_001250082.1 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_615938.3 | XM_615938.3 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_616244.3 | XM_616244.3 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| NP_001070366.1 | NM_001076898.1 | MGC139676 | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_591400.3 | XM_591400.3 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_001252146.1 | XM_001252145.1 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| NP_001069652.1 | NM_001076184.1 | MGC138047 | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_591106.3 | XM_591106.3 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_585734.1 | XM_585734.3 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_604746.3 | XM_604746.3 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_001252985.1 | XM_001252984.1 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| NP_001015603.1 | NM_001015603.1 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_582418.3 | XM_582418.3 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_616664.3 | XM_616664.3 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_872869.2 | XM_867776.2 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_614451.3 | XM_614451.3 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_610976.3 | XM_610976.3 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_587191.3 | XM_587191.3 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| NP_899666.1 | XM_183407.2 | MGC128993 | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_612526.3 | XM_612526.3 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| NP_001033160.2 | NM_001038071.2 | MGC134398 | MGC140486 | - | - | - | - | - | - | - | - | - | - | - |
| NP_001077162.1 | NM_001083693.1 | MGC151903 | - | - | - | - | - | - | - | - | - | - | - | - |
| NP_001092508.1 | NM_001099038.1 | MGC140244 | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_002700545.1 | XM_002700499.1 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| NP_001029217.1 | NM_001034045.1 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_001254724.1 | XM_001254723.3 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| NP_001092541.1 | NM_001099071.1 | MGC159463 | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_585134.3 | XM_585134.3 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_613548.2 | XM_613548.3 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_001253285.1 | XM_001253284.1 | ABLL | - | - | - | - | - | - | - | - | - | - | - | - |
| NP_776310.2 | NM_173885.2 | ACK | MGC137695 | - | - | - | - | - | - | - | - | - | - | - |
| XP_881345.1 | XM_876252.2 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_616782.3 | XM_616782.3 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_594754.3 | XM_594754.3 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_580552.3 | XM_580552.3 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_001253887.1 | XM_001253886.1 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| XP_869603.2 | XM_864510.2 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| NP_001068865.1 | NM_001075397.1 | MGC142896 | - | - | - | - | - | - | - | - | - | - | - | - |
| NP_001030183.1 | NM_001035011.1 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| NP_001069480.2 | NM_001076012.2 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| NP_001077189.1 | NM_001083720.1 | MGC140218 | - | - | - | - | - | - | - | - | - | - | - | - |
| Accession | Accession | Accession |
|-----------|-----------|-----------|
| XP_592211.3 | XM_592211.3 |   |
| NP_001096575.1 | NM_001103105.1 | MGC143211 |
| XP_002703751.1 | XM_002703705.1 |   |
| XP_604305.2 | XM_604305.3 | 525946 |
| XP_594054.3 | XM_594054.3 | - |
| XP_590380.3 | XM_590380.3 | - |
| XP_618140.3 | XM_618140.3 | - |
| NP_001076910.1 | NM_001083441.1 |   |
| XP_618422.3 | XM_618422.3 | - |
| XP_001788053.1 | XM_001788001.2 | - |
| XP_611161.3 | XM_611161.3 | - |
| XP_595537.3 | XM_595537.3 | - |
| XP_614602.3 | XM_614602.3 | - |
| XP_875687.2 | XM_870594.2 | - |
| NP_001178427.1 | NM_001191498.1 |   |
| XP_613645.2 | XM_613645.3 | - |
| XP_874493.2 | XM_869400.2 | - |
| NP_001091536.2 | NM_001098067.1 |   |
| NP_001068718.2 | NM_001075250.2 | FADK |
| NP_001095722.1 | NM_001102252.1 | MGC139227 |
| NP_001178265.1 | NM_001191336.1 |   |
| NP_001027471.1 | NM_001032300.1 | - |
| NP_001103677.1 | NM_001110207.1 | MGC151817 |
| XP_885574.2 | XM_880481.2 | FGFR |
| NP_776743.1 | NM_174318.3 | - |
| XP_602166.3 | XM_602166.3 | - |
| XP_606794.3 | XM_606794.3 | - |
| XP_590552.2 | XM_590552.3 | ir-A |
| XP_001254386.1 | XM_001254385.1 | - |
| XP_001790676.2 | XM_001790624.2 |   |
| XP_002689649.1 | XM_002689603.1 | - |
| XP_002704759.1 | XM_002704713.1 |   |
| NP_001107236.1 | NM_001113764.1 | - |
| XP_588863.3 | XM_588863.3 | - |
| XP_589779.3 | XM_589779.3 | - |
| NP_001013017.2 | NM_001012999.2 | HGFR|MGC166072|c-met |
| XP_603857.3 | XM_603857.3 | - |
| XP_591182.3 | XM_591182.3 | - |
| XP_590263.3 | XM_590263.3 | - |
| XP_612028.3 | XM_612028.3 | c-kit |
| XP_590921.3 | XM_590921.3 | - |
| NP_001069364.2 | NM_001075896.2 |   |
| XP_002703399.1 | XM_002703353.1 |   |
| XP_001789312.2 | XM_001789260.2 | - |
| NP_001098934.2 | NM_001105464.2 |   |
| XP_001249767.1 | XM_001249766.1 | - |
| Accession     | Forward          | Reverse          | Gene      |
|---------------|------------------|------------------|-----------|
| NP_001069436.1| NM_001075968.1   | MGC142356        |
| XP_608273.2   | XM_608273.2      | -                |
| NP_001092461.1| NM_001098991.1   | MGC159776        |
| XP_586141.3   | XM_586141.3      | -                |
| NP_001071440.1| NM_001077972.1   | -                |
| NP_001103664.1| NM_001110194.1   | -                |
| NP_001029506.1| NM_001034334.1   | MGC126900        |
| XP_614963.2   | XM_614963.3      | -                |
| NP_001104274.1| NM_001110804.1   | -                |
| XP_600086.3   | XM_600086.3      | -                |
| NP_001094530.1| NM_001110106.1   | -                |
| NP_001032542.1| NM_001037465.1   | MGC127145        |
| XP_870655.1   | XM_865562.2      | -                |
| NP_001179636.1| NM_001192707.1   | -                |
| NP_001029761.1| NM_001034589.1   | MGC126902        |
| NP_001098858.1| NM_001105388.1   | MGC165932        |
| XP_580898.3   | XM_580898.3      | -                |
| XP_870050.2   | XM_864957.2      | -                |
| NP_776390.1   | NM_173965.2      | TIE              |
| NP_776389.1   | NM_173964.2      | MGC139569        |
| XP_591681.3   | XM_591681.3      | SYTK1            |
| XP_613650.2   | XM_613650.3      | TRKA             |
| XP_002696558.1| XM_002696512.1   | -                |
| NP_001178061.1| NM_001191132.1   | VEGFR1           |
| NP_001178273.1| NM_001191344.1   | -                |
| NP_001103470.1| NM_001110000.1   | VEGFR2|flk-1     |
| NP_001035645.1| NM_001040555.1   | -                |
| NP_001069164.1| NM_001075696.1   | IRAK-2           |
| XP_587469.2   | XM_587469.3      | -                |
| NP_001069466.1| NM_001075998.1   | IRAK-4|MGC137816 |
| XP_002698230.1| XM_002698184.1   | -                |
| NP_001033187.1| NM_001038098.1   | MGC134164        |
| XP_606040.2   | XM_606040.3      | -                |
| XP_590674.3   | XM_590674.3      | -                |
| XP_591774.3   | XM_591774.3      | -                |
| XP_615760.3   | XM_615760.3      | -                |
| XP_001250856.1| XM_001250855.1   | MGC152244        |
| NP_001095323.1| NM_001101853.1   | MGC179376        |
| XP_002691037.1| XM_002690991.1   | -                |
| XP_001249388.1| XM_001249387.1   | -                |
| NP_001095461.1| NM_001101991.1   | MGC165851        |
| XP_873070.2   | XM_867977.2      | -                |
| XP_870499.1   | XM_865406.2      | -                |
| NP_001075064.1| NM_001081595.1   | MGC154981        |
| NP_001014964.1| NM_001014964.1   | MGC128775        |
| XP_002687048.1| XM_002687002.1   | -                |
| XP_001788801.1| XM_001788749.1   | -                |
| Accession   | Reference Accession | ID       |
|-------------|---------------------|----------|
| XP_874651.2 | XM_869558.2         |          |
| NP_001095975.1 | NM_001102505.1 | MGC165882 |
| NP_001093797.1 | NM_001100327.1 |          |
| NP_001030184.1 | NM_001035012.1 | MGC127532 |
| NP_001029782.1 | NM_001034610.1 | MGC127456 |
| NP_001095354.1 | NM_001101884.1 | MGC152488 |
| NP_001076948.1 | NM_001083479.1 | MGC139457 |
| NP_788836.2 | NM_176663.3        | ActR-IA  |
| XP_586402.3 | XM_586402.3        |          |
| XP_616508.3 | XM_616508.3        |          |
| NP_001070268.1 | NM_001076800.1 | BMPR-IA  |
| NP_001098798.1 | NM_001105328.1 | ALK6|BMP15|BMPR-IB|BMPRIB |
| NP_777046.1 | NM_174621.2        |          |
| NP_776652.1 | NM_174227.3        | ACVR2    |
| NP_776920.1 | NM_174495.2        | ActR-IIB|ActRIIB |
| XP_617592.3 | XM_617592.3        | bmprii   |
| XP_615445.2 | XM_615445.3        |          |
| NP_001029865.1 | NM_001034693.1 | MGC129022 |
| XP_001256760.1 | XM_001256759.1 |          |
| Description                                                                 |
|----------------------------------------------------------------------------|
| v-akt murine thymoma viral oncogene homolog 1                             |
| v-akt murine thymoma viral oncogene homolog 2                             |
| v-akt murine thymoma viral oncogene homolog 3                             |
| CDC42 binding protein kinase gamma                                          |
| CDC42 binding protein kinase alpha (DMPK-like)                            |
| Rho-associated, coiled-coil containing protein kinase 1                    |
| Rho-associated, coiled-coil containing protein kinase 2                    |
| adrenergic, beta, receptor kinase 1                                        |
| adrenergic, beta, receptor kinase 2                                        |
| G protein-coupled receptor kinase 4                                        |
| G protein-coupled receptor kinase 5                                        |
| G protein-coupled receptor kinase 7                                        |
| G protein-coupled receptor kinase 1                                        |
| microtubule associated serine/threonine kinase 1                          |
| microtubule associated serine/threonine kinase 3                          |
| microtubule associated serine/threonine kinase-like                       |
| LATS, large tumor suppressor, homolog 1 (Drosophila)                      |
| LATS, large tumor suppressor, homolog 2 (Drosophila)                      |
| serine/threonine kinase 38                                                |
| serine/threonine kinase 38 like                                           |
| protein kinase, cAMP-dependent, catalytic, alpha                          |
| protein kinase, cAMP-dependent, catalytic, beta                          |
| protein kinase, X-linked                                                  |
| 3-phosphoinositide dependent protein kinase-1                             |
| protein kinase C, iota                                                    |
| protein kinase C, zeta                                                    |
| protein kinase C, alpha                                                   |
| protein kinase C, beta 1                                                  |
| protein kinase C, gamma                                                   |
| protein kinase C, delta                                                   |
| protein kinase C, epsilon                                                 |
| protein kinase C, eta                                                     |
| protein kinase C, theta                                                   |
| protein kinase, cGMP-dependent, type I                                    |
| protein kinase, cGMP-dependent, type II                                   |
| protein kinase N1                                                         |
| protein kinase N2                                                         |
| protein kinase N3                                                         |
| ribosomal protein S6 kinase, 90kDa, polypeptide 5                         |
| ribosomal protein S6 kinase, 90kDa, polypeptide 4                         |
| ribosomal protein S6 kinase, 70kDa, polypeptide 1                         |
| ribosomal protein S6 kinase, 70kDa, polypeptide 2                         |
| Protein Name                                                                 | Description                                                                                           |
|----------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------|
| ribosomal protein S6 kinase, 90kDa, polypeptide 2                           |                                                                                                       |
| ribosomal protein S6 kinase, 90kDa, polypeptide 3                           |                                                                                                       |
| ribosomal protein S6 kinase, 90kDa, polypeptide 1                           |                                                                                                       |
| ribosomal protein S6 kinase, 90kDa, polypeptide 6                           |                                                                                                       |
| ribosomal protein S6 kinase, 52kDa, polypeptide 1                          |                                                                                                       |
| ribosomal protein S6 kinase-like 1                                          |                                                                                                       |
| similar to Putative serine/threonine-protein kinase F31E3.2                |                                                                                                       |
| serum/glucocorticoid regulated kinase 1                                     |                                                                                                       |
| serum/glucocorticoid regulated kinase 2                                     |                                                                                                       |
| serum/glucocorticoid regulated kinase family, member 3                      |                                                                                                       |
| serine/threonine kinase 32A                                                |                                                                                                       |
| serine/threonine kinase 32B                                                |                                                                                                       |
| serine/threonine kinase 32C                                                |                                                                                                       |
| twinfilin, actin-binding protein, homolog 1 (Drosophila)                   |                                                                                                       |
| twinfilin, actin-binding protein, homolog 2 (Drosophila)                   |                                                                                                       |
| chaperone, ABC1 activity of bc1 complex homolog (S. pombe)                 |                                                                                                       |
| aarF domain containing kinase 4                                             |                                                                                                       |
| aarF domain containing kinase 1                                             |                                                                                                       |
| aarF domain containing kinase 5                                             |                                                                                                       |
| aarF domain containing kinase 2                                             |                                                                                                       |
| transient receptor potential cation channel, subfamily M, member 7         |                                                                                                       |
| transient receptor potential cation channel, subfamily M, member 6         |                                                                                                       |
| eukaryotic elongation factor-2 kinase                                      |                                                                                                       |
| alpha-kinase 2                                                             |                                                                                                       |
| alpha-kinase 1                                                             |                                                                                                       |
| breakpoint cluster region                                                   |                                                                                                       |
| bromodomain containing 2                                                   |                                                                                                       |
| bromodomain containing 3                                                   |                                                                                                       |
| bromodomain containing 4                                                   |                                                                                                       |
| bromodomain, testis-specific                                                |                                                                                                       |
| Fas-activated serine/threonine kinase                                       |                                                                                                       |
| serine/threonine kinase 19                                                 |                                                                                                       |
| heat shock 22kDa protein 8                                                  |                                                                                                       |
| branched chain ketoacid dehydrogenase kinase                               |                                                                                                       |
| pyruvate dehydrogenase kinase, isozyme 1                                   |                                                                                                       |
| pyruvate dehydrogenase kinase, isozyme 2                                   |                                                                                                       |
| pyruvate dehydrogenase kinase, isozyme 3                                   |                                                                                                       |
| pyruvate dehydrogenase kinase, isozyme 4                                   |                                                                                                       |
| ataxia telangiectasia mutated                                               |                                                                                                       |
| ataxia telangiectasia and Rad3 related                                    |                                                                                                       |
| protein kinase, DNA-activated, catalytic polypeptide                       |                                                                                                       |
| mechanismic target of rapamycin (serine/threonine kinase)                  |                                                                                                       |
| SMG1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)    |                                                                                                       |
| transformation/transcription domain-associated protein                     |                                                                                                       |
| RIO kinase 1 (yeast)                                                       |                                                                                                       |
| RIO kinase 2 (yeast)                                                       |                                                                                                       |
| RIO kinase 3 (yeast)                                                       |                                                                                                       |
| TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 250kDa |                                                                                                       |
| tripartite motif-containing 33                                              |                                                                                                       |
| Name                                                                 | Description                                                                 |
|----------------------------------------------------------------------|------------------------------------------------------------------------------|
| tripartite motif-containing 24                                       |                                                                              |
| calcium/calmodulin-dependent protein kinase I                        |                                                                              |
| pregnancy upregulated non-ubiquitously expressed CaM kinase          |                                                                              |
| similar to Calcium/calmodulin-dependent protein kinase ID            |                                                                              |
| calcium/calmodulin-dependent protein kinase IG                       |                                                                              |
| calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha    |                                                                              |
| calcium/calmodulin-dependent protein kinase (CaM kinase) II beta     |                                                                              |
| calcium/calmodulin-dependent protein kinase (CaM kinase) II delta     |                                                                              |
| calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma    |                                                                              |
| similar to Calcium/calmodulin-dependent protein kinase type IV (CAM kinase-GR) (CaMK IV) | |
| protein kinase, AMP-activated, alpha 1 catalytic subunit              |                                                                              |
| BR serine/threonine kinase 1                                         |                                                                              |
| BR serine/threonine kinase 2                                         |                                                                              |
| CHK1 checkpoint homolog (S. pombe)                                   |                                                                              |
| hormonally upregulated Neu-associated kinase                         |                                                                              |
| serine/threonine kinase 11                                           |                                                                              |
| MAP/microtubule affinity-regulating kinase 1                         |                                                                              |
| MAP/microtubule affinity-regulating kinase 2                         |                                                                              |
| MAP/microtubule affinity-regulating kinase 3                         |                                                                              |
| MAP/microtubule affinity-regulating kinase 4                         |                                                                              |
| hypothetical LOC618482                                               |                                                                              |
| maternal embryonic leucine zipper kinase                             |                                                                              |
| hypothetical LOC530210                                               |                                                                              |
| NUAK family, SNF1-like kinase, 1                                     |                                                                              |
| NUAK family, SNF1-like kinase, 2                                     |                                                                              |
| PAS domain containing serine/threonine kinase                        |                                                                              |
| SNF1-like kinase 2                                                   |                                                                              |
| similar to KIAA0999 protein                                          |                                                                              |
| SNF related kinase                                                   |                                                                              |
| serine/threonine kinase 40                                           |                                                                              |
| serine/threonine kinase 33                                           |                                                                              |
| CaM kinase-like vesicle-associated                                   |                                                                              |
| calcium/calmodulin-dependent serine protein kinase (MAGUK family)    |                                                                              |
| death-associated protein kinase 1                                    |                                                                              |
| death-associated protein kinase 2                                    |                                                                              |
| death-associated protein kinase 3                                    |                                                                              |
| serine/threonine kinase 17a                                          |                                                                              |
| serine/threonine kinase 17b                                          |                                                                              |
| doublecortin-like kinase 2                                           |                                                                              |
| doublecortin-like kinase 3                                           |                                                                              |
| mitogen-activated protein kinase-activated protein kinase 2           |                                                                              |
| mitogen-activated protein kinase-activated protein kinase 3           |                                                                              |
| mitogen-activated protein kinase-activated protein kinase 5           |                                                                              |
| MAP kinase interacting serine/threonine kinase 1                     |                                                                              |
| MAP kinase interacting serine/threonine kinase 2                     |                                                                              |
| myosin light chain kinase 3                                           |                                                                              |
| Protein Name                                           |
|--------------------------------------------------------|
| myosin light chain kinase family, member 4             |
| myosin light chain kinase 2                            |
| myosin light chain kinase                              |
| titin                                                  |
| phosphorylase kinase, gamma 1 (muscle)                 |
| phosphorylase kinase, gamma 2 (testis)                 |
| pim-1 oncogene                                         |
| pim-2 oncogene                                         |
| serine/threonine protein kinase pim-3-like              |
| protein kinase D1                                      |
| protein kinase D2                                      |
| protein kinase D3                                      |
| protein serine kinase H1                               |
| CHK2 checkpoint homolog (S. pombe)                     |
| tribbles homolog 1 (Drosophila)                        |
| tribbles homolog 2 (Drosophila)                        |
| tribbles homolog 3 (Drosophila)                        |
| obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF |
| SPEG complex locus                                     |
| kalirin, RhoGEF kinase                                 |
| triple functional domain (PTPRF interacting)           |
| testis-specific serine kinase 6                        |
| testis-specific serine kinase 2                        |
| testis-specific serine kinase 3                        |
| testis-specific serine kinase 4                        |
| similar to testis-specific serine kinase 5             |
| casein kinase 1, alpha 1                               |
| casein kinase I beta                                   |
| casein kinase 1, delta                                 |
| casein kinase 1, epsilon                               |
| casein kinase 1, gamma 1                               |
| casein kinase 1, gamma 2                               |
| tau tubulin kinase 2                                   |
| vaccinia related kinase 1                              |
| vaccinia related kinase 2                              |
| vaccinia related kinase 3                              |
| cell division cycle 2, G1 to S and G2 to M            |
| cyclin-dependent kinase 2                              |
| cyclin-dependent kinase 3                              |
| cyclin-dependent kinase 10                             |
| cyclin-dependent kinase 4                              |
| cyclin-dependent kinase 6                              |
| cyclin-dependent kinase 5                              |
| cyclin-dependent kinase 7                              |
| cell division cycle 2-like 6 (CDK8-like)               |
| cyclin-dependent kinase 8                              |
| cyclin-dependent kinase 9                              |
| Gene Name                                                                 | Function/Description                                                                 |
|--------------------------------------------------------------------------|---------------------------------------------------------------------------------------|
| cell division cycle 2-like 5 (cholinesterase-related cell division controller) |                                                                                        |
| Cdc2-related kinase, arginine/serine-rich                                  |                                                                                        |
| cell division cycle 2-like 1 (PITSLRE proteins)                           |                                                                                        |
| PCTAIRE protein kinase 1                                                  |                                                                                        |
| PCTAIRE protein kinase 2                                                  |                                                                                        |
| PCTAIRE protein kinase 3                                                  |                                                                                        |
| cyclin-dependent kinase 14                                                |                                                                                        |
| cyclin-dependent kinase 15                                                |                                                                                        |
| cell cycle related kinase                                                |                                                                                        |
| cyclin-dependent kinase-like 1 (CDC2-related kinase)                     |                                                                                        |
| cyclin-dependent kinase-like 2 (CDC2-related kinase)                     |                                                                                        |
| cyclin-dependent kinase-like 3                                            |                                                                                        |
| cyclin-dependent kinase-like 4                                            |                                                                                        |
| CDC-like kinase 1                                                         |                                                                                        |
| CDC-like kinase 2                                                         |                                                                                        |
| CDC-like kinase 3                                                         |                                                                                        |
| CDC-like kinase 4                                                         |                                                                                        |
| dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A         |                                                                                        |
| dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B         |                                                                                        |
| similar to Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 |                                                                                        |
| dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3          |                                                                                        |
| hypothetical LOC531276                                                    |                                                                                        |
| homeodomain interacting protein kinase 1                                 |                                                                                        |
| homeodomain interacting protein kinase 2                                 |                                                                                        |
| homeodomain interacting protein kinase 3                                 |                                                                                        |
| homeodomain interacting protein kinase 4                                 |                                                                                        |
| PRP4 pre-mRNA processing factor 4 homolog B (yeast)                      |                                                                                        |
| glycogen synthase kinase 3 alpha                                         |                                                                                        |
| glycogen synthase kinase 3 beta                                         |                                                                                        |
| mitogen-activated protein kinase 3                                       |                                                                                        |
| mitogen-activated protein kinase 1                                       |                                                                                        |
| mitogen-activated protein kinase 6                                       |                                                                                        |
| mitogen-activated protein kinase 4                                       |                                                                                        |
| mitogen-activated protein kinase 7                                       |                                                                                        |
| mitogen-activated protein kinase 15                                      |                                                                                        |
| mitogen-activated protein kinase 8                                       |                                                                                        |
| mitogen-activated protein kinase 9                                       |                                                                                        |
| mitogen-activated protein kinase 10                                      |                                                                                        |
| nemo-like kinase                                                         |                                                                                        |
| mitogen-activated protein kinase 14                                      |                                                                                        |
| mitogen-activated protein kinase 11                                      |                                                                                        |
| mitogen-activated protein kinase 13                                      |                                                                                        |
| mitogen-activated protein kinase 12                                      |                                                                                        |
| intestinal cell (MAK-like) kinase                                       |                                                                                        |
| male germ cell-associated kinase                                         |                                                                                        |
| renal tumor antigen                                                      |                                                                                        |
| SFRS protein kinase 3                                                     |                                                                                        |
| SFRS protein kinase 1                                                     |                                                                                        |
| SFRS protein kinase 2                                                     |                                                                                        |
| Protein Name                                                                 | Description                                                                 |
|----------------------------------------------------------------------------|-----------------------------------------------------------------------------|
| aurora kinase A                                                             |                                                                             |
| aurora kinase B                                                              |                                                                             |
| aurora kinase C                                                              |                                                                             |
| BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)                 |                                                                             |
| BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)            |                                                                             |
| TP53 regulating kinase                                                      |                                                                             |
| calcium/calmodulin-dependent protein kinase kinase 1, alpha                 |                                                                             |
| calcium/calmodulin-dependent protein kinase kinase 2, beta                  |                                                                             |
| cell division cycle 7 homolog (S. cerevisiae)                              |                                                                             |
| casein kinase 2, alpha 1 polypeptide                                        |                                                                             |
| casein kinase 2, alpha prime polypeptide                                    |                                                                             |
| germ cell associated 2 (haspin)                                             |                                                                             |
| conserved helix-loop-helix ubiquitous kinase                               |                                                                             |
| inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta  |                                                                             |
| inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon|                                                                             |
| TANK-binding kinase 1                                                       |                                                                             |
| v-mos Moloney murine sarcoma viral oncogene homolog                          |                                                                             |
| AP2 associated kinase 1                                                      |                                                                             |
| cyclin G associated kinase                                                  |                                                                             |
| serine/threonine kinase 16                                                  |                                                                             |
| NIMA (never in mitosis gene a)-related kinase 10                            |                                                                             |
| NIMA (never in mitosis gene a)-related kinase 11                            |                                                                             |
| NIMA (never in mitosis gene a)-related kinase 2                             |                                                                             |
| NIMA (never in mitosis gene a)-related kinase 3                             |                                                                             |
| NIMA (never in mitosis gene a)-related kinase 4                             |                                                                             |
| NIMA (never in mitosis gene a)-related kinase 5                             |                                                                             |
| NIMA (never in mitosis gene a)-related kinase 6                             |                                                                             |
| NIMA (never in mitosis gene a)-related kinase 7                             |                                                                             |
| NIMA (never in mitosis gene a)-related kinase 8                             |                                                                             |
| NIMA (never in mitosis gene a)-related kinase 9                             |                                                                             |
| similar to SH3-binding kinase                                               |                                                                             |
| SH3-binding domain kinase family, member 2                                  |                                                                             |
| similar to protein kinase                                                   |                                                                             |
| PTEN induced putative kinase 1                                              |                                                                             |
| serine/threonine kinase 35                                                  |                                                                             |
| PDLIM1 interacting kinase 1 like                                            |                                                                             |
| similar to Gene model 1082, (NCBI)                                          |                                                                             |
| testis expressed 14                                                         |                                                                             |
| nuclear receptor binding protein 1                                          |                                                                             |
| nuclear receptor binding protein 2                                          |                                                                             |
| U2AF homology motif (UHM) kinase 1                                          |                                                                             |
| ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent)                |                                                                             |
| hypothetical LOC614899                                                     |                                                                             |
| Gene Name                                                                 | Molecular Function                                                                 |
|--------------------------------------------------------------------------|-------------------------------------------------------------------------------------|
| hypothetical LOC514490                                                  | serine/threonine kinase 31                                                         |
| protein kinase domain containing, cytoplasmic homolog (mouse)            | receptor interacting protein kinase 5                                              |
| eukaryotic translation initiation factor 2-alpha kinase 3                |                                                                                   |
| eukaryotic translation initiation factor 2-alpha kinase 1                |                                                                                   |
| eukaryotic translation initiation factor 2-alpha kinase 2                |                                                                                   |
| polo-like kinase 1 (Drosophila)                                         |                                                                                   |
| polo-like kinase 2 (Drosophila)                                         |                                                                                   |
| polo-like kinase 3 (Drosophila)                                         |                                                                                   |
| polo-like kinase 4                                                      |                                                                                   |
| similar to Serine/threonine-protein kinase PLK5 (Polo-like kinase 5) (PLK-5) |                                                                                   |
| SCY1-like 1 (S. cerevisiae)                                             |                                                                                   |
| SCY1-like 2 (S. cerevisiae)                                             |                                                                                   |
| SCY1-like 3 (S. cerevisiae)                                             |                                                                                   |
| PX domain containing serine/threonine kinase                            |                                                                                   |
| TBC1 domain containing kinase                                           |                                                                                   |
| tousled-like kinase 1                                                   |                                                                                   |
| tousled-like kinase 2                                                   |                                                                                   |
| PDZ binding kinase                                                      |                                                                                   |
| TTK protein kinase                                                      |                                                                                   |
| serine/threonine kinase 36, fused homolog (Drosophila)                  |                                                                                   |
| unc-51-like kinase 1 (C. elegans)                                       |                                                                                   |
| unc-51-like kinase 2 (C. elegans)                                       |                                                                                   |
| unc-51-like kinase 3 (C. elegans)                                       |                                                                                   |
| unc-51-like kinase 4 (C. elegans)                                       |                                                                                   |
| phosphoinositide-3-kinase, regulatory subunit 4                          |                                                                                   |
| protein kinase, membrane associated tyrosine/threonine 1                |                                                                                   |
| WEE1 homolog (S. pombe)                                                 |                                                                                   |
| WEE1 homolog 2 (S. pombe)                                               |                                                                                   |
| WNK lysine deficient protein kinase 1                                   |                                                                                   |
| WNK lysine deficient protein kinase 2                                   |                                                                                   |
| WNK lysine deficient protein kinase 3                                   |                                                                                   |
| natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic peptide receptor A) |                                                                                   |
| natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B) |                                                                                   |
| guanylate cyclase 2D, membrane (retina-specific)                        |                                                                                   |
| guanylate cyclase 2F, retinal                                           |                                                                                   |
| guanylate cyclase 2C (heat stable enterotoxin receptor)                 |                                                                                   |
| mitogen-activated protein kinase kinase 1                               |                                                                                   |
| mitogen-activated protein kinase kinase 2                               |                                                                                   |
| mitogen-activated protein kinase kinase 3                               |                                                                                   |
| mitogen-activated protein kinase kinase 4                               |                                                                                   |
| mitogen-activated protein kinase kinase 5                               |                                                                                   |
| mitogen-activated protein kinase kinase 6                               |                                                                                   |
| mitogen-activated protein kinase kinase 15                              |                                                                                   |
| yeast Sps1/Ste20-related kinase 4 (S. cerevisiae)                       |                                                                                   |
| serine threonine kinase 39 (STE20/SPS1 homolog, yeast)                 |                                                                                   |
| Protein Name                                                                 |
|----------------------------------------------------------------------------|
| mitogen-activated protein kinase kinase kinase kinase 2                     |
| mitogen-activated protein kinase kinase kinase kinase 1                     |
| mitogen-activated protein kinase kinase kinase kinase 5                     |
| mitogen-activated protein kinase kinase kinase kinase kinase 3              |
| TRAF2 and NCK interacting kinase                                            |
| misshapen-like kinase 1 (zebrafish)                                         |
| Nik related kinase                                                           |
| serine/threonine kinase 4                                                   |
| serine/threonine kinase 3 (STE20 homolog, yeast)                            |
| myosin IIIA                                                                  |
| myosin IIIB                                                                  |
| p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)                    |
| similar to serine/threonine kinase                                           |
| p21 (CDKN1A)-activated kinase 3                                              |
| p21(CDKN1A)-activated kinase 4                                               |
| p21(CDKN1A)-activated kinase 7                                               |
| p21(CDKN1A)-activated kinase 6                                               |
| serine/threonine kinase 10                                                   |
| STE20-like kinase (yeast)                                                    |
| protein kinase LYK5                                                          |
| STE20-related kinase adaptor beta                                            |
| TAO kinase 1                                                                 |
| TAO kinase 2                                                                 |
| TAO kinase 3                                                                 |
| serine/threonine kinase 24 (STE20 homolog, yeast)-like                      |
| serine/threonine protein kinase MST4                                         |
| serine/threonine kinase 25 (STE20 homolog, yeast)                           |
| mitogen-activated protein kinase kinase 1                                   |
| mitogen-activated protein kinase kinase 2                                   |
| mitogen-activated protein kinase kinase 3                                   |
| mitogen-activated protein kinase kinase 4                                   |
| mitogen-activated protein kinase kinase 5                                   |
| mitogen-activated protein kinase kinase 6                                   |
| mitogen-activated protein kinase kinase 7                                   |
| mitogen-activated protein kinase kinase 8                                   |
| mitogen-activated protein kinase kinase kinase kinase kinase 14             |
| c-abl oncogene 1, receptor tyrosine kinase                                  |
| v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene) |
| activated p21cdc42Hs kinase                                                 |
| tyrosine kinase, non-receptor, 1                                             |
| anaplastic lymphoma receptor tyrosine kinase                                |
| AXL receptor tyrosine kinase                                                |
| c-mer proto-oncogene tyrosine kinase                                        |
| TYRO3 protein tyrosine kinase                                               |
| PTK7 protein tyrosine kinase                                                |
| c-src tyrosine kinase                                                       |
| megakaryocyte-associated tyrosine kinase                                     |
| discoidin domain receptor tyrosine kinase 1                                 |
| discoidin domain receptor tyrosine kinase 2                                 |
| Protein Name                                                                 | Description                                                                                     |
|----------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------|
| epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) |                                                                                                 |
| v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)          |                                                                                                 |
| v-erb-a erythroblastic leukemia viral oncogene homolog 4                    |                                                                                                 |
| EPH receptor A1                                                            |                                                                                                 |
| EPH receptor A10                                                           |                                                                                                 |
| EPH receptor A2                                                            |                                                                                                 |
| EPH receptor A3                                                            |                                                                                                 |
| EPH receptor A4                                                            |                                                                                                 |
| EPH receptor A5                                                            |                                                                                                 |
| EPH receptor A6                                                            |                                                                                                 |
| EPH receptor A7                                                            |                                                                                                 |
| EPH receptor A8                                                            |                                                                                                 |
| EPH receptor B1                                                            |                                                                                                 |
| similar to protein tyrosine kinase                                         |                                                                                                 |
| EPH receptor B2                                                            |                                                                                                 |
| EPH receptor B3                                                            |                                                                                                 |
| EPH receptor B4                                                            |                                                                                                 |
| EPH receptor B6                                                            |                                                                                                 |
| PTK2 protein tyrosine kinase 2                                              |                                                                                                 |
| PTK2B protein tyrosine kinase 2 beta                                       |                                                                                                 |
| fer (fps/fes related) tyrosine kinase                                      |                                                                                                 |
| feline sarcoma oncogene                                                    |                                                                                                 |
| fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome) |                                                                                                 |
| acteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer |                                                                                                 |
| fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) |                                                                                                 |
| fibroblast growth factor receptor 4                                        |                                                                                                 |
| insulin-like growth factor 1 receptor                                      |                                                                                                 |
| insulin receptor                                                          |                                                                                                 |
| insulin receptor-related receptor                                         |                                                                                                 |
| Janus kinase 1                                                            |                                                                                                 |
| Janus kinase 2 (a protein tyrosine kinase)                                 |                                                                                                 |
| similar to Janus kinase 3                                                  |                                                                                                 |
| tyrosine kinase 2                                                          |                                                                                                 |
| apoptosis-associated tyrosine kinase                                       |                                                                                                 |
| lemur tyrosine kinase 2                                                    |                                                                                                 |
| met proto-oncogene (hepatocyte growth factor receptor)                     |                                                                                                 |
| macrophage stimulating 1 receptor (c-met-related tyrosine kinase)          |                                                                                                 |
| muscle, skeletal, receptor tyrosine kinase                                |                                                                                                 |
| fms-related tyrosine kinase 3                                              |                                                                                                 |
| v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog              |                                                                                                 |
| platelet-derived growth factor receptor, alpha polypeptide                 |                                                                                                 |
| platelet-derived growth factor receptor, beta polypeptide                  |                                                                                                 |
| ret proto-oncogene                                                         |                                                                                                 |
| receptor tyrosine kinase-like orphan receptor 1                            |                                                                                                 |
| receptor tyrosine kinase-like orphan receptor 2                            |                                                                                                 |
| RYK receptor-like tyrosine kinase                                         |                                                                                                 |
| Name                                                                 | Function                                                                                           |
|----------------------------------------------------------------------|---------------------------------------------------------------------------------------------------|
| B lymphoid tyrosine kinase                                           |                                                                                                   |
| PTK6 protein tyrosine kinase 6                                       |                                                                                                   |
| Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog        |                                                                                                   |
| fyn-related kinase                                                  |                                                                                                   |
| FYN oncogene related to SRC, FGR, YES                               |                                                                                                   |
| hemopoietic cell kinase                                             |                                                                                                   |
| lymphocyte-specific protein tyrosine kinase                         |                                                                                                   |
| v-yes-1 Yamaguchi sarcoma viral related oncogene homolog             |                                                                                                   |
| v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)    |                                                                                                   |
| src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites |                                                                                                   |
| v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1                   |                                                                                                   |
| spleen tyrosine kinase                                              |                                                                                                   |
| zeta-chain (TCR) associated protein kinase 70kDa                    |                                                                                                   |
| BMX non-receptor tyrosine kinase                                    |                                                                                                   |
| Bruton agammaglobulinemia tyrosine kinase                           |                                                                                                   |
| IL2-inducible T-cell kinase                                         |                                                                                                   |
| tec protein tyrosine kinase                                         |                                                                                                   |
| TXK tyrosine kinase                                                 |                                                                                                   |
| tyrosine kinase with immunoglobulin-like and EGF-like domains 1      |                                                                                                   |
| TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal) |                                                                                                   |
| serine/threonine/tyrosine kinase 1                                  |                                                                                                   |
| neurotrophic tyrosine kinase, receptor, type 1                      |                                                                                                   |
| neurotrophic tyrosine kinase, receptor, type 3                      |                                                                                                   |
| fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor) |                                                                                                   |
| fms-related tyrosine kinase 4                                       |                                                                                                   |
| kinase insert domain receptor (a type III receptor tyrosine kinase)  |                                                                                                   |
| interleukin-1 receptor-associated kinase 1                          |                                                                                                   |
| interleukin-1 receptor-associated kinase 2                          |                                                                                                   |
| interleukin-1 receptor-associated kinase 3                          |                                                                                                   |
| interleukin-1 receptor-associated kinase 4                          |                                                                                                   |
| LIM domain kinase 1                                                  |                                                                                                   |
| LIM domain kinase 2                                                  |                                                                                                   |
| testis-specific kinase 1                                             |                                                                                                   |
| testis-specific kinase 2                                             |                                                                                                   |
| leucine-rich repeat kinase 1                                         |                                                                                                   |
| leucine-rich repeat kinase 2                                         |                                                                                                   |
| TNNI3 interacting kinase                                            |                                                                                                   |
| mitogen-activated protein kinase kinase kinase 13                   |                                                                                                   |
| mitogen-activated protein kinase kinase kinase 9                    |                                                                                                   |
| mitogen-activated protein kinase kinase kinase 10                   |                                                                                                   |
| mitogen-activated protein kinase kinase kinase 11                   |                                                                                                   |
| similar to mixed lineage kinase 4 (KIAA1804)                        |                                                                                                   |
| sterile alpha motif and leucine zipper containing kinase AZK         |                                                                                                   |
| mitogen-activated protein kinase kinase kinase 7                    |                                                                                                   |
| v-raf murine sarcoma 3611 viral oncogene homolog                     |                                                                                                   |
| v-raf murine sarcoma viral oncogene homolog B1                       |                                                                                                   |
| kinase suppressor of ras 1                                           |                                                                                                   |
| Kinase Name |
|-------------|
| kinase suppressor of ras 2 |
| v-raf-1 murine leukemia viral oncogene homolog 1 |
| receptor-interacting serine-threonine kinase 4 |
| receptor (TNFRSF)-interacting serine-threonine kinase 1 |
| receptor-interacting serine-threonine kinase 2 |
| receptor-interacting serine-threonine kinase 3 |
| activin A receptor type II-like 1 |
| activin A receptor, type I |
| activin A receptor, type IB |
| activin A receptor, type IC |
| bone morphogenetic protein receptor, type IA |
| bone morphogenetic protein receptor, type IB |
| transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa) |
| activin A receptor, type IIA |
| activin A receptor, type IIB |
| bone morphogenetic protein receptor, type II (serine/threonine kinase) |
| transforming growth factor, beta receptor II (70/80kDa) |
| integrin-linked kinase |
| mixed lineage kinase domain-like |
| Chr | cDNA length | ORF length | Protein size | kinase domain (KD)n size |
|-----|-------------|------------|--------------|-------------------------|
| 21  | 1691        | 1443       | 480          | 259                     |
| 18  | 3460        | 1446       | 481          | 258                     |
| 16  | 1776        | 1440       | 479          | 258                     |
| 18  | 2434        | 1857       | 618          | 269                     |
| 29  | 5018        | 4632       | 1543         | 266                     |
| 16  | 5265        | 5265       | 1754         | 267                     |
| 21  | 6560        | 5271       | 1756         | 267                     |
| 24  | 4793        | 4104       | 1367         | 263                     |
| 11  | 5053        | 4167       | 1388         | 263                     |
| 17  | 5837        | NA         | 1820         | 110                     |
| 29  | 2520        | 2070       | 689          | 263                     |
| 17  | 2791        | 2067       | 688          | 263                     |
| 6   | 1752        | 1752       | 583          | 263                     |
| 26  | 2539        | 1773       | 590          | 263                     |
| 7   | 2853        | 1725       | 574          | 259                     |
| 1   | 2227        | 1659       | 552          | 264                     |
| 12  | 2898        | 1686       | 561          | 266                     |
| 7   | 4719        | 4719       | 1572         | 274                     |
| 3   | 5414        | 5136       | 1711         | 274                     |
| 7   | 5651        | 4101       | 1366         | 274                     |
| 20  | 7677        | 7302       | 2433         | 274                     |
| 13  | 2736        | 2643       | 880          | 276                     |
| 3   | 795         | 795        | 264          | 161                     |
| 9   | 7537        | 3372       | 1123         | 306                     |
| 12  | 4733        | 3048       | 1015         | 305                     |
| 23  | 3545        | 1398       | 465          | 294                     |
| 5   | 4209        | 1395       | 464          | 294                     |
| 7   | 2522        | 1056       | 351          | 255                     |
| 3   | 1750        | 1056       | 351          | 255                     |
| X   | 1139        | 957        | 318          | 255                     |
| 25  | 1820        | 1605       | 534          | 265                     |
| 1   | 2813        | 1791       | 596          | 269                     |
| 16  | 2240        | 1785       | 594          | 267                     |
| 19  | 2324        | 2019       | 672          | 259                     |
| 25  | 2955        | 2022       | 673          | 259                     |
| 18  | 3032        | 2094       | 697          | 264                     |
| 22  | 3019        | 2031       | 676          | 255                     |
| 11  | 5491        | 2214       | 737          | 261                     |
| 10  | 2389        | 2049       | 682          | 260                     |
| 13  | 3181        | 2121       | 706          | 255                     |
| 26  | 2775        | 2016       | 671          | 260                     |
| 6   | 2289        | 2289       | 762          | 259                     |
| 7   | 3059        | 2835       | 944          | 260                     |
| 3   | 3226        | 2946       | 981          | 260                     |
| 11  | 3386        | 2661       | 886          | 260                     |
| 10  | 4103        | 2346       | 781          | 270                     |
| 29  | 3061        | 2316       | 771          | 269                     |
| 19  | 1585        | 1584       | 527          | 262                     |
| 29  | 1791        | 1560       | 519          | 262                     |
| 9  | 3605 | 2202 | 733  | 260   |
|----|------|------|------|-------|
| X  | 2927 | 2223 | 740  | 260   |
| 2  | 3157 | 2208 | 735  | 260   |
| X  | 2635 | 2235 | 744  | 258   |
| 16 | 4415 | 3186 | 1061 | 232   |
| 10 | 3608 | 1326 | 441  | 283   |
| 19 | 1628 | 819  | 272  | 171   |
| 9  | 2382 | 1296 | 431  | 258   |
| 13 | 1755 | 1104 | 367  | 258   |
| 14 | 3363 | 1473 | 490  | 258   |
| 7  | 1852 | 1101 | 366  | 259   |
| 6  | 1479 | 1479 | 492  | 261   |
| 26 | 3409 | 2889 | 962  | 261   |
| 5  | 1242 | 1053 | 350  | NA    |
| 22 | 1614 | 1050 | 349  | NA    |
| 16 | 2903 | 1947 | 648  | NA    |
| 18 | 2149 | 1578 | 525  | NA    |
| 10 | 2274 | 1572 | 523  | NA    |
| 14 | 1927 | 1743 | 580  | NA    |
| 4  | 2160 | 1878 | 625  | NA    |
| 10 | 7214 | 5601 | 1866 | NA    |
| 8  | 6756 | 6480 | 2159 | NA    |
| 25 | 5774 | 2172 | 723  | NA    |
| 21 | 5352 | NA   | 1783 | NA    |
| 24 | 6916 | 6360 | 2119 | NA    |
| 6  | 4289 | 3774 | 1257 | NA    |
| 17 | 3127 | 2967 | 988  | NA    |
| 23 | 2412 | 2412 | 803  | NA    |
| 11 | 3093 | 2169 | 722  | NA    |
| 7  | 5608 | 4107 | 1368 | NA    |
| 3  | 2936 | 2808 | 935  | NA    |
| 4  | 1829 | 1632 | 543  | NA    |
| 23 | 2416 | 510  | 169  | NA    |
| 17 | 1906 | 591  | 196  | NA    |
| 25 | 1872 | 1239 | 412  | NA    |
| 2  | 3859 | 1317 | 438  | NA    |
| 19 | 2277 | 1032 | 343  | NA    |
| X  | 2082 | 1248 | 415  | NA    |
| 4  | 3805 | 1224 | 407  | NA    |
| 15 | 9406 | 9165 | 3054 | NA    |
| 1  | 8268 | 7935 | 2644 | NA    |
| 14 | 12953| 12375| 4124 | NA    |
| 16 | 8303 | 7656 | 2551 | NA    |
| 25 | 15784| 10977| 3658 | NA    |
| 25 | 12190| 11496| 3831 | NA    |
| 23 | 1952 | NA   | 544  | NA    |
| 7  | 1871 | 1656 | 551  | NA    |
| 24 | 4335 | 1560 | 519  | NA    |
| X  | 7765 | 6090 | 2029 | NA    |
| 3  | 3622 | 3330 | 1109 | NA    |
| 18  | 2934 | 2202  | 733   | NA   |
|-----|------|-------|-------|------|
| 4   | 3365 | 2808  | 935   | NA   |
| 22  | 1456 | 1113  | 370   | 257  |
| X   | 1410 | 1029  | 342   | 256  |
| 13  | 1510 | 1140  | 379   | 272  |
| 16  | 2357 | 1425  | 474   | 255  |
| 7   | 3032 | 1437  | 478   | 259  |
| 4   | 1912 | 1629  | 542   | 259  |
| 6   | 1537 | 1500  | 499   | 259  |
| 28  | 1780 | 1488  | 495   | 259  |
| 10  | 1532 | 1392  | 463   | 255  |
| 20  | 1698 | 1698  | 565   | 268  |
| 3   | 2153 | 1659  | 552   | 253  |
| 18  | 3018 | 2481  | 826   | 252  |
| 29  | 2175 | 2175  | 724   | 265  |
| 29  | 2276 | 1431  | 476   | 257  |
| 1   | 2028 | 2028  | 675   | 261  |
| 7   | 1623 | 1326  | 441   | 264  |
| 16  | 2681 | 2388  | 795   | 252  |
| 29  | 2274 | 2274  | 757   | 252  |
| 21  | 2995 | 2379  | 792   | 252  |
| 18  | 1947 | 1329  | 442   | 252  |
| 14  | 1518 | 1518  | 505   | 250  |
| 8   | 2445 | 1953  | 650   | 253  |
| 20  | 2122 | 1311  | 436   | 252  |
| 5   | 2227 | 1989  | 662   | 252  |
| 16  | 1476 | 1476  | 491   | 251  |
| 3   | 4495 | 4128  | 1375  | 253  |
| 15  | 3639 | 2721  | 906   | 252  |
| 15  | 6891 | 3945  | 1314  | 252  |
| 1   | 1797 | NA    | 599   | 255  |
| 22  | 5000 | 2085  | 694   | 254  |
| 3   | 1749 | 1311  | 436   | 195  |
| 15  | 2228 | 1461  | 486   | 266  |
| 22  | 2932 | 1515  | 504   | 263  |
| X   | 3302 | 2727  | 908   | 265  |
| 8   | 2519 | 4293  | 1430  | 263  |
| 10  | 1579 | 1452  | 483   | 263  |
| 7   | 3120 | 1365  | 454   | 263  |
| 4   | 1760 | 1245  | 414   | 261  |
| 2   | 1577 | 1119  | 372   | 260  |
| 12  | 1296 | NA    | 431   | 258  |
| 17  | 2304 | 2304  | 767   | 258  |
| 22  | 2607 | 2607  | 868   | 258  |
| 16  | 1747 | 1212  | 403   | 262  |
| 22  | 2654 | 1155  | 384   | 261  |
| 17  | 1751 | 1419  | 472   | 285  |
| 3   | 2553 | 1263  | 420   | 286  |
| 7   | 1504 | 1395  | 464   | 286  |
| 18  | 2457 | 2361  | 786   | 256  |
|   |     |     |     |     |
|---|-----|-----|-----|-----|
| 23 | 1206| 1206| 401 | 256 |
| 13 | 2249| 1872| 623 | 256 |
|   1 | 3983| 3531| 1176| 256 |
| 2  | 5   | NA  | NA  | 255 |
| 25 | 2042| 1164| 387 | 269 |
| 25 | 1717| 1221| 406 | 268 |
| 23 | 2753| 942 | 313 | 253 |
| X  | 2155| 1233| 410 | 255 |
| 5  | 1888| 981 | 326 | 254 |
| 21 | 3323| 2553| 850 | 257 |
| 18 | 2894| 2652| 883 | 257 |
| 11 | 3173| 2673| 890 | 257 |
| 18 | 3390| 1275| 424 | 258 |
| 17 | 1992| 1605| 534 | 267 |
| 14 | 3504| 1119| 372 | 245 |
| 11 | 3047| 1032| 343 | 245 |
| 13 | 1988| 1074| 357 | 245 |
| 7  | 5737| 5643| 1880| 254 |
| 2  | 10000| 9846| 3281| 254 |
| 1  | 8961| 8961| 2986| 255 |
| 20 | 4672| 4212| 1403| 255 |
| 7  | 1350| 822 | 273 | 256 |
| 17 | 1459| 1104| 367 | 261 |
| 17 | 1548| 1077| 358 | 261 |
| 2  | 1240| 810 | 269 | 256 |
| 10 | 1220| 1017| 338 | 281 |
| 14 | 1639| 1188| 395 | 277 |
| 7  | 1429| 978 | 325 | 261 |
| X  | 1903| 1011| 336 | 261 |
| 19 | 3533| 1230| 409 | 261 |
| 5  | 2133| 1401| 466 | 261 |
| 10 | 1924| 1314| 437 | 264 |
| 7  | 2383| 1245| 414 | 263 |
| 7  | 4603| 1341| 446 | 262 |
| 23 | 3834| 3834| 1277| 254 |
| 10 | 5466| 3732| 1243| 256 |
| 5  | 1525| 1191| 396 | 267 |
| 11 | 2106| 1296| 431 | 264 |
| 18 | 1956| 1356| 451 | 240 |
| 28 | 1258| 894 | 297 | 284 |
| 5  | 1369| 897 | 298 | 283 |
| 19 | 1576| 918 | 305 | 283 |
| 18 | 1644| 1086| 361 | 285 |
| 5  | 1369| 912 | 303 | 290 |
| 4  | 1619| 981 | 326 | 288 |
| 4  | 1100| 879 | 292 | 283 |
| 20 | 1376| 1041| 346 | 284 |
| 9  | 2895| 1503| 500 | 316 |
| 12 | 2484| 1332| 443 | 293 |
| 11 | 1747| 1119| 372 | 297 |
| 4  | 7268 | 4539 | 1512  | 294  |
|----|------|------|-------|------|
| 19 | 5981 | 4473 | 1490  | 294  |
| 16 | 2916 | 2316 | 771   | 286  |
| X  | 3105 | 1491 | 496   | 282  |
| 5  | 3625 | 1572 | 523   | 282  |
| 16 | 2847 | 1416 | 471   | 282  |
| 4  | 1605 | 1486 | 494   | 285  |
| 2  | 1305 | 1305 | 434   | 285  |
| 8  | 2119 | 1041 | 346   | 285  |
| 10 | 1889 | 1059 | 352   | 284  |
| 6  | 2549 | 1710 | 569   | 284  |
| 7  | 1776 | 1776 | 591   | 283  |
| 11 | 1216 | 948  | 315   | 283  |
| X  | 2949 | 2949 | 982   | 285  |
| 2  | 1831 | 1458 | 485   | 317  |
| 3  | 2131 | 1500 | 499   | 317  |
| 21 | 1901 | 1473 | 490   | 317  |
| 7  | 2081 | 1446 | 481   | 316  |
| 1  | 5114 | 2292 | 763   | 321  |
| 18 | 2567 | 2067 | 688   | 321  |
| 5  | 1800 | 1800 | 599   | 314  |
| 16 | 2180 | 1764 | 587   | 314  |
| 5  | 1914 | 1914 | 637   | 297  |
| 3  | 3645 | 3645 | 1214  | 331  |
| 4  | 3606 | 3573 | 1190  | 329  |
| 15 | 4874 | 3651 | 1216  | 329  |
| 18 | 3360 | 1851 | 616   | 337  |
| 23 | 4163 | 3027 | 1008  | 313  |
| 18 | 2506 | 1488 | 495   | 285  |
| 1  | 1861 | 1299 | 432   | 298  |
| 25 | 2135 | 1089 | 362   | 289  |
| 17 | 1272 | 1083 | 360   | 289  |
| 10 | 3901 | 2169 | 722   | 297  |
| 24 | 1755 | 1080 | 359   | 265  |
| 19 | 3054 | 2346 | 781   | 293  |
| 14 | 1959 | 1611 | 536   | 292  |
| 28 | 3047 | 1284 | 427   | 296  |
| 7  | 4602 | 1275 | 424   | 296  |
| 6  | 2913 | 1281 | 426   | 296  |
| 19 | 4073 | 1584 | 527   | 290  |
| 23 | 4284 | 1083 | 360   | 285  |
| 5  | 2290 | 1056 | 351   | 272  |
| 23 | 1402 | 1101 | 366   | 284  |
| 5  | 1727 | 1104 | 367   | 285  |
| 23 | 4005 | 1887 | 628   | 281  |
| 23 | 2257 | 1872 | 623   | 281  |
| 21 | 1731 | 1302 | 433   | 282  |
| X  | 2100 | 1698 | 565   | 486  |
| 23 | 4291 | 1968 | 655   | 574  |
| 4  | 5185 | 2133 | 710   | 606  |
|   |     |     |     |     |
|---|-----|-----|-----|-----|
| 13| 2000| 1209| 402 | 251 |
| 19| 2164| 1035| 344 | 251 |
| 18| 1071| 915 | 304 | 251 |
| 20| 1053| 1053| 350 | 233 |
| 11| 3750| 3237| 1078| 269 |
| 10| 4018| 3189| 1062| 265 |
| 13| 1406| 762 | 253 | 220 |
| 19| 2043| 1518| 505 | 285 |
| 17| 1957| 1740| 579 | 282 |
|  3| 3466| 1731| 576 | 514 |
| 13| 2328| 1176| 391 | 285 |
| 18| 1529| 1053| 350 | 286 |
| 19| 2999| 2346| 781 | 314 |
| 26| 3442| 2223| 740 | 274 |
| 27| 3490| 2271| 756 | 275 |
| 16| 3106| 2157| 718 | 318 |
|  5| 3348| 2190| 729 | 296 |
| 19| 2955| 2931| 976 | 262 |
| 25| 2937| 2778| 925 | 262 |
| 14| 1130| 1023| 340 | 272 |
| 11| 3195| 2877| 958 | 275 |
|  6| 3437| 3375| 1124| 291 |
|  6| 4394| 3807| 1268| 274 |
|  2| 1482| 918 | 305 | 271 |
|  8| 1272| NA  | 424 | 255 |
| 22| 2505| 2505| 834 | 246 |
|  1| 1731| 1731| 576 | 259 |
| 16| 2142| 1338| 445 | 264 |
| 12| 2089| 1488| 495 | 254 |
| 22| 3480| 2364| 787 | 256 |
| 12| 1644| 1644| 547 | 256 |
| 11| 2550| 942 | 313 | 261 |
| 16| 1680| 912 | 303 | 262 |
| 19| 2147| 2097| 698 | 255 |
| 10| 5508| 2934| 977 | 257 |
| 25| 1077| 1077| 358 | 265 |
| 18| 1503| 1503| 500 | 264 |
| 18| 1095| 1095| 364 | 262 |
|  2| 2971| 1767| 588 | 352 |
| 27| 4155| NA  | 1384| 313 |
| 21| 4647| 4647| 1548| 337 |
| 13| 1540| 1209| 402 | 329 |
|  2| 1394| 1290| 429 | 333 |
| 18| 2025| 2025| 674 | 111 |
| 19| 4808| 4482| 1493| 305 |
| 11| 2165| 1608| 535 | 264 |
| 14| 3298| 1500| 499 | 270 |
|  3| 2115| 1260| 419 | 282 |
| 16| 2779| 2172| 723 | 110 |
| 11| 1965| 1965| 654 | 266 |
|   |     |     |     |     |
|---|-----|-----|-----|-----|
| 27| 3345| 1053| 350 | 251 |
| 4 | 2922| 2922| 973 | 237 |
| 11| 2142| 1482| 493 | 228 |
| 16| 5138| 2787| 928 | 264 |
| 10| 5179| 4956| 1651| 412 |
| 11| 4607| 3348| 1115| 484 |
| 25| 2860| 1899| 632 | 418 |
| 11| 2267| 1602| 533 | 256 |
| 25| 2187| 1809| 602 | 253 |
| 20| 2903| 2058| 685 | 253 |
| 3 | 2371| 1944| 647 | 253 |
| 17| 3583| 2682| 893 | 254 |
| 7 | 1941| 1941| 646 | 255 |
| 29| 2644| 2424| 807 | 231 |
| 5 | 5581| 2790| 929 | 296 |
| 16| 2907| 2259| 752 | 221 |
| 22| 2927| 1740| 579 | 248 |
| 6 | 2931| 2931| 976 | 256 |
| 2 | 3897| 2289| 762 | 279 |
| 19| 3037| 2313| 770 | 280 |
| 8 | 1972| 975 | 324 | 288 |
| 9 | 2971| 2571| 856 | 266 |
| 2 | 4460| 3948| 1315| 251 |
| 17| 3805| 3168| 1055| 263 |
| 19| 3522| 3114| 1037| 264 |
| 21| 2562| 1419| 472 | 257 |
| 22| 3788| 3678| 1225| 277 |
| 1 | 4994| 4077| 1358| 284 |
| 25| 2579| 1494| 497 | 250 |
| 15| 2561| 1269| 422 | 271 |
| 4 | 1701| 1701| 566 | 275 |
| 5 | 8732| NA  | 2118| 226 |
| 8 | 6855| 6681| 2226| 259 |
| Un| 2460| NA  | 700 | 259 |
| 19| 4010| 3660| 1219| 259 |
| 3 | 3818| 3195| 1064| 269 |
| 8 | 3276| 3144| 1047| 270 |
| 19| 4594| 3333| 1110| 274 |
| X | 5956| 3312| 1103| 280 |
| 5 | 3772| 3219| 1072| 273 |
| 20| 4881| 4530| 1509| 268 |
| 2 | 3025| 1863| 620 | 261 |
| 19| 2187| 1851| 616 | 261 |
| 9 | 5630| 4662| 1553| 259 |
| 9 | 5283| 4101| 1366| 261 |
| 2 | 4109| 3888| 1295| 254 |
| X | 5876| 4473| 1490| 256 |
| 2 | 3984| 3984| 1327| 264 |
| 22| 1833| 1584| 527 | 275 |
| 2 | 3229| 1614| 537 | 275 |
|    |      |      |      |      |
|----|------|------|------|------|
| 29 | 2885 | 2466 | 821  | 258  |
| 18 | 2653 | 2463 | 820  | 258  |
| 10 | 4458 | 2541 | 846  | 258  |
| 11 | 4184 | 2685 | 894  | 258  |
| 11 | 4312 | 3999 | 1332 | 267  |
|  1 | 6668 | 3918 | 1305 | 248  |
| 19 | 4916 | 3933 | 1310 | 265  |
| X  | 5847 | 4761 | 1586 | 289  |
| 13 | 1911 | 1464 | 487  | 252  |
| 14 | 3034 | 1830 | 609  | 252  |
| 13 | 4908 | 4908 | 1635 | 267  |
|  2 | 2985 | 2985 | 994  | 267  |
| 29 | 3079 | 1635 | 544  | 252  |
|  9 | 4292 | 1038 | 345  | 252  |
| X  | 2336 | 1635 | 544  | 252  |
| 18 | 2616 | 1782 | 593  | 252  |
| 13 | 2511 | 2160 | 719  | 252  |
| 10 | 3868 | 2046 | 681  | 252  |
| 20 | 5256 | 2904 | 967  | 259  |
| 26 | 3176 | 2967 | 988  | 259  |
| 19 | 2294 | 1122 | 373  | 311  |
|  2 | 2001 | 1299 | 432  | 312  |
| 19 | 6255 | 3006 | 1001 | 254  |
| 25 | 4145 | 3150 | 1049 | 254  |
| 17 | 4101 | 2697 | 898  | 254  |
| 12 | 1744 | 1302 | 433  | 251  |
| X  | 1743 | 1365 | 454  | 251  |
|  3 | 1618 | 1284 | 427  | 251  |
| 10 | 2376 | 1182 | 393  | 294  |
|  7 | 1633 | 1203 | 400  | 298  |
| 19 | 2233 | 1044 | 347  | 262  |
| 19 | 3848 | 1239 | 412  | 266  |
| 10 | 1311 | 1311 | 436  | 253  |
| 19 | 1527 | 1005 | 334  | 262  |
|  7 | 3524 | 1407 | 468  | 261  |
| 13 | 2553 | 1407 | 468  | 253  |
| 19 | 4323 | 2862 | 953  | 267  |
| 11 | 3952 | 3456 | 1151 | 252  |
| 16 | 3539 | 3441 | 1146 | 252  |
|  1 | 4276 | 3216 | 1071 | 260  |
| 19 | 2611 | 1992 | 663  | 262  |
| 11 | 4866 | 4866 | 1621 | 270  |
| 18 | 4510 | 3012 | 1003 | 269  |
| 11 | 3474 | 2928 | 975  | 266  |
| 10 | 3746 | 2670 | 889  | 262  |
| 23 | 4281 | 3450 | 1149 | 266  |
| 21 | 2105 | 1353 | 450  | 246  |
|  7 | 1895 | 1458 | 485  | 244  |
| 23 | 3770 | 2748 | 915  | 295  |
|  3 | 3105 | 2568 | 855  | 287  |
|   |      |      |      |      |
|---|------|------|------|------|
| 22| 3633 | 3633 | 1210 | 258  |
| 19| 3786 | 3786 | 1261 | 258  |
|  5| 5448 | 4011 | 1336 | 257  |
|  2| 3459 | 2190 | 1152 | 258  |
|  4| 3207 | 2952 |  983 | 260  |
|  3| 3027 | 3027 | 1008 | 255  |
|  2| 3264 | 2928 |  975 | 257  |
|  1| 3050 | 2955 |  984 | 257  |
|  2| 3313 | 2973 |  990 | 257  |
|  6| 1712 |   NA |  569 | 257  |
|  1| 3182 |   NA | 1059 | 300  |
|  9| 3321 | 2997 |  998 | 257  |
|  2| 3156 | 3156 | 1051 | 258  |
|  1| 3830 | 2889 |  962 | 260  |
|  3|  504 |  504 |  167 |   85 |
|  2| 3886 | 2898 |  965 | 260  |
|  1| 3784 | 2994 |  997 | 260  |
| 25| 3975 | 3021 | 1006 | 285  |
|  4| 3175 | 2979 |  992 | 247  |
| 14| 4541 | 3186 | 1061 | 264  |
|  8| 4131 | 3030 | 1009 | 260  |
|  7| 2636 | 2469 |  822 | 254  |
|  X|  516 |   NA |  172 |  138 |
| 21| 2739 | 2469 |  822 | 256  |
| 27| 3400 | 2463 |  820 | 277  |
| 26| 3944 | 2469 |  822 | 277  |
|  6| 2562 | 2409 |  802 | 277  |
|  7| 2974 | 2403 |  800 | 277  |
| 21| 4483 | 3615 | 1204 | 270  |
|  7| 4770 | 3876 | 1291 | 268  |
|  3| 3906 | 3906 | 1301 | 270  |
|  3| 4331 | 3477 | 1158 | 278  |
|  8| 4695 | 3399 | 1132 | 278  |
|  7| 3775 | 3318 | 1105 | 283  |
|  7| 5781 | 3558 | 1185 | 266  |
| 19| 4706 | 4104 | 1367 | 274  |
| 25| 4751 |   NA | 1422 | 275  |
| 18| 4631 |   NA | 1431 | 320  |
|  4| 4823 | 4155 | 1384 | 261  |
| 22| 4489 | 4206 | 1401 | 253  |
|  8| 3259 | 2610 |  869 | 281  |
| 12| 3416 | 2925 |  974 | 334  |
|  7| 3825 | 2895 |  964 | 330  |
|  6| 5078 | 2967 |  988 | 336  |
|  6| 3270 | 3270 | 1089 | 358  |
|  7| 4452 | 3312 | 1103 | 359  |
| 28| 3541 | 3342 | 1113 | 284  |
|  3| 3299 | 2727 |  908 | 307  |
|  8| 4006 | 2823 |  940 | 307  |
|  1| 2593 | 1617 |  538 | 267  |
|   |     |     |     |     |
|---|-----|-----|-----|-----|
| 8 | 660 | 660 | 219 | 218 |
| 8 | 2114| 1506| 501 | 251 |
| 13| 1353| 1353| 450 | 253 |
| 2 | 2195| 1584| 527 | 250 |
| 9 | 3436| 1545| 514 | 258 |
| 9 | 2409| 1614| 537 | 250 |
| 13| 2046| 1512| 503 | 251 |
| 2 | 2080| 1530| 509 | 251 |
| 14| 2750| 1539| 512 | 252 |
| 13| 1697| 1629| 542 | 249 |
| 13| 1485| 1485| 494 | 251 |
| 24| 4997| 1626| 541 | 250 |
| 8 | 2532| 1818| 605 | 249 |
| 11| 3947| 1854| 617 | 249 |
| X | 1965| 1965| 654 | 252 |
| X | 2577| 1980| 659 | 252 |
| 7 | 4393| 1863| 620 | 250 |
| 6 | 2538| 1956| 651 | 250 |
| 6 | 2312| 1584| 527 | 252 |
| 3 | 3631| 3411| 1136| 269 |
| 8 | 4625| 3378| 1125| 269 |
| 5 | 1592| 1269| 422 | 269 |
| 3 | 2603| 2388| 795 | 275 |
| 8 | 3538| 2514| 837 | 273 |
| 21| 3380| 2478| 825 | 272 |
| 12| 4080| 4080| 1359| 328 |
| 7 | 4383| 4068| 1355| 325 |
| 6 | 5998| 4071| 1356| 327 |
| X | 2215| 2157| 718 | 310 |
| 22| 2823| 1866| 621 | 268 |
| 5 | 2177| 1743| 580 | 279 |
| 5 | 2590| 1386| 461 | 269 |
| 25| 3086| 1944| 647 | 266 |
| 17| 2274| 1917| 638 | 271 |
| 8 | 2192| 1893| 630 | 258 |
| 3 | 1569| 1569| 522 | 260 |
| 21| 6561| 6048| 2015| 283 |
| 5 | 7871| 7608| 2535| 246 |
| 3 | 3020| 2508| 835 | 261 |
| 5 | 3332| 2685| 894 | 239 |
| 1 | 3425| 2901| 966 | 240 |
| 10| 3312| 3312| 1103| 260 |
| 18| 1077| 1077| 358 | 193 |
| 29| 3595| 2595| 864 | 260 |
| 28| 3147| 3147| 1048| 275 |
| 2 | 2778| 2403| 800 | 244 |
| 9 | 3388| 1740| 579 | 248 |
| X | 2355| 1821| 606 | 258 |
| 4 | 2492| 2298| 765 | 260 |
| 19| 2913| 2334| 777 | 264 |
|   |     |     |     |     |
|---|-----|-----|-----|-----|
| 17| 1836| 1836| 611 | 262 |
| 22| 3209| 2007| 668 | 260 |
|   | 3794| 2358| 785 | 264 |
| 23| 2403| 1998| 665 | 269 |
| 14| 1688| 1623| 540 | 267 |
| 10| 1802| 1512| 503 | 261 |
| 15| 1884| NA  | 628 | 215 |
|   | 2494| 1512| 503 | 288 |
| 2 | 2808| 1530| 509 | 288 |
|   | 2578| 1518| 505 | 288 |
| 2 | 1662| 1479| 492 | 288 |
| 28| 4059| 1599| 532 | 288 |
| 6 | 3498| 1509| 502 | 288 |
| 8 | 2060| 1500| 499 | 288 |
| 2 | 4428| 1542| 513 | 281 |
| 22| 1833| 1539| 512 | 291 |
| 2 | 3823| 2745| 914 | 307 |
| 5 | 1716| 1716| 571 | 312 |
| 22| 4280| 1704| 567 | 295 |
| 15| 1701| 1359| 452 | 257 |
| 18| 2323| 1407| 468 | 263 |
| 14| 759 | 759 | 252 | 177 |
| VAIK | HRD | DFG | Catalytic activity |
|------|-----|-----|--------------------|
| YAMK | YRD | DFG | Active             |
| YAMK | YRD | DFG | Active             |
| YAMK | YRD | DFG | Active             |
| YAMK | HRD | DFG | Active             |
| FAMK | HRD | DFG | Active             |
| FAMK | HRD | DFG | Active             |
| YAMK | HRD | DFG | Active             |
| YAMK | HRD | DFD | Active             |
| ---   | HRD | DFG | Inactive           |
| YATK  | HRD | DFG | Active             |
| YAMK  | HRD | DFG | Active             |
| YAMK  | HRD | DFG | Active             |
| YAMK  | HRD | DFG | Active             |
| YAMK  | YRD | DFG | Active             |
| YAMK  | YRD | DFG | Active             |
| YAMK  | YRD | DFG | Active             |
| FALK  | YRD | DFG | Active             |
| YAIK  | HRD | DFG | Active             |
| YAMK  | YRD | DFG | Active             |
| YAMK  | YRD | DFG | Active             |
| YAIK  | YRD | DFG | Active             |
| YAVK  | YRD | DFG | Active             |
| YAIK  | YRD | DFG | Active             |
| YAVK  | YRD | DFG | Active             |
| FAIK  | YRD | DFG | Active             |
| YAVK  | YRD | DFG | Active             |
| FAIK  | YRD | DFG | Active             |
| FAMK  | YRD | DFG | Active             |
| FAIK  | YRD | DFG | Active             |
| FAMK  | YRD | DFG | Active             |
| FAIK  | YRD | DFG | Active             |
| FAIK  | YRD | DFG | Active             |
| YAIK  | YRD | DFG | Active             |
| YAMK  | YRD | DFG | Active             |
| FAMK  | YRD | DFG | Active             |
| YAIK  | YRD | DFG | Active             |
| YAMK  | YRD | DFG | Active             |
| FAMK  | YRD | DFG | Active             |
| YAMK  | YRD | DFG | Active             |
| YAMK  | YRD | DFG | Active             |
| YAMK  | YRD | DFG | Active             |
| YAMK  | YRD | DFG | Active             |
| YAMK  | YRD | DFG | Active             |
| YAMK  | YRD | DFG | Active             |
|     |     |     |     |
|-----|-----|-----|-----|
| YAMK | YRD | DFG | Active |
| YAMK | YRD | DFG | Active |
| YAMK | YRD | DFG | Active |
| YAMK | YRD | DFG | Active |
| LKTE | CRD | YFS | Inactive |
| LHLE | CRD | YFG | Inactive |
| FAVK | HRD | DFG | Active |
| YAVK | YRD | DFG | Active |
| YAVK | YRD | DFG | Active |
| YAVK | YRD | DFG | Active |
| YMNK | HRD | DFN | Active |
| YAMK | HRD | DFN | Active |
| YAMK | HRD | DFN | Active |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
| FLVK | IGDRH | DFG | Active |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
|      |     |     | Atypical |
| Code  | Location | Status | Notes |
|-------|----------|--------|-------|
| VAIK  | HRD      | DFG    | Active|
| VALK  | HRD      | DFG    | Active|
| FAVK  | HRD      | DFG    | Active|
| FALK  | HRD      | DFG    | Active|
| YAAK  | HRD      | DFG    | Active|
| YAAK  | HRD      | DFG    | Active|
| YAAK  | HRD      | DFG    | Active|
| YALK  | HRD      | DFG    | Active|
| VAVK  | HRD      | DFG    | Active|
| VAVK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| RAVK  | HKD      | DLG    | Active|
| VAVK  | HRD      | DFG    | Active|
| VAVK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| VAIK  | HRD      | DFG    | Active|
| HTCK  | HRN      | DFH    | Inactive|
| FAVK  | HRD      | GFG    | Inactive|
| YAAK  | HFD      | DFG    | Active|
| YAAK  | HFD      | DFG    | Active|
| YAAK  | HFD      | DFG    | Active|
| FAAK  | HLD      | DFG    | Active|
| YAAK  | HLD      | DFG    | Active|
| YALK  | HRD      | DFG    | Active|
| FALK  | HRD      | DFG    | Active|
| YAMK  | HRD      | DFG    | Active|
| FALK  | HRD      | DFG    | Active|
| CALK  | HRD      | DFG    | Active|
| FALK  | HRD      | DFG    | Active|
| YAVK  | HRD      | DLG    | Active|
| YAVK  | HRD      | DLG    | Active|
| LAAK  | HLD      | DFG    | Active|
| LAAK | HLD | DFG | Active |
|------|-----|-----|--------|
| LAAK | HLD | DFG | Active |
| WAGK | HLD | DFG | Active |
| YMAK | HFD | EFG | Inactive |
| YAVK | HRD | DFG | Active |
| FAVK | HRD | DFG | Active |
| VAIK | HRD | DFG | Active |
| VAIK | HRD | DFG | Active |
| VAVK | HCD | DFG | Active |
| VAIK | HCD | DFG | Active |
| VAIK | HRD | DFG | Active |
| VAIK | HRD | DFG | Active |
| LRCK | LGD | SLE | Inactive |
| LVCK | LRD | SLE | Inactive |
| YICK | LRD | NLE | Inactive |
| CAAK | HLD | DFG | Active |
| FAAK | HLD | DFG | Active |
| VAVK | HLD | DLE | Active |
| VAIK | HRD | DFG | Active |
| VAVK | HRD | DFG | Active |
| VAIK | HRD | DFG | Active |
| VAIK | HRD | DFG | Active |
| VAIK | GRD | DFG | Active |
| VAIK | HRD | DFG | Active |
| VAVK | HRD | DFG | Active |
| VAIK | HRD | DFG | Active |
| VAIK | HRD | DFG | Active |
| VAIK | HRD | DFG | Active |
| VAIK | HRD | DFG | Active |
| VALK | HRD | DFG | Active |
| VALK | HRD | DFG | Active |
| CVVK | HGD | DYG | Active |
| HVIK | HGD | DYG | Active |
| HQDK | HGN | GYG | Inactive |
| VAMK | HRD | DFG | Active |
| VALK | HRD | DFG | Active |
| VALK | HRD | DFG | Active |
| VALK | HRD | DFG | Active |
| VALK | HRD | DFG | Active |
| VALK | HRD | DFG | Active |
| VALK | HRD | DFG | Active |
| VALK | HRD | DFG | Active |
| VALK | HRD | DMG | Active |
| YALK | HRD | DMG | Active |
| YALK | HRD | DFG | Active |
| VALK | HRD | DFG | Active |
| VALK | HRD | DFG | Active |
|------|-----|-----|--------|
| VALK | HRD | DFG | Active |
| VALK | HRD | DFG | Active |
| VALK | HRD | DFG | Active |
| VALK | HRD | DFG | Active |
| VALK | HRD | DFG | Active |
| VALK | HRD | DFG | Active |
| VAIR | HRD | DFG | Active |
| VAIR | HRD | DFG | Active |
| VELK | HRD | DFG | Active |
| VAVK | HTD | DFG | Active |
| VALK | HTD | DWG | Active |
| VALK | HTD | DFG | Active |
| VAVK | HTD | DFG | Active |
| VAIR | HCD | DFG | Active |
| VAIR | HCD | DFG | Active |
| VALK | HCD | DFG | Active |
| VALK | HCD | DFG | Active |
| VAIR | HAD | DFG | Active |
| VAIR | HAD | DFG | Active |
| VAIR | HAD | DFG | Active |
| VAVK | HAD | DFG | Active |
| VAIR | HAD | DFG | Active |
| VAIR | HAD | DFG | Active |
| VAVK | HAD | DFG | Active |
| VAIR | HRD | DFG | Active |
| VAIR | HRD | DFG | Active |
| VAVK | HRD | DFG | Active |
| VAVK | HRD | DFG | Active |
| VALK | HRD | DFG | Active |
| VALK | HRD | DFG | Active |
| VAVK | HRD | DFG | Active |
| VAVK | HRD | DFG | Active |
| VALK | HRD | DFG | Active |
| VAMK | HTD | DLG | Active |
| VAMK | HTD | DLG | Active |
| LALK   | HRD   | DFG   | Active |
|-------|-------|-------|--------|
| VALK  | HRD   | DFG   | Active |
| VALK  | HRD   | DFG   | Active |
| VTLK  | RRD   | LIS   | Inactive |
| FALK  | HGD   | DLG   | Active |
| TIIK  | HGD   | DFS   | Active |
| AVVK  | HGD   | DFG   | Active |
| YAMK  | HRD   | DFG   | Active |
| YAMK  | HRD   | DFG   | Active |
| IALK  | HRD   | DFG   | Active |
| VVVK  | HRD   | DWG   | Active |
| VVVK  | HRD   | DWG   | Active |
| VALK  | HRD   | TLN   | Inactive |
| IAIK  | HRD   | DLG   | Active |
| IAIK  | HRD   | DLG   | Active |
| VAVK  | HRD   | DFG   | Active |
| FAIK  | HRD   | DFG   | Active |
| VAVK  | HRD   | DFG   | Active |
| VAVK  | HRD   | DFG   | Active |
| CALK  | HRD   | DFG   | Active |
| YALK  | HRD   | DFG   | Active |
| YALK  | HRD   | DFG   | Active |
| YVIK  | HRD   | DFG   | Active |
| LAMK  | HRD   | DFG   | Active |
| KVLK  | HRD   | DFG   | Active |
| LVWK  | HRD   | DFG   | Active |
| FAMK  | HRD   | DFG   | Active |
| YVIK  | HRD   | DLG   | Active |
| CVIK  | HRD   | DFG   | Active |
| VALK  | HRD   | DLG   | Active |
| VALK  | HRD   | DLG   | Active |
| VIIFK | HRD   | DFG   | Active |
| VVVK  | HRD   | DYG   | Active |
| MALK  | HRD   | DFG   | Active |
| LALK  | YRD   | DFG   | Active |
| VALK  | HAD   | DLG   | Active |
| LAIK  | HRD   | DFG   | Active |
| YAVK  | HRD   | NFL   | Inactive |
| YAVK  | HCD   | NFS   | Inactive |
| VAVK  | HRD   | DFG   | Active |
| VAVK  | HRD   | DFG   | Active |
| VKAK  |       |       | partial |
| VTKV  | HRS   | NLE   | Inactive |
| VVWN  | HGN   | VAP   | Inactive |
| VVWN  | HGN   | VWH   | Inactive |
| GALK  | HAD   | DFG   | Active |
| VAVK  | HQD   | DFD   | Active |
| TKVK  | HRN   | DLS   | Inactive |
| R | C  | S  | A  |
|---|----|----|----|
| VALS | TRV | NFS | Inactive |
| ILLK | HGS | DFD | Inactive |
| VALK | LLD | DLD | Active |
| CALK | HRD | DLG | Active |
| YAVK | HRD | DFG | Active |
| YAIK | HRD | DFG | Active |
| YVIK | HRD | DFG | Active |
| FAGK | HRD | DFG | Active |
| YAAK | HRD | DFG | Active |
| YAVK | HRD | DFG | Active |
| VAIK | HRD | DFG | Active |
| FALK | HRD | DLG | Active |
| VSIF | HNN | GLD | Inactive |
| VAVF | HGN | GFD | Inactive |
| ASVF | ARD | GME | Inactive |
| LVLS | YGH | DLE | Inactive |
| LTPN | HRA | KFG | Inactive |
| AAVK | HYD | DFG | Active |
| VAVK | HYD | DFG | Active |
| WAVK | HGD | DVG | Active |
| HAIK | HSD | DFG | Active |
| VALK | HRD | DFG | Active |
| VAVK | HRD | DFG | Active |
| VAIK | HRD | DFG | Active |
| VAIL | HGD | DYG | Inactive |
| VPIK | HGS | DYG | Inactive |
| VWLK | HGR | DHG | Inactive |
| VILK | HGR | DYG | Inactive |
| MAVK | HRD | DFG | Active |
| LAVK | HRD | DFG | Active |
| LASK | HRD | DFG | Active |
| MAMK | HRD | DFG | Active |
| IAIAK | HRD | DFG | Active |
| IAIAK | HRD | DFG | Active |
| IAIAK | HRD | DFG | Active |
| IAIAK | HRD | DFG | Active |
| VAIAK | HRD | DFG | Active |
| VAIAK | HRD | DFG | Active |
| Code  | Type | Status |
|-------|------|--------|
| AAVK  | HRD  | DFG    | Active |
| VALK  | HRD  | DFG    | Active |
| AAVK  | HRD  | DFG    | Active |
| AAIK  | HRD  | DFG    | Active |
| AAIK  | HRD  | DFG    | Active |
| AAIK  | HRD  | DFG    | Active |
| TAVK  | HRD  | DFG    | Active |
| VAIK  | HRD  | DFG    | Active |
| AAVK  | HRD  | DFG    | Active |
| VAIK  | HRD  | DFG    | Active |
| VAIK  | HRD  | DFG    | Active |
| VAVK  | HRD  | DFG    | Active |
| VAVK  | HRD  | DFG    | Active |
| AAKA  | HRD  | DFG    | Active |
| AAKA  | HRD  | DFG    | Active |
| VTVR  | HRS  | GLR    | Inactive |
| VTIK  | HRS  | GLS    | Inactive |
| VAIK  | HRD  | DFG    | Active |
| VAIK  | HRD  | DFG    | Active |
| VAIK  | HRD  | DFG    | Active |
| VAIK  | HRD  | DFG    | Active |
| VAIK  | HRD  | DFG    | Active |
| VAIK  | HRD  | DFG    | Active |
| MARK  | HRD  | DFG    | Active |
| MARK  | HRD  | DFG    | Active |
| MAVK  | HRD  | DFG    | Active |
| MAVK  | HRD  | DFG    | Active |
| MAVK  | HRD  | DFG    | Active |
| MAVK  | HRD  | DFG    | Active |
| MAVK  | HRD  | DFG    | Active |
| IAUK  | HRD  | DFG    | Active |
| MACK  | HHD  | DFG    | Active |
| CAVK  | HGD  | DFG    | Active |
| VAVK  | HRD  | DFG    | Active |
| VAVK  | HRD  | DFG    | Active |
| VAVK  | HRD  | DFG    | Active |
| VAVK  | HRD  | DFG    | Active |
| VAVK  | HRD  | DFG    | Active |
| VAVK  | HRD  | DFG    | Active |
| VAVK  | HRD  | DFG    | Active |
| VAVK  | HRD  | DFG    | Active |
| VAVK  | HRD  | DFG    | Active |
| VAVK  | HRD  | DFG    | Active |
| VAVK  | HRD  | DFG    | Active |
| VAVK  | HRD  | DFG    | Active |
| VAVK  | HRD  | DFG    | Active |
| Code  | Code  | Code  | Status |
|-------|-------|-------|--------|
| VAIK  | HRD   | DFG   | Active |
| VAIK  | HRD   | DFG   | Active |
| VCIR  | HRN   | DFG   | Inactive |
| VAIK  | HRD   | DFG   | Active |
| VAIK  | HRD   | DFG   | Active |
| VAIK  | HRD   | DFG   | Active |
| VAIK  | HRD   | DFG   | Active |
| VAIK  | HRD   | DFG   | Active |
| VAIK  | HRD   | DFG   | Active |
| VAVH  | HRG   | GFG   | Inactive |
| VAIK  | HRD   | DFG   | Active |
| VAIK  | HRD   | DFG   | Active |
| partial |       |       |         |
| VAIK  | HRD   | DFG   | Active |
| VAIK  | HRD   | DFG   | Active |
| VAIK  | HRD   | DFG   | Active |
| VAIK  | HRD   | DFG   | Active |
| VAIQ  | HRS   | RLG   | Inactive |
| VAIK  | HRD   | DFG   | Active |
| VAVK  | HRD   | DFG   | Active |
| VAVK  | HRD   | DFG   | Active |
| VAVK  | HRD   | DFG   | Active |
| VAVK  | HRD   | DFG   | Active |
| VAVK  | HRD   | DFG   | Active |
| VAVK  | HRD   | DFG   | Active |
| VAVK  | HRD   | DFG   | Active |
| VAVK  | HRD   | DFG   | Active |
| VAVK  | HRD   | DFG   | Active |
| VAVK  | HRD   | DFG   | Active |
| VAVK  | HSD   | DYG   | Active |
| VVVK  | HSD   | DYG   | Active |
| VVVK  | HSD   | DYG   | Active |
| CAIK  | HRD   | DFG   | Active |
| CAVK  | HRD   | DFG   | Active |
| VAVK  | HRD   | DFG   | Active |
| VAVK  | HRD   | DFG   | Active |
| VAVK  | HRD   | DFG   | Active |
| VAVK  | HRD   | DFG   | Active |
| VAVK  | HRD   | DFG   | Active |
| VAVK  | HRD   | DFG   | Active |
| AFVK  | HKD   | DNA   | Active |
| Sequence | Side 1 | Side 2 | Activity |
|----------|--------|--------|----------|
| AFVK     | HQD    | DNA    | Active   |
| VAIK     | HRD    | DFG    | Active   |
| VAIK     | HRD    | DFG    | Active   |
| VAVK     | HRD    | DFG    | Active   |
| VAVK     | HRD    | DFG    | Active   |
| VAIK     | HRD    | DFG    | Active   |
| VAVK     | HRD    | DFG    | Active   |
| VAIK     | HRD    | DFG    | Active   |
| VAVK     | HRD    | DFG    | Active   |
| VAIK     | HRD    | DFG    | Active   |
| VAVK     | HRD    | DFG    | Active   |
| VAIK     | HRD    | DFG    | Active   |
| AAIK     | HRD    | DFG    | Active   |
| AAIK     | HRD    | DFG    | Active   |
| VTLK     | HGD    | GLG    | Inactive |
| VAVK     | HRD    | DFG    | Active   |
| VAVK     | HRD    | DFG    | Active   |
| VAVK     | HRD    | DFG    | Active   |
| VAVK     | HRD    | DFG    | Active   |
| VAVK     | HRD    | DFG    | Active   |
| VAVK     | HRD    | DFG    | Active   |
| YAVK     | HGD    | DFG    | Active   |
| FVFK     | HSN    | HSM    | Inactive |
| YAIK     | CGS    | DFA    | Inactive |
| VAVK     | HRD    | DFG    | Active   |
| QAIK     | HRD    | DFG    | Active   |
| QAIK     | HRD    | DFG    | Active   |
| MVLK     | HRD    | DFG    | Active   |
| NVHK     | HRD    | DFG    | Active   |
| VAVK     | FCD    | DYG    | Active   |
| VAVK     | YRD    | DYG    | Active   |
| VAIK     | HRD    | DFG    | Active   |
| VAVK     | HRD    | DFG    | Active   |
| VAIK     | HRD    | DFG    | Active   |
| VAVK     | HRD    | DFG    | Active   |
| VAVK     | HRD    | DFG    | Active   |
| VAVK     | HRD    | DFG    | Active   |
| VAVK     | HRD    | DFG    | Active   |
| VAVK     | HRD    | DFG    | Active   |
| VAIK     | HRD    | DFG    | Active   |
| VAVK     | HRD    | DFG    | Active   |
| VAVK     | HRD    | DFG    | Active   |
| VAIR     | HKD    | DFG    | Inactive |
| VAIR | HKD  | DFG  | Inactive |
|------|------|------|----------|
| VAVK | HRD  | DFG  | Active   |
| LAIK | HLD  | DFG  | Active   |
| VILK | HRD  | DLG  | Active   |
| VAVK | HHD  | DFG  | Active   |
| VAVK | HRD  | DFG  | Active   |
| VAVK | HRD  | DLG  | Active   |
| VAVK | HRD  | DLG  | Active   |
| VAVK | HRD  | DLG  | Active   |
| EAAK | HLD  | DFG  | Active   |
| VAVK | HRD  | DFG  | Active   |
| VAVK | HRD  | DFG  | Active   |
| VAVK | HRD  | DFG  | Active   |
| VAVK | HRD  | DFG  | Active   |
| VAVK | HRD  | DFG  | Active   |
| VAVK | HRD  | DFG  | Active   |
| IVVK | RHA  | ---  | Inactive |
| VAIK | HRN  | ELS  | Inactive |
|      |      | partial |
| Ensemble Pep | Gene | Transcript | % identity in KD |
|--------------|------|------------|------------------|
|              |      |            | 97,7             |
|              |      |            | 100              |
|              |      |            | 100              |
| ENSBTAP00000015459 | ENSBTAG00000011639 | ENSBTAT00000015459 | 96,7             |
|              |      |            | 99,3             |
|              |      |            | 98,5             |
|              |      |            | 100              |
|              |      |            | 98,1             |
|              |      |            | 91,7             |
|              |      |            | 100              |
|              |      |            | 96,6             |
|              |      |            | 84,8             |
| ENSBTAP00000001500 | ENSBTAG0000001126 | ENSBTAT0000001500 | 98,9             |
|              |      |            | 93,2             |
|              |      |            | 91,3             |
|              |      |            | 88,7             |
| ENSBTAP00000007991 |      |            | 97,8             |
|              |      |            | 99,3             |
|              |      |            | 97,8             |
|              |      |            | 100              |
| ENSBTAP00000018430 | ENSBTAG00000013876 | ENSBTAT00000018430 | 92,4             |
|              |      |            | 98,7             |
|              |      |            | 96,4             |
|              |      |            | 99,7             |
|              |      |            | 99,3             |
|              |      |            | 99,6             |
|              |      |            | 100              |
|              |      |            | 89,9             |
|              |      |            | 98,8             |
|              |      |            | 100              |
| ENSBTAP00000024029 | ENSBTAG00000018049 | ENSBTAT00000024029 | 99,6             |
| ENSBTAP00000023654 | ENSBTAG00000017788 | ENSBTAT00000023654 | 99,2             |
|              |      |            | 99,6             |
|              |      |            | 99,2             |
|              |      |            | 88,6             |
|              |      |            | 99,6             |
|              |      |            | 98,5             |
|              |      |            | 98,4             |
|              |      |            | 100              |
|              |      |            | 99,2             |
|              |      |            | 99,2             |
| ENSBTAP00000045293 | ENSBTAG00000033983 | ENSBTAT00000048212 | 99,2             |
|              |      |            | 94,2             |
|              |      |            | 96,3             |
| ENSBTAP00000020910 |      |            | 97,4             |
|              |      |            | 100              |
| ENSBTAP00000043326 | ENSBTAG00000014351 | ENSBTAT00000045990 | 98,1             |
| Gene ID                  | ENSBTAG00000022777 | ENSBTAT00000029173 | 98.8 |
|-------------------------|------------------|-------------------|------|
| ENSBTAP00000029173      |                  |                   | 96.9 |
| ENSBTAP00000039020      |                  |                   | 99.6 |
| ENSBTAP00000019220      |                  |                   | 81.9 |
| ENSBTAP00000013805      |                  |                   | 95.3 |
| ENSBTAP00000010716      |                  |                   | 93.9 |
| ENSBTAP00000032957      |                  |                   | 94.2 |
| ENSBTAP00000018325      |                  |                   | 98.1 |
| ENSBTAP00000015445      |                  |                   | 96.9 |
| Gene1       | Gene2                   | Gene3                   | Value1 | Value2 | Value3 | Value4 | Value5 | Value6 | Value7 | Value8 | Value9 | Value10 |
|------------|-------------------------|-------------------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|---------|
| ENSBTAP00000008354 | ENSBTAG00000006359 | ENSBTAT00000008354     | 93,4   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 97,7   |        |        |        |        |        |        |        |        |         |
| ENSBTAP00000007991 | ENSBTAG00000006080 | ENSBTAT00000007991     | 98,9   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 96,5   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 94,8   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 98,1   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 98,8   |        |        |        |        |        |        |        |        |         |
| ENSBTAP00000009545 | ENSBTAG00000007256 | ENSBTAT00000009545     | 94,5   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 96,9   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 100    |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 98,4   |        |        |        |        |        |        |        |        |         |
| ENSBTAP00000009942 | ENSBTAG00000007556 | ENSBTAT00000009942     | 99,6   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 100    |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 95,5   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 98,3   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 99,6   |        |        |        |        |        |        |        |        |         |
| ENSBTAP00000008672 | ENSBTAG00000006601 | ENSBTAT00000008672     | 88,9   |        |        |        |        |        |        |        |        |         |
| ENSBTAP00000001378 | ENSBTAG00000001037 | ENSBTAT00000001378     | 86,8   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 94,9   |        |        |        |        |        |        |        |        |         |
| ENSBTAP00000010653 | ENSBTAG00000008098 | ENSBTAT00000010653     | 100    |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 93,3   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 98,4   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 92,7   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 93,9   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 96,1   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 97,9   |        |        |        |        |        |        |        |        |         |
| ENSBTAP00000015986 | ENSBTAG00000012047 | ENSBTAT00000015986     | 100    |        |        |        |        |        |        |        |        |         |
| ENSBTAP00000027857 | ENSBTAG00000020904 | ENSBTAT00000027857     | 100    |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 100    |        |        |        |        |        |        |        |        |         |
| ENSBTAP00000024657 | ENSBTAG00000018524 | ENSBTAT00000024657     | 99,2   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 99,2   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 99,2   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 99,6   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 99,6   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 95,5   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 90,9   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 82,5   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 98,9   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 98,6   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 91,2   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 96,1   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 97,9   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 99     |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 99,6   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 97,9   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 100    |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 94,3   |        |        |        |        |        |        |        |        |         |
|            |                         |                         | 98,3   |        |        |        |        |        |        |        |        |         |
| ENSBTAP000000000016 | ENSBTAG000000000013 | ENSBTAT000000000016 | 99,7 |
|---------------------|---------------------|---------------------|------|
|                     |                     |                     | 99,3 |
|                     |                     |                     | 97,9 |
|                     |                     |                     | 98,6 |
|                     |                     | ENSBTAT000000000016 | 97,9 |
|                     |                     |                     | 92,6 |
|                     |                     |                     | 100  |
|                     |                     |                     | 93   |
|                     |                     |                     | 92,6 |
|                     |                     |                     | 96,1 |
|                     |                     |                     | 96,1 |
|                     |                     |                     | 95,8 |
|                     |                     |                     | 95,8 |
|                     |                     |                     | 89,4 |
|                     |                     |                     | 97,2 |
|                     |                     |                     | 100  |
| ENSBTAP000000026195 | ENSBTAG00000032234  | ENSBTAT00000026195  | 99,7 |
| ENSBTAP00000026189  | ENSBTAG00000019652  | ENSBTAT00000026189  | 99,7 |
|                     |                     |                     | 100  |
|                     |                     |                     | 96,8 |
|                     |                     |                     | 93,9 |
|                     |                     |                     | 99,1 |
|                     |                     |                     | 99,7 |
|                     |                     |                     | 98,2 |
|                     |                     |                     | 98,3 |
|                     |                     |                     | 100  |
| ENSBTAP00000015200  | ENSBTAG0000011437   | ENSBTAT0000015200   | 98,2 |
|                     |                     |                     | 95,6 |
|                     |                     |                     | 98,6 |
|                     |                     |                     | 100  |
|                     |                     |                     | 99,7 |
|                     |                     |                     | 97   |
|                     |                     |                     | 99   |
|                     |                     |                     | 80   |
|                     |                     |                     | 99,7 |
| ENSBTAP0000000744   | ENSBTAG000000570    | ENSBTAT0000000744   | 99,7 |
|                     |                     |                     | 100  |
|                     |                     |                     | 100  |
|                     |                     |                     | 100  |
|                     |                     |                     | 89,8 |
|                     |                     |                     | 95,4 |
|                     |                     |                     | 94,7 |
|                     |                     |                     | 98,2 |
|                     |                     |                     | 99,3 |
| ENSBTAP00000032957  | ENSBTAG000012114    | ENSBTAT000033031    | 91,8 |
|                     |                     |                     | 91,4 |
|                     |                     |                     | 95,3 |
|                     |                     |                     | 96,5 |
| Gene ID            | Gene ID            | Gene ID            |
|-------------------|-------------------|-------------------|
| ENSBTAP00000023740 | ENSBTAG00000017860 | ENSBTAT00000023740 |
|                   |                   |                   |
|                   |                   |                   |
| ENSBTAP00000009441 | ENSBTAG00000007173 | ENSBTAT00000009441 |
|                   |                   |                   |
|                   |                   |                   |
| ENSBTAP00000017759 | ENSBTAG00000013347 | ENSBTAT00000017759 |
|                   |                   |                   |
|                   |                   |                   |
| ENSBTAP0000002122  | ENSBTAG00000001618 | ENSBTAT0000002122  |
|                   |                   |                   |
|                   |                   |                   |
| ENSBTAP00000025471 |                   |                   |
|                   |                   |                   |
|                   |                   |                   |
| ENSBTAP00000029056 | ENSBTAG00000021798 | ENSBTAT00000029056 |
|                   |                   |                   |
|                   |                   |                   |
| ENSBTAP00000013238 | ENSBTAG00000010030 | ENSBTAT00000013238 |
|                   |                   |                   |
|                   |                   |                   |
| ENSBTAP00000018603 | ENSBTAG00000014000 | ENSBTAT00000018603 |
|                   |                   |                   |
|                   |                   |                   |
| ENSBTAP00000035173 | ENSBTAG00000010979 | ENSBTAT00000035295 |
|                   |                   |                   |
| Accession               | Accession               | Accession               | Score |
|------------------------|------------------------|------------------------|-------|
| ENSBTAP00000013549     | ENSBTAG00000010254     | ENSBTAT00000013549     | 99,6  |
| ENSBTAP00000015051     | ENSBTAG00000011322     | ENSBTAT00000015051     | 97,4  |
| ENSBTAP00000042917     | ENSBTAG00000010639     | ENSBTAT00000045536     | 98,1  |
| ENSBTAP00000019139     | ENSBTAG00000014393     | ENSBTAT00000019139     | 99,2  |
| ENSBTAP00000046377     | ENSBTAG00000035028     | ENSBTAT00000049489     | 100   |
| ENSBTAP00000040257     | ENSBTAG00000030201     | ENSBTAT00000042621     | 98,5  |
| ENSBTAP00000018713     | ENSBTAG00000014064     | ENSBTAT00000018713     | 98,5  |
| ENSBTAP00000020866     | ENSBTAG00000015713     | ENSBTAT00000020866     | 94,7  |
| ENSBTAP00000021631     | ENSBTAG00000016260     | ENSBTAT00000021631     | 96,3  |
| ENSBTAP00000013808     | ENSBTAG00000010460     | ENSBTAT00000013808     | 97,2  |
| ENSBTAP00000012197 | ENSBTAG00000009258 | ENSBTAT00000012197 |
|--------------------|-------------------|-------------------|
|                    |                   | 94,4              |
|                    |                   | 85                |
|                    |                   | 92,4              |
|                    |                   | 96,1              |
|                    |                   | 99,6              |
|                    |                   | 96,8              |
|                    |                   | 97,2              |
|                    |                   | 99,6              |
| ENSBTAP00000022534 | ENSBTAG00000016943| ENSBTAT00000022534|
|                    |                   | 99,2              |
|                    |                   | 84,1              |
|                    |                   | 100               |
|                    |                   | 98                |
|                    |                   | 96,4              |
| ENSBTAP00000022347 | ENSBTAG00000016799| ENSBTAT00000022347|
|                    |                   | 94                |
|                    |                   | 99,2              |
|                    |                   | 96,8              |
|                    |                   | 96,8              |
|                    |                   | 89,3              |
|                    |                   | 99,3              |
|                    |                   | 100               |
|                    |                   | 79,4              |
|                    |                   | 98,9              |
|                    |                   | 100               |
| ENSBTAP00000015530 | ENSBTAG00000010408| ENSBTAT00000015530|
|                    |                   | 100               |
|                    |                   | 95,7              |
|                    |                   | 92,3              |
|                    |                   | 96                |
|                    |                   | 87,4              |
|                    |                   | 82,8              |
|                    |                   | 89,2              |
|                    |                   | 94,1              |
|                    |                   | 99,2              |
|                    |                   | 95,9              |
|                    |                   | 96,5              |
|                    |                   | 85,4              |
| ENSBTAP00000030935 | ENSBTAG00000003325| ENSBTAT00000030970|
|                    |                   | 95,1              |
|                    |                   | 98                |
|                    |                   | 97,7              |
| ENSBTAP00000010292 | ENSBTAG00000007825| ENSBTAT00000010292|
|                    |                   | 99,2              |
| ENSBTAP00000004466 | ENSBTAG00000030977| ENSBTAT00000004466|
|                    |                   | 99,6              |
|                    |                   | 98,8              |
|                    |                   | 98,5              |
|                    |                   | 99,2              |
|                    |                   | 96,4              |
|                    |                   | 100               |
|                    |                   | 100               |
|                    |                   | 99,2              |
|                    |                   | 100               |
|                    |                   | 97,7              |
| ENSBTAP00000009766 | ENSBTAG00000007428 | ENSBTAT00000009766 | 94,8 |
|-------------------|-------------------|-------------------|------|
| 71,9              |                   |                   |      |
| ENSBTAP00000012302| ENSBTAG00000009343| ENSBTAT00000012302| 75,3 |
|                   |                   |                   | 98,3 |
|                   |                   |                   | 100  |
|                   |                   |                   | 100  |
| ENSBTAP00000022500| ENSBTAG00000016915| ENSBTAT00000022500| 99,3 |
|                   |                   |                   | 99,3 |
|                   |                   |                   | 99,7 |
| ENSBTAP00000025356| ENSBTAG00000019049| ENSBTAT00000025356| 99,7 |
|                   |                   |                   | 100  |
|                   |                   |                   | 99   |
| ENSBTAP00000024657|                   |                   | 99,7 |
|                   |                   |                   | 89,7 |
| ENSBTAP00000031759| ENSBTAG00000012016| ENSBTAT00000031813| 97   |
|                   |                   |                   | 99,2 |
|                   |                   |                   | 71,5 |
| % identity in Protein | Comments            |
|-----------------------|--------------------|
| 96,3                  |                    |
| 98,1                  |                    |
| 100                   |                    |
| 80,1                  |                    |
| 84,5                  | Insertion in human |
| 97                    | Insertion in human |
| 90,3                  | Deletion in human  |
| 93,9                  |                    |
| 97,8                  |                    |
| 97,2                  |                    |
| 98                    |                    |
| 95,3                  |                    |
| 75,6                  |                    |
| 97,1                  |                    |
| 87,4                  | Insertion/Deletion |
| 85,4                  |                    |
| 83                    |                    |
| 94,6                  | Insertion in human |
| 85,9                  | Insertion in human |
| 87,8                  | Deletion in human  |
| 73,6                  |                    |
| 83,8                  |                    |
| 94,9                  |                    |
| 70,5                  | Insertion in human |
| 99,4                  |                    |
| 99,1                  |                    |
| 99,4                  |                    |
| 98,9                  |                    |
| 85,6                  | Insertion in human |
| 92,3                  |                    |
| 99,1                  |                    |
| 93,1                  |                    |
| 97,8                  |                    |
| 98,4                  |                    |
| 98                    |                    |
| 87,7                  |                    |
| 99,2                  |                    |
| 98                    |                    |
| 95,9                  |                    |
| 88,5                  | Insertion in human |
| 97,2                  |                    |
| 95,4                  |                    |
| 97                    |                    |
| 89,1                  |                    |
| 90,9                  |                    |
| 95,7                  |                    |
| 99,4                  |                    |
| 93,4                  |                    |
|     | Insertion in human | Deletion in human | Insertion/Deletion |
|-----|-------------------|-------------------|-------------------|
| 96,7|                   |                   |                   |
| 99,9|                   |                   |                   |
| 98,9|                   |                   |                   |
| 96,1|                   |                   |                   |
| 88,5| Insertion in human|                   |                   |
| 72,9| Insertion in human|                   |                   |
| 81,9| Insertion in human|                   |                   |
| 96,8|                   |                   |                   |
| 95,9|                   |                   |                   |
| 98  |                   |                   |                   |
| 91,8|                   |                   |                   |
| 84,1|                   |                   |                   |
| 89,5| Deletion in human |                   |                   |
| 94,9|                   |                   |                   |
| 95,1|                   |                   |                   |
| 87,3|                   |                   |                   |
| 87  |                   |                   |                   |
| 87,6|                   |                   |                   |
| 83,8|                   |                   |                   |
| 78,4|                   |                   |                   |
| 96  |                   |                   |                   |
| 83,8| Deletion in human |                   |                   |
| 91,2|                   |                   |                   |
| 73,8| Insertion in human|                   |                   |
| 57,5| Insertion/Deletion |                   |                   |
| 74,4| Deletion in human |                   |                   |
| 89,1| Insertion in human|                   |                   |
| 97,4|                   |                   |                   |
| 93,5|                   |                   |                   |
| 96,4| Deletion in human |                   |                   |
| 79,2| Insertion in human|                   |                   |
| 90,7| Insertion in human|                   |                   |
| 79,2| Insertion in human|                   |                   |
| 95,9|                   |                   |                   |
| 96,4|                   |                   |                   |
| 94,7|                   |                   |                   |
| 97,4|                   |                   |                   |
| 96,4|                   |                   |                   |
| 90,8| Insertion in human|                   |                   |
| 89,8|                   |                   |                   |
| 93,4|                   |                   |                   |
| 77,8|                   |                   |                   |
| 99,5|                   |                   |                   |
| 98,7|                   |                   |                   |
| 97,8|                   |                   |                   |
| 88,4|                   |                   |                   |
| 87,1|                   |                   |                   |
| 95,8|                   |                   |                   |
| 97,1| Deletion in human |                   |                   |
| 47,7| Insertion/Deletion |                   |                   |
| Position | Modification       |
|----------|-------------------|
| 95,5     | Insertion in human|
| 49,3     | Insertion/Deletion|
| 95,7     |                   |
| 91       |                   |
| 85,3     | Insertion/Deletion|
| 91,4     |                   |
| 99,6     |                   |
| 98,9     |                   |
| 99,4     |                   |
| 95,6     | Insertion in human|
| 81,4     | Insertion in human|
| 96,5     | Deletion in human |
| 97,6     |                   |
| 99,1     | Deletion in human |
| 90,4     | Deletion in human |
| 95,8     |                   |
| 85,7     | Insertion in human|
| 84,6     | Deletion in human |
| 95,5     |                   |
| 97,6     |                   |
| 86,6     | Deletion in human |
| 98       | Insertion in human|
| 89,4     |                   |
| 93,8     |                   |
| 93,7     |                   |
| 80       | Insertion/Deletion|
| 64       | Deletion in human |
| 87,9     |                   |
| 89,6     | Insertion in human|
| 84,5     | Insertion in human|
| 90       | Insertion in human|
| 96,1     |                   |
| 75       |                   |
| 93,3     |                   |
| 97,5     | Deletion in human |
| 94,8     |                   |
| 93,2     | Deletion in human |
| 94,9     |                   |
| 89,4     |                   |
| 93       |                   |
| 89,4     |                   |
| 95,6     | Insertion/Deletion|
| 76,5     | Deletion in human |
| 92,8     |                   |
| 95,9     |                   |
| 96,6     |                   |
| 91,2     |                   |
| 95,1     | Deletion in human |
| 66,5     | Insertion in human|
|   |   |   |
|---|---|---|
| 80,9 | Deletion in human |   |
| 80,6 |   | Deletion in human |
| 74,4 | Insertion in human |   |
| 94,3 |   | Insertion in human |
| 96,3 |   |   |
| 98,7 |   |   |
| 84,1 |   |   |
| 94,8 |   |   |
| 93,5 | Insertion in human |   |
| 94,5 |   |   |
| 97,6 |   |   |
| 97,9 | Insertion in human |   |
| 86 |   | Insertion in human |
| 96,8 |   |   |
| 99,1 |   |   |
| 81,3 |   |   |
| 66,9 | Insertion in human |   |
| 91,7 |   |   |
| 97,1 | Deletion in human |   |
| 80,2 | Insertion in human |   |
| 98,2 |   |   |
| 84,1 |   |   |
| 90,8 |   |   |
| 95,9 |   |   |
| 85,3 | Deletion in human |   |
| 99,7 |   |   |
| 97,6 | Deletion in human |   |
| 98,7 | Deletion in human |   |
| 96 |   |   |
| 95,7 |   |   |
| 98,4 |   |   |
| 88,6 |   |   |
| 91,2 |   |   |
| 90,9 |   |   |
| 73,7 |   |   |
| 72,8 | Insertion in human |   |
| 98,7 |   |   |
| 98,7 |   |   |
| 88,5 |   |   |
| 93,1 |   |   |
| 97 |   |   |
| 97,5 |   |   |
| 99,7 |   |   |
| 96,8 |   |   |
| 98 |   |   |
| 93,3 |   |   |
| 98,4 |   |   |
| 96,1 |  |
| 93,8 |  |
| 93,6 | Insertion in human |
| 98 |  |
| 98,5 |  |
| 86,3 | Insertion in human |
| 98,2 |  |
| 90,4 |  |
| 92,5 |  |
| 89,7 | Insertion in human |
| 76,8 | Deletion in human |
| 86,3 | Deletion in human |
| 93,1 | Insertion in human |
| 84,7 | Insertion in human |
| 93,2 |  |
| 98,6 |  |
| 98,2 |  |
| 90,9 | Insertion in human |
| 98,4 | Deletion in human |
| 98,7 |  |
| 98,2 |  |
| 92,5 |  |
| 80,5 | Insertion in human |
| 98 |  |
| 96,7 |  |
| 94,5 |  |
| 76,2 | Deletion in human |
| 96,9 |  |
| 92,9 |  |
| 95,6 | Deletion in human |
| 93,1 | Insertion in human |
| 99,7 |  |
| 97,6 |  |
| 96,1 | Insertion in human |
| 88,4 | Insertion in human |
| 67,4 | Insertion in human |
| 99,2 | Deletion in human |
| 99,5 |  |
| 99,2 | Insertion/Deletion |
| 100 |  |
| 100 |  |
| 90,3 | Insertion in human |
| 94,8 |  |
| 92,9 |  |
| 91,5 |  |
| 87 |  |
| 79,8 |  |
| 89,9 | Deletion in human |
| 95,6 |  |
| 96,5 |  |
| Position | Event          |
|----------|----------------|
| 88,9     | Insertion in human |
| 93       | Insertion in human |
| 80,6     | Insertion in human |
| 78,6     | Insertion in human |
| 88,8     | Insertion in human |
| 88,2     | Insertion in human |
| 91,1     | Insertion in human |
| 90,2     | Insertion in human |
| 89,1     | Insertion in human |
| 99,7     | Insertion in human |
| 99,1     | Insertion in human |
| 70,9     | Insertion in human |
| 96,5     | Insertion in human |
| 93,3     | Insertion in human |
| 88       | Insertion in human |
| 97,1     | Insertion in human |
| 93,3     | Insertion in human |
| 85,4     | Insertion in human |
| 68,6     | Insertion in human |
| 94,4     | Insertion/Deletion |
| 81,6     | Insertion/Deletion |
| 78,6     | Insertion in human |
| 91,8     | Insertion in human |
| 89,9     | Insertion in human |
| 90,2     | Insertion in human |
| 80,1     | Insertion in human |
| 92,8     | Insertion in human |
| 84,4     | Insertion in human |
| 76,6     | Insertion in human |
| 90,4     | Insertion in human |
| 95,9     | Insertion in human |
| 98       | Insertion in human |
| 93,2     | Insertion in human |
| 96,1     | Insertion in human |
| 89,5     | Insertion in human |
| 77,7     | Insertion in human |
| 82,5     | Insertion in human |
| 85,4     | Insertion in human |
| 78,5     | Deletion in human |
| 90,4     | Insertion in human |
| 97,3     | Insertion in human |
| 99,4     | Deletion in human |
| 56,2     | Insertion/Deletion |
| 72,4     | Deletion in human |
| 99,4     | Insertion in human |
| 91,3     | Insertion in human |
| 99,5     | Insertion in human |
| 69,6     | Insertion in human |
| 54,5     | Deletion in human |
|    |          |                  |
|----|----------|-----------------|
| 76,4 |         |                  |
| 82,5 |         |                  |
| 95,1 |         |                  |
| 93,8 |         |                  |
| 89,4 |         |                  |
| 89,3 |         |                  |
| 80,4 |         |                  |
| 61,6 | Insertion in human |          |
| 94,9 |         |                  |
| 98,1 |         |                  |
| 92,1 |         |                  |
| 82,4 | Insertion in human |          |
| 91,5 |         |                  |
| 96,1 | Insertion in human |          |
| 70,6 | Insertion/Deletion |          |
| 94,6 |         |                  |
| 94,9 | Deletion in human |          |
| 94,7 | Insertion in human |          |
| 96,8 | Deletion in human |          |
| 88,9 |         |                  |
| 85,5 |         |                  |
| 88,2 |         |                  |
| 89,6 |         |                  |
| 86,8 |         |                  |
| 97  |         |                  |
| 83,2 | Deletion in human |          |
| 96,6 |         |                  |
| 87,5 | Insertion/Deletion |          |
| 91,9 |         |                  |
| 73  |         |                  |
| 81  |         |                  |
| 77,5 |         |                  |
| 92,3 |         |                  |
| 87  |         |                  |
| 92,6 |         |                  |
| 98,3 |         |                  |
| 86,6 | Deletion in human |          |
| 89,6 |         |                  |
| 85,3 |         |                  |
| 93,3 |         |                  |
| 95,6 |         |                  |
| 96,9 |         |                  |
| 91,5 | Insertion in human |          |
| 95  | Insertion in human |          |
| 87,4 |         |                  |
| 83,1 |         |                  |
| 79,6 | Deletion in human |          |
| 97,2 |         |                  |
| 95,6 | Insertion in human |          |
| 94.4 | Deletion in human |
| 89.7 | Deletion in human |
| 97.1 | Deletion in human |
| 85   | Insertion in human |
| 98.7 | Insertion in human |
| 97.3 | Insertion in human |
| 99.6 | Deletion in human |
| 93.8 | Deletion in human |
| 94   | Insertion/Deletion |
| 94.9 | Deletion in human |
| 95.9 | Deletion in human |
| 96   | Deletion in human |
| 94.1 | Deletion in human |
| 82.7 | Deletion in human |
| 81.3 | Deletion in human |
| 91.7 | Deletion in human |
| 94.1 | Deletion in human |
| 98.7 | Deletion in human |
| 93.4 | Deletion in human |
| 90.8 | Deletion in human |
| 97.2 | Deletion in human |
| Value | Description               |
|-------|---------------------------|
| 87,6  |                           |
| 91,3  | Deletion in human         |
| 93,1  |                           |
| 96,8  | Insertion in human        |
| 84    | Insertion/Deletion        |
| 91,3  |                           |
| 92,9  |                           |
| 97,3  |                           |
| 97,9  |                           |
| 97,7  |                           |
| 98    | Deletion in human         |
| 98,2  |                           |
| 97,3  | Deletion in human         |
| 96,5  |                           |
| 98,4  | Insertion in human        |
| 98    |                           |
| 93,7  | Deletion in human         |
| 91,7  | Insertion in human        |
| 95,3  | Deletion in human         |
| 95,5  |                           |
| 94,8  |                           |
| 92,5  |                           |
| 98,5  |                           |
| 93,9  |                           |
| 93,1  |                           |
| 92,4  |                           |
| 97,7  | Insertion in human        |
| 83,1  | Insertion in human        |
| 92,9  |                           |
| 96    |                           |
| 94,8  |                           |
| 87,9  |                           |
| 81,6  |                           |
| 74,4  |                           |
| 73,8  |                           |
| 88    | Insertion in human        |
| 89,5  |                           |
| 80,1  |                           |
| 94    |                           |
| 90,7  |                           |
| 83,1  |                           |
| 87,2  |                           |
| 94,1  |                           |
| 90,7  |                           |
| 87,2  |                           |
| 97,9  |                           |
| 93,5  |                           |
| 97,2  | Insertion in human        |
|   |   |   |
|---|---|---|
| 86,6 | Insertion in human |   |
| 81,2 |   |   |
| 90 |   |   |
| 87 | Deletion in human |   |
| 99,6 |   |   |
| 90,9 |   |   |
| 96,3 |   |   |
| 96,9 |   |   |
| 97 | Deletion in human |   |
| 76,9 |   |   |
| 96,9 |   |   |
| 88,4 | Insertion in human |   |
| 93,4 |   |   |
| 89,1 | Insertion in human |   |
| 98,6 |   |   |
| 95,5 |   |   |
| 86,7 |   |   |
| 89 |   |   |
| 92,8 |   |   |
| 94,9 |   |   |
| 75,6 |   |   |
| 92,7 |   |   |
| 94,2 |   |   |
| 97,5 |   |   |
| 83,7 | Deletion in human |   |
| 87,6 | Deletion in human |   |
| 91,1 |   |   |
| 80,4 |   |   |
| 77,6 |   |   |
| 80,7 |   |   |
| 89,2 |   |   |
| 97,5 |   |   |
| 92,2 |   |   |
| 94,3 |   |   |
| 78,1 | Insertion/Deletion |   |
| 86,1 |   |   |
| 86,3 | Insertion/Deletion |   |
| 96,5 |   |   |
| 92,6 | Deletion in human |   |
| 93,8 |   |   |
| 94,8 | Insertion in human |   |
| 79 | Insertion in human |   |
| 92,6 |   |   |
| 80,2 | Deletion in human |   |
| 92,5 |   |   |
| 94,7 | Insertion in human |   |
| 96,5 |   |   |
| 97,8 | Insertion/Deletion |   |
| 89,3 | Insertion in human |   |
|     |                  |
|-----|-----------------|
| 83.5| Insertion in human |
| 94.8| Deletion in human |
| 89.9|                 |
| 74.4|                 |
| 86.7|                 |
| 61.7| Insertion/Deletion |
| 66.1| Insertion in human |
| 90.5|                 |
| 99.2|                 |
| 94.3|                 |
| 93.5|                 |
| 97.9|                 |
| 98.6|                 |
| 96.4| Insertion in human |
| 98.6|                 |
| 97.9|                 |
| 96.5| Insertion in human |
| 80.7|                 |
| 91.5|                 |
| 99.3|                 |
| 63.6|                 |