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Geographical distribution and molecular insights into abamectin and milbemectin cross-resistance in European field populations of *Tetranychus urticae*

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Abstract

BACKGROUND: Milbemectin and abamectin are frequently used to control the spider mite *Tetranychus urticae*. The development of abamectin resistance in this major pest has become an increasing problem worldwide, potentially compromising the use of milbemectin. In this study, a large collection of European field populations was screened for milbemectin and abamectin resistance, allowing to thoroughly evaluate any potential cross-resistance risk, and both target-site and metabolic resistance mechanisms were investigated.

RESULTS: High to very high levels of abamectin resistance were found in one third of all populations, while milbemectin resistance levels were low for most populations. The occurrence of well-known target-site resistance mutations in glutamate-gated chloride channels (G314D in GluCl1 and G326E in GluCl3) was documented in the most resistant populations. However, a new mutation, I321T in GluCl3, was also uncovered in three resistant populations. A differential gene-expression analysis revealed the overexpression of detoxification genes, more specifically cytochrome P450 monooxygenase (P450) and UDP-glycosyltransferase (UGT) genes. Subsequently, multiple UGTs were functionally expressed, and their capability to glycosylate abamectin and milbemectin, was tested and confirmed.

CONCLUSIONS: We found a clear correlation between abamectin and milbemectin resistance in European populations of *T. urticae*, but as milbemectin resistance levels were low, the observed cross-resistance is probably not of operational importance. The presence of target-site resistance mutations in GluCl genes was confirmed in most but not all resistant populations. Gene-expression analysis andr functional characterization of P450s and UGTs suggests that also metabolic abamectin resistance mechanisms are common in European *T. urticae* populations.

Keywords: ivermectin, macrocyclic lactone; UGTs, P450, molecular diagnostic, transcriptomics

1 INTRODUCTION

Milbemectin (70:30 milbemycin A4/A3) and abamectin (80:20 avermectin B1a/B1b) are major fermentation-based compounds derived from the soil actinomycetes *Streptomyces hygroscopicus* subsp. *Aureolacrimosus* and *Streptomyces avermitilis*, respectively. They belong to a family of compounds, the milbemycins and the avermectins, that exhibit strong insecticidal, nematicidal, and acaricidal activity.[1–3] Milbemectin and abamectin are both 16-membered macrolides and thus structurally very similar, but differ in a bisoleandrosyl substituent appended to the C13 position of the macrolide ring, which is only present in avermectins but not milbemycins.[4]

Milbemectin and abamectin are amongst the most frequently used compounds to control phytophagous pests, but are also used extensively as anthelmintics in animal and human health.[3] One of the main targeted phytophagous pests is the two-spotted spider mite, *Tetranychus urticae* (Arhropoda: Chelicerata: Acari: Tetranychidae). This species is a highly polyphagous herbivore and an important agricultural pest worldwide that causes severe damages to many economically important crops. It is also notorious for its ability to rapidly develop acaricide resistance.[5–7]

Abamectin has been used in agriculture for more than 30 years, mainly to control phytophagous mites such as *T. urticae*.[8] Only quite recently, abamectin resistance has been repeatedly reported and was partially investigated in a number of *T. urticae* populations from several regions worldwide.[9–15] In contrast, milbemectin has been applied more recently in European fields, and to a much lesser scale according to the EU Pesticides database. Reports of milbemectin resistance are still very limited, as well as studies investigating the potential risk of cross-resistance between milbemectin and abamectin, that are chemically related with a shared mode of action.[16,17]

Both target-site resistance as increased metabolism have been previously linked to resistance against abamectin.[7] The glutamate-gated chloride channel (GluCl), the gamma amino butyric acid (GABA)-gated chloride channel (GABA) and the histamine-gated chloride channel (HisCl) all interact with avermectins and ivermectins in insects and nematodes,[17–22] although GluCl is considered the main target-site in arthropods.[23] Interestingly, in contrast to insect genomes that harbor a single gene, five to six orthologous GluCl genes have been described in tetranychid mites (*T. urticae*, *Tetranychus lintearius* and *Tetranychus evansi*).[7] The mutations G314D in GluCl1 and G326E in GluCl3 have been associated with abamectin resistance in *T. urticae* by backcrossing and F2 screens by independent studies.[24,25] Remarkably, functional validation by two electrode voltage-clamp electrophysiology in *Xenopus* oocytes revealed that G326E reduced abamectin sensitivity of *Plutella xylostella* GluCl by more than 400-fold[26] or, in case of *T. urticae* GluCl3, completely abolished the agonistic activity of abamectin or milbemycin A4.[27] Further, a G329D mutant of a *Haemonchus contortus* GluCl, corresponding to the G314D mutation reported for *T. urticae* GluCl1, was unable to bind milbemycin A4.[28] Surprisingly, marker assisted backcrossing of the G326E mutation in a susceptible genetic background, revealed that the mutation alone or in combination with G314D, exhibited only a weak phenotype in isogenic lines of *T. urticae*. Nevertheless, as avermectins and milbemycins target the same channels, the potential risk of cross-resistance by these or other target-site mutations is evident and should be further examined. It is however not clear how frequently target-site resistance mutations occur in European *T. urticae* populations, nor what the magnitude might be of target-site based cross-resistance and whether it is of operational importance.

Besides target-site resistance, increased metabolism has been linked with resistance against macrocyclic lactones. Both synergism experiments, gene-expression analysis, as well as dedicated assays with functionally expressed proteins have pointed towards the involvement of cytochrome P450s (P450s).[29–32] Recombinant CYP392A16, a P450 overexpressed in an abamectin resistant strain, was shown to metabolize abamectin to a non-toxic metabolite.[33] In addition, glutathione-S-transferases (GSTs) have also been associated with abamectin resistance in this pest[30,34] and most recently, the uridine diphosphate (UDP)-glycosyltransferases (UGTs) were suggested to play a role in abamectin conjugation and resistance.[35,36] Although much less studied in arthropods as a resistance-conferring enzyme, UGTs are known to add a sugar moiety to lipophilic xenobiotics, resulting in more hydrophilic compounds which facilitates excretion or sequestration. To what extent these or other enzymes also confer cross-resistance, alone or in combination with target-site mutations, is still largely unknown.

The main aim of this study is to investigate abamectin and milbemectin (cross)-resistance patterns in a large survey of 32 European populations and investigate the molecular mechanism that underlie abamectin and milbemectin resistance. Populations were screened for the presence of target site (GluCl) mutations and genome wide transcriptomic profiling was performed for a selection of populations to identify detoxification enzymes that might play a role in resistance. Finally, we recombinantly expressed some key UGTs and determined their ability to glycosylate both abamectin and milbemectin to further confirm their potential role in resistance.

2 MATERIALS AND METHODS

2.1 Samples

During 2017 and 2018, thirty-two *T. urticae* field populations were collected from nine countries in Europe, both in greenhouses and open field. Populations from both the green and red colour morph were collected (Fig. 1). The sample names (abbreviations of the country of origin, numbered in order of arrival in the lab), locations and host plants are shown in Table S1. All *T. urticae* strains were maintained on non-sprayed kidney bean leaves (*Phaseolus vulgaris* L. cv. “Prelude”) under laboratory conditions (25±1°C, 60% relative humidity, and 16:8 hr light: dark photoperiod).

2.2 Toxicity Bioassays

Toxicity bioassays were carried out with commercially formulated abamectin (Vertimec 18 g/L EC) and milbemectin (Milbeknock 9.3 g/L EC). About 20-30 young adult female mites were transferred to 9-cm^2 bean leaf disks and sprayed (0.8 ml) with serial pesticide dilutions at 1 bar pressure in a custom built spray tower, as previously described.[37] For each pesticide, at least five concentrations were tested causing a mortality between 20 and 80% 24h after treatment (four technical replicates per concentration). LC_{50} and LC_{90} values and their 95% confidence limits were determined with PoloPlus (LeOra Software, Berkeley, CA, USA, 2006).[38,39]

2.3 DNA and RNA isolation

Genomic DNA was extracted from approximately 200 *T. urticae* female adults as described earlier by Van Leeuwen et al. (2008). RNA was extracted from a pool of 100-120 adult females using the RNeasy plus mini kit (Qiagen). Four independent RNA extractions were performed for each population. The concentration and integrity of the RNA and DNA samples was assessed by a DeNovix DS-11 spectrophotometer (DeNovix, Willmington, DE, USA) and by running a 2µl aliquot on 1% or 2% agarose gels.

2.4 Detection of resistance associated point mutations

PCR amplification of the GluCl gene fragments carrying the mutations was performed as earlier described by Dermauw *et al.*[24] The primer sequences used are listed in Table S2. PCR-products were purified using E.Z.N.A. Cycle Pure Kit (Omega Bio-Tek) and were sequenced (LGC genomics, Germany). All sequenced data was analysed using BioEdit version 7.0.5.2.[40]

2.5 RNA-seq

Illumina libraries were constructed with the TruSeq Stranded mRNA Library Preparation Kit with polyA selection (Illumina, USA), and the resulting libraries were sequenced on an Illumina HiSeq 3000 (strain UK6) or HiSeq 2500 instrument (all other strains), to generate strand-specific, paired-end reads with a length of 150 bp and 125 bp, respectively. Library construction and sequencing were performed at the NXTGNT sequencing platform (Ghent University, Ghent, Belgium) and the High-Throughput Genomics and Bioinformatic Analysis Shared Resource of the Huntsman Cancer Institute (University of Utah, Salt Lake City, UT, USA). Prior to read mapping, the quality of reads was verified using FastQC version 0.11.4 (https://www.bioinformatics.babraham.ac.uk/projects/fastqc/), no reads were tagged as poor quality.

2.6 Differential expression (DE) analysis and principal component analysis (PCA)

RNA reads were aligned to the *T. urticae* three-chromosome assembly[41] using STAR 2.5.3a with a 2-pass mode and the maximum intron size of 20kb, without the use of the GFF annotation. SAMtools 1.9 was used for indexing and merging the BAM files. Read counts were performed by HTSeq 0.11.2[42] using the GFF annotation version of 23 June 2016.[41]

A PCA was created as described by Love *et al.*[43] Briefly, read counts were first normalized using the regularized-logarithm (rlog) transformation implemented in the DESeq2[44] R-package. A PCA was then performed using the R-packages stats (version 3.5.1) and ggplot2 (version 3.2.1) with the 1000 most variable genes across all RNA-seq samples. A differential expression (DE) analysis was performed using the R-package limma (voom) 3.38.3. Differentially expressed genes (DEGs, fold change (FC) ≥ 2 and a Benjamini-Hochberg adjusted p-value (FDR) < 0.05) were determined pairwise between susceptible and resistant mite populations: IT2 versus RO1, UK6 versus RO1 and ES1 versus IT3. Those genes that were more than four-fold differentially expressed in all three pairwise comparisons were considered as the core set of differentially expressed genes related to abamectin resistance.

Secondly, as part of an alternative approach, all five strains were analysed together with a linear model using limma 3.38.3.[45] In line with the pairwise comparisons, 'resistant' compared to 'susceptible' was used as the contrast in the design of the DE analysis. However, instead of making only comparisons between strains with the same colour morph, a correction was now implemented in the model design for a different background (green/red morph) by using a blocking factor.

Finally, gene expression heatmaps were generated by using the resulting FC values of the three pairwise DE comparisons and the R-packages limma 3.38.3 and gplots 3.0.1.1. Gene lists of the metabolic detoxification families were obtained from Snoeck *et al.*[46] Genes with no FC ≥ 1 in all three pairwise DE comparisons were not included in the heatplots. Additionally, genes were clustered using a Euclidean distance metric and Ward's method.

2.7 Cloning, functional expression and purification of recombinant UGTs

The design of expression constructs and the procedure for protein expression in *E.coli* was carried out as described in Snoeck and Pavlidi *et al.*[36] with slight modifications. Briefly, total RNA was extracted from IT2 and ES1 strains, reverse transcribed using Maxima first strand cDNA synthesis kit (Thermo scientific) and amplified with primers specific for *tetur02g09830* from IT2 and *tetur05g05060* from ES1, using Phusion high fidelity DNA polymerase. Amplification conditions were 98°C for 30sec, followed by 30 cycles of 98 °C for 10 sec, 60°C for 30s, 72°C for 45 sec and a final extension at 72°C for 5 min. The PCR product was purified and ligated into pJET /Blunt 2.0 vector and heat-shocked into *Escherichia coli*. Based on a colony PCR, 5 positive colonies were grown, plasmids extracted and sent for sequencing (LGC genomics, Germany). A clone with the correct DNA sequence was used to order codon optimized constructs in pET100/D-TOPO vector from GenScript (The Netherlands). Protein expression conditions were optimized to maximize protein yields. For large scale protein production in 1L cultures, transformed *E. coli* BL21(DE3) STAR cells were grown at 37°C with shaking at 250rpm until an OD_{600nm} = 0.6 was reached. The cultures were cooled to 16°C, then expression was induced with 0.4 mM IPTG and incubated overnight at 16°C with shaking at 180 rpm. The cells were harvested by centrifugation at 8000 g for 10 minutes, re-suspended in 20 mL sodium phosphate buffer (PBS) pH 7.5 and lysed with 200µg / mL lysozyme for 30 minutes at 37°C. To complete the lysis process, 40 mL lysis buffer (100 mM PBS pH 7.5, 500 mM NaCl, 10 mM imidazole, 20 mM β-mercaptoethanol (β-ME), 0.5 mM PMSF, 2% glycerol) was added, followed by sonication on ice. Cell lysate was centrifuged at 8000 g for 30 minutes and the supernatant was loaded onto NiNTA column equilibrated with 100 Mm PBS buffer containing 500 mM NaCl and 20 mM imidazole. Unbound protein was washed with PBS buffer containing 500mM NaCl and varying concentrations of imidazole (25 mM to 50 mM). The protein was eluted using 100mM imidazole in 100mM PBS and 500 mM NaCl, desalted and concentrated using pierce protein concentrators (Thermo scientific) with a cutoff of 10kDa. Protein concentration was determined using Bradford assay with BSA standard.[47] Protein purity was verified with 12 % SDS-PAGE gel and a western blot with anti-His-tag antibody (Thermo Fisher Scientific, Belgium). The purified protein was stored at -20 °C with addition of glycerol to a final concentration of 25 %.

The recombinant UGTs, tetur05g05050 and tetur02g09850, were provided by Snoeck and Pavlidi *et al.*[36]

2.8 Activity assays and determination of specificities for model substrates

UGT activity was determined against the model substrate p-nitrophenol[48] (Sigma-Aldrich) as described earlier by Snoeck and Pavlidi *et al.*[36] Depletion of p-nitrophenol was measured spectrophotometrically (400nm) in three independent replicates while using 96-well plates (Greiner Bio-One, Belgium) and a Biotek EON microplate spectrophotometer (Biotek, France).

2.9 UGT incubation and UDP-glo glycosyltransferase assay

Incubation was performed as described earlier by Snoeck and Pavlidi *et al.*[36] In short, 50 µM abamectin (CAS number 71751-41-2, Sigma–Aldrich) or milbemectin (SanBio, Uden, the Netherlands), 0.1µg enzyme and 400 µM UDP-glucose were incubated in a total reaction volume of 125µL containing 0.1 M sodium phosphate buffer (pH 7.5) and 16.7 mM $MgCl_2$ at 25°C for 1 h. Negative controls used for the calculations consisted of all reaction components except the substrate (abamectin/milbemectin). Additionally, negative controls were incorporated in the experiments which contained all reaction components except the enzyme or UDP-glucose.

The formation of free-UDP by the glycosyltransferase reaction was quantified with the UDP-Glo™ glycosyltransferase assay (Promega) as described in Snoeck and Pavlidi *et al.* (2019). This assay detects the free-UDP release by converting free-UDP to ATP which results in the generation of light in a luciferase reaction with white, flat bottom 96-(chimney)-well lumitrac medium binding assay plate (Greiner Bio-One). Subsequently, luminescence was measured in Relative Luminescence Units (RLU) in triplicates with a Tecan infinet M200 plate reader (Tecan). An alternative incubation set-up was used for all experiments with tetur05g05050 since the enzyme had a relatively low activity against the model substrate p-nitrophenol. The only difference in set-up in comparison to the other three UGTs was the amount of enzyme, which was elevated to 1 µg instead of 0.1 ug.

2.10 Figure editing

CorelDRAW Home & Student ×7, R and SigmaPlot 12.0 software were used to process and edit the figures.

3 RESULTS

3.1 Resistance levels and stability of resistance to milbemectin and abamectin in *T. urticae* field populations

Compared to an acaricide susceptible reference strain, ten out of the thirty-two *T. urticae* field populations exhibited resistance against abamectin, with resistance ratios (RRs) ranging from 30- to 1600-fold (Table 1). In contrast, RRs of milbemectin only reached 136- and 203-fold for the most resistant populations, UK6 and IT2. These two populations also showed very high RRs for abamectin, 958- and 1655-fold respectively.

The LC_{90} values of both acaricides are shown for all field populations in Fig. 2 in combination with a correlation analysis. A concentration of 10 mg a.i. /L (advised field rate) milbemectin could theoretically control almost all mite populations, except ES1, UK6 and IT2, while the advised field dose of abamectin (18 mg a.i./L) would not be sufficient to control 10 out of 32 populations. The correlation analysis between the $\log_{10}$ values of the LC_{90} values of milbemectin and albemectin was performed with populations that had LC_{90} values over 1 mg a.i./L (19 populations) for both compounds, and resulted in a correlation coefficient (R^2) of 0.8071 (Fig. 2).

Five resistant populations were kept in the lab on bean leaves without selection pressure for approximately one year, after which the toxicity for abamectin and milbemectin were re-evaluated. This revealed that RRs were highly stable (Table 2). For two populations (UK1 and ES1), despite the lack of selection pressure, the resistance levels were even higher in comparison to the year before.

3.2 GluCl resistance mutation detection

Milbemectin and abamectin resistance has previously been linked to two mutations in the GluCl channels, G314D and G326E.[24,25,27] All the populations were PCR-screened for these GluCl target-site mutations using DNA from approximately 200 individuals as a template. The G314D (GGT->GAT) and G326E (GGA->GAA) mutation was fixed in the IT2 population while a G326E mutation was fixed in the UK6 population and segregating in the ES3 population. In addition, a new potential target-site mutation, I321T (ATT->ACT) in GluCl3, was fixed in multiple red colour morph resistant populations (IT1, IT5 and IT6), while in the ES1 population three segregating mutations, I321T (ATT->ACT), V327A (GTC->GCC) and L329F (CTT->TTT) were identified (Fig. 3).

3.3 RNA-seq and principal component analysis (PCA)

Five populations were selected for Illumina sequencing based on their resistance levels against abamectin and milbemectin (and observed cross-resistance), the host plant they were sampled from, and their body colour phenotype (red or green morph). The IT2, UK6 and ES1 population had the highest abamectin and milbemectin resistance levels. RO1 and IT3 were selected since they were both susceptible strains but with a different colour morph. Among the sequenced populations, IT2, UK6 and RO1 were green colour morphs and ES1 and IT3 were red colour morphs. The set-up of the pairwise comparisons can be found in Table S3.

Illumina sequencing generated on average of 18 million strand-specific paired end reads per sample. Alignment of RNA-seq reads against the *T. urticae* annotation resulted in an overall mapping rate of uniquely mapped reads of 81.13% across all sequenced samples (Table S4). Reads of each population are available in the Gene-Expression Omnibus (GEO) repository with accession number [accession number will be provided upon acceptance].

The PCA revealed that 44.1% of the total variation could be explained by principal component 1 (PC1) while 20.6% could be explained by PC2 (Fig. 4A). Replicates clustered by population, further confirming the sample quality. The two green-coloured resistant populations (IT2 and UK6) were positioned close together and far away from the green-coloured susceptible strain RO1 for PC1. Similarly, the red-coloured resistant strain ES1 was clearly separated from the red-coloured susceptible strain IT3 for both PCs.

3.4 Differential gene expression analysis

The limma package with the voom method was used to analyse differential gene expression patterns in pairwise comparisons between the resistant and susceptible *T. urticea* strains (IT2 vs RO1, UK6 vs RO1 and ES1 vs IT3) ($\log_2|FC| \geq 1$ and a $FDR < 0.05$). We found 410 and 312 genes significantly over-expressed by two-fold or more, while 189 and 344 genes were significantly under-expressed by two-fold or more in IT2 and UK6 compared to the susceptible strain RO1, respectively. In the comparison of ES1 vs IT3, there are 269 and 226 genes over- or under-expressed, respectively. Remarkably, two cys-loop ligand-gated ion channel genes, *tetur02g11020* and *tetur02g11170* (*T. urticae* homologs of *Drosophila* CG12344), were overexpressed among all comparisons ($\log_2$FC between 1 and 5.7). The subunits they encode seem most related to those of vertebrate glycine-gated channels (GlyR alpha subunits), but their function in insects and mites is not well studied.

Forty-seven genes were more than four-fold overexpressed in all pairwise comparisons (Fig. 4B). These 47 “core” overexpressed genes include ten P450s, four UGTs, three carboxyl/cholinesterase (CCEs), two intradiol ring-cleavage dioxygenase (ID-RCDs), three short-chain dehydrogenases/reductases (SDRs), and one lipase/lipoxygenase (PLAT/LH2) among other genes (Table 4). We also performed an alternative differential expression analysis, based on a linear model with a blocking factor (green/red morph), resulting in 177 over- and 159 underexpressed genes ($\log_2|FC| \geq 2$ and a $FDR < 0.05$) (Table S6). In line with the pairwise comparison approach, both *tetur02g11020* and *tetur02g11170* were overexpressed ($\log_2$FC of 4.3 and 1.2, respectively). In addition, 43 of the 47 shared “core” overexpressed genes were also overexpressed in this alternative analysis (Table 3, Table S6).

As shown in Fig. 5, multiple P450s and several UGTs were also strongly overexpressed in some or all resistant mite populations. Gene expression heatmaps for ID-RCDs, GSTs, SDRs and CCEs can be found in Fig. S1.

3.5 Cloning, heterologous expression and purification of *T. urticae* UGTs

Coding sequences of two UGTs were successfully cloned into pJET/Blunt 2.0 expression vector and inspection of cloned sequences did not reveal any sequencing errors. IPTG induction of expression resulted in good levels of protein production. Although most of the expressed protein was found in the insoluble fraction, the remaining yield in the soluble fraction was sufficient to allow efficient metal affinity purification of recombinant enzymes.

The overall amount of recombinant UGTs tetur05g05060 and tetur02g09830 was 1 and 3 mg derived from 1L bacterial cultures, respectively. All four UGTs (tetur05g05060 and tetur02g09830 (this study) and tetur02g09850 and tetur05g05050[36] were successfully purified close to homogeneity, as verified by obtaining a main band of the expected size after both SDS-PAGE as well as a Western-blot with anti-His-tag primary antibodies (Fig. S2).

The four recombinant UGTs (tetur05g05050, tetur05g05060, tetur02g09830 and tetur02g09850) were assayed towards the model substrate p-nitrophenol to investigate whether they exhibited UDP glycosyltransferase activity (Fig. S3). Three recombinant UGTs (tetur02g09830, tetur02g09850 and tetur05g05060) were capable of conjugating p-nitrophenol (between 56 and 92% depletion of UDP at a concentration of 100 micrograms of UGT enzyme). In line with Snoeck and Pavlidi *et al.*[36], tetur05g05050 only showed low conjugation activity towards p-nitrophenol (8% depletion of UDP at 100 microgram of enzyme).

3.6 UDP glycosyltransferase activity

Three out of four recombinant *T. urticae* UGTs (tetur05g05060, tetur02g09830 and tetur02g09850) could glycosylate abamectin. Incubation with tetur02g09830 resulted in the highest amount of released free-UDP (~glycosylation), 6.08μM. In contrast, milbemectin was only glycosylated by tetur02g09850. Tetur05g05050 showed no activity towards both macrocyclic lactones (Table 4).

4 DISCUSSION

Milbemectin and abamectin are two frequently applied acaricides in the control of spider mites. Based on the LC_{90} values of thirty-two *T. urticae* field populations determined in this study, advised field doses of milbemectin (10 mg a.i. /L) seems still efficient to control the majority of *T. urticae* field populations in Europe. This is in contrast to abamectin, where a field dose (18 mg a.i. /L) would only be able to control two-thirds of our sampled populations. Only two strains were highly resistant to milbemectin (IT2: RR= 203 and UK6: RR=136) and exactly these strains exhibited extreme high resistance to abamectin, with RRs reaching 958- and 1655-fold, suggesting cross-resistance. However, both LC_{50} values and RRs were markedly lower for milbemectin in comparison to abamectin. The field dose of milbemectin will most likely still control all except three populations from this study, and to what extent the current observed milbemectin resistance is of operational importance is still questionable. A link between abamectin and milbemectin toxicity and some level of cross-resistance was also clear from a correlation analysis including all populations with LC_{90} values higher than 1 mg a.i./ L (Fig. 2). Together, this suggests that the extensive use of abamectin might compromise milbemectin efficacy in the long run. Resistance against both macrocyclic lactones was stable over the course of one year in the laboratory (Table 2). This observed stability of abamectin and milbemectin resistance is in accordance with the findings of Stumpf & Nauen 2002, were an abamectin resistant strain (NL-00) from roses showed stable resistance after being maintained for six months in the lab without selection pressure.[31] In contrast, studies from Sato *et al.* and Nicastro *et al.* revealed instabilities of abamectin and milbemectin resistance after laboratory selection,[14,16] pointing towards different mechanism selected in the field and the laboratory.[49–51]

The macrocyclic lactones milbemectin and abamectin are structurally strongly related and share GluCls as the main target-site.[52] Hence, the risk for cross-resistance observed in this study, and suggested earlier,[14,16,27] could both be due to both target-site changes affecting binding of both molecules, as well as a common metabolic detoxification pathway. A number of target-site mutations *in T. urticae* GluCl channels (G314D and G326E) were previously associated with milbemectin and abamectin resistance,[24,25] and have been functionally validated.[26–28] Several studies have reported the absence or only low frequency of these target-site mutation in *T. urticae* field populations worldwide,[10,15,32,53,54] but toxicity data of both abamectin and milbemectin is often lacking in these screening studies. It is therefore not yet clear to what extent they are a reliable marker of resistance. Remarkably, we confirmed in this study that both target-site mutations are relatively common, as detected in 3 out of 7 most resistant populations (Fig. 2, Fig. 3). Their presence in only the most resistant populations might be explained by the observation that both mutations carry a fitness cost, and hence their presence might reflect continuous selection in the field, further rising resistance ratio's[55,56] (Fig. 3). Thus, the detection of these mutations is predictive of very high resistance levels, even if not present in all resistant populations. This was also confirmed by a recent study in China, where six out of seven field strains with extensive abamectin application history contained both mutations.[10] However, regardless of the association with resistance, it remains unclear to what extent the mutations contribute to the phenotype, as introgression by marker-assisted backcrossing revealed only low levels of resistance in isogenic lines.[38] The potential mechanisms explaining this discrepancy might be complex, as channels typically consist of potentially different combinations of five subunits, as discussed in Riga *et al.*[38], and one cannot exclude even that heteromeric channel assembly occurs, consisting of both GluCl and GABACl subunits.[57,58] Of particular note, two cys-loop ligand gated ion channel subunit genes (*tetur02g11020* and *tetur02g11170*), were overexpressed in all resistant *T. urticae* strains (Table S6). These genes encode homologues of *Drosophila* CG12344, which is predicted to be an orthologue of human glycine receptors but has only been poorly characterized.[59,60] Ivermectin is known as an agonist of human glycine receptors, but these receptors are 100-fold less sensitive to ivermectin compared to invertebrate GluCls as they lack the TM3 glycine residue at a position corresponding to G314/G326 in *T. urticae* GluCl1/GluCl3.[24,61,62] Speculatively, this might suggest that heteromeric channels are formed, consisting of these overexpressed subunits, hereby reducing abamectin binding. In the cases described above, it is clear that simple introgression of a GluCl resistance mutation in a single subunit, might not convey the full phenotype, and this merits further investigation.

In addition to well-known target-site GluCl mutations, we also discovered a potential new target-site mutation, I321T in GluCl3, present in four resistant strains of the red colour morph (ES1, IT1, IT5 and IT6) (Fig. 2, Fig. 3). This mutation is adjacent to A309V, a previously reported abamectin resistance mutation in *P. xylostella* [26], and adjacent to one of the *Caenorhabditis elegans* GluClα TM3 residues that, based on the GluClα crystal structure, was predicted to be involved in ivermectin binding[63] (Fig. 3). Interestingly, GluCl3 of ES1 also carried a V327G mutation, adjacent to the important G326 residue, and a leucine to phenylalanine mutation at residue 329. Interestingly, the corresponding residue in *Caenorhabditis elegans* GluClα was also predicted to be involved in ivermectin binding (Supplemental Fig. 8 in Hibbs *et al.* [63]), while an L315F mutant of *Musca domestica* GluCl and L319F mutant of *Bombyx mori* GluCl (corresponding to L329F in *T.urticae* GluCl3) showed reduced sensitivity to ivermectin[64,65], suggesting the L329F mutation might also contribute to the high abamectin resistance levels of population ES1. However, these three newly identified mutations await further functional validation. In the light of cross-resistance, it is remarkable to notice that the presence or absence of resistance mutations does not seem to impact the correlation of toxicity (Fig. 2, Fig. 3), suggesting alternative mechanisms at play. This is also suggested from the fact that although functional expression in oocytes of the G326E mutant of GluCl3 reveals equally strong effects of abamectin and milbemycin on channel activation[27], there are still large differences in toxicity between compounds in strain IT2 and UK6 that harbour these mutations (Fig.2).

Indeed, as some strains with high resistance levels did not harbour any mutations, and mutations alone might not explain the full resistance phenotype[38], we also investigated increased metabolism/transport as potential resistance mechanism. Increased detoxification by metabolism was previously linked to abamectin resistance in diverse species, including spider mites. Hence, we selected five *T. urticae* field strains and performed a genome-wide transcriptomic study to identify specific genes involved in resistance. We selected strains based on colour morph, host plant sampled and resistance status (Table 1, Table S1), in attempt to provide genetically relevant comparisons to uncover gene-expression differences only related to resistance. Not surprisingly, our analysis (Table 3) revealed that multiple P450s were among the most highly overexpressed DEGs. Oxidative metabolism was earlier reported as a principal resistance mechanism against abamectin for multiple pests, such as the Colorado potato beetle [*Leptinotarsa decemlineata* (Say) (Coleoptera: Chrysomelidae)] and the house fly [*Musca domestica* Linnaeus (Diptera: Muscidae)].[21] For *T. urticae,* several P450 genes - *CYP392D2*, *CYP392D8*, *CYP392D10*, *CYP392A11* and *CYP392A16* - were reported to be overexpressed in abamectin resistant strains.[29,32,33] In addition, CYP392A16 was functionally expressed and *in vitro* assays showed that it could metabolize abamectin to a non-toxic metabolite. In line with previous studies, *CYP392A12*, *CYP392E8* and *CYP392Dn* were highly overexpressed in all resistant strains (Table 4), suggesting that P450-mediated metabolic resistance is also contributing to the high resistance levels observed in many strains from different crops throughout Europe. Unfortunately, in contrast to CYP392A16, we did not succeed in functionally expressing P450s from the D-family.

Next to P450s, UGTs were strongly represented in the pairwise comparisons DEGs (tetur02g09830, tetur05g00070, tetur05g05050 and tetur05g05060). Recently, a high-throughput substrate screening of both plant secondary metabolites and pesticides revealed that tetur02g09850 was able to glycosylate abamectin, whereas milbemectin was not tested.[36] Here two *T. urticae* UGTs, tetur02g09830 and tetur05g05060, were functionally expressed and together with enzyme stocks of tetur02g09850 and tetur05g05050 from this previous study, tested for glycosylation activity towards abamectin and milbemectin. Tetur02g09850 was included because the protein sequence was highly similar to tetur02g09830 (Fig. S5) and it was previously shown to glycosylate abamectin.[36] In addition, its encoding gene was also overexpressed in all pairwise resistant-susceptible comparisons (Table S6), albeit at lower level.

The result of activity assays showed that three out of four recombinant UGTs were able to glycosylate abamectin, the highest glycosylation activity was detected for tetur02g09830 (Table 4). Milbemectin, on the other hand, could only be metabolized by tetur02g09850. It is remarkable that despite the very high protein similarity of tetur02g09830 and tetur02g09850, different substrate preferences are evident. An aligment including UGT50A1 (*Bombyx mori*), UGT50A2 (*Helicoverpa armigera*) and UGT2B7 (*Homo sapiens*) and indication of all currently known important residues (catalytic residues and residues interacting with the sugar donor) [66–68] is presented in Figure S5. There are no differences between tetur02g09830 and tetur02g09850 except for one different residue in the sugar donor binding region, but to what extent this might contribute to substrate specificity is unclear. In addition, proteins were recombinantly expressed in *E. coli*, which does not allow correct glycosylation, which might be needed for the correct interpretation of this observation. This can also be the reason for the lack of activity of the recombinant tetur05g05050.

Last, gene-expression analysis has previously associated TuGSTd14 (tetur29g00220) with abamectin resistance, and functional expression has revealed interactions between this GST and abamectin in inhibition assays with model substrates.[34] Although TuGSTd14 is not in our key list (Table 3), it is higher expressed in all comparisons (Table S6) with $\log_2$FC of 2.41, 1.28, 2.04 and 1.93 in comparisons IT2 vs RO1, UK6 vs RO1, ES1 vs IT3 and in the list predicted by the linear model, respectively. This further supports a role of this GST in abamectin and milbemectin resistance.

5 CONCLUSION

In conclusion, using an exceptionally wide collection of field populations from Europe, we were able to determine resistance levels to abamectin and milbemectin, and thoroughly evaluate any potential cross-resistance risk. We found high to very high levels of resistance to abamectin in one third of the examined populations. Although there was clearly a correlation between abamectin and milbemectin toxicity, resistance levels to milbemectin were low and in most cases probably not of operational importance. In search of the molecular mechanisms of cross-resistance, we sequenced all GluCl target-site genes, and found both previously reported mutations, as well as new mutations in GluCl3, in the majority of the highly resistant strains. However, as these mutations were not found in all resistant strains, the overall correlation of toxicity between abamectin and milbemectin points towards metabolism as the likely cause for cross-resistance. We therefore also investigated the role of metabolic detoxification by gene expression profiling. This revealed the association of a number of P450s, of which one was previously shown to metabolise abamectin. In addition, the role of UGT-mediated metabolic detoxification in resistance against macrocyclic lactones was further corroborated by *in vitro* enzyme activity assays.

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SUPPORTING INFORMATION

Supporting information might be found in the online version of this article.

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FIGURES

Figure 1. The major geographic distribution of *T. urticae* populations collected from 8 countries in Europe. For detailed information about collection date, collection site and host plant species see Table S1.

Figure 2. LC_{90} values of milbemectin and abamectin in field populations. The advised field doses (*) are indicated with dashed lines (10 mg a.i. /L for milbemectin and 18 mg a.i. /L for abamectin). Red colour morph populations are underlined, while green colour morph populations are not underlined. The presence of the G326E, G314D, I321T or V327A/L329F mutation in either GluCl1 or GluCl3 is indicated by a filled circle, hollow circle, black rhombus and a cross, respectively. Those strains used in the differential gene expression analysis are indicated in blue font. A correlation analysis (top left) between the $\log_{10}$ values of the LC_{90}s of milbemectin and abamectin was performed with populations that had an LC_{90} value of more than 1 mg a.i. /L (19 populations) for both compounds.

Figure 3. Mutations in transmembrane domain 3 of GluCl1 and GluCl3 subunits of *T. urticae* strains investigated in this study. Alignment of transmembrane domain 3 (TM3) of GluCl1 and GluCl3 subunits of *T. urticae* strains ROI, UK6, ES1, ES3, IT1, IT2, IT5 and IT6 with TM3 of *Drosophila melanogaster* and *Plutella xylostella* GluCl and TM3 of *C. elegans* GluClα. Previously reported abamectin resistance mutations, G314D and/or G326E are indicated by a red arrow and red font.[24,27] A new mutation I321T mutation in four abamectin resistant *T. urticae* strains (ES1, IT1, IT5 and IT6) is indicated by a blue arrow and a blue font, while the V327A and L329F mutation found in ES1 is indicated by a green arrow and green font. Underlined residues indicate the position of *C. elegans* GluCl*α* residues that, based on the GluCl*α* crystal structure, were shown to be involved in ivermectin binding.[63] An 80% threshold was used for identity (black background) and similarity shading (grey background). Abbreviation of species names: Tu, *T. urticae*; Ce, *C. elegans*; Dm, *D. melanogaster*; Px, *P. xylostella*.

Figure 4. Principal component analysis (PCA) and differential gene expression analysis. (A) PCA analysis of gene expression among five populations of*T. urticae*. (B) Differential expressed genes (DEGs; red, overexpressed; blue underexpressed) between three resistant and two susceptible *T. urticae* strains ($\log_2|FC|\geq1$, $FDR < 0.05$). For a list of DEGs, see Table 3 and Table S6.

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TABLES

Table 1. LC$_{50}$ values of milbemectin and abamectin for 32 *T. urticae* field populations in Europe

	Milbemectin			Abamectin		
Populations[a]	**Slope(±SE)**	**LC$_{50}$(95% CI) /mg L^{-1}**	**RR**[b]	**Slope(±SE)**	**LC$_{50}$(95% CI) /mg L^{-1}**	**RR**[b]
IT2	3.14 (±0.32)	35.87 (31.48-40.37)	203.8	2.69 (±0.23)	151.44 (134.25-169.53)	958.51
UK6	2.34 (±0.24)	23.94 (16.87-30.40)	136.04	2.38 (±0.22)	261.56 (210.94-312.41)	1655.43
ES1*	3.10 (±0.26)	4.10 (3.35-4.91)	23.28	2.53 (±0.18)	78.59 (67.63-90.84)	497.39
BE1	2.72 (±0.27)	3.71 (3.04-4.35)	21.07	2.32 (±0.25)	41.95 (36.01-48.06)	265.5
UK2	2.01 (±0.18)	3.46 (2.97-4.04)	19.66	2.82 (±0.20)	7.40 (6.42- 8.48)	46.86
IT6*	3.10 (±0.23)	3.12 (2.78-3.46)	17.74	3.33 (±0.22)	24.96 (22.76-27.20)	157.99
IT5*	3.74 (±0.30)	2.99 (2.67-3.32)	16.98	4.28 (±0.13)	14.26 (12.45-16.15)	90.22
UK1	1.71 (±0.13)	2.31 (1.87-2.90)	13.15	1.50 (±0.14)	17.02 (13.79-21.27)	107.71
IT1*	3.98 (±0.36)	2.07 (1.85-2.30)	11.77	3.31 (±0.32)	14.64 (12.08-17.12)	92.65
DE1	2.94 (±0.25)	0.99 (0.86-1.15)	5.65	2.75 (±0.22)	1.56 (1.40-1.74)	9.89
NL2	2.73 (±0.24)	0.92 (0.79-1.05)	5.23	2.83 (±0.21)	3.96 (3.52-4.40)	25.08
UK4	2.68 (±0.20)	0.89 (0.62-1.24)	5.06	1.82 (±0.13)	1.72 (1.46-2.02)	10.87
NL1	4.15 (±0.37)	0.82 (0.72-0.93)	4.69	2.23 (±0.20)	3.25 (2.79-3.77)	20.59
ES2*	3.22 (±0.26)	0.80 (0.73-0.88)	4.56	4.55 (±0.42)	0.35 (0.31-0.38)	2.2
DE3	2.79 (±0.29)	0.77 (0.66-0.90)	4.39	2.15 (±0.18)	0.86 (0.73-0.99)	5.41
IT4	2.87 (±0.27)	0.76 (0.68-0.85)	4.33	2.19 (±0.19)	1.27 (1.09-1.47)	8.01
DE5	2.89 (±0.26)	0.76 (0.65-0.86)	4.29	1.83 (±0.21)	1.47 (1.19-1.77)	9.29
ES3	2.62 (±0.25)	0.73 (0.64-0.83)	4.14	1.86 (±0.15)	11.82 (9.20-15.13)	74.84
RO2	4.04 (±0.43)	0.59 (0.54-0.36)	3.33	4.07 (±0.48)	0.48 (0.42-0.53)	3.01
DE7	4.10 (±0.41)	0.54 (0.48-0.60)	3.09	8.18 (±0.84)	0.68 (0.64-0.71)	4.28
DE2	3.25 (±0.30)	0.53 (0.47-0.59)	3.02	3.35 (±0.30)	1.52 (1.34-1.68)	9.59
UK5	3.68 (±0.30)	0.53 (0.48-0.58)	3.02	3.34 (±0.24)	0.23 (0.20-0.25)	1.44
DE4	2.99 (±0.23)	0.42 (0.38-0.46)	2.39	1.98 (±0.16)	0.28 (0.24-0.32)	1.76
DE6	4.17 (±0.36)	0.38 (0.35-0.42)	2.19	1.97 (±0.18)	1.36 (1.18-1.56)	8.58
IT7*	5.05 (±0.40)	0.36 (0.33-0.39)	2.04	4.42 (±0.40)	0.22 (0.20-0.24)	1.39
BE3	3.32 (±0.42)	0.35 (0.30-0.40)	2.00	3.35 (±0.29)	0.34 (0.24-0.46)	2.13
RO1	3.25 (±0.29)	0.33 (0.29-0.37)	1.87	5.53 (±0.69)	0.12 (0.11-0.13)	0.74
POL2	4.15 (±0.44)	0.31 (0.27-0.34)	1.76	3.16 (±0.28)	0.23 (0.19-0.27)	1.44
POL1	2.58 (±0.25)	0.25 (0.22-0.28)	1.41	3.89 (±0.43)	0.27 (0.23-0.30)	1.68
IT3*	2.73 (±0.28)	0.24 (0.17-0.29)	1.36	3.24 (±0.24)	0.14 (0.13-0.16)	0.91
BE2	2.81 (±0.25)	0.20 (0.18-0.23)	1.14	3.46 (±0.34)	0.34 (0.30-0.38)	2.18
UK3	4.55 (±0.42)	0.18 (0.16-0.19)	1.00	4.38 (±0.35)	0.16 (0.14-0.18)	1.00

[a] those populations indicated with an asterisk are red color morphs while all other populations are green color morphs

[b] RR(Resistance ratio)= LC50 of a population/LC50 of the UK3 strain;

The strains with grey shade were selected to do RNA-seq.

Table 2. Resistance stability assessment of 5 selected populations

Populations	Date of tested	Milbemectin LC50 (95% CI) / mg L^{-1}	Abamectin LC50 (95% CI) / mg L^{-1}
UK1	Jan/2019	3.05 (2.46-3.79)	84.92 (74.78-96.34)
	Aug/2017	2.31 (1.87-2.90)	17.02 (13.79-21.27)
UK2	Jan/2019	3.43 (2.99-3.90)	10.13 (8.92-11.37)
	Aug/2017	3.46 (2.97-4.04)	7.40 (6.42-8.48)
ES1	Jan/2019	2.51 (2.22-2.82)	131.25 (115.03-150.74)
	Aug/2017	4.10 (3.35-4.91)	78.59 (67.63-90.84)
IT1	Jan/2019	1.47 (1.29-1.68)	15.77 (13.20-18.70)
	Aug/2017	2.07(1.85-2.30)	14.64 (12.08-17.12)
IT2	Jan/2019	34.80 (18.33-49.61)	110.189 (93.116-130.160)
	Jan/2018	35.87 (31.48-40.37)	151.445 (134.252-169.530)

Table 3. Shared overexpressed genes in the three resistant-susceptible comparisons

Genes were sorted based on their gene description. See supporting information Table S4 for a list of shared underexpressed genes. For a list of all differentially expressed genes see Table S6.

T. urticae **gene ID**	**Description**	**log_2FC**			*** Linear Model**
		IT2 vs RO1	**UK6 vs RO1**	**ES1 vs IT3**	
tetur03g00970	Cytochrome P450 (CYP392A11)	8.18	6.58	4.38	6.25
tetur03g00830	Cytochrome P450 (CYP392A12)	4.99	3.78	8.01	5.89
tetur06g04520	Cytochrome P450 (CYP392A16)	4.52	2.95	3.19	3.51
tetur03g04990	Cytochrome P450 (CYP392D2)	10.35	9.06	8.16	9.29
tetur03g05020	Cytochrome P450 (CYP392D5p)	8.72	7.00	10.31	N/A
tetur03g05070	Cytochrome P450 (CYP392D8)	13.36	11.30	5.97	9.74
tetur03g05110	Cytochrome P450 (CYP392D10p)	7.68	6.80	4.23	5.94
tetur03g05100	Cytochrome P450 (CYP392Dn)	6.04	3.60	6.23	5.92
tetur27g00350	Cytochrome P450 (CYP392E8)	4.73	4.11	2.10	3.50
tetur27g00220	Cytochrome P450 probable pseudogene	4.99	3.94	4.70	4.56
tetur02g09830	UDP-glycosyltransferase (teturUGT10)	4.35	2.69	3.16	3.38
tetur05g00070	UDP-glycosyltransferase (teturUGT21)	4.80	3.33	2.31	3.42
tetur05g05050	UDP-glycosyltransferase (teturUGT28)	3.84	4.24	8.06	5.55
tetur05g05060	UDP-glycosyltransferase(teturUGT29)	5.11	5.63	6.91	6.11
tetur11g05770	Carboxyl/cholinesterase (TuCCE35)	6.05	5.14	4.10	5.28
tetur29g00930	Carboxyl/cholinesterase (TuCCE58)	3.59	2.25	3.41	3.13
tetur29g00940	Carboxyl/cholinesterase (TuCCE59)	3.95	2.22	2.11	2.73
tetur19g02300	Intradiol ring-cleavage dioxygenase	7.50	2.05	3.17	N/A
tetur13g04550	Intradiol ring-cleavage dioxygenase	7.41	4.76	4.96	5.68
tetur06g04970	Short-chain dehydrogenase/reductase	6.52	2.89	6.31	N/A
tetur12g00570	Short-chain dehydrogenase/reductase	4.12	2.91	2.32	3.16
tetur12g00590	Short-chain dehydrogenase/reductase	6.02	4.28	2.65	4.20
tetur04g00770	Small Secreted Protein (Family F)	9.47	7.72	2.16	5.97
tetur04g09479	Small Secreted Protein (Family F)	10.61	9.49	2.36	7.46
tetur04g09459	Small Secreted Protein (Family F)	12.01	10.33	4.18	8.20
tetur01g13120	Leucine-rich repeat domain	6.19	5.60	7.64	6.64
tetur07g02420	Leucine-rich repeat domain	4.35	4.19	7.01	5.68
tetur34g00160	Leucine-rich repeat domain	2.63	2.72	6.17	4.02
tetur16g03490	Antigen B membrane protein	10.14	5.39	6.06	N/A
tetur12g03950	Serine protease (SP29)	3.28	2.41	2.12	2.54
tetur11g05740	Lipase/lipooxygenase; PLAT/LH2	3.89	4.15	2.10	3.19
tetur02g14741	BTB/Kelch-associated	4.81	3.71	9.43	6.56
tetur24g00770	BTB/POZ-like	2.81	3.70	5.81	4.38
tetur13g04170	GE26306	6.86	4.94	2.91	4.69
tetur31g02020	Apple-like	3.17	3.16	8.59	5.41
tetur03g02760	Scramblase	3.18	3.09	5.29	3.93
tetur08g05010	Cathepsin B (TuPap-11)	4.24	3.07	2.03	3.00
tetur28g01360	Wannes-Thomas Secreted Protein 2	2.34	2.72	2.11	2.38
tetur01g01500	Apolipo protein D precursor (putative)	3.40	2.58	3.91	3.37
tetur17g03440	Domain of unknown function DUF3421	2.10	2.82	3.91	3.04
tetur06g01100	Hypothetical protein	2.64	3.24	3.04	3.01
tetur12g00580	Hypothetical protein	4.18	4.37	4.03	4.11
tetur04g90885	Hypothetical protein	5.72	4.04	3.61	4.63
tetur02g14280	Hypothetical protein	2.59	2.54	2.66	2.60
tetur06g91354	Hypothetical protein	2.12	3.36	3.15	2.94
tetur21g01410	Hypothetical protein	4.96	4.65	3.04	4.10
tetur47g00220	Hypothetical protein	5.97	5.10	4.70	5.10

* The log_2FC of these 47 genes in the linear model analysis.

N/A: the gene was not detected as a differential expressed gene in the linear model analysis.

Table 4. The enzyme characteristics of four UGTs in combination with abamectin and milbemectin

	free-UDP (μM ± SE)			
	tetur05g05050	tetur05g05060	tetur02g09830	tetur02g09850
abamectin	nd	1.52 (± 0.19)	6.08 (± 0.61)	1.73 (± 0.14)
milbemectin	nd	nd	nd	4.84 (± 0.18)

nd: No glycosylation detected.

SUPPLEMENTAL FIGURES

Figure S1. Expression heatmaps of genes coding for ID-RCD, GSTs, SDRs and CCEs. Genes with a $\log_2|FC| \geq 1$ in at least one of the three resistant versus susceptible comparisons (IT2 vs RO1, UK6 vs RO1 and ES1 vs IT3) are shown in the heatmap. *T. urticae* gene IDs are shown on the right.

Figure S2. SDS-PAGE and western blot of the purified fractions of the recombinantly expressed *T. urticae* UGTs. (A) stain free SDS-PAGE gel. (B) western blot. 1: precision plus unstained protein standard. 2: tetur05g05050. 3: tetur05g05060. 4: tetur02g09830. 5: tetur02g09850. 6: precision plus protein standards (all blue).

Figure S3. Validation of UGT activity towards p-nitrophenol. P-nitrophenol (OD 400 nm) spectrophotometrical measurement after incubation with the respective recombinant *T. urticae* UGT enzyme. Values represent the mean of three replicates ± SD.

Figure S4. Standard curve glycosyltransferase assay. Free-UDP standard curve, Relative Luminescence Units (RLU) in function of free-UDP (range of 0-25µM). Values represent the mean of three replicates ± SD. The regression line ($R^2=0.9964$) was added to the plot as well as the 99% confidence interval.

Figure S5. Multiple alignment of 7 UGTs. There are 4 *T. urticae* UGTs, UGT50A1 (Gnenbank ID: JQ070272) from *Bombyx mori*, UGT50A2 (Gnenbank ID: JQ070228) from *Helicoverpa armigera* and UGT2B7 (NCBI Reference Sequence: NP_001065) from *Homo sapiens*. Important catalytic residues, H and D are indicated by red asterisks (∗) under the alignment. SDBR refers to sugar donor binding region and several important residues interacting with the sugar donor are indicated by red dots (•) under the alignment by comparison with a human UGT2B7 crystal structure[67,68] and UGTs from *B. mori* and *H. armigera.*[66]

SUPPLEMENTAL TABLES

Table S1. Detailed information of collected *T. urticae* populations

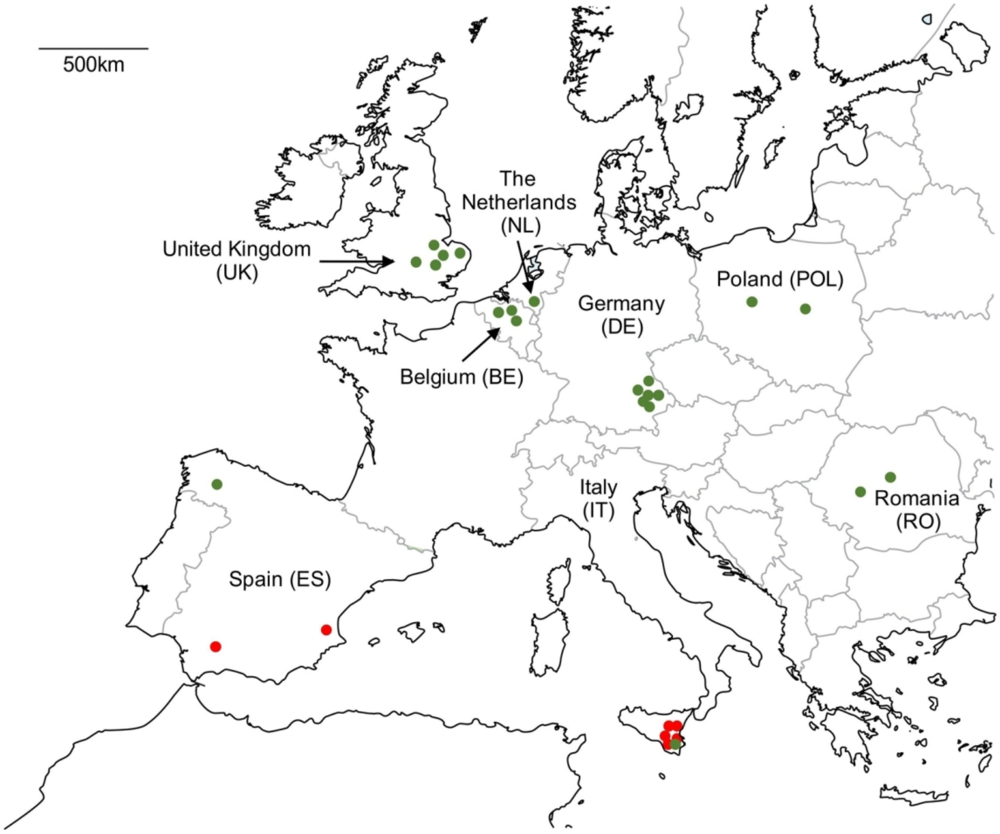
Table S2. Primers used in this study

Table S3. Information of selected populations for differential expression analysis (IT2vsRO1, UK6vsRO1 and ES1vsIT3)

Table S4. Read statistics for RNAseq samples of three resistant (IT2, UK6 and ES1) and two susceptible populations (RO1 and IT3) of *T. urticae*

Table S5. Twelve shared underexpressed (“core”) genes in the three resistant-susceptible comparisons combined with the linear model analysis

Table S6. Differentially expressed genes (DEGs) determined by either pairwise comparison between resistant (IT2, UK6 and ES1) and susceptible *T. urticae* populations (RO1 and IT3) or determined by using a multiple-factor linear model analysis (including all populations in one analysis).



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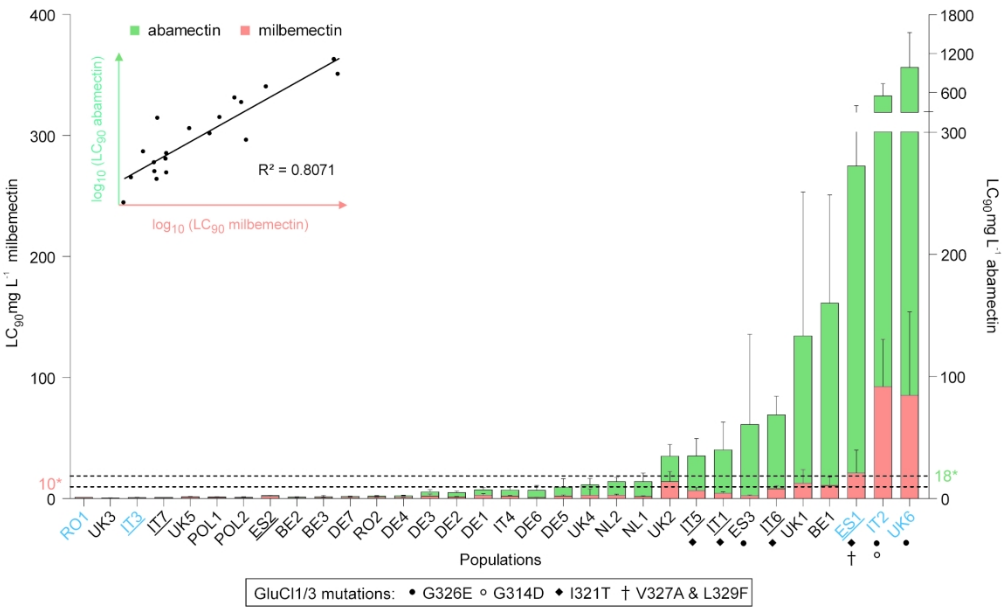

Figure 2. LC90 values of milbemectin and abamectin in field populations. The advised field doses (*) are indicated with dashed lines (10 mg a.i. /L for milbemectin and 18 mg a.i. /L for abamectin). Red colour morph populations are underlined, while green colour morph populations are not underlined. The presence of the G326E, G314D, I321T or V327A/L329F mutation in either GluCl1 or GluCl3 is indicated by a filled circle, hollow circle, black rhombus and a cross, respectively. Those strains used in the differential gene expression analysis are indicated in blue font. A correlation analysis (top left) between the log10 values of the LC90s of milbemectin and abamectin was performed with populations that had an LC90 value of more than 1 mg a.i. /L (19 populations) for both compounds

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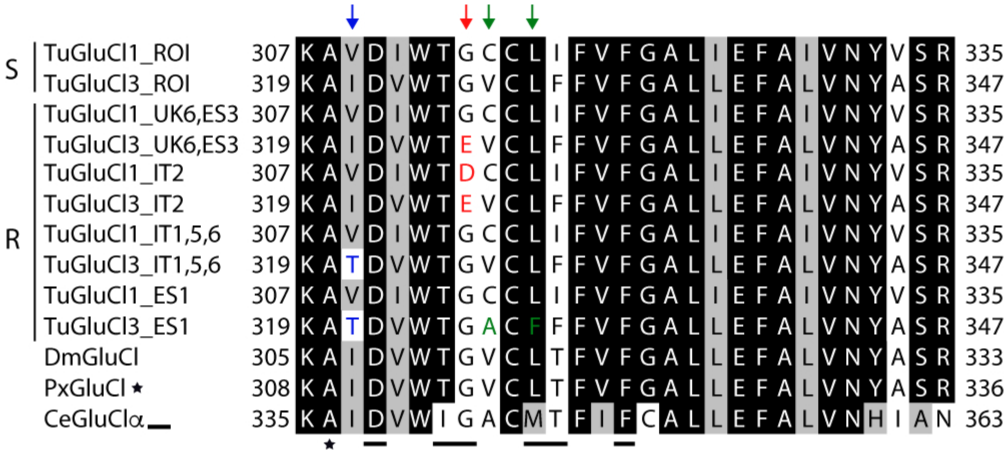

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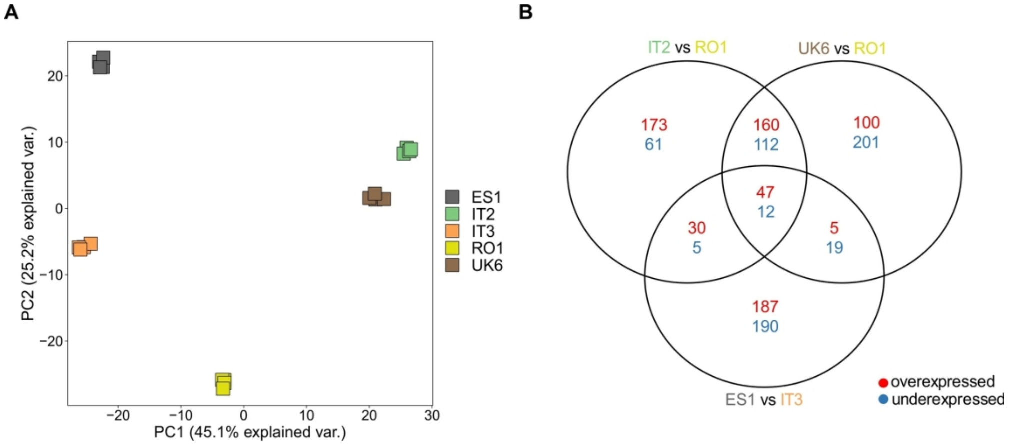

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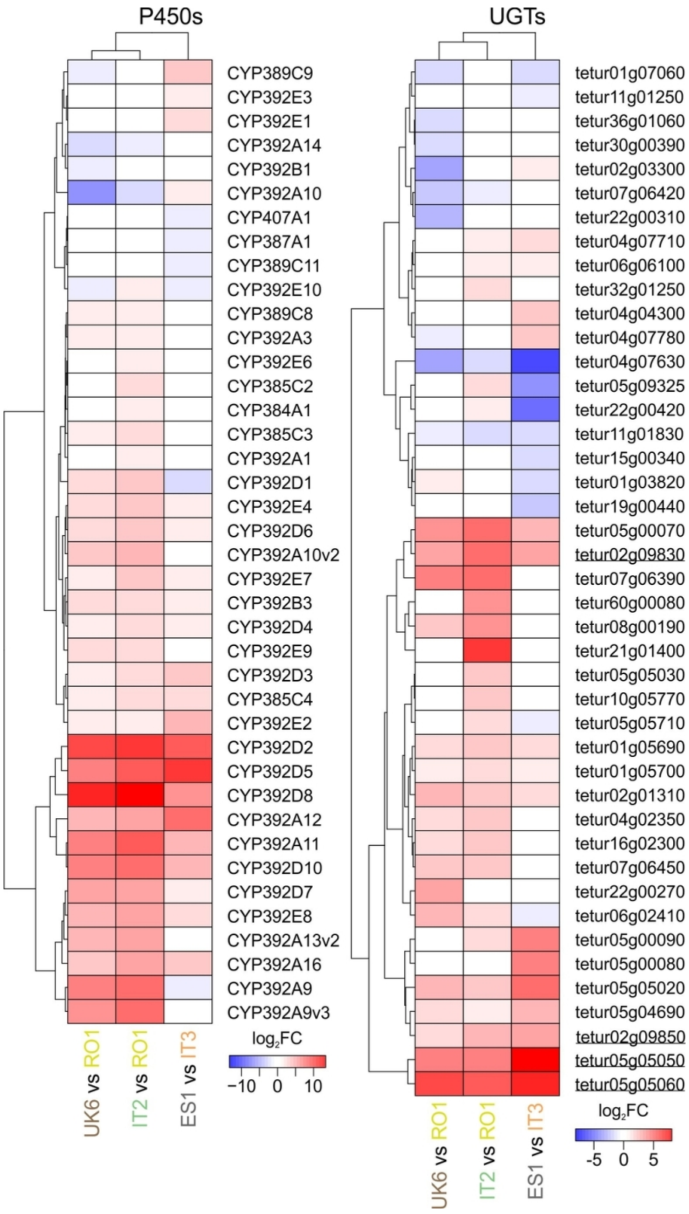

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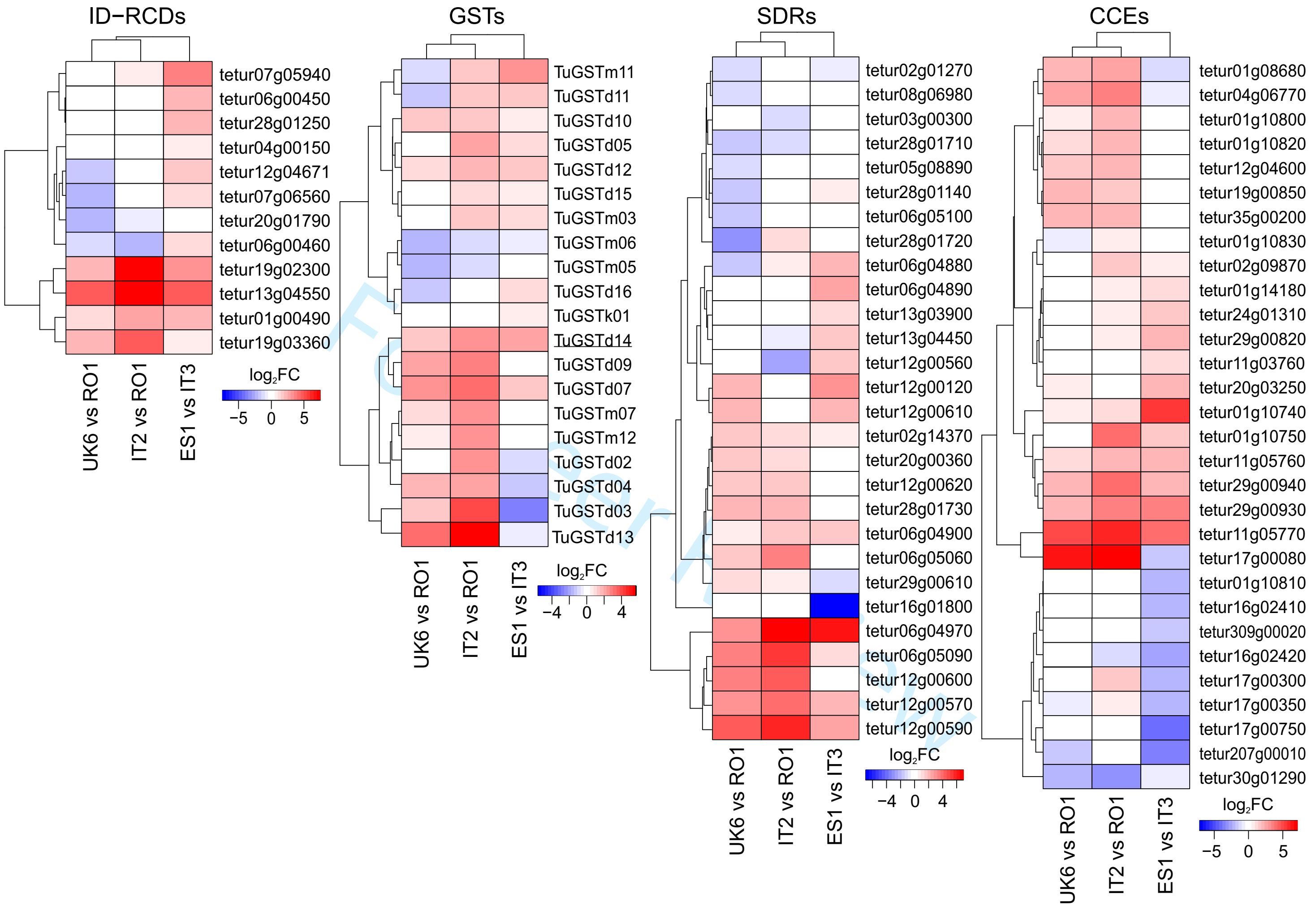
85x149mm (300 x 300 DPI)

Geographical distribution and molecular insights into abamectin and milbemectin cross-resistance in European field populations of *Tetranychus urticae*

Wenxin Xue, Simon Snoeck, Christine Njiru, Emre Inak, Wannes Dermauw, Thomas Van Leeuwen

Supplementary Figures



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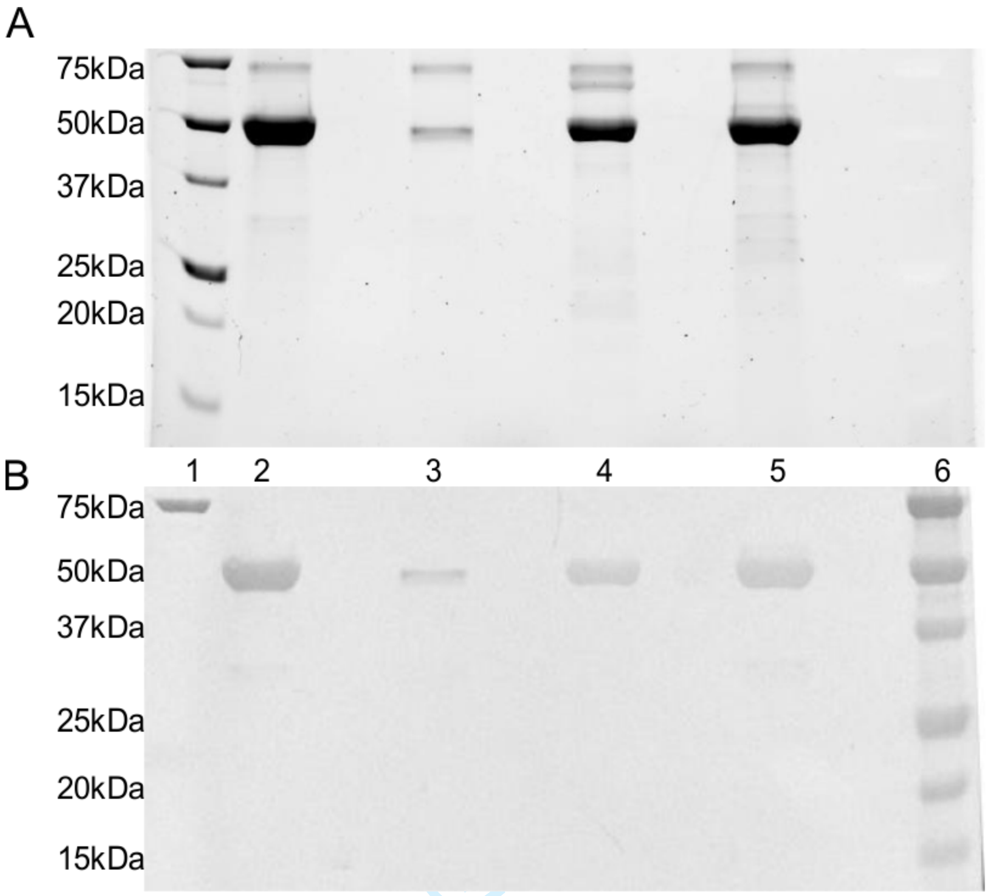

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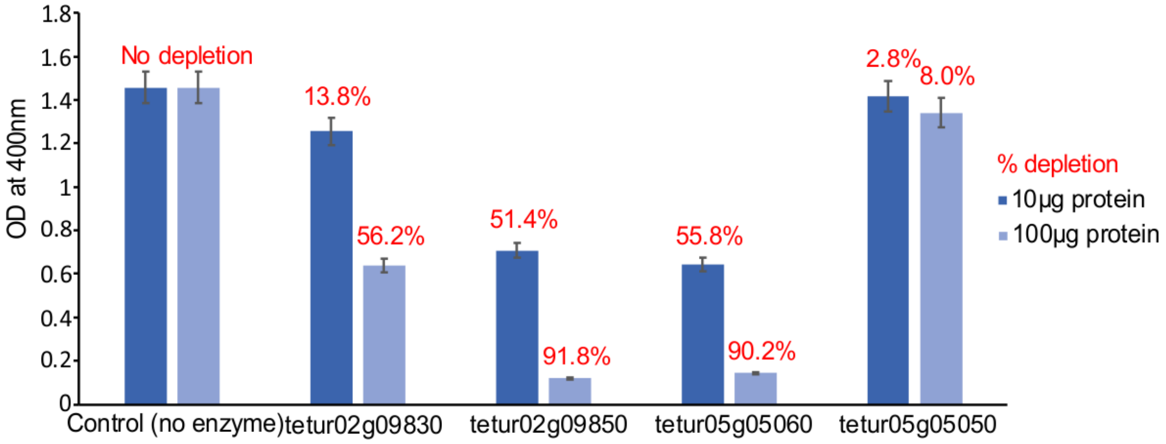

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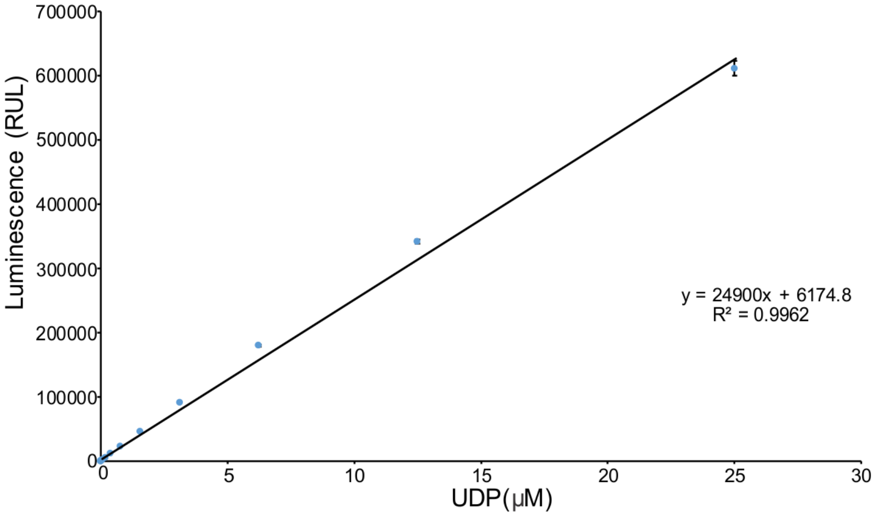

Figure S4. Standard curve glycosyltransferase assay. Free-UDP standard curve, Relative Luminescence Units (RLU) in function of free-UDP (range of 0-25μM). Values represent the mean of three replicates ± SD. The regression line (R^2=0.9964) was added to the plot as well as the 99% confidence interval.

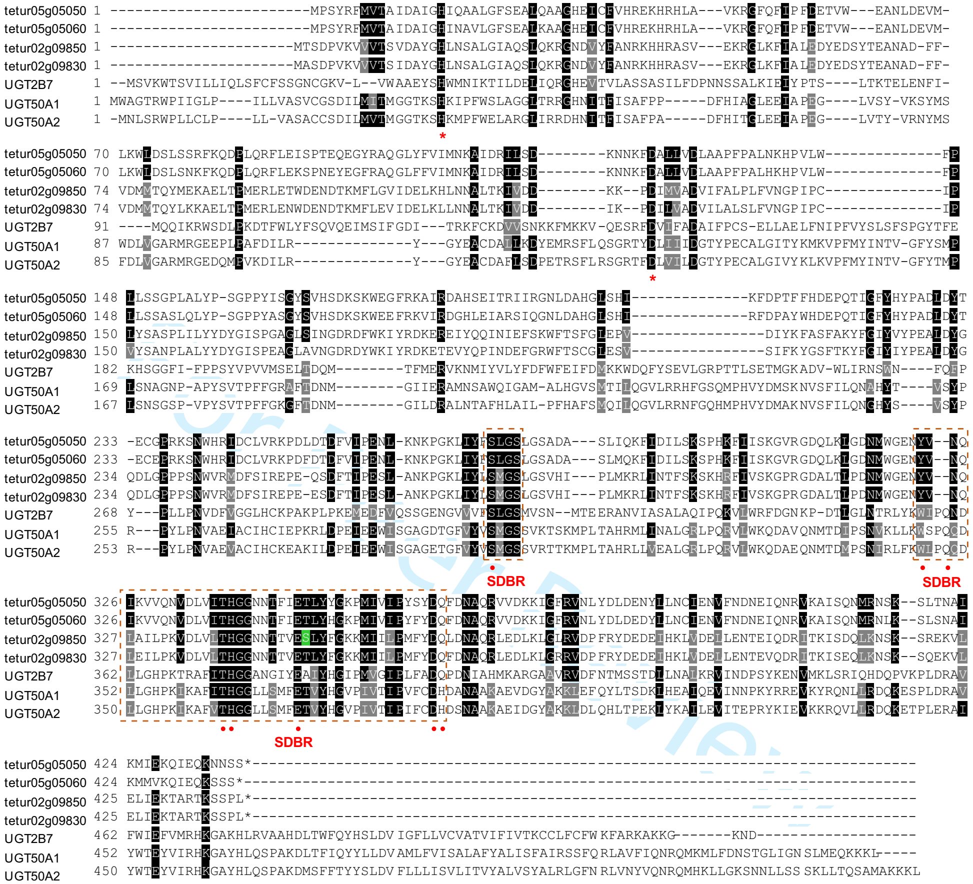

Figure S5. Multiple alignment of 7 UGTs. There are 4 *T. urticae* UGTs, UGT50A1 (Gnenbank ID: JQ070272) from *Bombyx mori*, UGT50A2 (Gnenbank ID: JQ070228) from *Helicoverpa armigera* and UGT2B7 (NCBI Reference Sequence: NP_001065) from *Homo sapiens*. Important catalytic residues, H and D are indicated by red asterisks (∗) under the alignment. SDBR refers to sugar donor binding region and several important residues interacting with the sugar donor are indicated by red dots (•) under the alignment by comparison with a human UGT2B7 crystal structure[67,68] and UGTs from *B. mori* and *H. armigera.*[66]

Table S1. Detailed information of collected *T. urticae* populations

Populations	Collection date	Country	City	Host plant
UK1	5/3/2017	United Kingdom	Nazeing	Cucumber
UK2	5/17/2017	United Kingdom	Worcestershire	Strawberry
ES1	5/23/2017	Spain	Sevilla	Strawberry
IT1	6/5/2017	Italia	Granieri	Cornation
IT2	6/5/2017	Italia	Comiso	Rose
UK3	5/30/2017	United Kingdom	Ruskington	Cucumber
UK4	6/5/2017	United Kingdom	Tunstead	Strawberry
DE1	6/28/2017	Germany	Attenhofen	Hops
DE2	7/10/2017	Germany	Au in der Hallertau	Hops
DE3	7/10/2017	Germany	Nandlstadt	Hops
DE4	7/10/2017	Germany	Nandlstadt	Hops
IT3	7/25/2017	Italy	Motta Sant'Anastasia	Citrus
RO1	7/25/2017	Romania	Blaj	Rose
DE5	5/14/2018	Germany	Neustadt an der Donau	Hops
IT4	5/21/2018	Italy	Maniace	Strawberry
IT5	5/22/2018	Italy	Granieri	Carnation
IT6	5/22/2018	Italy	Vittoria	Gerbera
BE1	5/24/2018	Belgium	Merelbeke	Rose
UK5	5/29/2018	United Kingdom	Double Yew Nursery	Lonicera
UK6	5/29/2018	United Kingdom	Double Yew Nursery	Euphorbia
RO2	7/4/2018	Romania	Balta	Rose
NL1	7/10/2018	The Netherlands	Meterik	Strawberry
POL1	8/7/2018	Poland	Wilcze srednie	Malus Domestica
POL2	8/7/2018	Poland	Dobiecin	Malus Domestica
DE6	8/14/2018	Germany	Volkenschwand	Hops
DE7	8/14/2018	Germany	Motzing	Potato
ES2	8/23/2018	Spain	Benimuslem	Citrus
NL2	9/4/2018	The Netherlands	Meterik	Strawberry
IT7	9/12/2018	Italy	San Giuseppe La Rena	Tangerine
BE2	9/14/2018	Belgium	Tienen	Potato
BE3	9/14/2018	Belgium	Jodoigne	Potato
ES3	9/10/2018	Spain	Monforte de Lemos	Strawberry

Red morph has been coloured red

Table S2. Primers used in this study

Tetur-ID	Primer name	Sequence (5’ - 3’)	
tetur02g04080	Tu_GluCl1_dia_F	TTGGATTGACCCTAACTCAGCA	(Dermauw et al. 2012)
	Tu_GluCl1_dia_R	TTGCACCAACAATTCCTTGA	
tetur08g04990	Tu_GluCl2_dia_F	TCATCGTCTCTTGGGTCTCC	
	Tu_GluCl2_dia_R	CCCATCGTCGTTGATACCTT	
tetur10g03090	Tu_GluCl3_dia_F	CCGGGTCAGTCTTGGTGTTA	
	Tu_GluCl3_dia_R	CACCACCAAGAACCTGTTGA	
tetur22g02450	Tu_GluCl4_dia_F	TATTCCAGCCCGAGTTTCAC	
	Tu_GluCl4_dia_R	AATCGGAGGTTGACTTGGTG	
tetur36g00090	Tu_GluCl5_dia_F	ATGTTGGTCATCGTTTCGTG	
	Tu_GluCl5_dia_R	AATCGGGATTGAATTTGCTG	
tetur05g05060	Tu05g05060_F	GCAATGCCTTCATATCGTTTTATGG	This study
	Tu05g05060_R	GCGCTCAAGATGAACTTTTTTGTTC	
tetur02g09830	Tu02g09830_F	TAAGCAATGGCCAGTGATCCAGTA	This Study
	Tu02g09830_R	CGCACGTTAAAGAGGAGACGATTT	

Table S3. Information of selected populations for differential expression analysis (IT2vsRO

	IT2	RO1	UK6
Type	Green	Green	Green
Host plant	Rose	Rose	Euphorbia
Location	Italy	Romania	The United Kingdom
LC 50(95% CI) /mg L-1 (Abamectin)	151.445	0.117	261.558
LC 50(95% CI) /mg L-1 (Milbemectin)	35.869	0.355	23.944

1, UK6vsRO1 and ES1vsIT3)

ES1	IT3
Red	Red
Strawberry	Citrus
Spain	Italy
73.444	0.141
4.073	0.205

Table S4 - Read st

RNAseq sample	number of reads
IT2_1	13586162
IT2_2	19027450
IT2_3	17966251
IT2_4	17510230
UK6_1	18361253
UK6_2	11699324
UK6_3	13797807
UK6_4	12490313
ES1_1	22761429
ES1_2	19794033
ES1_3	21391535
ES1_4	22904037
RO1_1	21754879
RO1_2	21906392
RO1_3	21657866
RO1_4	25868899
IT3_1	18084877
IT3_2	17068017
IT3_3	20777591
IT3_4	19343645
average	18887599
standard error of the mean	

atistics for RNAseq samples of three resistant populations (IT2, UK6 and

% overall alignment rate with *T. urticae* three-chromosome assembly
77.84%
78.78%
80.88%
77.32%
84.15%
84.05%
82.05%
81.68%
83.51%
79.82%
82.79%
83.53%
82.09%
84.16%
83.88%
85.56%
82.26%
60.47%
84.35%
83.52%
81.13%
1.19990542

ES1) and two susceptible strains (RO1 and IT3) of *T. urticae*

total number of reads/population or strain	average % overall alignment rate/population
68090093	78.71%
56348697	82.98%
86851034	82.41%
91188036	83.92%
75274130	77.65%

Table S5. Twelve shared underexpressed (“core”) ge

Gene ID	Description
tetur486g00010	DNA replication factor Cdt1
tetur21g02540	Steroid dehydrogenase
tetur17g02440	Similar to neprilysin; partial
tetur10g05570	Hypothetical protein
tetur07g91894	Leucine-rich repeat domain
tetur11g90924	Hypothetical protein
tetur14g03240	Hypothetical protein
tetur432g00010	Hypothetical protein
tetur486g00030	Nse4
tetur02g07590	Aldo-keto reductase family E
tetur65g00010	Leucine-rich repeat domain
tetur09g05220	Hypothetical protein

***** The Log_2FC of these 47 genes in the linear model analysis.

N/A: the gene was not detected as a differential expressed gene in the linear model analys enes in the three resistant-susceptible comparisons combined with the linear model analysis

Log$_2$FC		
IT2vsRO1	**UK6vsRO1**	**ES1vsIT3**
-4.09	-2.54	-3.44
-2.96	-3.88	-2.73
-3.73	-3.52	-3.76
-2.26	-2.7	-2.59
-4.79	-7.11	-4.76
-2.18	-8.64	-8.4
-4.2	-4.12	-3.15
-4.82	-6.61	-4.7
-3.28	-2.01	-2.25
-3.02	-3.13	-7.09
-2.67	-3.56	-2.5
-2.69	-2.96	-2.42

sis.

* Linear Model
-3.13
-3.52
-3.63
-2.5
-6.15
-7.79
-3.69
-5.59
-2.3
-4.74
-2.99
-2.75

Gene ID	$\log_2FC$
tetur03g05070	13.363214
tetur04g09459	12.005085
tetur07g04400	11.156148
tetur66g00060	10.656017
tetur04g09479	10.611798
tetur05g92600	10.393957
tetur03g04990	10.350371
tetur02g14470	10.174349
tetur16g03490	10.135975
tetur02g14420	10.087345
tetur04g09489	9.7728581
tetur04g00770	9.4728526
tetur28g92005	9.3735903
tetur243g00010	9.3499576
tetur06g02030	9.3476873
tetur14g01700	9.3008521
tetur14g00070	9.1436615
tetur11g05730	8.9457294
tetur10g05590	8.8706179
tetur14g00110	8.8085654
tetur651g00010	8.7525543
tetur15g01810	8.7501465
tetur03g05020	8.7205934
tetur30g00110	8.6620827
tetur02g12340	8.557002
tetur86g00060	8.5539733
tetur12g91729	8.4614971
tetur01g16463	8.4430286
tetur09g04540	8.3421721
tetur23g00210	8.2480847
tetur01g12600	8.2470863
tetur03g00970	8.18322
tetur02g14440	8.1127948
tetur07g02630	7.8325291
tetur14g04233	7.741339
tetur12g03210	7.6841837
tetur03g05110	7.6777391
tetur02g09200	7.6364615
tetur19g02300	7.5047973
tetur03g09040	7.4900282
tetur03g04360	7.4854964
tetur13g04550	7.4102634
tetur47g00090	7.3901025
tetur02g14330	7.3699484
tetur07g05770	7.3172425
tetur05g06440	7.2847067
tetur01g04940	7.2163469
tetur10g02890	7.2070518
tetur28g01460	7.2047246
tetur10g05854	7.1905803
tetur20g01380	7.1509494
tetur17g00080	7.1248022

tetur24g92198	7.0780544
tetur21g01370	6.9826354
tetur03g00950	6.882411
tetur06g02270	6.8784602
tetur13g04170	6.8646721
tetur30g01360	6.8576436
tetur09g00820	6.831013
tetur01g12400	6.7668247
tetur03g00980	6.7408336
tetur01g10110	6.7325744
tetur02g15041	6.706296
tetur26g00550	6.6886231
tetur13g00610	6.6555965
tetur02g11000	6.5789818
tetur28g92008	6.5685553
tetur21g00340	6.5231913
tetur06g04970	6.5195247
tetur05g06420	6.5099219
tetur07g07730	6.4862966
tetur09g07580	6.4766005
tetur67g00010	6.4748563
tetur28g00670	6.4282401
tetur315g90211	6.4048583
tetur40g00030	6.3519142
tetur83g90373	6.3464812
tetur01g02610	6.3401893
tetur02g07770	6.3089759
tetur09g03740	6.2907498
tetur02g05670	6.2241714
tetur03g10033	6.187382
tetur01g13120	6.1859281
tetur28g00660	6.1785168
tetur24g00510	6.1013683
tetur08g05850	6.0922203
tetur11g05770	6.0531613
tetur05g06470	6.0517835
tetur03g05100	6.0424397
tetur12g00590	6.0164148
tetur21g01400	6.0081227
tetur05g02230	5.9845176
tetur47g00220	5.973005
tetur143g00020	5.910817
tetur09g92864	5.8180066
tetur47g00120	5.7945508
tetur03g10063	5.7792086
tetur04g90885	5.7210201
tetur02g11020	5.6980951
tetur14g03970	5.6697716
tetur26g01510	5.6148064
tetur02g07750	5.5743647
tetur31g00880	5.4926951
tetur21g01360	5.4488462
tetur01g15540	5.4277306
tetur07g02230	5.4236042
tetur06g05090	5.3578777
tetur11g04080	5.3022426

tetur17g03410	5.295009
tetur26g00540	5.2612446
tetur03g00020	5.2012545
tetur05g05060	5.1088751
tetur540g00010	5.0808789
tetur17g03950	5.0770316
tetur06g02040	5.0269884
tetur27g00220	4.9948225
tetur03g00830	4.986917
tetur668g00010	4.9602483
tetur21g01410	4.9601604
tetur128g00020	4.9558483
tetur24g00160	4.9549847
tetur17g03530	4.9328191
tetur28g01030	4.8775935
tetur19g03360	4.8707518
tetur02g12360	4.8163814
tetur02g14741	4.813587
tetur05g00070	4.8011064
tetur120g00040	4.7958402
tetur13g00650	4.7734583
tetur06g01610	4.7620414
tetur171g90421	4.7438402
tetur05g00160	4.7300136
tetur27g00350	4.7285894
tetur20g00470	4.6377068
tetur03g09961	4.6201123
tetur09g92915	4.6064768
tetur01g11990	4.5937679
tetur174g00010	4.5864502
tetur03g05040	4.5469272
tetur05g06430	4.5453062
tetur06g04520	4.5227782
tetur03g06580	4.5106509
tetur10g02870	4.505872
tetur36g91067	4.5035249
tetur24g02680	4.4913596
tetur07g06390	4.4756319
tetur12g00600	4.414205
tetur02g14460	4.3927641
tetur01g05740	4.3855216
tetur01g06730	4.3560883
tetur07g02420	4.3542617
tetur02g09830	4.3475743
tetur23g00880	4.3423951
tetur33g01520	4.3240532
tetur03g09510	4.300706
tetur14g04180	4.2991434
tetur26g02903	4.2614127
tetur24g00200	4.2463457
tetur08g05010	4.237352
tetur36g00530	4.2071989
tetur01g01510	4.1930533
tetur03g00780	4.1902187
tetur06g04920	4.1871219
tetur12g00580	4.1849835

tetur10g05690	4.1319811
tetur12g00570	4.1244628
tetur184g00040	4.1201182
tetur188g00040	4.1179505
tetur01g10750	4.0607469
tetur02g08720	4.0488597
tetur24g00170	4.0142412
tetur06g04960	4.0097117
tetur11g05410	3.9542211
tetur01g13610	3.9485866
tetur29g00940	3.9470114
tetur21g03340	3.8887215
tetur11g05740	3.8867058
tetur11g04480	3.8598667
tetur03g07460	3.8477872
tetur05g05050	3.8457752
tetur28g01330	3.8125686
tetur08g05990	3.7973004
tetur01g02480	3.7588393
tetur01g08280	3.7439863
tetur26g00560	3.7321719
tetur09g92920	3.7283848
tetur10g92068	3.7252845
tetur02g14400	3.7026938
tetur16g03680	3.6942036
tetur14g03880	3.6809984
tetur20g01190	3.6724747
tetur466g00030	3.6608167
tetur08g00190	3.6452419
tetur04g06770	3.6143935
tetur24g00520	3.6091664
tetur29g00930	3.5907186
tetur26g00370	3.576066
tetur03g07490	3.5374838
tetur11g00720	3.5146549
tetur03g05880	3.5119278
tetur01g15500	3.5034755
tetur28g00580	3.5020791
tetur12g00740	3.4860759
tetur02g07760	3.4844634
tetur01g15490	3.4752053
tetur60g00080	3.4590752
tetur31g01950	3.4411963
tetur02g14410	3.4197675
tetur03g04370	3.4047399
tetur01g01500	3.4002847
tetur89g00020	3.3771871
tetur04g02440	3.3733341
tetur10g04020	3.3433234
tetur03g05030	3.3399624
tetur13g01210	3.3195772
tetur06g05060	3.3176334
tetur16g03200	3.3128076
tetur17g00660	3.3116618
tetur28g00630	3.2966785
tetur05g07750	3.2891805

tetur03g08160	3.2853142
tetur19g03010	3.2771053
tetur12g03950	3.2760461
tetur11g05720	3.2756572
tetur17g03540	3.2651272
tetur02g14540	3.2487941
tetur380g00010	3.2383003
tetur02g06900	3.2329257
tetur04g90883	3.2299594
tetur128g00030	3.2269206
tetur123g00050	3.2234887
tetur01g13600	3.2136636
tetur30g00080	3.2038329
tetur24g00860	3.1819518
tetur03g02760	3.1776547
tetur32g00960	3.1762069
tetur31g02020	3.1700396
tetur614g00010	3.1200391
tetur55g00120	3.1020418
tetur07g04960	3.1018103
tetur23g91461	3.0734696
tetur19g00500	3.0718605
tetur03g07510	3.0632043
tetur11g05440	3.0619129
tetur04g06160	3.049359
tetur25g00410	3.047418
tetur06g03470	3.0359318
tetur08g07760	3.0191815
tetur26g01450	3.0183447
tetur21g03010	3.0106544
tetur09g01020	3.0044944
tetur20g02200	2.9587888
tetur35g00180	2.955873
tetur26g02801	2.9556669
tetur305g00010	2.9459286
tetur66g00070	2.93856
tetur20g00450	2.9286358
tetur27g02598	2.9196527
tetur557g00020	2.9113649
tetur30g01810	2.910609
tetur16g01140	2.9041862
tetur24g00440	2.8927445
tetur06g01690	2.8913162
tetur13g02590	2.8904374
tetur20g00440	2.8890323
tetur06g02130	2.8871918
tetur23g02020	2.8855787
tetur23g00260	2.8731851
tetur05g92637	2.8646268
tetur06g04940	2.8554364
tetur30g01750	2.8426169
tetur08g06030	2.839866
tetur02g04900	2.838551
tetur11g00780	2.8345225
tetur27g00340	2.824116
tetur16g02250	2.8201355

tetur04g05540	2.8159055
tetur08g07170	2.8123606
tetur106g00050	2.8109295
tetur24g00770	2.809631
tetur318g00010	2.8063527
tetur20g00010	2.8061588
tetur01g14350	2.7528073
tetur14g03800	2.7511313
tetur20g00020	2.7467171
tetur06g91385	2.7414299
tetur22g02780	2.736296
tetur24g01030	2.6940975
tetur04g02380	2.6928194
tetur30g01110	2.6873094
tetur11g90914	2.6840187
tetur13g92965	2.6831119
tetur02g11030	2.6806212
tetur12g03940	2.6722823
tetur90g00030	2.6593529
tetur28g02510	2.6395742
tetur06g01100	2.637778
tetur34g00160	2.6265146
tetur16g03330	2.6264871
tetur01g03110	2.6142202
tetur30g01790	2.6086632
tetur24g02580	2.6066562
tetur43g00580	2.6060428
tetur01g00490	2.6011296
tetur02g14280	2.5913196
tetur07g05900	2.588671
tetur154g00010	2.5616979
tetur09g04470	2.5603909
tetur01g03880	2.5580561
tetur30g00100	2.557605
tetur28g01420	2.5527183
tetur04g03910	2.5432489
tetur04g08760	2.5299192
tetur06g03070	2.526795
tetur06g04980	2.5200599
tetur31g00830	2.5140506
tetur22g01210	2.5075383
tetur04g00760	2.4941547
tetur03g00400	2.4930838
tetur08g07790	2.4853903
tetur05g05240	2.4813056
tetur01g08680	2.4768374
tetur09g00610	2.4652932
tetur17g03420	2.46381
tetur01g11780	2.4389165
tetur05g05300	2.4378107
tetur507g00010	2.4299938
tetur06g01700	2.4267324
tetur01g02470	2.4265251
tetur136g00040	2.4259629
tetur23g01820	2.423919
tetur33g01630	2.4108937

tetur29g00220	2.4087894
tetur437g00030	2.4035553
tetur18g01260	2.3945425
tetur11g05540	2.3945017
tetur04g00790	2.3847703
tetur02g10370	2.3825676
tetur22g02040	2.3816114
tetur30g01270	2.3755715
tetur11g01020	2.3726112
tetur03g09880	2.371773
tetur24g00830	2.3713151
tetur01g10820	2.3619878
tetur12g02110	2.3609979
tetur16g03420	2.3450201
tetur06g04580	2.3420072
tetur28g01360	2.3400844
tetur02g14561	2.339338
tetur13g04350	2.335091
tetur02g09850	2.3151351
tetur30g00090	2.3081253
tetur21g00410	2.306085
tetur19g02880	2.3042425
tetur437g00010	2.298563
tetur09g00490	2.2912121
tetur01g05730	2.2902268
tetur63g00030	2.290039
tetur01g12480	2.2862107
tetur11g05760	2.2817689
tetur35g00190	2.2768734
tetur15g00280	2.2556864
tetur30g01740	2.2552461
tetur12g04600	2.2462275
tetur24g01970	2.245917
tetur03g05000	2.2435236
tetur208g00020	2.2353491
tetur02g13050	2.2175299
tetur17g03390	2.2153667
tetur18g01440	2.2147278
tetur02g09730	2.212932
tetur24g00220	2.2047657
tetur46g00010	2.1825899
tetur36g00010	2.1789595
tetur01g02510	2.1785481
tetur14g03760	2.1759951
tetur11g04470	2.1715405
tetur08g04870	2.16911
tetur28g01730	2.1640976
tetur01g02500	2.1622477
tetur08g03270	2.1608725
tetur06g01570	2.1509627
tetur615g00020	2.1448484
tetur01g10800	2.1408956
tetur06g91354	2.1223548
tetur07g06710	2.1141459
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tetur04g92244	-1.197631
tetur22g02270	-1.19887
tetur16g02420	-1.199865
tetur641g00010	-1.202699
tetur11g00760	-1.204009
tetur08g02700	-1.204585
tetur01g01140	-1.207157
tetur01g08180	-1.207209
tetur09g01930	-1.207816
tetur09g01720	-1.208586
tetur10g04390	-1.208785
tetur01g09190	-1.210556
tetur03g09360	-1.215466
tetur55g00100	-1.219321
tetur17g02630	-1.222088
tetur14g03670	-1.224827
tetur01g07120	-1.228337
tetur35g01100	-1.230786
tetur122g00010	-1.232411
tetur547g00010	-1.233013
tetur20g00750	-1.234302
tetur30g01550	-1.235774
tetur05g92632	-1.236156
tetur03g06820	-1.23995
tetur08g04040	-1.24169
tetur02g92502	-1.256975
tetur15g02090	-1.259307
tetur352g00020	-1.259383
tetur05g04710	-1.259763
tetur04g92241	-1.261477
tetur18g01750	-1.262088
tetur01g02690	-1.264595
tetur08g06210	-1.265283
tetur28g00280	-1.26984
tetur30g01240	-1.276674
tetur06g03420	-1.278981
tetur01g02900	-1.280687

tetur11g05200	-1.2831
tetur43g00020	-1.283985
tetur30g02080	-1.285675
tetur306g00010	-1.286169
tetur01g13290	-1.28626
tetur01g16010	-1.287134
tetur02g04760	-1.287377
tetur01g09260	-1.289886
tetur26g00490	-1.294028
tetur30g01250	-1.29516
tetur07g03790	-1.29793
tetur02g00510	-1.297963
tetur04g00270	-1.30222
tetur03g02200	-1.305556
tetur07g03210	-1.308371
tetur18g02050	-1.310009
tetur08g07340	-1.312792
tetur17g01150	-1.314439
tetur35g00310	-1.315856
tetur22g01100	-1.316173
tetur28g00780	-1.320466
tetur01g04860	-1.321401
tetur37g00540	-1.323535
tetur10g03160	-1.327039
tetur18g02510	-1.333508
tetur05g05640	-1.336139
tetur20g01390	-1.336648
tetur03g08460	-1.346959
tetur32g02040	-1.349422
tetur31g00640	-1.353421
tetur13g92982	-1.360394
tetur23g02150	-1.362545
tetur06g03280	-1.362864
tetur32g90860	-1.363095
tetur02g15167	-1.367297
tetur08g00240	-1.36893
tetur10g03600	-1.370983
tetur39g00230	-1.372697
tetur11g01830	-1.376632
tetur28g02430	-1.377836
tetur01g12820	-1.378658
tetur01g14730	-1.380094
tetur05g03650	-1.382256
tetur06g00230	-1.384662
tetur06g00610	-1.388841
tetur13g04678	-1.39261
tetur29g01610	-1.3929
tetur24g01280	-1.396811
tetur02g02390	-1.398804
tetur17g03590	-1.400587
tetur09g04760	-1.401315
tetur06g00550	-1.410002
tetur01g10910	-1.410451
tetur39g00730	-1.412956
tetur17g00850	-1.413199
tetur04g02530	-1.417041

tetur04g00810	-1.417947
tetur10g04000	-1.429444
tetur04g01270	-1.432683
tetur04g07630	-1.433226
tetur91g00020	-1.433625
tetur11g04810	-1.434919
tetur01g14390	-1.441643
tetur02g07220	-1.451959
tetur07g08040	-1.453993
tetur20g00970	-1.461533
tetur15g02070	-1.464065
tetur23g00480	-1.485121
tetur192g00020	-1.485453
tetur12g02340	-1.493155
tetur08g07940	-1.496916
tetur13g02500	-1.49702
tetur09g05140	-1.497063
tetur07g06700	-1.502292
tetur02g05970	-1.50406
tetur90g00050	-1.504968
tetur05g00130	-1.505732
tetur16g03240	-1.507405
tetur126g00010	-1.50922
tetur20g01650	-1.514592
tetur02g03070	-1.515659
tetur24g00950	-1.516855
tetur29g00540	-1.523501
tetur01g00610	-1.526462
tetur32g00690	-1.537869
tetur14g03770	-1.538569
tetur06g04150	-1.545743
tetur12g91730	-1.552923
tetur16g02820	-1.554985
tetur36g00190	-1.55818
tetur04g90877	-1.560856
tetur02g13900	-1.566066
tetur04g09509	-1.570774
tetur10g04820	-1.57306
tetur18g01090	-1.573341
tetur19g02270	-1.573468
tetur14g01100	-1.580494
tetur13g02150	-1.586959
tetur11g90913	-1.590123
tetur11g05660	-1.601409
tetur07g06750	-1.603946
tetur19g00200	-1.605871
tetur10g00740	-1.610033
tetur10g03590	-1.612769
tetur04g03720	-1.613909
tetur15g03640	-1.614305
tetur23g91467	-1.617826
tetur17g00510	-1.626901
tetur39g00780	-1.638081
tetur21g03160	-1.638775
tetur11g01910	-1.645155
tetur12g02810	-1.658446

tetur14g92990	-1.664475
tetur27g01280	-1.665783
tetur04g02830	-1.667584
tetur11g05010	-1.668217
tetur20g01200	-1.677573
tetur66g00140	-1.678777
tetur04g06870	-1.691118
tetur06g00420	-1.692401
tetur77g00040	-1.695125
tetur01g09840	-1.705036
tetur01g00860	-1.705745
tetur58g90065	-1.707998
tetur352g00040	-1.710118
tetur03g00200	-1.722813
tetur05g02680	-1.722813
tetur17g03720	-1.724908
tetur516g00020	-1.725243
tetur14g02720	-1.727702
tetur05g05600	-1.729114
tetur11g05220	-1.732826
tetur03g06170	-1.744157
tetur07g06740	-1.746144
tetur55g00160	-1.749994
tetur07g01420	-1.757789
tetur136g00050	-1.768719
tetur01g03020	-1.778019
tetur02g04810	-1.779605
tetur30g00420	-1.781651
tetur20g00400	-1.786519
tetur08g02000	-1.791016
tetur01g00530	-1.792125
tetur12g02350	-1.811195
tetur19g00790	-1.811875
tetur18g02300	-1.822835
tetur02g02400	-1.824178
tetur07g07010	-1.824489
tetur37g00560	-1.83178
tetur02g13120	-1.845226
tetur149g00010	-1.868915
tetur03g06800	-1.882389
tetur46g00020	-1.8946
tetur11g04600	-1.896205
tetur02g90622	-1.898251
tetur22g02640	-1.898819
tetur06g03380	-1.901151
tetur07g03400	-1.908037
tetur01g08070	-1.91162
tetur03g91543	-1.918594
tetur29g00990	-1.931817
tetur12g02130	-1.937139
tetur31g00900	-1.94899
tetur18g00810	-1.958557
tetur03g00280	-1.961037
tetur28g01130	-1.965768
tetur02g03100	-1.967685
tetur31g01890	-1.971177

tetur13g01730	-1.978066
tetur03g03730	-1.979468
tetur17g92128	-1.979918
tetur09g05700	-1.983851
tetur03g09921	-1.989778
tetur03g03070	-1.998939
tetur17g92120	-2.004458
tetur30g01100	-2.005969
tetur03g07820	-2.007019
tetur06g91386	-2.011564
tetur05g03090	-2.027963
tetur41g00160	-2.036476
tetur19g92445	-2.044461
tetur03g00560	-2.054586
tetur20g00700	-2.065769
tetur01g05310	-2.082117
tetur03g91512	-2.109361
tetur16g00850	-2.110199
tetur01g05230	-2.111455
tetur13g02600	-2.112972
tetur01g00410	-2.113995
tetur06g01390	-2.119821
tetur01g07180	-2.120283
tetur14g03810	-2.153529
tetur06g02440	-2.154935
tetur230g00010	-2.159612
tetur233g00040	-2.160721
tetur11g00200	-2.16406
tetur02g13070	-2.164207
tetur191g00020	-2.170787
tetur11g90924	-2.181696
tetur06g02610	-2.191375
tetur31g00630	-2.211227
tetur01g07710	-2.211824
tetur16g03570	-2.225387
tetur11g01550	-2.235947
tetur10g05570	-2.265612
tetur03g07240	-2.301918
tetur22g02730	-2.305326
tetur09g03090	-2.308313
tetur27g00680	-2.319099
tetur05g05610	-2.320994
tetur03g00290	-2.321236
tetur50g00070	-2.326838
tetur06g06650	-2.347026
tetur02g14140	-2.35654
tetur30g00680	-2.361083
tetur16g03790	-2.374189
tetur01g08700	-2.374795
tetur01g16350	-2.376688
tetur21g01500	-2.382555
tetur72g00010	-2.410104
tetur12g00560	-2.424402
tetur01g08100	-2.425932
tetur16g03590	-2.430176
tetur05g02100	-2.442204

tetur48g00020	-2.454873
tetur06g00460	-2.458423
tetur05g01550	-2.464606
tetur07g02270	-2.467967
tetur04g03360	-2.483162
tetur29g01670	-2.49327
tetur31g00690	-2.515818
tetur08g03130	-2.543304
tetur07g00810	-2.546849
tetur08g06700	-2.550362
tetur11g05450	-2.605327
tetur02g05250	-2.608661
tetur20g00480	-2.621647
tetur02g13810	-2.632959
tetur01g16874	-2.644084
tetur01g01010	-2.665288
tetur65g00010	-2.673824
tetur09g05220	-2.693775
tetur11g03880	-2.716937
tetur05g05100	-2.718808
tetur09g00900	-2.72009
tetur01g10450	-2.744164
tetur33g90843	-2.796794
tetur92g00010	-2.818237
tetur248g00020	-2.82567
tetur01g12410	-2.83869
tetur21g03250	-2.843421
tetur07g05930	-2.854912
tetur07g07950	-2.866217
tetur30g01290	-2.892984
tetur20g00570	-2.89946
tetur35g01090	-2.914944
tetur22g00890	-2.916948
tetur28g01070	-2.930929
tetur08g03200	-2.950423
tetur01g10950	-2.954589
tetur21g02540	-2.956741
tetur04g03040	-2.960382
tetur16g00100	-2.973
tetur01g05850	-2.974494
tetur207g00020	-2.978102
tetur02g07590	-3.02016
tetur04g08890	-3.092958
tetur09g01070	-3.10023
tetur14g02600	-3.103741
tetur19g01180	-3.103749
tetur03g00940	-3.116682
tetur134g00010	-3.118065
tetur18g02750	-3.173573
tetur06g02590	-3.181761
tetur23g01620	-3.198369
tetur05g02480	-3.231041
tetur06g03050	-3.239657
tetur486g00030	-3.275514
tetur01g01000	-3.305838
tetur511g00010	-3.369185

tetur07g07890	-3.369874
tetur43g00480	-3.419737
tetur11g00940	-3.42582
tetur30g01320	-3.427427
tetur22g01220	-3.440844
tetur20g01410	-3.47329
tetur12g03180	-3.503995
tetur02g09760	-3.513471
tetur184g00010	-3.539662
tetur06g05830	-3.541093
tetur31g00860	-3.544793
tetur03g09750	-3.591559
tetur23g00240	-3.60054
tetur92g00020	-3.609597
tetur48g00120	-3.624537
tetur07g03950	-3.624702
tetur01g04360	-3.680336
tetur07g02410	-3.705219
tetur06g06630	-3.709757
tetur17g02440	-3.728411
tetur30g01300	-3.790186
tetur23g00250	-3.795402
tetur13g02000	-3.808691
tetur30g00690	-3.900521
tetur32g00050	-3.933386
tetur657g00010	-3.960137
tetur154g00030	-3.9682
tetur09g01050	-3.994659
tetur343g00010	-3.998912
tetur149g00020	-4.004587
tetur366g00010	-4.044561
tetur486g00010	-4.088706
tetur34g00090	-4.09115
tetur28g00610	-4.111158
tetur22g01050	-4.174322
tetur14g03240	-4.196749
tetur10g05824	-4.265204
tetur02g04730	-4.3049
tetur30g00700	-4.338525
tetur01g08370	-4.378357
tetur415g00010	-4.403639
tetur03g08450	-4.467794
tetur04g06430	-4.598966
tetur16g04149	-4.613529
tetur20g01420	-4.628876
tetur63g90083	-4.642672
tetur02g07550	-4.644652
tetur30g00730	-4.645842
tetur08g05980	-4.652555
tetur14g03250	-4.655617
tetur508g00010	-4.690914
tetur12g04641	-4.701746
tetur02g05310	-4.770444
tetur07g91894	-4.794402
tetur432g00010	-4.81835
tetur522g00010	-4.836644

tetur21g00780	-4.871341
tetur12g02790	-4.886002
tetur607g00010	-4.906851
tetur22g02170	-4.933183
tetur18g00510	-5.003119
tetur13g03320	-5.190037
tetur192g00010	-5.367158
tetur11g05710	-5.511477
tetur02g02690	-5.527651
tetur08g04090	-5.601077
tetur14g02490	-5.73827
tetur08g04020	-5.864771
tetur03g07880	-6.056953
tetur04g02230	-6.101201
tetur01g91139	-6.124019
tetur04g06440	-6.409309
tetur09g04730	-6.426557
tetur48g00050	-6.429798
tetur06g03010	-6.486429
tetur12g02850	-6.544122
tetur511g00020	-6.751401
tetur36g91078	-6.807423
tetur28g01340	-6.830353
tetur20g00740	-7.105912
tetur44g00301	-7.136039
tetur28g00590	-7.420942
tetur17g01910	-8.080266
tetur27g00290	-8.995821

Table S6 - Differentially expressed genes (DEGs) and significantly over/underexpressed genes between thre

IT2 vs RO

description
CYP392D8 Cytochrome P450 - CYP392D8
SSPF2 Small Secreted Protein; Family F hypothetical protein
Immunoglobulin-like fold
SP45_2 Serine protease SP47 Serine protease
SSPF3 Small Secreted Protein; Family F hypothetical protein
hypothetical protein
CYP392D2 Cytochrome P450 - CYP392D2
Hypothetical protein
antigen B membrane protein
Hypothetical protein
SSPF4 Small Secreted Protein; Family F hypothetical protein
SSPF1 Small Secreted Protein; Family F transporter; AcrB/AcrD/AcrF family protein transporter; AcrB/AcrD/A
hypothetical protein
Hypothetical protein
SLIT-ROBO Rho GTPase activating protein 2
MDL14 Immunoglobulin E-set Immunoglobulin E-set
Hypothetical protein
PLAT11 PLAT/LH2 domain PLAT/LH2 domain PLAT/LH2 domain PLAT/LH2 domain PLAT/LH2 domain
HNTX-XIV-3.2 precursor
Hypothetical protein
ribosomal protein S12
partitioning defective 6 homolog beta
CYP392D5p Cytochrome P450 - CYP392D5p probable pseudogene
exosome complex exonuclease RRP46
BTB/Kelch-associated
SSPF6 Calycin-like Calycin-like
hypothetical protein
TuPap-18 Peptidase C1A, papain C-terminal Peptidase C1A, papain C-terminal
TuPap-58 Cathepsin L
DDM9-19 Domain of unknown function DUF3421 Domain of unknown function DUF3421
Hypothetical protein
CYP392A11 Cytochrome P450 - CYP392A11 CYP392A11v2 Cytochrome P450 - CYP392A11v2
Hypothetical protein
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like
hypothetical protein
Hypothetical protein
CYP392D10p Cytochrome P450 - CYP392D10p probable pseudogene
Hypothetical protein
intradiol ring-cleavage dioxygenase
NAT10 Acyl-CoA N-acyltransferase Acyl-CoA N-acyltransferase
Hypothetical protein
Intradiol ring-cleavage dioxygenase, core Intradiol ring-cleavage dioxygenase, core
CYP392A9 Cytochrome P450 - CYP392A9
CYP392A9v2 Cytochrome P450 - CYP392A9v2
Scramblase
Tudor domain
Hypothetical protein
Hypothetical protein
potential DNA-binding protein C17orf49
hypothetical protein
Hypothetical protein
TuCCE44 Carboxyl/cholinesterase TuCCE-38 Carboxyl/cholinesterase

hypothetical protein
undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase
Hypothetical protein
Hypothetical protein
GE26306
hypothetical protein StAA4_21417
hypothetical protein
Hypothetical protein
Hypothetical protein
Hypothetical protein
BTB/Kelch-associated BTB/Kelch-associated
UNCoordinated family member
Hypothetical protein
Hypothetical protein
hypothetical protein
Hypothetical protein
3-oxoacyl-acyl-carrier-protein reductase
Hypothetical protein
Hypothetical protein
hypothetical protein
Cytochrome P450
PLC-like phosphodiesterase, TIM beta/alpha-barrel domain
hypothetical protein
Major facilitator superfamily; general substrate transporter
hypothetical protein
MDL4 Immunoglobulin E-set Immunoglobulin E-set
Glycoside hydrolase; subgroup; catalytic core
WTTMP1 Wannes-Thomas type-I single-pass transmembrane protein type-I single-pass transmembrane prote
GI21111

RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like
PLC-like phosphodiesterase, TIM beta/alpha-barrel domain
Hypothetical protein
Lipase
TuCCE35 Carboxyl/cholinesterase TuCCE35 Carboxylesterase; type B TuCCE34 Carboxylesterase; type B Tu
Zinc finger, DksA/TraR C4-type conserved site
CYP392Dn Cytochrome P450, conserved site CYP Cytochrome P450, conserved site Cytochrome P450, con
C-factor
UGT UDP-glycosyltransferase; teturUGT58p UGT UDP-glycosyltransferase; teturUGT58 UDP-glycosyltransfe
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like
Hypothetical protein
SSPF8 Small Secretory Protein; Family F hypothetical protein
hypothetical protein
Hypothetical protein
SSPB3 Small Secreted Protein; Family B hypothetical protein
hypothetical protein
Tu_12344.2 cys-loop ligand-gated ion channel Tu_12344.2 ligand-gated ion channel glycine receptor-like E3
ACYPI009414
TuGSTd13 Glutathione S-transferase; class delta
adenylate cyclase
ApoD27 Invertebrate colouration protein Invertebrate colouration protein
PB1 Bromo adjacent homology BAH domain Bromo adjacent homology BAH domain
Hypothetical protein
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like
short chain dehydrogenase
Hypothetical protein

DDM9-12 Domain of unknown function DUF3421 Domain of unknown function DUF3421
UNCoordinated family member
CYP392A13v2 Cytochrome P450 - CYP392A13v2
UGT UDP-glycosyltransferase; teturUGT29 UGT UDP-glycosyltransferase Glycosyltransferase; MGT
puromycin-sensitive aminopeptidase
Hypothetical protein
Hypothetical protein
CYP probable pse Cytochrome P450 probable pseudogene
CYP392A12 Cytochrome P450 - CYP392A12
selenophosphate synthetase 1
Hypothetical protein
Protease inhibitor I4; serpin
Hypothetical protein
Epididymal secretory protein E1 precursor
Fibroin Hypothetical protein
Intradiol ring-cleavage dioxygenase, core Intradiol ring-cleavage dioxygenase, core Intradiol ring-cleavage dio
BTB/Kelch-associated BTB/Kelch-associated
BTB/Kelch-associated
UGT UDP-glycosyltransferase; teturUGT21 UGT UDP-glycosyltransferase Glycosyltransferase; MGT
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like
SPU1 Secreted peptide of unknown function Hypothetical protein
ApoDR9 Calycin-like ApoDR9 Calycin-like Calycin-like
hypothetical protein
hypothetical protein GrBNV_gp28
CYP392E8 Cytochrome P450 - CYP392E8
conserved hypothetical protein
CYP392D7 Cytochrome P450, conserved site Cytochrome P450, conserved site
hypothetical protein
DNA-binding SAP
Proteinase inhibitor; propeptide
Cytochrome P450 - fragment na Cytochrome P450 -
Cytidine deaminase-like
CYP392A16 Cytochrome P450 - CYP392A16
Hypothetical protein
Hypothetical protein
hypothetical protein
Protein of unknown function DUF2362
UGT UDP-glycosyltransferase; teturUGT36 UGT UDP-glycosyltransferase Glycosyltransferase; MGT
C-factor
PAN/Apple domain
ApoD29 Apolipoprotein D precursor lipoprotein Blc
SP18 Serine protease
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like
UGT UDP-glycosyltransferase; teturUGT10 UGT UDP-glycosyltransferase Glycosyltransferase; MGT
TuPap-30 Cathepsin L
PAN/Apple domain
hypothetical pro hypothetical protein ABCCinc-02 ABC-transporter; class C; incomplete;

Leucine-rich repeat domain, L domain-like
Apple-like
TuPap-11 Cathepsin B
palmitoyl-protein thioesterase 1
Apolipoprotein D precursor; putative Calycin GH10331
PREDICTED: similar to adenylate cyclase
3-oxoacyl-acyl-carrier-protein reductase
Hypothetical protein

Replication fork protection component Swi3
C-signal
PREDICTED: UDP glucuronosyltransferase 2B10 isoform 1
Hypothetical protein
TuCCE04 Carboxyl/cholinesterase TuCCE-04 Carboxyl/cholinesterase
PREDICTED: RNA-dependent RNA polymerase Family family member
photosystem II CP47 protein
short-chain dehydrogenase/reductase SDR
PREDICTED: similar to adenylate cyclase
IAP Proteinase inhibitor I32; inhibitor of apoptosis IAP Proteinase inhibitor I32; inhibitor of apoptosis   Proteinas
TuCCE50 Carboxyl/cholinesterase TuCCE-50 Carboxyl/cholinesterase
Calycin-like
PLAT9 Lipase/lipooxygenase; PLAT/LH2   Lipase/lipooxygenase; PLAT/LH2   Lipase/lipooxygenase; PLAT/LH2
Kelch-type beta propeller
TuABCC-07 ABC-transporter; class C;
UGT UDP-glycosyltransferase; teturUGT28 UGT UDP-glycosyltransferase   Glycosyltransferase; MGT
WTSP1a Wannes-Thomas Secreted Protein 1 WTSP1b Wannes-Thomas Secreted Protein 1 WTSP1a Wanne
Rhodopsin-like receptor
TuGSTd03 Glutathione S-transferase; class delta
Nuclear hormone receptor, ligand-binding domain
PREDICTED: similar to Low-density lipoprotein receptor-related protein 1B precursor
hypothetical protein
hypothetical protein
CYP392A10v2 Cytochrome P450 - CYP392A10v2
TuPap-31 Cathepsin L
chitinase
UNC93-like protein MFSD11
RNI Unknown_Fbox_Gene, truncated RNI Unknown_Fbox_Gene RNI Unknown_Fbox_Gene   Unknown_Fbo
UGT UDP-glycosyltransferase; teturUGT40 UGT UDP-glycosyltransferase   Glycosyltransferase
TuCCE25 Carboxyl/cholinesterase TuCCE-25 Carboxyl/cholinesterase
WD40 repeat, conserved site
TuCCE58 Carboxyl/cholinesterase TuCCE-49 Carboxyl/cholinesterase
Thioredoxin-like fold
TuABCC-08 ABC-transporter; class C;
PREDICTED: similar to limkain b1
LYSI1 putative I-type Lysozyme; possibly a pseudogene LYSI1 putative cytosolic I-type Lysozyme LYSI1 I-typ
Hypothetical protein
phosphatidylinositol-4-phosphate 5-kinase; type I; alpha
Hypothetical protein
adenylate cyclase; putative
Hypothetical protein
UGT UDP-glycosyltransferase; teturUGT78p UGT UDP-glycosyltransferase; teturUGT78 UGT UDP-glycosyltr
mismatch repair protein pms1 homologue; putative
TuLeg-14 Legumain
GH15585
Apolipoprotein D precursor; putative   PREDICTED: apolipoprotein D-like; partial
Hypothetical protein
PREDICTED: similar to adenylate cyclase
beta-tubulin
CYP392D6 Cytochrome P450 - CYP392D6 na Cytochrome P450 -
Hypothetical protein
short-chain dehydrogenase/reductase SDR
PREDICTED: similar to adenylate cyclase
protein Red
FCOL Fibrillar collagen precursor   collagen alpha-1
autophagy-related protein 101

cardioacceleratory peptide receptor
Hypothetical protein
SP29 Serine protease SP45_3 Serine protease SP29 Serine protease
PLAT10 Lipase/lipooxygenase; PLAT/LH2 Lipase/lipooxygenase; PLAT/LH2 Lipase/lipooxygenase; PLAT/LH
Hypothetical protein
TuPap-43 Cathepsin L
Nucleotide-binding alpha-beta plait domain
inositol monophosphatase 3 inositol monophosphatase 3
hypothetical protein
serpin 3 inhibitory serine protease inhibitor
TuPap-56 Cathepsin L
solute carrier family 35 member B1 solute carrier family 35 member B1
39S ribosomal protein L51; mitochondrial precursor
kelch-like 18
Scramblase
Hypothetical protein
Apple-like
Hypothetical protein
TuPap-24 Cathepsin B
Phosphatidic acid phosphatase type 2/haloperoxidase
hypothetical protein
Hypothetical protein
TuIR3 Chemosensing Ionotropic Receptor : IR25A homolog TuIR3 TuIR1 paralog IR 8 ionotropic olfactory glut
PLAT8 Lipase/lipooxygenase; PLAT/LH2 Lipase/lipooxygenase; PLAT/LH2 Lipase/lipooxygenase; PLAT/LH2
bZIP_2 thyrotroph embryonic factor bZIP_2 Basic region leucine zipper
Hypothetical protein
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like
Hypothetical protein
TuGSTd07 Glutathione S-transferase; class delta
Hypothetical protein
Hypothetical protein
MYL1;2 Myosin regulatory light chain; isoform1 Myosin regulatory light chain 2; smooth muscle isoform
CCEincTu13 Carboxyl/cholinesterase; incomplete CCEincTu15 Carboxyl/cholinesterase; incomplete CCEincTu
TuGSTd09 Glutathione S-transferase, C-terminal TuGSTd09 Glutathione S-transferase, C-terminal Glutathion
Hypothetical protein
SP45 Serine protease
conserved hypothetical protein
CYP392E4 Cytochrome P450, E-class, group I CYP392E4 Cytochrome P450, E-class, group I Cytochrome P
methylenetetrahydrofolate dehydrogenase methylenetetrahydrofolate dehydrogenase
PREDICTED: hypothetical protein
Hypothetical protein
unnamed protein product
Glycoside hydrolase; subgroup; catalytic core
NAGLT1a Major facilitator superfamily; general substrate transporter Major facilitator superfamily; general subs
Nose resistant-to-fluoxetine protein, N-terminal
ApoD6 Apolipoprotein D polycalin
Hypothetical protein
CYP392D1 Cytochrome P450 - CYP392D1
hypothetical protein
3-oxoacyl-acyl-carrier-protein reductase
PREDICTED: hypothetical protein
TuLeg-16 Legumain
PREDICTED: similar to Bsdc1 protein
PREDICTED: similar to limkain b1
CYP392E7 Cytochrome P450 - CYP392E7
SP26/M Low-density lipoprotein LDL receptor class A repeat SP26 Low-density lipoprotein LDL receptor class

TuABCC-13 ABC-transporter; class C TuABCC-13 ABC-transporter; class C;
Helix-loop-helix DNA-binding
PREDICTED: similar to Y41C4A.8   PREDICTED: similar to Y41C4A.8   PREDICTED: similar to Y41C4A.8
BTB/POZ-like
Hypothetical protein
Hypothetical protein
Transcription initiation factor TFIID subunit 10   Transcription initiation factor TFIID subunit 10
PREDICTED: similar to PMP1 protein
Hypothetical protein
hypothetical protein
Insect antifreeze protein
ApoD99 apolipoprotein D   apolipoprotein D
TLDc
Hypothetical protein
hypothetical protein
hypothetical protein
proteasome assembly chaperone 2   proteasome assembly chaperone 2
SP28 Serine protease
medium-chain specific acyl-CoA dehydrogenase; mitochondrial precursor
Aldehyde dehydrogenase; N-terminal
Hypothetical protein
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
SPH5 Serine protease homologue SPH Serine protease homologue
Tetratricopeptide repeat
hypothetical protein
CCEincTu10 Carboxyl/cholinesterase; incomplete CCEincTu10 Carboxylesterase; type B CCEincTu11 Carbox
Hypothetical protein
intradiol ring-cleavage dioxygenase
Hypothetical protein
phospholipid scramblase 2
Hypothetical protein
TuPap-55 Cathepsin L-like
Methyltransferase type 11
protein kinase   protein kinase
TuPap-22 Cathepsin B-like
SSPG2 Small secreted protein; Family G   Hypothetical protein
Scv4 scavenger receptor activity
ApoDR5 Calycin-like ApoDR5 Calycin-like   Calycin-like
short-chain dehydrogenase/reductase SDR
methyl-accepting chemotaxis sensory transducer
PREDICTED: similar to peritrophin 1   PREDICTED: similar to peritrophin 1
ribosomal protein S7
Hypothetical protein
Hypothetical protein
TuGSTm07 Glutathione S-transferase; class mu
TuCCE01 Carboxyl/cholinesterase TuCCE-01 Carboxyl/cholinesterase
Disintegrin domain
DDM9-11 Domain of unknown function DUF3421   Domain of unknown function DUF3421
Hypothetical protein
TuGSTm12 Glutathione S-transferase; class mu
aldo/keto reductase   aldo/keto reductase
Glycoside hydrolase; subgroup; catalytic core
TuGSTd02 Glutathione S-transferase, C-terminal   Glutathione S-transferase, C-terminal   Glutathione S-transfe
Hypothetical protein
Tetratricopeptide repeat
Hypothetical protein

TuGSTd14 Glutathione S-transferase; class delta

Cytochrome P450, conserved site

cathepsin A

CYP385C3 Cytochrome P450 - CYP385C3

GBA1 Glycoside hydrolase; subgroup; catalytic core   Glycoside hydrolase; subgroup; catalytic core

Double-stranded RNA binding

TeturLY6_UPAR18 LY6_UPAR protein   Three finger domain protein TFD   Hypothetical protein

Hypothetical protein

Hypothetical protein

TuABCC-11 ABC-transporter; class C;

BTB/POZ-like

TuCCE08 Carboxyl/cholinesterase TuCCE-08 Carboxyl/cholinesterase

conserved unknown protein

beta-mannosidase   beta-mannosidase

Hypothetical protein

WTSP2 Wannes-Thomas Secreted Protein 2   Hypothetical protein

Diacylglycerol/phorbol-ester binding   Diacylglycerol/phorbol-ester binding

PREDICTED: similar to F55A4.8a

UGT UDP-glycosyltransferase; teturUGT11 UGT UDP-glycosyltransferase   Glycosyltransferase; MGT

Hypothetical protein

sodium-dependent glucose transporter 1

Hypothetical protein

Hypothetical protein

DDM9-10 Domain of unknown function DUF3421   Domain of unknown function DUF3421

ApoD28 Apolipoprotein D precursor   apolipoprotein D

Insect antifreeze protein

Hypothetical protein

TuCCE34 Carboxyl/cholinesterase TuCCE33 Carboxyl/cholinesterase TuCCE-33 Carboxyl/cholinesterase

CCEincTu14 Carboxyl/cholinesterase; incomplete CCEincTu15 Carboxyl/cholinesterase; incomplete CCEinc-2

L-galactose dehydrogenase

PREDICTED: hypothetical protein

TuCCE37 Carboxyl/cholinesterase TuCCE-35 Carboxyl/cholinesterase

solute carrier family 22 member 4

CYP392D3 Cytochrome P450 - CYP392D3

Mitochondrial substrate/solute carrier

Hypothetical protein

DDM9-17 Domain of unknown function DUF3421   Domain of unknown function DUF3421

Peptidase M16; core

adenylosuccinate lyase

Hypothetical protein

PLAT7 Lipase/lipooxygenase; PLAT/LH2   Lipase/lipooxygenase; PLAT/LH2   Lipase/lipooxygenase; PLAT/LH2

Hypothetical protein

TuGSTd05 Glutathione S-transferase; class delta

PREDICTED: hypothetical protein; partial

serum amyloid A protein-like

PREDICTED: similar to adenylate cyclase   PREDICTED: similar to adenylate cyclase

3-oxoacyl-acyl-carrier-protein reductase

TuGSTd04 Glutathione S-transferase; class delta

Alkaline phosphatase-like, alpha/beta/alpha

Glycoside hydrolase; subgroup; catalytic core

PREDICTED: similar to PMP1 protein

TuCCE06 Carboxyl/cholinesterase TuCCE-06 Carboxyl/cholinesterase

hypothetical protein

PREDICTED: sodium-dependent glucose transporter 1-like; partial

TuCCE65 Carboxyl/cholinesterase TuCCE-55 Carboxyl/cholinesterase

hypothetical protein

CYP392B3 Cytochrome P450 - CYP392B3
PREDICTED: solute carrier family 2   PREDICTED: solute carrier family 2
DDM9-13 Domain of unknown function DUF3421   Domain of unknown function DUF3421
Major facilitator superfamily domain
mutS protein homolog 4
TuPap-29 Cathepsin L
Galactose oxidase/kelch; beta-propeller
PHYH
adenylate cyclase
PREDICTED: similar to adenylate cyclase
Chibby family
PREDICTED: similar to apical endosomal glycoprotein
Hypothetical protein
Hypothetical protein
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
multidrug resistance-associated protein 1
SLCP4 Secreted low complexity protein; putative
BTB/Kelch-associated
UGT UDP-glycosyltransferase; teturUGT13 UGT UDP-glycosyltransferase   glycosyltransferase; MGT family
patched sphingolipid transporter
spectrin; alpha; non-erythrocytic 1
CHT5 chitinase   chitinase
UNCoordinated family member
PREDICTED: similar to adenylate cyclase
Hypothetical protein
hatching enzyme   hatching enzyme
Hypothetical protein
Hypothetical protein
HR96-like h HR96-like nuclear receptor h NR1/3 member Possible NR1 or NR3 member? NR2/3 member Pos
Plexin domain-containing protein
Hypothetical protein
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
Low-density lipoprotein LDL receptor class A repeat
glycogen debranching enzyme
UGT UDP-glycosyltransferase; teturUGT26 UGT UDP-glycosyltransferase   Glycosyltransferase; MGT

dopa decarboxylase   dopa decarboxylase
CYP385C2 Cytochrome P450 - CYP385C2
Hypothetical protein
BTB/Kelch-associated   BTB/Kelch-associated
TPAN-4 3-Pan modules Cell Surface Protein; antigen-2   Hypothetical protein
PLAT17 PLAT/LH2 domain   PLAT/LH2 domain   PLAT/LH2 domain
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
FAD-dependent pyridine nucleotide-disulphide oxidoreductase
scavenger receptor class B; member 2
CYP392A14P Cytochrome P450 pseudogene CYP probable pse Cytochrome P450 fragment - probable pseud
AP complex subunit beta
hypothetical protein
UGT UDP-glycosyltransferase; teturUGT27 UGT UDP-glycosyltransferase   Glycosyltransferase; MGT
TuPap-57 Cathepsin L-like TuPap-57 Cathepsin L-like
WTSP1b Wannes-Thomas Secreted Protein 1 WTSP1a Wannes-Thomas Secreted Protein 1   Hypothetical pro
Hypothetical protein
WD40 repeat
TPAN-53 PAN/Apple domain   PAN/Apple domain
CYP392D4 Cytochrome P450 - CYP392D4
CYP-pseudogene Cytochrome P450 - probable pseudogene

S-adenosyl-L-methionine-dependent methyltransferase
Tetraspanin/Peripherin
Complement control module
CYP385C4 Cytochrome P450 - CYP385C4
UGT UDP-glycosyltransferase; teturUGT39 UGT UDP-glycosyltransferase   Glycosyltransferase; MGT
Nuclear hormone receptor; ligand-binding
TuABCC-26 ABC-transporter; class C;
CYP392E9 Cytochrome P450 - CYP392E9
Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
hypothetical protein
sorbitol dehydrogenase
C-factor
hypothetical protein
phosphotyrosyl phosphatase activator   phosphotyrosyl phosphatase activator   phosphotyrosyl phosphatase act
PLAT16 Lipase/lipooxygenase; PLAT/LH2   Lipase/lipooxygenase; PLAT/LH2   Lipase/lipooxygenase; PLAT/LH
TuABCG-06 ABC-transporter; class G TuABCG-04 ABC-transporter; class G;
Hypothetical protein
Hypothetical protein
TuCCE49 Acetyl-cholinesterase TuCCE-41-AChE Acetyl-cholinesterase
CYP392E6 Cytochrome P450 - CYP392E6
N-alpha-acetyltransferase 15; NatA auxiliary subunit   N-alpha-acetyltransferase 15; NatA auxiliary subunit
Sec1-like protein
MAM
bromodomain-containing protein 7
hypothetical protein
SIFa Neuropeptide precursor
Hypothetical protein
hypothetical protein
BTB/Kelch-associated
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
hypothetical protein
serpin 3 inhibitory serine protease inhibitor
Apple-like
PREDICTED: similar to ECM 18   PREDICTED: similar to ECM 18
3-oxoacyl-acyl-carrier-protein reductase
Ankyrin repeat domain-containing protein 13   Ankyrin repeat domain-containing protein 13
Hypothetical protein
GTP-binding protein Rit1
Nerve growth factor-related
GF11962
UGT UDP-glucuronosyl/UDP-glucosyltransferase MGT1 UDP-glucuronosyl/UDP-glucosyltransferase MGT1 Ul
Hypothetical protein
SAPS domain family; member 3
TuABCH-09 ABC-transporter; class H pABC-14 ABC-transporter; putative;
Hypothetical protein
Glycoside hydrolase; subgroup; catalytic core
Major facilitator superfamily domain
UGT UDP-glucuronosyl/UDP-glucosyltransferase UGT UDP-glucuronosyl/UDP-glucosyltransferase   UDP-gluc
hypothetical protein
Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like   Leucine-rich repeat dom
TuCCE45 Carboxyl/cholinesterase TuCCE-39 Carboxyl/cholinesterase
RDRP-2 RNA-directed RNA polymerase 2
Hypothetical protein
hypothetical protein
hypothetical protein
TuGSTd12 Glutathione S-transferase; class delta

Scramblase
Hypothetical protein
innexin; putative
UGT UDP-glycosyltransferase; teturUGT02 UGT UDP-glycosyltransferase   Glycosyltransferase; MGT
Hypothetical protein
HMW kininogen
TuPap-42 Cathepsin L
Lipocalin family conserved site   Lipocalin family conserved site
Hypothetical protein
UGT UDP-glycosyltransferase; teturUGT06 UGT UDP-glycosyltransferase   rhamnosyltransferase I; subunit B
sialin; putative
TuPap-26 Cathepsin B
Hypothetical protein
TuCCE17 Carboxyl/cholinesterase TuCCE-17 Carboxyl/cholinesterase
DM DM DNA-binding domain
TuPap-47 Peptidase C1A; papain C-terminal TuPap-45 Peptidase C1A; papain C-terminal   Peptidase C1A; pa
PREDICTED: similar to limkain b1
TuPap-10 Cathepsin B
SSPA1 Small Secreted Protein; family A   Hypothetical protein
DDM9-6 Domain of unknown function DUF3421   Domain of unknown function DUF3421
SPH3 Serine protease homologue SPH Serine protease homologue
Insect antifreeze protein
serpin 2 plasmodium-related inhibitory serine protease inhibitor
phytoene dehydrogenase
Hypothetical protein
Hypothetical protein
Fibroin   Fibrion   Hypothetical protein
Hypothetical protein
hypothetical protein
Leukocyte elastase inhibitor
Fibroin   Hypothetical protein
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
lipase 1 precursor   lipase 1 precursor
Hypothetical protein
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
Hypothetical protein
PLAT2 Lipase/lipooxygenase; PLAT/LH2 PLAT2 Lipase/lipooxygenase; PLAT/LH2   Lipase/lipooxygenase; PL
poly
Ganglioside GM2 activator
Hypothetical protein
conserved hypothetical protein
RNA-directed DNA polymerase
TuPap-17 Cathepsin B
UGT UDP-glucuronosyl/UDP-glucosyltransferase UGT UDP-glucuronosyl/UDP-glucosyltransferase MGT2 UD
calcyclin binding protein
Tudor domain
TuPap-52 Cathepsin L
CYP392E5p Cytochrome P450 - CYP392E5p probable pseudogene
Peptidase M12B; ADAM/reprolysin
glucosylceramidase precursor
PREDICTED: similar to adenylate cyclase
PREDICTED: similar to lycopene cyclase / phytoene synthase
Hypothetical protein
protein LTV1 homolog
TPAN-5 Apple-like TPAN-5 Apple-like PAN1 Apple-like   Apple-like
TuABCG-13 ABC-transporter; class G TuABCG-11 ABC-transporter; class G;

CH11 chitinase   chitinase
Collagen IV; non-collagenous
nhr-48 Nuclear hormone receptor, ligand-binding domain   Nuclear hormone receptor, ligand-binding domain
Hypothetical protein
PREDICTED: similar to inorganic phosphate cotransporter; putative
CYP389C8 Cytochrome P450 - CYP389C8
Hypothetical protein
ab-hydrolase associated lipase region family protein
Ubiquitin-fold modifier-conjugating enzyme 1
Major facilitator superfamily; general substrate transporter
TuLeg-17 Legumain
sialin
glucosylceramidase; putative
Six-bladed beta-propeller; TolB-like
51 kDA subunit c NADH-quinone oxidoreductase; 51 kDa subunit;
CD63 antigen
Vg2 Lipid transport protein, beta-sheet shell   Lipid transport protein, beta-sheet shell
CYP384A1 Cytochrome P450 - CYP384A1
Ganglioside GM2 activator
mitochondrial sodium/hydrogen exchanger NHA2
BTB/Kelch-associated
DDM9-22 Domain of unknown function DUF3421   Domain of unknown function DUF3421
LZY1;5 Conserved zygote-specific protein homologue LZY1;5 Conserved zygote-specific protein LZY1;5 Cons
Dgri Nuclear hormone receptor, ligand-binding domain   Nuclear hormone receptor, ligand-binding domain
Leukocyte elastase inhibitor
frataxin
Hypothetical protein
Hypothetical protein
Hypothetical protein
rRNA-processing protein FCF1 homolog   rRNA-processing protein FCF1 homolog
Hypothetical protein
Major facilitator superfamily; general substrate transporter
antigen B membrane protein
Hypothetical protein
SPH35 Serine protease homologue
Nuclear hormone receptor, ligand-binding domain
SSPB1 Small Secreted Protein; Family B   Hypothetical protein
BTB/Kelch-associated
TLDc
Hypothetical protein
adenylate cyclase
Hypothetical protein
hypothetical protein
SPH7 Serine protease homologue SPH Serine protease homologue
PREDICTED: hypothetical protein
AGO-1G ortholog of Argonaute-1 Drosophila melanogaster
serine carboxypeptidase; putative   serine carboxypeptidase; putative
Hypothetical protein
MAM
TuLeg-13 Legumain
TuPap-6 Cathepsin B
Leukocyte elastase inhibitor
PREDICTED: similar to adenylate cyclase
Hypothetical protein
Hypothetical protein
LAC3 Immunoglobulin Family Cell Adhesion Molecule; putative Lachesin   lachesin; putative

beta-lactamase-like protein 2
E3 ubiquitin-protein ligase MARCH5
timeless
Hypothetical protein
nuclear receptor coactivator 6
phosphoglucomutase   phosphoglucomutase
palmitoyl protein thioesterase family protein   palmitoyl protein thioesterase family protein
UGT UDP-glycosyltransferase; teturUGT23 UGT UDP-glycosyltransferase   Glycosyltransferase; MGT

beta-tubulin
phosphatidylethanolamine-binding protein
PREDICTED: similar to TRAF6
laminin subunit gamma-1 precursor
Proteinase/amylase inhibitor domain
ApoD3 Apolipoprotein D   apolipoprotein D
TuABCC-31 ABC-transporter; class C TuABCC-37 ABC-transporter; class C TuABCC-37 ABC-transporter AB
TuGSTm11 Glutathione S-transferase; class mu
Hypothetical protein
gem-associated protein; putative
lipase 1
Alpha/Beta hydrolase fold
Glycoside hydrolase; subgroup; catalytic core
Hypothetical protein
Glycoside hydrolase; subgroup; catalytic core
RST Immunoglobulin subtype RST Immunoglobulin subtype   Immunoglobulin subtype
hypothetical protein Bbu156a_O16
sialin
Solute carrier family 35 member F3/F4
Hypothetical protein
short-chain dehydrogenase/reductase SDR
Hypothetical protein
beta-mannosidase
TuABCC-38 ABC-transporter; class C TuABCC-39 ABC-transporter; class C ABCCinc-07 ABC-transporter; cla
Apolipoprotein D precursor; putative
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
phosphatidylinositol 3-kinase regulatory subunit gamma
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
Hypothetical protein
UGT UDP-glycosyltransferase; teturUGT31 UGT UDP-glycosyltransferase   rhamnosyltransferase I; subunit B
TuGSTd11 Glutathione S-transferase; class delta TuGSTd11 Glutathione S-transferase; class delta
Ferritin/ribonucleotide reductase-like
Insulin-like growth factor-binding protein; IGFBP
Alpha/Beta hydrolase fold
viral A-type inclusion protein
elongator complex protein 1
Dicer-2 Dicer-2; homolog of Drosophila melanogaster DCL2
Cystatin domain
PREDICTED: similar to ENSANGP00000012602
Transferrin-like domain
PREDICTED: 3-hydroxybutyrate dehydrogenase; type 1-like
CYP392A1 Cytochrome P450 - CYP392A1
MD-2-related lipid-recognition domain
Apple-like
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
PLXDC2 Plexin-like fold   Plexin-like fold
PLAT12 Lipase/lipooxygenase; PLAT/LH2   Lipase/lipooxygenase; PLAT/LH2   Lipase/lipooxygenase; PLAT/LH

MIER1 Mesoderm induction early response protein mesoderm induction early response 1; family member 3
TuABCC-35 ABC-transporter; class C TuABCC-34 ABC-transporter; class C;
phospholipid hydroperoxide glutathione peroxidase
Glycoside hydrolase; subgroup; catalytic core
short chain dehydrogenase/reductase family 16C; member 5
TuGSTm03 Glutathione S-transferase; class mu
PREDICTED: si:dkey-88l16.3 PREDICTED: si:dkey-88l16.3
Glycoside hydrolase; subgroup; catalytic core
SSPA9 Small Secreted Protein; family A Hypothetical protein
Vg1 vitellogenin; partial sequence Vit vitellogenin; partial sequence vitellogenin vitellogenin
M-phase inducer phosphatase
TuPap-15 Cathepsin B
BolA-2 BolA-like protein BolA-like protein
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like
GRSP12 Glycine-rich secreted protein GYGSP3 Secreted protein with GYG repeats Hypothetical protein
long-chain fatty acid transport protein 1
Hypothetical protein
Domain of unknown function DUF21
PREDICTED: similar to adenylate cyclase
conserved hypothetical protein
ApoD26 apolipoprotein D precursor apolipoprotein D
parkin
TuPap-44 Cathepsin L
ApoD11 Apolipoprotein D precursor PREDICTED: similar to apolipoprotein D
TPAN-52 3-Pan modules Cell Surface Protein; Antigen-B homolog Apple-like
RNA-dependent RNA polymerase, eukaryotic-type
peroxinectin; putative
PREDICTED: similar to kelch-like 12
PREDICTED: similar to glucose dehydrogenase
Hypothetical protein
Hypothetical protein
atrial natriuretic peptide receptor 2 precursor
Hypothetical protein
UGT UDP-glycosyltransferase; teturUGT03 UGT UDP-glycosyltransferase Glycosyltransferase; MGT
TuGSTd10 Glutathione S-transferase, C-terminal TuGSTd10 Glutathione S-transferase, C-terminal Glutathion
ornithine aminotransferase
Hypothetical protein
CDK5 and ABL1 enzyme substrate 1/2 CDK5 and ABL1 enzyme substrate 1/2
CAM calmodulin calmodulin
TuABCC-32 ABC-transporter; class C TuABCC-31 ABC-transporter; class C;
Hypothetical protein
puromycin-sensitive aminopeptidase puromycin-sensitive aminopeptidase
Tubeta2 Neurotransmitter-gated ion-channel Neurotransmitter-gated ion-channel
hypothetical protein
Hypothetical protein
macrolide glycosyltransferase
Hypothetical protein
Hypothetical protein
PREDICTED: similar to leucine rich protein; putative PREDICTED: similar to leucine rich protein; putative
Conserved hypothetical protein CHP02464
PREDICTED: minichromosome maintenance complex component 3 associated protein
nhr-48 Nuclear hormone receptor, ligand-binding domain Nuclear hormone receptor, ligand-binding domain
Armadillo-type fold
Kelch-type beta propeller
Hypothetical protein

FAD/NADP-binding domain
GI21111
selenophosphate synthetase 2   selenophosphate synthetase 2
Outer membrane chaperone Skp OmpH
beta-galactosidase
TuLeg-5 Legumain
UGT UDP-glycosyltransferase; teturUGT33   UDP-glycosyltransferase; teturUGT33   UDP-glycosyltransferase;
PREDICTED: UTP6; small subunit   PREDICTED: UTP6; small subunit
Concanavalin A-like lectin/glucanase
minor tail protein gp26-like
hypothetical protein
mitochondrial ribosomal protein S17   mitochondrial ribosomal protein S17
Fibronectin; type III
Hypothetical protein
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
CYP392E2 Cytochrome P450 - CYP392E2
Hypothetical protein
Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
lethal
AGO-1B ortholog of Argonaute-1 Drosophila melanogaster
AkrA Aldo-keto reductase family A   alcohol dehydrogenase
Hypothetical protein
Cation/H+ exchanger
Hypothetical protein
Hypothetical protein
Hypothetical protein
PREDICTED: similar to solute carrier family 5
Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase   Glyoxalase/Bleomycin resistance pro
UNCoordinated family member
CuffL3 Cutoff-like protein HPA1c Hypothetical Protein of Unknown Function Conserved in Arthropods   Hypothe
Hypothetical protein
adenylate cyclase
Hypothetical protein
Peptidase S60; transferrin lactoferrin
CPD CPD photolyase   CPD photolyase
Hypothetical protein
lethal
Peptidase M14; carboxypeptidase A
BTB/Kelch-associated   BTB/Kelch-associated
peroxisomal acyl-coenzyme A oxidase 1
Hypothetical protein
regucalcin
UGT UDP-glycosyltransferase; teturUGT75 UGT UDP-glycosyltransferase   glycosyltransferase; MGT family
transmembrane protein 189
Conserved hypothetical protein CHP02464
nidogen 1
hormone-sensitive lipase
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
Leucine-rich repeat domain, L domain-like
SSPE2 Small Secreted Protein; Family E   Hypothetical protein
Tu_12344.3 cys-loop ligand-gated ion channel   glycine receptor subunit beta precursor
D-3-phosphoglycerate dehydrogenase
Hypothetical protein
PREDICTED: similar to galactosamine
Hypothetical protein
guanine nucleotide-binding protein G

kynureninase   kynureninase
TuABCG-12 ABC-transporter; class G TuABCG-10 ABC-transporter; class G;
PREDICTED: dedicator of cytokinesis 2
Hypothetical protein
Peptidase S60; transferrin lactoferrin
spondin-1 precursor   spondin-1 precursor
MECP2 Methyl-CpG binding protein 2/3, C-terminal domain mbd2 Methyl-CpG binding protein 2/3, C-terminal c
PREDICTED: similar to ileal sodium-dependent bile acid transporter
Hypothetical protein
Adhesion molecule CD36
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
hypothetical protein
Rap/ran-GAP
hypothetical protein
hypothetical protein
Nab NGFI-A-binding protein homolog NGFI-A- homolog NGFI-A-binding protein 1   NGFI-A-binding protein 1
Histone deacetylase complex subunit SAP18
TuPap-38 Cathepsin L
Hypothetical protein
SP6/C Serine proteases, trypsin family, histidine active site
Saposin type A
P-loop containing nucleoside triphosphate hydrolase
deoxyribonuclease II
Glycoside hydrolase; family 30
Six-bladed beta-propeller; TolB-like
Tubulin-tyrosine ligase
Alpha/Beta hydrolase fold
TuABCC-02 ABC-transporter; class C;
sialin
zf zinc finger protein
Hypothetical protein
short-chain dehydrogenase/reductase SDR
Probable dimethyladenosine transferase
TuABCC-14 ABC-transporter; class C TuABCC-14 ABC-transporter; class C;
Vitamin D3 receptor; putative
Hypothetical protein
UGT UDP-glucuronosyl/UDP-glucosyltransferase UGT UDP-glucuronosyl/UDP-glucosyltransferase   UDP-gluc
PREDICTED: similar to Glucosylceramidase precursor
Thyroglobulin type-1
hypothetical protein
choline/ethanolamine kinase
UGT UDP-glycosyltransferase; teturUGT35 UGT UDP-glycosyltransferase   glycosyltransferase; MGT family
conserved hypothetical protein
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
conserved hypothetical protein
GF11309
PREDICTED: similar to adenylate cyclase
TuGSTd15 Glutathione S-transferase; class delta
Hypothetical protein
TuCPI-8 Cystatin domain   Cystatin domain
PREDICTED: hypothetical protein
TFDP1 transcription factor Dp-1
Conserved hypothetical protein CHP02464
SON DNA-binding protein isoform F
Flavin reductase
Hypothetical protein

Hypothetical protein
hypothetical protein
Tetraspanin/Peripherin
Nucleotide-binding; alpha-beta plait
Hypothetical protein
SP14/2P Serine protease; polyserase
Hypothetical protein
Dgri hormone receptor 96   NR1 nuclear receptor
TuPap-16 Cathepsin B
ApoD5 apolipoprotein D   apolipoprotein D; putative
Cyt-b5 Cytochrome b5
TuCCE03 Carboxyl/cholinesterase TuCCE-03 Carboxyl/cholinesterase
autophagy-related protein 101
Fatty acyl-CoA reductase
DEAH
Hypothetical protein
Immunodominant surface protein, Ehrlichia tandem repeat-containing
Hypothetical protein
Oxidoreductase-like, N-terminal
lachesin; putative
OSP2b Orphan secreted protein OSP2a Orphan secreted protein   Hypothetical protein

MOSPD2a PapD-like   PapD-like
PREDICTED: solute carrier family 2
Hypothetical protein
Hypothetical protein
CCAP-R 2 GPCR; cardioacceleratory peptide receptor
Hypothetical protein
Hypothetical protein
Hypothetical protein
CPR X cuticle protein; putative CP X cuticle protein; putative   cuticle protein; putative   cuticle protein; putative
Zinc finger; C2H2-type
aromatic amino acid decarboxylase
chitinase
HYP5 hypothetical protein
agrin   agrin
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
hypothetical protein
Dynamin GTPase effector
F-box only protein 9
3-oxoacyl-acyl-carrier-protein reductase
P-loop containing nucleoside triphosphate hydrolase
RhoGAP
hypothetical protein
CTPS1 CTP synthase 1   CTP synthase 1
tyrosinase
RNI Leucine-rich repeat domain, L domain-like HYP1b Leucine-rich repeat domain, L domain-like   Leucine-rich
PREDICTED: similar to CG33978 CG33978-PA
CuffL8 Cutoff-like protein   protein Dom3Z
Nuclear hormone receptor, ligand-binding domain
GRSP8 Glycine-rich secreted protein   Hypothetical protein
Hypothetical protein
Hypothetical protein
Hypothetical protein
TPAN-3 3-Pan module Cell Surface Protein; antigen-2 PANR-3 Pan module-related Cell Surface Protein; antige
hypothetical protein

Pleckstrin-homology domain PH domain/Phosphotyrosine-binding domain PTB
3-oxoacyl-acyl-carrier-protein reductase
amino acid transporter
TuABCH-08 P-loop containing nucleoside triphosphate hydrolase TuABCH-08 P-loop containing nucleoside trip
hypothetical protein
Hypothetical protein
Hypothetical protein
Short-chain dehydrogenase/reductase SDR
TuPap-25 Cathepsin B-like
Hypothetical protein
PIGS Gas2-like target of Notch; pickled eggs homolog.   PREDICTED: growth arrest-specific 2 like 2
Hypothetical protein
Galactose oxidase/kelch; beta-propeller
Hypothetical protein
Hypothetical protein
carboxypeptidase D
CYP392A14 Cytochrome P450 - CYP392A14
CBF-like protein
Hypothetical protein
ApoDR1 Calycin-like ApoDR1 Calycin-like   Calycin-like
CREB-binding protein
Hypothetical protein
Hypothetical protein
5'-nucleotidase
hypothetical protein
Hypothetical protein
Hypothetical protein
putative glycosylhydrolase
LZY1;2 Conserved zygote-specific protein homologue LZY1;2 Conserved zygote-specific protein LZY1;2 Cons
Hypothetical protein
hypothetical protein
PREDICTED: transmembrane inner ear-like
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
Leucine-rich repeat domain, L domain-like
SMAD domain, Dwarfin-type
Hypothetical protein
PREDICTED: similar to AGAP003567-PA
ApoD21 Apolipoprotein D precursor ApoD21 Apolipoprotein precursor   Lipocalin family protein
Histone H4
Hypothetical protein
Hypothetical protein
CPAP 12 cuticular protein analogous to peritrophins 1-A
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
Hypothetical protein
sorbitol dehydrogenase
Hypothetical protein
Trafficking protein particle complex subunit 5   Trafficking protein particle complex subunit 5
Galactose-binding domain-like
Hypothetical protein
Hypothetical protein
Hypothetical protein
PrtA Chitin binding protein; peritrophin-A   Chitin binding protein; peritrophin-A
cytochrome b
Hypothetical protein
Hypothetical protein
HAUS augmin-like complex subunit 6, N-terminal

Hypothetical protein
collagen alpha-1
Hypothetical protein
DnaJ
TuENaC133 Na+ channel/degenerin ENaC/DEG family protein Tu_ENaC133 Na+ channel/degenerin ENaC/DE
hypothetical protein
Hypothetical protein
hypothetical protein
RYamide Receptor G-protein coupled neuropeptide receptor; homologous to Drosophila receptor CG5811; whic
Hypothetical protein
Hypothetical protein
ApoD23 Apolipoprotein D precursor   apolipoprotein D
Hypothetical protein
Hypothetical protein
Awh Zinc finger, LIM-type Homeobox Zinc finger, LIM-type
PREDICTED: similar to Glucosylceramidase precursor
Reeler domain
GE10869
Hypothetical protein
hypothetical protein
Hypothetical protein
TuCCE43 Carboxyl/cholinesterase TuCCE43 Carboxyl/cholinesterase; incomplete CCEinc-12 Carboxyl/choline
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
Hypothetical protein
ADP-ribosylation factor related protein 1
Hypothetical protein
Leucine-rich repeat domain, L domain-like
TuABCG-10 ABC-transporter; class G TuABCG-08 ABC-transporter; class G;
aminopeptidase
Outer membrane protein Iml2/Tetratricopeptide repeat protein 39
Hypothetical protein
TuENaC122 Na+ channel, amiloride-sensitive Tu_ENaC122 Na+ channel, amiloride-sensitive   Na+ channel, a
TuPap-27 Cathepsin B
Hypothetical protein
PREDICTED: similar to shavenoid CG13209-PA
Hypothetical protein
Hypothetical protein
Hypothetical protein
variable lymphocyte receptor A
Hypothetical protein
TuIR1 Chemosensing Ionotropic Receptor : IR25A homolog TuIR1 IR25A homolog IR 5 ionotropic glutamate r
hypothetical protein
Hypothetical protein
PREDICTED: similar to microtubule binding protein; putative
hypothetical protein
solute carrier family 6
Hypothetical protein
TuLeg-8 Legumain
hypothetical protein
Hypothetical protein
dissatisfaction dissatisfaction homolog [Tetranychus urticae] dissatisfaction   dissatisfaction homolog [Tetranych
TuENaC118 Na+ channel, amiloride-sensitive Tu_ENaC118 Na+ channel, amiloride-sensitive   Na+ channel, a
Zinc finger, RING/FYVE/PHD-type
Hypothetical protein
Hypothetical protein
Shisa family

TuABCA-05 ABC-transporter; class A;
Vg4 Vitellogenin 4
cation efflux protein/ zinc transporter
apoptosis regulator BAX
SSPA5 Small Secreted Protein; family A   Hypothetical protein
Superoxide dismutase; copper/zinc binding
Klf5 Zinc finger, C2H2-like   Zinc finger, C2H2-like
CPR 60 Putative cuticle protein CPR B Putative cuticle protein CPR B Putative cuticle protein
Six-bladed beta-propeller; TolB-like
protein kinase
BolA-2 BolA-like protein   BolA-like protein
neprilysin
Hypothetical protein
Hypothetical protein
PREDICTED: Bardet-Biedl syndrome 9
GE13940
elongase; putative
Hypothetical protein
huntingtin
nucleoprotein
TuABCH-17 ABC-transporter; class H pABC-27 ABC-transporter; putative;
Hypothetical protein
Hypothetical protein
Cupredoxin
Hypothetical protein
HESP3 Highly Expressed Secreted Protein Family   Hypothetical protein
Hypothetical protein
Hypothetical protein
Hypothetical protein
Hypothetical protein
hypothetical protein
Hypothetical protein
Uncharacterised domain KxDL   Uncharacterised domain KxDL
hypothetical protein
SP68 Serine proteases, trypsin family, histidine active site   Serine proteases, trypsin family, histidine active site
Nose resistant-to-fluoxetine protein; N-terminal
Hypothetical protein
UNC93-like protein MFSD11
UGT UDP-glycosyltransferase; teturUGT52 UGT UDP-glycosyltransferase   Glycosyltransferase; MGT
CynS cyanate lyase; cyanase   cyanate hydratase
CPR 28 cuticle protein
Hypothetical protein
RPL19 ribosomal protein L19   ribosomal protein L19
Hypothetical protein
Rho GTPase activation protein

60S ribosomal protein L35
ATP-sensitive inward rectifier potassium channel 12
zinc finger protein 183   zinc finger protein 183
Hypothetical protein
Hypothetical protein
Homeobox protein SIX1, N-terminal SD domain
bacterioferritin
vitellogenin1
Glycoside hydrolase; subgroup; catalytic core
Mitochondrial substrate/solute carrier

RPS7 ribosomal protein S7   ribosomal protein S7
Carbohydrate-binding-like fold
Tetratricopeptide-like helical domain
UGT UDP-glycosyltransferase; teturUGT16 UGT UDP-glycosyltransferase MGT4 Glycosyltransferase; MGT
calmodulin
phytoene dehydrogenase
Hypothetical protein
Galactose-binding domain-like

Hypothetical protein
sine oculis-binding protein homolog
Hypothetical protein
PREDICTED: similar to organic cation transporter   PREDICTED: similar to organic cation transporter
Hypothetical protein
lethal
Cysteine peptidase, asparagine active site
galactokinase
BCDO2-1 Beta;beta-carotene 9';10'-oxygenase; CMO-II BCO2-1 Beta;beta-carotene 9';10'-oxygenase; CMO-II
Glycosyl transferase; family 31
GK22478
IarsP isoleucyl-tRNA synthetase; pseudogene   isoleucyl-tRNA synthetase; cytoplasmic
PAN/Apple domain
Zinc finger, C2H2-like
tubulin gamma-1 chain
TuOsp1 orphan secreted protein Osp1 orphan secreted protein   Hypothetical protein
Alpha/Beta hydrolase fold
Hypothetical protein
Hypothetical protein
RNA polymerase-associated protein LEO1
Golgi-associated plant pathogenesis-related protein 1
GnRH-R3 G-protein coupled neuropeptide receptor
Leucine-rich repeat domain, L domain-like
Hypothetical protein
PREDICTED: similar to CG18549 CG18549-PA
hypothetical protein
Hypothetical protein
SOD1 Superoxide dismutase Cu/Zn / superoxide dismutase copper chaperone   Superoxide dismutase Cu/Zn /
Protease inhibitor I4; serpin
Rfx4 Winged helix-turn-helix DNA-binding domain RFX_DNA_binding Winged helix-turn-helix DNA-binding don
Hypothetical protein
GG20998
candidate tumor suppressor protein
hypothetical protein
hypothetical protein Y39G10AR.18
glutaryl-CoA dehydrogenase
GK24554
PREDICTED: similar to lipase 1
Hypothetical protein
Lklf krueppel-like factor 2
origin recognition complex subunit 2
hypothetical protein
lipase 1 precursor
vitellogenin1
ApoDR10 Calycin-like   Calycin-like
TuENaC93 Na+ channel, amiloride-sensitive Tu_ENaC93 Na+ channel, amiloride-sensitive   Na+ channel, amil
ovo ovo ovo Zinc finger; C2H2 type

hypothetical protein
suppressor of Ty 3 homolog
FUCTCb alpha-1;3-fucosyltransferase C
Hypothetical protein
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like
hypothetical protein
Hypothetical protein
PREDICTED: similar to otoferlin
Hypothetical protein
PREDICTED: similar to AHNAK nucleoprotein isoform 1
ribosomal protein S12
hypothetical protein
Hypothetical protein
lethal
PREDICTED: UTP6; small subunit
Hypothetical protein
Vg1 von Willebrand factor, type D domain Vg1 von Willebrand factor, type D domain von Willebrand factor, ty
Hypothetical protein
HESP2 Highly expressed secreted protein family Hypothetical protein
SP39 Serine protease
Hypothetical protein
Major facilitator superfamily; general substrate transporter
potential DNA-binding protein C17orf49
paraxis Myc-type, basic helix-loop-helix bHLH domain HLH Myc-type, basic helix-loop-helix bHLH domain
Hypothetical protein
Hesr-1/Hey1 bHLH protein Hesr-1/Hey1
Hypothetical protein
mitochondrial intermembrane space import and assembly protein 40
PREDICTED: similar to Bardet-Biedl syndrome 7
Alkaline phosphatase-like, alpha/beta/alpha
Hypothetical protein
Hypothetical protein
ABC transporter; permease/ATP-binding protein
Hypothetical protein
beta-mannosidase beta-mannosidase
Hypothetical protein
dentin sialophosphoprotein precursor
PMS1
UNCoordinated family member
U6 snRNA-associated Sm-like protein LSm5
Hypothetical protein
tRNA
hypothetical protein
Insect antifreeze protein
Hypothetical protein
Hypothetical protein
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like
hypothetical protein
CCEincTu18 Carboxyl/cholinesterase; incomplete esterase
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like
ApoD22 Apolipoprotein D precursor Lipocalin family protein
Hypothetical protein
zinc carboxypeptidase
short chain dehydrogenase
Bicarbonate transporter; eukaryotic
Hypothetical protein

Hypothetical protein
PE-PGRS family protein
hypothetical protein
Alkaline phosphatase-like, alpha/beta/alpha
Fibroin hypothetical protein
Hypothetical protein
hypothetical protein
Plexin-like fold
UNCoordinated family member
hypothetical protein
Hypothetical protein
phosphatidylcholine-sterol acyltransferase
hypothetical protein
Bardet-Biedl syndrome 1 protein
Hypothetical protein
E2f4 E2F transcription factor, CC-MB domain E2F_TDP E2F transcription factor, CC-MB domain
hypothetical protein
Carboxypeptidase-like, regulatory domain
TuPap-20 Cathepsin B
NAGLT1b Major facilitator superfamily; general substrate transporter Major facilitator superfamily; general subs
Clusterin-associated protein-1
Hypothetical protein
Gfi1b growth factor independent protein 1B zf-C2H2 Zinc finger; C2H2 type
Concanavalin A-like lectin/glucanase
protein kinase C alpha type
beta-1;4-galactosyltransferase
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like
Hypothetical protein
antigen B membrane protein
Kelch-type beta propeller
hypothetical protein
TuLeg-6 Legumain
Armadillo-type fold
Hypothetical protein
antigen B membrane protein
SRSP1 Serine-rich secreted protein LSPA1 Large secreted protein; family A LSPA1 Large secreted protein; fa
Hypothetical protein
Apple-like
Insect antifreeze protein
Hypothetical protein
peritrophic membrane chitin binding protein; putative
HESP1 Highly expressed secreted protein family HESP1 Highly expressed secreted protein family 1 Hypothet
hypothetical protein
DEAD/DEAH box DNA helicase
TuPap-19 Cystatin domain Cystatin domain
antigen B membrane protein
PREDICTED: similar to CG13913 CG13913-PA
CYP392A10 Cytochrome P450 - CYP392A10
DEAD
Fibroin Hypothetical protein
Bromo adjacent homology BAH domain
PREDICTED: similar to Glucosylceramidase precursor
putative oxidoreductase protein
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like
Hypothetical protein
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like

WASH complex subunit strumpellin   WASH complex subunit strumpellin
intradiol ring-cleavage dioxygenase
Hypothetical protein
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
TuGR99 Chemosensory Receptor; Gustatory receptor family   Hypothetical protein
isoamyl acetate-hydrolyzing esterase 1 homolog
Cysteine peptidase, asparagine active site
TuENaC08 Na+ channel, amiloride-sensitive ENaC08 Na+ channel, amiloride-sensitive ENaC8 Na+ channel,
LRRP1 Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
Hypothetical protein
Csp1f conserved secreted protein 1   Hypothetical protein
SSPG1 Small secreted protein; Family G   Hypothetical protein
conserved hypothetical protein
RecName: Full
Fibroin   hypothetical protein
OSP1a Orphan Secreted protein OSP1 Orphan Secreted protein   Hypothetical protein
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
Hypothetical protein
Zinc finger, C2H2-like
major facilitator superfamily MFS_1
Hypothetical protein
Hypothetical protein
hypothetical protein
Fibroin new   Hypothetical protein
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
Hypothetical protein
Hypothetical protein
intradiol ring-cleavage dioxygenase
Leucine-rich repeat domain, L domain-like
TuCCE61 Carboxyl/cholinesterase TuCCE-51 Carboxyl/cholinesterase
Hypothetical protein
Sodium/calcium exchanger membrane region SPHp5 Sodium/calcium exchanger membrane region
Hypothetical protein
short chain dehydrogenase
Hypothetical protein
TMCO7 RNA polymerase II assembly factor Rtp1, C-terminal   RNA polymerase II assembly factor Rtp1, C-term
steroid dehydrogenase
Hypothetical protein
MAP4K3 mitogen-activated protein kinase kinase kinase kinase 3 partial   mitogen-activated protein kinase kina
exostosin-1
CCEincTu16 Carboxyl/cholinesterase; incomplete CCEinc-26 Carboxyl/cholinesterase; incomplete
AkrE2 Aldo-keto reductase family E; member 2; likely a pseudogene   aldo-keto reductase
Fibroin   Hypothetical protein
phosphatidylinositol 3-kinase regulatory subunit gamma
Hypothetical protein
TuGR306 Chemosensory Receptor; Gustatory receptor family   Hypothetical protein
sodium-dependent multivitamin transporter
Hypothetical protein
IMP   IMP
SPH43 Serine protease homologue
BTB/POZ-like
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
PLAT14 PLAT/LH2 domain   PLAT/LH2 domain   PLAT/LH2 domain
Nse4
OSP2a Orphan secreted protein   Hypothetical protein
Uncharacterized oxidoreductase yqjQ   Uncharacterized oxidoreductase yqjQ

RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
TuENaC05 Putative amiloride-sensitive sodium channel ENaC05 Putative amiloride-sensitive sodium channel
LKAP32 Limkain-b1;
lysosomal alpha-glucosidase precursor
D13
Hypothetical protein
BTB/Kelch-associated
adenylosuccinate lyase
Hypothetical protein
unnamed protein product
High mobility group; HMG1/HMG2
PREDICTED: Cdt1 protein-like
UNCoordinated family member
Hypothetical fibroin new   Hypothetical protein
WASH complex subunit strumpellin
acylamino-acid-releasing enzyme
dUTPase deoxyuridine 5'-triphosphate nucleotidohydrolase   deoxyuridine 5'-triphosphate nucleotidohydrolase
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
TuCPI-20 Cystatin   hypothetical protein
PREDICTED: similar to neprilysin; partial
S-adenosyl-L-methionine-dependent methyltransferase
UNCoordinated family member   UNCoordinated family member
Hypothetical protein
DDM9-21 Domain of unknown function DUF3421   Domain of unknown function DUF3421
SSPF15 Small Secreted Protein; Family F   Hypothetical protein
lambda-crystallin homolog
Domain of unknown function DUF814   Domain of unknown function DUF814
Hypothetical protein
Six-bladed beta-propeller; TolB-like
jnk/sapk-associated protein   jnk/sapk-associated protein
Hypothetical protein
DNA replication factor Cdt1, C-terminal
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
PLC-like phosphodiesterase, TIM beta/alpha-barrel domain
Mitochondrial import inner membrane translocase subunit Tim13
Hypothetical protein
Protoporphyrinogen oxidase, C-terminal domain
Hypothetical protein
Apple-like
RNI Leucine-rich repeat domain, L domain-like   Leucine-rich repeat domain, L domain-like
TuLeg-18 Legumain TuLeg-18 Legumain;
Hypothetical protein
hatching enzyme
hypothetical protein
Hypothetical protein
hypothetical protein
aldo-keto reductase
Hypothetical protein
TuLeg-22 Legumain-like; pseudogene
Hypothetical protein
alanyl-tRNA synthetase
WD40/YVTN repeat-like-containing domain
Hypothetical protein
Leucine-rich repeat domain, L domain-like
Hypothetical protein
SFRS protein kinase 1

Hypothetical protein
ovo ovo zf-C2H2 Zinc finger; C2H2 type
Phosphoribosyltransferase-like Phosphoribosyltransferase-like
PLAT13 PLAT single domain protein PLAT/LH2 single domain protein; related Hypothetical protein
Hypothetical protein
Zinc finger, RING/FYVE/PHD-type Zinc finger, RING/FYVE/PHD-type
phospholipase A2 precursor; putative
PREDICTED: UDP-Gal:betaGlcNAc beta 1;3-galactosyltransferase 1-like
K Homology domain, type 1
Endonuclease/exonuclease/phosphatase
Hypothetical protein
IQ calmodulin-binding region
TuGSTinc03 Glutathione-S-transferase; incomplete;
pseudogene of 04g02210 ferrochelatase ferrochelatase
hypothetical protein
Hypothetical protein
ApoD20 Apolipoprotein D precursor PREDICTED: apolipoprotein D-like
WASH complex subunit strumpellin
PLATp2 PLAT/LH2 domain PLAT/LH2 domain
ovo ovo zf-C2H2 Zinc finger; C2H2 type
partitioning defective 6 homolog beta
hypothetical protein
cathepsin B
Hypothetical protein
SSPF16 Small Secreted Protein; family F hypothetical protein
PLC-like phosphodiesterase; TIM beta/alpha-barrel domain
ADP-ribosylation factor GTPase-activating protein 1
Hypothetical protein

stant populations (IT2, UK

P.Value	adj.P.Val
6.89E-11	4.16E-09
1.04E-12	2.05E-10
1.93E-14	1.24E-11
0.0001296	0.0006552
9.37E-10	3.33E-08
8.93E-14	3.61E-11
5.39E-13	1.33E-10
5.69E-09	1.48E-07
4.31E-10	1.79E-08
3.39E-10	1.47E-08
1.95E-13	6.89E-11
9.70E-16	1.91E-12
3.71E-14	1.91E-11
2.98E-13	8.63E-11
1.57E-12	2.87E-10
1.02E-09	3.60E-08
8.44E-12	1.02E-09
4.18E-08	7.60E-07
6.82E-12	8.67E-10
3.19E-13	8.80E-11
2.11E-11	1.69E-09
1.23E-11	1.25E-09
9.77E-12	1.09E-09
2.28E-11	1.79E-09
5.07E-10	2.01E-08
2.73E-08	5.29E-07
5.13E-12	6.83E-10
8.96E-09	2.10E-07
1.36E-08	2.98E-07
1.83E-12	3.16E-10
2.28E-12	3.66E-10
4.33E-19	4.90E-15
3.92E-11	2.71E-09
1.53E-11	1.44E-09
6.61E-10	2.49E-08
7.72E-13	1.76E-10
1.61E-11	1.47E-09
7.79E-13	1.76E-10
1.19E-15	1.93E-12
5.33E-09	1.41E-07
3.43E-10	1.48E-08
4.73E-15	4.87E-12
1.23E-10	6.47E-09
5.63E-09	1.47E-07
5.65E-12	7.43E-10
7.76E-11	4.51E-09
1.60E-11	1.47E-09
1.99E-10	9.64E-09
1.85E-12	3.16E-10
1.23E-10	6.47E-09
4.48E-11	2.99E-09
4.22E-08	7.63E-07

1.27E-11	1.29E-09
2.90E-10	1.29E-08
9.09E-06	6.73E-05
1.81E-07	2.51E-06
1.60E-13	6.05E-11
1.68E-11	1.51E-09
3.64E-12	5.17E-10
1.40E-08	3.05E-07
2.10E-07	2.83E-06
2.53E-11	1.96E-09
8.62E-09	2.04E-07
7.97E-13	1.77E-10
3.43E-11	2.41E-09
1.66E-11	1.51E-09
8.83E-10	3.17E-08
1.67E-10	8.24E-09
1.23E-10	6.47E-09
1.40E-10	7.18E-09
6.92E-11	4.16E-09
6.99E-08	1.14E-06
5.74E-09	1.49E-07
3.46E-11	2.42E-09
1.74E-11	1.55E-09
4.96E-08	8.74E-07
1.26E-08	2.79E-07
5.01E-11	3.24E-09
6.93E-10	2.57E-08
8.53E-15	6.89E-12
1.05E-09	3.66E-08
2.38E-09	7.14E-08
4.86E-10	1.97E-08
1.80E-10	8.79E-09
1.12E-07	1.70E-06
8.85E-11	5.03E-09
2.74E-08	5.30E-07
4.61E-10	1.89E-08
6.81E-10	2.55E-08
2.70E-12	4.18E-10
5.99E-10	2.28E-08
1.88E-09	5.98E-08
2.36E-10	1.11E-08
1.14E-11	1.19E-09
3.32E-13	8.93E-11
1.50E-09	4.93E-08
4.77E-12	6.42E-10
1.14E-11	1.19E-09
1.45E-11	1.38E-09
1.30E-09	4.34E-08
4.41E-09	1.20E-07
4.93E-09	1.32E-07
7.54E-09	1.84E-07
2.41E-07	3.14E-06
2.38E-09	7.14E-08
3.70E-08	6.77E-07
9.71E-10	3.45E-08
1.06E-09	3.71E-08

2.25E-07	2.97E-06
2.46E-07	3.20E-06
2.31E-14	1.24E-11
1.72E-08	3.59E-07
2.02E-13	6.93E-11
3.15E-07	3.99E-06
2.36E-10	1.11E-08
1.39E-16	5.26E-13
1.01E-15	1.91E-12
4.44E-11	2.99E-09
2.15E-14	1.24E-11
1.91E-07	2.63E-06
3.52E-12	5.17E-10
2.28E-14	1.24E-11
1.21E-11	1.25E-09
4.10E-15	4.64E-12
2.97E-08	5.66E-07
2.93E-11	2.17E-09
1.52E-10	7.62E-09
5.36E-09	1.41E-07
2.05E-12	3.36E-10
5.24E-07	6.03E-06
5.96E-10	2.27E-08
1.31E-10	6.83E-09
7.57E-16	1.91E-12
9.24E-08	1.43E-06
5.49E-08	9.40E-07
2.26E-09	6.89E-08
6.50E-09	1.63E-07
4.54E-07	5.39E-06
4.10E-09	1.14E-07
1.34E-07	1.98E-06
4.85E-18	2.74E-14
2.03E-10	9.76E-09
2.31E-08	4.58E-07
9.44E-07	9.89E-06
9.34E-13	1.98E-10
1.32E-08	2.91E-07
1.54E-08	3.29E-07
3.28E-08	6.11E-07
5.20E-14	2.35E-11
3.35E-06	2.85E-05
5.80E-11	3.57E-09
3.18E-13	8.80E-11
3.70E-07	4.51E-06
5.02E-08	8.80E-07
8.86E-08	1.38E-06
9.49E-07	9.93E-06
2.66E-11	2.02E-09
3.66E-12	5.17E-10
5.19E-14	2.35E-11
1.67E-08	3.52E-07
2.79E-10	1.25E-08
2.76E-10	1.24E-08
7.90E-08	1.26E-06
4.07E-07	4.88E-06

8.36E-11	4.80E-09
4.31E-14	2.12E-11
2.01E-08	4.07E-07
4.11E-12	5.62E-10
2.52E-10	1.15E-08
1.09E-09	3.74E-08
4.20E-08	7.62E-07
1.68E-06	1.61E-05
1.21E-09	4.10E-08
6.82E-10	2.55E-08
8.03E-15	6.89E-12
2.15E-06	1.98E-05
2.54E-07	3.29E-06
9.82E-13	1.98E-10
2.30E-12	3.66E-10
7.85E-08	1.26E-06
7.54E-10	2.77E-08
8.32E-08	1.32E-06
2.40E-11	1.87E-09
1.08E-10	5.86E-09
1.04E-09	3.66E-08
8.29E-08	1.32E-06
2.00E-07	2.71E-06
2.90E-11	2.16E-09
3.17E-08	5.97E-07
1.13E-07	1.71E-06
1.45E-10	7.30E-09
6.36E-08	1.05E-06
1.12E-08	2.54E-07
1.93E-08	3.95E-07
9.22E-12	1.06E-09
2.79E-13	8.54E-11
3.22E-06	2.76E-05
9.69E-11	5.35E-09
9.87E-09	2.27E-07
5.51E-07	6.32E-06
5.07E-07	5.88E-06
1.24E-12	2.33E-10
1.57E-09	5.14E-08
5.00E-10	2.01E-08
3.13E-08	5.91E-07
1.09E-07	1.65E-06
7.64E-13	1.76E-10
1.91E-05	0.0001267
4.95E-07	5.77E-06
6.99E-11	4.19E-09
1.60E-14	1.21E-11
5.63E-08	9.61E-07
2.66E-11	2.02E-09
2.46E-07	3.20E-06
4.21E-11	2.89E-09
4.20E-09	1.16E-07
9.38E-09	2.18E-07
1.95E-12	3.24E-10
6.49E-08	1.07E-06
1.38E-15	1.95E-12

2.48E-06	2.24E-05
7.01E-07	7.76E-06
4.36E-11	2.96E-09
2.35E-09	7.09E-08
7.67E-07	8.32E-06
1.44E-11	1.38E-09
2.13E-06	1.96E-05
7.06E-09	1.74E-07
3.46E-07	4.31E-06
2.29E-09	6.94E-08
2.06E-14	1.24E-11
4.48E-09	1.21E-07
3.98E-07	4.82E-06
1.66E-09	5.41E-08
7.81E-08	1.26E-06
2.76E-12	4.22E-10
5.00E-10	2.01E-08
6.36E-08	1.05E-06
2.68E-13	8.54E-11
6.50E-07	7.29E-06
1.69E-07	2.38E-06
7.52E-13	1.76E-10
3.72E-07	4.53E-06
0.0004116	0.0017691
4.83E-07	5.67E-06
5.42E-07	6.23E-06
5.33E-08	9.21E-07
3.10E-08	5.87E-07
1.60E-10	7.98E-09
1.35E-07	2.00E-06
3.49E-09	9.99E-08
2.24E-09	6.86E-08
6.52E-09	1.63E-07
1.85E-11	1.59E-09
7.25E-06	5.55E-05
2.20E-10	1.05E-08
6.27E-08	1.04E-06
1.98E-11	1.66E-09
6.06E-08	1.02E-06
1.03E-06	1.06E-05
1.90E-08	3.90E-07
1.05E-05	7.64E-05
1.07E-09	3.72E-08
1.62E-05	0.0001102
1.43E-07	2.08E-06
3.61E-10	1.54E-08
2.31E-07	3.04E-06
1.87E-12	3.17E-10
2.59E-06	2.30E-05
1.15E-09	3.93E-08
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8.44E-15	6.89E-12
2.02E-10	9.75E-09
4.07E-08	7.43E-07
6.52E-14	2.73E-11
4.01E-09	1.12E-07

1.36E-08	2.98E-07
8.79E-09	2.07E-07
6.19E-09	1.57E-07
4.94E-07	5.77E-06
4.72E-07	5.55E-06
3.25E-10	1.43E-08
4.13E-12	5.62E-10
8.15E-08	1.30E-06
3.53E-11	2.45E-09
9.46E-08	1.46E-06
2.33E-08	4.59E-07
3.94E-13	1.04E-10
1.30E-13	5.07E-11
1.05E-06	1.08E-05
2.92E-10	1.30E-08
1.92E-08	3.93E-07
2.54E-10	1.16E-08
1.80E-08	3.74E-07
1.18E-10	6.30E-09
6.17E-09	1.57E-07
2.37E-05	0.0001524
3.18E-08	5.98E-07
4.97E-07	5.78E-06
7.68E-08	1.24E-06
5.66E-09	1.48E-07
2.58E-06	2.30E-05
1.09E-11	1.17E-09
4.84E-11	3.18E-09
5.69E-11	3.53E-09
4.34E-11	2.96E-09
0.0011381	0.0041545
1.20E-08	2.68E-07
3.01E-09	8.76E-08
2.46E-08	4.83E-07
8.55E-12	1.02E-09
7.71E-09	1.87E-07
9.47E-12	1.07E-09
9.92E-07	1.03E-05
1.22E-10	6.47E-09
1.19E-05	8.45E-05
3.65E-09	1.04E-07
2.39E-10	1.11E-08
3.30E-08	6.12E-07
4.90E-11	3.20E-09
2.41E-07	3.14E-06
1.88E-07	2.60E-06
5.50E-08	9.40E-07
1.34E-07	1.98E-06
5.80E-11	3.57E-09
1.36E-09	4.51E-08
1.03E-11	1.14E-09
2.08E-10	9.96E-09
1.72E-13	6.29E-11
9.55E-09	2.21E-07
2.08E-09	6.48E-08
7.56E-08	1.23E-06

2.11E-11	1.69E-09
3.21E-07	4.05E-06
2.90E-13	8.63E-11
4.70E-10	1.92E-08
2.25E-09	6.87E-08
5.89E-14	2.56E-11
1.25E-08	2.78E-07
2.54E-06	2.27E-05
7.07E-07	7.82E-06
2.56E-11	1.97E-09
6.55E-10	2.47E-08
5.03E-10	2.01E-08
1.41E-11	1.37E-09
1.98E-09	6.23E-08
2.84E-05	0.0001774
2.01E-08	4.07E-07
2.39E-10	1.11E-08
5.00E-11	3.24E-09
5.96E-12	7.76E-10
1.66E-07	2.36E-06
3.69E-08	6.76E-07
2.87E-08	5.51E-07
2.03E-09	6.37E-08
2.33E-07	3.06E-06
2.15E-11	1.70E-09
1.21E-06	1.21E-05
0.0005765	0.0023367
1.13E-07	1.72E-06
2.54E-09	7.54E-08
8.71E-12	1.03E-09
3.27E-11	2.34E-09
3.91E-09	1.10E-07
3.12E-06	2.69E-05
2.89E-12	4.37E-10
2.49E-13	8.27E-11
7.87E-12	9.79E-10
1.55E-08	3.30E-07
4.91E-08	8.67E-07
1.23E-05	8.71E-05
3.43E-11	2.41E-09
1.70E-08	3.56E-07
1.89E-07	2.61E-06
4.54E-11	3.00E-09
4.45E-05	0.0002625
5.27E-11	3.33E-09
2.10E-05	0.0001371
9.63E-11	5.35E-09
9.53E-11	5.34E-09
2.76E-06	2.44E-05
1.62E-05	0.0001098
8.35E-07	9.00E-06
5.05E-11	3.25E-09
2.97E-08	5.66E-07
3.54E-09	1.01E-07
8.31E-09	1.99E-07
2.14E-07	2.86E-06

1.05E-10	5.75E-09
3.05E-11	2.22E-09
2.04E-09	6.37E-08
1.05E-11	1.14E-09
1.03E-11	1.14E-09
6.22E-06	4.88E-05
9.19E-07	9.67E-06
2.23E-07	2.95E-06
2.46E-12	3.86E-10
1.10E-06	1.13E-05
1.54E-06	1.50E-05
1.53E-07	2.21E-06
3.38E-11	2.40E-09
4.32E-08	7.77E-07
9.83E-09	2.26E-07
1.94E-06	1.83E-05
1.48E-10	7.46E-09
1.85E-07	2.56E-06
5.38E-08	9.25E-07
3.67E-06	3.08E-05
1.12E-05	8.09E-05
2.46E-10	1.13E-08
1.80E-11	1.57E-09
1.45E-08	3.14E-07
2.49E-06	2.24E-05
1.89E-09	5.99E-08
1.96E-06	1.84E-05
6.49E-06	5.07E-05
6.31E-09	1.60E-07
7.62E-10	2.78E-08
5.61E-07	6.42E-06
9.72E-07	1.01E-05
1.71E-08	3.58E-07
4.33E-13	1.11E-10
3.34E-07	4.18E-06
2.41E-10	1.12E-08
3.10E-11	2.25E-09
4.86E-13	1.22E-10
3.23E-10	1.42E-08
3.50E-07	4.34E-06
1.61E-11	1.47E-09
1.14E-06	1.16E-05
1.47E-05	0.0001014
9.72E-13	1.98E-10
1.31E-12	2.43E-10
1.41E-10	7.20E-09
1.12E-09	3.84E-08
3.38E-06	2.88E-05
4.02E-05	0.0002403
4.17E-10	1.74E-08
2.35E-07	3.08E-06
1.52E-08	3.27E-07
6.17E-09	1.57E-07
3.62E-09	1.03E-07
1.17E-09	3.98E-08
5.69E-06	4.53E-05

1.73E-07	2.42E-06
4.47E-07	5.32E-06
2.13E-09	6.61E-08
7.93E-08	1.27E-06
8.60E-07	9.19E-06
2.71E-09	7.96E-08
2.76E-13	8.54E-11
3.83E-06	3.20E-05
4.69E-08	8.29E-07
1.90E-05	0.0001264
0.0001641	0.000806
6.11E-09	1.56E-07
4.04E-05	0.0002418
2.49E-06	2.24E-05
8.77E-07	9.31E-06
0.0001572	0.0007756
3.68E-07	4.50E-06
1.97E-05	0.0001303
9.06E-09	2.12E-07
2.77E-11	2.09E-09
1.19E-12	2.32E-10
1.17E-06	1.19E-05
2.13E-09	6.61E-08
1.91E-05	0.0001267
5.38E-06	4.31E-05
2.11E-07	2.84E-06
1.57E-05	0.0001071
4.04E-07	4.86E-06
3.43E-05	0.0002095
8.57E-07	9.17E-06
0.0001016	0.0005297
6.94E-08	1.14E-06
1.33E-06	1.32E-05
4.45E-08	7.95E-07
9.47E-09	2.20E-07
2.42E-06	2.20E-05
4.52E-07	5.37E-06
1.18E-08	2.65E-07
1.56E-05	0.0001069
3.45E-05	0.0002106
9.17E-06	6.78E-05
1.20E-06	1.20E-05
2.44E-06	2.21E-05
2.26E-07	2.98E-06
5.09E-10	2.01E-08
1.06E-11	1.15E-09
4.01E-05	0.0002401
6.75E-11	4.11E-09
2.15E-07	2.87E-06
0.0001462	0.0007282
0.0003416	0.0015114
7.82E-07	8.48E-06
1.86E-05	0.0001241
5.23E-06	4.21E-05
1.72E-05	0.0001159
4.06E-10	1.71E-08

0.0002698	0.00124
8.33E-06	6.23E-05
0.0001915	0.0009201
1.52E-08	3.27E-07
2.53E-06	2.26E-05
1.94E-06	1.82E-05
8.21E-12	1.01E-09
4.31E-07	5.14E-06
0.000786	0.0030462
8.33E-08	1.32E-06
0.0005838	0.002358
5.95E-11	3.64E-09
2.62E-07	3.38E-06
2.95E-10	1.30E-08
3.30E-07	4.14E-06
5.99E-08	1.01E-06
7.36E-08	1.20E-06
1.25E-08	2.78E-07
3.93E-07	4.76E-06
2.17E-08	4.34E-07
5.96E-08	1.01E-06
3.17E-06	2.73E-05
0.0001182	0.000604
3.91E-10	1.66E-08
7.77E-11	4.51E-09
6.55E-06	5.11E-05
1.55E-06	1.50E-05
2.32E-06	2.11E-05
2.83E-08	5.44E-07
2.54E-08	4.95E-07
0.0016303	0.0056385
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5.32E-08	9.20E-07
8.95E-12	1.04E-09
2.41E-09	7.19E-08
1.74E-09	5.64E-08
8.35E-11	4.80E-09
1.43E-05	9.89E-05
8.97E-11	5.07E-09
2.04E-11	1.69E-09
0.0015163	0.005314
2.06E-05	0.0001351
1.84E-11	1.59E-09
1.50E-05	0.0001034
6.04E-08	1.02E-06
1.56E-07	2.24E-06
1.22E-12	2.33E-10
8.14E-09	1.95E-07
4.14E-06	3.42E-05
8.86E-07	9.38E-06
1.77E-08	3.69E-07
1.14E-10	6.15E-09
0.0004287	0.0018299
1.08E-06	1.11E-05
7.61E-12	9.56E-10
2.80E-06	2.47E-05

2.39E-06	2.17E-05
1.37E-08	3.00E-07
7.34E-10	2.71E-08
6.66E-07	7.45E-06
7.27E-07	7.98E-06
3.30E-06	2.82E-05
7.26E-06	5.56E-05
7.64E-09	1.86E-07
4.41E-05	0.0002606
3.32E-10	1.45E-08
1.97E-09	6.23E-08
0.0006153	0.0024651
3.05E-07	3.88E-06
1.61E-06	1.55E-05
1.70E-12	3.06E-10
9.94E-07	1.03E-05
1.19E-09	4.03E-08
4.89E-10	1.98E-08
1.32E-11	1.33E-09
4.44E-05	0.000262
1.58E-06	1.54E-05
6.10E-09	1.56E-07
0.000202	0.0009632
1.23E-05	8.74E-05
4.34E-09	1.19E-07
3.02E-07	3.85E-06
5.62E-10	2.18E-08
5.51E-11	3.47E-09
0.0003529	0.0015564
1.41E-08	3.08E-07
1.52E-07	2.19E-06
7.07E-06	5.45E-05
1.02E-06	1.05E-05
5.47E-10	2.13E-08
8.16E-09	1.96E-07
5.73E-06	4.55E-05
2.91E-09	8.50E-08
1.44E-06	1.41E-05
4.64E-08	8.24E-07
2.62E-05	0.0001659
1.41E-07	2.05E-06
6.80E-09	1.69E-07
8.97E-07	9.45E-06
2.63E-06	2.33E-05
4.58E-05	0.0002692
5.79E-10	2.22E-08
5.14E-11	3.28E-09
2.20E-10	1.05E-08
1.05E-07	1.60E-06
1.67E-07	2.36E-06
9.08E-10	3.25E-08
0.0001167	0.0005971
2.81E-11	2.10E-09
0.0165189	0.0380999
9.66E-07	1.01E-05
1.19E-06	1.20E-05

6.45E-09	1.62E-07
5.09E-09	1.35E-07
1.75E-08	3.64E-07
6.72E-06	5.22E-05
1.30E-10	6.82E-09
8.68E-09	2.05E-07
6.15E-05	0.0003457
3.94E-06	3.27E-05
0.0013593	0.004845
2.27E-06	2.07E-05
1.26E-07	1.89E-06
5.93E-06	4.68E-05
0.0004659	0.0019563
0.0042567	0.0124725
0.0009791	0.0036678
1.16E-06	1.18E-05
2.86E-06	2.50E-05
0.0178784	0.0406305
1.34E-10	6.94E-09
1.02E-07	1.57E-06
5.16E-11	3.28E-09
1.30E-05	9.11E-05
2.35E-10	1.11E-08
8.99E-05	0.0004766
8.80E-11	5.03E-09
9.31E-10	3.32E-08
8.43E-05	0.0004513
2.60E-08	5.06E-07
9.41E-07	9.87E-06
6.40E-05	0.0003574
1.62E-08	3.43E-07
6.05E-06	4.76E-05
1.93E-07	2.64E-06
1.19E-06	1.20E-05
0.0003656	0.0016064
4.88E-07	5.71E-06
0.0001035	0.0005378
0.0001492	0.0007414
7.41E-09	1.82E-07
1.04E-07	1.59E-06
1.01E-08	2.32E-07
3.22E-07	4.06E-06
1.09E-10	5.89E-09
4.54E-09	1.22E-07
3.77E-05	0.0002274
7.37E-11	4.34E-09
1.61E-07	2.30E-06
1.74E-05	0.0001174
6.06E-08	1.02E-06
2.08E-08	4.17E-07
0.0032348	0.0099635
0.001045	0.0038761
1.01E-05	7.37E-05
1.89E-06	1.79E-05
7.23E-09	1.78E-07
8.36E-10	3.04E-08

8.82E-07	9.34E-06
6.32E-09	1.60E-07
3.90E-10	1.66E-08
6.11E-07	6.92E-06
0.0002574	0.0011915
8.42E-07	9.05E-06
4.27E-08	7.71E-07
4.66E-08	8.27E-07
2.65E-06	2.35E-05
1.17E-08	2.63E-07
0.0004876	0.0020363
1.44E-10	7.30E-09
1.18E-06	1.19E-05
5.69E-06	4.53E-05
2.73E-06	2.42E-05
1.06E-07	1.61E-06
9.89E-11	5.43E-09
4.25E-08	7.68E-07
3.32E-06	2.83E-05
0.0007452	0.002911
1.65E-06	1.59E-05
3.40E-09	9.76E-08
8.56E-09	2.04E-07
0.0021585	0.007109
0.0003455	0.0015269
2.15E-09	6.63E-08
8.02E-06	6.04E-05
6.55E-07	7.33E-06
7.52E-09	1.84E-07
1.04E-05	7.55E-05
4.44E-09	1.21E-07
4.95E-09	1.32E-07
2.38E-06	2.17E-05
0.0004413	0.0018712
1.35E-05	9.43E-05
0.0001083	0.0005599
5.37E-10	2.10E-08
1.42E-05	9.81E-05
5.80E-05	0.0003289
5.75E-07	6.56E-06
3.71E-05	0.0002247
4.66E-06	3.80E-05
6.04E-08	1.02E-06
0.0002533	0.0011777
3.31E-07	4.15E-06
0.000787	0.0030491
0.001523	0.0053344
1.76E-06	1.68E-05
2.17E-09	6.67E-08
0.0003615	0.0015918
8.78E-07	9.31E-06
3.70E-07	4.51E-06
2.19E-05	0.0001427
1.56E-09	5.12E-08
1.72E-08	3.59E-07
3.41E-08	6.29E-07

2.92E-05	0.0001815
2.04E-06	1.90E-05
1.91E-05	0.0001267
0.0002099	0.0009952
2.15E-09	6.63E-08
3.75E-09	1.06E-07
2.66E-06	2.36E-05
2.89E-06	2.52E-05
6.17E-10	2.33E-08
4.63E-07	5.48E-06
6.11E-05	0.0003443
1.68E-05	0.0001133
6.35E-05	0.0003547
1.03E-09	3.61E-08
4.76E-05	0.0002777
8.72E-08	1.37E-06
3.20E-08	6.00E-07
0.0001403	0.0007017
4.43E-08	7.93E-07
4.99E-06	4.04E-05
3.99E-09	1.12E-07
7.15E-06	5.51E-05
1.55E-07	2.23E-06
1.28E-07	1.91E-06
2.54E-05	0.0001616
4.37E-07	5.22E-06
3.22E-09	9.34E-08
1.63E-09	5.31E-08
5.10E-09	1.35E-07
1.05E-08	2.38E-07
9.71E-06	7.12E-05
0.0013656	0.0048611
3.11E-07	3.94E-06
1.22E-07	1.83E-06
1.49E-06	1.46E-05
3.62E-07	4.45E-06
8.93E-07	9.43E-06
7.18E-05	0.0003945
2.88E-06	2.52E-05
8.08E-06	6.08E-05
1.68E-07	2.37E-06
1.58E-05	0.0001082
3.61E-08	6.63E-07
5.11E-05	0.000295
1.17E-05	8.37E-05
1.90E-09	6.03E-08
2.12E-08	4.24E-07
5.63E-05	0.000321
1.11E-05	8.04E-05
7.66E-07	8.32E-06
2.20E-05	0.0001431
0.0003338	0.0014845
1.60E-06	1.55E-05
2.70E-05	0.00017
2.48E-06	2.24E-05
0.0001689	0.0008265

2.82E-06	2.48E-05
1.26E-09	4.22E-08
0.000403	0.0017375
6.00E-06	4.73E-05
4.97E-05	0.0002887
0.000366	0.0016068
6.11E-07	6.92E-06
8.64E-07	9.20E-06
5.62E-09	1.47E-07
2.58E-10	1.17E-08
5.51E-05	0.000316
0.0007609	0.002961
1.38E-07	2.03E-06
7.32E-08	1.19E-06
1.20E-05	8.49E-05
5.45E-08	9.34E-07
8.49E-06	6.33E-05
4.48E-09	1.21E-07
1.61E-08	3.42E-07
0.0003136	0.0014091
1.08E-09	3.74E-08
7.66E-05	0.0004175
0.000254	0.0011795
0.0013241	0.0047298
9.13E-06	6.76E-05
0.0001116	0.0005734
0.0003145	0.0014122
1.32E-07	1.96E-06
7.25E-07	7.97E-06
4.84E-07	5.67E-06
2.70E-07	3.48E-06
2.11E-06	1.96E-05
1.73E-07	2.42E-06
1.66E-08	3.52E-07
1.70E-07	2.40E-06
2.52E-06	2.26E-05
1.84E-09	5.90E-08
2.85E-07	3.66E-06
4.18E-06	3.45E-05
1.36E-05	9.48E-05
1.61E-07	2.30E-06
6.01E-08	1.02E-06
2.10E-08	4.21E-07
2.78E-05	0.000174
0.0001594	0.0007845
1.72E-09	5.59E-08
1.20E-08	2.69E-07
1.36E-05	9.46E-05
1.20E-07	1.81E-06
1.07E-06	1.11E-05
2.10E-05	0.0001373
2.33E-09	7.06E-08
1.97E-05	0.0001302
0.000307	0.0013861
1.63E-07	2.32E-06
6.27E-05	0.0003514

1.95E-05	0.0001288
6.57E-05	0.0003652
6.43E-08	1.06E-06
0.000238	0.0011136
0.0001869	0.0009011
8.80E-08	1.38E-06
0.0070876	0.0191046
0.0005066	0.0020956
8.27E-08	1.31E-06
1.91E-05	0.0001267
1.45E-07	2.11E-06
5.74E-10	2.21E-08
2.57E-10	1.17E-08
9.33E-08	1.45E-06
4.92E-05	0.0002861
3.13E-05	0.0001932
4.03E-06	3.34E-05
2.00E-08	4.06E-07
0.0003081	0.0013888
7.95E-07	8.60E-06
1.91E-07	2.62E-06
0.0079337	0.0209608
2.78E-05	0.0001741
2.85E-08	5.48E-07
2.82E-06	2.48E-05
1.81E-05	0.0001211
0.0001532	0.0007584
0.0021637	0.0071198
0.0001703	0.0008323
1.02E-05	7.41E-05
0.0005625	0.0022907
1.80E-06	1.71E-05
7.38E-07	8.07E-06
0.0001066	0.0005521
6.43E-07	7.24E-06
9.43E-06	6.94E-05
3.85E-06	3.21E-05
0.0021529	0.0070946
9.18E-05	0.0004858
8.95E-08	1.40E-06
0.0010456	0.0038771
0.0022775	0.0074318
7.05E-07	7.80E-06
0.0004078	0.0017543
3.60E-07	4.44E-06
0.0003217	0.0014391
3.00E-07	3.83E-06
3.04E-06	2.63E-05
9.31E-06	6.86E-05
3.76E-05	0.0002274
0.0008603	0.003289
5.06E-05	0.0002932
0.0003736	0.0016329
7.80E-05	0.0004246
3.26E-05	0.0002001
0.0036052	0.0108731

1.29E-05	9.08E-05
1.13E-06	1.16E-05
2.67E-05	0.0001683
0.0005431	0.0022218
0.0009006	0.0034214
1.06E-06	1.09E-05
6.29E-05	0.0003523
4.03E-07	4.85E-06
6.29E-05	0.0003523
0.0009027	0.0034269
5.96E-08	1.01E-06
0.001126	0.0041158
0.0014972	0.0052553
4.90E-06	3.97E-05
1.38E-06	1.36E-05
3.35E-09	9.64E-08
3.82E-07	4.64E-06
0.0012798	0.0045935
7.31E-06	5.58E-05
4.27E-05	0.0002529
0.0015363	0.0053665
1.22E-08	2.72E-07
1.01E-07	1.55E-06
6.70E-05	0.0003711
0.0139768	0.0332952
0.0002963	0.0013457
1.24E-05	8.74E-05
1.22E-06	1.22E-05
5.29E-06	4.24E-05
0.003053	0.0094963
0.0001171	0.0005987
0.0006201	0.002482
0.0006417	0.0025561
3.49E-07	4.34E-06
9.73E-05	0.0005108
9.94E-06	7.26E-05
1.82E-08	3.76E-07
1.10E-05	7.96E-05
8.66E-10	3.13E-08
5.43E-05	0.0003116
2.08E-06	1.93E-05
2.14E-07	2.86E-06
1.82E-07	2.53E-06
0.0007804	0.0030277
9.85E-07	1.03E-05
1.40E-07	2.05E-06
0.0003126	0.0014049
0.0001399	0.0007004
0.0003947	0.0017063
6.77E-09	1.69E-07
3.49E-07	4.34E-06
4.34E-05	0.0002566
0.0015896	0.0055247
6.11E-05	0.0003443
3.98E-05	0.0002382
3.57E-06	3.00E-05

0.0002237	0.0010517
0.0001598	0.0007861
5.57E-05	0.0003185
7.48E-06	5.69E-05
8.63E-06	6.42E-05
8.87E-09	2.09E-07
0.007158	0.0192282
0.0002183	0.0010301
1.14E-05	8.20E-05
4.13E-05	0.0002461
5.80E-08	9.84E-07
3.29E-08	6.11E-07
0.0039188	0.0116606
3.53E-05	0.000215
1.49E-07	2.15E-06
3.22E-08	6.02E-07
0.0052306	0.0147934
0.0001571	0.0007754
0.0013992	0.0049651
0.0008887	0.0033829
0.0006907	0.0027253
0.0001097	0.0005651
0.0001703	0.0008323
7.75E-06	5.85E-05
8.32E-05	0.0004461
0.0006545	0.0026025
3.08E-06	2.66E-05
5.72E-06	4.54E-05
5.07E-10	2.01E-08
0.0002977	0.0013506
2.03E-06	1.89E-05
0.0015714	0.0054698
1.80E-09	5.79E-08
0.0010784	0.0039792
2.32E-06	2.11E-05
0.0030753	0.009558
6.94E-08	1.14E-06
7.55E-05	0.0004119
3.63E-07	4.46E-06
0.0095826	0.0244218
1.24E-05	8.76E-05
0.0004974	0.0020661
2.11E-05	0.0001377
7.56E-06	5.74E-05
0.0004575	0.0019283
1.61E-06	1.55E-05
7.27E-06	5.56E-05
2.91E-05	0.000181
0.0002563	0.0011883
7.30E-05	0.0003995
1.89E-06	1.79E-05
2.58E-05	0.000164
1.08E-05	7.81E-05
4.33E-09	1.19E-07
0.0011222	0.0041032
2.58E-07	3.34E-06

8.74E-08	1.37E-06
1.04E-08	2.38E-07
2.94E-08	5.62E-07
0.0004754	0.0019911
1.98E-07	2.70E-06
8.83E-05	0.0004689
0.001108	0.0040672
6.97E-06	5.39E-05
1.62E-08	3.43E-07
1.89E-07	2.61E-06
8.64E-06	6.42E-05
0.0003962	0.001712
0.0001923	0.0009233
2.09E-05	0.0001369
1.84E-07	2.55E-06
8.71E-09	2.06E-07
1.02E-05	7.42E-05
0.0003772	0.0016459
0.0006493	0.0025848
2.49E-09	7.42E-08
0.0003276	0.0014622
0.0007558	0.0029439
8.01E-05	0.0004339
2.49E-05	0.0001591
4.10E-06	3.39E-05
1.89E-08	3.90E-07
3.70E-09	1.05E-07
8.24E-06	6.17E-05
6.07E-06	4.77E-05
1.18E-08	2.66E-07
0.0004239	0.0018112
6.03E-07	6.85E-06
5.03E-07	5.85E-06
0.0028258	0.0089099
0.0008209	0.0031609
1.28E-05	8.96E-05
0.0005095	0.0021054
9.64E-11	5.35E-09
2.31E-07	3.04E-06
3.74E-05	0.0002264
0.0201159	0.0449569
0.0011008	0.0040458
4.55E-09	1.23E-07
4.34E-09	1.19E-07
0.0001527	0.000757
3.19E-07	4.02E-06
1.63E-05	0.0001108
7.02E-06	5.42E-05
4.85E-10	1.97E-08
1.04E-07	1.59E-06
0.0004886	0.0020397
1.24E-05	8.77E-05
0.0003096	0.0013938
9.65E-09	2.23E-07
3.26E-09	9.43E-08
8.82E-10	3.17E-08

4.57E-10	1.88E-08
8.84E-05	0.0004693
5.43E-07	6.23E-06
2.55E-06	2.28E-05
2.71E-06	2.40E-05
0.0037742	0.0112927
5.49E-05	0.000315
0.0005673	0.0023068
6.46E-05	0.0003602
6.50E-05	0.0003621
0.0008634	0.0032998
4.26E-06	3.50E-05
1.44E-05	9.97E-05
1.20E-05	8.54E-05
1.35E-07	2.00E-06
3.58E-10	1.54E-08
7.22E-07	7.94E-06
0.0001881	0.0009055
5.68E-09	1.48E-07
7.21E-08	1.18E-06
1.39E-06	1.37E-05
1.00E-05	7.32E-05
1.77E-05	0.0001186
0.000169	0.0008265
6.29E-06	4.94E-05
1.70E-05	0.0001149
8.48E-06	6.32E-05
9.97E-07	1.04E-05
0.0003758	0.0016423
8.21E-07	8.86E-06
1.88E-07	2.60E-06
1.32E-06	1.31E-05
0.000129	0.0006525
5.24E-06	4.22E-05
1.32E-05	9.23E-05
2.55E-06	2.28E-05
3.59E-05	0.0002183
4.13E-08	7.53E-07
3.52E-07	4.36E-06
5.01E-05	0.0002903
2.44E-06	2.21E-05
1.38E-07	2.03E-06
1.13E-05	8.14E-05
1.07E-05	7.73E-05
1.42E-11	1.37E-09
1.37E-06	1.35E-05
3.90E-05	0.0002342
8.05E-06	6.06E-05
0.0005162	0.0021283
9.93E-05	0.0005192
9.69E-06	7.11E-05
5.18E-10	2.04E-08
2.99E-05	0.0001855
0.0003302	0.0014711
1.43E-06	1.41E-05
5.59E-07	6.40E-06

1.56E-07	2.23E-06
8.51E-12	1.02E-09
6.29E-07	7.10E-06
0.0004673	0.0019618
2.96E-06	2.58E-05
8.80E-05	0.0004677
8.55E-05	0.0004565
2.20E-08	4.38E-07
1.20E-06	1.21E-05
8.54E-06	6.36E-05
4.28E-09	1.18E-07
3.08E-07	3.92E-06
2.05E-05	0.0001348
8.51E-07	9.13E-06
4.23E-07	5.08E-06
1.25E-09	4.18E-08
3.43E-06	2.91E-05
2.36E-06	2.14E-05
6.50E-07	7.29E-06
1.04E-07	1.59E-06
5.01E-06	4.05E-05
2.28E-09	6.94E-08
1.55E-07	2.23E-06
1.50E-05	0.000103
2.66E-05	0.0001677
0.0003975	0.0017162
2.30E-06	2.10E-05
5.12E-08	8.96E-07
1.17E-06	1.19E-05
4.32E-05	0.0002561
3.30E-09	9.52E-08
0.0002179	0.0010285
1.34E-06	1.33E-05
5.77E-05	0.0003273
7.17E-09	1.77E-07
2.96E-05	0.0001835
1.88E-10	9.19E-09
3.33E-06	2.84E-05
1.97E-06	1.85E-05
5.13E-06	4.14E-05
5.81E-06	4.60E-05
1.75E-05	0.0001178
2.85E-09	8.37E-08
3.13E-06	2.70E-05
6.87E-07	7.64E-06
5.70E-10	2.20E-08
4.69E-05	0.0002742
4.92E-09	1.32E-07
2.89E-05	0.0001798
9.64E-09	2.23E-07
1.38E-06	1.36E-05
6.13E-06	4.81E-05
8.08E-08	1.29E-06
2.08E-11	1.69E-09
5.40E-08	9.26E-07
6.89E-05	0.0003805

1.98E-09	6.23E-08
5.32E-10	2.08E-08
1.70E-05	0.0001149
3.09E-07	3.93E-06
6.39E-05	0.0003565
6.01E-09	1.55E-07
2.81E-05	0.0001755
2.21E-07	2.94E-06
4.45E-05	0.0002623
8.78E-08	1.38E-06
8.86E-05	0.00047
4.15E-05	0.0002472
1.25E-05	8.81E-05
1.55E-05	0.0001059
1.16E-06	1.18E-05
6.88E-05	0.0003799
7.14E-07	7.88E-06
3.60E-07	4.44E-06
3.71E-07	4.52E-06
2.87E-05	0.0001788
3.06E-06	2.65E-05
7.38E-05	0.0004035
1.36E-07	2.01E-06
3.41E-08	6.29E-07
4.20E-09	1.16E-07
1.60E-05	0.0001089
2.82E-06	2.48E-05
3.61E-07	4.45E-06
8.88E-07	9.38E-06
1.53E-08	3.29E-07
1.53E-06	1.49E-05
3.62E-07	4.45E-06
1.18E-11	1.22E-09
2.47E-05	0.0001578
9.67E-06	7.10E-05
2.08E-06	1.93E-05
6.38E-07	7.18E-06
1.71E-07	2.40E-06
0.0001441	0.0007193
7.62E-11	4.47E-09
0.0039615	0.0117475
1.04E-08	2.38E-07
1.17E-07	1.76E-06
2.43E-08	4.79E-07
5.55E-05	0.0003175
5.51E-09	1.45E-07
2.72E-10	1.23E-08
1.77E-09	5.70E-08
2.15E-11	1.70E-09
2.92E-06	2.55E-05
2.76E-05	0.0001731
8.10E-05	0.0004377
6.60E-06	5.14E-05
4.38E-07	5.22E-06
2.59E-05	0.0001647
6.17E-07	6.97E-06

9.14E-11	5.15E-09
7.10E-08	1.16E-06
9.68E-05	0.0005084
1.43E-09	4.72E-08
1.69E-08	3.55E-07
2.48E-06	2.24E-05
7.64E-07	8.31E-06
1.35E-05	9.45E-05
2.26E-05	0.0001463
3.89E-05	0.0002337
8.41E-07	9.05E-06
2.83E-06	2.49E-05
8.32E-07	8.98E-06
5.22E-06	4.21E-05
2.86E-06	2.50E-05
5.25E-10	2.06E-08
6.40E-09	1.61E-07
5.73E-08	9.76E-07
4.24E-10	1.76E-08
3.04E-06	2.63E-05
6.80E-08	1.12E-06
5.81E-09	1.50E-07
1.74E-07	2.43E-06
1.82E-12	3.16E-10
6.16E-07	6.97E-06
9.92E-08	1.53E-06
1.62E-06	1.56E-05
2.72E-08	5.28E-07
3.42E-06	2.90E-05
8.28E-13	1.80E-10
3.25E-07	4.08E-06
1.41E-11	1.37E-09
8.58E-07	9.17E-06
1.14E-07	1.72E-06
9.21E-08	1.43E-06
1.91E-11	1.62E-09
5.27E-06	4.24E-05
1.08E-07	1.65E-06
3.99E-07	4.82E-06
2.03E-07	2.74E-06
6.32E-08	1.05E-06
4.49E-11	2.99E-09
3.57E-12	5.17E-10
2.67E-09	7.86E-08
1.07E-06	1.11E-05
4.45E-06	3.65E-05
7.08E-07	7.82E-06
4.62E-08	8.22E-07
1.17E-07	1.76E-06
6.69E-05	0.0003708
2.39E-09	7.14E-08
8.52E-07	9.13E-06
5.43E-05	0.0003116
3.12E-07	3.95E-06
1.42E-10	7.25E-09
2.54E-08	4.96E-07

2.00E-07	2.71E-06
1.53E-07	2.21E-06
1.94E-11	1.64E-09
1.38E-10	7.10E-09
5.25E-08	9.14E-07
3.46E-12	5.15E-10
7.04E-10	2.60E-08
2.04E-08	4.11E-07
3.33E-08	6.17E-07
2.11E-11	1.69E-09
1.65E-06	1.59E-05
1.32E-07	1.96E-06
6.52E-07	7.30E-06
2.43E-10	1.12E-08
7.02E-09	1.74E-07
4.06E-12	5.62E-10
5.00E-08	8.79E-07
1.19E-05	8.45E-05
0.0001766	0.0008577
8.03E-06	6.05E-05
2.08E-11	1.69E-09
2.10E-07	2.83E-06
1.33E-08	2.93E-07
3.10E-08	5.87E-07
9.78E-07	1.02E-05
6.77E-12	8.67E-10
1.09E-08	2.46E-07
3.44E-07	4.29E-06
5.29E-08	9.19E-07
2.59E-08	5.04E-07
1.65E-07	2.35E-06
2.95E-09	8.59E-08
4.33E-08	7.77E-07
1.27E-08	2.81E-07
2.82E-08	5.44E-07
1.85E-09	5.92E-08
8.60E-09	2.04E-07
8.74E-08	1.37E-06
1.13E-09	3.85E-08
1.59E-06	1.54E-05
9.48E-13	1.98E-10
1.37E-11	1.36E-09
5.04E-07	5.86E-06
9.47E-12	1.07E-09
3.82E-15	4.64E-12
6.78E-07	7.56E-06
5.14E-08	8.99E-07
1.68E-08	3.54E-07
6.99E-09	1.74E-07
1.62E-10	8.02E-09
4.53E-10	1.87E-08
4.08E-10	1.71E-08
3.52E-10	1.52E-08
1.78E-11	1.57E-09
1.01E-09	3.56E-08
9.22E-09	2.15E-07

4.06E-07	4.88E-06
5.21E-07	6.01E-06
2.27E-08	4.50E-07
2.98E-07	3.81E-06
1.79E-07	2.49E-06
1.33E-08	2.92E-07
3.35E-10	1.46E-08
1.23E-09	4.14E-08
2.98E-11	2.19E-09
5.55E-11	3.47E-09
9.95E-09	2.28E-07
1.73E-10	8.52E-09
1.45E-08	3.14E-07
3.42E-08	6.29E-07
4.05E-10	1.71E-08
7.04E-11	4.19E-09
1.71E-14	1.21E-11
7.09E-11	4.20E-09
3.27E-11	2.34E-09
7.57E-10	2.77E-08
4.65E-09	1.25E-07
2.65E-09	7.83E-08
1.69E-09	5.49E-08
6.84E-10	2.55E-08
1.82E-08	3.76E-07
1.86E-11	1.59E-09
1.10E-09	3.77E-08
1.60E-11	1.47E-09

6 and ES1) and two susceptible strains (RO1 and IT3) of *T.* ***urticae***

ipr_ALL
IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
NA
NA
IPR001254*Serine proteases, trypsin domain, IPR001314*Peptidase S1A, chymotrypsin family, IPR0
IPR012674*Calycin
NA
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
NA
NA
NA
NA
IPR012674*Calycin
IPR000998*MAM domain, IPR013320*Concanavalin A-like lectin/glucanase domain
NA
NA
IPR003172*MD-2-related lipid-recognition domain, IPR014756*Immunoglobulin E-set
NA
NA
NA
NA
IPR029064*50S ribosomal protein L30e-like, IPR000530*Ribosomal protein S12e, IPR004038*Ribos
IPR001478*PDZ domain, IPR000270*PB1 domain, IPR034876*Partitioning defective protein 6
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR027408*PNPase/RNase PH domain, IPR020568*Ribosomal protein S5 domain 2-type fold, IPR0
IPR011705*BTB/Kelch-associated, IPR011333*SKP1/BTB/POZ domain
IPR012674*Calycin
NA
IPR012599*Peptidase C1A, propeptide, IPR000668*Peptidase C1A, papain C-terminal, IPR013128*
IPR013201*Cathepsin propeptide inhibitor domain (I29)
IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat
NA
IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
NA
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
NA
NA
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
NA
IPR015889*Intradiol ring-cleavage dioxygenase, core
IPR007807*Helicase domain, IPR032672*TmcA/NAT10/Kre33, IPR027992*Possible tRNA binding d
NA
IPR015889*Intradiol ring-cleavage dioxygenase, core
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
IPR005552*Scramblase
IPR002999*Tudor domain
NA
NA
NA
NA
NA
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B

NA
NA
NA
NA
NA
NA
NA
NA
NA
NA
IPR011705*BTB/Kelch-associated, IPR028764*Kelch repeat and BTB domain-containing protein 8, I
IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR011042*Six-bladed beta-prope
NA
NA
NA
NA
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
NA
NA
NA
IPR001128*Cytochrome P450
IPR017946*PLC-like phosphodiesterase, TIM beta/alpha-barrel domain
NA
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR024483*Protein of unknown function DUF2700
IPR003172*MD-2-related lipid-recognition domain, IPR014756*Immunoglobulin E-set
IPR033453*Glycosyl hydrolase family 30, TIM-barrel domain, IPR033452*Glycosyl hydrolase family 3
NA
IPR031968*VASt domain
NA
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR017946*PLC-like phosphodiesterase, TIM beta/alpha-barrel domain
NA
IPR029058*Alpha/Beta hydrolase fold, IPR000734*Triacylglycerol lipase family, IPR013818*Lipase/vi
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
NA
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
NA
NA
NA
NA
NA
IPR003609*PAN/Apple domain
IPR006202*Neurotransmitter-gated ion-channel ligand-binding domain, IPR006028*Gamma-aminobu
NA
IPR010987*Glutathione S-transferase, C-terminal-like, IPR004045*Glutathione S-transferase, N-term
IPR020846*Major facilitator superfamily domain
IPR022271*Lipocalin, ApoD type, IPR012674*Calycin, IPR002345*Lipocalin, IPR003057*Invertebrat
IPR001025*Bromo adjacent homology (BAH) domain
NA
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
NA

IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat
IPR002172*Low-density lipoprotein (LDL) receptor class A repeat
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR007235*Glycosyl transferase, family 28, C-terminal, IPR002213*UDP-glucuronosyl/UDP-glucosylt
NA
NA
NA
IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
NA
NA
IPR023796*Serpin domain, IPR000215*Serpin family
NA
IPR014756*Immunoglobulin E-set, IPR003172*MD-2-related lipid-recognition domain
NA
IPR015889*Intradiol ring-cleavage dioxygenase, core
IPR028764*Kelch repeat and BTB domain-containing protein 8, IPR011705*BTB/Kelch-associated
IPR011333*SKP1/BTB/POZ domain, IPR011705*BTB/Kelch-associated
IPR007235*Glycosyl transferase, family 28, C-terminal, IPR002213*UDP-glucuronosyl/UDP-glucosylt
IPR032675*Leucine-rich repeat domain, L domain-like
NA
IPR000566*Lipocalin/cytosolic fatty-acid binding domain, IPR012674*Calycin
IPR031968*VASt domain
NA
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
NA
IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
NA
IPR006568*PSP, proline-rich, IPR003034*SAP domain, IPR007180*Domain of unknown function DU
IPR009020*Protease propeptides/proteinase inhibitor I9
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
NA
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
NA
NA
NA
IPR019311*Protein of unknown function DUF2362
IPR007235*Glycosyl transferase, family 28, C-terminal
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
NA
IPR003057*Invertebrate colouration protein, IPR022271*Lipocalin, ApoD type, IPR012674*Calycin, IF
IPR001314*Peptidase S1A, chymotrypsin family, IPR009003*Peptidase S1, PA clan, IPR001254*Ser
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR006326*UDP-glycosyltransferase, MGT, IPR007235*Glycosyl transferase, family 28, C-terminal, I
IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A, IPR013201*Cathepsin pr
IPR003609*PAN/Apple domain
NA
NA
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
NA
IPR000668*Peptidase C1A, papain C-terminal, IPR012599*Peptidase C1A, propeptide, IPR013128*F
IPR029058*Alpha/Beta hydrolase fold, IPR002472*Palmitoyl protein thioesterase, IPR030294*Palmito
IPR012674*Calycin
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
NA

IPR012923*Chromosome segregation in meiosis protein 3, IPR019393*WASH complex, subunit strur
IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
NA
NA
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
NA
NA
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR001370*BIR repeat, IPR006568*PSP, proline-rich, IPR007180*Domain of unknown function DUF
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR012674*Calycin
NA
IPR006652*Kelch repeat type 1, IPR015915*Kelch-type beta propeller, IPR011498*Kelch repeat type
IPR011527*ABC transporter type 1, transmembrane domain, IPR027417*P-loop containing nucleosid
IPR007235*Glycosyl transferase, family 28, C-terminal
NA
IPR001096*Peptidase C13, legumain
IPR004046*Glutathione S-transferase, C-terminal, IPR004045*Glutathione S-transferase, N-terminal,
IPR000536*Nuclear hormone receptor, ligand-binding domain
IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR011042*Six-bladed beta-prope
NA
NA
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR013201*Cathepsin propeptide inhibitor domain (I29), IPR000668*Peptidase C1A, papain C-termin
IPR029070*Chitinase insertion domain, IPR001223*Glycoside hydrolase family 18, catalytic domain,
IPR020846*Major facilitator superfamily domain, IPR010291*Ion channel regulatory protein, UNC-93
IPR032675*Leucine-rich repeat domain, L domain-like
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
IPR002018*Carboxylesterase, type B, IPR029058*Alpha/Beta hydrolase fold
IPR015943*WD40/YVTN repeat-like-containing domain, IPR017986*WD40-repeat-containing domain
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR012336*Thioredoxin-like fold, IPR013766*Thioredoxin domain
IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR011527*ABC transporter type 1
IPR029060*PIN domain-like, IPR024768*Meiosis regulator and mRNA stability factor 1, IPR021139*
IPR008597*Invertebrate-type lysozyme
NA
IPR002498*Phosphatidylinositol-4-phosphate 5-kinase, core, IPR027483*Phosphatidylinositol-4-phos
NA
NA
NA
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
NA
IPR001096*Peptidase C13, legumain
IPR020846*Major facilitator superfamily domain
IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain
NA
IPR020846*Major facilitator superfamily domain
IPR003008*Tubulin/FtsZ, GTPase domain, IPR000217*Tubulin, IPR002453*Beta tubulin, IPR008280
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
NA
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
IPR020846*Major facilitator superfamily domain
IPR012916*RED-like, N-terminal
IPR008160*Collagen triple helix repeat, IPR000885*Fibrillar collagen, C-terminal, IPR014716*Fibrino
IPR012445*Autophagy-related protein 101

IPR000276*G protein-coupled receptor, rhodopsin-like
NA
IPR001314*Peptidase S1A, chymotrypsin family, IPR001254*Serine proteases, trypsin domain, IPR0
NA
NA
IPR013128*Peptidase C1A, IPR000668*Peptidase C1A, papain C-terminal
IPR000504*RNA recognition motif domain
IPR000760*Inositol monophosphatase-like
IPR003609*PAN/Apple domain
IPR023796*Serpin domain, IPR000215*Serpin family
IPR013201*Cathepsin propeptide inhibitor domain (I29), IPR000668*Peptidase C1A, papain C-termin
IPR013657*UAA transporter
IPR019373*Ribosomal protein L51, mitochondrial
IPR000210*BTB/POZ domain, IPR011333*SKP1/BTB/POZ domain
IPR005552*Scramblase
NA
IPR003609*PAN/Apple domain
NA
IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A, IPR012599*Peptidase C
IPR000326*Phosphatidic acid phosphatase type 2/haloperoxidase
NA
NA
IPR001320*Ionotropic glutamate receptor, IPR019594*Ionotropic glutamate receptor, L-glutamate an
IPR001024*PLAT/LH2 domain
IPR004827*Basic-leucine zipper domain, IPR007588*Zinc finger, FLYWCH-type
NA
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
NA
IPR004046*Glutathione S-transferase, C-terminal, IPR010987*Glutathione S-transferase, C-terminal-
NA
NA
IPR002048*EF-hand domain, IPR011992*EF-hand domain pair
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR004045*Glutathione S-transferase, N-terminal, IPR012336*Thioredoxin-like fold, IPR010987*Glut
NA
IPR001254*Serine proteases, trypsin domain, IPR001314*Peptidase S1A, chymotrypsin family, IPR0
NA
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR016040*NAD(P)-binding domain, IPR020631*Tetrahydrofolate dehydrogenase/cyclohydrolase, N
NA
NA
IPR034638*Atypical kinase COQ8B
IPR001139*Glycoside hydrolase family 30, IPR033453*Glycosyl hydrolase family 30, TIM-barrel dom
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR006621*Nose resistant-to-fluoxetine protein, N-terminal
IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain, IPR022271*Lipocalin,
NA
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
NA
IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
NA
IPR001096*Peptidase C13, legumain
NA
IPR024768*Meiosis regulator and mRNA stability factor 1, IPR021139*NYN domain, limkain-b1-type,
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR001254*Serine proteases, tryp

IPR011527*ABC transporter type 1, transmembrane domain, IPR003439*ABC transporter-like, IPR00
IPR011598*Myc-type, basic helix-loop-helix (bHLH) domain, IPR015943*WD40/YVTN repeat-like-cor
IPR021454*Protein of unknown function DUF3105
IPR011333*SKP1/BTB/POZ domain, IPR000210*BTB/POZ domain, IPR028764*Kelch repeat and BT
NA
NA
NA
NA
NA
IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain
NA
IPR022271*Lipocalin, ApoD type, IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid bindi
IPR006571*TLDc domain
NA
NA
NA
IPR019151*Proteasome assembly chaperone 2
IPR001254*Serine proteases, trypsin domain, IPR001314*Peptidase S1A, chymotrypsin family, IPR0
IPR009075*Acyl-CoA dehydrogenase/oxidase C-terminal, IPR013786*Acyl-CoA dehydrogenase/oxid
IPR016161*Aldehyde/histidinol dehydrogenase, IPR015590*Aldehyde dehydrogenase domain, IPR0
NA
IPR032675*Leucine-rich repeat domain, L domain-like
IPR009003*Peptidase S1, PA clan, IPR001254*Serine proteases, trypsin domain
IPR011990*Tetratricopeptide-like helical domain
NA
IPR002018*Carboxylesterase, type B, IPR029058*Alpha/Beta hydrolase fold
NA
IPR015889*Intradiol ring-cleavage dioxygenase, core
NA
IPR005552*Scramblase
NA
IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A
IPR029063*S-adenosyl-L-methionine-dependent methyltransferase, IPR013216*Methyltransferase ty
IPR000408*Regulator of chromosome condensation, RCC1, IPR000719*Protein kinase domain, IPR
IPR012599*Peptidase C1A, propeptide, IPR000668*Peptidase C1A, papain C-terminal, IPR013128*
NA
IPR002159*CD36 family
IPR012674*Calycin
IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
NA
IPR002557*Chitin binding domain
IPR000554*Ribosomal protein S7e
NA
NA
IPR012336*Thioredoxin-like fold, IPR010987*Glutathione S-transferase, C-terminal-like, IPR004045*
IPR002018*Carboxylesterase, type B, IPR029058*Alpha/Beta hydrolase fold
IPR001762*Disintegrin domain
IPR024518*Domain of unknown function DUF3421
NA
IPR004046*Glutathione S-transferase, C-terminal, IPR003081*Glutathione S-transferase, Mu class, I
IPR023210*NADP-dependent oxidoreductase domain
IPR017853*Glycoside hydrolase superfamily, IPR033453*Glycosyl hydrolase family 30, TIM-barrel d
IPR004046*Glutathione S-transferase, C-terminal, IPR004045*Glutathione S-transferase, N-terminal,
NA
IPR011990*Tetratricopeptide-like helical domain, IPR019734*Tetratricopeptide repeat
NA

IPR004046*Glutathione S-transferase, C-terminal, IPR004045*Glutathione S-transferase, N-terminal,
IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
IPR029058*Alpha/Beta hydrolase fold, IPR001563*Peptidase S10, serine carboxypeptidase
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR001139*Glycoside hydrolase family 30, IPR017853*Glycoside hydrolase superfamily, IPR033452
IPR014720*Double-stranded RNA-binding domain
NA
NA
NA
IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR030247*Canalicular multispecifi
IPR000210*BTB/POZ domain, IPR011705*BTB/Kelch-associated, IPR011333*SKP1/BTB/POZ doma
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
NA
IPR008979*Galactose-binding domain-like, IPR013783*Immunoglobulin-like fold, IPR017853*Glycosi
NA
NA
IPR015727*Protein kinase C mu-related, IPR002219*Protein kinase C-like, phorbol ester/diacylglycer
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily, IPR001958
IPR007235*Glycosyl transferase, family 28, C-terminal, IPR002213*UDP-glucuronosyl/UDP-glucosylt
NA
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
NA
NA
IPR024518*Domain of unknown function DUF3421
IPR002345*Lipocalin, IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain, I
NA
NA
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR023210*NADP-dependent oxidoreductase domain
NA
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR020846*Major facilitator superfamily domain, IPR005828*Major facilitator, sugar transporter-like
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR023395*Mitochondrial carrier domain, IPR018108*Mitochondrial substrate/solute carrier, IPR0020
NA
IPR006616*DM9 repeat, IPR024518*Domain of unknown function DUF3421
IPR011249*Metalloenzyme, LuxS/M16 peptidase-like, IPR013578*Peptidase M16C associated
IPR008948*L-Aspartase-like
NA
IPR001024*PLAT/LH2 domain
NA
IPR004046*Glutathione S-transferase, C-terminal, IPR012336*Thioredoxin-like fold, IPR010987*Glut
NA
NA
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
IPR004045*Glutathione S-transferase, N-terminal, IPR004046*Glutathione S-transferase, C-terminal,
IPR004245*Protein of unknown function DUF229, IPR017849*Alkaline phosphatase-like, alpha/beta/
IPR001139*Glycoside hydrolase family 30, IPR033453*Glycosyl hydrolase family 30, TIM-barrel dom
NA
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
NA
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
NA

IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I

IPR020846*Major facilitator superfamily domain, IPR003663*Sugar/inositol transporter, IPR005828*M

IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat

IPR011701*Major facilitator superfamily, IPR020846*Major facilitator superfamily domain

IPR000432*DNA mismatch repair protein MutS, C-terminal, IPR007860*DNA mismatch repair protein

IPR013201*Cathepsin propeptide inhibitor domain (I29), IPR000668*Peptidase C1A, papain C-termin

IPR015915*Kelch-type beta propeller, IPR000210*BTB/POZ domain, IPR011705*BTB/Kelch-associa

IPR008775*Phytanoyl-CoA dioxygenase

IPR020846*Major facilitator superfamily domain

IPR020846*Major facilitator superfamily domain

IPR028118*Chibby family

IPR013320*Concanavalin A-like lectin/glucanase domain, IPR000998*MAM domain

NA

NA

IPR032675*Leucine-rich repeat domain, L domain-like

NA

NA

IPR011333*SKP1/BTB/POZ domain, IPR011705*BTB/Kelch-associated

IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase

IPR032190*Niemann-Pick C1, N-terminal

NA

IPR011583*Chitinase II, IPR029070*Chitinase insertion domain, IPR017853*Glycoside hydrolase su

IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR011042*Six-bladed beta-prope

IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily

NA

IPR001506*Peptidase M12A, IPR024079*Metallopeptidase, catalytic domain, IPR006026*Peptidase,

NA

NA

IPR001628*Zinc finger, nuclear hormone receptor-type, IPR013088*Zinc finger, NHR/GATA-type, IP

IPR031152*Plexin domain-containing protein

NA

IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like

IPR013320*Concanavalin A-like lectin/glucanase domain, IPR002172*Low-density lipoprotein (LDL)

IPR032788*Glycogen debranching enzyme, central domain, IPR029436*Eukaryotic glycogen debran

IPR007235*Glycosyl transferase, family 28, C-terminal, IPR002213*UDP-glucuronosyl/UDP-glucosyl

NA

IPR015421*Pyridoxal phosphate-dependent transferase, major region, subdomain 1, IPR015424*Pyri

IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I

NA

IPR011705*BTB/Kelch-associated, IPR011333*SKP1/BTB/POZ domain, IPR011042*Six-bladed beta

NA

NA

IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like

IPR023753*FAD/NAD(P)-binding domain

IPR002159*CD36 family

IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450

IPR008152*Clathrin adaptor, alpha/beta/gamma-adaptin, appendage, Ig-like subdomain, IPR013041*

IPR011990*Tetratricopeptide-like helical domain

IPR007235*Glycosyl transferase, family 28, C-terminal

IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A, IPR013201*Cathepsin pr

NA

NA

IPR001680*WD40 repeat, IPR017986*WD40-repeat-containing domain, IPR015943*WD40/YVTN re

IPR003609*PAN/Apple domain

IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I

IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I

IPR029063*S-adenosyl-L-methionine-dependent methyltransferase, IPR013216*Methyltransferase ty
IPR000301*Tetraspanin, IPR008952*Tetraspanin, EC2 domain, IPR018499*Tetraspanin/Peripherin
IPR000436*Sushi/SCR/CCP domain
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
NA
IPR000536*Nuclear hormone receptor, ligand-binding domain
IPR011527*ABC transporter type 1, transmembrane domain, IPR003439*ABC transporter-like, IPR0
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
NA
IPR020843*Polyketide synthase, enoylreductase domain, IPR016040*NAD(P)-binding domain, IPR0
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
NA
IPR004327*Phosphotyrosyl phosphatase activator, PTPA
IPR001024*PLAT/LH2 domain
IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR013525*ABC-2 type transporter
NA
NA
IPR000997*Cholinesterase, IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, ty
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR011990*Tetratricopeptide-like helical domain, IPR021183*N-terminal acetyltransferase A, auxiliar
IPR001619*Sec1-like protein
IPR000998*MAM domain, IPR013320*Concanavalin A-like lectin/glucanase domain, IPR002172*Low
NA
NA
NA
NA
IPR011705*BTB/Kelch-associated
IPR011705*BTB/Kelch-associated, IPR028764*Kelch repeat and BTB domain-containing protein 8, I
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
NA
IPR023796*Serpin domain, IPR000215*Serpin family
IPR003609*PAN/Apple domain
IPR002919*Trypsin Inhibitor-like, cysteine rich domain
IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
IPR021832*Ankyrin repeat domain-containing protein 13
NA
IPR001806*Small GTPase superfamily, IPR020849*Small GTPase superfamily, Ras type, IPR02741
IPR029034*Cystine-knot cytokine, IPR002072*Nerve growth factor-related
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
NA
NA
IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR003593*AAA+ ATPase domain,
NA
IPR001139*Glycoside hydrolase family 30, IPR033452*Glycosyl hydrolase family 30, beta sandwich
IPR011701*Major facilitator superfamily, IPR020846*Major facilitator superfamily domain
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
NA
IPR032675*Leucine-rich repeat domain, L domain-like
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR007855*RNA-dependent RNA polymerase, eukaryotic-type
NA
NA
NA
IPR004045*Glutathione S-transferase, N-terminal, IPR004046*Glutathione S-transferase, C-terminal,

IPR005552*Scramblase
NA
IPR000990*Innexin
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase, IPR007235*Glycosyl transferase, family 28,
NA
IPR002395*HMW kininogen
IPR013128*Peptidase C1A, IPR013201*Cathepsin propeptide inhibitor domain (I29), IPR000668*Pep
IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain
NA
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase, IPR007235*Glycosyl transferase, family 28,
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR013128*Peptidase C1A, IPR012599*Peptidase C1A, propeptide, IPR000668*Peptidase C1A, pap
NA
IPR002018*Carboxylesterase, type B, IPR029058*Alpha/Beta hydrolase fold
IPR001275*DM DNA-binding domain, IPR026607*DMRT/protein doublesex/protein male abnormal 3
IPR000668*Peptidase C1A, papain C-terminal, IPR013201*Cathepsin propeptide inhibitor domain (I2
IPR024768*Meiosis regulator and mRNA stability factor 1, IPR021139*NYN domain, limkain-b1-type,
IPR013128*Peptidase C1A, IPR000668*Peptidase C1A, papain C-terminal
NA
IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat
IPR009003*Peptidase S1, PA clan, IPR001254*Serine proteases, trypsin domain
NA
IPR023796*Serpin domain, IPR000215*Serpin family
IPR023753*FAD/NAD(P)-binding domain, IPR014105*Carotenoid/retinoid oxidoreductase, IPR00293
NA
NA
NA
NA
NA
IPR023796*Serpin domain, IPR000215*Serpin family
NA
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR029058*Alpha/Beta hydrolase fold, IPR006693*Partial AB-hydrolase lipase domain, IPR000073*
IPR023352*Membrane associated eicosanoid/glutathione metabolism-like domain
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
NA
IPR001024*PLAT/LH2 domain
IPR012337*Ribonuclease H-like domain, IPR006941*Ribonuclease CAF1
IPR028996*Ganglioside GM2 activator, IPR003172*MD-2-related lipid-recognition domain
NA
NA
NA
IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A, IPR012599*Peptidase C
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
IPR007052*CS domain, IPR008978*HSP20-like chaperone, IPR007699*SGS domain
IPR002999*Tudor domain
IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A, IPR013201*Cathepsin pr
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR001590*Peptidase M12B, ADAM/reprolysin, IPR002870*Peptidase M12B, propeptide, IPR02407
IPR001139*Glycoside hydrolase family 30, IPR033452*Glycosyl hydrolase family 30, beta sandwich
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR002060*Squalene/phytoene synthase, IPR017825*Lycopene cyclase domain, IPR008949*Isopre
NA
IPR007307*Low temperature viability protein
IPR003609*PAN/Apple domain
IPR003439*ABC transporter-like, IPR003593*AAA+ ATPase domain, IPR013525*ABC-2 type transp

IPR002557*Chitin binding domain, IPR029070*Chitinase insertion domain, IPR001223*Glycoside hy
IPR001442*Collagen IV, non-collagenous, IPR016187*C-type lectin fold
IPR000536*Nuclear hormone receptor, ligand-binding domain
NA
IPR011701*Major facilitator superfamily, IPR020846*Major facilitator superfamily domain
IPR001128*Cytochrome P450, IPR002403*Cytochrome P450, E-class, group IV
NA
IPR006693*Partial AB-hydrolase lipase domain, IPR000073*Alpha/beta hydrolase fold-1, IPR029058
IPR014806*Ubiquitin-fold modifier-conjugating enzyme 1, IPR016135*Ubiquitin-conjugating enzyme/
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR001096*Peptidase C13, legumain
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR001139*Glycoside hydrolase family 30, IPR033452*Glycosyl hydrolase family 30, beta sandwich
IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR000033*LDLR class B repeat,
IPR011538*NADH-ubiquinone oxidoreductase 51kDa subunit, FMN-binding domain, IPR011537*NA
IPR008952*Tetraspanin, EC2 domain, IPR018499*Tetraspanin/Peripherin
IPR015819*Lipid transport protein, beta-sheet shell, IPR015255*Vitellinogen, open beta-sheet, IPR00
IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
IPR028996*Ganglioside GM2 activator, IPR003172*MD-2-related lipid-recognition domain
IPR006153*Cation/H+ exchanger
IPR011333*SKP1/BTB/POZ domain, IPR011705*BTB/Kelch-associated
IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat
NA
IPR000536*Nuclear hormone receptor, ligand-binding domain
IPR000215*Serpin family, IPR023796*Serpin domain
IPR002908*Frataxin/CyaY, IPR017789*Frataxin
NA
NA
NA
IPR029060*PIN domain-like, IPR006984*rRNA-processing protein Fcf1/Utp23
NA
IPR009357*Solute carrier family 52, riboflavin transporter
NA
IPR028996*Ganglioside GM2 activator
IPR001254*Serine proteases, trypsin domain, IPR009003*Peptidase S1, PA clan
IPR000536*Nuclear hormone receptor, ligand-binding domain
NA
IPR011705*BTB/Kelch-associated, IPR028764*Kelch repeat and BTB domain-containing protein 8
IPR006571*TLDc domain
NA
IPR020846*Major facilitator superfamily domain
NA
NA
IPR001254*Serine proteases, trypsin domain, IPR009003*Peptidase S1, PA clan
IPR031139*RPGRIP1 family
IPR003165*Piwi domain, IPR003100*PAZ domain, IPR012337*Ribonuclease H-like domain, IPR032
IPR001563*Peptidase S10, serine carboxypeptidase, IPR029058*Alpha/Beta hydrolase fold
NA
IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR013320*Concanavalin A-like le
IPR001096*Peptidase C13, legumain
IPR000668*Peptidase C1A, papain C-terminal, IPR012599*Peptidase C1A, propeptide, IPR013128*
IPR023796*Serpin domain, IPR000215*Serpin family
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
NA
NA
IPR007110*Immunoglobulin-like domain, IPR013783*Immunoglobulin-like fold, IPR003599*Immunog

IPR001279*Metallo-beta-lactamase
IPR033275*E3 ubiquitin-protein ligase MARCH-like
IPR006906*Timeless protein
NA
IPR032715*Nuclear receptor coactivator 6, putative nucleic acid-binding region, IPR026638*Nuclear
IPR016055*Alpha-D-phosphohexomutase, alpha/beta/alpha I/II/III, IPR005844*Alpha-D-phosphohex
IPR030294*Palmitoyl-protein thioesterase 1, IPR002472*Palmitoyl protein thioesterase, IPR029058*
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase, IPR006326*UDP-glycosyltransferase, MGT,
NA
IPR003008*Tubulin/FtsZ, GTPase domain, IPR000217*Tubulin, IPR018316*Tubulin/FtsZ, 2-layer sa
IPR008914*Phosphatidylethanolamine-binding protein
IPR013083*Zinc finger, RING/FYVE/PHD-type, IPR008974*TRAF-like, IPR001293*Zinc finger, TRAF
IPR008979*Galactose-binding domain-like, IPR008211*Laminin, N-terminal, IPR002049*Laminin EG
NA
IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain, IPR022271*Lipocalin,
IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR003593*AAA+ ATPase domain,
IPR004045*Glutathione S-transferase, N-terminal, IPR012336*Thioredoxin-like fold, IPR004046*Glut
NA
NA
IPR006693*Partial AB-hydrolase lipase domain, IPR029058*Alpha/Beta hydrolase fold, IPR000073*
IPR029058*Alpha/Beta hydrolase fold, IPR025483*Lipase, eukaryotic, IPR000073*Alpha/beta hydrol
IPR033452*Glycosyl hydrolase family 30, beta sandwich domain, IPR033453*Glycosyl hydrolase fam
NA
IPR017853*Glycoside hydrolase superfamily, IPR001139*Glycoside hydrolase family 30, IPR033452
IPR013783*Immunoglobulin-like fold, IPR003599*Immunoglobulin subtype, IPR007110*Immunoglobu
NA
IPR011701*Major facilitator superfamily, IPR020846*Major facilitator superfamily domain
IPR026505*Solute carrier family 35 member F3/F4
NA
IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
NA
IPR013783*Immunoglobulin-like fold, IPR008979*Galactose-binding domain-like, IPR017853*Glycos
IPR003439*ABC transporter-like, IPR003593*AAA+ ATPase domain, IPR027417*P-loop containing n
IPR000566*Lipocalin/cytosolic fatty-acid binding domain, IPR012674*Calycin
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR000980*SH2 domain, IPR001720*PI3K p85/p55 subunit, IPR032498*PI3K p85 subunit, inter-SH2
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
NA
IPR007235*Glycosyl transferase, family 28, C-terminal
IPR004045*Glutathione S-transferase, N-terminal, IPR010987*Glutathione S-transferase, C-terminal-
IPR000358*Ribonucleotide reductase small subunit family, IPR009078*Ferritin-like superfamily, IPR0
IPR002350*Kazal domain, IPR013783*Immunoglobulin-like fold, IPR003599*Immunoglobulin subtype
IPR029058*Alpha/Beta hydrolase fold, IPR006693*Partial AB-hydrolase lipase domain
NA
IPR006849*Elongator complex subunit Iki3, IPR015943*WD40/YVTN repeat-like-containing domain,
IPR000999*Ribonuclease III domain, IPR027417*P-loop containing nucleoside triphosphate hydrolas
IPR000010*Cystatin domain
IPR011705*BTB/Kelch-associated, IPR011333*SKP1/BTB/POZ domain
IPR001156*Transferrin-like domain
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR028996*Ganglioside GM2 activator, IPR003172*MD-2-related lipid-recognition domain
IPR003609*PAN/Apple domain
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR031152*Plexin domain-containing protein
IPR001024*PLAT/LH2 domain

IPR000949*ELM2 domain, IPR009057*Homeobox domain-like, IPR001005*SANT/Myb domain
IPR005292*Multi drug resistance-associated protein, IPR011527*ABC transporter type 1, transmemb
IPR000889*Glutathione peroxidase, IPR012336*Thioredoxin-like fold
IPR033453*Glycosyl hydrolase family 30, TIM-barrel domain, IPR001139*Glycoside hydrolase family
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
IPR010987*Glutathione S-transferase, C-terminal-like, IPR004046*Glutathione S-transferase, C-term
IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR011042*Six-bladed beta-prope
IPR033452*Glycosyl hydrolase family 30, beta sandwich domain, IPR017853*Glycoside hydrolase su
NA
IPR001747*Lipid transport protein, N-terminal, IPR015819*Lipid transport protein, beta-sheet shell, I
IPR000751*M-phase inducer phosphatase, IPR001763*Rhodanese-like domain
IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A, IPR012599*Peptidase C
IPR002634*BolA protein
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
NA
IPR000873*AMP-dependent synthetase/ligase
NA
IPR002550*Domain of unknown function DUF21
IPR020846*Major facilitator superfamily domain
NA
IPR000566*Lipocalin/cytosolic fatty-acid binding domain, IPR002446*Lipocalin, bacterial, IPR002345
IPR029071*Ubiquitin-related domain, IPR031127*E3 ubiquitin ligase RBR family, IPR002867*IBR do
IPR000668*Peptidase C1A, papain C-terminal, IPR013201*Cathepsin propeptide inhibitor domain (I2
IPR000566*Lipocalin/cytosolic fatty-acid binding domain, IPR022271*Lipocalin, ApoD type, IPR01267
IPR003609*PAN/Apple domain
IPR007855*RNA-dependent RNA polymerase, eukaryotic-type
IPR010255*Haem peroxidase, IPR019791*Haem peroxidase, animal type
IPR011333*SKP1/BTB/POZ domain, IPR000210*BTB/POZ domain, IPR028764*Kelch repeat and BT
IPR000172*Glucose-methanol-choline oxidoreductase, N-terminal, IPR007867*Glucose-methanol-ch
NA
NA
IPR001054*Adenylyl cyclase class-3/4/guanylyl cyclase, IPR029787*Nucleotide cyclase
NA
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase, IPR007235*Glycosyl transferase, family 28,
IPR012336*Thioredoxin-like fold, IPR010987*Glutathione S-transferase, C-terminal-like, IPR004045*
IPR005814*Aminotransferase class-III, IPR015422*Pyridoxal phosphate-dependent transferase, sub
NA
NA
IPR011992*EF-hand domain pair
IPR011527*ABC transporter type 1, transmembrane domain, IPR027417*P-loop containing nucleosid
NA
IPR034016*Aminopeptidase N-type, IPR014782*Peptidase M1, membrane alanine aminopeptidase,
IPR006029*Neurotransmitter-gated ion-channel transmembrane domain, IPR006201*Neurotransmitte
NA
NA
NA
NA
NA
NA
IPR012816*NADAR
IPR005062*SAC3/GANP/THP3
IPR000536*Nuclear hormone receptor, ligand-binding domain
IPR016024*Armadillo-type fold
IPR011705*BTB/Kelch-associated, IPR015915*Kelch-type beta propeller
NA

IPR023753*FAD/NAD(P)-binding domain
IPR031968*VASt domain
IPR004536*Selenophosphate synthetase, IPR010918*AIR synthase-related protein, C-terminal doma
IPR002999*Tudor domain
IPR008979*Galactose-binding domain-like, IPR026283*Beta-galactosidase 1-like, IPR031330*Glycos
IPR001096*Peptidase C13, legumain
NA
IPR013949*U3 small nucleolar RNA-associated protein 6, IPR011990*Tetratricopeptide-like helical d
IPR013320*Concanavalin A-like lectin/glucanase domain
NA
NA
IPR000266*Ribosomal protein S17/S11, IPR012340*Nucleic acid-binding, OB-fold
IPR003961*Fibronectin type III, IPR013783*Immunoglobulin-like fold, IPR002602*Domain of unknow
IPR028996*Ganglioside GM2 activator
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR001128*Cytochrome P450
NA
IPR032675*Leucine-rich repeat domain, L domain-like
IPR031107*Small heat shock protein HSP20, IPR002068*Alpha crystallin/Hsp20 domain, IPR008978
IPR012337*Ribonuclease H-like domain, IPR003100*PAZ domain, IPR003165*Piwi domain, IPR032
IPR023210*NADP-dependent oxidoreductase domain, IPR020471*Aldo/keto reductase
NA
IPR006153*Cation/H+ exchanger
NA
NA
NA
IPR001734*Sodium/solute symporter
IPR029068*Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase
IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR007110*Immunoglobulin-like d
NA
NA
IPR020846*Major facilitator superfamily domain
NA
IPR001156*Transferrin-like domain, IPR016357*Transferrin
IPR006050*DNA photolyase, N-terminal, IPR005101*Cryptochrome/DNA photolyase, FAD-binding d
NA
IPR008978*HSP20-like chaperone, IPR031107*Small heat shock protein HSP20, IPR001436*Alpha
IPR000834*Peptidase M14, carboxypeptidase A, IPR034223*Insect gut carboxypeptidase-like, carbo
IPR011333*SKP1/BTB/POZ domain, IPR011705*BTB/Kelch-associated
IPR009075*Acyl-CoA dehydrogenase/oxidase C-terminal, IPR002655*Acyl-CoA oxidase, C-terminal
NA
IPR005511*Senescence marker protein-30 (SMP-30), IPR013658*SMP-30/Gluconolactonase/LRE-li
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
IPR019547*B domain of TMEM189, localisation domain
IPR012816*NADAR
IPR000716*Thyroglobulin type-1
IPR013094*Alpha/beta hydrolase fold-3, IPR029058*Alpha/Beta hydrolase fold
IPR032675*Leucine-rich repeat domain, L domain-like
IPR032675*Leucine-rich repeat domain, L domain-like
NA
IPR006202*Neurotransmitter-gated ion-channel ligand-binding domain, IPR006029*Neurotransmitter-
IPR016040*NAD(P)-binding domain, IPR006140*D-isomer specific 2-hydroxyacid dehydrogenase, N
NA
IPR017849*Alkaline phosphatase-like, alpha/beta/alpha, IPR017850*Alkaline-phosphatase-like, core
NA
IPR001019*Guanine nucleotide binding protein (G-protein), alpha subunit, IPR011025*G protein alph

IPR015421*Pyridoxal phosphate-dependent transferase, major region, subdomain 1, IPR010111*Kyn
IPR013525*ABC-2 type transporter, IPR003593*AAA+ ATPase domain, IPR027417*P-loop containin
IPR027007*DHR-1 domain, IPR026791*Dedicator of cytokinesis, IPR026799*Dedicator of cytokinesi
NA
IPR001156*Transferrin-like domain, IPR016357*Transferrin
IPR002223*Pancreatic trypsin inhibitor Kunitz domain, IPR009465*Spondin, N-terminal, IPR000884*
IPR032343*Methyl-CpG-binding domain protein 2/3, p55-binding region, IPR001739*Methyl-CpG DN
IPR002657*Bile acid:sodium symporter/arsenical resistance protein Acr3, IPR030203*Solute carrier
IPR006149*EB domain
IPR002159*CD36 family, IPR005428*CD36/scavenger receptor class B member 1
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
NA
IPR001781*Zinc finger, LIM-type, IPR011333*SKP1/BTB/POZ domain, IPR000331*Rap GTPase acti
IPR011012*Longin-like domain, IPR028565*Mu homology domain, IPR022775*AP complex, mu/sigm
NA
IPR006989*NAB co-repressor, domain, IPR006988*Nab, N-terminal
IPR010516*Sin3 associated polypeptide p18
IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A, IPR013201*Cathepsin pr
NA
IPR001314*Peptidase S1A, chymotrypsin family, IPR009003*Peptidase S1, PA clan, IPR001254*Ser
IPR008139*Saposin B type domain, IPR011001*Saposin-like, IPR003119*Saposin A-type domain, IP
IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR001752*Kinesin motor domain
IPR004947*Deoxyribonuclease II
IPR001139*Glycoside hydrolase family 30
IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR011042*Six-bladed beta-prope
IPR004344*Tubulin-tyrosine ligase/Tubulin polyglutamylase
IPR029058*Alpha/Beta hydrolase fold, IPR006693*Partial AB-hydrolase lipase domain
IPR005292*Multi drug resistance-associated protein, IPR011527*ABC transporter type 1, transmemb
IPR011701*Major facilitator superfamily, IPR020846*Major facilitator superfamily domain
IPR013087*Zinc finger C2H2-type
NA
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
IPR029063*S-adenosyl-L-methionine-dependent methyltransferase, IPR001737*Ribosomal RNA ade
IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR011527*ABC transporter type 1
IPR000536*Nuclear hormone receptor, ligand-binding domain
NA
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
IPR033452*Glycosyl hydrolase family 30, beta sandwich domain, IPR001139*Glycoside hydrolase fa
IPR000716*Thyroglobulin type-1
NA
IPR011009*Protein kinase-like domain
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
NA
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
NA
NA
IPR011701*Major facilitator superfamily, IPR020846*Major facilitator superfamily domain
IPR004046*Glutathione S-transferase, C-terminal, IPR010987*Glutathione S-transferase, C-terminal-
NA
IPR000010*Cystatin domain
NA
IPR014889*Transcription factor DP, C-terminal, IPR011991*Winged helix-turn-helix DNA-binding dom
IPR012816*NADAR
IPR014720*Double-stranded RNA-binding domain, IPR000467*G-patch domain
IPR016040*NAD(P)-binding domain
NA

NA

NA

IPR018499*Tetraspanin/Peripherin, IPR008952*Tetraspanin, EC2 domain

IPR000504*RNA recognition motif domain, IPR034237*FOX1, RNA recognition motif

NA

IPR001254*Serine proteases, trypsin domain, IPR009003*Peptidase S1, PA clan, IPR001314*Peptid

NA

IPR000536*Nuclear hormone receptor, ligand-binding domain

IPR013128*Peptidase C1A, IPR012599*Peptidase C1A, propeptide, IPR000668*Peptidase C1A, pap

IPR022271*Lipocalin, ApoD type, IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid bindi

IPR001199*Cytochrome b5-like heme/steroid binding domain

IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B

IPR012445*Autophagy-related protein 101

IPR026055*Fatty acyl-CoA reductase, IPR016040*NAD(P)-binding domain, IPR033640*Fatty acyl-C

IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR001650*Helicase, C-terminal, I

NA

IPR016024*Armadillo-type fold

NA

IPR019180*Oxidoreductase-like, N-terminal

IPR007110*Immunoglobulin-like domain, IPR013783*Immunoglobulin-like fold, IPR003598*Immunog

NA

NA

IPR001251*CRAL-TRIO lipid binding domain, IPR000535*Major sperm protein (MSP) domain, IPR00

IPR005828*Major facilitator, sugar transporter-like, IPR020846*Major facilitator superfamily domain,

NA

NA

IPR000276*G protein-coupled receptor, rhodopsin-like

NA

NA

NA

IPR000618*Insect cuticle protein

NA

IPR015424*Pyridoxal phosphate-dependent transferase, IPR010977*Aromatic-L-amino-acid decarbo

IPR001223*Glycoside hydrolase family 18, catalytic domain, IPR002557*Chitin binding domain, IPR0

NA

IPR013320*Concanavalin A-like lectin/glucanase domain, IPR000742*EGF-like domain, IPR003645*

IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like

NA

IPR022812*Dynamin superfamily, IPR003130*Dynamin GTPase effector, IPR000375*Dynamin centr

IPR001810*F-box domain

IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR

IPR014001*Helicase superfamily 1/2, ATP-binding domain, IPR027417*P-loop containing nucleoside

IPR001478*PDZ domain, IPR000198*Rho GTPase-activating protein domain, IPR000008*C2 domai

NA

IPR029062*Class I glutamine amidotransferase-like, IPR004468*CTP synthase, IPR033828*CTP sy

IPR008922*Uncharacterised domain, di-copper centre, IPR002227*Tyrosinase copper-binding domai

IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain

IPR001881*EGF-like calcium-binding domain, IPR000082*SEA domain, IPR011398*Fibrillin

NA

IPR000536*Nuclear hormone receptor, ligand-binding domain

NA

NA

NA

NA

NA

NA

IPR011993*PH domain-like, IPR001849*Pleckstrin homology domain
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
IPR013057*Amino acid transporter, transmembrane domain
IPR003593*AAA+ ATPase domain, IPR003439*ABC transporter-like, IPR027417*P-loop containing n
NA
NA
NA
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A, IPR012599*Peptidase C
NA
IPR001715*Calponin homology domain, IPR003108*Gas2-related domain, IPR029931*GAS2-like pro
NA
IPR015915*Kelch-type beta propeller
NA
NA
IPR008969*Carboxypeptidase-like, regulatory domain, IPR027062*Carboxypeptidase M, IPR000834
IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
NA
NA
IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain
IPR003101*Coactivator CBP, KIX domain
NA
NA
IPR006179*5'-Nucleotidase/apyrase, IPR029052*Metallo-dependent phosphatase-like, IPR008334*5
NA
NA
NA
IPR001139*Glycoside hydrolase family 30, IPR017853*Glycoside hydrolase superfamily
NA
NA
IPR006667*SLC41 divalent cation transporters, integral membrane domain
IPR032006*Transmembrane inner ear expressed protein
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR001132*SMAD domain, Dwarfin-type, IPR008984*SMAD/FHA domain, IPR017855*SMAD domai
NA
IPR024135*Ragulator complex protein LAMTOR5
IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain, IPR002345*Lipocalin, I
IPR001951*Histone H4, IPR035425*CENP-T/Histone H4, histone fold, IPR009072*Histone-fold
NA
NA
IPR002557*Chitin binding domain
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
NA
IPR016040*NAD(P)-binding domain, IPR011032*GroES-like, IPR013149*Alcohol dehydrogenase, C-
NA
IPR024096*NO signalling/Golgi transport ligand-binding domain, IPR016696*TRAPP I complex, subu
IPR008979*Galactose-binding domain-like
NA
NA
NA
IPR002557*Chitin binding domain
NA
NA
NA
IPR011011*Zinc finger, FYVE/PHD-type, IPR000306*FYVE zinc finger, IPR028163*HAUS augmin-lik

NA
IPR010515*Collagenase NC10/endostatin, IPR016187*C-type lectin fold, IPR016186*C-type lectin-lik
NA
IPR008971*HSP40/DnaJ peptide-binding, IPR002939*Chaperone DnaJ, C-terminal
IPR001873*Epithelial sodium channel
NA
NA
NA
IPR000276*G protein-coupled receptor, rhodopsin-like, IPR000611*Neuropeptide Y receptor family
NA
NA
IPR003057*Invertebrate colouration protein, IPR022271*Lipocalin, ApoD type, IPR000566*Lipocalin/
NA
NA
IPR001356*Homeobox domain, IPR001781*Zinc finger, LIM-type, IPR009057*Homeobox domain-like
IPR017853*Glycoside hydrolase superfamily, IPR001139*Glycoside hydrolase family 30, IPR033453
IPR002861*Reeler domain
NA
NA
NA
NA
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
NA
IPR006689*Small GTPase superfamily, ARF/SAR type, IPR027417*P-loop containing nucleoside trip
NA
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
NA
IPR024571*ERAP1-like C-terminal domain, IPR014782*Peptidase M1, membrane alanine aminopept
IPR011990*Tetratricopeptide-like helical domain, IPR019412*Outer membrane protein Iml2/Tetratric
NA
IPR001873*Epithelial sodium channel
IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A, IPR012599*Peptidase C
NA
NA
NA
NA
NA
IPR032675*Leucine-rich repeat domain, L domain-like, IPR003591*Leucine-rich repeat, typical subty
NA
IPR001508*Ionotropic glutamate receptor, metazoa, IPR001320*Ionotropic glutamate receptor, IPR0
NA
NA
IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR000048*IQ motif, EF-hand bindi
IPR019443*FMP27, C-terminal
IPR000175*Sodium:neurotransmitter symporter
NA
IPR001096*Peptidase C13, legumain
IPR001926*Tryptophan synthase beta subunit-like PLP-dependent enzyme
NA
IPR000536*Nuclear hormone receptor, ligand-binding domain, IPR001628*Zinc finger, nuclear horm
IPR001873*Epithelial sodium channel
IPR013083*Zinc finger, RING/FYVE/PHD-type, IPR011011*Zinc finger, FYVE/PHD-type
NA
NA
IPR026910*Shisa family

IPR003439*ABC transporter-like, IPR026082*ABC transporter A, ABCA, IPR027417*P-loop containin
NA
IPR002524*Cation efflux protein, IPR027470*Cation efflux protein, cytoplasmic domain
IPR026298*Blc2 family
NA
IPR001424*Superoxide dismutase, copper/zinc binding domain
IPR013087*Zinc finger C2H2-type
IPR000618*Insect cuticle protein
IPR011042*Six-bladed beta-propeller, TolB-like, IPR000033*LDLR class B repeat
IPR000719*Protein kinase domain, IPR009091*Regulator of chromosome condensation 1/beta-lactar
IPR002634*BolA protein
IPR024079*Metallopeptidase, catalytic domain, IPR000718*Peptidase M13, IPR018497*Peptidase M
NA
NA
IPR028074*PTHB1, C-terminal domain, IPR017986*WD40-repeat-containing domain, IPR026511*Pa
NA
NA
NA
NA
IPR023330*Rhabdovirus nucleocapsid, N-terminal, IPR000448*Rhabdovirus nucleocapsid, IPR02333
IPR003439*ABC transporter-like, IPR003593*AAA+ ATPase domain, IPR027417*P-loop containing n
NA
NA
IPR019545*DM13 domain, IPR005018*DOMON domain
NA
NA
NA
NA
NA
NA
NA
NA
IPR019371*Uncharacterised domain KxDL
NA
IPR009003*Peptidase S1, PA clan, IPR001254*Serine proteases, trypsin domain, IPR001314*Peptid
IPR006621*Nose resistant-to-fluoxetine protein, N-terminal, IPR002656*Acyltransferase 3
NA
IPR020846*Major facilitator superfamily domain, IPR010291*Ion channel regulatory protein, UNC-93
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
IPR010982*Lambda repressor-like, DNA-binding domain, IPR003712*Cyanate lyase, C-terminal, IPR
IPR000618*Insect cuticle protein
NA
IPR000196*Ribosomal protein L19/L19e, IPR015973*Ribosomal protein L19/L19e, domain 2, IPR015
NA
IPR008936*Rho GTPase activation protein, IPR000198*Rho GTPase-activating protein domain
IPR008979*Galactose-binding domain-like
IPR001854*Ribosomal protein L29/L36
IPR016449*Potassium channel, inwardly rectifying, Kir, IPR014756*Immunoglobulin E-set, IPR01351
IPR000571*Zinc finger, CCCH-type, IPR001841*Zinc finger, RING-type, IPR013083*Zinc finger, RIN
NA
NA
IPR001356*Homeobox domain, IPR031701*Homeobox protein SIX1, N-terminal SD domain, IPR009
NA
NA
IPR033453*Glycosyl hydrolase family 30, TIM-barrel domain, IPR033452*Glycosyl hydrolase family 3
IPR023395*Mitochondrial carrier domain, IPR018108*Mitochondrial substrate/solute carrier, IPR0020

IPR000554*Ribosomal protein S7e
IPR013784*Carbohydrate-binding-like fold, IPR019008*Domain of unknown function DUF2012
IPR015943*WD40/YVTN repeat-like-containing domain, IPR011990*Tetratricopeptide-like helical don
IPR007235*Glycosyl transferase, family 28, C-terminal
IPR002048*EF-hand domain, IPR011992*EF-hand domain pair
IPR014105*Carotenoid/retinoid oxidoreductase, IPR023753*FAD/NAD(P)-binding domain, IPR00293
NA
IPR008979*Galactose-binding domain-like
NA
NA
IPR026092*Retinoic acid-induced protein 2/sine oculis-binding protein homologue
NA
IPR020846*Major facilitator superfamily domain, IPR005828*Major facilitator, sugar transporter-like
NA
IPR001436*Alpha crystallin/Heat shock protein, IPR008978*HSP20-like chaperone, IPR031107*Sma
IPR013201*Cathepsin propeptide inhibitor domain (I29), IPR000668*Peptidase C1A, papain C-termin
NA
IPR004294*Carotenoid oxygenase
IPR002659*Glycosyl transferase, family 31
IPR006621*Nose resistant-to-fluoxetine protein, N-terminal, IPR009075*Acyl-CoA dehydrogenase/ox
IPR002300*Aminoacyl-tRNA synthetase, class Ia, IPR009008*Valyl/Leucyl/Isoleucyl-tRNA synthetase
NA
NA
IPR000217*Tubulin, IPR008280*Tubulin/FtsZ, C-terminal, IPR002454*Gamma tubulin, IPR003008*T
NA
IPR029058*Alpha/Beta hydrolase fold
NA
NA
IPR007149*Leo1-like protein
IPR001283*Cysteine-rich secretory protein, allergen V5/Tpx-1-related, IPR014044*CAP domain, IPR
IPR000276*G protein-coupled receptor, rhodopsin-like
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
NA
IPR010291*Ion channel regulatory protein, UNC-93, IPR020846*Major facilitator superfamily domain
NA
NA
IPR001424*Superoxide dismutase, copper/zinc binding domain
IPR000215*Serpin family, IPR023796*Serpin domain
IPR011991*Winged helix-turn-helix DNA-binding domain, IPR003150*DNA-binding RFX-type winged
NA
NA
IPR008949*Isoprenoid synthase domain
NA
NA
IPR013786*Acyl-CoA dehydrogenase/oxidase, N-terminal, IPR009075*Acyl-CoA dehydrogenase/oxic
IPR009075*Acyl-CoA dehydrogenase/oxidase C-terminal, IPR006621*Nose resistant-to-fluoxetine pr
IPR025483*Lipase, eukaryotic, IPR029058*Alpha/Beta hydrolase fold, IPR006693*Partial AB-hydrola
NA
IPR013087*Zinc finger C2H2-type
IPR007220*Origin recognition complex, subunit 2
NA
IPR029058*Alpha/Beta hydrolase fold, IPR000073*Alpha/beta hydrolase fold-1
NA
IPR012674*Calycin
IPR001873*Epithelial sodium channel
IPR013087*Zinc finger C2H2-type, IPR027755*Transcription factor Ovo-like, IPR013083*Zinc finger,

NA
IPR003195*Transcription initiation factor IID, subunit 13, IPR009072*Histone-fold
IPR031481*Fucosyltransferase, N-terminal, IPR001503*Glycosyl transferase family 10
NA
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
NA
NA
IPR000008*C2 domain, IPR012968*Ferlin domain, IPR012561*Ferlin B-domain, IPR032362*Ferlin, C
NA
NA
IPR029064*50S ribosomal protein L30e-like, IPR000530*Ribosomal protein S12e, IPR004038*Ribos
NA
NA
IPR001436*Alpha crystallin/Heat shock protein, IPR031107*Small heat shock protein HSP20, IPR00
IPR011990*Tetratricopeptide-like helical domain, IPR013949*U3 small nucleolar RNA-associated pro
NA
IPR001846*von Willebrand factor, type D domain
NA
NA
IPR001254*Serine proteases, trypsin domain, IPR001314*Peptidase S1A, chymotrypsin family, IPR0
NA
IPR020846*Major facilitator superfamily domain
NA
IPR032665*Helix-loop-helix protein delilah, IPR011598*Myc-type, basic helix-loop-helix (bHLH) doma
NA
IPR003650*Orange domain, IPR011598*Myc-type, basic helix-loop-helix (bHLH) domain
NA
IPR010625*CHCH
IPR017986*WD40-repeat-containing domain, IPR015943*WD40/YVTN repeat-like-containing domain
IPR017850*Alkaline-phosphatase-like, core domain, IPR004245*Protein of unknown function DUF22
NA
NA
NA
NA
IPR013783*Immunoglobulin-like fold, IPR017853*Glycoside hydrolase superfamily
NA
IPR019314*BLOC-1-related complex subunit 6
IPR028831*DNA mismatch repair protein Pms1
IPR019143*JNK/Rab-associated protein-1, N-terminal
IPR010920*LSM domain, IPR033871*Sm-like protein LSm5, IPR001163*LSM domain, eukaryotic/arc
NA
IPR025714*Methyltransferase domain, IPR010280*(Uracil-5)-methyltransferase family, IPR029063*S
NA
NA
NA
NA
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR011705*BTB/Kelch-associated
NA
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR000566*Lipocalin/cytosolic fatty-acid binding domain, IPR012674*Calycin, IPR002345*Lipocalin, I
NA
IPR034223*Insect gut carboxypeptidase-like, carboxypeptidase domain, IPR000834*Peptidase M14,
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
IPR011531*Bicarbonate transporter, C-terminal, IPR003020*Bicarbonate transporter, eukaryotic
NA

NA
NA
NA
IPR004245*Protein of unknown function DUF229, IPR017850*Alkaline-phosphatase-like, core domai
NA
NA
IPR016186*C-type lectin-like/link domain, IPR001304*C-type lectin-like, IPR016187*C-type lectin fold
IPR031152*Plexin domain-containing protein
IPR002490*V-type ATPase, V0 complex, 116kDa subunit family
NA
NA
IPR029058*Alpha/Beta hydrolase fold, IPR003386*Lecithin:cholesterol/phospholipid:diacylglycerol ac
NA
IPR015943*WD40/YVTN repeat-like-containing domain, IPR032728*Bardet-Biedl syndrome 1, N-tern
NA
IPR003316*E2F/DP family, winged-helix DNA-binding domain, IPR015633*E2F Family, IPR028312*
IPR003609*PAN/Apple domain
IPR008969*Carboxypeptidase-like, regulatory domain
IPR012599*Peptidase C1A, propeptide, IPR000668*Peptidase C1A, papain C-terminal, IPR013128*
NA
IPR019366*Clusterin-associated protein-1
NA
IPR013087*Zinc finger C2H2-type
IPR013320*Concanavalin A-like lectin/glucanase domain
IPR002219*Protein kinase C-like, phorbol ester/diacylglycerol-binding domain, IPR015727*Protein ki
IPR029044*Nucleotide-diphospho-sugar transferases, IPR003859*Beta-1,4-galactosyltransferase, IP
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
NA
NA
IPR015915*Kelch-type beta propeller
IPR024768*Meiosis regulator and mRNA stability factor 1
IPR001096*Peptidase C13, legumain
IPR016024*Armadillo-type fold
NA
NA
NA
NA
NA
NA
NA
IPR002509*NodB homology domain, IPR011330*Glycoside hydrolase/deacetylase, beta/alpha-barrel
NA
NA
IPR001650*Helicase, C-terminal, IPR004179*Sec63 domain, IPR027417*P-loop containing nucleosi
IPR000010*Cystatin domain
NA
IPR016024*Armadillo-type fold, IPR010472*Formin, FH3 domain, IPR010473*Formin, GTPase-bindi
IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
IPR011545*DEAD/DEAH box helicase domain, IPR014001*Helicase superfamily 1/2, ATP-binding d
NA
IPR009071*High mobility group box domain, IPR001025*Bromo adjacent homology (BAH) domain
NA
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
NA
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like

IPR019393*WASH complex, subunit strumpellin
IPR015889*Intradiol ring-cleavage dioxygenase, core
NA
IPR032675*Leucine-rich repeat domain, L domain-like
NA
IPR013830*SGNH hydrolase-type esterase domain
NA
NA
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
NA
NA
NA
NA
NA
NA
NA
IPR032675*Leucine-rich repeat domain, L domain-like
NA
IPR013087*Zinc finger C2H2-type
IPR011701*Major facilitator superfamily, IPR020846*Major facilitator superfamily domain
NA
NA
NA
NA
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
NA
NA
IPR015889*Intradiol ring-cleavage dioxygenase, core
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
NA
IPR004837*Sodium/calcium exchanger membrane region, IPR004481*Sodium/potassium/calcium ex
NA
IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
NA
IPR011989*Armadillo-like helical, IPR016024*Armadillo-type fold, IPR019451*RNA polymerase II ass
NA
NA
IPR021160*Mitogen-activated protein (MAP) kinase kinase kinase kinase, IPR011009*Protein kinase
IPR012496*TMC
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR023210*NADP-dependent oxidoreductase domain, IPR020471*Aldo/keto reductase
NA
IPR000980*SH2 domain, IPR001720*PI3K p85/p55 subunit, IPR032498*PI3K p85 subunit, inter-SH2
NA
NA
NA
NA
IPR001093*IMP dehydrogenase/GMP reductase, IPR013785*Aldolase-type TIM barrel
IPR009003*Peptidase S1, PA clan, IPR001254*Serine proteases, trypsin domain
IPR011705*BTB/Kelch-associated, IPR011333*SKP1/BTB/POZ domain, IPR000210*BTB/POZ doma
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
NA
IPR014854*Non-structural maintenance of chromosome element 4, C-terminal, IPR027786*Nse4/EID
NA
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain

IPR032675*Leucine-rich repeat domain, L domain-like
NA
NA
IPR011013*Galactose mutarotase-like domain, IPR031727*Galactose mutarotase, N-terminal barrel,
IPR000219*Dbl homology (DH) domain
NA
IPR011333*SKP1/BTB/POZ domain, IPR011705*BTB/Kelch-associated
IPR008948*L-Aspartase-like
NA
NA
NA
IPR032054*DNA replication factor Cdt1, C-terminal
IPR019143*JNK/Rab-associated protein-1, N-terminal
NA
IPR019393*WASH complex, subunit strumpellin
IPR029058*Alpha/Beta hydrolase fold, IPR001375*Peptidase S9, prolyl oligopeptidase, catalytic dom
IPR029054*dUTPase-like, IPR008181*Deoxyuridine triphosphate nucleotidohydrolase, IPR033704*d
IPR032675*Leucine-rich repeat domain, L domain-like
IPR000010*Cystatin domain
IPR008753*Peptidase M13, N-terminal domain, IPR000718*Peptidase M13, IPR029736*Endothelin-
IPR029063*S-adenosyl-L-methionine-dependent methyltransferase, IPR025714*Methyltransferase d
IPR026054*Nuclear pore complex protein, IPR019143*JNK/Rab-associated protein-1, N-terminal
NA
IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat
NA
IPR006176*3-hydroxyacyl-CoA dehydrogenase, NAD binding, IPR016040*NAD(P)-binding domain, I
IPR008532*Domain of unknown function DUF814
NA
NA
IPR019143*JNK/Rab-associated protein-1, N-terminal
NA
IPR032054*DNA replication factor Cdt1, C-terminal
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR017946*PLC-like phosphodiesterase, TIM beta/alpha-barrel domain
IPR035427*Tim10/FAM136A-like domain, IPR004217*Tim10-like
NA
NA
NA
NA
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR001096*Peptidase C13, legumain
NA
IPR001506*Peptidase M12A, IPR024079*Metallopeptidase, catalytic domain
NA
NA
NA
IPR023210*NADP-dependent oxidoreductase domain, IPR020471*Aldo/keto reductase
NA
IPR001096*Peptidase C13, legumain
NA
IPR002318*Alanine-tRNA ligase, class IIc, IPR018162*Alanine-tRNA ligase, class IIc, anti-codon-bin
IPR015943*WD40/YVTN repeat-like-containing domain, IPR017986*WD40-repeat-containing domain
NA
IPR032675*Leucine-rich repeat domain, L domain-like
NA
IPR011009*Protein kinase-like domain, IPR000719*Protein kinase domain

NA
IPR013083*Zinc finger, RING/FYVE/PHD-type, IPR027775*C2H2- zinc finger protein family subset, II
IPR029057*Phosphoribosyltransferase-like, IPR029933*Uridine-cytidine kinase-like 1
NA
NA
IPR011011*Zinc finger, FYVE/PHD-type, IPR013083*Zinc finger, RING/FYVE/PHD-type
IPR016090*Phospholipase A2 domain
IPR002659*Glycosyl transferase, family 31
IPR004087*K Homology domain, IPR004088*K Homology domain, type 1
IPR005135*Endonuclease/exonuclease/phosphatase
NA
IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR000048*IQ motif, EF-hand bindi
IPR012336*Thioredoxin-like fold, IPR004045*Glutathione S-transferase, N-terminal, IPR010987*Glut
NA
NA
NA
IPR012674*Calycin, IPR002345*Lipocalin, IPR003057*Invertebrate colouration protein, IPR000566*L
IPR019393*WASH complex, subunit strumpellin
NA
IPR013087*Zinc finger C2H2-type, IPR013083*Zinc finger, RING/FYVE/PHD-type, IPR027775*C2H2
IPR001478*PDZ domain, IPR034876*Partitioning defective protein 6, IPR000270*PB1 domain
NA
IPR000668*Peptidase C1A, papain C-terminal
NA
NA
NA
IPR001164*Arf GTPase activating protein, IPR013328*6-phosphogluconate dehydrogenase, domain
NA

)09003*Peptidase S1, PA clan

omal protein L7Ae/L30e/S12e/Gadd45

)1247*Exoribonuclease, phosphorolytic domain 1, IPR015847*Exoribonuclease, phosphorolytic domain 2

Peptidase C1A

omain, IPR013562*tRNA(Met) cytidine acetyltransferase TmcA, N-terminal, IPR000182*GNAT domain, IPR01

PR011333*SKP1/BTB/POZ domain

eller, TolB-like, IPR000033*LDLR class B repeat

30, beta sandwich domain, IPR001139*Glycoside hydrolase family 30, IPR017853*Glycoside hydrolase super

itellogenin

utyric acid A receptor/Glycine receptor alpha, IPR006029*Neurotransmitter-gated ion-channel transmembrane

inal, IPR004046*Glutathione S-transferase, C-terminal, IPR012336*Thioredoxin-like fold

e colouration protein, IPR000566*Lipocalin/cytosolic fatty-acid binding domain transferase

transferase, IPR006326*UDP-glycosyltransferase, MGT

IF382

PR002345*Lipocalin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain
rine proteases, trypsin domain

IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
ropeptide inhibitor domain (I29)

Peptidase C1A
oyl-protein thioesterase 1

mpellin

382

e 2

de triphosphate hydrolase, IPR003593*AAA+ ATPase domain, IPR030247*Canalicular multispecific organic ar

, IPR012336*Thioredoxin-like fold, IPR010987*Glutathione S-transferase, C-terminal-like

eller, TolB-like, IPR000033*LDLR class B repeat

nal, IPR013128*Peptidase C1A

IPR017853*Glycoside hydrolase superfamily

n, IPR012952*BING4, C-terminal domain

, transmembrane domain, IPR030247*Canalicular multispecific organic anion transporter 1, IPR003439*ABC

NYN domain, limkain-b1-type

sphate 5-kinase, C-terminal, IPR023610*Phosphatidylinositol-4-phosphate 5-kinase

)*Tubulin/FtsZ, C-terminal, IPR018316*Tubulin/FtsZ, 2-layer sandwich domain

gen, alpha/beta/gamma chain, C-terminal globular, subdomain 1, IPR001007*VWFC domain

09003*Peptidase S1, PA clan

ıal, IPR013128*Peptidase C1A

1A, propeptide

d glycine-binding domain

-like, IPR012336*Thioredoxin-like fold, IPR004045*Glutathione S-transferase, N-terminal

athione S-transferase, C-terminal-like, IPR004046*Glutathione S-transferase, C-terminal

09003*Peptidase S1, PA clan

AD(P)-binding domain, IPR000672*Tetrahydrofolate dehydrogenase/cyclohydrolase

ıain, IPR033452*Glycosyl hydrolase family 30, beta sandwich domain, IPR017853*Glycoside hydrolase superf

ApoD type

IPR029060*PIN domain-like

ısin domain, IPR009003*Peptidase S1, PA clan, IPR000859*CUB domain, IPR001314*Peptidase S1A, chymo

03593*AAA+ ATPase domain, IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR030247*C
ntaining domain

TB domain-containing protein 8, IPR011705*BTB/Kelch-associated

ng domain, IPR003057*Invertebrate colouration protein

009003*Peptidase S1, PA clan
lase, N-terminal, IPR009100*Acyl-CoA dehydrogenase/oxidase, N-terminal and middle domain, IPR006091*A
16162*Aldehyde dehydrogenase N-terminal domain

ype 11
011009*Protein kinase-like domain, IPR009091*Regulator of chromosome condensation 1/beta-lactamase-inh
Peptidase C1A

Glutathione S-transferase, N-terminal, IPR004046*Glutathione S-transferase, C-terminal

PR012336*Thioredoxin-like fold, IPR004045*Glutathione S-transferase, N-terminal, IPR010987*Glutathione S

omain, IPR001139*Glycoside hydrolase family 30, IPR033452*Glycosyl hydrolase family 30, beta sandwich d
, IPR012336*Thioredoxin-like fold, IPR010987*Glutathione S-transferase, C-terminal-like

, IPR010987*Glutathione S-transferase, C-terminal-like, IPR012336*Thioredoxin-like fold

*Glycosyl hydrolase family 30, beta sandwich domain, IPR033453*Glycosyl hydrolase family 30, TIM-barrel dc

ic organic anion transporter 1, IPR003439*ABC transporter-like, IPR011527*ABC transporter type 1, transmer
ain

ide hydrolase superfamily

rol-binding domain, IPR020454*Diacylglycerol/phorbol-ester binding
3*Tetracycline resistance protein TetA/multidrug resistance protein MdtG
transferase, IPR006326*UDP-glycosyltransferase, MGT

IPR022271*Lipocalin, ApoD type, IPR003057*Invertebrate colouration protein

)67*Mitochondrial carrier protein

athione S-transferase, C-terminal-like, IPR004045*Glutathione S-transferase, N-terminal

, IPR010987*Glutathione S-transferase, C-terminal-like, IPR012336*Thioredoxin-like fold
alpha, IPR017850*Alkaline-phosphatase-like, core domain
ıain, IPR017853*Glycoside hydrolase superfamily, IPR033452*Glycosyl hydrolase family 30, beta sandwich dc

Major facilitator, sugar transporter-like

ı MutS, connector domain, IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR007696*DNA
ıal, IPR013128*Peptidase C1A
ıted, IPR011333*SKP1/BTB/POZ domain

perfamily, IPR001223*Glycoside hydrolase family 18, catalytic domain
eller, TolB-like, IPR000033*LDLR class B repeat

metallopeptidase

R000536*Nuclear hormone receptor, ligand-binding domain

receptor class A repeat, IPR000998*MAM domain
ching enzyme, N-terminal domain, IPR008928*Six-hairpin glycosidase-like, IPR032792*Glycogen debranching
transferase

idoxal phosphate-dependent transferase, IPR010977*Aromatic-L-amino-acid decarboxylase, IPR002129*Pyri

ı-propeller, TolB-like

*Coatomer/clathrin adaptor appendage, Ig-like subdomain, IPR015151*Beta-adaptin appendage, C-terminal su

ropeptide inhibitor domain (I29)

peat-like-containing domain

ype 11

30247*Canalicular multispecific organic anion transporter 1, IPR003593*AAA+ ATPase domain, IPR027417*P

13149*Alcohol dehydrogenase, C-terminal, IPR011032*GroES-like, IPR013154*Alcohol dehydrogenase, N-te

r, IPR003439*ABC transporter-like, IPR003593*AAA+ ATPase domain

pe B

y subunit

v-density lipoprotein (LDL) receptor class A repeat

PR011333*SKP1/BTB/POZ domain

7*P-loop containing nucleoside triphosphate hydrolase

, IPR003439*ABC transporter-like

domain, IPR017853*Glycoside hydrolase superfamily, IPR033453*Glycosyl hydrolase family 30, TIM-barrel do

, IPR012336*Thioredoxin-like fold, IPR010987*Glutathione S-transferase, C-terminal-like

C-terminal

›tidase C1A, papain C-terminal

C-terminal

›ain C-terminal

29), IPR013128*Peptidase C1A
IPR029060*PIN domain-like

›7*Amine oxidase

Alpha/beta hydrolase fold-1

1A, propeptide

ropeptide inhibitor domain (I29), IPR015644*Peptidase C1A, cathepsin K

9*Metallopeptidase, catalytic domain, IPR000884*Thrombospondin type-1 (TSP1) repeat
domain, IPR017853*Glycoside hydrolase superfamily, IPR033453*Glycosyl hydrolase family 30, TIM-barrel dc

noid synthase domain

›rter, IPR027417*P-loop containing nucleoside triphosphate hydrolase

drolase family 18, catalytic domain, IPR017853*Glycoside hydrolase superfamily, IPR011583*Chitinase II

*Alpha/Beta hydrolase fold, IPR025483*Lipase, eukaryotic

RWD-like

domain, IPR033453*Glycosyl hydrolase family 30, TIM-barrel domain, IPR017853*Glycoside hydrolase superf

IPR011042*Six-bladed beta-propeller, TolB-like

DH ubiquinone oxidoreductase, F subunit, IPR019575*NADH-ubiquinone oxidoreductase 51kDa subunit, iron-

01846*von Willebrand factor, type D domain, IPR001747*Lipid transport protein, N-terminal, IPR015816*Vitelli

474*Protein argonaute, N-terminal

ectin/glucanase domain, IPR000998*MAM domain

Peptidase C1A

lobulin subtype, IPR003598*Immunoglobulin subtype 2, IPR013098*Immunoglobulin I-set

receptor coactivator 6
omutase, alpha/beta/alpha domain I
Alpha/Beta hydrolase fold
, IPR007235*Glycosyl transferase, family 28, C-terminal

ndwich domain, IPR002453*Beta tubulin, IPR008280*Tubulin/FtsZ, C-terminal

-type
F domain

ApoD type
, IPR011527*ABC transporter type 1, transmembrane domain, IPR003439*ABC transporter-like
athione S-transferase, C-terminal, IPR010987*Glutathione S-transferase, C-terminal-like

lpha/beta hydrolase fold-1
ase fold-1
ily 30, TIM-barrel domain, IPR001139*Glycoside hydrolase family 30, IPR017853*Glycoside hydrolase super

*Glycosyl hydrolase family 30, beta sandwich domain, IPR033453*Glycosyl hydrolase family 30, TIM-barrel d
ulin-like domain, IPR003598*Immunoglobulin subtype 2, IPR013162*CD80-like, immunoglobulin C2-set

ide hydrolase superfamily
ucleoside triphosphate hydrolase, IPR011527*ABC transporter type 1, transmembrane domain, IPR030247*

domain, IPR035022*PI3K p85 subunit, N-terminal SH2 domain

-like, IPR012336*Thioredoxin-like fold, IPR004046*Glutathione S-transferase, C-terminal
33909*Ribonucleotide reductase small subunit
e, IPR000867*Insulin-like growth factor-binding protein, IGFBP, IPR011390*Insulin-like growth factor binding

IPR017986*WD40-repeat-containing domain
se, IPR003100*PAZ domain, IPR005034*Dicer dimerisation domain, IPR001650*Helicase, C-terminal, IPR014

brane domain, IPR030247*Canalicular multispecific organic anion transporter 1, IPR003593*AAA+ ATPase doi

30, IPR017853*Glycoside hydrolase superfamily

inal, IPR012336*Thioredoxin-like fold, IPR004045*Glutathione S-transferase, N-terminal
eller, TolB-like
uperfamily, IPR001139*Glycoside hydrolase family 30, IPR033453*Glycosyl hydrolase family 30, TIM-barrel dc

PR015816*Vitellinogen, beta-sheet N-terminal

1A, propeptide

*Lipocalin, IPR022271*Lipocalin, ApoD type, IPR012674*Calycin
main, IPR003977*E3 ubiquitin-protein ligase parkin
29), IPR013128*Peptidase C1A
74*Calycin

TB domain-containing protein 8, IPR011705*BTB/Kelch-associated
holine oxidoreductase, C-terminal, IPR012132*Glucose-methanol-choline oxidoreductase, IPR023753*FAD/NA

C-terminal
Glutathione S-transferase, N-terminal, IPR004046*Glutathione S-transferase, C-terminal
domain 2, IPR015424*Pyridoxal phosphate-dependent transferase, IPR015421*Pyridoxal phosphate-depende

de triphosphate hydrolase, IPR003439*ABC transporter-like, IPR003593*AAA+ ATPase domain

N-terminal, IPR001930*Peptidase M1, alanine aminopeptidase/leukotriene A4 hydrolase
er-gated ion-channel, IPR006202*Neurotransmitter-gated ion-channel ligand-binding domain

ain

side hydrolase 35, catalytic domain, IPR001944*Glycoside hydrolase, family 35, IPR017853*Glycoside hydrola

omain

n function DB

3*HSP20-like chaperone, IPR001436*Alpha crystallin/Heat shock protein
474*Protein argonaute, N-terminal, IPR014811*Argonaute, linker 1 domain

lomain, IPR013783*Immunoglobulin-like fold, IPR003598*Immunoglobulin subtype 2, IPR003599*Immunoglob

omain, IPR008148*DNA photolyase class 2, IPR014729*Rossmann-like alpha/beta/alpha sandwich fold

crystallin/Heat shock protein, IPR002068*Alpha crystallin/Hsp20 domain
xypeptidase domain

ke region, IPR011042*Six-bladed beta-propeller, TolB-like

-gated ion-channel transmembrane domain, IPR006028*Gamma-aminobutyric acid A receptor/Glycine recept
AD-binding domain

domain, IPR000917*Sulfatase, N-terminal

a subunit, helical insertion, IPR001408*G-protein alpha subunit, group I, IPR027417*P-loop containing nucleo

ureninase, IPR015424*Pyridoxal phosphate-dependent transferase, IPR015422*Pyridoxal phosphate-depen
g nucleoside triphosphate hydrolase, IPR003439*ABC transporter-like
s protein 2, IPR000008*C2 domain

Thrombospondin type-1 (TSP1) repeat, IPR002861*Reeler domain
A binding, IPR016177*DNA-binding domain, IPR025884*Methyl-CpG binding protein 2/3, C-terminal domain
family 10 member 6, IPR004710*Bile acid:sodium symporter

ivating protein domain
a subunit, IPR001392*Clathrin adaptor, mu subunit

ropeptide inhibitor domain (I29)

rine proteases, trypsin domain
PR008138*Saposin B type, region 2, IPR008373*Saposin, IPR007856*Saposin-like type B, region 1

eller, TolB-like, IPR000033*LDLR class B repeat

rane domain, IPR003439*ABC transporter-like, IPR030247*Canalicular multispecific organic anion transporte

enine methyltransferase KsgA/Erm, IPR011530*Ribosomal RNA adenine dimethylase, IPR020598*Ribosomal
, transmembrane domain, IPR003439*ABC transporter-like, IPR003593*AAA+ ATPase domain

mily 30, IPR033453*Glycosyl hydrolase family 30, TIM-barrel domain, IPR017853*Glycoside hydrolase superf

-like, IPR004045*Glutathione S-transferase, N-terminal, IPR012336*Thioredoxin-like fold

main, IPR003316*E2F/DP family, winged-helix DNA-binding domain, IPR015648*Transcription factor DP lase S1A, chymotrypsin family

ɔain C-terminal
ng domain

ɔA reductase, C-terminal, IPR013120*Male sterility, NAD-binding
PR007502*Helicase-associated domain, IPR014001*Helicase superfamily 1/2, ATP-binding domain, IPR0203

globulin subtype 2, IPR003599*Immunoglobulin subtype, IPR013098*Immunoglobulin I-set

)8962*PapD-like, IPR013783*Immunoglobulin-like fold
IPR003663*Sugar/inositol transporter

oxylase, IPR015421*Pyridoxal phosphate-dependent transferase, major region, subdomain 1, IPR002129*Pyri
)17853*Glycoside hydrolase superfamily

Follistatin-like, N-terminal, IPR002350*Kazal domain, IPR009030*Growth factor receptor cysteine-rich domain

al domain, IPR030556*Dynamin-1-like protein

triphosphate hydrolase, IPR001650*Helicase, C-terminal, IPR016197*Chromo domain-like, IPR023780*Chro
ı, IPR008936*Rho GTPase activation protein

ıthase GATase domain, IPR017926*Glutamine amidotransferase, IPR027417*P-loop containing nucleoside tr
in

ıucleoside triphosphate hydrolase

1A, propeptide

otein 1

*Peptidase M14, carboxypeptidase A

'-Nucleotidase, C-terminal, IPR004843*Calcineurin-like phosphoesterase domain, ApaH type

n-like

IPR022271*Lipocalin, ApoD type, IPR003057*Invertebrate colouration protein

-terminal, IPR013154*Alcohol dehydrogenase, N-terminal, IPR020843*Polyketide synthase, enoylreductase dc

unit 5, IPR007194*Transport protein particle (TRAPP) component

‹e complex subunit 6, N-terminal, IPR026797*HAUS augmin-like complex subunit 6, IPR021565*Rabenosyn, I ke/link domain, IPR008160*Collagen triple helix repeat

cytosolic fatty-acid binding domain, IPR012674*Calycin, IPR002345*Lipocalin

e

*Glycosyl hydrolase family 30, TIM-barrel domain, IPR033452*Glycosyl hydrolase family 30, beta sandwich do

hosphate hydrolase, IPR005225*Small GTP-binding protein domain

tidase, N-terminal, IPR034016*Aminopeptidase N-type, IPR001930*Peptidase M1, alanine aminopeptidase/leu

opeptide repeat protein 39

1A, propeptide

pe, IPR001611*Leucine-rich repeat

13099*Potassium channel domain, IPR019594*Ionotropic glutamate receptor, L-glutamate and glycine-binding

ing site, IPR029955*Abnormal spindle-like microcephaly-associated protein

one receptor-type, IPR003068*Transcription factor COUP, IPR001723*Nuclear hormone receptor, IPR013088 ıg nucleoside triphosphate hydrolase, IPR003593*AAA+ ATPase domain

mase-inhibitor protein II, IPR011009*Protein kinase-like domain, IPR000408*Regulator of chromosome conde

113, C-terminal domain, IPR030082*Neprilysin-21, IPR008753*Peptidase M13, N-terminal domain

ırathyroid hormone-responsive B1, IPR015943*WD40/YVTN repeat-like-containing domain, IPR028073*PTHE

31*Rhabdovirus nucleocapsid, C-terminal
ıucleoside triphosphate hydrolase

lase S1A, chymotrypsin family

R008076*Cyanate hydratase

5974*Ribosomal protein L19/L19e, domain 3, IPR033935*Ribosomal protein L19, eukaryotic, IPR015972*Ribc

18*Potassium channel, inwardly rectifying, Kir, cytoplasmic
G/FYVE/PHD-type

057*Homeobox domain-like

30, beta sandwich domain, IPR017853*Glycoside hydrolase superfamily, IPR001139*Glycoside hydrolase fam
067*Mitochondrial carrier protein

nain, IPR017986*WD40-repeat-containing domain

37*Amine oxidase

ll heat shock protein HSP20, IPR002068*Alpha crystallin/Hsp20 domain

nal, IPR013128*Peptidase C1A

idase C-terminal

e, editing domain

ubulin/FtsZ, GTPase domain, IPR018316*Tubulin/FtsZ, 2-layer sandwich domain

R034113*Golgi-associated plant pathogenesis-related protein 1, SCP domain

-helix domain

dase C-terminal, IPR009100*Acyl-CoA dehydrogenase/oxidase, N-terminal and middle domain, IPR006091*A

otein, N-terminal

ase lipase domain

RING/FYVE/PHD-type, IPR027775*C2H2- zinc finger protein family subset

C-terminal domain

omal protein L7Ae/L30e/S12e/Gadd45

8978*HSP20-like chaperone, IPR002068*Alpha crystallin/Hsp20 domain
otein 6

09003*Peptidase S1, PA clan

ain

n
9, IPR017849*Alkaline phosphatase-like, alpha/beta/alpha

chaea-type

-adenosyl-L-methionine-dependent methyltransferase

IPR003057*Invertebrate colouration protein, IPR022271*Lipocalin, ApoD type

carboxypeptidase A

n, IPR017849*Alkaline phosphatase-like, alpha/beta/alpha

d

cyltransferase

minal, IPR028784*Bardet-Biedl syndrome 1 protein, IPR017986*WD40-repeat-containing domain

Transcription factor E2F4, IPR011991*Winged helix-turn-helix DNA-binding domain, IPR032198*E2F transcrip

Peptidase C1A

nase C mu-related, IPR020454*Diacylglycerol/phorbol-ester binding

PR027995*Galactosyltransferase, N-terminal, IPR027791*Galactosyltransferase, C-terminal

l

de triphosphate hydrolase

ng domain, IPR011989*Armadillo-like helical

omain, IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR001650*Helicase, C-terminal changer

sembly factor Rtp1, C-terminal

-like domain, IPR001180*Citron homology (CNH) domain, IPR000719*Protein kinase domain

domain, IPR035022*PI3K p85 subunit, N-terminal SH2 domain

in

family

IPR017853*Glycoside hydrolase superfamily, IPR000322*Glycoside hydrolase family 31, IPR025887*Glycosi

ıain
UTPase, trimeric

converting enzyme-like 1
omain

PR008927*6-phosphogluconate dehydrogenase C-terminal domain-like, IPR013328*6-phosphogluconate deh

ding domain, IPR018164*Alanyl-tRNA synthetase, class IIc, N-terminal
ı, IPR001680*WD40 repeat

PR013087*Zinc finger C2H2-type

ing site

athione S-transferase, C-terminal-like

Lipocalin/cytosolic fatty-acid binding domain, IPR022271*Lipocalin, ApoD type

2- zinc finger protein family subset

2, IPR008927*6-phosphogluconate dehydrogenase C-terminal domain-like, IPR029154*3-hydroxyisobutyrate

6181*Acyl-CoA N-acyltransferase

family

domain, IPR006201*Neurotransmitter-gated ion-channel

nion transporter 1, IPR003439*ABC transporter-like

transporter-like, IPR003593*AAA+ ATPase domain

family

trypsin family

Canalicular multispecific organic anion transporter 1

cyl-CoA oxidase/dehydrogenase, central domain

ibitor protein II

-transferase, C-terminal-like

omain

omain

mbrane domain, IPR003593*AAA+ ATPase domain

omain

mismatch repair protein MutS, core, IPR017261*DNA mismatch repair protein MutS/MSH, IPR007861*DNA

g enzyme, glucanotransferase domain, IPR006421*Glycogen debranching enzyme, metazoa, IPR017853*Gly

doxal phosphate-dependent decarboxylase, IPR015422*Pyridoxal phosphate-dependent transferase, subdom

ubdomain, IPR013037*Clathrin adaptor, beta-adaptin, appendage, Ig-like subdomain, IPR009028*Coatomer/

P-loop containing nucleoside triphosphate hydrolase

rminal

omain

omain

family

sulphur binding domain, IPR019554*Soluble ligand binding domain

inogen, beta-sheet N-terminal, IPR011030*Vitellinogen, superhelical

family

omain

Canalicular multispecific organic anion transporter 1

protein-related protein (IGFBP-rP), MAC25, IPR013098*Immunoglobulin I-set, IPR009030*Growth factor recep

001*Helicase superfamily 1/2, ATP-binding domain, IPR011545*DEAD/DEAH box helicase domain

omain, IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR003439*ABC transporter-like

omain

AD(P)-binding domain

ent transferase, major region, subdomain 1, IPR034758*Ornithine aminotransferase, mitochondrial, IPR01016 ase superfamily

ulin subtype

or alpha, IPR006201*Neurotransmitter-gated ion-channel

side triphosphate hydrolase

dent transferase, subdomain 2, IPR000192*Aminotransferase class V domain

r 1, IPR003593*AAA+ ATPase domain, IPR027417*P-loop containing nucleoside triphosphate hydrolase

RNA adenine methylase transferase, N-terminal

family

38*SMN complex, gem-associated protein 7

doxal phosphate-dependent decarboxylase, IPR015422*Pyridoxal phosphate-dependent transferase, subdom

ı, IPR001791*Laminin G domain, IPR002049*Laminin EGF domain

ɔmo domain, IPR000330*SNF2-related, N-terminal domain, IPR000953*Chromo/chromo shadow domain, IPR

riphosphate hydrolase, IPR017456*CTP synthase, N-terminal

omain

Rab binding domain, IPR013083*Zinc finger, RING/FYVE/PHD-type

omain

ukotriene A4 hydrolase

g domain

*Zinc finger, NHR/GATA-type

ensation, RCC1

31, N-terminal domain

osomal protein L19/L19e, domain 1

ily 30

cyl-CoA oxidase/dehydrogenase, central domain

ption factor, CC-MB domain

ide hydrolase family 31, N-terminal domain, IPR000519*P-type trefoil domain

ıydrogenase, domain 2, IPR006108*3-hydroxyacyl-CoA dehydrogenase, C-terminal dehydrogenase, NAD-binding domain, IPR011548*3-hydroxyisobutyrate dehydrogenase

mismatch repair protein MutS, clamp

ycoside hydrolase superfamily, IPR010401*Glycogen debranching enzyme, IPR032790*Glycogen debranching

nain 2

calthrin adaptor appendage, C-terminal subdomain, IPR026739*AP complex subunit beta

otor cysteine-rich domain, IPR007110*Immunoglobulin-like domain

4*Ornithine aminotransferase

ıain 2

006576*BRK domain

g enzyme, C-terminal

Table S6 -

Gene ID	$\log_2$FC
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tetur04g09479	9.490102736
tetur02g14440	9.358088546
tetur03g04990	9.057781803
tetur14g01700	8.838004051
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tetur11g05730	8.800439508
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tetur02g09200	8.503476884
tetur04g09489	8.326315821
tetur01g16463	8.291540249
tetur12g03210	8.082951533
tetur07g04400	8.054111618
tetur651g00010	7.998725309
tetur01g11990	7.967646934
tetur14g04233	7.830868531
tetur24g92198	7.766216485
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tetur04g00770	7.718795837
tetur05g06400	7.612366493
tetur23g00210	7.577578267
tetur05g06440	7.509922136
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tetur30g00110	7.270725509
tetur20g01380	7.196816477
tetur14g00070	7.056171335
tetur10g02890	7.009067201
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tetur11g90924	-8.63667662
tetur03g08460	-8.75614476
tetur27g00290	-9.00056134
tetur28g01480	-9.7730236

Differentially expressed genes (DEGs) and significantly over/underexpressed genes between three resistar

	UK6 vs RO1
description	P.Value
CYP392D8 Cytochrome P450 - CYP392D8	1.60E-12
Hypothetical protein	1.23E-10
SSPF2 Small Secreted Protein; Family F hypothetical protein	1.07E-13
Hypothetical protein	5.52E-16
Hypothetical protein	2.24E-11
hypothetical protein	1.93E-14
SSPF3 Small Secreted Protein; Family F hypothetical protein	1.92E-12
Hypothetical protein	5.33E-11
CYP392D2 Cytochrome P450 - CYP392D2	1.52E-15
MDL14 Immunoglobulin E-set Immunoglobulin E-set	5.99E-12
hypothetical protein	1.04E-12
PLAT11 PLAT/LH2 domain PLAT/LH2 domain PLAT/LH2 domain PLAT/LH2 domain PL	7.66E-11
partitioning defective 6 homolog beta	7.66E-13
SLIT-ROBO Rho GTPase activating protein 2	1.64E-14
Hypothetical protein	6.36E-14
SSPF4 Small Secreted Protein; Family F hypothetical protein	6.77E-14
TuPap-18 Peptidase C1A, papain C-terminal Peptidase C1A, papain C-terminal	3.37E-06
Hypothetical protein	3.28E-14
Immunoglobulin-like fold	7.41E-14
ribosomal protein S12	1.50E-12
DNA-binding SAP	4.76E-14
hypothetical protein	2.58E-11
hypothetical protein	9.70E-12
SP45_2 Serine protease SP47 Serine protease	9.18E-09
hypothetical protein	3.18E-11
SSPF1 Small Secreted Protein; Family F transporter; AcrB/AcrD/AcrF family protein transp	4.21E-16
Hypothetical protein	9.97E-14
DDM9-19 Domain of unknown function DUF3421 Domain of unknown function DUF3421	8.77E-13
Tudor domain	9.65E-13
BTB/Kelch-associated	9.25E-10
exosome complex exonuclease RRP46	8.42E-12
Hypothetical protein	2.41E-13
Hypothetical protein	2.37E-13
Hypothetical protein	1.85E-11
CYP392D5p Cytochrome P450 - CYP392D5p probable pseudogene	9.93E-12
NAT10 Acyl-CoA N-acyltransferase Acyl-CoA N-acyltransferase	6.54E-10
Hypothetical protein	6.20E-10
Hypothetical protein	1.27E-11
CYP392D10p Cytochrome P450 - CYP392D10p probable pseudogene	4.66E-13
Hypothetical protein	1.55E-12
Hypothetical protein	7.21E-12
Short-chain dehydrogenase/reductase SDR	2.33E-10
CYP392A11 Cytochrome P450 - CYP392A11 CYP392A11v2 Cytochrome P450 - CYP392A1	4.30E-20
CYP392A9 Cytochrome P450 - CYP392A9	3.25E-10

Scramblase	5.52E-12
Pyruvate kinase; C-terminal-like	1.87E-12
hypothetical protein StAA4_21417	8.96E-13
Hypothetical protein	1.31E-14
ApoD27 Invertebrate colouration protein Invertebrate colouration protein	8.02E-10
TuCCE44 Carboxyl/cholinesterase TuCCE-38 Carboxyl/cholinesterase	1.24E-10
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	2.04E-10
PB1 Bromo adjacent homology BAH domain Bromo adjacent homology BAH domain	2.19E-09
Hypothetical protein	4.35E-12
nitrilase homolog 1	3.22E-10
WTTMP1 Wannes-Thomas type-I single-pass transmembrane protein type-I single-pass trar	3.15E-14
SSPF6 Calycin-like Calycin-like	1.16E-11
UGT UDP-glycosyltransferase; teturUGT29 UGT UDP-glycosyltransferase Glycosyltransfera	1.81E-13
CYP392A9v2 Cytochrome P450 - CYP392A9v2	1.26E-08
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	2.34E-10
Curculin-like mannose-binding lectin	1.67E-09
hypothetical protein	6.60E-10
Fibroin Hypothetical protein	1.12E-13
PAN/Apple domain	3.10E-10
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	1.85E-09
antigen B membrane protein	7.78E-09
GI21111	1.61E-09
	1.40E-09
Hypothetical protein	2.92E-10
Tu_12344.2 cys-loop ligand-gated ion channel Tu_12344.2 ligand-gated ion channel glycine	1.22E-10
TuCCE35 Carboxyl/cholinesterase TuCCE35 Carboxylesterase; type B TuCCE34 Carboxyle	3.52E-11
Hypothetical protein	4.25E-11
photosystem II CP47 protein	7.25E-10
Apple-like	1.69E-15
Hypothetical protein	5.73E-10
hypothetical protein	2.77E-09
V-type proton ATPase subunit d 2	2.93E-12
CYP392D7 Cytochrome P450, conserved site Cytochrome P450, conserved site	4.69E-10
GE26306	3.32E-12
hypothetical protein	9.20E-10
SP18 Serine protease	2.16E-07
Protein phosphatase 2A; regulatory B subunit; B56	1.35E-09
CCEincTu10 Carboxyl/cholinesterase; incomplete CCEincTu10 Carboxylesterase; type B CC	1.01E-10
Intradiol ring-cleavage dioxygenase, core Intradiol ring-cleavage dioxygenase, core	1.89E-12
Hypothetical protein	5.54E-17
Hypothetical protein	2.04E-12
WTSP1a Wannes-Thomas Secreted Protein 1 WTSP1b Wannes-Thomas Secreted Protein 1	2.64E-14
Hypothetical protein	2.15E-17
Major facilitator superfamily; general substrate transporter	9.53E-10
Hypothetical protein	1.24E-07
PAN/Apple domain	2.42E-09
conserved hypothetical protein	1.58E-08

BTB/Kelch-associated BTB/Kelch-associated	3.15E-07
Leucine-rich repeat domain, L domain-like	7.79E-14
hypothetical protein GrBNV_gp28	1.05E-11
Hypothetical protein	3.41E-10
Hypothetical protein	7.01E-09
Hypothetical protein	1.05E-08
BTB/Kelch-associated BTB/Kelch-associated	7.29E-08
IAP Proteinase inhibitor I32; inhibitor of apoptosis IAP Proteinase inhibitor I32; inhibitor of ap	9.73E-13
Hypothetical protein	9.78E-07
C-factor	3.41E-10
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	3.74E-09
UGT UDP-glycosyltransferase; teturUGT28 UGT UDP-glycosyltransferase Glycosyltransfer	3.60E-09
selenophosphate synthetase 1	2.09E-10
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	6.86E-10
Fibroin partial Fibrion Hypothetical protein	4.18E-08
UGT UDP-glycosyltransferase; teturUGT36 UGT UDP-glycosyltransferase Glycosyltransfer	2.98E-11
PLAT9 Lipase/lipooxygenase; PLAT/LH2 Lipase/lipooxygenase; PLAT/LH2 Lipase/lipooxy	2.96E-13
ADP/ATP translocase	1.10E-12
CYP392E8 Cytochrome P450 - CYP392E8	2.15E-18
CYP392A13v2 Cytochrome P450 - CYP392A13v2	3.61E-13
FCOL Fibrillar collagen precursor collagen alpha-1	2.23E-10
hypothetical protein	1.02E-10
V-type proton ATPase subunit d 2 V-type proton ATPase subunit d 2	5.32E-12
TuPap-30 Cathepsin L	6.15E-08
CYP probable pse Cytochrome P450 probable pseudogene	1.61E-17
Hypothetical protein	1.16E-09
Hypothetical protein	1.53E-13
phosphatidylinositol-4-phosphate 5-kinase; type I; alpha	7.04E-15
PREDICTED: similar to limkain b1	4.97E-10
Hypothetical protein	4.38E-08
CYP392A12 Cytochrome P450 - CYP392A12	5.82E-15
Apolipoprotein D precursor; putative Calycin GH10331	5.56E-13
BTB/Kelch-associated	8.67E-11
hypothetical protein	3.72E-09
BTB/POZ-like	1.69E-09
puromycin-sensitive aminopeptidase	1.41E-11
CYP392Dn Cytochrome P450, conserved site CYP Cytochrome P450, conserved site Cyto	7.61E-07
hypothetical protein	2.72E-08
Hypothetical protein	3.01E-09
C-factor	1.11E-08
kelch-like 18	3.29E-07
Protein of unknown function DUF2362	1.28E-11
short chain dehydrogenase	1.42E-11
SSPF8 Small Secretory Protein; Family F hypothetical protein	4.84E-10
phosphatidylinositol-4-phosphate 5-kinase; type I; alpha phosphatidylinositol-4-phosphate 5-	8.99E-07
Hypothetical protein	1.22E-08
Fibroin hypothetical protein	1.24E-09

hypothetical protein	6.81E-11
UGT UDP-glycosyltransferase; teturUGT21 UGT UDP-glycosyltransferase Glycosyltransfera	1.93E-09
WTSP12 Wannes-Thomas Secreted Protein 12 Hypothetical protein	9.17E-07
DDM9-12 Domain of unknown function DUF3421 Domain of unknown function DUF3421	1.78E-05
Hypothetical protein	1.28E-08
mismatch repair protein pms1 homologue; putative	2.52E-11
4-nitrophenylphosphatase	5.51E-07
Hypothetical protein	6.20E-07
RNA-directed DNA polymerase	1.81E-10
Hypothetical protein	1.06E-12
beta-tubulin	4.15E-13
Fibroin Hypothetical protein	2.64E-05
TuGSTd13 Glutathione S-transferase; class delta	5.52E-09
Apple-like	2.24E-11
WD40 repeat, conserved site	1.08E-11
apoptosis regulator BAX apoptosis regulator BAX	1.22E-08
PREDICTED: similar to Y41C4A.8 PREDICTED: similar to Y41C4A.8 PREDICTED: similar	5.84E-10
hypothetical protein	1.02E-06
Chibby family	1.93E-09
PREDICTED: similar to adenylate cyclase	6.88E-09
TuLeg-14 Legumain	6.94E-07
Scramblase	1.48E-08
solute carrier family 35 member B1 solute carrier family 35 member B1	2.15E-10
TuPap-11 Cathepsin B	1.88E-14
Hypothetical protein	2.99E-07
DNA repair protein xp-c / rad4 DNA repair protein xp-c / rad4	6.14E-07
CYP392A10v2 Cytochrome P450 - CYP392A10v2	1.12E-12
Aldehyde dehydrogenase; N-terminal	2.24E-11
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	2.77E-10
Hypothetical protein	3.19E-08
SSPB3 Small Secreted Protein; Family B hypothetical protein	9.88E-11
SLCP4 Secreted low complexity protein; putative	1.07E-14
Hypothetical protein	3.62E-07
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	3.10E-10
Nuclear hormone receptor, ligand-binding domain	6.08E-10
CYP392A16 Cytochrome P450 - CYP392A16	3.52E-17
hypothetical protein	1.17E-09
C-signal	1.92E-13
intraflagellar transport protein 81 homolog	2.45E-07
3-oxoacyl-acyl-carrier-protein reductase	3.88E-10
mitochondrial sodium/hydrogen exchanger NHA2	8.49E-09
PREDICTED: RNA-dependent RNA polymerase Family family member	2.53E-08
ApoDR5 Calycin-like ApoDR5 Calycin-like Calycin-like	3.34E-08
hypothetical protein	4.92E-12
Hypothetical protein	8.40E-14
Hypothetical protein	2.60E-07
Hypothetical protein	2.57E-13

DDM9-13 Domain of unknown function DUF3421 Domain of unknown function DUF3421	1.71E-13
MDL4 Immunoglobulin E-set Immunoglobulin E-set	2.21E-07
medium-chain specific acyl-CoA dehydrogenase; mitochondrial precursor	1.21E-14
UGT UDP-glycosyltransferase; teturUGT59 UGT UDP-glycosyltransferase glycosyl transfer	2.49E-06
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	2.30E-06
GBA1 Glycoside hydrolase; subgroup; catalytic core Glycoside hydrolase; subgroup; catalyti	2.26E-12
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	7.20E-09
WTSP2 Wannes-Thomas Secreted Protein 2 Hypothetical protein	1.22E-11
UGT UDP-glycosyltransferase; teturUGT10 UGT UDP-glycosyltransferase Glycosyltransfer	1.82E-14
Peptidase M16; core	4.24E-11
Vg2 Lipid transport protein, beta-sheet shell Lipid transport protein, beta-sheet shell	3.77E-14
CYP392D6 Cytochrome P450 - CYP392D6 na Cytochrome P450 -	1.16E-08
TuPap-22 Cathepsin B-like	1.91E-13
Ubiquitin-fold modifier-conjugating enzyme 1	8.27E-10
Hypothetical protein	6.21E-08
MYL1;2 Myosin regulatory light chain; isoform1 Myosin regulatory light chain 2; smooth mus	1.34E-09
Hypothetical protein	2.75E-09
CRAL-TRIO lipid binding domain	1.65E-05
Hypothetical protein	6.31E-09
TuPap-56 Cathepsin L	1.07E-16
TuCCE25 Carboxyl/cholinesterase TuCCE-25 Carboxyl/cholinesterase	6.86E-10
Helix-loop-helix DNA-binding	3.58E-09
serpin 3 inhibitory serine protease inhibitor	8.07E-10
UNC93-like protein MFSD11	2.22E-09
Apolipoprotein D precursor; putative PREDICTED: apolipoprotein D-like; partial	5.91E-13
Hypothetical protein	8.45E-07
hypothetical protein	2.62E-11
Hypothetical protein	8.36E-07
TuPap-6 Cathepsin B	9.90E-15
Hypothetical protein	1.71E-11
RDRP-2 RNA-directed RNA polymerase 2	1.68E-10
hypothetical protein	1.88E-09
Hypothetical protein	4.63E-09
Transcription initiation factor TFIID subunit 10 Transcription initiation factor TFIID subunit 10	1.04E-12
UGT UDP-glycosyltransferase; teturUGT33 UDP-glycosyltransferase; teturUGT33 UDP-gly	1.57E-09
kelch-like 18	1.00E-08
Hypothetical protein	6.94E-07
CYP392E9 Cytochrome P450 - CYP392E9	4.97E-10
PLAT10 Lipase/lipooxygenase; PLAT/LH2 Lipase/lipooxygenase; PLAT/LH2 Lipase/lipooxy	2.93E-11
Replication fork protection component Swi3	1.03E-07
UGT UDP-glycosyltransferase; teturUGT26 UGT UDP-glycosyltransferase Glycosyltransfer	1.37E-10
Hypothetical protein	2.81E-08
Hypothetical protein	8.87E-07
Kelch-type beta propeller	3.91E-11
odd Protein odd-skipped	5.55E-08
intraflagellar transport protein 81 homolog	2.79E-07
Hypothetical protein	2.63E-06

unnamed protein product	1.11E-11
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	1.68E-07
Zinc finger, C2H2	3.15E-08
SP29 Serine protease SP45_3 Serine protease SP29 Serine protease	2.06E-10
TuPap-19 Cystatin domain Cystatin domain	4.73E-10
phospholipid scramblase 2	1.44E-11
Sec39 domain	7.22E-07
protein kinase protein kinase	2.08E-09
WD40 repeat	2.77E-11
Leucine-rich repeat domain, L domain-like	2.62E-07
Hypothetical protein	2.42E-06
PREDICTED: brefeldin A-inhibited guanine nucleotide-exchange protein 3	1.01E-10
Tudor domain	5.44E-11
Hypothetical protein	1.97E-11
P-loop containing nucleoside triphosphate hydrolase	3.22E-10
autophagy-related protein 101	1.97E-13
Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like Leucir	6.78E-07
PREDICTED: similar to adenylate cyclase	2.19E-06
kynureninase kynureninase	9.70E-12
serum amyloid A protein-like	6.11E-13
TuGSTd07 Glutathione S-transferase; class delta	8.83E-11
Intradiol ring-cleavage dioxygenase, core Intradiol ring-cleavage dioxygenase, core Intradiol	1.57E-11
Hypothetical protein	2.37E-07
Hypothetical protein	2.29E-05
transmembrane protein 181 transmembrane protein 181	2.09E-08
Hypothetical protein	2.08E-07
UGT UDP-glycosyltransferase; teturUGT06 UGT UDP-glycosyltransferase rhamnosyltransf	2.98E-12
MIER1 Mesoderm induction early response protein mesoderm induction early response 1; fa	5.56E-11
Hypothetical protein	1.24E-09
PLAT8 Lipase/lipooxygenase; PLAT/LH2 Lipase/lipooxygenase; PLAT/LH2 Lipase/lipooxyg	6.99E-08
Glycoside hydrolase; subgroup; catalytic core	6.75E-09
TuPap-48 Cathepsin L	4.28E-07
CYP392D1 Cytochrome P450 - CYP392D1	6.69E-12
Dgri Nuclear hormone receptor, ligand-binding domain Nuclear hormone receptor, ligand-bin	8.84E-09
conserved hypothetical protein	2.23E-09
Hypothetical protein	8.15E-12
Mif2/CENP-C cupin domain	3.14E-07
TuCCE58 Carboxyl/cholinesterase TuCCE-49 Carboxyl/cholinesterase	3.03E-11
PREDICTED: similar to adenylate cyclase	5.46E-09
Major facilitator superfamily domain	5.60E-08
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	1.25E-09
ApoD6 Apolipoprotein D polycalin	9.24E-07
TuCCE50 Carboxyl/cholinesterase TuCCE-50 Carboxyl/cholinesterase	3.39E-13
ApoDR8 Calycin-like Calycin-like	1.45E-06
sorbitol dehydrogenase	1.56E-08
hypothetical protein	2.00E-06
BTB/POZ-like	9.29E-09

TuLeg-16 Legumain	4.57E-15
N-alpha-acetyltransferase 15; NatA auxiliary subunit N-alpha-acetyltransferase 15; NatA auxi	2.37E-15
hypothetical protein	2.38E-11
3-oxoacyl-acyl-carrier-protein reductase	5.88E-14
hypothetical protein	9.48E-08
conserved hypothetical protein	7.99E-07
C-factor	1.74E-06
Methyltransferase type 11	4.31E-09
ApoD29 Apolipoprotein D precursor lipoprotein Blc	5.85E-10
phosphotyrosyl phosphatase activator phosphotyrosyl phosphatase activator phosphotyrosy	2.14E-08
PREDICTED: myeloid/lymphoid or mixed-lineage leukemia 2 PREDICTED: myeloid/lymphoic	4.18E-08
hypothetical protein	6.54E-10
Mid1-interacting protein 1 Mid1-interacting protein 1	9.41E-07
CYP392E4 Cytochrome P450, E-class, group I CYP392E4 Cytochrome P450, E-class, grour	1.11E-10
DM DM DNA-binding domain	1.36E-09
PREDICTED: similar to adenylate cyclase	1.45E-07
Hypothetical protein	1.67E-07
hypothetical protein	6.52E-08
PREDICTED: similar to Bsdc1 protein	5.41E-09
Galactose oxidase/kelch; beta-propeller	1.75E-07
Hypothetical protein	5.12E-06
Nuclear hormone receptor, ligand-binding domain	2.13E-10
intradiol ring-cleavage dioxygenase	4.46E-07
Nose resistant-to-fluoxetine protein, N-terminal	7.33E-06
serpin 3 inhibitory serine protease inhibitor	5.14E-10
Hypothetical protein	3.50E-13
Leukocyte elastase inhibitor	1.23E-12
Hypothetical protein	2.40E-07
adenylate cyclase	1.01E-05
TuGSTd09 Glutathione S-transferase, C-terminal TuGSTd09 Glutathione S-transferase, C-te	3.47E-11
glycogen debranching enzyme	1.58E-13
TuCCE49 Acetyl-cholinesterase TuCCE-41-AChE Acetyl-cholinesterase	5.12E-11
TuCCE65 Carboxyl/cholinesterase TuCCE-55 Carboxyl/cholinesterase	1.80E-08
DDM9-20 Domain of unknown function DUF3421 Domain of unknown function DUF3421	1.53E-06
PREDICTED: similar to limkain b1	8.45E-06
Hypothetical protein	9.58E-08
TuCCE01 Carboxyl/cholinesterase TuCCE-01 Carboxyl/cholinesterase	1.30E-07
short-chain dehydrogenase/reductase SDR	1.46E-10
TuABCC-11 ABC-transporter; class C;	7.88E-11
Hypothetical protein	1.91E-08
Low-density lipoprotein LDL receptor class A repeat	5.26E-09
Hypothetical protein	4.14E-10
Hypothetical protein	6.44E-07
Hypothetical protein	7.41E-06
Epididymal secretory protein E1 precursor	4.69E-11
hypothetical protein	5.19E-06
UGT UDP-glycosyltransferase; teturUGT40 UGT UDP-glycosyltransferase Glycosyltransfera	2.13E-06

CYP392B3 Cytochrome P450 - CYP392B3	2.29E-11
Hypothetical protein	5.41E-05
Hypothetical protein	1.99E-11
protein LTV1 homolog	7.94E-09
PREDICTED: similar to limkain b1	5.07E-06
hmx3 Homeobox protein HMX3	2.76E-11
CHT5 chitinase chitinase	3.22E-11
Hypothetical protein	8.82E-06
Peptidase S60; transferrin lactoferrin	3.88E-09
hypothetical protein	1.37E-05
UGT UDP-glycosyltransferase; teturUGT39 UGT UDP-glycosyltransferase Glycosyltransfer	7.67E-07
ribosomal protein S7	2.58E-10
Plexin domain-containing protein	9.87E-11
Calponin-like actin-binding	6.98E-05
Hypothetical protein	2.01E-07
bromodomain-containing protein 7	2.32E-06
TuPap-24 Cathepsin B	5.19E-11
Hypothetical protein	5.74E-06
NAGLT1a Major facilitator superfamily; general substrate transporter Major facilitator superf	3.75E-05
Lipocalin family conserved site Lipocalin family conserved site	4.73E-09
Hypothetical protein	1.43E-11
PREDICTED: hypothetical protein	9.38E-11
Hypothetical protein	1.33E-06
Tnc extracellular matrix protein Tenectin flocculin flocculin	4.05E-07
conserved unknown protein	2.95E-09
PLAT14 PLAT/LH2 domain PLAT/LH2 domain PLAT/LH2 domain	6.32E-06
hypothetical protein	3.60E-10
conserved hypothetical protein	5.95E-06
Nab NGFI-A-binding protein homolog NGFI-A- homolog NGFI-A-binding protein 1 NGFI-A-	8.41E-12
Hypothetical protein	3.19E-08
hypothetical protein	3.66E-10
PLAT7 Lipase/lipooxygenase; PLAT/LH2 Lipase/lipooxygenase; PLAT/LH2 Lipase/lipooxy	1.08E-09
Hypothetical protein	7.95E-08
SP28 Serine protease	5.10E-07
Sec1-like protein	1.09E-06
RNA-dependent RNA polymerase, eukaryotic-type	7.51E-07
conserved hypothetical protein	0.0003039
hypothetical protein	1.92E-07
TuPap-43 Cathepsin L	1.23E-08
Leucine-rich repeat domain, L domain-like	5.42E-06
Nucleotide-binding; alpha-beta plait	7.70E-08
proteasome assembly chaperone 2 proteasome assembly chaperone 2	1.52E-07
Glycoside hydrolase; subgroup; catalytic core	8.11E-10
Hypothetical protein	4.18E-11
Vg1 vitellogenin; partial sequence Vit vitellogenin; partial sequence vitellogenin vitellogeni	2.17E-08
protein Red	3.09E-08
PREDICTED: similar to SFRS protein kinase 2 PREDICTED: similar to SFRS protein kinase	3.38E-09

FAD-dependent pyridine nucleotide-disulphide oxidoreductase	8.90E-15
TuGSTd04 Glutathione S-transferase; class delta	1.45E-11
myosin heavy chain myosin heavy chain	1.60E-06
PREDICTED: similar to peritrophin 1 PREDICTED: similar to peritrophin 1	1.11E-07
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	1.28E-07
Armadillo-type fold	1.90E-08
Hypothetical protein	4.43E-11
GI21111	1.04E-07
Hypothetical protein	3.80E-06
UNCoordinated family member	6.72E-11
viral A-type inclusion protein	2.04E-11
SP26/M Low-density lipoprotein LDL receptor class A repeat SP26 Low-density lipoprotein LI	6.79E-07
TuABCC-26 ABC-transporter; class C;	4.20E-13
Double-stranded RNA binding	1.10E-12
Hypothetical protein	8.52E-08
Hypothetical protein	1.59E-11
Hypothetical protein	4.78E-10
hypothetical protein	1.96E-14
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	3.80E-08
hypothetical protein	8.25E-06
Hypothetical protein	1.65E-06
Hypothetical protein	3.47E-10
IQ calmodulin-binding region	1.72E-13
hypothetical protein	1.05E-07
MAM	6.33E-08
Phosphatidylinositol transfer protein-like; N-terminal	3.01E-07
SSPA1 Small Secreted Protein; family A Hypothetical protein	6.14E-10
ovo ovo ovo Zinc finger; C2H2 type	5.22E-09
iro Homeobox, conserved site Homeobox, conserved site	8.29E-11
Hypothetical protein	4.18E-08
PREDICTED: similar to CG31534 CG31534-PA	4.45E-09
hypothetical protein	5.39E-07
PREDICTED: similar to fragile site-associated protein PREDICTED: similar to fragile site-ass	1.63E-08
Hypothetical protein	4.33E-07
AP complex subunit beta	4.29E-10
Tubulin-tyrosine ligase	1.42E-07
FY-rich; N-terminal subgroup	6.87E-09
Hypothetical protein	1.47E-10
Hypothetical protein	7.12E-08
ECMP2 endonuclease-chitinase multifunctional protein chitinase	7.21E-12
Src homology-3; region	1.70E-11
PREDICTED: similar to leucine rich protein; putative PREDICTED: similar to leucine rich prot	4.13E-06
hypothetical protein	1.50E-06
nej nejire nej zf-TAZ CREB-binding protein homolog zf-TAZ TAZ zinc finger	1.30E-09
PREDICTED: hypothetical protein	1.86E-05
Hypothetical protein	2.84E-05
PREDICTED: 3-hydroxybutyrate dehydrogenase; type 1-like	1.57E-10

Histone deacetylase complex subunit SAP18	1.83E-08
ENSANGG00000014888 protein	1.66E-07
Hypothetical protein	2.44E-08
Hypothetical protein	6.44E-05
TuABCC-21 ABC-transporter; class C;	3.33E-10
Niemann-Pick C1 protein	6.40E-12
threonine dehydratase	1.80E-05
hypothetical protein	1.11E-09
short-chain dehydrogenase/reductase SDR	2.45E-05
serine/threonine protein kinase	2.17E-11
TuCCE37 Carboxyl/cholinesterase TuCCE-35 Carboxyl/cholinesterase	5.43E-08
Glycoside hydrolase; subgroup; catalytic core	1.46E-07
hypothetical protein IscW_ISCW017229	1.80E-10
Spz3 Cystine-knot cytokine	4.65E-08
Hypothetical protein	1.19E-07
hypothetical protein AaeL_AAEL007290	1.48E-07
Pleckstrin homology domain	3.96E-07
Peptidase S60; transferrin lactoferrin	5.05E-11
PREDICTED: similar to adenylate cyclase	1.27E-12
MUscle Attachment abnormal family member	9.01E-10
Hypothetical protein	2.19E-08
C-factor	1.50E-08
LSM domain, eukaryotic/archaea-type	1.71E-05
RecName: Full	1.14E-07
P-loop containing nucleoside triphosphate hydrolase	9.18E-10
Collagen IV; non-collagenous	7.54E-09
Hypothetical protein	1.19E-05
Hypothetical protein	1.05E-10
Transferrin family, iron binding site	3.82E-08
SIFa Neuropeptide precursor	1.10E-06
Prefoldin	2.80E-05
Hypothetical protein	5.03E-10
TuGSTd03 Glutathione S-transferase; class delta	6.93E-06
PREDICTED: similar to adenylate cyclase	2.22E-05
CPR 23 cuticle protein	6.09E-10
PREDICTED: UTP6; small subunit PREDICTED: UTP6; small subunit	1.54E-08
TuABCA-03 ABC-transporter; class A;	7.01E-11
Hypothetical protein	3.26E-09
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	1.25E-10
DM DNA-binding domain	2.60E-06
nucleolin protein Nsr1; putative	4.15E-10
Hypothetical protein	1.33E-08
short chain dehydrogenase/reductase family 16C; member 5	7.63E-09
PREDICTED: similar to astakine	1.26E-09
Tu_12344.3 cys-loop ligand-gated ion channel glycine receptor subunit beta precursor	2.44E-07
HR38 1 Hormone Receptor 38 1	1.22E-08
SLS Titin; Kettin I-connectin	1.16E-06

PREDICTED: similar to adenylate cyclase	4.74E-06
PREDICTED: similar to inorganic phosphate cotransporter; putative	2.63E-06
Hypothetical protein	1.11E-05
nuclear receptor coactivator 6	4.80E-12
transcription factor protein	0.0001008
Aldehyde dehydrogenase; N-terminal	5.51E-10
Armadillo-type fold	2.64E-09
PREDICTED: dachsous 1	3.41E-11
neurofibromin	2.56E-10
HR96-like h HR96-like nuclear receptor h NR1/3 member Possible NR1 or NR3 member? N	2.55E-08
BTB/Kelch-associated	6.20E-05
Tetraspanin/Peripherin	1.34E-10
PREDICTED: similar to limkain b1	1.21E-05
Hypothetical protein	1.64E-05
Diacylglycerol/phorbol-ester binding Diacylglycerol/phorbol-ester binding	2.84E-09
Hypothetical protein	3.11E-10
frataxin	4.47E-07
hybrid sensory histidine kinase in two-component regulatory system with EvgA	9.74E-05
dystrophin	6.73E-09
Centrosomal protein of 290kDa	6.96E-06
PREDICTED: similar to adenylate cyclase	3.51E-08
beta-mannosidase beta-mannosidase	1.77E-06
Kelch-type beta propeller	2.37E-07
Tu_GluCl6 cys-loop ligand-gated ion channel; possible allelic variant of tetur36g00090 TuGlu	2.55E-05
FoxN1 winged helix/forkhead transcription factor FoxN1/4a	0.0001608
PREDICTED: similar to Brg1	3.02E-05
Homeobox Zinc finger, C2H2-like Homeobox Zinc finger, C2H2-like Homeobox Zinc finger,	3.30E-09
nuclear factor related to kappa-B-binding protein	2.40E-09
hypothetical protein	3.08E-09
Fibroin hypothetical protein	4.88E-07
GE10168	2.56E-06
Pleckstrin homology	2.17E-08
UGT UDP-glycosyltransferase; teturUGT11 UGT UDP-glycosyltransferase Glycosyltransfer	1.56E-11
WTSP8 Wannes-Thomas Secreted Protein 8 Hypothetical protein	1.37E-10
Scv4 scavenger receptor activity	7.91E-09
conserved hypothetical protein	4.48E-06
Fibronectin; type III	4.64E-06
UGT UDP-glucuronosyl/UDP-glucosyltransferase UGT UDP-glucuronosyl/UDP-glucosyltrans	1.01E-10
rRNA-processing protein FCF1 homolog rRNA-processing protein FCF1 homolog	1.17E-07
latrophilin-like receptor	2.94E-06
Fibroin Fibrion Hypothetical protein	0.000136
Hypothetical protein	9.36E-05
DDT Zinc finger, PHD-type, conserved site DDT Zinc finger, PHD-type, conserved site	1.24E-09
Hypothetical protein	8.44E-08
hypothetical protein	1.36E-05
EF-Hand 1, calcium-binding site	1.47E-05
CUB	2.77E-08

Glycoside hydrolase; subgroup; catalytic core	1.02E-11
Hypothetical protein	3.75E-07
Hypothetical protein	1.43E-06
51 kDA subunit c NADH-quinone oxidoreductase; 51 kDa subunit;	8.36E-13
Transmembrane protein 223	4.77E-05
beta-spectrin	4.64E-10
zf-C2H2 Zinc finger; C2H2 type	2.17E-09
PH domain-like	1.97E-08
CYP385C3 Cytochrome P450 - CYP385C3	3.11E-07
PREDICTED: similar to E1a binding protein P400	1.24E-09
CYP392D3 Cytochrome P450 - CYP392D3	5.12E-11
PREDICTED: similar to Glucosylceramidase precursor PREDICTED: similar to Glucosylcera	2.12E-08
Mid1-interacting protein 1	1.44E-06
N Notch	5.85E-10
scavenger receptor class B; member 2	6.97E-11
TuABCC-08 ABC-transporter; class C;	2.39E-08
TeturLY6_UPAR13 LY6_UPAR protein Three finger domain protein TFD conserved hypoth	5.28E-06
GTF3C3 general transcription factor 3C polypeptide 3 general transcription factor 3C polype	4.46E-09
Voltage-dependent calcium channel, alpha-1 subunit, IQ domain	2.67E-08
BolA-2 BolA-like protein BolA-like protein	1.12E-06
SLCP1 Secreted low-complexity protein of unknown function hypothetical protein	7.42E-06
ALS similar to Acid labile subunit leucine-rich transmembrane protein; putative	7.41E-08
MAP1B protein MAP1B protein	5.13E-06
BTB/Kelch-associated	1.53E-06
Apple-like	4.04E-07
PREDICTED: similar to galactosamine	4.49E-07
AT-rich interactive domain-containing protein 5B	1.46E-08
PREDICTED: similar to Chaoptin precursor	3.58E-09
regulator of G-protein signaling 19	5.36E-06
TEP1	2.67E-07
polycomb complex protein BMI-1	4.79E-07
GTP-binding protein Rit1	2.29E-06
lambda-crystallin homolog	2.26E-10
TuGSTd14 Glutathione S-transferase; class delta	1.36E-08
Zinc finger, FYVE-related	2.17E-09
S-adenosyl-L-methionine-dependent methyltransferase	1.10E-06
hypothetical protein	3.04E-08
sialin	0.0045876
INneXin family member	0.0002535
Pre-SET zinc-binding sub-group	3.62E-10
LAC3 Immunoglobulin Family Cell Adhesion Molecule; putative Lachesin lachesin; putative	6.76E-07
Cytoskeleton-associated protein; CAP-Gly	6.20E-05
bone morphogenetic protein 1	6.11E-05
WTSP1b Wannes-Thomas Secreted Protein 1 WTSP1a Wannes-Thomas Secreted Protein 1	0.0001586
cytoplasmic polyadenylation element-binding protein 4	1.67E-06
Leucine-rich repeat; cysteine-containing subtype	6.15E-06
Hypothetical protein	6.05E-09

AT rich interactive domain 1A	7.45E-08
CYP389C8 Cytochrome P450 - CYP389C8	5.58E-06
Hypothetical protein	3.23E-08
Hypothetical protein	4.06E-06
Hypothetical protein	2.05E-12
MECP2 Methyl-CpG binding protein 2/3, C-terminal domain mbd2 Methyl-CpG binding protei	8.61E-09
PREDICTED: similar to fragile site-associated protein PREDICTED: similar to fragile site-ass	1.23E-07
spatacsin	8.44E-09
Hypothetical protein	1.55E-05
CHKB2 Choline/ethanolamine kinase; putative	3.58E-08
hypothetical protein	1.18E-05
Hypothetical protein	1.13E-06
WD40/YVTN repeat-like-containing domain	1.56E-10
LPHN2;1 Latrophilin-2; Calcium-independent alpha-latrotoxin receptor 2 PREDICTED: simila	1.56E-09
PLEKH1 Pleckstrin-homology domain PH domain/Phosphotyrosine-binding domain PTB PLEI	5.00E-08
ANKRD17 Ankyrin repeat-containing domain Ankyrin repeat-containing domain	5.04E-10
Hypothetical protein	1.68E-05
zinc finger protein 687 zinc finger protein 687	5.22E-10
Hypothetical protein	5.88E-10
GF11962	0.0001549
large proline-rich protein BAT2 large proline-rich protein BAT2	4.48E-07
cathepsin A	2.42E-11
TuPap-57 Cathepsin L-like TuPap-57 Cathepsin L-like	4.73E-09
Hypothetical protein	8.17E-06
Ror2 transmembrane receptor protein tyrosine kinase activity	6.95E-08
Dve dve; Ortholog of Drosophila melanogaster defective proventriculus dve dve; Ortholog of	1.17E-08
Vtg1 Lipid transport protein, beta-sheet shell Lipid transport protein, beta-sheet shell	2.25E-09
Peptidase S1, trypsin family, active site Peptidase S1, trypsin family, active site	5.27E-08
long-chain fatty acid transport protein 1	4.51E-12
Hypothetical protein	1.77E-06
PDZ2PH Pleckstrin-homology domain PH domain/Phosphotyrosine-binding domain PTB Ple	0.0003552
IGEGFSP Immunoglobulin-like fold Immunoglobulin-like fold	4.23E-05
Spatacsin	9.67E-07
hypothetical protein	5.16E-11
hypothetical protein DDB_G0288123	3.14E-09
Hypothetical protein	9.74E-05
NRT2 PIWI-related; RNA binding NRT2 RNA binding	1.65E-08
Hypothetical protein	8.08E-09
mediator of RNA polymerase II transcription; subunit 12 homolog	1.20E-09
DNA repair protein xp-c / rad4	1.65E-08
SCRT1 scratch homolog 1; zinc finger protein zf-C2H2 Zinc finger; C2H2 type	0.0002893
ss PAS fold-3 HLH PAS fold-3	7.78E-05
timeless	6.60E-09
	4.68E-10
DESP1 Cellulosome enzyme, dockerin type I DESP1 Cellulosome enzyme, dockerin type I D	1.78E-09
mutS protein homolog 4	7.46E-10
Hypothetical protein	3.81E-06

sialin; putative	2.35E-08
Hypothetical protein	1.30E-05
serine/threonine-protein kinase LATS1	2.59E-10
PREDICTED: ash1 PREDICTED: ash1	7.68E-11
TuCCE08 Carboxyl/cholinesterase TuCCE-08 Carboxyl/cholinesterase	1.49E-06
rfx5 Winged helix-turn-helix DNA-binding domain RFX_DNA_binding Winged helix-turn-helix	1.71E-08
hypothetical protein	9.89E-05
Hypothetical protein	1.10E-08
NEDD8-conjugating enzyme Ubc12	1.71E-07
cell wall surface anchor family protein	2.18E-10
PREDICTED: similar to NHL	8.75E-07
N Notch notch PREDICTED: neurogenic locus notch homolog protein 2-like	5.43E-09
atrial natriuretic peptide receptor 2 precursor	2.93E-06
intradiol ring-cleavage dioxygenase	2.21E-07
Hypothetical protein	2.46E-09
ase achaete-scute homolog 2 achaete-scute homolog 2	5.09E-05
P-loop containing nucleoside triphosphate hydrolase	5.56E-06
Hypothetical protein	0.0018335
PREDICTED: similar to CG18076-PB	2.71E-08
Hypothetical protein	3.47E-05
PREDICTED: similar to F-box/LRR-repeat protein 10	9.90E-10
integrin; alpha V	1.89E-08
Zinc finger; LIM-type	1.81E-07
DOCK10 Dedicator of cytokinesis protein 10/Zizimin-3 homologue.	1.57E-10
neurofilament-H; putative	1.25E-11
Leukocyte elastase inhibitor	1.35E-06
Nucleotide-binding alpha-beta plait domain	8.13E-07
PREDICTED: similar to glucose dehydrogenase	3.19E-05
transmembrane channel-like protein 3	0.001259
MobKL3 MOB kinase activator family MOB kinase activator family	2.64E-09
dynein heavy chain	7.29E-09
Hypothetical protein	2.34E-09
Hypothetical protein	0.0003109
Glycoside hydrolase; family 30	0.0006601
conserved hypothetical protein	1.81E-09
hypothetical protein	3.60E-10
Hypothetical protein	6.02E-06
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	0.0001965
DDM9-17 Domain of unknown function DUF3421 Domain of unknown function DUF3421	3.51E-05
Glycoside hydrolase/deacetylase, beta/alpha-barrel	2.86E-07
Armadillo-type fold	3.61E-10
transporter	2.23E-05
Hypothetical protein	5.15E-07
Zinc finger, C2H2	6.97E-08
Glutathione synthase, substrate-binding, eukaryotic	7.95E-10
dentin sialophosphoprotein precursor dentin sialophosphoprotein precursor	7.46E-07
Zinc finger, LIM-type	2.77E-09

Hypothetical protein	3.74E-07
ApoD3 Apolipoprotein D apolipoprotein D	0.0017233
Endoglin/CD105 antigen	1.27E-09
cAMP-specific 3;5-cyclic phosphodiesterase; putative cAMP-specific 3;5-cyclic phosphodiest	9.06E-07
TuCCE34 Carboxyl/cholinesterase TuCCE33 Carboxyl/cholinesterase TuCCE-33 Carboxyl/c	4.91E-07
PROS Homeobox protein Prospero	9.46E-08
SAPS domain family; member 3	0.0001814
Zinc finger; RING-type	1.44E-07
Hypothetical protein	8.40E-08
Hypothetical protein	8.00E-06
PREDICTED: remodeling and spacing factor 1	5.81E-09
zf-C2H2 Zinc finger; C2H2 type	1.67E-10
TumGRI mGluR-I GRM1 Metabotropic glutamate receptor homologue IR 3 ionotropic glutam	5.76E-05
Hypothetical protein	4.85E-05
mitochondrial ribosomal protein S31	4.08E-07
hypothetical protein	5.81E-07
TuABCC-14 ABC-transporter; class C TuABCC-14 ABC-transporter; class C;	3.47E-09
stan	3.40E-09
UGT UDP-glycosyltransferase; teturUGT13 UGT UDP-glycosyltransferase glycosyltransfera	3.24E-05
protein O-mannosyl-transferase 2	8.94E-10
Sterile alpha motif homology	1.14E-09
TuABCC-28 ABC-transporter; class C;	1.14E-06
nuclear receptor co-repressor 1	7.08E-10
CYP392E7 Cytochrome P450 - CYP392E7	1.11E-09
zf-C2H2 Zinc finger; C2H2 type zf-C2H2 Zinc finger; C2H2 type	4.01E-07
Hypothetical protein	1.08E-06
Hypothetical protein	8.70E-06
PIK-related kinase	2.84E-08
conserved hypothetical protein	1.32E-06
TuGSTd10 Glutathione S-transferase, C-terminal TuGSTd10 Glutathione S-transferase, C-te	3.50E-05
PhosphoLipase C family member	2.09E-10
TuABCA-06 ABC-transporter; class A;	1.69E-08
TuPap-7 Cathepsin B	6.81E-10
Hypothetical protein	9.06E-06
hypothetical protein	3.38E-09
CYP392A3 Cytochrome P450 - CYP392A3	0.0008119
DGK2 diacylglycerol kinase zeta homolog diacylglycerol kinase zeta	3.49E-07
TuPap-5 Cathepsin B	4.28E-10
PREDICTED: similar to myosin IIIA	4.71E-08
TuGSTm07 Glutathione S-transferase; class mu	0.0009203
zf-C2H2 Zinc finger; C2H2 type	8.49E-07
Hypothetical protein	8.42E-10
hypothetical protein	0.0002923
Membrane insertion protein; OxaA/YidC	2.68E-05
Protein of unknown function DUF2181	1.85E-08
PREDICTED: similar to arginine-glutamic acid dipeptide	6.05E-09
APC Armadillo-type fold APC Armadillo-type fold	1.31E-07

P-loop containing nucleoside triphosphate hydrolase P-loop containing nucleoside triphospha	4.11E-05
CG18265	8.56E-09
Hypothetical protein	1.94E-05
UGT UDP-glycosyltransferase; teturUGT02 UGT UDP-glycosyltransferase Glycosyltransfera	1.09E-07
chloride channel protein 2	1.52E-10
UGT UDP-glycosyltransferase; teturUGT25 UGT UDP-glycosyltransferase Glycosyltransfera	3.08E-08
GYF	5.02E-09
RE19971p RE19971p	2.62E-07
Cation channel complex component UNC80, N-terminal	1.45E-05
TuABCC-13 ABC-transporter; class C TuABCC-13 ABC-transporter; class C;	3.52E-06
TuPap-53 Cathepsin L	9.45E-06
ATP-NAD kinase; PpnK-type; all-beta	2.95E-06
SON DNA-binding protein isoform F	3.55E-06
hypothetical protein	7.01E-05
PREDICTED: similar to splicing factor u2af large subunit	1.39E-06
rutabaga	1.29E-09
Leucine-rich repeat; ribonuclease inhibitor subtype	1.76E-08
PREDICTED: signal-induced proliferation-associated 1 like 1	9.43E-09
Zinc finger; PHD-finger	4.99E-08
lipase 1 precursor lipase 1 precursor	2.06E-07
Zinc finger; C2H2-type	8.94E-06
disabled homolog 1 disabled homolog 1	4.13E-10
hormone-sensitive lipase	5.54E-10
hypothetical protein	2.27E-06
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	8.37E-09
Nose resistant-to-fluoxetine protein, N-terminal	0.0001587
PREDICTED: dedicator of cytokinesis 2	6.58E-09
Hypothetical protein	9.47E-08
Alpha/Beta hydrolase fold	6.16E-10
CAM calmodulin calmodulin	4.37E-06
TuPap-36 Cathepsin L	5.55E-09
Hypothetical protein	2.22E-08
Short-chain dehydrogenase/reductase SDR	1.51E-05
Hypothetical protein	6.52E-05
PREDICTED: sodium-dependent glucose transporter 1-like; partial	2.94E-06
RAB35; member RAS oncogene family	7.24E-05
Zinc finger FYVE domain-containing protein 26 Zinc finger FYVE domain-containing protein 2	2.20E-09
Hypothetical protein	8.34E-08
Apx/Shrm Domain 2	1.81E-08
PREDICTED: similar to Neural-cadherin precursor	3.20E-10
HBR Immunoglobulin/major histocompatibility complex, conserved site Immunoglobulin/majc	2.64E-07
Hypothetical protein	0.0001607
secreted protein; putative	1.29E-05
PREDICTED: similar to MRAS2; putative	6.16E-08
Alpha/Beta hydrolase fold	0.0006536
Ptx Homeobox, conserved site Homeobox Homeobox, conserved site	1.03E-05
Tu_Rdl1 cys-loop ligand-gated ion channel; Rdl-homolog TuGABA-01 GABA gated chloride c	1.73E-06

TuABCC-07 ABC-transporter; class C;	2.98E-08
PREDICTED: similar to TRAF6	2.93E-05
glycerol kinase	3.37E-07
CCEincTu14 Carboxyl/cholinesterase; incomplete CCEincTu15 Carboxyl/cholinesterase; inc	2.42E-05
Tetratricopeptide repeat	8.95E-06
carbamoylphosphate synthetase/aspartate transcarbamylase/dihydroorotase	4.36E-08
sna snail; zinc finger protein snail snail zinc finger protein	4.50E-07
TPAN-1 3-Pan modules Cell Surface Protein; antigen-2 PANR-1 Pan module-related Cell Su	1.62E-10
Armadillo-type fold	3.90E-09
Hypothetical protein	0.0010603
Rap/ran-GAP	3.37E-08
Hypothetical protein	0.0004112
TRP-interacting helix, InaF motif TRP-interacting helix, InaF motif	3.42E-06
latrophilin-like receptor	2.38E-10
Hypothetical protein	0.0009901
PREDICTED: similar to Activating signal cointegrator 1 complex subunit 3	3.47E-08
bifunctional aminoacyl-tRNA synthetase	7.62E-09
TLDc	4.94E-09
Hypothetical protein	3.90E-06
E2f4 E2F transcription factor, CC-MB domain E2F_TDP E2F transcription factor, CC-MB do	4.73E-10
Ribosomal protein L53, mitochondrial	1.15E-05
PREDICTED: similar to synaptotagmin XIV	4.10E-07
Histone deacetylase superfamily	2.03E-07
Hypothetical protein	2.07E-08
PHD finger protein 20	8.45E-07
zf-C2H2 zinc finger protein zf-C2H2 Zinc finger; C2H2 type	3.26E-08
HECW2 E3 ubiquitin-protein ligase	6.41E-10
phosphatidylethanolamine-binding protein	3.87E-05
Hypothetical protein	4.01E-07
Mediator complex, subunit Med1	8.64E-09
zinc finger prot zinc finger protein; u-shaped u-shaped	2.99E-08
CYP385C4 Cytochrome P450 - CYP385C4	1.19E-05
PREDICTED: hypothetical protein PREDICTED: hypothetical protein	1.10E-09
Fibroin Hypothetical protein	1.85E-05
Pleckstrin-homology domain PH domain/Phosphotyrosine-binding domain PTB	4.67E-07
hypothetical protein	6.40E-08
Hypothetical protein	0.0007612
Hypothetical protein	0.0005625
ApoD4 Apolipoprotein D chlorophyllide A binding protein precursor	0.0016141
hypothetical protein	1.13E-07
scribbled homolog	1.34E-09
Leukocyte elastase inhibitor	0.0020967
PDZ/DHR/GLGF	1.48E-05
leucine-rich transmembrane protein; putative	3.56E-06
hypothetical protein	8.63E-08
Mediator complex, subunit Med13, N-terminal, metazoa/fungi	2.16E-06
BTB/Kelch-associated BTB/Kelch-associated	0.000112

Hypothetical protein	9.14E-07
DNA repair protein RAD51 homolog 1	5.17E-06
Hypothetical protein	1.19E-05
Leucine-rich repeat domain, L domain-like	5.21E-05
Hypothetical protein	1.27E-06
PREDICTED: similar to ECM 18	3.02E-07
ARAP1 protein	3.59E-10
Peptidase C54	4.83E-09
Nbea neurobeachin; rugose protein neurobeachin neurobeachin	1.09E-08
Hypothetical protein	8.11E-06
glucosylceramidase; putative	1.76E-06
hypothetical protein	1.26E-06
Ankyrin repeat	5.32E-09
DNA topoisomerase 2-alpha DNA topoisomerase 2-alpha	1.29E-10
F-box WD 40 protein	1.30E-08
Acyltransferase 3	0.0003973
sox17 High mobility group box domain High mobility group box domain	5.52E-07
Hypothetical protein	3.44E-06
Tl-2 Toll-like receptor	3.03E-08
CYP392D4 Cytochrome P450 - CYP392D4	7.52E-07
Major facilitator superfamily associated domain	5.56E-07
PREDICTED: hypothetical protein	4.04E-08
WD40 repeat	3.88E-09
docking protein 4 docking protein 4	1.56E-07
Kr-2 Kr-2; Ortholog of Drosophila melanogaster Kruppel Kr-2 Kr-2; Ortholog of Drosophila me	8.84E-08
gamma-glutamyl hydrolase precursor	5.00E-08
Hypothetical protein	0.0004212
Hypothetical protein	4.73E-06
Fibroin Hypothetical protein	0.0002106
Tl-1 Toll-like receptor	1.14E-07
TFDP1 transcription factor Dp-1	5.09E-10
4-hydroxy-3-methylbut-2-enyl diphosphate reductase	4.17E-06
WD and tetratricopeptide repeats protein 1	3.36E-09
PAS	7.77E-09
GW182 M domain	1.64E-08
microtubule-actin crosslinking factor 1	1.05E-09
PREDICTED: phosphodiesterase 11A	3.52E-08
PREDICTED: similar to ubiquitin specific peptidase 9; X-linked; isoform 2	2.31E-08
Hypothetical protein	0.0003411
Hypothetical protein	1.10E-08
	3.13E-05
ribosomal protein S12	9.25E-08
AN1-type zinc finger protein 6	2.69E-09
Hypothetical protein	2.33E-06
Peptidyl-prolyl cis-trans isomerase; FKBP-type	1.44E-09
Ndufa4 NADH-ubiquinone reductase complex 1 MLRQ subunit-4 PREDICTED: NADH dehy	1.15E-07
Tubby C-terminal-like domain	3.86E-06

Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	3.28E-06
Hypothetical protein	4.48E-06
Proteasome subunit beta type-4 precursor	1.03E-09
Snf7 family	4.89E-09
ribosomal protein S3	4.03E-10
ribosomal protein L28	9.95E-10
Hypothetical protein	2.59E-07
PREDICTED: NADH dehydrogenase	1.05E-08
troponin I	4.00E-06
OSP2a Orphan secreted protein Hypothetical protein	8.94E-10
muscular protein 20	5.36E-06
SAC3/GANP/THP3	8.95E-07
Transport protein XK	1.85E-10
PREDICTED: similar to Prenyl	1.30E-08
DAP1 DAP1/DAPL1 VWF1 DAP1/DAPL1 DAP1/DAPL1	7.37E-10
Deoxyribonuclease II family protein	1.89E-07
39S ribosomal protein L16; mitochondrial precursor	5.50E-10
small subunit ribosomal protein 14	4.66E-10
TMP21-related	7.45E-09
protein AATF	4.75E-08
hypothetical protein	2.50E-07
Hypothetical protein	4.13E-05
3-hydroxyacyl-CoA dehydrogenase	1.58E-08
Acyl-CoA N-acyltransferase Acyl-CoA N-acyltransferase	7.06E-05
Hypothetical protein	0.000968
hypothetical protein	1.04E-05
TuENaC118 Na+ channel, amiloride-sensitive Tu_ENaC118 Na+ channel, amiloride-sensitiv	8.03E-06
PAR14 peptidyl-prolyl cis-trans isomerase NIMA-interacting 4; Parvulin-14; Rotamase Pin4	1.30E-08
PREDICTED: similar to ubiquinol-cytochrome c reductase; complex III subunit VII	4.92E-08
PSST NADH dehydrogenase; PSST subunit	3.55E-09
Hypothetical protein	7.06E-06
hypothetical protein	3.58E-06
Vg3 Vitellogenin 3 Vg3a Vitellogenin 3a Vg3 Vitellogenin 3 Vg3 Vitellogenin 3	3.82E-09
Acyl-CoA N-acyltransferase	1.54E-06
vesicular glutamate transporter 1	9.97E-06
myosin alkali light chain	6.33E-07
Hypothetical protein	0.0001204
Csp1c conserved secreted protein 1 Hypothetical protein	4.74E-10
Insulin-like growth factor-binding protein; IGFBP	2.12E-05
SCP-like extracellular	4.36E-07
F-box only protein 47	0.0034004
L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase L-aminoadip	0.0001303
GM2 activator protein	7.66E-11
Hypothetical protein	0.0016986
survival of motor neuron protein-interacting protein 1	9.37E-09
PREDICTED: similar to Kuzbanian-like CG1964-PA	9.81E-06
cuticle protein; putative	0.0002563

Major facilitator superfamily; general substrate transporter	1.75E-08
Active regulator of SIRT1	3.85E-06
troponin i troponin i	1.05E-05
LRRP1 Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	0.0005082
PREDICTED: solute carrier family 6 PREDICTED: solute carrier family 6	0.0005899
Hypothetical protein	2.48E-06
HEY2 hairy/enhancer-of-split related with YRPW motif 2	2.38E-06
Hypothetical protein	1.24E-08
Srrm2 protein	8.06E-10
Activated RNA polymerase II transcriptional coactivator p15	2.60E-08
PREDICTED: filamin B; beta	8.16E-07
ARF/SAR superfamily	7.55E-10
Cystatin domain	4.15E-07
Hypothetical protein	4.80E-10
exosome complex RNA-binding protein Rrp42	1.28E-06
CCAP-R 2 GPCR; cardioacceleratory peptide receptor	1.32E-05
exosome complex RNA-binding protein Rrp42	8.14E-09
D-3-phosphoglycerate dehydrogenase	9.06E-12
group 3 secretory phospholipase A2 precursor	2.81E-07
ATP synthase subunit delta; mitochondrial precursor	1.75E-08
Hypothetical protein	0.0006348
Hypothetical protein	0.0003121
eukaryotic translation initiation factor 4E	2.91E-06
Hypothetical protein	0.0010169
SGT1; suppressor of G2 allele of SKP1	3.11E-07
Insulin-like growth factor binding protein, N-terminal	1.86E-09
Immunoglobulin-like fold Immunoglobulin-like fold	1.12E-06
hypothetical protein	5.23E-08
grn likely ortholog of Dm grain transcription factor	8.03E-07
CDK5 and ABL1 enzyme substrate 1/2 CDK5 and ABL1 enzyme substrate 1/2	0.0004717
GRSP4 Glycine-rich secreted protein SSPD2 Small secreted peptide Hypothetical protein	0.0235354
Hypothetical protein	3.28E-05
jagunal	8.85E-09
RPGR	1.39E-08
C12orf31 homolog	1.13E-07
CYP392E10 Cytochrome P450 - CYP392E10	0.0009641
28S ribosomal protein S11; mitochondrial precursor	5.36E-07
Hypothetical protein	1.33E-08
Hypothetical protein	4.88E-05
MTCP1	8.62E-09
RAB5-interacting protein	1.05E-06
dynactin subunit 5	3.97E-07
conserved hypothetical protein	0.0001598
DNA-directed RNA polymerases I; II; and III subunit RPABC3	4.75E-09
dehydrogenase/reductase SDR family member 7 dehydrogenase/reductase SDR family mem	4.50E-09
Hypothetical protein	0.0005456
Zinc finger; C2H2-like	8.32E-07

Ato2 Protein atonal/lin-32 Atoh1a Protein atonal/lin-32 HLH Protein atonal/lin-32	5.86E-08
NGF1 Nerve growth factor-related Nerve growth factor-related	0.0002119
HCSP2 Hypothetical Cell Surface Protein Hypothetical protein	6.36E-07
CPR 16 cuticle protein	2.31E-06
hemolysin-type calcium-binding region	2.44E-07
Endoglin/CD105 antigen	2.71E-06
NADH-ubiquinone oxidoreductase ashi subunit	1.31E-08
EGF-like protein EGF-like protein	3.88E-07
GTP1/OBG	2.70E-05
eukaryotic translation initiation factor 6 eukaryotic translation initiation factor 6	5.49E-05
BCDO2-3 Beta;beta-carotene 9';10'-oxygenase; CMO-II BCO2-3 Beta;beta-carotene 9';10'-o	4.07E-05
Hypothetical protein	2.19E-05
Nuclear hormone receptor, ligand-binding domain	1.41E-05
Hypothetical protein	5.27E-10
U6 snRNA-associated Sm-like protein LSm4	7.42E-07
PREDICTED: similar to mitochondrial ribosomal protein S10	4.55E-08
glutaryl-CoA dehydrogenase	4.55E-10
Histone H4	1.42E-10
cytochrome b	0.0009407
cytoplasmic dynein 2 light intermediate chain 1	0.0008439
Hypothetical protein	0.0003635
Programmed cell death protein 5	2.14E-08
Lipocalin family protein	1.63E-07
muscular protein 20	1.09E-07
PREDICTED: similar to glucose dehydrogenase	7.54E-07
Hypothetical protein	2.00E-06
PHF5-like	3.53E-08
TuENaC133 Na+ channel/degenerin ENaC/DEG family protein Tu_ENaC133 Na+ channel/d	9.22E-06
Fcf2 pre-rRNA processing	4.48E-08
40S ribosomal protein S3a	8.11E-12
diphthamide biosynthesis protein; putative	1.85E-08
Manganese/iron superoxide dismutase; C-terminal	3.74E-09
Hypothetical protein	6.95E-09
Hypothetical protein	1.18E-06
60S ribosomal protein L27	1.15E-08
anaphase promoting complex subunit 11	4.17E-08
Hypothetical protein	1.83E-05
troponin i	3.04E-05
Hypothetical protein	4.59E-08
Hypothetical protein	3.46E-06
Cellular retinaldehyde-binding/triple function; C-terminal	9.33E-07
Hypothetical protein	0.0001636
TuABCH-17 ABC-transporter; class H pABC-27 ABC-transporter; putative;	0.000945
hypothetical protein	0.0001233
short-chain dehydrogenase/reductase SDR	5.71E-09
Myosin regulatory light chain 2; smooth muscle isoform	1.34E-07
Hypothetical protein	8.67E-08

Golgin subfamily A member 5	1.52E-09
ATP synthase E chain	5.39E-09
hypothetical protein	0.0018897
N-alpha-acetyltransferase 50; NatE catalytic subunit	5.91E-09
nucleoside diphosphate kinase B	6.18E-09
conserved hypothetical protein conserved hypothetical protein	3.92E-06
Hypothetical protein	2.46E-07
lambda-crystallin homolog	4.97E-10
PREDICTED: similar to mediator complex; subunit; putative	5.69E-07
hypothetical protein	0.005574
NPC2 Immunoglobulin E-set Immunoglobulin E-set	1.51E-09
Hypothetical protein	2.23E-05
guanosine 5'-monophosphate oxidoreductase	5.15E-09
hypothetical protein	4.17E-05
POMP Proteasome maturation protein	2.84E-07
ribosomal protein S18	3.39E-09
hypothetical protein	9.53E-09
DEAH	1.61E-06
Hypothetical protein	2.50E-10
LZY1;4 Conserved zygote-specific protein homologue LZY1;4 Conserved zygote-specific pro	8.70E-07
Low molecular weight phosphotyrosine protein phosphatase	1.66E-08
hypothetical protein	0.0001734
UPF0139 membrane protein C19orf56 homolog	2.10E-09
PREDICTED: similar to KIAA1919	0.0005258
hypothetical protein	0.0002678
Phytanoyl-CoA dioxygenase	2.30E-07
Hypothetical protein	2.39E-05
secreted salivary gland peptide; putative	0.0006959
ribosomal protein L12	2.85E-10
Hypothetical protein	1.45E-06
conserved hypothetical protein	2.94E-09
hypothetical protein	7.46E-07
ribosomal protein S16 ribosomal protein S16	2.86E-10
Molybdenum cofactor sulfurase, C-terminal	4.40E-10
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	6.53E-07
Protein of unknown function DUF1674	2.33E-07
MevPPD Diphosphomevalonate decarboxylase	3.81E-11
acid phosphatase-1	6.06E-08
Protein of unknown function DUF3128 Protein of unknown function DUF3128	1.89E-08
peroxisomal acyl-coenzyme A oxidase 3	1.13E-07
GRSP7 Glycine-rich secreted protein GRSP7 Glycine-rich secreted protein Hypothetical prc	1.98E-05
mitochondrial ribosomal protein S17	1.62E-07
Kelch-type beta propeller	2.37E-07
elongation of very long chain fatty acids protein 6	0.0001292
huntingtin interacting protein K	1.10E-08
Serine/threonine-protein kinase, active site	6.47E-05
PTPL1 Protein tyrosine phosphatase-like protein	4.78E-10

conserved oligomeric Golgi complex subunit 7	0.0002505
PREDICTED: similar to CG13913 CG13913-PA	1.76E-08
Hypothetical protein	3.64E-10
30S ribosomal protein S16	2.44E-07
Hypothetical protein	9.55E-09
G protein coupled receptor	1.18E-06
hypothetical protein	2.82E-06
Hypothetical protein	2.15E-08
tyrosinase	7.34E-05
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	2.12E-08
methyltransferase type 11 methyltransferase type 11	4.53E-09
Protein of unknown function DUF1358	5.48E-06
SUZ domain	1.98E-08
U6 snRNA-associated Sm-like protein LSm8	8.49E-08
Six-bladed beta-propeller; TolB-like	1.87E-10
Histone H2A.Z	6.30E-11
RNA-binding protein 8A	3.66E-09
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	0.0002206
PREDICTED: similar to CG12400 CG12400-PA	1.72E-08
SPH43 Serine protease homologue	0.0032676
SMAD domain, Dwarfin-type	5.74E-06
60S ribosomal protein L18a	1.84E-10
PE-PGRS family protein	3.98E-08
Hypothetical protein dentin sialophosphoprotein precursor	1.47E-07
Hypothetical protein	1.24E-05
PREDICTED: rCG19957-like	2.69E-07
PREDICTED: ribosomal protein L35a-like	2.12E-09
Hypothetical protein	5.11E-09
Hypothetical protein	2.11E-07
Hypothetical protein	3.12E-07
Hypothetical protein	0.0002311
NADH-ubiquinone oxidoreductase; chain 4L	3.35E-07
Small EDRK-rich factor 2	1.68E-06
TuGSTd16 Glutathione S-transferase; class delta	3.87E-06
GRSP8 Glycine-rich secreted protein Hypothetical protein	0.0017122
AGAP002847-PA	4.09E-11
PB1 protein PB1 protein	0.0003206
SSPF2 Small Secreted Protein; family F PRSP1 Proline-rich Secreted Protein Hypothetical	2.79E-11
PREDICTED: similar to mitochondrial ribosomal protein L40 CG5242-PA	2.67E-09
inositol 2-dehydrogenase	1.33E-08
NADH dehydrogenase	5.01E-07
intraflagellar transport protein 20 homolog	0.0001586
Galactose-binding domain-like	1.71E-06
Receptor expression-enhancing protein 5	3.72E-12
PREDICTED: similar to glucose dehydrogenase	0.000747
Small nuclear ribonucleoprotein Sm D2	1.24E-07
NHP2-like protein 1 NHP2-like protein 1	4.39E-07

40S ribosomal protein S2	3.70E-11
Hypothetical protein	0.0001814
PREDICTED: aquaporin-like	1.56E-07
MDL8 Immunoglobulin E-set Immunoglobulin E-set	5.65E-11
Hypothetical protein	1.62E-07
Agrin NtA	2.09E-06
Mitogen-activated protein-binding protein-interacting protein	5.35E-08
Hypothetical protein	0.0008105
Hypothetical protein	0.0002634
Hypothetical protein	3.12E-07
SPC25 Microsomal signal peptidase 25 kDa subunit. SPC25 Microsomal signal peptidase 25	6.25E-11
G-protein beta WD-40 repeat; region	1.91E-06
BET1 homolog	1.26E-08
CPAP 7 cuticular protein analogous to peritrophins 1-A	8.19E-06
Transmembrane protein 167 precursor	1.26E-07
DNA-directed RNA polymerase II subunit RPB4	3.65E-08
ribosomal protein S5	1.26E-10
lambda-crystallin homolog	2.51E-09
transmembrane protein 93	3.43E-07
HYP59 Hypothetical protein ZFC4-1 Protein with two C4-type Zn finger modules; maybe a ps	3.04E-08
Splicing factor 3B; subunit 5	1.90E-07
dehydratase	8.93E-06
PRA1 family protein 3	2.07E-11
hypothetical protein	1.24E-07
Hypothetical protein	0.0005203
Hypothetical protein	6.59E-09
PREDICTED: hCG1994130-like	2.86E-11
Hypothetical protein	4.62E-07
40S ribosomal protein S9	3.86E-11
PrtA Chitin binding protein; peritrophin-A Chitin binding protein; peritrophin-A	9.26E-06
ATP synthase subunit f; mitochondrial	1.24E-10
60S ribosomal protein L17	6.66E-11
hypothetical protein	5.70E-05
vacuolar protein sorting-associated protein VTA1 homolog	1.09E-10
Uev1A ubiquitin-protein ligase activity	1.64E-10
conserved oligomeric Golgi complex subunit 7	1.91E-05
MD-2-related lipid-recognition domain	3.15E-08
Hypothetical protein	8.38E-06
PREDICTED: similar to isolog of yeast sui1 and rice gos2; putative	6.51E-11
Hypothetical protein	4.56E-10
dolichyl pyrophosphate Man9GlcNAc2 alpha-1;3-glucosyltransferase	0.0003107
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	6.74E-05
Tubeta3 cys-loop ligand-gated ion channel; nicotinic acetylcholine receptor subunit beta 3 A	0.0001186
ribosomal protein L13	7.67E-11
phenylalanine hydroxylase phenylalanine hydroxylase	2.61E-09
Major facilitator superfamily; general substrate transporter Major facilitator superfamily; gener	7.91E-10
60S ribosomal protein L14	1.41E-09

dihydrofolate reductase dihydrofolate reductase	3.92E-07
Alpha/Beta hydrolase fold	1.98E-08
Hypothetical protein	6.06E-10
Sterile alpha motif homology	2.76E-06
Mitochondrial import inner membrane translocase subunit Tim16 Mitochondrial import inner n	1.81E-07
Immunodominant surface protein, Ehrlichia tandem repeat-containing	6.58E-10
HCSP1a Hypothetical Cell Surface Protein HCSP1 Hypothetical Cell Surface Protein HCSP1	9.57E-07
Hypothetical protein	2.70E-06
calcium release-activated calcium channel protein 1	1.46E-06
MOSPD2a PapD-like PapD-like	1.49E-06
GRSP16 Glycine-rich secreted protein Hypothetical protein	0.0059509
NADH dehydrogenase 1 alpha subcomplex subunit 13	1.62E-09
Hypothetical protein	7.48E-09
intradiol ring-cleavage dioxygenase	2.11E-06
Hypothetical protein	0.0001694
Tetratricopeptide-like helical domain	6.57E-07
Ribosomal protein S32, mitochondrial	7.11E-08
Protein kinase-like domain	1.03E-07
Chitin binding protein; peritrophin-A	1.80E-05
Domain of unknown function DUF2236	1.35E-06
Protein Pet100	5.78E-08
c-fos AP-1 transcription factor AP-1 transcription factor	1.50E-11
Hypothetical protein	8.85E-05
Cyclin-dependent kinases regulatory subunit 1	8.07E-10
Hypothetical protein	2.67E-05
peptidyl-tRNA hydrolase	4.15E-07
DSS1/SEM1	1.70E-06
outer membrane lipoprotein Blc	1.32E-09
Hypothetical protein	2.82E-06
PREDICTED: similar to limkain b1	1.90E-07
PREDICTED: transmembrane inner ear-like	0.0008748
ATG4 autophagy related 4 homolog A	4.88E-12
transmembrane protein 17	0.0006095
UGT UDP-glycosyltransferase; teturUGT71 UGT UDP-glycosyltransferase glycosyl transfer	3.96E-06
Hypothetical protein	6.37E-10
Cytochrome c oxidase subunit VIc	1.16E-08
PREDICTED: similar to ECM 18 PREDICTED: similar to ECM 18	6.45E-06
dual oxidase maturation factor 1	1.11E-08
M-phase phosphoprotein 6	1.44E-06
Immunoglobulin E-set	2.62E-06
ribosomal protein L13	3.84E-07
chitinase	2.38E-12
MSX-2 Ribosomal protein L13 domain Ribosomal protein L13 domain	1.25E-09
ribosomal protein L55; putative	1.39E-08
TuABCG-11 ABC-transporter; class G TuABCG-09 ABC-transporter; class G;	2.59E-09
Hypothetical protein	0.0006307
signal peptidase complex subunit 1	2.54E-08

agrin agrin	6.09E-06
dopamine receptor D2	2.00E-07
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	4.64E-09
eukaryotic translation initiation factor 4E	2.14E-11
TeturLY6_UPAR15 LY6_UPAR protein Three finger domain protein TFD Hypothetical prote	0.0002105
TGF-beta-inducible nuclear protein 1	1.12E-10
solute carrier family 6	4.60E-07
Hypothetical neuropeptide precursor hypothetical protein	0.0001084
TuGSTd11 Glutathione S-transferase; class delta TuGSTd11 Glutathione S-transferase; clas	4.02E-08
Hypothetical protein	1.14E-09
phosphatidylethanolamine-binding protein	5.52E-09
NijA homologue of insect Ninjurin A ninjurin a	2.50E-06
40S ribosomal protein S11	1.40E-10
AkrB2 Aldo/keto reductase/potassium channel subunit beta Aldo/keto reductase/potassium c	2.48E-11
Uncharacterised domain KxDL Uncharacterised domain KxDL	7.72E-08
Hypothetical protein	1.88E-06
TiTiN family member	2.37E-07
Hypothetical protein	0.0005549
Hypothetical protein	1.55E-06
Hypothetical protein	0.0001311
Hypothetical protein	0.0001951
TeturLY6_UPAR20 LY6_UPAR protein Three finger domain protein TFD conserved hypoth	1.88E-08
adenylate kinase 1	6.10E-07
NADH dehydrogenase	3.15E-09
40S ribosomal protein S19	1.07E-10
Oxidoreductase-like, N-terminal Oxidoreductase-like, N-terminal	1.67E-05
MDL9 Immunoglobulin E-set Immunoglobulin E-set	4.17E-13
Hypothetical protein	8.88E-11
Hypothetical protein	0.0001703
Zinc finger; C2H2-type	1.20E-08
Roc1a Roc1a RING-box protein 1	1.63E-09
Hypothetical protein	0.0001984
hypothetical protein	1.49E-07
PREDICTED: ectonucleotide pyrophosphatase/phosphodiesterase 5	2.32E-11
Hypothetical protein	9.50E-06
membrane glycoprotein LIG-1; putative membrane glycoprotein LIG-1; putative	4.49E-05
Hypothetical protein	4.68E-05
cysteine synthase A	2.25E-11
RecName: Full	0.0001605
Hypothetical protein	2.42E-07
Pleckstrin-homology domain PH domain/Phosphotyrosine-binding domain PTB	1.68E-06
GK24554	1.44E-06
cysteine and glycine-rich protein 3	4.68E-08
ADP-ribosylation factor related protein 1	1.13E-05
nucleoprotein	4.19E-11
P-loop containing nucleoside triphosphate hydrolase	3.31E-08
UNCoordinated family member	1.57E-09

Arginase	7.58E-09
MD-2-related lipid-recognition domain	0.001003
Ribosomal protein L21e, conserved site	7.52E-11
Hypothetical protein	1.59E-07
Hypothetical protein	7.61E-09
Citrate synthase-like; core	5.22E-11
trafficking protein particle complex subunit 2	1.29E-06
hatching enzyme	1.10E-05
Sm-like protein Lsm7/snRNP-G	4.26E-09
U6 snRNA-associated Sm-like protein LSm2	1.50E-06
Hypothetical protein	2.43E-05
Hypothetical protein	0.0001668
hypothetical protein	3.82E-11
signal peptidase I	5.96E-08
Hypothetical protein	3.65E-10
putative gut cathepsin L-like cysteine protease	2.16E-07
dimethylaniline monooxygenase dimethylaniline monooxygenase	6.77E-05
ribosomal protein S10	4.37E-11
PLAT4 PLAT single domain protein PLAT/LH2 single domain protein; related Hypothetical	2.24E-12
Hypothetical protein	1.17E-05
CBSP1 Chitin binding domain Chitin binding domain	6.38E-08
H/ACA ribonucleoprotein complex subunit 3 H/ACA ribonucleoprotein complex subunit 3	4.03E-07
Hypothetical protein	1.99E-05
Hypothetical protein	3.15E-08
Hypothetical protein	2.43E-06
CYP389C9 Cytochrome P450 - CYP389C9	6.39E-06
Hypothetical protein	8.91E-10
Hypothetical protein	8.80E-11
lethal	5.15E-06
zinc carboxypeptidase	5.00E-07
thioredoxin	1.82E-09
Glycosyl transferase; family 31	9.97E-10
BCDO2-1 Beta;beta-carotene 9';10'-oxygenase; CMO-II BCO2-1 Beta;beta-carotene 9';10'-o	0.0001354
Signal recognition particle 9 kDa protein Signal recognition particle 9 kDa protein	1.32E-09
FUCTCb alpha-1;3-fucosyltransferase C	3.74E-07
PREDICTED: protein tyrosine phosphatase 4a1-like	1.36E-09
Hypothetical protein	2.27E-05
Vg5 Vitellogenin 5	5.37E-12
NADH dehydrogenase iron-sulfur protein 6; mitochondrial precursor	3.78E-10
CD63 antigen	3.27E-05
glutathione peroxidase	5.00E-05
Hypothetical protein	9.88E-05
Hypothetical protein	2.52E-05
DDM9-5 Domain of unknown function DUF3421 Domain of unknown function DUF3421	2.11E-06
peptidyl-prolyl cis-trans isomerase	0.0004904
Hypothetical protein	2.48E-06
Hypothetical protein	2.94E-05

Mitochondrial 28S ribosomal protein S33	5.95E-09
solute carrier family 25	3.03E-10
40S ribosomal protein S30	2.56E-11
Mitochondrial import inner membrane translocase subunit Tim13	1.76E-08
archease archease	6.61E-09
hypothetical protein	4.48E-05
MICOS complex subunit Mic13	4.94E-11
CPAP 12 cuticular protein analogous to peritrophins 1-A	7.66E-10
60S ribosomal protein L11	1.57E-10
hypothetical protein	5.90E-09
Hypothetical protein	1.69E-08
TuENaC91 Na+ channel, amiloride-sensitive ENaC91 Na+ channel, amiloride-sensitive Na+	0.0001031
UGT UDP-glycosyltransferase; teturUGT77 UGT UDP-glycosyltransferase glycosyltransfera	1.51E-10
PREDICTED: similar to Williams-Beuren syndrome chromosome region 27-like	4.54E-11
51 kDa subunit c NADH-quinone oxidoreductase; 51 kDa subunit	3.88E-10
Hypothetical protein	1.65E-05
60S ribosomal protein L31	1.54E-09
LKAP32 Limkain-b1;	1.41E-09
DRAP deaminase	1.37E-07
Hypothetical protein	0.0003822
CRAL-TRIO lipid binding domain	1.28E-07
patched patched	2.42E-12
Enhancer of rudimentary homolog	1.05E-09
tropomyosin	9.24E-06
Hemopexin-like repeats	8.79E-05
WASH complex subunit strumpellin	8.82E-08
Small EDRK-rich factor 2	3.00E-09
Hypothetical protein	1.31E-08
Probable protein BRICK1	7.05E-07
lipase 1 precursor	2.77E-10
Hypothetical protein	0.0001895
Hypothetical protein	0.0002039
transcription initiation factor TFIID subunit 11 transcription initiation factor TFIID subunit 11	5.13E-07
SSPF15 Small Secreted Protein; Family F Hypothetical protein	1.09E-05
Hypothetical protein	3.59E-08
CPAP 10 cuticular protein analogous to peritrophins 1-A	5.99E-08
Translocon-associated protein subunit delta precursor	2.50E-10
Hypothetical protein	1.22E-05
Cytochrome c oxidase assembly protein PET191	3.44E-08
hypothetical protein	1.88E-06
GRSP1 Glycine-rich secreted protein Hypothetical protein	0.0002709
CPR 6 cuticle protein CPR 6 cuticle protein	9.97E-05
Hypothetical protein	9.48E-07
deoxyribose-phosphate aldolase	1.96E-06
Cytochrome c oxidase; subunit VIa	6.02E-11
U6 snRNA-associated Sm-like protein LSm5	7.67E-06
Translocon-associated protein subunit gamma	1.52E-11

DBI / ACBP Diazepam Binding Inhibitor DBI aka Acyl-CoA binding protein ACBP	1.94E-08
cytochrome c oxidase polypeptide VIII	2.49E-06
Lklf krueppel-like factor 2	0.0002637
Zinc finger, RING/FYVE/PHD-type	3.71E-07
Hypothetical protein	2.59E-08
PREDICTED: similar to CG12400 CG12400-PA	5.75E-08
High mobility group; HMG1/HMG2	6.18E-05
Hypothetical protein	0.0001011
PREDICTED: similar to Glucosylceramidase precursor	4.26E-05
hypothetical protein	9.77E-10
suppressor of Ty 3 homolog	7.45E-13
TF2H5 General transcription factor IIH subunit 5 General transcription factor IIH subunit 5	4.16E-08
mitochondrial import receptor subunit TOM40 homolog mitochondrial import receptor subunit	1.27E-08
Hypothetical protein	0.0004708
Hypothetical protein	9.30E-05
UGT UDP-glucuronosyl/UDP-glucosyltransferase UGT UDP-glucuronosyl/UDP-glucosyltrans	6.33E-08
PREDICTED: similar to AGAP011648-PA	1.44E-05
SSPB4 Small secreted protein; family B Hypothetical protein	5.16E-11
Hypothetical protein	7.56E-05
PPIL3 Cyclophilin-type peptidyl-prolyl cis-trans isomerase, conserved site PPIL3 Cyclophilin-	4.42E-08
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	1.40E-07
cysteine and glycine-rich protein 3	2.48E-10
SPH35 Serine protease homologue	4.56E-09
hypothetical protein	8.23E-07
alpha-glucosidase	5.41E-09
sodium-dependent glucose transporter 1	8.30E-05
Cytochrome b-c1 complex subunit 6; mitochondrial precursor	1.63E-11
40S ribosomal protein S27	3.70E-11
pathogenesis-related maize seed protein	6.30E-07
BTB/POZ-like	1.93E-06
TeturLY6_UPAR8 LY6_UPAR protein Three finger domain protein TFD conserved hypothe	2.83E-06
3-oxoacyl-acyl-carrier-protein reductase	1.10E-08
hypothetical protein	3.72E-08
Hypothetical protein	1.50E-06
Hypothetical protein	0.0001902
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	2.13E-08
Ubiquinol-cytochrome C reductase complex; 6.4kDa protein	2.62E-09
Hypothetical protein	4.66E-06
Hypothetical protein	1.65E-06
DNA-directed RNA polymerases I; II; and III subunit RPABC5	4.40E-06
40S ribosomal protein S15	1.51E-11
prefoldin subunit 6	5.26E-09
Hypothetical protein	3.35E-09
elongase; putative	5.55E-07
hypothetical protein	2.15E-06
P-loop containing nucleoside triphosphate hydrolase	1.03E-07
Hypothetical protein	5.80E-09

CYP392B1 Cytochrome P450 - CYP392B1	4.82E-05
hlx H2.0-like homeobox protein	6.72E-06
TuOsp1 orphan secreted protein Osp1 orphan secreted protein Hypothetical protein	5.64E-06
Hypothetical protein	5.91E-13
Ribosomal protein L34e, conserved site	1.48E-10
PREDICTED: similar to FYVE-finger-containing Rab5 effector protein rabenosyn-5	7.42E-11
SAP domain-containing ribonucleoprotein	5.99E-11
Pyruvate kinase; barrel	2.46E-09
Hypothetical protein	1.58E-07
sodium-dependent multivitamin transporter	1.27E-06
Hypothetical protein	6.22E-09
Hypothetical protein	1.63E-08
Hypothetical protein	4.80E-06
Stress-associated endoplasmic reticulum protein 1	1.34E-10
CuffL5 Cutoff-like protein CuffL5 Cutoff-like protein Hypothetical protein	1.39E-06
Vacuolar ATP synthase subunit e 1	9.23E-09
C-type lectin-like	4.27E-08
ribosomal protein S26	1.20E-11
PREDICTED: similar to AGAP003567-PA	4.38E-11
Hypothetical protein	1.43E-08
SSPA5 Small Secreted Protein; family A Hypothetical protein	2.23E-09
LYR motif-containing protein 1	9.42E-09
Male sterility, NAD-binding	1.29E-07
lysosomal alpha-glucosidase precursor	1.04E-09
Mpv17/PMP22	7.73E-06
MDL12 Immunoglobulin E-set Immunoglobulin E-set	1.42E-11
Hypothetical protein	1.06E-08
hypothetical protein	2.25E-05
Hypothetical protein	3.81E-07
40S ribosomal protein S20	2.82E-10
TuCPI-20 Cystatin hypothetical protein	5.69E-05
Vitellinogen, open beta-sheet, subdomain 1	4.03E-09
hydroxymethylglutaryl-CoA lyase	1.12E-10
Hypothetical protein	9.61E-10
3-oxoacyl-acyl-carrier-protein reductase	0.0002169
DnaJ	2.02E-07
Hypothetical protein	6.49E-05
GK22478	2.73E-08
Apple-like	5.79E-08
Uncharacterised protein family UPF0390	3.91E-10
TuGR99 Chemosensory Receptor; Gustatory receptor family Hypothetical protein	6.70E-08
RPB7 DNA-directed RNA polymerases I; II; and III 7kDa polypeptide	2.88E-09
peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	5.38E-06
zeta-sarcoglycan	2.38E-05
Phospholipase B-like	1.07E-10
3-oxoacyl-acyl-carrier-protein reductase	1.37E-05
SSPC3 Small Secreted Protein; family C Hypothetical protein	0.0011311

Galactose-binding domain-like	5.39E-05
Hypothetical protein	1.77E-08
Hypothetical protein	4.19E-08
60S ribosomal protein L35 60S ribosomal protein L35	1.62E-11
Hypothetical protein	6.92E-09
Mannose-6-phosphate receptor; binding	3.77E-10
Intradiol ring-cleavage dioxygenase, C-terminal Intradiol ring-cleavage dioxygenase, C-termi	1.36E-11
Hypothetical protein	3.30E-05
Hypothetical protein	7.58E-10
TuGSTm05 Glutathione S-transferase; class mu	4.26E-08
40S ribosomal protein S23	4.09E-11
SJCHGC06741 protein	5.49E-07
short-chain dehydrogenase/reductase SDR short-chain dehydrogenase/reductase SDR	9.30E-06
TuENaC122 Na+ channel, amiloride-sensitive Tu_ENaC122 Na+ channel, amiloride-sensitiv	4.33E-05
vitellogenin1	1.79E-12
ribosomal protein L26	1.65E-11
phosphoglucomutase phosphoglucomutase	2.15E-07
elongase; putative	1.64E-08
Hypothetical protein	5.20E-11
LSM domain, eukaryotic/archaea-type	9.85E-09
GRSP11 Glycine-rich secreted protein GYGSP1 Secreted protein with GYG repeats Hypoth	8.24E-11
Hypothetical protein	4.48E-10
Protease inhibitor I4; serpin	1.03E-10
PREDICTED: similar to peritrophin 1 PREDICTED: similar to peritrophin 1	1.76E-06
protein transport protein Sec61 subunit beta	1.29E-11
Mitochondrial 28S ribosomal protein S21	2.52E-10
protein-tyrosine sulfotransferase 2 protein-tyrosine sulfotransferase 2	1.73E-12
ubiquitin	3.37E-11
Rtf1; Paf1/RNA polymerase II complex component; homolog	1.45E-07
P-loop containing nucleoside triphosphate hydrolase	4.29E-09
PROM prominin-like	2.38E-09
Leucine-rich repeat domain, L domain-like	1.12E-07
60S ribosomal protein L44	6.80E-11
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	3.88E-09
Hypothetical protein	1.15E-06
Protein of unknown function DUF1075	2.09E-08
Ubiquitin-fold modifier-conjugating enzyme 1	4.00E-08
saccharopine dehydrogenase	1.52E-08
Hypothetical protein	6.56E-06
Protein-tyrosine phosphatase; low molecular weight	1.24E-09
Complex 1 LYR protein	3.46E-08
Ubiquinol-cytochrome C reductase; UQCRX/QCR9-like	3.54E-10
lethal	2.05E-09
SSPD Small Secreted Protein; Family D; hypothetical Hypothetical protein	3.48E-11
Hypothetical protein	8.73E-05
U6 snRNA-associated Sm-like protein LSm3	2.24E-10
ATP synthase subunit g; mitochondrial	3.20E-11

Hypothetical protein	2.03E-08
apolipoprotein D	3.92E-08
Major facilitator superfamily; general substrate transporter	9.31E-10
DnaJ	4.75E-09
TuPap-32 Cathepsin L	4.54E-12
hypothetical protein	2.53E-07
nematoblast-specific protein	1.11E-09
Hypothetical protein	6.16E-07
Hypothetical protein	1.70E-08
hypothetical protein	4.73E-10
Hypothetical protein	6.05E-09
viral A-type inclusion protein	6.52E-10
Concanavalin A-like lectin/glucanase	1.68E-06
TuABCA-05 ABC-transporter; class A;	1.93E-09
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	8.82E-06
BTB/Kelch-associated	1.45E-11
BolA-2 BolA-like protein BolA-like protein	7.76E-08
Hypothetical protein	2.99E-06
lethal	2.08E-12
Hypothetical protein	0.0003042
Hypothetical protein	7.35E-08
Hypothetical protein	5.20E-09
Hypothetical protein	1.62E-09
Hypothetical protein	2.51E-05
Hypothetical protein	2.64E-07
Renin receptor-like	5.12E-11
TPAN-3 3-Pan module Cell Surface Protein; antigen-2 PANR-3 Pan module-related Cell Surf	3.36E-08
Hypothetical protein	1.22E-07
Insect antifreeze protein	5.17E-07
Hypothetical protein	5.05E-07
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	7.18E-09
Hypothetical protein	5.49E-10
Alkaline phosphatase-like, alpha/beta/alpha	5.33E-08
S-adenosyl-L-methionine-dependent methyltransferase	1.95E-05
TuGSTm06 Glutathione S-transferase; class mu	2.89E-11
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	2.16E-06
LZY1;5 Conserved zygote-specific protein homologue LZY1;5 Conserved zygote-specific pro	1.29E-06
immediate early response 3-interacting protein 1	3.44E-09
Myosin regulatory light chain 2; smooth muscle isoform	1.81E-10
TuCCE70 Carboxyl/cholinesterase TuCCE-60 Carboxyl/cholinesterase	9.50E-12
CSPCA1 CUB domain CUB domain	7.67E-06
PREDICTED: similar to AGAP011635-PA	2.05E-11
Hypothetical protein	6.43E-06
PREDICTED: similar to Bardet-Biedl syndrome 7	1.15E-07
sodium-dependent phosphate transport protein 2B	5.81E-09
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	4.44E-09
26S proteasome non-ATPase regulatory subunit 9	6.09E-09

Translation machinery associated TMA7	4.19E-10
antigen B membrane protein	8.45E-06
Bromo adjacent homology BAH domain	6.76E-05
ApoD22 Apolipoprotein D precursor Lipocalin family protein	8.65E-06
	2.34E-06
hypothetical protein	5.90E-06
Myosin regulatory light chain 2; smooth muscle isoform	2.35E-09
Hypothetical protein	1.38E-10
MGR2 homolog	2.25E-09
mago mago nashi mago nashi	2.55E-10
Hypothetical protein	5.25E-06
ApoD21 Apolipoprotein D precursor ApoD21 Apolipoprotein precursor Lipocalin family prote	8.65E-09
CYP392A14 Cytochrome P450 - CYP392A14	2.46E-10
MDL2 Immunoglobulin E-set Immunoglobulin E-set	2.18E-08
Protein of unknown function DUF3743	1.09E-08
copper chaperone copper chaperone	1.03E-08
TuPap-14 Cathepsin B	4.52E-06
Insect antifreeze protein Insect antifreeze protein	1.19E-09
transketolase	3.82E-06
CPR X cuticle protein; putative CP X cuticle protein; putative cuticle protein; putative cuticl	1.50E-06
aryl hydrocarbon receptor nuclear translocator	5.96E-08
hypothetical protein IscW_ISCW011638	7.75E-10
aldose 1-epimerase	4.26E-10
Hypothetical protein	1.01E-06
40S ribosomal protein S13 40S ribosomal protein S13	8.71E-12
60S ribosomal protein L22	6.93E-11
60S ribosomal protein L30	4.72E-12
LZY1;3 conserved zygote-specific protein homologue LZY1;3 conserved zygote-specific prot	4.85E-09
Hypothetical protein	7.40E-05
zinc/iron transporter; putative zinc/iron transporter; putative	5.78E-08
Hypothetical protein	1.16E-06
LMPT Zinc finger, LIM-type Zinc finger, LIM-type	4.67E-08
Granulin	1.29E-11
fumarylacetoacetase	7.40E-15
Alpha/Beta hydrolase fold	8.74E-07
PREDICTED: coiled-coil-helix-coiled-coil-helix domain-containing protein 8-like	3.24E-07
Hypothetical protein	3.07E-05
large subunit ribosomal protein 23 large subunit ribosomal protein 23	3.05E-11
Hypothetical protein	8.94E-06
Hypothetical protein	2.22E-05
Hypothetical protein	2.69E-05
	2.32E-07
Cysteine peptidase, asparagine active site	5.14E-13
dolichyl-phosphate mannosyltransferase polypeptide 3	7.10E-08
BTB	1.30E-07
Hypothetical protein	1.19E-11
ATP-sensitive inward rectifier potassium channel 12	8.72E-08

Hypothetical protein	2.02E-11
Hypothetical protein	1.45E-11
Hypothetical protein	9.75E-10
zinc finger protein 183 zinc finger protein 183	3.08E-13
Hypothetical protein	1.17E-10
ATP synthase lipid-binding protein; mitochondrial precursor	1.91E-12
TuENaC08 Na+ channel, amiloride-sensitive ENaC08 Na+ channel, amiloride-sensitive ENa(	4.63E-06
Rp49 Ribosomal protein 49	6.29E-12
candidate tumor suppressor protein	7.75E-10
CTPS1 CTP synthase 1 CTP synthase 1	2.36E-11
metallothionein	8.52E-12
Hypothetical protein	1.27E-06
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	7.71E-07
Fibronectin; type III-like fold	3.17E-10
Hypothetical protein	1.57E-06
GE13940	1.99E-12
ATP synthase subunit epsilon; mitochondrial	4.14E-08
dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 4	3.11E-07
Hypothetical protein	1.26E-06
short chain dehydrogenase	1.87E-12
SPH7 Serine protease homologue SPH Serine protease homologue	1.16E-06
Hypothetical protein	1.90E-11
26S proteasome non-ATPase regulatory subunit 7	1.14E-09
Selenoprotein SelK/SelG	2.84E-11
Hypothetical protein	6.07E-07
Hypothetical protein	0.0007345
Golgi-associated plant pathogenesis-related protein 1	6.48E-10
LZY1;2 Conserved zygote-specific protein homologue LZY1;2 Conserved zygote-specific pro	8.48E-10
Translation initiation factor eIF-2B subunit alpha Translation initiation factor eIF-2B subunit al	3.70E-05
Hypothetical protein	4.03E-09
GRSP10 Glycine-rich secreted protein GYGSP2 Secreted protein with GYG repeats Hypoth	3.33E-09
protein kinase	3.02E-10
Tyrosyl-DNA phosphodiesterase	6.13E-06
CPR G Putative cuticle protein	3.66E-06
Hypothetical protein	8.19E-10
Hypothetical protein	6.48E-07
Cox20/FAM36A	6.40E-10
Hypothetical protein	7.36E-06
PREDICTED: filamin B; beta	7.61E-06
Hypothetical protein	3.80E-12
Hypothetical protein	8.31E-13
SRSP1 Serine-rich secreted protein LSPA1 Large secreted protein; family A LSPA1 Large s(	7.58E-07
Hypothetical protein	1.60E-11
galactokinase	3.13E-09
Hypothetical protein	1.59E-11
Myeloma-overexpressed 2-like	3.70E-10
serpin 9 inhibitory serine protease inhibitor	1.94E-05

Hypothetical protein	1.10E-08
Nse4	1.49E-08
50S ribosomal protein L14	5.61E-07
mitochondrial intermembrane space import and assembly protein 40	1.43E-09
60S ribosomal protein L36	1.47E-11
Protein-tyrosine phosphatase-like	4.63E-05
Leucine-rich repeat domain, L domain-like	1.54E-09
SERP Secreted Protein with 8aa repeat structure Hypothetical protein	7.90E-07
Hypothetical protein	8.93E-06
Cytochrome c oxidase assembly factor 3, mitochondrial	3.81E-09
Reeler domain	9.76E-06
Rpf2p Brix domain Brix domain	7.66E-07
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	7.20E-05
Hypothetical protein	1.50E-06
RPS7 ribosomal protein S7 ribosomal protein S7	7.44E-15
intradiol ring-cleavage dioxygenase	1.31E-11
SacC1 Levanase; Beta-D-fructofuranosidase; secreted levanase	2.38E-09
Hypothetical protein	2.93E-10
Hypothetical protein	5.11E-08
PREDICTED: hypothetical protein	4.50E-08
CG1950-PA	8.03E-12
Concanavalin A-like lectin/glucanase	8.43E-10
Hypothetical protein	2.46E-08
Hypothetical protein	1.56E-06
SP68 Serine proteases, trypsin family, histidine active site Serine proteases, trypsin family, h	7.60E-06
Carbohydrate-binding-like fold	2.17E-07
UGT UDP-glycosyltransferase; teturUGT37 UGT UDP-glycosyltransferase Glycosyltransfera	4.18E-07
HAUS augmin-like complex subunit 6, N-terminal	5.80E-09
Intradiol ring-cleavage dioxygenase, core Intradiol ring-cleavage dioxygenase, core Intradiol	2.01E-08
CPAP 3 cuticular protein analogous to peritrophins 1-A	1.26E-09
hypothetical protein	8.36E-07
CHT7 chitinase chitinase	2.98E-06
exostosin-1	4.61E-08
tubulin gamma-1 chain	2.79E-06
TMCO7 RNA polymerase II assembly factor Rtp1, C-terminal RNA polymerase II assembly f	8.18E-13
TuPap-55 Cathepsin L-like	4.13E-07
40S ribosomal protein S21	1.43E-12
60S ribosomal protein L37	1.01E-12
SSPG1 Small secreted protein; Family G Hypothetical protein	1.02E-08
SP22 Serine protease	5.84E-07
Hypothetical protein	4.86E-08
Signal recognition particle 14 kDa protein	4.66E-10
lipase 1 precursor	0.000101
ubiquitin-conjugating enzyme E2 G2	2.00E-09
SP39 Serine protease	1.43E-09
Hypothetical protein	1.34E-06
lipophorin receptor	2.29E-08

Hypothetical protein	7.91E-12
WASH complex subunit strumpellin	7.53E-10
sensory box protein/histidinol phosphate phosphatase family protein	3.65E-10
UNCoordinated family member	4.03E-08
hypothetical protein	1.59E-13
zf-C2H2 Zinc finger; C2H2 type	1.67E-07
hypothetical protein	1.93E-05
PREDICTED: Sec61 gamma subunit-like PREDICTED: Sec61 gamma subunit-like	9.79E-11
short-chain dehydrogenase/reductase SDR	2.28E-06
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	3.42E-08
Hypothetical protein	2.55E-06
CREB-binding protein	2.87E-06
FAD/NADP-binding domain	7.12E-08
hypothetical protein	1.54E-08
Hypothetical protein	6.82E-07
Hypothetical protein	4.92E-11
Zinc finger, C2H2-like	2.02E-11
40S ribosomal protein S17	2.82E-13
hypothetical protein	6.58E-08
PREDICTED: UTP6; small subunit	8.23E-10
TuCCE61 Carboxyl/cholinesterase TuCCE-51 Carboxyl/cholinesterase	1.26E-12
small subunit of serine palmitoyltransferase A	2.72E-08
Hypothetical protein	2.07E-06
Hypothetical protein	4.93E-07
Sodium/calcium exchanger membrane region SPHp5 Sodium/calcium exchanger membrane	1.74E-13
Nucleotide-binding; alpha-beta plait	6.51E-11
Hypothetical protein	2.00E-11
Hypothetical protein	6.29E-07
Rfx4 Winged helix-turn-helix DNA-binding domain RFX_DNA_binding Winged helix-turn-helix	5.56E-10
PREDICTED: similar to lipase 1	3.69E-07
NAGLT1b Major facilitator superfamily; general substrate transporter Major facilitator superfa	2.83E-07
Major facilitator superfamily; general substrate transporter	2.62E-14
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	1.43E-07
Hypothetical protein	7.56E-11
UGT UDP-glycosyltransferase; teturUGT60 UGT UDP-glycosyltransferase glycosyl transfer	3.65E-09
paraxis Myc-type, basic helix-loop-helix bHLH domain HLH Myc-type, basic helix-loop-helix b	1.86E-07
hypothetical protein	1.66E-08
Hypothetical protein	5.80E-10
PREDICTED: Sec61 gamma subunit-like	4.32E-12
Six-bladed beta-propeller; TolB-like	7.53E-13
Dynamin GTPase effector	1.09E-08
PMS1	3.70E-06
Hypothetical protein	7.14E-09
antigen B membrane protein	4.79E-10
Hypothetical protein	0.0040106
GG18546	2.35E-09
ribosomal protein S25	3.12E-13

GE10869	9.40E-08
CPR 30 cuticle protein	4.00E-09
CD63 antigen	4.07E-07
S-adenosyl-L-methionine-dependent methyltransferase	1.44E-13
Apoptosis regulator; Bcl-2; BH	6.35E-10
Putative scavenger receptor cysteine-rich protein PREDICTED: similar to ECM 18	1.56E-15
UBL5 Ubiquitin-like protein 5	8.14E-08
Hypothetical protein	5.76E-12
PREDICTED: similar to kelch-like 12	1.40E-09
DSS1/SEM1	1.16E-06
PREDICTED: Cdt1 protein-like	5.92E-10
TuLeg-18 Legumain TuLeg-18 Legumain;	1.59E-14
TuPap-3 Cathepsin B	2.08E-11
PREDICTED: cytochrome c oxidase subunit 7C; mitochondrial-like	3.26E-12
hypothetical protein	2.03E-06
Reactive oxygen species modulator 1	3.31E-10
PAN/Apple domain	9.24E-07
Hypothetical protein	1.40E-09
HCP1 Hypothetical Cuticular Protein HPR1 Hypothetical Cuticular Protein Hypothetical prot	2.70E-06
hypothetical protein	1.75E-11
Hypothetical protein	1.39E-09
DNA replication factor Cdt1, C-terminal	6.32E-08
Hypothetical protein	1.47E-08
Hypothetical protein	6.04E-06
Bicarbonate transporter; eukaryotic	9.65E-10
mitochondrial malate dehydrogenase 2; NAD	7.01E-14
Csp1f conserved secreted protein 1 Hypothetical protein	4.54E-09
major facilitator superfamily MFS_1	6.20E-06
Proteasome subunit alpha type-1	1.00E-06
gsx2 GS homeobox 2	2.72E-10
beta-1;4-galactosyltransferase	0.0001113
Fatty acyl-CoA reductase	4.61E-13
PREDICTED: hypothetical protein	3.52E-14
Hypothetical protein	2.60E-10
S-adenosyl-L-methionine-dependent methyltransferase	4.78E-07
Hypothetical protein	2.64E-10
ApoDR10 Calycin-like Calycin-like	2.75E-06
Protein of unknown function DUF543	8.01E-12
Hypothetical protein	0.0001239
Hypothetical protein	3.91E-10
GRSP3 Glycine-rich secreted protein SSPD1 Small secreted peptide Hypothetical protein	0.0002078
Hypothetical protein	7.70E-08
UNCoordinated family member UNCoordinated family member	4.61E-09
Hypothetical protein	3.84E-09
E2f4 E2F transcription factor, CC-MB domain E2F_TDP E2F transcription factor, CC-MB don	1.64E-07
phytoene dehydrogenase	1.19E-05
large subunit ribosomal protein 29 large subunit ribosomal protein 29	7.12E-11

60S ribosomal protein L38	1.28E-12
dimethylaniline monooxygenase	5.12E-08
hypothetical protein	5.39E-10
Gfi1b growth factor independent protein 1B zf-C2H2 Zinc finger; C2H2 type	1.87E-09
CPR 51 Cuticle secreted protein; putative CPR1 Cuticle secreted protein; putative CPR1 Cu	2.07E-06
hypothetical protein	3.60E-08
Alpha/Beta hydrolase fold	3.46E-08
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	8.39E-07
variable lymphocyte receptor A	1.04E-10
UGT UDP-glycosyltransferase; teturUGT09 UGT UDP-glycosyltransferase Glycosyltransfer	8.12E-10
short-chain dehydrogenase/reductase SDR	2.86E-09
DDM9-21 Domain of unknown function DUF3421 Domain of unknown function DUF3421	4.31E-08
SJCHGC06741 protein	2.60E-10
Zinc finger, CXXC-type	4.00E-09
N-acylneuraminate cytidylyltransferase	1.54E-09
Hypothetical protein	1.63E-07
Hypothetical protein	1.57E-08
PREDICTED: hypothetical protein	3.99E-06
short chain dehydrogenase	1.05E-08
Fibroin Hypothetical protein	7.68E-09
Hypothetical protein	4.21E-09
GRSP5 Glycine-rich secreted protein Hypothetical protein	9.09E-06
UGT UDP-glycosyltransferase; teturUGT16 UGT UDP-glycosyltransferase MGT4 Glycosyltr	8.67E-10
Hypothetical protein	4.42E-10
Clusterin-associated protein-1	5.78E-08
Glycoside hydrolase; subgroup; catalytic core	2.21E-13
vitellogenin1	1.91E-08
hypothetical protein	1.80E-06
Hypothetical protein	9.51E-08
TuCPI-4 Cystatin	6.57E-12
Hypothetical protein	4.29E-08
ABC transporter; permease/ATP-binding protein	3.91E-09
Hypothetical protein	0.0010263
conserved hypothetical protein	1.70E-07
Hypothetical protein	6.72E-13
aldo-keto reductase	6.76E-08
SSPA9 Small Secreted Protein; family A Hypothetical protein	1.96E-07
ApoD23 Apolipoprotein D precursor apolipoprotein D	5.99E-14
adenylosuccinate lyase	2.87E-09
Der f 2 allergen	1.33E-12
Hypothetical protein	3.03E-10
Hypothetical protein	5.10E-07
Protein of unknown function DUF4817	3.92E-13
Hypothetical protein	7.57E-11
UNCoordinated family member	1.93E-07
calmodulin	1.06E-08
TuENaC05 Putative amiloride-sensitive sodium channel ENaC05 Putative amiloride-sensitive	4.12E-09

RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	5.67E-09
T-complex protein 1 subunit zeta T-complex protein 1 subunit zeta	3.38E-11
NHP2-like protein 1	1.25E-10
Hypothetical protein	1.19E-06
jnk/sapk-associated protein jnk/sapk-associated protein	4.74E-08
phosphatidylcholine-sterol acyltransferase	3.62E-07
AkrE2 Aldo-keto reductase family E; member 2; likely a pseudogene aldo-keto reductase	5.73E-13
Ribosomal protein S28e conserved site	1.09E-13
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	3.33E-08
Zinc finger, C2H2-like	5.45E-09
TuPap-4 Cathepsin B	5.26E-12
Hypothetical protein	2.88E-09
Hypothetical protein	7.29E-10
PAN/Apple domain	2.42E-09
Hypothetical protein	1.30E-07
	2.39E-07
hypothetical protein	1.06E-07
hypothetical protein	2.97E-09
FATE/Miff/Tango-11	2.39E-09
Hypothetical protein	9.67E-07
unnamed protein product	1.11E-12
Hypothetical protein	1.38E-15
Zinc finger, RING/FYVE/PHD-type Zinc finger, RING/FYVE/PHD-type	2.85E-10
Cysteine peptidase, asparagine active site	3.76E-09
apoptosis regulator BAX	2.17E-05
ribosomal protein L41	1.47E-13
hypothetical protein	3.18E-10
GG20998	6.28E-07
60S ribosomal protein L37a	7.75E-13
5'-nucleotidase	7.98E-10
GE10869	2.92E-11
hypothetical protein	1.38E-07
TuGR306 Chemosensory Receptor; Gustatory receptor family Hypothetical protein	1.61E-05
antigen B membrane protein	6.64E-08
protein kinase C alpha type	1.12E-12
hypothetical protein	7.91E-09
Hypothetical protein	1.50E-12
chaperone protein DnaJ	4.07E-07
hypothetical protein	9.14E-09
Apple-like	3.09E-11
PREDICTED: similar to neprilysin; partial	1.08E-08
Uncharacterised domain KLRAQ/TTKRSYEDQ, C-terminal	5.94E-09
CPR 26 cuticle protein	2.58E-06
acylamino-acid-releasing enzyme	1.55E-13
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	2.96E-11
TuLeg-22 Legumain-like; pseudogene	4.49E-11
40S ribosomal protein S29	3.10E-13

Hypothetical protein	2.23E-11
Mitochondrial import inner membrane translocase subunit Tim13	1.32E-09
Insect antifreeze protein	1.83E-05
HCP2 Hypothetical Cuticular Protein Hypothetical protein	0.0011817
CCEincTu16 Carboxyl/cholinesterase; incomplete CCEinc-26 Carboxyl/cholinesterase; incon	5.12E-11
hypothetical protein	2.21E-07
Protein kinase-like domain	3.89E-07
Trafficking protein particle complex subunit 5 Trafficking protein particle complex subunit 5	3.57E-08
eukaryotic translation initiation factor 6	1.12E-09
Hypothetical protein	7.12E-15
steroid dehydrogenase	2.34E-07
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	1.36E-08
Hypothetical protein	4.60E-09
D13	2.68E-09
Plexin-like fold	7.99E-10
spectrin; alpha; non-erythrocytic 1	1.33E-11
Hypothetical protein	1.48E-09
phospholipase A2 precursor; putative	5.65E-14
Hypothetical protein	1.62E-12
PLATp2 PLAT/LH2 domain PLAT/LH2 domain	6.58E-08
UNCoordinated family member	2.29E-08
Hypothetical protein	7.07E-15
CPR 28 cuticle protein	7.15E-05
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	1.07E-08
Oxidoreductase-like, N-terminal	4.79E-09
	4.63E-09
Protoporphyrinogen oxidase, C-terminal domain	3.72E-10
TuCPI-5 Cystatin	1.70E-15
Hypothetical protein	6.73E-09
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	1.40E-09
Hypothetical protein	9.56E-14
PREDICTED: similar to Sialin	4.32E-08
Hypothetical protein	4.03E-08
hypothetical protein	1.28E-09
Leucine-rich repeat domain, L domain-like	4.44E-09
Smg-6 homolog; nonsense mediated mRNA decay factor	1.56E-09
Insect antifreeze protein	2.22E-08
Hypothetical protein	3.67E-09
MZT2b MOZART2 family MOZART2 family	6.72E-09
WD40/YVTN repeat-like-containing domain	5.83E-11
origin recognition complex subunit 2	1.44E-08
Hypothetical protein	2.42E-11
Prolyl 4-hydroxylase; alpha subunit	1.78E-09
NUDIX hydrolase	7.18E-10
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	2.77E-10
pseudogene of 04g02210 ferrochelatase ferrochelatase	1.33E-09
Hypothetical protein	2.06E-08

Carboxypeptidase-like, regulatory domain	4.92E-10
TuPap-27 Cathepsin B	9.31E-15
Hypothetical protein	6.66E-11
ADP-ribosylation factor GTPase-activating protein 1	2.54E-10
Hypothetical protein	4.01E-10
Hypothetical protein	1.96E-09
SFRS protein kinase 1	1.21E-10
TuLeg-6 Legumain	3.05E-08
IarsP isoleucyl-tRNA synthetase; pseudogene isoleucyl-tRNA synthetase; cytoplasmic	2.41E-09
PLAT13 PLAT single domain protein PLAT/LH2 single domain protein; related Hypothetical	7.49E-08
hypothetical protein	1.03E-08
Nose resistant-to-fluoxetine protein; N-terminal	4.08E-10
Hypothetical protein	2.24E-09
hypothetical protein	6.99E-08
ApoD20 Apolipoprotein D precursor PREDICTED: apolipoprotein D-like	2.78E-16
Insect antifreeze protein	4.19E-09
CYP392A10 Cytochrome P450 - CYP392A10	5.94E-12
PLC-like phosphodiesterase, TIM beta/alpha-barrel domain	3.40E-09
CCEincTu18 Carboxyl/cholinesterase; incomplete esterase	2.49E-11
RPL39 ribosomal protein L39 ribosomal protein L39	5.05E-14
hypothetical protein	8.80E-08
alanyl-tRNA synthetase	1.32E-10
CPR 22 cuticle protein	5.64E-05
Hypothetical protein	5.03E-15
ovo ovo zf-C2H2 Zinc finger; C2H2 type	1.70E-09
Hypothetical protein	1.61E-09
ApoDR1 Calycin-like ApoDR1 Calycin-like Calycin-like	7.78E-10
Endonuclease/exonuclease/phosphatase	4.01E-10
PREDICTED: UDP-Gal:betaGlcNAc beta 1;3-galactosyltransferase 1-like	9.57E-11
IQ calmodulin-binding region	4.63E-10
hypothetical protein	4.47E-10
ovo ovo zf-C2H2 Zinc finger; C2H2 type	2.28E-10
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	3.09E-10
intradiol ring-cleavage dioxygenase	3.79E-11
Hypothetical protein	3.00E-12
PIN domain-like	2.36E-10
Hypothetical protein	4.41E-11
TuGSTinc03 Glutathione-S-transferase; incomplete;	1.28E-09
hypothetical protein	5.32E-11
SSPF16 Small Secreted Protein; family F hypothetical protein	2.02E-09
cathepsin B	4.42E-11
Hypothetical protein	1.08E-10
hypothetical protein	8.36E-10
Leucine-rich repeat domain, L domain-like	1.12E-11
Hypothetical protein	2.05E-17
Uncharacterized oxidoreductase yqjQ Uncharacterized oxidoreductase yqjQ	1.14E-10
Phosphoribosyltransferase-like Phosphoribosyltransferase-like	1.49E-10

hypothetical protein	2.36E-13
Hypothetical protein	8.80E-13
DnaJ	4.39E-10
Hypothetical protein	1.12E-11
TuPap-10 Cathepsin B	1.44E-12
dUTPase deoxyuridine 5'-triphosphate nucleotidohydrolase deoxyuridine 5'-triphosphate nuc	6.48E-11
partitioning defective 6 homolog beta	4.65E-12
K Homology domain, type 1	1.77E-12
PLC-like phosphodiesterase; TIM beta/alpha-barrel domain	2.37E-12
Six-bladed beta-propeller; TolB-like	3.96E-12
hypothetical protein	1.13E-11
Hypothetical protein	2.19E-11
Hypothetical protein	8.88E-15
Stress-associated endoplasmic reticulum protein 1	4.78E-13

nt populations (IT2, UK6 and ES1) and two susceptible strains (RO1 and IT3) of *T. urticae*

adj.P.Val	ipr_ALL
1.36E-10	IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
3.56E-09	NA
2.07E-11	NA
5.67E-13	NA
9.93E-10	NA
5.82E-12	IPR000998*MAM domain, IPR013320*Concanavalin A-like lectin/glucanase domain
1.53E-10	IPR012674*Calycin
1.85E-09	NA
1.20E-12	IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
3.88E-10	IPR003172*MD-2-related lipid-recognition domain, IPR014756*Immunoglobulin E-set
1.02E-10	NA
2.44E-09	NA
8.40E-11	IPR001478*PDZ domain, IPR000270*PB1 domain, IPR034876*Partitioning defective protein 6
5.43E-12	NA
1.44E-11	NA
1.50E-11	NA
1.24E-05	IPR012599*Peptidase C1A, propeptide, IPR000668*Peptidase C1A, papain C-terminal, IPR01312
8.82E-12	NA
1.58E-11	NA
1.31E-10	IPR029064*50S ribosomal protein L30e-like, IPR000530*Ribosomal protein S12e, IPR004038*Rib
1.19E-11	IPR006568*PSP, proline-rich, IPR003034*SAP domain, IPR007180*Domain of unknown function
1.09E-09	NA
5.67E-10	NA
9.53E-08	IPR001254*Serine proteases, trypsin domain, IPR001314*Peptidase S1A, chymotrypsin family, IP
1.27E-09	NA
4.75E-13	IPR012674*Calycin
1.97E-11	NA
9.11E-11	IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat
9.81E-11	IPR002999*Tudor domain
1.61E-08	IPR011705*BTB/Kelch-associated, IPR011333*SKP1/BTB/POZ domain
5.08E-10	IPR027408*PNPase/RNase PH domain, IPR020568*Ribosomal protein S5 domain 2-type fold, IPR
3.54E-11	NA
3.52E-11	NA
8.79E-10	NA
5.78E-10	IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
1.23E-08	IPR007807*Helicase domain, IPR032672*TmcA/NAT10/Kre33, IPR027992*Possible tRNA binding
1.19E-08	NA
6.92E-10	NA
5.71E-11	IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
1.34E-10	NA
4.52E-10	NA
5.94E-09	IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
4.85E-16	IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
7.56E-09	IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I

3.64E-10	IPR005552*Scramblase
1.53E-10	NA
9.19E-11	NA
4.62E-12	NA
1.45E-08	IPR022271*Lipocalin, ApoD type, IPR012674*Calycin, IPR002345*Lipocalin, IPR003057*Invertebra
3.59E-09	IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
5.35E-09	IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
3.09E-08	IPR001025*Bromo adjacent homology (BAH) domain
3.07E-10	NA
7.52E-09	IPR003010*Carbon-nitrogen hydrolase
8.68E-12	NA
6.47E-10	IPR012674*Calycin
2.92E-11	IPR007235*Glycosyl transferase, family 28, C-terminal, IPR002213*UDP-glucuronosyl/UDP-glucos
1.21E-07	IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
5.97E-09	IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
2.51E-08	NA
1.24E-08	NA
2.10E-11	NA
7.33E-09	NA
2.72E-08	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
8.28E-08	NA
2.43E-08	IPR031968*VASt domain
2.19E-08	NA
7.00E-09	NA
3.56E-09	IPR006202*Neurotransmitter-gated ion-channel ligand-binding domain, IPR006028*Gamma-amino
1.37E-09	IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
1.58E-09	NA
1.34E-08	NA
1.20E-12	NA
1.13E-08	NA
3.69E-08	NA
2.19E-10	IPR002843*ATPase, V0 complex, c/d subunit, IPR016727*ATPase, V0 complex, subunit d, IPR03
9.75E-09	IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
2.41E-10	NA
1.60E-08	IPR024483*Protein of unknown function DUF2700
1.20E-06	IPR001314*Peptidase S1A, chymotrypsin family, IPR009003*Peptidase S1, PA clan, IPR001254*S
2.13E-08	IPR002554*Protein phosphatase 2A, regulatory B subunit, B56, IPR016024*Armadillo-type fold
3.07E-09	IPR002018*Carboxylesterase, type B, IPR029058*Alpha/Beta hydrolase fold
1.53E-10	IPR015889*Intradiol ring-cleavage dioxygenase, core
8.94E-14	NA
1.60E-10	NA
7.45E-12	NA
4.86E-14	NA
1.65E-08	IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
7.65E-07	NA
3.31E-08	NA
1.45E-07	NA

1.63E-06	IPR011705*BTB/Kelch-associated, IPR028764*Kelch repeat and BTB domain-containing protein 8,
1.63E-11	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
6.07E-10	NA
7.88E-09	NA
7.66E-08	NA
1.06E-07	NA
4.87E-07	IPR028764*Kelch repeat and BTB domain-containing protein 8, IPR011705*BTB/Kelch-associated
9.81E-11	IPR001370*BIR repeat, IPR006568*PSP, proline-rich, IPR007180*Domain of unknown function DU
4.31E-06	NA
7.88E-09	IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
4.70E-08	IPR032675*Leucine-rich repeat domain, L domain-like
4.56E-08	IPR007235*Glycosyl transferase, family 28, C-terminal
5.45E-09	NA
1.28E-08	IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
3.12E-07	NA
1.21E-09	IPR007235*Glycosyl transferase, family 28, C-terminal
4.17E-11	NA
1.05E-10	IPR023395*Mitochondrial carrier domain, IPR018108*Mitochondrial substrate/solute carrier, IPR00
1.21E-14	IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
4.74E-11	IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
5.75E-09	IPR008160*Collagen triple helix repeat, IPR000885*Fibrillar collagen, C-terminal, IPR014716*Fibri
3.09E-09	IPR003609*PAN/Apple domain
3.55E-10	IPR035067*V-type ATPase subunit c domain, IPR016727*ATPase, V0 complex, subunit d, IPR002
4.24E-07	IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A, IPR013201*Cathepsin
4.86E-14	IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
1.91E-08	NA
2.72E-11	NA
3.36E-12	IPR002498*Phosphatidylinositol-4-phosphate 5-kinase, core, IPR027483*Phosphatidylinositol-4-ph
1.01E-08	IPR029060*PIN domain-like, IPR024768*Meiosis regulator and mRNA stability factor 1, IPR02113
3.23E-07	NA
3.29E-12	IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
6.61E-11	IPR012674*Calycin
2.71E-09	IPR011333*SKP1/BTB/POZ domain, IPR011705*BTB/Kelch-associated
4.68E-08	IPR031968*VASt domain
2.53E-08	IPR011333*SKP1/BTB/POZ domain, IPR000210*BTB/POZ domain, IPR028764*Kelch repeat and
7.41E-10	NA
3.48E-06	IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
2.20E-07	IPR003609*PAN/Apple domain
3.94E-08	NA
1.10E-07	IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
1.70E-06	IPR000210*BTB/POZ domain, IPR011333*SKP1/BTB/POZ domain, IPR011705*BTB/Kelch-associ
6.92E-10	IPR019311*Protein of unknown function DUF2362
7.41E-10	IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
9.87E-09	NA
4.01E-06	IPR023610*Phosphatidylinositol-4-phosphate 5-kinase, IPR002498*Phosphatidylinositol-4-phosph
1.18E-07	NA
2.02E-08	NA

2.24E-09	NA
2.81E-08	IPR007235*Glycosyl transferase, family 28, C-terminal, IPR002213*UDP-glucuronosyl/UDP-glucos
4.09E-06	NA
5.33E-05	IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat
1.22E-07	NA
1.07E-09	NA
2.64E-06	IPR023214*HAD-like domain
2.93E-06	NA
4.82E-09	NA
1.04E-10	NA
5.26E-11	IPR003008*Tubulin/FtsZ, GTPase domain, IPR000217*Tubulin, IPR002453*Beta tubulin, IPR0082
7.51E-05	NA
6.35E-08	IPR010987*Glutathione S-transferase, C-terminal-like, IPR004045*Glutathione S-transferase, N-ter
9.93E-10	IPR003609*PAN/Apple domain
6.16E-10	IPR015943*WD40/YVTN repeat-like-containing domain, IPR017986*WD40-repeat-containing doma
1.18E-07	IPR026298*Blc2 family
1.14E-08	IPR021454*Protein of unknown function DUF3105
4.46E-06	NA
2.82E-08	IPR028118*Chibby family
7.55E-08	IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
3.22E-06	IPR001096*Peptidase C13, legumain
1.38E-07	IPR005552*Scramblase
5.57E-09	IPR013657*UAA transporter
5.82E-12	IPR000668*Peptidase C1A, papain C-terminal, IPR012599*Peptidase C1A, propeptide, IPR013128
1.57E-06	NA
2.91E-06	IPR004583*DNA repair protein Rad4, IPR018328*Rad4 beta-hairpin domain 3, IPR018327*Rad4 b
1.05E-10	IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
9.93E-10	IPR016161*Aldehyde/histidinol dehydrogenase, IPR015590*Aldehyde dehydrogenase domain, IPR
6.72E-09	IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
2.52E-07	NA
3.02E-09	NA
4.04E-12	NA
1.85E-06	NA
7.33E-09	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
1.17E-08	IPR000536*Nuclear hormone receptor, ligand-binding domain
6.63E-14	IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
1.93E-08	IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain
3.01E-11	IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
1.33E-06	IPR029600*Intraflagellar transport protein 81
8.58E-09	IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
8.93E-08	IPR006153*Cation/H+ exchanger
2.09E-07	NA
2.61E-07	IPR012674*Calycin
3.33E-10	NA
1.72E-11	NA
1.40E-06	NA
3.71E-11	NA

2.85E-11	IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat
1.22E-06	IPR003172*MD-2-related lipid-recognition domain, IPR014756*Immunoglobulin E-set
4.40E-12	IPR009075*Acyl-CoA dehydrogenase/oxidase C-terminal, IPR013786*Acyl-CoA dehydrogenase/ox
9.54E-06	IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
8.90E-06	IPR032675*Leucine-rich repeat domain, L domain-like
1.73E-10	IPR001139*Glycoside hydrolase family 30, IPR017853*Glycoside hydrolase superfamily, IPR03345
7.83E-08	IPR032675*Leucine-rich repeat domain, L domain-like
6.75E-10	NA
5.82E-12	IPR006326*UDP-glycosyltransferase, MGT, IPR007235*Glycosyl transferase, family 28, C-terminal
1.58E-09	IPR011249*Metalloenzyme, LuxS/M16 peptidase-like, IPR013578*Peptidase M16C associated
9.66E-12	IPR015819*Lipid transport protein, beta-sheet shell, IPR015255*Vitellinogen, open beta-sheet, IPR
1.14E-07	IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
3.01E-11	IPR012599*Peptidase C1A, propeptide, IPR000668*Peptidase C1A, papain C-terminal, IPR013128
1.47E-08	IPR014806*Ubiquitin-fold modifier-conjugating enzyme 1, IPR016135*Ubiquitin-conjugating enzym
4.27E-07	NA
2.11E-08	IPR002048*EF-hand domain, IPR011992*EF-hand domain pair
3.68E-08	NA
4.99E-05	IPR001251*CRAL-TRIO lipid binding domain, IPR011074*CRAL/TRIO, N-terminal domain
7.05E-08	NA
1.51E-13	IPR013201*Cathepsin propeptide inhibitor domain (I29), IPR000668*Peptidase C1A, papain C-term
1.28E-08	IPR002018*Carboxylesterase, type B, IPR029058*Alpha/Beta hydrolase fold
4.54E-08	IPR011598*Myc-type, basic helix-loop-helix (bHLH) domain, IPR015943*WD40/YVTN repeat-like-c
1.45E-08	IPR023796*Serpin domain, IPR000215*Serpin family
3.12E-08	IPR020846*Major facilitator superfamily domain, IPR010291*Ion channel regulatory protein, UNC-9
6.81E-11	IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain
3.81E-06	NA
1.10E-09	NA
3.78E-06	NA
3.85E-12	IPR000668*Peptidase C1A, papain C-terminal, IPR012599*Peptidase C1A, propeptide, IPR013128
8.20E-10	NA
4.52E-09	IPR007855*RNA-dependent RNA polymerase, eukaryotic-type
2.75E-08	NA
5.52E-08	NA
1.02E-10	NA
2.38E-08	NA
1.03E-07	IPR000210*BTB/POZ domain, IPR011333*SKP1/BTB/POZ domain
3.22E-06	NA
1.01E-08	IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
1.20E-09	NA
6.52E-07	IPR012923*Chromosome segregation in meiosis protein 3, IPR019393*WASH complex, subunit str
3.87E-09	IPR007235*Glycosyl transferase, family 28, C-terminal, IPR002213*UDP-glucuronosyl/UDP-glucos
2.26E-07	NA
3.96E-06	NA
1.49E-09	IPR006652*Kelch repeat type 1, IPR015915*Kelch-type beta propeller, IPR011498*Kelch repeat ty
3.91E-07	IPR013087*Zinc finger C2H2-type
1.48E-06	IPR029600*Intraflagellar transport protein 81
1.00E-05	NA

6.32E-10	IPR026746*Nucleolar protein 4-like
9.77E-07	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
2.49E-07	NA
5.39E-09	IPR001314*Peptidase S1A, chymotrypsin family, IPR001254*Serine proteases, trypsin domain, IP
9.77E-09	IPR000010*Cystatin domain
7.43E-10	IPR005552*Scramblase
3.33E-06	IPR013244*Sec39 domain
2.97E-08	IPR000408*Regulator of chromosome condensation, RCC1, IPR000719*Protein kinase domain, IP
1.16E-09	IPR001680*WD40 repeat, IPR017986*WD40-repeat-containing domain, IPR015943*WD40/YVTN r
1.41E-06	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
9.32E-06	NA
3.06E-09	IPR011989*Armadillo-like helical, IPR000904*Sec7 domain, IPR015403*Sec7, C-terminal, IPR023
1.88E-09	IPR002999*Tudor domain
9.27E-10	NA
7.52E-09	IPR001650*Helicase, C-terminal, IPR023780*Chromo domain, IPR000330*SNF2-related, N-termin
3.05E-11	IPR012445*Autophagy-related protein 101
3.16E-06	IPR032675*Leucine-rich repeat domain, L domain-like
8.53E-06	IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
5.67E-10	IPR015421*Pyridoxal phosphate-dependent transferase, major region, subdomain 1, IPR010111*K
6.97E-11	NA
2.75E-09	IPR004046*Glutathione S-transferase, C-terminal, IPR010987*Glutathione S-transferase, C-termin
7.78E-10	IPR015889*Intradiol ring-cleavage dioxygenase, core
1.29E-06	NA
6.65E-05	NA
1.79E-07	NA
1.16E-06	NA
2.21E-10	IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase, IPR007235*Glycosyl transferase, family 2
1.92E-09	IPR000949*ELM2 domain, IPR009057*Homeobox domain-like, IPR001005*SANT/Myb domain
2.02E-08	NA
4.70E-07	IPR001024*PLAT/LH2 domain
7.43E-08	IPR001139*Glycoside hydrolase family 30, IPR033453*Glycosyl hydrolase family 30, TIM-barrel do
2.13E-06	IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A
4.24E-10	IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
9.23E-08	IPR000536*Nuclear hormone receptor, ligand-binding domain
3.13E-08	NA
4.97E-10	NA
1.63E-06	IPR025974*Mif2/CENP-C cupin domain
1.23E-09	IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
6.29E-08	IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
3.94E-07	IPR011701*Major facilitator superfamily, IPR020846*Major facilitator superfamily domain
2.02E-08	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
4.11E-06	IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain, IPR022271*Lipocalin
4.56E-11	IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
5.99E-06	IPR012674*Calycin
1.44E-07	IPR020843*Polyketide synthase, enoylreductase domain, IPR016040*NAD(P)-binding domain, IPR
7.91E-06	NA
9.63E-08	IPR000210*BTB/POZ domain, IPR011705*BTB/Kelch-associated, IPR011333*SKP1/BTB/POZ do

2.87E-12	IPR001096*Peptidase C13, legumain
1.57E-12	IPR011990*Tetratricopeptide-like helical domain, IPR021183*N-terminal acetyltransferase A, auxili
1.03E-09	NA
1.38E-11	IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
6.07E-07	NA
3.64E-06	NA
6.99E-06	IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
5.24E-08	IPR029063*S-adenosyl-L-methionine-dependent methyltransferase, IPR013216*Methyltransferase
1.14E-08	IPR003057*Invertebrate colouration protein, IPR022271*Lipocalin, ApoD type, IPR012674*Calycin,
1.81E-07	IPR004327*Phosphotyrosyl phosphatase activator, PTPA
3.12E-07	IPR011011*Zinc finger, FYVE/PHD-type, IPR001965*Zinc finger, PHD-type, IPR013083*Zinc finge
1.23E-08	NA
4.18E-06	IPR009786*Spot 14 family
3.28E-09	IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
2.13E-08	IPR001275*DM DNA-binding domain, IPR026607*DMRT/protein doublesex/protein male abnormal
8.68E-07	IPR020846*Major facilitator superfamily domain
9.71E-07	NA
4.44E-07	NA
6.26E-08	NA
1.01E-06	IPR015915*Kelch-type beta propeller, IPR000210*BTB/POZ domain, IPR011705*BTB/Kelch-asso
1.79E-05	NA
5.52E-09	IPR000536*Nuclear hormone receptor, ligand-binding domain
2.20E-06	IPR015889*Intradiol ring-cleavage dioxygenase, core
2.44E-05	IPR006621*Nose resistant-to-fluoxetine protein, N-terminal
1.03E-08	IPR023796*Serpin domain, IPR000215*Serpin family
4.65E-11	IPR028996*Ganglioside GM2 activator
1.14E-10	IPR000215*Serpin family, IPR023796*Serpin domain
1.31E-06	NA
3.22E-05	IPR020846*Major facilitator superfamily domain
1.36E-09	IPR004045*Glutathione S-transferase, N-terminal, IPR012336*Thioredoxin-like fold, IPR010987*G
2.72E-11	IPR032788*Glycogen debranching enzyme, central domain, IPR029436*Eukaryotic glycogen debra
1.82E-09	IPR000997*Cholinesterase, IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase,
1.60E-07	IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
6.29E-06	IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat
2.76E-05	IPR024768*Meiosis regulator and mRNA stability factor 1, IPR029060*PIN domain-like, IPR02113
6.13E-07	NA
7.90E-07	IPR002018*Carboxylesterase, type B, IPR029058*Alpha/Beta hydrolase fold
4.07E-09	IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
2.49E-09	IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR030247*Canalicular multispe
1.66E-07	NA
6.13E-08	IPR013320*Concanavalin A-like lectin/glucanase domain, IPR002172*Low-density lipoprotein (LDL
8.93E-09	NA
3.02E-06	NA
2.45E-05	NA
1.70E-09	IPR014756*Immunoglobulin E-set, IPR003172*MD-2-related lipid-recognition domain
1.81E-05	NA
8.34E-06	IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase

1.01E-09	IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
0.0001413	NA
9.32E-10	NA
8.42E-08	IPR007307*Low temperature viability protein
1.78E-05	IPR024768*Meiosis regulator and mRNA stability factor 1, IPR021139*NYN domain, limkain-b1-typ
1.16E-09	IPR020479*Homeobox domain, metazoa, IPR009057*Homeobox domain-like, IPR001356*Homeob
1.28E-09	IPR011583*Chitinase II, IPR029070*Chitinase insertion domain, IPR017853*Glycoside hydrolase s
2.86E-05	NA
4.81E-08	IPR001156*Transferrin-like domain, IPR016357*Transferrin
4.23E-05	NA
3.50E-06	NA
6.38E-09	IPR000554*Ribosomal protein S7e
3.02E-09	IPR031152*Plexin domain-containing protein
0.0001782	IPR001715*Calponin homology domain, IPR030265*Nesprin-1
1.13E-06	NA
8.96E-06	NA
1.82E-09	IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A, IPR012599*Peptidase
1.97E-05	NA
0.0001023	IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
5.63E-08	IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain
7.42E-10	NA
2.90E-09	NA
5.60E-06	NA
2.03E-06	NA
3.89E-08	NA
2.14E-05	NA
8.17E-09	NA
2.03E-05	NA
5.08E-10	IPR006989*NAB co-repressor, domain, IPR006988*Nab, N-terminal
2.52E-07	NA
8.20E-09	NA
1.81E-08	IPR001024*PLAT/LH2 domain
5.22E-07	NA
2.47E-06	IPR001254*Serine proteases, trypsin domain, IPR001314*Peptidase S1A, chymotrypsin family, IPR
4.73E-06	IPR001619*Sec1-like protein
3.45E-06	IPR007855*RNA-dependent RNA polymerase, eukaryotic-type
0.0006688	NA
1.09E-06	NA
1.19E-07	IPR013128*Peptidase C1A, IPR000668*Peptidase C1A, papain C-terminal
1.87E-05	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
5.08E-07	IPR034192*SREK1, RNA recognition motif 2, IPR000504*RNA recognition motif domain
9.02E-07	IPR019151*Proteasome assembly chaperone 2
1.45E-08	IPR017853*Glycoside hydrolase superfamily, IPR033453*Glycosyl hydrolase family 30, TIM-barrel
1.57E-09	NA
1.83E-07	IPR001747*Lipid transport protein, N-terminal, IPR015819*Lipid transport protein, beta-sheet shell,
2.45E-07	IPR012916*RED-like, N-terminal
4.34E-08	IPR000719*Protein kinase domain, IPR011009*Protein kinase-like domain

3.72E-12	IPR023753*FAD/NAD(P)-binding domain
7.43E-10	IPR004045*Glutathione S-transferase, N-terminal, IPR004046*Glutathione S-transferase, C-termin
6.53E-06	IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR001609*Myosin head, motor
6.94E-07	IPR002557*Chitin binding domain
7.82E-07	IPR032675*Leucine-rich repeat domain, L domain-like
1.66E-07	IPR024855*UNC79
1.62E-09	NA
6.56E-07	IPR031968*VASt domain
1.38E-05	NA
2.22E-09	IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR011042*Six-bladed beta-pro
9.40E-10	NA
3.16E-06	IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR001254*Serine proteases, tr
5.26E-11	IPR011527*ABC transporter type 1, transmembrane domain, IPR003439*ABC transporter-like, IPR
1.05E-10	IPR014720*Double-stranded RNA-binding domain
5.55E-07	NA
7.80E-10	NA
9.79E-09	NA
5.82E-12	NA
2.89E-07	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
2.70E-05	NA
6.70E-06	NA
7.99E-09	NA
2.85E-11	IPR013783*Immunoglobulin-like fold, IPR027417*P-loop containing nucleoside triphosphate hydrol
6.61E-07	IPR011705*BTB/Kelch-associated
4.33E-07	IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR013320*Concanavalin A-like
1.58E-06	IPR001251*CRAL-TRIO lipid binding domain, IPR011074*CRAL/TRIO, N-terminal domain
1.18E-08	NA
6.09E-08	IPR013087*Zinc finger C2H2-type, IPR027755*Transcription factor Ovo-like, IPR013083*Zinc finge
2.60E-09	IPR001356*Homeobox domain, IPR008422*Homeobox KN domain, IPR009057*Homeobox domai
3.12E-07	NA
5.37E-08	IPR031865*Domain of unknown function DUF4757
2.59E-06	NA
1.50E-07	IPR018863*Fragile site-associated protein, C-terminal, IPR033616*Protein KIAA1109
2.15E-06	NA
9.15E-09	IPR008152*Clathrin adaptor, alpha/beta/gamma-adaptin, appendage, Ig-like subdomain, IPR01304
8.55E-07	IPR004344*Tubulin-tyrosine ligase/Tubulin polyglutamylase
7.55E-08	IPR001214*SET domain, IPR003889*FY-rich, C-terminal, IPR003888*FY-rich, N-terminal, IPR0036
4.07E-09	NA
4.77E-07	NA
4.52E-10	IPR020821*Extracellular Endonuclease, subunit A, IPR002557*Chitin binding domain, IPR001002*
8.18E-10	IPR001452*SH3 domain, IPR018556*Domain of unknown function DUF2013
1.48E-05	NA
6.16E-06	NA
2.08E-08	IPR000197*Zinc finger, TAZ-type, IPR013178*Histone acetyltransferase Rtt109/CBP, IPR000433*
5.52E-05	NA
8.01E-05	NA
4.28E-09	IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain

1.62E-07	IPR010516*Sin3 associated polypeptide p18
9.70E-07	IPR025946*CABIT domain
2.02E-07	NA
0.0001658	NA
7.72E-09	IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR003593*AAA+ ATPase domai
4.10E-10	IPR004765*Niemann-Pick C type protein, IPR032190*Niemann-Pick C1, N-terminal, IPR003392*Pı
5.38E-05	NA
1.85E-08	NA
7.04E-05	IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
9.79E-10	IPR000719*Protein kinase domain, IPR011009*Protein kinase-like domain
3.84E-07	IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
8.72E-07	IPR001139*Glycoside hydrolase family 30, IPR033453*Glycosyl hydrolase family 30, TIM-barrel do
4.82E-09	NA
3.38E-07	IPR032104*Spaetzle, IPR029034*Cystine-knot cytokine
7.35E-07	NA
8.84E-07	NA
2.00E-06	IPR030737*IQ motif and SEC7 domain-containing protein 1, IPR011993*PH domain-like, IPR0337
1.82E-09	IPR001156*Transferrin-like domain, IPR016357*Transferrin
1.15E-10	IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
1.57E-08	IPR000082*SEA domain
1.85E-07	NA
1.40E-07	IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
5.14E-05	IPR001163*LSM domain, eukaryotic/archaea-type, IPR010920*LSM domain
7.11E-07	NA
1.60E-08	IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR014012*Helicase/SANT-asso
8.13E-08	IPR001442*Collagen IV, non-collagenous, IPR016187*C-type lectin fold
3.72E-05	NA
3.16E-09	NA
2.90E-07	IPR001156*Transferrin-like domain
4.75E-06	NA
7.91E-05	IPR019323*Active zone protein ELKS
1.02E-08	NA
2.32E-05	IPR004046*Glutathione S-transferase, C-terminal, IPR004045*Glutathione S-transferase, N-termin
6.46E-05	IPR020846*Major facilitator superfamily domain
1.17E-08	IPR000618*Insect cuticle protein
1.43E-07	IPR013949*U3 small nucleolar RNA-associated protein 6, IPR011990*Tetratricopeptide-like helical
2.29E-09	IPR003439*ABC transporter-like, IPR003593*AAA+ ATPase domain, IPR026082*ABC transporter
4.21E-08	NA
3.59E-09	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
9.91E-06	IPR001275*DM DNA-binding domain
8.93E-09	NA
1.26E-07	NA
8.18E-08	IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
2.03E-08	NA
1.33E-06	IPR006202*Neurotransmitter-gated ion-channel ligand-binding domain, IPR006029*Neurotransmitt
1.18E-07	IPR003070*Orphan nuclear receptor, IPR013088*Zinc finger, NHR/GATA-type, IPR000536*Nuclea
4.98E-06	IPR007110*Immunoglobulin-like domain, IPR001452*SH3 domain, IPR035524*Titin, invertebrate, I

1.67E-05	IPR020846*Major facilitator superfamily domain
1.00E-05	IPR011701*Major facilitator superfamily, IPR020846*Major facilitator superfamily domain
3.49E-05	NA
3.29E-10	IPR032715*Nuclear receptor coactivator 6, putative nucleic acid-binding region, IPR026638*Nuclea
0.0002479	IPR028316*Transcription factor E2F5, IPR032198*E2F transcription factor, CC-MB domain, IPR01
1.09E-08	IPR016161*Aldehyde/histidinol dehydrogenase, IPR016162*Aldehyde dehydrogenase N-terminal d
3.55E-08	IPR011989*Armadillo-like helical, IPR000569*HECT domain, IPR018123*WWE domain, subgroup,
1.34E-09	IPR015919*Cadherin-like, IPR002126*Cadherin
6.36E-09	IPR001251*CRAL-TRIO lipid binding domain, IPR001936*Ras GTPase-activating protein, IPR0089
2.10E-07	IPR001628*Zinc finger, nuclear hormone receptor-type, IPR013088*Zinc finger, NHR/GATA-type, I
0.0001601	IPR011705*BTB/Kelch-associated, IPR028764*Kelch repeat and BTB domain-containing protein 8,
3.80E-09	IPR018499*Tetraspanin/Peripherin, IPR008952*Tetraspanin, EC2 domain
3.78E-05	IPR024768*Meiosis regulator and mRNA stability factor 1, IPR021139*NYN domain, limkain-b1-typ
4.95E-05	NA
3.78E-08	IPR015727*Protein kinase C mu-related, IPR002219*Protein kinase C-like, phorbol ester/diacylglyc
7.34E-09	NA
2.21E-06	IPR002908*Frataxin/CyaY, IPR017789*Frataxin
0.0002407	NA
7.42E-08	IPR000433*Zinc finger, ZZ-type, IPR015153*EF-hand domain, type 1, IPR001202*WW domain, IP
2.32E-05	IPR026201*Centrosomal protein of 290kDa
2.71E-07	IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
7.12E-06	IPR008979*Galactose-binding domain-like, IPR013783*Immunoglobulin-like fold, IPR017853*Glyco
1.29E-06	IPR011705*BTB/Kelch-associated, IPR000210*BTB/POZ domain, IPR015915*Kelch-type beta prop
7.29E-05	IPR006202*Neurotransmitter-gated ion-channel ligand-binding domain, IPR006029*Neurotransmitt
0.0003771	IPR001766*Fork head domain, IPR011991*Winged helix-turn-helix DNA-binding domain
8.44E-05	IPR014978*Glutamine-Leucine-Glutamine, QLQ
4.26E-08	IPR013087*Zinc finger C2H2-type, IPR009057*Homeobox domain-like, IPR001356*Homeobox do
3.30E-08	IPR024867*Nuclear factor related to kappa-B-binding protein, IPR025220*NFRKB winged helix-like
4.01E-08	NA
2.38E-06	NA
9.79E-06	NA
1.83E-07	IPR011993*PH domain-like, IPR001849*Pleckstrin homology domain
7.76E-10	IPR007235*Glycosyl transferase, family 28, C-terminal, IPR002213*UDP-glucuronosyl/UDP-glucos
3.86E-09	NA
8.40E-08	IPR002159*CD36 family
1.59E-05	NA
1.64E-05	IPR003961*Fibronectin type III, IPR013783*Immunoglobulin-like fold, IPR002602*Domain of unkno
3.06E-09	IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
7.28E-07	IPR029060*PIN domain-like, IPR006984*rRNA-processing protein Fcf1/Utp23
1.10E-05	NA
0.0003244	NA
0.0002323	NA
2.02E-08	IPR018501*DDT domain, IPR011011*Zinc finger, FYVE/PHD-type, IPR013083*Zinc finger, RING/F
5.52E-07	IPR015943*WD40/YVTN repeat-like-containing domain
4.20E-05	NA
4.51E-05	IPR002048*EF-hand domain, IPR011992*EF-hand domain pair
2.24E-07	IPR000859*CUB domain

5.90E-10	IPR001139*Glycoside hydrolase family 30, IPR033452*Glycosyl hydrolase family 30, beta sandwic
1.91E-06	NA
5.95E-06	NA
8.82E-11	IPR011538*NADH-ubiquinone oxidoreductase 51kDa subunit, FMN-binding domain, IPR011537*N
0.0001265	IPR026100*Transmembrane protein 223
9.72E-09	IPR001715*Calponin homology domain, IPR016343*Spectrin, beta subunit, IPR001849*Pleckstrin
3.07E-08	IPR013087*Zinc finger C2H2-type, IPR013083*Zinc finger, RING/FYVE/PHD-type
1.71E-07	IPR011993*PH domain-like
1.62E-06	IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
2.02E-08	IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR000330*SNF2-related, N-ter
1.82E-09	IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
1.81E-07	IPR001139*Glycoside hydrolase family 30, IPR017853*Glycoside hydrolase superfamily, IPR03345
5.97E-06	IPR009786*Spot 14 family
1.14E-08	IPR000800*Notch domain, IPR013032*EGF-like, conserved site, IPR020683*Ankyrin repeat-contai
2.28E-09	IPR002159*CD36 family
1.98E-07	IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR011527*ABC transporter type
1.83E-05	NA
5.37E-08	IPR011990*Tetratricopeptide-like helical domain, IPR019734*Tetratricopeptide repeat
2.18E-07	IPR014873*Voltage-dependent calcium channel, alpha-1 subunit, IQ domain, IPR002077*Voltage-
4.83E-06	IPR002634*BolA protein
2.46E-05	NA
4.93E-07	IPR032675*Leucine-rich repeat domain, L domain-like, IPR003591*Leucine-rich repeat, typical sub
1.79E-05	IPR026074*Microtubule associated protein 1
6.28E-06	IPR011705*BTB/Kelch-associated, IPR028764*Kelch repeat and BTB domain-containing protein 8
2.03E-06	NA
2.21E-06	IPR017849*Alkaline phosphatase-like, alpha/beta/alpha, IPR017850*Alkaline-phosphatase-like, co
1.37E-07	IPR001606*ARID DNA-binding domain, IPR030408*AT-rich interactive domain-containing protein 5
4.54E-08	IPR032675*Leucine-rich repeat domain, L domain-like, IPR001611*Leucine-rich repeat, IPR003591
1.86E-05	IPR016137*RGS domain, IPR024066*RGS, subdomain 1
1.42E-06	IPR002890*Alpha-2-macroglobulin, N-terminal
2.34E-06	IPR013083*Zinc finger, RING/FYVE/PHD-type, IPR018957*Zinc finger, C3HC4 RING-type, IPR011
8.88E-06	IPR001806*Small GTPase superfamily, IPR020849*Small GTPase superfamily, Ras type, IPR0274
5.79E-09	IPR013328*6-phosphogluconate dehydrogenase, domain 2, IPR008927*6-phosphogluconate dehy
1.29E-07	IPR004046*Glutathione S-transferase, C-terminal, IPR004045*Glutathione S-transferase, N-termin
3.07E-08	IPR000306*FYVE zinc finger, IPR000409*BEACH domain, IPR013083*Zinc finger, RING/FYVE/PH
4.75E-06	IPR029063*S-adenosyl-L-methionine-dependent methyltransferase, IPR013216*Methyltransferase
2.42E-07	NA
0.0078319	IPR020846*Major facilitator superfamily domain
0.0005677	IPR000990*Innexin
8.17E-09	IPR001214*SET domain, IPR001739*Methyl-CpG DNA binding, IPR016177*DNA-binding domain,
3.15E-06	IPR007110*Immunoglobulin-like domain, IPR013783*Immunoglobulin-like fold, IPR003599*Immun
0.0001601	IPR000938*CAP Gly-rich domain
0.0001581	IPR000859*CUB domain, IPR000742*EGF-like domain, IPR001881*EGF-like calcium-binding dom
0.0003727	NA
6.75E-06	NA
2.09E-05	IPR032675*Leucine-rich repeat domain, L domain-like
6.82E-08	NA

4.96E-07	NA
1.92E-05	IPR001128*Cytochrome P450, IPR002403*Cytochrome P450, E-class, group IV
2.54E-07	NA
1.46E-05	NA
1.60E-10	NA
9.03E-08	IPR032343*Methyl-CpG-binding domain protein 2/3, p55-binding region, IPR001739*Methyl-CpG D
7.57E-07	IPR033616*Protein KIAA1109
8.89E-08	IPR028103*Spatacsin
4.71E-05	NA
2.76E-07	IPR011009*Protein kinase-like domain
3.70E-05	IPR001478*PDZ domain
4.86E-06	NA
4.28E-09	IPR015943*WD40/YVTN repeat-like-containing domain, IPR017986*WD40-repeat-containing doma
2.37E-08	IPR000832*GPCR, family 2, secretin-like, IPR000203*GPS motif, IPR000922*D-galactoside/L-rhan
3.58E-07	IPR001849*Pleckstrin homology domain, IPR011993*PH domain-like
1.02E-08	IPR020683*Ankyrin repeat-containing domain, IPR002110*Ankyrin repeat, IPR004088*K Homolog
5.06E-05	NA
1.04E-08	IPR013083*Zinc finger, RING/FYVE/PHD-type, IPR013087*Zinc finger C2H2-type
1.14E-08	NA
0.000365	IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
2.21E-06	IPR033184*Protein PRRC2
1.04E-09	IPR029058*Alpha/Beta hydrolase fold, IPR001563*Peptidase S10, serine carboxypeptidase
5.63E-08	IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A, IPR013201*Cathepsin
2.68E-05	NA
4.68E-07	IPR000001*Kringle, IPR001245*Serine-threonine/tyrosine-protein kinase, catalytic domain, IPR020
1.14E-07	IPR001356*Homeobox domain, IPR009057*Homeobox domain-like, IPR032392*SATB, ubiquitin-li
3.15E-08	IPR015255*Vitellinogen, open beta-sheet, IPR011030*Vitellinogen, superhelical, IPR015817*Vitelli
3.75E-07	NA
3.16E-10	IPR000873*AMP-dependent synthetase/ligase
7.11E-06	NA
0.0007687	IPR011993*PH domain-like, IPR001478*PDZ domain, IPR001849*Pleckstrin homology domain
0.0001137	IPR003599*Immunoglobulin subtype, IPR007110*Immunoglobulin-like domain, IPR013106*Immun
4.26E-06	NA
1.82E-09	IPR010987*Glutathione S-transferase, C-terminal-like, IPR026928*Failed axon connections, IPR03
4.08E-08	NA
0.0002407	NA
1.51E-07	IPR003165*Piwi domain, IPR003100*PAZ domain, IPR012337*Ribonuclease H-like domain
8.55E-08	NA
1.97E-08	IPR021990*Mediator complex, subunit Med12, LCEWAV-domain, IPR019035*Mediator complex, s
1.51E-07	IPR018327*Rad4 beta-hairpin domain 2, IPR004583*DNA repair protein Rad4, IPR018328*Rad4 b
0.0006396	IPR013087*Zinc finger C2H2-type
0.0001964	IPR011598*Myc-type, basic helix-loop-helix (bHLH) domain, IPR000014*PAS domain, IPR013767*
7.32E-08	IPR006906*Timeless protein
9.74E-09	NA
2.64E-08	IPR023346*Lysozyme-like domain, IPR008597*Invertebrate-type lysozyme
1.37E-08	IPR000432*DNA mismatch repair protein MutS, C-terminal, IPR007860*DNA mismatch repair prote
1.38E-05	NA

1.95E-07	IPR011701*Major facilitator superfamily, IPR020846*Major facilitator superfamily domain
4.03E-05	NA
6.38E-09	IPR000719*Protein kinase domain, IPR028741*Serine/threonine-protein kinase LATS1/ Warts, IPR
2.44E-09	IPR006560*AWS domain, IPR001214*SET domain
6.16E-06	IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
1.54E-07	IPR003150*DNA-binding RFX-type winged-helix domain, IPR011991*Winged helix-turn-helix DNA-
0.000244	NA
1.09E-07	NA
9.92E-07	IPR000608*Ubiquitin-conjugating enzyme E2, IPR016135*Ubiquitin-conjugating enzyme/RWD-like
5.64E-09	NA
3.92E-06	IPR018957*Zinc finger, C3HC4 RING-type, IPR013083*Zinc finger, RING/FYVE/PHD-type
6.28E-08	NA
1.09E-05	IPR001054*Adenylyl cyclase class-3/4/guanylyl cyclase, IPR029787*Nucleotide cyclase
1.22E-06	IPR015889*Intradiol ring-cleavage dioxygenase, core
3.36E-08	NA
0.000134	IPR011598*Myc-type, basic helix-loop-helix (bHLH) domain, IPR015660*Achaete-scute transcriptio
1.92E-05	IPR014001*Helicase superfamily 1/2, ATP-binding domain, IPR027417*P-loop containing nucleosi
0.0034114	NA
2.20E-07	IPR002017*Spectrin repeat, IPR018159*Spectrin/alpha-actinin
9.55E-05	NA
1.69E-08	IPR003347*JmjC domain
1.66E-07	IPR013519*Integrin alpha beta-propellor, IPR013517*FG-GAP repeat, IPR000413*Integrin alpha c
1.04E-06	NA
4.28E-09	IPR026791*Dedicator of cytokinesis, IPR010703*Dedicator of cytokinesis, C-terminal, IPR011993*
6.87E-10	NA
5.68E-06	IPR023796*Serpin domain, IPR000215*Serpin family
3.70E-06	IPR000504*RNA recognition motif domain
8.87E-05	IPR000172*Glucose-methanol-choline oxidoreductase, N-terminal, IPR007867*Glucose-methanol-
0.0024207	IPR012496*TMC
3.55E-08	IPR005301*MOB kinase activator family
7.91E-08	IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR013594*Dynein heavy chain,
3.25E-08	NA
0.000682	NA
0.0013489	IPR001139*Glycoside hydrolase family 30
2.67E-08	NA
8.17E-09	IPR001650*Helicase, C-terminal, IPR027417*P-loop containing nucleoside triphosphate hydrolase
2.05E-05	NA
0.0004513	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
9.65E-05	IPR006616*DM9 repeat, IPR024518*Domain of unknown function DUF3421
1.51E-06	IPR002509*NodB homology domain, IPR011330*Glycoside hydrolase/deacetylase, beta/alpha-barr
8.17E-09	IPR016024*Armadillo-type fold
6.50E-05	NA
2.49E-06	NA
4.69E-07	NA
1.44E-08	IPR004887*Glutathione synthase, substrate-binding, eukaryotic
3.43E-06	NA
3.69E-08	NA

1.91E-06	NA
0.0032251	IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain, IPR022271*Lipocalin
2.04E-08	IPR001507*Zona pellucida domain
4.04E-06	IPR002073*3'5'-cyclic nucleotide phosphodiesterase, catalytic domain
2.39E-06	IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
6.06E-07	IPR023082*Homeo-prospero domain, IPR009057*Homeobox domain-like
0.0004197	NA
8.61E-07	IPR001452*SH3 domain, IPR001841*Zinc finger, RING-type, IPR013083*Zinc finger, RING/FYVE/
5.49E-07	NA
2.63E-05	NA
6.59E-08	IPR013083*Zinc finger, RING/FYVE/PHD-type, IPR028938*Remodeling and spacing factor 1, IPR0
4.51E-09	IPR009057*Homeobox domain-like, IPR013087*Zinc finger C2H2-type, IPR000949*ELM2 domain,
0.0001499	IPR028082*Periplasmic binding protein-like I, IPR000337*GPCR, family 3, IPR000162*GPCR, fami
0.0001284	NA
2.04E-06	IPR026299*Mitochondrial 28S ribosomal protein S31
2.77E-06	NA
4.42E-08	IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR011527*ABC transporter type
4.35E-08	IPR015919*Cadherin-like, IPR000742*EGF-like domain, IPR001791*Laminin G domain, IPR01332
8.97E-05	IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
1.56E-08	IPR027005*Glycosyltransferase 39-like, IPR016093*MIR motif, IPR003342*Glycosyl transferase fa
1.88E-08	IPR013761*Sterile alpha motif/pointed domain, IPR001660*Sterile alpha motif domain
4.89E-06	IPR003439*ABC transporter-like, IPR027417*P-loop containing nucleoside triphosphate hydrolase,
1.32E-08	IPR031557*N-CoR, GPS2-interacting domain, IPR009057*Homeobox domain-like, IPR001005*SA
1.85E-08	IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
2.01E-06	IPR000210*BTB/POZ domain, IPR011333*SKP1/BTB/POZ domain, IPR013087*Zinc finger C2H2-
4.69E-06	NA
2.83E-05	IPR011990*Tetratricopeptide-like helical domain
2.28E-07	IPR016024*Armadillo-type fold, IPR000403*Phosphatidylinositol 3-/4-kinase, catalytic domain, IPR
5.54E-06	NA
9.62E-05	IPR012336*Thioredoxin-like fold, IPR010987*Glutathione S-transferase, C-terminal-like, IPR00404
5.44E-09	IPR000008*C2 domain, IPR011992*EF-hand domain pair, IPR029071*Ubiquitin-related domain, IP
1.53E-07	IPR026082*ABC transporter A, ABCA, IPR003439*ABC transporter-like, IPR027417*P-loop contai
1.27E-08	IPR000668*Peptidase C1A, papain C-terminal, IPR012599*Peptidase C1A, propeptide, IPR013128
2.93E-05	NA
4.34E-08	IPR011012*Longin-like domain, IPR028565*Mu homology domain, IPR022775*AP complex, mu/si
0.0016249	IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
1.79E-06	IPR002219*Protein kinase C-like, phorbol ester/diacylglycerol-binding domain, IPR001206*Diacylgl
9.14E-09	IPR013128*Peptidase C1A, IPR000668*Peptidase C1A, papain C-terminal, IPR012599*Peptidase
3.41E-07	IPR001609*Myosin head, motor domain, IPR027417*P-loop containing nucleoside triphosphate hy
0.0018193	IPR012336*Thioredoxin-like fold, IPR010987*Glutathione S-transferase, C-terminal-like, IPR00404
3.83E-06	IPR013087*Zinc finger C2H2-type, IPR000210*BTB/POZ domain, IPR011333*SKP1/BTB/POZ do
1.49E-08	NA
0.0006455	NA
7.63E-05	IPR001708*Membrane insertase OXA1/ALB3/YidC
1.63E-07	IPR019356*Protein of unknown function DUF2181
6.82E-08	IPR000949*ELM2 domain, IPR009057*Homeobox domain-like, IPR002951*Atrophin-like, IPR0010
7.98E-07	IPR026818*Adenomatous polyposis coli (APC) family, IPR011989*Armadillo-like helical, IPR0160

0.0001109	IPR023780*Chromo domain, IPR016197*Chromo domain-like, IPR027417*P-loop containing nucle
9.00E-08	IPR013087*Zinc finger C2H2-type
5.75E-05	NA
6.81E-07	IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase, IPR007235*Glycosyl transferase, family 2
4.17E-09	IPR001807*Chloride channel, voltage gated, IPR014743*Chloride channel, core
2.45E-07	IPR007235*Glycosyl transferase, family 28, C-terminal, IPR002213*UDP-glucuronosyl/UDP-glucos
5.88E-08	IPR003169*GYF domain, IPR035445*GYF-like domain
1.41E-06	NA
4.45E-05	IPR031542*Cation channel complex component UNC80, N-terminal
1.29E-05	IPR011527*ABC transporter type 1, transmembrane domain, IPR003439*ABC transporter-like, IPR
3.04E-05	IPR013201*Cathepsin propeptide inhibitor domain (I29), IPR000668*Peptidase C1A, papain C-term
1.10E-05	IPR002504*NAD kinase, IPR017437*ATP-NAD kinase, PpnK-type, all-beta, IPR017438*Inorganic
1.30E-05	IPR014720*Double-stranded RNA-binding domain, IPR000467*G-patch domain
0.0001789	NA
5.82E-06	IPR000504*RNA recognition motif domain
2.07E-08	IPR001054*Adenylyl cyclase class-3/4/guanylyl cyclase, IPR029787*Nucleotide cyclase, IPR00939
1.57E-07	IPR032675*Leucine-rich repeat domain, L domain-like, IPR000483*Cysteine-rich flanking region, C
9.74E-08	IPR000331*Rap GTPase activating protein domain, IPR001478*PDZ domain
3.58E-07	NA
1.16E-06	IPR029058*Alpha/Beta hydrolase fold, IPR006693*Partial AB-hydrolase lipase domain, IPR000073
2.90E-05	NA
8.93E-09	IPR011993*PH domain-like, IPR006020*PTB/PI domain, IPR028761*Protein disabled, IPR015943*
1.09E-08	IPR013094*Alpha/beta hydrolase fold-3, IPR029058*Alpha/Beta hydrolase fold
8.82E-06	NA
8.82E-08	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
0.0003728	IPR006621*Nose resistant-to-fluoxetine protein, N-terminal
7.31E-08	IPR010703*Dedicator of cytokinesis, C-terminal, IPR000008*C2 domain, IPR026791*Dedicator of
6.06E-07	NA
1.18E-08	IPR029058*Alpha/Beta hydrolase fold, IPR006693*Partial AB-hydrolase lipase domain
1.56E-05	IPR011992*EF-hand domain pair
6.37E-08	IPR013201*Cathepsin propeptide inhibitor domain (I29), IPR000668*Peptidase C1A, papain C-term
1.87E-07	NA
4.61E-05	IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
0.0001676	NA
1.10E-05	IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
0.000184	IPR001806*Small GTPase superfamily, IPR027417*P-loop containing nucleoside triphosphate hydr
3.09E-08	IPR011011*Zinc finger, FYVE/PHD-type, IPR013083*Zinc finger, RING/FYVE/PHD-type, IPR00030
5.46E-07	NA
1.60E-07	IPR014799*Apx/Shrm Domain 2, IPR027685*Shroom family
7.51E-09	IPR015919*Cadherin-like, IPR001791*Laminin G domain, IPR000742*EGF-like domain, IPR00212
1.41E-06	IPR013783*Immunoglobulin-like fold, IPR003598*Immunoglobulin subtype 2, IPR013098*Immunog
0.0003769	NA
4.02E-05	IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR000863*Sulfotransferase dom
4.24E-07	IPR001806*Small GTPase superfamily, IPR020849*Small GTPase superfamily, Ras type, IPR0274
0.0013363	IPR029058*Alpha/Beta hydrolase fold, IPR006693*Partial AB-hydrolase lipase domain
3.28E-05	IPR009057*Homeobox domain-like, IPR001356*Homeobox domain
6.96E-06	IPR006029*Neurotransmitter-gated ion-channel transmembrane domain, IPR006201*Neurotransmi

2.38E-07	IPR011527*ABC transporter type 1, transmembrane domain, IPR027417*P-loop containing nucleos
8.23E-05	IPR013083*Zinc finger, RING/FYVE/PHD-type, IPR008974*TRAF-like, IPR001293*Zinc finger, TRA
1.73E-06	IPR018484*Carbohydrate kinase, FGGY, N-terminal
6.95E-05	IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
2.90E-05	IPR011990*Tetratricopeptide-like helical domain, IPR019734*Tetratricopeptide repeat
3.22E-07	IPR017926*Glutamine amidotransferase, IPR029062*Class I glutamine amidotransferase-like, IPR
2.22E-06	IPR013087*Zinc finger C2H2-type
4.40E-09	NA
4.83E-08	IPR012954*BP28, C-terminal domain, IPR016024*Armadillo-type fold, IPR022125*U3 small nucleo
0.0020708	NA
2.63E-07	IPR001781*Zinc finger, LIM-type, IPR011333*SKP1/BTB/POZ domain, IPR000331*Rap GTPase a
0.0008789	NA
1.26E-05	IPR029162*TRP-interacting helix, InaF motif
6.04E-09	IPR000203*GPS motif, IPR000832*GPCR, family 2, secretin-like, IPR032471*GAIN domain, N-term
0.0019437	NA
2.69E-07	IPR000008*C2 domain, IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR0140
8.18E-08	IPR011035*Ribosomal protein L25/Gln-tRNA synthetase, anti-codon-binding domain, IPR000924*G
5.80E-08	IPR006571*TLDc domain
1.41E-05	NA
9.77E-09	IPR003316*E2F/DP family, winged-helix DNA-binding domain, IPR011991*Winged helix-turn-helix
3.62E-05	IPR019716*Ribosomal protein L53, mitochondrial
2.05E-06	IPR000008*C2 domain
1.14E-06	IPR023801*Histone deacetylase domain, IPR000286*Histone deacetylase superfamily
1.78E-07	NA
3.81E-06	IPR002999*Tudor domain
2.56E-07	IPR013087*Zinc finger C2H2-type, IPR013083*Zinc finger, RING/FYVE/PHD-type
1.22E-08	IPR001202*WW domain, IPR000008*C2 domain, IPR000569*HECT domain
0.0001052	IPR008914*Phosphatidylethanolamine-binding protein
2.01E-06	NA
9.04E-08	IPR019680*Mediator complex, subunit Med1
2.39E-07	IPR013087*Zinc finger C2H2-type
3.72E-05	IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
1.84E-08	NA
5.49E-05	NA
2.29E-06	IPR011993*PH domain-like, IPR000219*Dbl homology (DH) domain
4.37E-07	NA
0.0015323	NA
0.0011633	NA
0.0030383	IPR012674*Calycin, IPR022271*Lipocalin, ApoD type, IPR003057*Invertebrate colouration protein,
7.05E-07	IPR029304*A-kinase anchor protein 2, C-terminal domain
2.11E-08	IPR001611*Leucine-rich repeat, IPR001478*PDZ domain, IPR032675*Leucine-rich repeat domain,
0.0038521	IPR023796*Serpin domain, IPR000215*Serpin family
4.52E-05	IPR001478*PDZ domain
1.30E-05	IPR032675*Leucine-rich repeat domain, L domain-like
5.62E-07	NA
8.45E-06	IPR021643*Mediator complex, subunit Med13, N-terminal, metazoa/fungi, IPR009401*Mediator com
0.0002724	IPR011705*BTB/Kelch-associated, IPR011333*SKP1/BTB/POZ domain, IPR011042*Six-bladed be

4.07E-06	NA
1.80E-05	IPR003593*AAA+ ATPase domain, IPR011940*Meiotic recombinase Dmc1, IPR016467*DNA reco
3.73E-05	NA
0.0001368	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
5.37E-06	NA
1.58E-06	IPR002919*Trypsin Inhibitor-like, cysteine rich domain
8.17E-09	IPR011993*PH domain-like, IPR000198*Rho GTPase-activating protein domain, IPR008936*Rho
5.70E-08	IPR005078*Peptidase C54
1.09E-07	IPR031570*Domain of unknown function DUF4704, IPR000409*BEACH domain, IPR011993*PH d
2.66E-05	NA
7.09E-06	IPR001139*Glycoside hydrolase family 30, IPR033452*Glycosyl hydrolase family 30, beta sandwic
5.36E-06	NA
6.19E-08	IPR011047*Quinoprotein alcohol dehydrogenase-like superfamily, IPR032675*Leucine-rich repeat
3.67E-09	IPR001241*DNA topoisomerase, type IIA, IPR013757*Type IIA DNA topoisomerase subunit A, alp
1.24E-07	IPR001810*F-box domain
0.000852	IPR002656*Acyltransferase 3
2.65E-06	IPR009071*High mobility group box domain
1.27E-05	NA
2.42E-07	IPR032675*Leucine-rich repeat domain, L domain-like, IPR003591*Leucine-rich repeat, typical sub
3.45E-06	IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
2.67E-06	IPR020846*Major facilitator superfamily domain, IPR024989*Major facilitator superfamily associate
3.04E-07	NA
4.82E-08	IPR001680*WD40 repeat, IPR017986*WD40-repeat-containing domain, IPR015943*WD40/YVTN
9.22E-07	IPR011993*PH domain-like, IPR001849*Pleckstrin homology domain, IPR002404*IRS-type PTB d
5.73E-07	IPR013083*Zinc finger, RING/FYVE/PHD-type, IPR013087*Zinc finger C2H2-type
3.58E-07	IPR029062*Class I glutamine amidotransferase-like, IPR015527*Peptidase C26, gamma-glutamyl
0.0008981	NA
1.67E-05	NA
0.0004802	NA
7.11E-07	IPR032675*Leucine-rich repeat domain, L domain-like, IPR000157*Toll/interleukin-1 receptor hom
1.02E-08	IPR014889*Transcription factor DP, C-terminal, IPR011991*Winged helix-turn-helix DNA-binding d
1.49E-05	NA
4.32E-08	IPR001680*WD40 repeat, IPR015943*WD40/YVTN repeat-like-containing domain, IPR011990*Tet
8.28E-08	IPR000014*PAS domain, IPR017426*Nuclear receptor coactivator
1.50E-07	IPR026805*GW182, middle domain, IPR033503*Protein Gawky
1.78E-08	IPR002017*Spectrin repeat, IPR018159*Spectrin/alpha-actinin
2.73E-07	IPR029016*GAF domain-like, IPR003018*GAF domain
1.93E-07	IPR001394*Peptidase C19, ubiquitin carboxyl-terminal hydrolase, IPR016024*Armadillo-type fold
0.0007418	NA
1.09E-07	NA
8.70E-05	NA
5.97E-07	IPR029064*50S ribosomal protein L30e-like, IPR000530*Ribosomal protein S12e, IPR004038*Rib
3.61E-08	IPR000058*Zinc finger, AN1-type
9.00E-06	NA
2.22E-08	IPR023566*Peptidyl-prolyl cis-trans isomerase, FKBP-type, IPR001179*FKBP-type peptidyl-prolyl
7.17E-07	IPR010530*NADH-ubiquinone reductase complex 1 MLRQ subunit
1.40E-05	IPR000007*Tubby, C-terminal, IPR025659*Tubby C-terminal-like domain

1.21E-05	IPR003038*DAD/Ost2
1.59E-05	NA
1.75E-08	IPR016295*Proteasome endopeptidase complex, beta subunit, IPR029055*Nucleophile aminohydr
5.75E-08	IPR005024*Snf7 family
8.81E-09	IPR005703*Ribosomal protein S3, eukaryotic/archaeal, IPR001351*Ribosomal protein S3, C-termi
1.69E-08	IPR002672*Ribosomal protein L28e, IPR029004*Ribosomal L28e/Mak16
1.39E-06	NA
1.06E-07	IPR009622*NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4
1.44E-05	IPR001978*Troponin
1.56E-08	NA
1.86E-05	IPR001715*Calponin homology domain, IPR003096*Smooth muscle protein/calponin
4.00E-06	IPR005062*SAC3/GANP/THP3
4.91E-09	IPR018629*XK-related protein
1.24E-07	IPR008949*Isoprenoid synthase domain, IPR000092*Polyprenyl synthetase
1.36E-08	IPR024130*DAP1/DAPL1
1.07E-06	IPR004947*Deoxyribonuclease II, IPR009567*Store-operated calcium entry-associated regulatory
1.09E-08	IPR016180*Ribosomal protein L10e/L16, IPR000114*Ribosomal protein L16
9.73E-09	IPR001971*Ribosomal protein S11
8.06E-08	IPR015720*TMP21-related, IPR009038*GOLD domain
3.43E-07	IPR008025*PKC-activated phosphatase-1 inhibitor
1.35E-06	NA
0.0001114	NA
1.46E-07	IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
0.00018	IPR016181*Acyl-CoA N-acyltransferase, IPR000182*GNAT domain
0.0019044	NA
3.32E-05	NA
2.64E-05	IPR001873*Epithelial sodium channel
1.24E-07	NA
3.53E-07	IPR004205*Cytochrome b-c1 complex subunit 8
4.52E-08	IPR006137*NADH:ubiquinone oxidoreductase-like, 20kDa subunit, IPR006138*NADH-ubiquinone
2.36E-05	NA
1.31E-05	NA
4.77E-08	IPR015819*Lipid transport protein, beta-sheet shell, IPR011030*Vitellinogen, superhelical, IPR001
6.30E-06	IPR000182*GNAT domain, IPR016181*Acyl-CoA N-acyltransferase
3.19E-05	IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
2.98E-06	IPR011992*EF-hand domain pair
0.000291	NA
9.77E-09	NA
6.22E-05	IPR002350*Kazal domain, IPR013783*Immunoglobulin-like fold, IPR003599*Immunoglobulin subty
2.16E-06	IPR014044*CAP domain, IPR034113*Golgi-associated plant pathogenesis-related protein 1, SCP
0.0059965	IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
0.0003126	IPR008278*4'-phosphopantetheinyl transferase superfamily
2.44E-09	IPR003172*MD-2-related lipid-recognition domain, IPR028996*Ganglioside GM2 activator
0.0031855	NA
9.70E-08	IPR035426*Gemin2/Brr1, IPR017364*Gem-associated protein 2
3.14E-05	NA
0.0005731	IPR000618*Insect cuticle protein

1.57E-07	IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
1.40E-05	IPR023262*Active regulator of SIRT1
3.32E-05	IPR001978*Troponin
0.0010631	IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
0.0012157	IPR000175*Sodium:neurotransmitter symporter
9.52E-06	NA
9.19E-06	IPR011598*Myc-type, basic helix-loop-helix (bHLH) domain, IPR003650*Orange domain
1.20E-07	NA
1.45E-08	IPR013170*mRNA splicing factor Cwf21 domain
2.13E-07	IPR009044*ssDNA-binding transcriptional regulator, IPR003173*Transcriptional coactivator p15 (P
3.70E-06	IPR014756*Immunoglobulin E-set, IPR013783*Immunoglobulin-like fold, IPR017868*Filamin/ABP2
1.39E-08	IPR005225*Small GTP-binding protein domain, IPR027417*P-loop containing nucleoside triphosph
2.07E-06	IPR000010*Cystatin domain
9.79E-09	NA
5.42E-06	IPR027408*PNPase/RNase PH domain, IPR015847*Exoribonuclease, phosphorolytic domain 2, IP
4.09E-05	IPR000276*G protein-coupled receptor, rhodopsin-like
8.61E-08	IPR020568*Ribosomal protein S5 domain 2-type fold, IPR015847*Exoribonuclease, phosphorolytic
5.38E-10	IPR006139*D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain, IPR006140*D-isome
1.49E-06	IPR016090*Phospholipase A2 domain
1.57E-07	IPR020546*ATP synthase, F1 complex, delta/epsilon subunit, N-terminal, IPR001469*ATP synthas
0.0012998	NA
0.0006844	NA
1.09E-05	IPR001040*Translation Initiation factor eIF- 4e, IPR023398*Translation Initiation factor eIF- 4e-like
0.0019935	NA
1.62E-06	IPR007699*SGS domain
2.73E-08	IPR009030*Growth factor receptor cysteine-rich domain
4.84E-06	IPR013106*Immunoglobulin V-set domain, IPR013783*Immunoglobulin-like fold, IPR013098*Immu
3.72E-07	NA
3.66E-06	IPR000679*Zinc finger, GATA-type, IPR016374*Transcription factor, GATA-2/3, IPR013088*Zinc fi
0.0009933	NA
0.0349563	NA
9.06E-05	NA
9.23E-08	IPR009787*Protein jagunal
1.30E-07	NA
7.03E-07	IPR018784*Learning associated protein 18-like
0.0018985	IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
2.58E-06	IPR001971*Ribosomal protein S11
1.26E-07	NA
0.000129	NA
9.04E-08	IPR009069*Cysteine alpha-hairpin motif superfamily, IPR010625*CHCH, IPR033620*Coiled-coil-he
4.59E-06	IPR029008*Rab5-interacting protein family, IPR010742*Rab5-interacting protein
2.00E-06	IPR001451*Hexapeptide repeat, IPR011004*Trimeric LpxA-like
0.0003754	NA
5.63E-08	IPR005570*RNA polymerase, Rpb8, IPR012340*Nucleic acid-binding, OB-fold
5.41E-08	IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
0.0011336	NA
3.77E-06	NA

4.08E-07	IPR011598*Myc-type, basic helix-loop-helix (bHLH) domain, IPR032664*Protein atonal/amos/lin-32
0.000483	IPR029034*Cystine-knot cytokine, IPR002072*Nerve growth factor-related
2.99E-06	NA
8.92E-06	IPR000618*Insect cuticle protein
1.33E-06	NA
1.03E-05	IPR001507*Zona pellucida domain, IPR003609*PAN/Apple domain
1.25E-07	IPR008699*NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8
1.97E-06	IPR001881*EGF-like calcium-binding domain, IPR001791*Laminin G domain, IPR000742*EGF-like
7.67E-05	IPR006073*GTP binding domain, IPR023179*GTP-binding protein, orthogonal bundle domain, IPR
0.0001435	IPR002769*Translation initiation factor IF6
0.0001101	IPR004294*Carotenoid oxygenase
6.39E-05	NA
4.33E-05	IPR000536*Nuclear hormone receptor, ligand-binding domain
1.05E-08	NA
3.42E-06	IPR001163*LSM domain, eukaryotic/archaea-type, IPR027141*Like-Sm (LSM) domain containing
3.32E-07	IPR027486*Ribosomal protein S10 domain
9.58E-09	IPR013786*Acyl-CoA dehydrogenase/oxidase, N-terminal, IPR009075*Acyl-CoA dehydrogenase/o
3.96E-09	IPR001951*Histone H4, IPR035425*CENP-T/Histone H4, histone fold, IPR009072*Histone-fold
0.0018565	NA
0.0016821	IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR022780*Dynein family light in
0.0007849	NA
1.81E-07	IPR002836*PDCD5-related protein
9.56E-07	IPR002446*Lipocalin, bacterial, IPR012674*Calycin, IPR002345*Lipocalin, IPR022271*Lipocalin, A
6.84E-07	IPR003096*Smooth muscle protein/calponin, IPR001997*Calponin/LIMCH1, IPR001715*Calponin
3.46E-06	IPR007867*Glucose-methanol-choline oxidoreductase, C-terminal, IPR023753*FAD/NAD(P)-bindin
7.91E-06	NA
2.73E-07	IPR005345*PHF5-like
2.98E-05	IPR001873*Epithelial sodium channel
3.28E-07	IPR014810*Fcf2 pre-rRNA processing
4.97E-10	IPR001593*Ribosomal protein S3Ae
1.63E-07	IPR010014*Diphthamide synthesis DHP2, eukaryotes, IPR016435*Diphthamide synthesis DPH1/D
4.70E-08	IPR019831*Manganese/iron superoxide dismutase, N-terminal, IPR001189*Manganese/iron super
7.60E-08	NA
5.06E-06	NA
1.13E-07	IPR008991*Translation protein SH3-like domain, IPR001141*Ribosomal protein L27e, IPR014722*
3.12E-07	IPR024991*Anaphase-promoting complex subunit 11, IPR013083*Zinc finger, RING/FYVE/PHD-ty
5.45E-05	NA
8.51E-05	IPR001978*Troponin
3.34E-07	NA
1.27E-05	NA
4.15E-06	NA
0.0003832	NA
0.0018642	IPR003439*ABC transporter-like, IPR003593*AAA+ ATPase domain, IPR027417*P-loop containin
0.0002971	NA
6.53E-08	IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
8.13E-07	IPR002048*EF-hand domain, IPR011992*EF-hand domain pair
5.64E-07	NA

2.33E-08	IPR006925*Vps16, C-terminal
6.25E-08	IPR008386*ATP synthase, F0 complex, subunit E, mitochondrial
0.0035055	NA
6.69E-08	IPR000182*GNAT domain, IPR016181*Acyl-CoA N-acyltransferase
6.92E-08	IPR001564*Nucleoside diphosphate kinase, IPR034907*Nucleoside diphosphate kinase-like domai
1.41E-05	NA
1.34E-06	NA
1.01E-08	IPR008927*6-phosphogluconate dehydrogenase C-terminal domain-like, IPR006176*3-hydroxyacy
2.72E-06	IPR011425*Mediator of RNA polymerase II transcription subunit 9
0.0093677	NA
2.32E-08	IPR003172*MD-2-related lipid-recognition domain, IPR014756*Immunoglobulin E-set
6.49E-05	NA
6.02E-08	IPR013785*Aldolase-type TIM barrel, IPR001093*IMP dehydrogenase/GMP reductase, IPR005993
0.0001123	NA
1.50E-06	IPR008012*Proteasome maturation factor Ump1
4.34E-08	IPR010979*Ribosomal protein S13-like, H2TH, IPR001892*Ribosomal protein S13, IPR027437*30
9.83E-08	IPR021019*Mediator complex, subunit Med30, metazoa
6.57E-06	IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR001650*Helicase, C-terminal,
6.27E-09	NA
3.90E-06	NA
1.51E-07	IPR023485*Phosphotyrosine protein phosphatase I superfamily, IPR017867*Protein-tyrosine phos
0.0004031	NA
3.00E-08	IPR005351*Uncharacterised protein family UPF0139
0.0010966	IPR020846*Major facilitator superfamily domain
0.0005958	IPR010541*Domain of unknown function DUF1115, IPR017359*Uncharacterised conserved protei
1.26E-06	IPR008775*Phytanoyl-CoA dioxygenase
6.89E-05	NA
0.0014167	NA
6.88E-09	IPR000911*Ribosomal protein L11/L12, IPR020784*Ribosomal protein L11, N-terminal, IPR020783
6.00E-06	NA
3.88E-08	NA
3.43E-06	NA
6.88E-09	IPR000754*Ribosomal protein S9, IPR014721*Ribosomal protein S5 domain 2-type fold, subgroup,
9.34E-09	IPR005302*Molybdenum cofactor sulfurase, C-terminal, IPR005303*MOSC, N-terminal beta barrel,
3.06E-06	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
1.28E-06	IPR012875*Protein of unknown function DUF1674
1.46E-09	IPR006204*GHMP kinase N-terminal domain, IPR014721*Ribosomal protein S5 domain 2-type fol
4.19E-07	IPR000560*Histidine phosphatase superfamily, clade-2, IPR029033*Histidine phosphatase superfa
1.65E-07	IPR021475*Protein of unknown function DUF3128
7.03E-07	IPR006091*Acyl-CoA oxidase/dehydrogenase, central domain, IPR002655*Acyl-CoA oxidase, C-te
5.84E-05	NA
9.51E-07	IPR012340*Nucleic acid-binding, OB-fold
1.29E-06	IPR015915*Kelch-type beta propeller
0.0003101	IPR002076*ELO family
1.09E-07	NA
0.0001666	IPR011009*Protein kinase-like domain, IPR000719*Protein kinase domain
9.79E-09	IPR007482*Protein-tyrosine phosphatase-like, PTPLA

0.0005616	IPR019335*Conserved oligomeric Golgi complex subunit 7
1.57E-07	IPR016024*Armadillo-type fold, IPR010472*Formin, FH3 domain, IPR010473*Formin, GTPase-bin
8.19E-09	NA
1.33E-06	IPR023803*Ribosomal protein S16 domain, IPR000307*Ribosomal protein S16
9.85E-08	NA
5.05E-06	IPR000276*G protein-coupled receptor, rhodopsin-like
1.06E-05	IPR001163*LSM domain, eukaryotic/archaea-type, IPR027078*Small nuclear ribonucleoprotein E,
1.82E-07	NA
0.0001861	IPR008922*Uncharacterised domain, di-copper centre, IPR002227*Tyrosinase copper-binding dom
1.80E-07	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
5.43E-08	IPR029063*S-adenosyl-L-methionine-dependent methyltransferase
1.89E-05	IPR009792*Transmembrane protein 242
1.71E-07	IPR024771*SUZ domain
5.54E-07	IPR034103*Sm-like protein Lsm8, IPR001163*LSM domain, eukaryotic/archaea-type, IPR010920*
4.93E-09	IPR011042*Six-bladed beta-propeller, TolB-like, IPR000033*LDLR class B repeat
2.13E-09	IPR007125*Histone H2A/H2B/H3, IPR002119*Histone H2A, IPR032454*Histone H2A, C-terminal
4.62E-08	IPR000504*RNA recognition motif domain, IPR008111*RNA-binding motif protein 8, IPR033744*R
0.0005004	IPR032675*Leucine-rich repeat domain, L domain-like
1.55E-07	IPR009423*NADH:ubiquinone oxidoreductase, subunit b14.5b
0.0057895	IPR009003*Peptidase S1, PA clan, IPR001254*Serine proteases, trypsin domain
1.97E-05	IPR001132*SMAD domain, Dwarfin-type, IPR008984*SMAD/FHA domain, IPR017855*SMAD dom
4.88E-09	IPR021138*60S ribosomal protein L18a/ L20, eukaryotes, IPR023573*Ribosomal protein 50S-L18
3.01E-07	NA
8.78E-07	NA
3.87E-05	NA
1.43E-06	IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
3.01E-08	IPR009000*Translation protein, beta-barrel domain, IPR001780*Ribosomal protein L35A
5.99E-08	NA
1.18E-06	NA
1.62E-06	NA
0.0005212	NA
1.73E-06	NA
6.79E-06	IPR007513*Uncharacterised protein family SERF
1.40E-05	IPR012336*Thioredoxin-like fold, IPR010987*Glutathione S-transferase, C-terminal-like, IPR00404
0.0032099	NA
1.55E-09	IPR014756*Immunoglobulin E-set, IPR003172*MD-2-related lipid-recognition domain
0.0007009	IPR001025*Bromo adjacent homology (BAH) domain
1.16E-09	NA
3.59E-08	IPR019192*Ribosomal protein L28/L40, mitochondrial
1.26E-07	IPR004104*Oxidoreductase, C-terminal, IPR016040*NAD(P)-binding domain, IPR000683*Oxidore
2.43E-06	IPR006806*ETC complex I subunit
0.0003727	IPR028172*Intraflagellar transport protein 20
6.91E-06	IPR008979*Galactose-binding domain-like
2.69E-10	IPR004345*TB2/DP1/HVA22-related protein
0.001506	IPR012132*Glucose-methanol-choline oxidoreductase, IPR000172*Glucose-methanol-choline oxid
7.64E-07	IPR027248*Small nuclear ribonucleoprotein Sm D2, IPR001163*LSM domain, eukaryotic/archaea-
2.17E-06	IPR029064*50S ribosomal protein L30e-like, IPR004038*Ribosomal protein L7Ae/L30e/S12e/Gadd

1.43E-09	IPR013810*Ribosomal protein S5, N-terminal, IPR020568*Ribosomal protein S5 domain 2-type fol
0.0004197	NA
9.21E-07	IPR031145*Invertebrate aquaporin-10, IPR023271*Aquaporin-like, IPR000425*Major intrinsic prote
1.94E-09	IPR003172*MD-2-related lipid-recognition domain, IPR014756*Immunoglobulin E-set
9.51E-07	NA
8.20E-06	IPR008993*Tissue inhibitor of metalloproteinases-like, OB-fold, IPR004850*NtA (N-terminal agrin)
3.79E-07	IPR004942*Roadblock/LAMTOR2 domain
0.001623	NA
0.0005875	NA
1.62E-06	NA
2.12E-09	IPR009582*Signal peptidase complex subunit 2
7.59E-06	IPR015943*WD40/YVTN repeat-like-containing domain, IPR017986*WD40-repeat-containing doma
1.21E-07	NA
2.68E-05	IPR002557*Chitin binding domain
7.71E-07	IPR009653*Protein kish
2.80E-07	IPR010997*HRDC-like, IPR005574*RNA polymerase II, Rpb4, IPR006590*RNA polymerase II, Rp
3.61E-09	IPR000235*Ribosomal protein S5/S7, IPR023798*Ribosomal protein S7 domain, IPR005716*Ribos
3.41E-08	IPR006176*3-hydroxyacyl-CoA dehydrogenase, NAD binding, IPR016040*NAD(P)-binding domain,
1.76E-06	IPR029008*Rab5-interacting protein family, IPR008504*ER membrane protein complex subunit 6
2.42E-07	NA
1.08E-06	IPR009846*Splicing factor 3B subunit 5/RDS3 complex subunit 10, IPR017089*Splicing factor 3B,
2.89E-05	IPR029069*HotDog domain, IPR002539*MaoC-like domain
9.44E-10	IPR004895*Prenylated rab acceptor PRA1
7.64E-07	NA
0.0010864	NA
7.32E-08	NA
1.18E-09	IPR000630*Ribosomal protein S8
2.27E-06	NA
1.47E-09	IPR022801*Ribosomal protein S4/S9, IPR002942*RNA-binding S4 domain, IPR005710*Ribosomal
2.98E-05	IPR002557*Chitin binding domain
3.58E-09	IPR019344*Mitochondrial F1-F0 ATP synthase subunit F, predicted
2.21E-09	IPR001063*Ribosomal protein L22/L17, IPR005721*Ribosomal protein L22/L17, eukaryotic/archae
0.0001483	NA
3.23E-09	IPR023175*Vacuolar protein sorting-associate protein Vta1/Callose synthase, N-terminal domain
4.44E-09	IPR000608*Ubiquitin-conjugating enzyme E2, IPR016135*Ubiquitin-conjugating enzyme/RWD-like
5.66E-05	IPR019335*Conserved oligomeric Golgi complex subunit 7
2.49E-07	NA
2.74E-05	NA
2.18E-09	IPR001950*SUI1 domain, IPR005874*Eukaryotic translation initiation factor SUI1
9.59E-09	NA
0.0006816	IPR004856*Glycosyl transferase, ALG6/ALG8
0.0001728	IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
0.0002871	IPR006202*Neurotransmitter-gated ion-channel ligand-binding domain, IPR006201*Neurotransmitt
2.44E-09	IPR001380*Ribosomal protein L13e, IPR034295*Ribosomal protein L13, eukaryotic
3.54E-08	IPR019774*Aromatic amino acid hydroxylase, C-terminal, IPR002912*ACT domain, IPR001273*Ar
1.44E-08	IPR011701*Major facilitator superfamily, IPR020846*Major facilitator superfamily domain
2.19E-08	IPR014722*Ribosomal protein L2 domain 2, IPR008991*Translation protein SH3-like domain, IPR0

1.98E-06	IPR024072*Dihydrofolate reductase-like domain, IPR012259*Dihydrofolate reductase, IPR001796*
1.71E-07	IPR000073*Alpha/beta hydrolase fold-1, IPR006693*Partial AB-hydrolase lipase domain, IPR0254
1.17E-08	NA
1.04E-05	IPR001660*Sterile alpha motif domain, IPR013761*Sterile alpha motif/pointed domain
1.04E-06	IPR000086*NUDIX hydrolase domain, IPR015797*NUDIX hydrolase domain-like
1.24E-08	IPR016024*Armadillo-type fold
4.24E-06	NA
1.02E-05	NA
6.04E-06	IPR012446*Calcium release-activated calcium channel protein
6.15E-06	IPR001251*CRAL-TRIO lipid binding domain, IPR000535*Major sperm protein (MSP) domain, IPR
0.0099384	NA
2.45E-08	IPR009346*GRIM-19
8.08E-08	NA
8.25E-06	IPR015889*Intradiol ring-cleavage dioxygenase, core
0.0003947	NA
3.08E-06	IPR015943*WD40/YVTN repeat-like-containing domain, IPR011990*Tetratricopeptide-like helical d
4.77E-07	IPR019346*Ribosomal protein S32, mitochondrial
6.54E-07	IPR000719*Protein kinase domain, IPR011009*Protein kinase-like domain
5.38E-05	IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR011330*Glycoside hydrolase
5.66E-06	IPR018713*Domain of unknown function DUF2236
4.04E-07	IPR018625*Protein Pet100
7.54E-10	IPR000837*AP-1 transcription factor, IPR004827*Basic-leucine zipper domain
0.0002208	NA
1.45E-08	IPR000789*Cyclin-dependent kinase, regulatory subunit
7.60E-05	NA
2.07E-06	IPR023476*Peptidyl-tRNA hydrolase II domain, IPR002833*Peptidyl-tRNA hydrolase, PTH2
6.86E-06	IPR007834*DSS1/SEM1
2.10E-08	IPR012674*Calycin, IPR003057*Invertebrate colouration protein, IPR000566*Lipocalin/cytosolic fat
1.06E-05	NA
1.08E-06	IPR021139*NYN domain, limkain-b1-type, IPR029060*PIN domain-like, IPR024768*Meiosis regula
0.0017378	IPR032006*Transmembrane inner ear expressed protein
3.32E-10	IPR005078*Peptidase C54, IPR011993*PH domain-like
0.0012532	IPR019184*Uncharacterised protein family, transmembrane-17
1.43E-05	IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
1.21E-08	NA
1.14E-07	IPR034884*Mitochondrial cytochrome c oxidase subunit VIc/VIIs
2.18E-05	IPR002919*Trypsin Inhibitor-like, cysteine rich domain
1.10E-07	IPR018469*Dual oxidase maturation factor
5.98E-06	IPR019324*M-phase phosphoprotein 6
9.98E-06	NA
1.95E-06	IPR034295*Ribosomal protein L13, eukaryotic, IPR001380*Ribosomal protein L13e
1.81E-10	IPR017853*Glycoside hydrolase superfamily
2.02E-08	IPR005822*Ribosomal protein L13
1.30E-07	IPR018615*Ribosomal protein L55, mitochondrial
3.51E-08	IPR003439*ABC transporter-like, IPR003593*AAA+ ATPase domain, IPR027417*P-loop containing
0.0012924	NA
2.09E-07	IPR009542*Microsomal signal peptidase 12kDa subunit

2.07E-05	IPR002350*Kazal domain, IPR002049*Laminin EGF domain
1.12E-06	IPR000276*G protein-coupled receptor, rhodopsin-like
5.53E-08	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
9.71E-10	IPR023398*Translation Initiation factor eIF- 4e-like, IPR001040*Translation Initiation factor eIF- 4e
0.0004801	NA
3.31E-09	IPR022309*Ribosomal protein S8e/ribosomal biogenesis NSA2
2.26E-06	IPR000175*Sodium:neurotransmitter symporter
0.0002646	NA
3.03E-07	IPR004045*Glutathione S-transferase, N-terminal, IPR010987*Glutathione S-transferase, C-termin
1.88E-08	NA
6.35E-08	IPR008914*Phosphatidylethanolamine-binding protein
9.56E-06	IPR007007*Ninjurin
3.93E-09	IPR000266*Ribosomal protein S17/S11, IPR012340*Nucleic acid-binding, OB-fold, IPR032440*40
1.06E-09	IPR020471*Aldo/keto reductase, IPR023210*NADP-dependent oxidoreductase domain
5.08E-07	IPR019371*Uncharacterised domain KxDL
7.49E-06	NA
1.29E-06	NA
0.0011486	NA
6.33E-06	NA
0.0003142	NA
0.0004486	NA
1.65E-07	NA
2.89E-06	IPR000850*Adenylate kinase/UMP-CMP kinase, IPR027417*P-loop containing nucleoside triphosp
4.09E-08	IPR008011*Complex 1 LYR protein
3.19E-09	IPR001266*Ribosomal protein S19e, IPR011991*Winged helix-turn-helix DNA-binding domain
5.04E-05	IPR019180*Oxidoreductase-like, N-terminal
5.26E-11	IPR003172*MD-2-related lipid-recognition domain, IPR014756*Immunoglobulin E-set
2.75E-09	NA
0.0003967	NA
1.17E-07	NA
2.46E-08	IPR024766*Zinc finger, RING-H2-type, IPR013083*Zinc finger, RING/FYVE/PHD-type
0.0004553	NA
8.90E-07	NA
1.01E-09	IPR017849*Alkaline phosphatase-like, alpha/beta/alpha, IPR002591*Type I phosphodiesterase/nuc
3.05E-05	NA
0.0001197	IPR032675*Leucine-rich repeat domain, L domain-like, IPR001611*Leucine-rich repeat
0.0001244	NA
9.93E-10	IPR001926*Tryptophan synthase beta subunit-like PLP-dependent enzyme
0.0003766	NA
1.32E-06	NA
6.79E-06	IPR011993*PH domain-like, IPR001849*Pleckstrin homology domain
5.98E-06	IPR009075*Acyl-CoA dehydrogenase/oxidase C-terminal, IPR006621*Nose resistant-to-fluoxetine
3.39E-07	IPR001781*Zinc finger, LIM-type
3.56E-05	IPR006689*Small GTPase superfamily, ARF/SAR type, IPR027417*P-loop containing nucleoside t
1.57E-09	IPR023330*Rhabdovirus nucleocapsid, N-terminal, IPR000448*Rhabdovirus nucleocapsid, IPR023
2.59E-07	IPR001752*Kinesin motor domain, IPR027417*P-loop containing nucleoside triphosphate hydrolas
2.38E-08	IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR007110*Immunoglobulin-like

8.15E-08	IPR006035*Ureohydrolase
0.0019681	IPR003172*MD-2-related lipid-recognition domain, IPR028996*Ganglioside GM2 activator
2.43E-09	IPR001147*Ribosomal protein L21e, IPR008991*Translation protein SH3-like domain
9.34E-07	NA
8.17E-08	NA
1.83E-09	IPR002020*Citrate synthase, IPR010109*Citrate synthase, eukaryotic-type, IPR016142*Citrate syn
5.45E-06	IPR006722*Trafficking protein particle complex subunit 2, IPR011012*Longin-like domain
3.49E-05	IPR001506*Peptidase M12A, IPR024079*Metallopeptidase, catalytic domain
5.20E-08	IPR017132*Sm-like protein Lsm7, IPR001163*LSM domain, eukaryotic/archaea-type, IPR010920*L
6.16E-06	IPR016654*U6 snRNA-associated Sm-like protein LSm2, IPR001163*LSM domain, eukaryotic/arch
7.00E-05	NA
0.0003895	NA
1.46E-09	NA
4.14E-07	IPR015927*Peptidase S24/S26A/S26B/S26C, IPR000223*Peptidase S26A, signal peptidase I, IPR
8.19E-09	NA
1.20E-06	IPR013201*Cathepsin propeptide inhibitor domain (I29), IPR013128*Peptidase C1A
0.0001734	IPR023753*FAD/NAD(P)-binding domain, IPR000960*Flavin monooxygenase FMO, IPR020946*Fl
1.62E-09	IPR011991*Winged helix-turn-helix DNA-binding domain, IPR005326*Plectin/S10, N-terminal
1.73E-10	NA
3.67E-05	NA
4.36E-07	IPR002557*Chitin binding domain
2.02E-06	IPR007264*H/ACA ribonucleoprotein complex, subunit Nop10
5.86E-05	NA
2.49E-07	NA
9.32E-06	NA
2.16E-05	IPR002403*Cytochrome P450, E-class, group IV, IPR001128*Cytochrome P450
1.56E-08	NA
2.74E-09	NA
1.80E-05	IPR001436*Alpha crystallin/Heat shock protein, IPR031107*Small heat shock protein HSP20, IPR0
2.43E-06	IPR034223*Insect gut carboxypeptidase-like, carboxypeptidase domain, IPR000834*Peptidase M1
2.68E-08	IPR005746*Thioredoxin, IPR013766*Thioredoxin domain, IPR012336*Thioredoxin-like fold
1.69E-08	IPR002659*Glycosyl transferase, family 31
0.0003234	IPR004294*Carotenoid oxygenase
2.10E-08	IPR009018*Signal recognition particle, SRP9/SRP14 subunit, IPR008832*Signal recognition particl
1.91E-06	IPR031481*Fucosyltransferase, N-terminal, IPR001503*Glycosyl transferase family 10
2.14E-08	IPR029021*Protein-tyrosine phosphatase-like, IPR000340*Dual specificity phosphatase, catalytic d
6.60E-05	NA
3.56E-10	IPR001747*Lipid transport protein, N-terminal, IPR011030*Vitellinogen, superhelical, IPR001846*v
8.39E-09	IPR019401*Zinc finger, CHCC-type
9.06E-05	IPR008952*Tetraspanin, EC2 domain, IPR000301*Tetraspanin, IPR018499*Tetraspanin/Peripherir
0.0001318	IPR000889*Glutathione peroxidase, IPR012336*Thioredoxin-like fold
0.0002439	NA
7.21E-05	NA
8.26E-06	IPR006616*DM9 repeat, IPR024518*Domain of unknown function DUF3421
0.0010302	IPR024936*Cyclophilin-type peptidyl-prolyl cis-trans isomerase, IPR002130*Cyclophilin-type peptid
9.51E-06	NA
8.24E-05	NA

6.72E-08	IPR013219*Ribosomal protein S27/S33, mitochondrial
7.23E-09	IPR023395*Mitochondrial carrier domain, IPR018108*Mitochondrial substrate/solute carrier, IPR00
1.09E-09	IPR006846*Ribosomal protein S30, IPR029071*Ubiquitin-related domain
1.57E-07	IPR004217*Tim10-like, IPR035427*Tim10/FAM136A-like domain, IPR001478*PDZ domain
7.33E-08	IPR023572*Archease domain, IPR002804*Archease
0.0001194	NA
1.78E-09	IPR026769*MICOS complex subunit Mic13
1.40E-08	IPR002557*Chitin binding domain
4.28E-09	IPR002132*Ribosomal protein L5, IPR022803*Ribosomal protein L5 domain, IPR031310*Ribosom
6.69E-08	IPR011705*BTB/Kelch-associated
1.53E-07	NA
0.000253	IPR001873*Epithelial sodium channel
4.16E-09	IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
1.65E-09	IPR029063*S-adenosyl-L-methionine-dependent methyltransferase, IPR013216*Methyltransferase
8.58E-09	IPR011538*NADH-ubiquinone oxidoreductase 51kDa subunit, FMN-binding domain, IPR019575*N
4.99E-05	NA
2.36E-08	IPR023621*Ribosomal protein L31e domain, IPR000054*Ribosomal protein L31e
2.19E-08	NA
8.29E-07	IPR006225*Pseudouridine synthase, RluC/RluD, IPR006145*Pseudouridine synthase, RsuA/RluB/
0.0008226	NA
7.84E-07	IPR001251*CRAL-TRIO lipid binding domain
1.82E-10	IPR000731*Sterol-sensing domain, IPR003392*Protein patched/dispatched
1.77E-08	IPR000781*Enhancer of rudimentary
2.98E-05	IPR000533*Tropomyosin
0.0002195	IPR000585*Hemopexin-like domain
5.72E-07	IPR019393*WASH complex, subunit strumpellin
3.94E-08	IPR007513*Uncharacterised protein family SERF
1.25E-07	NA
3.26E-06	IPR033378*Protein BRICK1
6.72E-09	IPR029058*Alpha/Beta hydrolase fold, IPR000073*Alpha/beta hydrolase fold-1
0.0004371	NA
0.0004665	NA
2.48E-06	IPR009072*Histone-fold, IPR006809*TAFII28-like protein
3.45E-05	NA
2.76E-07	NA
4.15E-07	IPR002557*Chitin binding domain
6.27E-09	IPR008855*Translocon-associated
3.81E-05	NA
2.68E-07	IPR018793*Cytochrome c oxidase assembly protein PET191
7.51E-06	NA
0.0006021	NA
0.0002457	IPR000618*Insect cuticle protein
4.20E-06	NA
7.76E-06	NA
2.05E-09	IPR001349*Cytochrome c oxidase, subunit VIa
2.53E-05	IPR010920*LSM domain, IPR033871*Sm-like protein LSm5, IPR001163*LSM domain, eukaryotic/
7.57E-10	IPR009779*Translocon-associated protein subunit gamma

1.69E-07	IPR000582*Acyl-CoA-binding protein, ACBP, IPR014352*FERM/acyl-CoA-binding protein, 3-helica
9.53E-06	IPR003205*Cytochrome c oxidase, subunit 8
0.0005881	IPR013087*Zinc finger C2H2-type
1.89E-06	IPR013083*Zinc finger, RING/FYVE/PHD-type, IPR011011*Zinc finger, FYVE/PHD-type
2.12E-07	NA
4.03E-07	IPR009423*NADH:ubiquinone oxidoreductase, subunit b14.5b
0.0001597	NA
0.0002485	NA
0.0001143	NA
1.67E-08	IPR027877*Small integral membrane protein 15
8.32E-11	IPR003195*Transcription initiation factor IID, subunit 13, IPR009072*Histone-fold
3.11E-07	IPR009400*TFIIH subunit TTDA/Tfb5
1.22E-07	IPR027246*Eukaryotic porin/Tom40
0.0009919	NA
0.0002311	NA
4.33E-07	IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
4.43E-05	IPR020635*Tyrosine-protein kinase, catalytic domain, IPR001245*Serine-threonine/tyrosine-protei
1.82E-09	NA
0.0001915	NA
3.25E-07	IPR024936*Cyclophilin-type peptidyl-prolyl cis-trans isomerase, IPR002130*Cyclophilin-type peptid
8.40E-07	IPR032675*Leucine-rich repeat domain, L domain-like
6.25E-09	IPR001781*Zinc finger, LIM-type
5.46E-08	IPR001254*Serine proteases, trypsin domain, IPR009003*Peptidase S1, PA clan
3.73E-06	NA
6.26E-08	IPR031984*Solute carrier family 3 member 2, N-terminal domain
0.000208	IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
7.92E-10	IPR003422*Cytochrome b-c1 complex, subunit 6, IPR023184*Ubiquinol-cytochrome C reductase h
1.43E-09	IPR000592*Ribosomal protein S27e, IPR011332*Zinc-binding ribosomal protein, IPR023407*Ribos
2.97E-06	IPR001283*Cysteine-rich secretory protein, allergen V5/Tpx-1-related, IPR014044*CAP domain, I
7.68E-06	IPR000210*BTB/POZ domain, IPR011705*BTB/Kelch-associated, IPR028764*Kelch repeat and B
1.07E-05	NA
1.09E-07	IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
2.84E-07	NA
6.17E-06	NA
0.0004385	NA
1.81E-07	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
3.54E-08	IPR015089*Cytochrome b-c1 complex subunit 10
1.65E-05	NA
6.69E-06	NA
1.57E-05	IPR000268*DNA-directed RNA polymerase, subunit N/Rpb10, IPR023580*RNA polymerase subuni
7.56E-10	IPR002222*Ribosomal protein S19/S15, IPR023575*Ribosomal protein S19, superfamily, IPR0057
6.13E-08	IPR002777*Prefoldin beta-like
4.31E-08	NA
2.66E-06	NA
8.40E-06	IPR009112*GTP cyclohydrolase I, feedback regulatory protein
6.54E-07	IPR015415*Vps4 oligomerisation, C-terminal, IPR027417*P-loop containing nucleoside triphosphat
6.59E-08	NA

0.0001276	IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
2.25E-05	IPR009057*Homeobox domain-like, IPR001356*Homeobox domain
1.94E-05	NA
6.81E-11	NA
4.10E-09	IPR008195*Ribosomal protein L34Ae
2.40E-09	IPR021565*Rabenosyn, Rab binding domain, IPR013083*Zinc finger, RING/FYVE/PHD-type, IPR0
2.04E-09	NA
3.36E-08	IPR011705*BTB/Kelch-associated, IPR011333*SKP1/BTB/POZ domain, IPR006652*Kelch repeat
9.29E-07	NA
5.36E-06	NA
6.96E-08	NA
1.50E-07	NA
1.69E-05	NA
3.80E-09	IPR010580*Stress-associated endoplasmic reticulum protein
5.81E-06	NA
9.57E-08	IPR008389*ATPase, V0 complex, subunit e1/e2
3.16E-07	IPR001304*C-type lectin-like, IPR016186*C-type lectin-like/link domain, IPR016187*C-type lectin f
6.65E-10	IPR000892*Ribosomal protein S26e
1.62E-09	IPR024135*Ragulator complex protein LAMTOR5
1.34E-07	NA
3.13E-08	NA
9.74E-08	IPR008011*Complex 1 LYR protein
7.88E-07	IPR013120*Male sterility, NAD-binding, IPR010920*LSM domain, IPR001163*LSM domain, eukary
1.76E-08	IPR011013*Galactose mutarotase-like domain, IPR031727*Galactose mutarotase, N-terminal barr
2.55E-05	IPR007248*Mpv17/PMP22
7.41E-10	IPR003172*MD-2-related lipid-recognition domain, IPR014756*Immunoglobulin E-set
1.07E-07	NA
6.55E-05	NA
1.94E-06	NA
6.82E-09	IPR001848*Ribosomal protein S10, IPR027486*Ribosomal protein S10 domain, IPR005729*Ribos
0.0001482	IPR000010*Cystatin domain
4.96E-08	IPR011030*Vitellinogen, superhelical, IPR001747*Lipid transport protein, N-terminal, IPR015817*V
3.31E-09	IPR000891*Pyruvate carboxyltransferase, IPR013785*Aldolase-type TIM barrel
1.65E-08	NA
0.0004931	IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
1.13E-06	IPR008971*HSP40/DnaJ peptide-binding, IPR002939*Chaperone DnaJ, C-terminal
0.0001669	NA
2.21E-07	IPR006621*Nose resistant-to-fluoxetine protein, N-terminal, IPR009075*Acyl-CoA dehydrogenase/
4.04E-07	NA
8.61E-09	IPR019034*Uncharacterised protein family UPF0390
4.53E-07	NA
3.82E-08	NA
1.86E-05	NA
6.87E-05	IPR006875*Sarcoglycan complex subunit protein
3.19E-09	IPR007000*Phospholipase B-like
4.21E-05	IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
0.0021964	NA

0.000141	IPR008979*Galactose-binding domain-like
1.58E-07	NA
3.12E-07	NA
7.90E-10	IPR001854*Ribosomal protein L29/L36
7.58E-08	NA
8.39E-09	IPR012913*Glucosidase II beta subunit-like, IPR009011*Mannose-6-phosphate receptor binding d
7.20E-10	IPR015889*Intradiol ring-cleavage dioxygenase, core, IPR000627*Intradiol ring-cleavage dioxygen
9.12E-05	NA
1.39E-08	NA
3.16E-07	IPR004045*Glutathione S-transferase, N-terminal, IPR010987*Glutathione S-transferase, C-termin
1.55E-09	IPR012340*Nucleic acid-binding, OB-fold, IPR005680*Ribosomal protein S23, eukaryotic/archaeal,
2.63E-06	IPR009866*NADH:ubiquinone oxidoreductase, subunit NDUFB4
3.00E-05	IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
0.0001158	IPR001873*Epithelial sodium channel
1.49E-10	NA
7.95E-10	IPR005756*Ribosomal protein L26/L24, eukaryotic/archaeal, IPR014722*Ribosomal protein L2 do
1.19E-06	IPR016055*Alpha-D-phosphohexomutase, alpha/beta/alpha I/II/III, IPR005844*Alpha-D-phosphohe
1.50E-07	IPR002076*ELO family
1.82E-09	NA
1.01E-07	IPR010920*LSM domain, IPR001163*LSM domain, eukaryotic/archaea-type, IPR034110*LSM do
2.59E-09	NA
9.45E-09	NA
3.10E-09	IPR000215*Serpin family, IPR023796*Serpin domain
7.08E-06	IPR002557*Chitin binding domain
6.94E-10	IPR030671*Protein transport Sec61-beta/Sbh, IPR016482*Protein transport protein SecG/Sec61-b
6.30E-09	IPR001911*Ribosomal protein S21
1.46E-10	IPR026634*Protein-tyrosine sulfotransferase, IPR027417*P-loop containing nucleoside triphosphat
1.33E-09	IPR029071*Ubiquitin-related domain, IPR011332*Zinc-binding ribosomal protein, IPR001975*Ribos
8.67E-07	NA
5.22E-08	IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR003191*Guanylate-binding pr
3.28E-08	IPR008795*Prominin
7.01E-07	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
2.24E-09	IPR000552*Ribosomal protein L44e, IPR011332*Zinc-binding ribosomal protein
4.81E-08	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
4.95E-06	NA
1.79E-07	IPR009432*Protein of unknown function DUF1075
3.02E-07	IPR014806*Ubiquitin-fold modifier-conjugating enzyme 1, IPR016135*Ubiquitin-conjugating enzym
1.41E-07	IPR007886*Alanine dehydrogenase/pyridine nucleotide transhydrogenase, N-terminal, IPR007698*
2.21E-05	NA
2.02E-08	IPR023476*Peptidyl-tRNA hydrolase II domain, IPR002833*Peptidyl-tRNA hydrolase, PTH2
2.69E-07	IPR008011*Complex 1 LYR protein
8.12E-09	IPR008027*Cytochrome b-c1 complex subunit 9
2.93E-08	IPR001436*Alpha crystallin/Heat shock protein, IPR008978*HSP20-like chaperone, IPR031107*S
1.36E-09	NA
0.0002181	NA
5.75E-09	IPR001163*LSM domain, eukaryotic/archaea-type, IPR010920*LSM domain, IPR034105*Sm-like
1.27E-09	IPR006808*ATP synthase, F0 complex, subunit G, mitochondrial, IPR016702*Mitochondrial ATP s

1.75E-07	NA
2.96E-07	IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain
1.62E-08	IPR013057*Amino acid transporter, transmembrane domain
5.63E-08	IPR001623*DnaJ domain
3.17E-10	IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A
1.37E-06	NA
1.85E-08	NA
2.91E-06	NA
1.53E-07	NA
9.77E-09	NA
6.82E-08	NA
1.23E-08	IPR029048*Heat shock protein 70kD, C-terminal domain
6.79E-06	IPR013320*Concanavalin A-like lectin/glucanase domain
2.81E-08	IPR003439*ABC transporter-like, IPR026082*ABC transporter A, ABCA, IPR027417*P-loop contair
2.86E-05	IPR032675*Leucine-rich repeat domain, L domain-like
7.43E-10	IPR011333*SKP1/BTB/POZ domain, IPR011705*BTB/Kelch-associated
5.11E-07	IPR002634*BolA protein
1.11E-05	NA
1.62E-10	IPR002068*Alpha crystallin/Hsp20 domain, IPR008978*HSP20-like chaperone, IPR031107*Small h
0.0006693	NA
4.90E-07	NA
6.07E-08	NA
2.45E-08	NA
7.19E-05	NA
1.41E-06	NA
1.82E-09	IPR012493*Renin receptor-like
2.62E-07	NA
7.54E-07	NA
2.50E-06	NA
2.45E-06	NA
7.83E-08	IPR032675*Leucine-rich repeat domain, L domain-like
1.09E-08	NA
3.78E-07	IPR004245*Protein of unknown function DUF229, IPR017850*Alkaline-phosphatase-like, core dom
5.76E-05	IPR029063*S-adenosyl-L-methionine-dependent methyltransferase
1.19E-09	IPR010987*Glutathione S-transferase, C-terminal-like, IPR012336*Thioredoxin-like fold, IPR00404
8.45E-06	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
5.45E-06	NA
4.40E-08	IPR013880*Yos1-like
4.83E-09	IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR000859*CUB domain
5.61E-10	IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
2.53E-05	IPR000859*CUB domain
9.40E-10	IPR021137*Ribosomal protein L35, IPR019338*Ribosomal protein L35, mitochondrial
2.17E-05	NA
7.17E-07	IPR017986*WD40-repeat-containing domain, IPR015943*WD40/YVTN repeat-like-containing doma
6.59E-08	IPR003841*Sodium-dependent phosphate transport protein, IPR030147*Sodium-dependent phospl
5.37E-08	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
6.85E-08	IPR035269*26S Proteasome non-ATPase regulatory subunit 9

9.00E-09	IPR015157*Translation machinery associated TMA7
2.75E-05	NA
0.0001732	IPR009071*High mobility group box domain, IPR001025*Bromo adjacent homology (BAH) domain
2.81E-05	IPR000566*Lipocalin/cytosolic fatty-acid binding domain, IPR012674*Calycin, IPR002345*Lipocalin
9.03E-06	NA
2.02E-05	NA
3.26E-08	IPR011992*EF-hand domain pair, IPR002048*EF-hand domain
3.88E-09	NA
3.15E-08	IPR018450*Romo1/Mgr2
6.34E-09	IPR004023*Mago nashi protein
1.83E-05	NA
9.05E-08	IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain, IPR002345*Lipocalin
6.22E-09	IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
1.84E-07	IPR014756*Immunoglobulin E-set, IPR003172*MD-2-related lipid-recognition domain
1.09E-07	IPR022214*Mitotic-spindle organizing protein 1
1.05E-07	IPR006121*Heavy metal-associated domain, HMA
1.60E-05	IPR013128*Peptidase C1A, IPR000668*Peptidase C1A, papain C-terminal, IPR012599*Peptidase
1.96E-08	NA
1.39E-05	IPR009014*Transketolase C-terminal/Pyruvate-ferredoxin oxidoreductase domain II, IPR033248*Tr
6.16E-06	IPR000618*Insect cuticle protein
4.14E-07	IPR001067*Nuclear translocator, IPR000014*PAS domain
1.41E-08	NA
9.12E-09	IPR014718*Glycoside hydrolase-type carbohydrate-binding, IPR011013*Galactose mutarotase-like
4.45E-06	NA
5.20E-10	IPR009068*S15/NS1, RNA-binding, IPR012606*Ribosomal protein S13/S15, N-terminal, IPR00058
2.27E-09	IPR002671*Ribosomal protein L22e
3.25E-10	IPR029064*50S ribosomal protein L30e-like, IPR004038*Ribosomal protein L7Ae/L30e/S12e/Gadd
5.71E-08	NA
0.0001876	NA
4.04E-07	IPR003689*Zinc/iron permease
4.96E-06	NA
3.39E-07	IPR001781*Zinc finger, LIM-type
6.94E-10	IPR000118*Granulin
3.36E-12	IPR011234*Fumarylacetoacetase, C-terminal-related, IPR015377*Fumarylacetoacetase, N-termina
3.92E-06	IPR029058*Alpha/Beta hydrolase fold, IPR006693*Partial AB-hydrolase lipase domain, IPR025483
1.67E-06	NA
8.56E-05	NA
1.23E-09	IPR000218*Ribosomal protein L14P
2.90E-05	NA
6.46E-05	NA
7.65E-05	NA
1.27E-06	NA
6.17E-11	IPR013201*Cathepsin propeptide inhibitor domain (I29), IPR000668*Peptidase C1A, papain C-term
4.77E-07	IPR013174*Dolichol-phosphate mannosyltransferase subunit 3
7.93E-07	IPR011705*BTB/Kelch-associated, IPR011333*SKP1/BTB/POZ domain, IPR012983*PHR, IPR000
6.61E-10	NA
5.67E-07	IPR016449*Potassium channel, inwardly rectifying, Kir, IPR014756*Immunoglobulin E-set, IPR013

9.35E-10	NA
7.43E-10	NA
1.67E-08	NA
4.24E-11	IPR000571*Zinc finger, CCCH-type, IPR001841*Zinc finger, RING-type, IPR013083*Zinc finger, RI
3.43E-09	NA
1.53E-10	IPR002379*V-ATPase proteolipid subunit C-like domain, IPR000454*ATP synthase, F0 complex, su
1.64E-05	NA
4.06E-10	IPR001515*Ribosomal protein L32e
1.41E-08	IPR008949*Isoprenoid synthase domain
1.03E-09	IPR029062*Class I glutamine amidotransferase-like, IPR004468*CTP synthase, IPR033828*CTP s
5.11E-10	NA
5.36E-06	NA
3.52E-06	IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
7.48E-09	IPR013783*Immunoglobulin-like fold, IPR003961*Fibronectin type III
6.43E-06	NA
1.59E-10	NA
3.11E-07	IPR006721*ATP synthase, F1 complex, epsilon subunit, mitochondrial
1.62E-06	IPR018943*Oligosaccaryltransferase
5.35E-06	NA
1.53E-10	IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
4.99E-06	IPR001254*Serine proteases, trypsin domain, IPR009003*Peptidase S1, PA clan
8.99E-10	NA
1.88E-08	IPR024969*Rpn11/EIF3F, C-terminal, IPR033858*26S Proteasome non-ATPase regulatory subunit
1.18E-09	IPR024491*Selenoprotein SelK/SelG
2.88E-06	NA
0.0014841	NA
1.23E-08	IPR001283*Cysteine-rich secretory protein, allergen V5/Tpx-1-related, IPR014044*CAP domain, IF
1.50E-08	NA
0.000101	IPR000649*Initiation factor 2B-related
4.96E-08	NA
4.29E-08	NA
7.21E-09	IPR000719*Protein kinase domain, IPR009091*Regulator of chromosome condensation 1/beta-lact
2.09E-05	IPR010347*Tyrosyl-DNA phosphodiesterase I, IPR027415*Tyrosyl-DNA phosphodiesterase C-term
1.34E-05	IPR000618*Insect cuticle protein
1.46E-08	NA
3.04E-06	NA
1.22E-08	IPR023242*FAM36A, IPR022533*Cox20/FAM36A
2.44E-05	NA
2.51E-05	IPR014756*Immunoglobulin E-set, IPR017868*Filamin/ABP280 repeat-like, IPR013783*Immunoglo
2.73E-10	NA
8.82E-11	NA
3.48E-06	NA
7.83E-10	NA
4.08E-08	NA
7.80E-10	NA
8.26E-09	IPR029391*Myeloma-overexpressed 2-like
5.73E-05	IPR023796*Serpin domain, IPR000215*Serpin family

1.09E-07	NA
1.39E-07	IPR014854*Non-structural maintenance of chromosome element 4, C-terminal, IPR027786*Nse4/E
2.69E-06	IPR000218*Ribosomal protein L14P
2.22E-08	IPR010625*CHCH
7.49E-10	IPR000509*Ribosomal protein L36e
0.0001232	IPR029021*Protein-tyrosine phosphatase-like, IPR020417*Atypical dual specificity phosphatase, IP
2.36E-08	IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
3.60E-06	NA
2.89E-05	NA
4.76E-08	IPR018628*Cytochrome c oxidase assembly factor 3, mitochondrial
3.13E-05	IPR002861*Reeler domain
3.50E-06	IPR007109*Brix domain
0.0001831	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
6.17E-06	NA
3.36E-12	IPR000554*Ribosomal protein S7e
7.03E-10	IPR015889*Intradiol ring-cleavage dioxygenase, core
3.29E-08	IPR023296*Glycosyl hydrolase, five-bladed beta-propellor domain, IPR013320*Concanavalin A-like
7.03E-09	NA
3.66E-07	NA
3.30E-07	NA
4.95E-10	IPR001578*Peptidase C12, ubiquitin carboxyl-terminal hydrolase, IPR017390*Ubiquitinyl hydrolase
1.49E-08	IPR013320*Concanavalin A-like lectin/glucanase domain
2.03E-07	NA
6.39E-06	NA
2.51E-05	IPR009003*Peptidase S1, PA clan, IPR001254*Serine proteases, trypsin domain, IPR001314*Pept
1.20E-06	IPR013784*Carbohydrate-binding-like fold, IPR019008*Domain of unknown function DUF2012
2.08E-06	IPR007235*Glycosyl transferase, family 28, C-terminal
6.59E-08	IPR011011*Zinc finger, FYVE/PHD-type, IPR000306*FYVE zinc finger, IPR028163*HAUS augmin-
1.73E-07	IPR015889*Intradiol ring-cleavage dioxygenase, core
2.04E-08	IPR002557*Chitin binding domain
3.79E-06	NA
1.11E-05	IPR017853*Glycoside hydrolase superfamily, IPR029070*Chitinase insertion domain, IPR011583*
3.36E-07	IPR012496*TMC
1.05E-05	IPR000217*Tubulin, IPR008280*Tubulin/FtsZ, C-terminal, IPR002454*Gamma tubulin, IPR003008*
8.79E-11	IPR011989*Armadillo-like helical, IPR016024*Armadillo-type fold, IPR019451*RNA polymerase II a
2.06E-06	IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A
1.27E-10	IPR001931*Ribosomal protein S21e
1.01E-10	IPR001569*Ribosomal protein L37e, IPR011332*Zinc-binding ribosomal protein, IPR011331*Ribos
1.04E-07	NA
2.78E-06	IPR001314*Peptidase S1A, chymotrypsin family, IPR001254*Serine proteases, trypsin domain, IP
3.50E-07	NA
9.73E-09	IPR003210*Signal recognition particle, SRP14 subunit, IPR009018*Signal recognition particle, SR
0.0002482	IPR029058*Alpha/Beta hydrolase fold
2.87E-08	IPR000608*Ubiquitin-conjugating enzyme E2, IPR016135*Ubiquitin-conjugating enzyme/RWD-like
2.22E-08	IPR001254*Serine proteases, trypsin domain, IPR001314*Peptidase S1A, chymotrypsin family, IP
5.65E-06	NA
1.92E-07	IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR011042*Six-bladed beta-prop

4.93E-10	NA
1.38E-08	IPR019393*WASH complex, subunit strumpellin
8.19E-09	NA
3.04E-07	IPR019143*JNK/Rab-associated protein-1, N-terminal
2.72E-11	NA
9.75E-07	NA
5.70E-05	NA
3.01E-09	IPR001901*Protein translocase complex, SecE/Sec61-gamma subunit, IPR023391*Protein transloc
8.85E-06	IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
2.66E-07	IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
9.74E-06	NA
1.08E-05	IPR003101*Coactivator CBP, KIX domain
4.77E-07	IPR023753*FAD/NAD(P)-binding domain
1.43E-07	NA
3.17E-06	NA
1.78E-09	NA
9.35E-10	IPR013087*Zinc finger C2H2-type
4.03E-11	IPR001210*Ribosomal protein S17e
4.48E-07	IPR006667*SLC41 divalent cation transporters, integral membrane domain
1.47E-08	IPR011990*Tetratricopeptide-like helical domain, IPR013949*U3 small nucleolar RNA-associated p
1.15E-10	IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
2.20E-07	IPR024512*Small subunit of serine palmitoyltransferase-like
8.15E-06	NA
2.40E-06	NA
2.85E-11	IPR004837*Sodium/calcium exchanger membrane region, IPR004481*Sodium/potassium/calcium
2.18E-09	IPR000504*RNA recognition motif domain
9.32E-10	NA
2.97E-06	NA
1.09E-08	IPR011991*Winged helix-turn-helix DNA-binding domain, IPR003150*DNA-binding RFX-type winge
1.89E-06	IPR025483*Lipase, eukaryotic, IPR029058*Alpha/Beta hydrolase fold, IPR006693*Partial AB-hydro
1.49E-06	NA
7.45E-12	IPR020846*Major facilitator superfamily domain
8.57E-07	IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
2.43E-09	NA
4.60E-08	IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase, IPR006326*UDP-glycosyltransferase, MG
1.06E-06	IPR032665*Helix-loop-helix protein delilah, IPR011598*Myc-type, basic helix-loop-helix (bHLH) do
1.51E-07	IPR003609*PAN/Apple domain
1.14E-08	NA
3.07E-10	IPR008158*Protein translocase SEC61 complex, gamma subunit, IPR001901*Protein translocase
8.33E-11	IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR011042*Six-bladed beta-pro
1.09E-07	IPR022812*Dynamin superfamily, IPR003130*Dynamin GTPase effector, IPR000375*Dynamin ce
1.35E-05	IPR028831*DNA mismatch repair protein Pms1
7.79E-08	NA
9.79E-09	NA
0.0069404	NA
3.26E-08	IPR011332*Zinc-binding ribosomal protein
4.24E-11	IPR004977*Ribosomal protein S25

6.05E-07	NA
4.93E-08	IPR000618*Insect cuticle protein
2.04E-06	IPR008952*Tetraspanin, EC2 domain, IPR018499*Tetraspanin/Peripherin
2.66E-11	IPR029063*S-adenosyl-L-methionine-dependent methyltransferase, IPR025714*Methyltransferase
1.21E-08	IPR026298*Blc2 family
1.20E-12	IPR002919*Trypsin Inhibitor-like, cysteine rich domain
5.34E-07	IPR000626*Ubiquitin domain, IPR029071*Ubiquitin-related domain
3.78E-10	NA
2.18E-08	IPR011333*SKP1/BTB/POZ domain, IPR000210*BTB/POZ domain, IPR028764*Kelch repeat and
4.99E-06	IPR007834*DSS1/SEM1
1.15E-08	IPR032054*DNA replication factor Cdt1, C-terminal
5.43E-12	IPR001096*Peptidase C13, legumain
9.48E-10	IPR012599*Peptidase C1A, propeptide, IPR000668*Peptidase C1A, papain C-terminal, IPR01312
2.39E-10	IPR004202*Cytochrome c oxidase subunit VIIc
8.01E-06	NA
7.69E-09	IPR018450*Romo1/Mgr2
4.11E-06	NA
2.18E-08	NA
1.02E-05	NA
8.32E-10	NA
2.18E-08	NA
4.33E-07	IPR032054*DNA replication factor Cdt1, C-terminal
1.37E-07	NA
2.06E-05	NA
1.65E-08	IPR011531*Bicarbonate transporter, C-terminal, IPR003020*Bicarbonate transporter, eukaryotic
1.52E-11	IPR001557*L-lactate/malate dehydrogenase, IPR010097*Malate dehydrogenase, type 1, IPR0223
5.44E-08	NA
2.10E-05	IPR011701*Major facilitator superfamily, IPR020846*Major facilitator superfamily domain
4.40E-06	IPR001353*Proteasome, subunit alpha/beta, IPR035144*Proteasome subunit alpha 1, IPR000426*
6.66E-09	IPR001356*Homeobox domain, IPR000047*Helix-turn-helix motif, IPR020479*Homeobox domain,
0.0002713	IPR029044*Nucleotide-diphospho-sugar transferases, IPR003859*Beta-1,4-galactosyltransferase,
5.71E-11	IPR026055*Fatty acyl-CoA reductase, IPR016040*NAD(P)-binding domain, IPR033640*Fatty acyl-
9.24E-12	NA
6.38E-09	NA
2.34E-06	IPR029063*S-adenosyl-L-methionine-dependent methyltransferase, IPR010342*Protein of unknow
6.48E-09	NA
1.04E-05	IPR012674*Calycin
4.95E-10	IPR007512*Protein of unknown function DUF543
0.0002983	NA
8.61E-09	NA
0.0004746	NA
5.08E-07	NA
5.50E-08	IPR026054*Nuclear pore complex protein, IPR019143*JNK/Rab-associated protein-1, N-terminal
4.79E-08	NA
9.59E-07	IPR003316*E2F/DP family, winged-helix DNA-binding domain, IPR015633*E2F Family, IPR02831
3.74E-05	IPR014105*Carotenoid/retinoid oxidoreductase, IPR023753*FAD/NAD(P)-binding domain, IPR002
2.32E-09	IPR002673*Ribosomal protein L29e

1.15E-10	IPR002675*Ribosomal protein L38e
3.66E-07	IPR020946*Flavin monooxygenase-like
1.07E-08	NA
2.74E-08	IPR013087*Zinc finger C2H2-type
8.14E-06	NA
2.77E-07	NA
2.69E-07	IPR029058*Alpha/Beta hydrolase fold
3.79E-06	IPR032675*Leucine-rich repeat domain, L domain-like
3.12E-09	IPR032675*Leucine-rich repeat domain, L domain-like, IPR003591*Leucine-rich repeat, typical sub
1.45E-08	IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase, IPR006326*UDP-glycosyltransferase, MG
3.80E-08	IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
3.18E-07	IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat
6.38E-09	IPR009866*NADH:ubiquinone oxidoreductase, subunit NDUFB4
4.93E-08	NA
2.35E-08	IPR029044*Nucleotide-diphospho-sugar transferases
9.56E-07	NA
1.45E-07	NA
1.44E-05	NA
1.06E-07	IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
8.22E-08	NA
5.14E-08	NA
2.94E-05	NA
1.53E-08	IPR007235*Glycosyl transferase, family 28, C-terminal
9.35E-09	NA
4.04E-07	IPR019366*Clusterin-associated protein-1
3.38E-11	IPR033453*Glycosyl hydrolase family 30, TIM-barrel domain, IPR033452*Glycosyl hydrolase family
1.66E-07	NA
7.23E-06	NA
6.08E-07	NA
4.19E-10	NA
3.17E-07	NA
4.83E-08	NA
0.0020101	NA
9.86E-07	NA
7.59E-11	NA
4.56E-07	IPR023210*NADP-dependent oxidoreductase domain, IPR020471*Aldo/keto reductase
1.11E-06	NA
1.38E-11	IPR003057*Invertebrate colouration protein, IPR022271*Lipocalin, ApoD type, IPR000566*Lipocali
3.80E-08	IPR008948*L-Aspartase-like
1.20E-10	IPR003172*MD-2-related lipid-recognition domain, IPR014756*Immunoglobulin E-set
7.22E-09	NA
2.47E-06	NA
5.09E-11	IPR032135*Protein of unknown function DUF4817
2.43E-09	NA
1.09E-06	IPR019143*JNK/Rab-associated protein-1, N-terminal
1.06E-07	IPR002048*EF-hand domain, IPR011992*EF-hand domain pair
5.06E-08	NA

6.49E-08	IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
1.33E-09	IPR027413*GroEL-like equatorial domain, IPR002423*Chaperonin Cpn60/TCP-1 family
3.59E-09	IPR029064*50S ribosomal protein L30e-like, IPR004038*Ribosomal protein L7Ae/L30e/S12e/Gadd
5.08E-06	NA
3.42E-07	IPR019143*JNK/Rab-associated protein-1, N-terminal
1.85E-06	IPR029058*Alpha/Beta hydrolase fold, IPR003386*Lecithin:cholesterol/phospholipid:diacylglycerol
6.74E-11	IPR023210*NADP-dependent oxidoreductase domain, IPR020471*Aldo/keto reductase
2.08E-11	IPR000289*Ribosomal protein S28e, IPR012340*Nucleic acid-binding, OB-fold
2.60E-07	IPR032675*Leucine-rich repeat domain, L domain-like
6.29E-08	NA
3.53E-10	IPR012599*Peptidase C1A, propeptide, IPR013128*Peptidase C1A, IPR000668*Peptidase C1A, p
3.82E-08	NA
1.35E-08	NA
3.31E-08	NA
7.92E-07	NA
1.30E-06	IPR008979*Galactose-binding domain-like
6.65E-07	IPR016186*C-type lectin-like/link domain, IPR001304*C-type lectin-like, IPR016187*C-type lectin f
3.91E-08	NA
3.29E-08	IPR008518*FATE/Miff/Tango-11
4.26E-06	NA
1.05E-10	NA
1.20E-12	NA
6.88E-09	IPR011011*Zinc finger, FYVE/PHD-type, IPR013083*Zinc finger, RING/FYVE/PHD-type
4.72E-08	NA
6.33E-05	IPR026298*Blc2 family
2.67E-11	IPR007836*Ribosomal protein L41
7.49E-09	NA
2.96E-06	NA
8.41E-11	IPR002674*Ribosomal protein L37ae, IPR011332*Zinc-binding ribosomal protein, IPR011331*Ribo
1.44E-08	IPR006179*5'-Nucleotidase/apyrase, IPR029052*Metallo-dependent phosphatase-like, IPR008334
1.20E-09	NA
8.34E-07	IPR001506*Peptidase M12A, IPR024079*Metallopeptidase, catalytic domain
4.87E-05	NA
4.50E-07	NA
1.05E-10	IPR002219*Protein kinase C-like, phorbol ester/diacylglycerol-binding domain, IPR015727*Protein
8.40E-08	NA
1.31E-10	NA
2.04E-06	IPR001623*DnaJ domain
9.50E-08	NA
1.24E-09	NA
1.08E-07	IPR008753*Peptidase M13, N-terminal domain, IPR000718*Peptidase M13, IPR029736*Endotheli
6.71E-08	IPR019348*Uncharacterised domain KLRAQ/TTKRSYEDQ, C-terminal
9.86E-06	IPR000618*Insect cuticle protein
2.72E-11	IPR029058*Alpha/Beta hydrolase fold, IPR001375*Peptidase S9, prolyl oligopeptidase, catalytic do
1.21E-09	IPR032675*Leucine-rich repeat domain, L domain-like
1.64E-09	IPR001096*Peptidase C13, legumain
4.24E-11	IPR001209*Ribosomal protein S14

9.93E-10	NA
2.10E-08	IPR035427*Tim10/FAM136A-like domain, IPR004217*Tim10-like
5.43E-05	NA
0.0022857	NA
1.82E-09	IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
1.22E-06	NA
1.97E-06	IPR011009*Protein kinase-like domain
2.76E-07	IPR024096*NO signalling/Golgi transport ligand-binding domain, IPR016696*TRAPP I complex, su
1.86E-08	IPR002769*Translation initiation factor IF6
3.36E-12	NA
1.28E-06	NA
1.29E-07	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
5.50E-08	NA
3.61E-08	IPR000219*Dbl homology (DH) domain
1.44E-08	IPR031152*Plexin domain-containing protein
7.11E-10	IPR012459*Ribosomal RNA-processing protein 15, IPR002017*Spectrin repeat, IPR018159*Spectr
2.28E-08	NA
1.36E-11	IPR016090*Phospholipase A2 domain
1.37E-10	NA
4.48E-07	NA
1.91E-07	IPR002490*V-type ATPase, V0 complex, 116kDa subunit family
3.36E-12	NA
0.0001819	IPR000618*Insect cuticle protein
1.08E-07	IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
5.65E-08	IPR019180*Oxidoreductase-like, N-terminal
5.52E-08	NA
8.31E-09	NA
1.20E-12	IPR000010*Cystatin domain, IPR027214*Cystatin
7.42E-08	NA
2.19E-08	IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
1.93E-11	NA
3.19E-07	IPR011701*Major facilitator superfamily, IPR020846*Major facilitator superfamily domain
3.04E-07	NA
2.05E-08	NA
5.37E-08	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
2.38E-08	IPR002716*PIN domain, IPR029060*PIN domain-like
1.87E-07	NA
4.62E-08	NA
7.42E-08	IPR024332*MOZART2 family
1.99E-09	IPR015943*WD40/YVTN repeat-like-containing domain, IPR017986*WD40-repeat-containing doma
1.35E-07	IPR007220*Origin recognition complex, subunit 2
1.04E-09	NA
2.64E-08	IPR006620*Prolyl 4-hydroxylase, alpha subunit
1.33E-08	IPR003563*7,8-dihydro-8-oxoguanine triphosphatase
6.72E-09	IPR032675*Leucine-rich repeat domain, L domain-like
2.11E-08	NA
1.77E-07	NA

1.00E-08	IPR008969*Carboxypeptidase-like, regulatory domain
3.75E-12	IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A, IPR012599*Peptidase
2.21E-09	NA
6.33E-09	IPR001164*Arf GTPase activating protein, IPR013328*6-phosphogluconate dehydrogenase, domai
8.80E-09	NA
2.83E-08	NA
3.53E-09	IPR011009*Protein kinase-like domain, IPR000719*Protein kinase domain
2.43E-07	IPR001096*Peptidase C13, legumain
3.31E-08	IPR002300*Aminoacyl-tRNA synthetase, class Ia, IPR009008*Valyl/Leucyl/Isoleucyl-tRNA syntheta
4.98E-07	NA
1.05E-07	NA
8.88E-09	IPR006621*Nose resistant-to-fluoxetine protein, N-terminal, IPR002656*Acyltransferase 3
3.14E-08	NA
4.70E-07	NA
3.48E-13	IPR012674*Calycin, IPR002345*Lipocalin, IPR003057*Invertebrate colouration protein, IPR000566
5.13E-08	NA
3.88E-10	IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
4.35E-08	IPR017946*PLC-like phosphodiesterase, TIM beta/alpha-barrel domain
1.07E-09	NA
1.24E-11	IPR023626*Ribosomal protein L39e domain, IPR000077*Ribosomal protein L39e
5.71E-07	NA
3.75E-09	IPR002318*Alanine-tRNA ligase, class IIc, IPR018162*Alanine-tRNA ligase, class IIc, anti-codon-bi
0.000147	IPR000618*Insect cuticle protein
2.99E-12	NA
2.54E-08	IPR013083*Zinc finger, RING/FYVE/PHD-type, IPR027775*C2H2- zinc finger protein family subset
2.43E-08	NA
1.42E-08	IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain
8.80E-09	IPR005135*Endonuclease/exonuclease/phosphatase
2.95E-09	IPR002659*Glycosyl transferase, family 31
9.71E-09	IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR000048*IQ motif, EF-hand bir
9.45E-09	NA
5.82E-09	IPR013087*Zinc finger C2H2-type, IPR013083*Zinc finger, RING/FYVE/PHD-type, IPR027775*C2H
7.33E-09	IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
1.46E-09	IPR015889*Intradiol ring-cleavage dioxygenase, core
2.21E-10	NA
5.99E-09	NA
1.62E-09	NA
2.05E-08	IPR012336*Thioredoxin-like fold, IPR004045*Glutathione S-transferase, N-terminal, IPR010987*Gl
1.85E-09	NA
2.90E-08	NA
1.62E-09	IPR000668*Peptidase C1A, papain C-terminal
3.22E-09	NA
1.48E-08	NA
6.32E-10	IPR032675*Leucine-rich repeat domain, L domain-like
4.86E-14	NA
3.34E-09	IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
4.12E-09	IPR029057*Phosphoribosyltransferase-like, IPR029933*Uridine-cytidine kinase-like 1

3.52E-11	NA
9.11E-11	NA
9.33E-09	IPR001623*DnaJ domain
6.32E-10	NA
1.27E-10	IPR013128*Peptidase C1A, IPR000668*Peptidase C1A, papain C-terminal
2.18E-09	IPR029054*dUTPase-like, IPR008181*Deoxyuridine triphosphate nucleotidohydrolase, IPR033704
3.22E-10	IPR001478*PDZ domain, IPR034876*Partitioning defective protein 6, IPR000270*PB1 domain
1.48E-10	IPR004087*K Homology domain, IPR004088*K Homology domain, type 1
1.81E-10	NA
2.83E-10	NA
6.32E-10	IPR024768*Meiosis regulator and mRNA stability factor 1
9.83E-10	NA
3.72E-12	NA
5.80E-11	IPR010580*Stress-associated endoplasmic reticulum protein

3*Peptidase C1A

osomal protein L7Ae/L30e/S12e/Gadd45

)UF382

R009003*Peptidase S1, PA clan

R001247*Exoribonuclease, phosphorolytic domain 1, IPR015847*Exoribonuclease, phosphorolytic do

domain, IPR013562*tRNA(Met) cytidine acetyltransferase TmcA, N-terminal, IPR000182*GNAT don ate colouration protein, IPR000566*Lipocalin/cytosolic fatty-acid binding domain

syltransferase

butyric acid A receptor/Glycine receptor alpha, IPR006029*Neurotransmitter-gated ion-channel trans

5067*V-type ATPase subunit c domain

Serine proteases, trypsin domain

, IPR011333*SKP1/BTB/POZ domain

JF382

2067*Mitochondrial carrier protein, IPR002113*Adenine nucleotide translocator 1

nogen, alpha/beta/gamma chain, C-terminal globular, subdomain 1, IPR001007*VWFC domain

2843*ATPase, V0 complex, c/d subunit

propeptide inhibitor domain (I29)

hosphate 5-kinase, C-terminal, IPR023610*Phosphatidylinositol-4-phosphate 5-kinase

9*NYN domain, limkain-b1-type

BTB domain-containing protein 8, IPR011705*BTB/Kelch-associated

ated

ate 5-kinase, core, IPR027483*Phosphatidylinositol-4-phosphate 5-kinase, C-terminal, IPR027484*Pl syltransferase, IPR006326*UDP-glycosyltransferase, MGT

80*Tubulin/FtsZ, C-terminal, IPR018316*Tubulin/FtsZ, 2-layer sandwich domain

rminal, IPR004046*Glutathione S-transferase, C-terminal, IPR012336*Thioredoxin-like fold

ain, IPR012952*BING4, C-terminal domain

3*Peptidase C1A

beta-hairpin domain 2

R016162*Aldehyde dehydrogenase N-terminal domain xidase, N-terminal, IPR009100*Acyl-CoA dehydrogenase/oxidase, N-terminal and middle domain, IP

52*Glycosyl hydrolase family 30, beta sandwich domain, IPR033453*Glycosyl hydrolase family 30, T

l, IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase

001846*von Willebrand factor, type D domain, IPR001747*Lipid transport protein, N-terminal, IPR01

3*Peptidase C1A

e/RWD-like

ninal, IPR013128*Peptidase C1A

containing domain

93

3*Peptidase C1A

rumpellin

yltransferase

pe 2

R009003*Peptidase S1, PA clan

R011009*Protein kinase-like domain, IPR009091*Regulator of chromosome condensation 1/beta-lac
repeat-like-containing domain

394*Sec7 domain, alpha orthogonal bundle, IPR016024*Armadillo-type fold

al domain, IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR000953*Chromo/ch

ynureninase, IPR015424*Pyridoxal phosphate-dependent transferase, IPR015422*Pyridoxal phosph

al-like, IPR012336*Thioredoxin-like fold, IPR004045*Glutathione S-transferase, N-terminal

8, C-terminal

main, IPR017853*Glycoside hydrolase superfamily, IPR033452*Glycosyl hydrolase family 30, beta s

, ApoD type

R013149*Alcohol dehydrogenase, C-terminal, IPR011032*GroES-like, IPR013154*Alcohol dehydroge

main

ary subunit

type 11

, IPR002345*Lipocalin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain

r, RING/FYVE/PHD-type, IPR015943*WD40/YVTN repeat-like-containing domain, IPR011990*Tetrat

3

iated, IPR011333*SKP1/BTB/POZ domain

lutathione S-transferase, C-terminal-like, IPR004046*Glutathione S-transferase, C-terminal

anching enzyme, N-terminal domain, IPR008928*Six-hairpin glycosidase-like, IPR032792*Glycogen

type B

*NYN domain, limkain-b1-type

cific organic anion transporter 1, IPR003439*ABC transporter-like, IPR011527*ABC transporter type

) receptor class A repeat, IPR000998*MAM domain e, IPR029060*PIN domain-like

box domain

superfamily, IPR001223*Glycoside hydrolase family 18, catalytic domain

C1A, propeptide

R009003*Peptidase S1, PA clan

domain, IPR001139*Glycoside hydrolase family 30, IPR033452*Glycosyl hydrolase family 30, beta

, IPR015816*Vitellinogen, beta-sheet N-terminal al, IPR010987*Glutathione S-transferase, C-terminal-like, IPR012336*Thioredoxin-like fold

domain

peller, TolB-like, IPR000033*LDLR class B repeat

ypsin domain, IPR009003*Peptidase S1, PA clan, IPR000859*CUB domain, IPR001314*Peptidase S

030247*Canalicular multispecific organic anion transporter 1, IPR003593*AAA+ ATPase domain, IP

ase, IPR011989*Armadillo-like helical, IPR031549*Abnormal spindle-like microcephaly-associated p

lectin/glucanase domain, IPR000998*MAM domain

er, RING/FYVE/PHD-type, IPR027775*C2H2- zinc finger protein family subset

n-like

41*Coatomer/clathrin adaptor appendage, Ig-like subdomain, IPR015151*Beta-adaptin appendage, C

616*Post-SET domain, IPR015722*Histone-lysine N-methyltransferase Trr

Chitin-binding, type 1, IPR017853*Glycoside hydrolase superfamily, IPR001604*DNA/RNA non-spec

Zinc finger, ZZ-type, IPR010303*CREB-binding protein/p300, atypical RING domain, IPR001487*Bro

in, IPR011527*ABC transporter type 1, transmembrane domain, IPR003439*ABC transporter-like
rotein patched/dispatched

omain, IPR033452*Glycosyl hydrolase family 30, beta sandwich domain, IPR017853*Glycoside hydro

42*IQ motif and SEC7 domain-containing protein, PH domain

ciated domain, IPR006576*BRK domain, IPR001487*Bromodomain, IPR000330*SNF2-related, N-te

al, IPR012336*Thioredoxin-like fold, IPR010987*Glutathione S-transferase, C-terminal-like

domain
A, ABCA, IPR027417*P-loop containing nucleoside triphosphate hydrolase

er-gated ion-channel transmembrane domain, IPR006028*Gamma-aminobutyric acid A receptor/Gly
r hormone receptor, ligand-binding domain, IPR001628*Zinc finger, nuclear hormone receptor-type,
IPR013098*Immunoglobulin I-set, IPR013783*Immunoglobulin-like fold, IPR003598*Immunoglobulin

ar receptor coactivator 6
5633*E2F Family
domain, IPR015590*Aldehyde dehydrogenase domain
, IPR016024*Armadillo-type fold, IPR004170*WWE domain

936*Rho GTPase activation protein, IPR016024*Armadillo-type fold, IPR028553*Neurofibromin
PR000536*Nuclear hormone receptor, ligand-binding domain
, IPR011333*SKP1/BTB/POZ domain

e, IPR029060*PIN domain-like

cerol-binding domain, IPR020454*Diacylglycerol/phorbol-ester binding

R018159*Spectrin/alpha-actinin, IPR015154*EF-hand domain, type 2, IPR011992*EF-hand domain

oside hydrolase superfamily
peller, IPR011333*SKP1/BTB/POZ domain
er-gated ion-channel transmembrane domain, IPR006201*Neurotransmitter-gated ion-channel, IPR

main
domain

syltransferase, IPR006326*UDP-glycosyltransferase, MGT

own function DB

FYVE/PHD-type, IPR001487*Bromodomain, IPR019787*Zinc finger, PHD-finger, IPR028941*WHIM2 h domain, IPR017853*Glycoside hydrolase superfamily, IPR033453*Glycosyl hydrolase family 30, T

ADH ubiquinone oxidoreductase, F subunit, IPR019575*NADH-ubiquinone oxidoreductase 51kDa su

homology domain, IPR011993*PH domain-like, IPR018159*Spectrin/alpha-actinin, IPR002017*Spec

ninal domain, IPR014001*Helicase superfamily 1/2, ATP-binding domain, IPR014012*Helicase/SAN

52*Glycosyl hydrolase family 30, beta sandwich domain, IPR033453*Glycosyl hydrolase family 30, T

ining domain, IPR000742*EGF-like domain, IPR008297*Notch, IPR002110*Ankyrin repeat, IPR0090

1, transmembrane domain, IPR030247*Canalicular multispecific organic anion transporter 1, IPR00

dependent calcium channel, alpha-1 subunit, IPR005821*Ion transport domain, IPR031649*Voltage-

type, IPR001611*Leucine-rich repeat

re domain, IPR000917*Sulfatase, N-terminal

B

1*Leucine-rich repeat, typical subtype

1990*Tetratricopeptide-like helical domain

417*P-loop containing nucleoside triphosphate hydrolase

drogenase C-terminal domain-like, IPR006108*3-hydroxyacyl-CoA dehydrogenase, C-terminal, IPR

al, IPR010987*Glutathione S-transferase, C-terminal-like, IPR012336*Thioredoxin-like fold

D-type, IPR011011*Zinc finger, FYVE/PHD-type, IPR001680*WD40 repeat, IPR013320*Concanava

type 11

IPR007728*Pre-SET domain

oglobulin subtype, IPR003598*Immunoglobulin subtype 2, IPR013098*Immunoglobulin I-set

ain

ƆNA binding, IPR016177*DNA-binding domain, IPR025884*Methyl-CpG binding protein 2/3, C-termir

ain, IPR001680*WD40 repeat

nnose binding SUEL lectin domain, IPR032471*GAIN domain, N-terminal

y domain, type 1, IPR004087*K Homology domain

propeptide inhibitor domain (I29)

)067*Frizzled domain, IPR020635*Tyrosine-protein kinase, catalytic domain, IPR013806*Kringle-like

ke oligomerisation domain

nogen, open beta-sheet, subdomain 1, IPR015819*Lipid transport protein, beta-sheet shell, IPR015

oglobulin V-set domain, IPR013783*Immunoglobulin-like fold

33468*Metaxin, glutathione S-transferase domain, IPR012336*Thioredoxin-like fold

ubunit Med12

eta-hairpin domain 3, IPR018326*Rad4 beta-hairpin domain 1, IPR018325*Rad4/PNGase transgluta

PAS fold, IPR013655*PAS fold-3

ein MutS, connector domain, IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR0

011009*Protein kinase-like domain

binding domain

n factor-related

de triphosphate hydrolase, IPR001650*Helicase, C-terminal, IPR016197*Chromo domain-like, IPR02

hain, IPR032695*Integrin domain, IPR013649*Integrin alpha-2

PH domain-like, IPR011989*Armadillo-like helical, IPR027007*DHR-1 domain, IPR001849*Pleckstri

choline oxidoreductase, C-terminal, IPR012132*Glucose-methanol-choline oxidoreductase, IPR0237

domain-1, IPR003593*AAA+ ATPase domain, IPR004273*Dynein heavy chain domain, IPR024317*

rel

, ApoD type

PHD-type

01965*Zinc finger, PHD-type, IPR019787*Zinc finger, PHD-finger, IPR011011*Zinc finger, FYVE/PH

IPR001005*SANT/Myb domain

ily 3, metabotropic glutamate receptor, IPR017978*GPCR family 3, C-terminal, IPR011500*GPCR, f

1, transmembrane domain, IPR003439*ABC transporter-like, IPR003593*AAA+ ATPase domain

0*Concanavalin A-like lectin/glucanase domain, IPR002049*Laminin EGF domain, IPR002126*Cadh

mily 39/83, IPR032421*Protein O-mannosyl-transferase, C-terminal four TM domain

, IPR003593*AAA+ ATPase domain, IPR011527*ABC transporter type 1, transmembrane domain, IF

NT/Myb domain

type, IPR011990*Tetratricopeptide-like helical domain

003152*FATC domain, IPR003151*PIK-related kinase, FAT, IPR011989*Armadillo-like helical, IPR0

5*Glutathione S-transferase, N-terminal, IPR004046*Glutathione S-transferase, C-terminal

R001711*Phospholipase C, phosphatidylinositol-specific, Y domain, IPR000909*Phosphatidylinosito

ning nucleoside triphosphate hydrolase, IPR003593*AAA+ ATPase domain

*Peptidase C1A

gma subunit, IPR001392*Clathrin adaptor, mu subunit

lycerol kinase, catalytic domain, IPR000756*Diacylglycerol kinase, accessory domain, IPR020683*A

C1A, propeptide

drolase, IPR000048*IQ motif, EF-hand binding site

5*Glutathione S-transferase, N-terminal, IPR004046*Glutathione S-transferase, C-terminal

nain, IPR008598*Drought induced 19 protein type, zinc-binding domain

05*SANT/Myb domain

24*Armadillo-type fold

eoside triphosphate hydrolase, IPR000953*Chromo/chromo shadow domain, IPR000330*SNF2-relate

28, C-terminal

syltransferase

R003593*AAA+ ATPase domain, IPR027417*P-loop containing nucleoside triphosphate hydrolase, IF

ninal, IPR013128*Peptidase C1A

polyphosphate/ATP-NAD kinase, domain 1, IPR016064*NAD kinase/diacylglycerol kinase-like domai

98*Adenylate cyclase, conserved domain, IPR032628*Adenylate cyclase, N-terminal

C-terminal, IPR001611*Leucine-rich repeat, IPR003591*Leucine-rich repeat, typical subtype

3*Alpha/beta hydrolase fold-1

*WD40/YVTN repeat-like-containing domain

cytokinesis, IPR011989*Armadillo-like helical, IPR027007*DHR-1 domain

ninal, IPR013128*Peptidase C1A

rolase

06*FYVE zinc finger

26*Cadherin, IPR001881*EGF-like calcium-binding domain, IPR027397*Catenin binding domain, IPR

globulin I-set, IPR007110*Immunoglobulin-like domain, IPR003961*Fibronectin type III, IPR003599*Ir

nain

417*P-loop containing nucleoside triphosphate hydrolase

itter-gated ion-channel, IPR006202*Neurotransmitter-gated ion-channel ligand-binding domain, IPR0 side triphosphate hydrolase, IPR003593*AAA+ ATPase domain, IPR030247*Canalicular multispecifi

AF-type

002474*Carbamoyl-phosphate synthase small subunit, N-terminal domain, IPR005479*Carbamoyl-p

olar RNA-associated protein 10, IPR011989*Armadillo-like helical

ctivating protein domain

minal, IPR000922*D-galactoside/L-rhamnose binding SUEL lectin domain

001*Helicase superfamily 1/2, ATP-binding domain, IPR011991*Winged helix-turn-helix DNA-binding

Glutamyl/glutaminyl-tRNA synthetase, IPR009068*S15/NS1, RNA-binding, IPR020056*Ribosomal pr

DNA-binding domain, IPR032198*E2F transcription factor, CC-MB domain, IPR028312*Transcriptio

, IPR000566*Lipocalin/cytosolic fatty-acid binding domain

, L domain-like

mplex, subunit Med13

eta-propeller, TolB-like

mbination and repair protein, RecA-like, IPR010995*DNA repair Rad51/transcription factor NusA, alp

GTPase activation protein, IPR001849*Pleckstrin homology domain, IPR029071*Ubiquitin-related do

omain-like, IPR010508*Domain of unknown function DUF1088, IPR016024*Armadillo-type fold, IPR

h domain, IPR033453*Glycosyl hydrolase family 30, TIM-barrel domain, IPR017853*Glycoside hydro

domain, L domain-like, IPR020683*Ankyrin repeat-containing domain, IPR011009*Protein kinase-lik

ha-helical domain, IPR006171*TOPRIM domain, IPR002205*DNA topoisomerase, type IIA, subunit

type, IPR001611*Leucine-rich repeat

d domain

repeat-like-containing domain

omain

hydrolase, IPR011697*Peptidase C26

ology (TIR) domain, IPR001611*Leucine-rich repeat, IPR000483*Cysteine-rich flanking region, C-ter

omain, IPR003316*E2F/DP family, winged-helix DNA-binding domain, IPR015648*Transcription fact

ratricopeptide-like helical domain, IPR017986*WD40-repeat-containing domain

osomal protein L7Ae/L30e/S12e/Gadd45

cis-trans isomerase domain

rolases, N-terminal, IPR001353*Proteasome, subunit alpha/beta

nal, IPR009019*K homology domain, prokaryotic type, IPR004044*K Homology domain, type 2, IPR(

factor

oxidoreductase, 20 Kd subunit

747*Lipid transport protein, N-terminal, IPR015816*Vitellinogen, beta-sheet N-terminal, IPR001846*v

ype, IPR000867*Insulin-like growth factor-binding protein, IGFBP, IPR011390*Insulin-like growth fact
domain, IPR001283*Cysteine-rich secretory protein, allergen V5/Tpx-1-related

C4)

280 repeat-like, IPR001298*Filamin/ABP280 repeat

hate hydrolase, IPR006689*Small GTPase superfamily, ARF/SAR type

PR001247*Exoribonuclease, phosphorolytic domain 1, IPR020568*Ribosomal protein S5 domain 2-ty

domain 2, IPR001247*Exoribonuclease, phosphorolytic domain 1, IPR027408*PNPase/RNase PH

er specific 2-hydroxyacid dehydrogenase, NAD-binding domain, IPR016040*NAD(P)-binding domain

se, F1 complex, delta/epsilon subunit

noglobulin I-set, IPR003599*Immunoglobulin subtype, IPR007110*Immunoglobulin-like domain, IPR

nger, NHR/GATA-type

elix-coiled-coil-helix domain-containing protein 1

2

e domain, IPR013320*Concanavalin A-like lectin/glucanase domain

014813*Guanine nucleotide-binding protein-like 3, N-terminal domain, IPR027417*P-loop containing

protein, LSm4/SmD1/SmD3, IPR010920*LSM domain, IPR034101*Sm-like protein Lsm4

xidase C-terminal, IPR009100*Acyl-CoA dehydrogenase/oxidase, N-terminal and middle domain, IP

termediate chain

ApoD type, IPR000566*Lipocalin/cytosolic fatty-acid binding domain

homology domain, IPR000557*Calponin repeat

ng domain, IPR012132*Glucose-methanol-choline oxidoreductase, IPR000172*Glucose-methanol-ch

PH2

oxide dismutase, IPR019832*Manganese/iron superoxide dismutase, C-terminal

Ribosomal protein L2 domain 2, IPR005824*KOW

pe

g nucleoside triphosphate hydrolase

in

/l-CoA dehydrogenase, NAD binding, IPR016040*NAD(P)-binding domain, IPR013328*6-phosphoglu

3*GMP reductase

s ribosomal protein S13, C-terminal

, IPR007502*Helicase-associated domain, IPR014001*Helicase superfamily 1/2, ATP-binding domai

phatase, low molecular weight, IPR002115*Protein-tyrosine phosphatase, low molecular weight, mar

ı UCP038021, RWD

3*Ribosomal protein L11, C-terminal

;, IPR020568*Ribosomal protein S5 domain 2-type fold

, IPR011037*Pyruvate kinase-like, insert domain

d, subgroup, IPR013750*GHMP kinase, C-terminal domain, IPR005935*Diphosphomevalonate/phos

amily

erminal, IPR012258*Acyl-CoA oxidase, IPR009075*Acyl-CoA dehydrogenase/oxidase C-terminal, IPI ding domain, IPR011989*Armadillo-like helical

IPR010920*LSM domain

ıain

LSM domain

domain, IPR009072*Histone-fold

BM8, RNA recognition motif

ıain-like

Ae/60S-L20/60S-L18A

6*Glutathione S-transferase, C-terminal, IPR004045*Glutathione S-transferase, N-terminal

ductase, N-terminal

loreductase, N-terminal, IPR023753*FAD/NAD(P)-binding domain, IPR007867*Glucose-methanol-ch

type, IPR010920*LSM domain

d45, IPR002415*H/ACA ribonucleoprotein complex, subunit Nhp2, eukaryote, IPR018492*Ribosomal d, IPR005324*Ribosomal protein S5, C-terminal, IPR000851*Ribosomal protein S5, IPR005711*Ribo

ein

domain, IPR002350*Kazal domain

ain, IPR001680*WD40 repeat

b4, core

somal protein S5/S7, eukaryotic/archaeal

, IPR008927*6-phosphogluconate dehydrogenase C-terminal domain-like, IPR013328*6-phosphoglu

subunit 5

l protein S4/S9, eukaryotic/archaeal

al

er-gated ion-channel

omatic amino acid hydroxylase

02784*Ribosomal protein L14e domain

'Dihydrofolate reductase domain

83*Lipase, eukaryotic, IPR029058*Alpha/Beta hydrolase fold

008962*PapD-like, IPR013783*Immunoglobulin-like fold

lomain, IPR017986*WD40-repeat-containing domain

e/deacetylase, beta/alpha-barrel, IPR002509*NodB homology domain, IPR002557*Chitin binding dor

tty-acid binding domain, IPR022271*Lipocalin, ApoD type

itor and mRNA stability factor 1

g nucleoside triphosphate hydrolase, IPR013525*ABC-2 type transporter al-like, IPR012336*Thioredoxin-like fold, IPR004046*Glutathione S-transferase, C-terminal

S ribosomal protein S11, N-terminal, IPR028333*Ribosomal protein S17, archaeal/eukaryotic

hate hydrolase

cleotide pyrophosphatase/phosphate transferase, IPR017850*Alkaline-phosphatase-like, core domai

protein, N-terminal

riphosphate hydrolase, IPR005225*Small GTP-binding protein domain

331*Rhabdovirus nucleocapsid, C-terminal

e

domain, IPR013783*Immunoglobulin-like fold, IPR003598*Immunoglobulin subtype 2, IPR003599*I ıthase-like, large alpha subdomain

LSM domain

ıaea-type, IPR010920*LSM domain

ː026730*Mitochondrial inner membrane protease subunit 1

lavin monooxygenase-like

)08978*HSP20-like chaperone, IPR002068*Alpha crystallin/Hsp20 domain

4, carboxypeptidase A

le, SRP9 subunit

lomain

on Willebrand factor, type D domain, IPR015819*Lipid transport protein, beta-sheet shell, IPR01525

ı

lyl-prolyl cis-trans isomerase domain, IPR029000*Cyclophilin-like domain

2067*Mitochondrial carrier protein

al protein L5, N-terminal, IPR031309*Ribosomal protein L5, C-terminal

type 11

ADH-ubiquinone oxidoreductase 51kDa subunit, iron-sulphur binding domain, IPR019554*Soluble li

C/D/E/F, IPR020103*Pseudouridine synthase, catalytic domain

archaea-type

ıl bundle

ı kinase, catalytic domain, IPR011009*Protein kinase-like domain

dyl-prolyl cis-trans isomerase domain, IPR029000*Cyclophilin-like domain

ıinge domain

somal protein S27e, zinc-binding domain

PR034113*Golgi-associated plant pathogenesis-related protein 1, SCP domain

TB domain-containing protein 8, IPR011333*SKP1/BTB/POZ domain

ıit RPB10

'13*Ribosomal protein S19A/S15e

te hydrolase, IPR003959*ATPase, AAA-type, core

)00306*FYVE zinc finger, IPR011011*Zinc finger, FYVE/PHD-type

type 1, IPR000210*BTB/POZ domain, IPR017096*BTB-kelch protein, IPR015915*Kelch-type beta pr

old

yotic/archaea-type

el, IPR017853*Glycoside hydrolase superfamily, IPR000322*Glycoside hydrolase family 31, IPR025

omal protein S10, eukaryotic/archaeal

/itellinogen, open beta-sheet, subdomain 1

oxidase C-terminal

omain
ase, C-terminal

al-like, IPR004046*Glutathione S-transferase, C-terminal, IPR012336*Thioredoxin-like fold
, IPR006032*Ribosomal protein S12/S23

nain 2, IPR008991*Translation protein SH3-like domain, IPR005824*KOW
exomutase, alpha/beta/alpha domain I

nain containing 1

eta/Sbh

te hydrolase
somal protein L40e, IPR000626*Ubiquitin domain

rotein, C-terminal, IPR015894*Guanylate-binding protein, N-terminal

e/RWD-like
*Alanine dehydrogenase/pyridine nucleotide transhydrogenase, NAD(H)-binding domain, IPR032095

nall heat shock protein HSP20, IPR002068*Alpha crystallin/Hsp20 domain

protein Lsm3
ynthase subunit g, animal

ning nucleoside triphosphate hydrolase, IPR003593*AAA+ ATPase domain

heat shock protein HSP20, IPR001436*Alpha crystallin/Heat shock protein

ain, IPR017849*Alkaline phosphatase-like, alpha/beta/alpha

5*Glutathione S-transferase, N-terminal, IPR004046*Glutathione S-transferase, C-terminal, IPR003C

ain

hate transporter NptA-like, IPR001509*NAD-dependent epimerase/dehydratase, IPR016040*NAD(P ı, IPR003057*Invertebrate colouration protein, IPR022271*Lipocalin, ApoD type

ı, IPR022271*Lipocalin, ApoD type, IPR003057*Invertebrate colouration protein

C1A, propeptide

ransketolase, C-terminal domain, IPR005474*Transketolase, N-terminal, IPR029061*Thiamin diphos

ɛ domain, IPR008183*Aldose 1-/Glucose-6-phosphate 1-epimerase, IPR015443*Aldose 1-epimerase

39*Ribosomal protein S15, IPR023029*Ribosomal protein S15P

d45

al, IPR005959*Fumarylacetoacetase

3*Lipase, eukaryotic

ninal, IPR013128*Peptidase C1A

)210*BTB/POZ domain

518*Potassium channel, inwardly rectifying, Kir, cytoplasmic

ING/FYVE/PHD-type

ubunit C

synthase GATase domain, IPR017926*Glutamine amidotransferase, IPR027417*P-loop containing nu

t 7/8

PR034113*Golgi-associated plant pathogenesis-related protein 1, SCP domain

tamase-inhibitor protein II, IPR011009*Protein kinase-like domain, IPR000408*Regulator of chromos
ninal domain

bulin-like fold, IPR001298*Filamin/ABP280 repeat

EID family

PR024950*Dual specificity phosphatase, IPR000340*Dual specificity phosphatase, catalytic domain,

e lectin/glucanase domain, IPR013148*Glycosyl hydrolase family 32, N-terminal, IPR013189*Glycosy

e, UCH37 type

tidase S1A, chymotrypsin family

-like complex subunit 6, N-terminal, IPR026797*HAUS augmin-like complex subunit 6, IPR021565*R

Chitinase II, IPR001223*Glycoside hydrolase family 18, catalytic domain

*Tubulin/FtsZ, GTPase domain, IPR018316*Tubulin/FtsZ, 2-layer sandwich domain

assembly factor Rtp1, C-terminal

somal protein L37ae/L37e

R009003*Peptidase S1, PA clan

P9/SRP14 subunit

R009003*Peptidase S1, PA clan

peller, TolB-like, IPR000033*LDLR class B repeat case SecE domain, IPR008158*Protein translocase SEC61 complex, gamma subunit

protein 6

exchanger

ed-helix domain

plase lipase domain

GT

main

complex, SecE/Sec61-gamma subunit, IPR023391*Protein translocase SecE domain

peller, TolB-like

ntral domain, IPR030556*Dynamin-1-like protein domain

BTB domain-containing protein 8, IPR011705*BTB/Kelch-associated

3*Peptidase C1A

83*Lactate/malate dehydrogenase, C-terminal, IPR015955*Lactate dehydrogenase/glycoside hydrola

*Proteasome alpha-subunit, N-terminal domain, IPR029055*Nucleophile aminohydrolases, N-termina

metazoa, IPR009057*Homeobox domain-like

IPR027995*Galactosyltransferase, N-terminal, IPR027791*Galactosyltransferase, C-terminal

CoA reductase, C-terminal, IPR013120*Male sterility, NAD-binding

n function DUF938

2*Transcription factor E2F4, IPR011991*Winged helix-turn-helix DNA-binding domain, IPR032198*E2

937*Amine oxidase

otype, IPR001611*Leucine-rich repeat

GT

y 30, beta sandwich domain, IPR017853*Glycoside hydrolase superfamily, IPR001139*Glycoside hy

n/cytosolic fatty-acid binding domain, IPR012674*Calycin, IPR002345*Lipocalin d45, IPR002415*H/ACA ribonucleoprotein complex, subunit Nhp2, eukaryote, IPR018492*Ribosomal

acyltransferase

apain C-terminal

old

osomal protein L37ae/L37e

*5'-Nucleotidase, C-terminal, IPR004843*Calcineurin-like phosphoesterase domain, ApaH type

kinase C mu-related, IPR020454*Diacylglycerol/phorbol-ester binding

n-converting enzyme-like 1

omain

ubunit 5, IPR007194*Transport protein particle (TRAPP) component

rin/alpha-actinin

ain, IPR001680*WD40 repeat

C1A, propeptide

in 2, IPR008927*6-phosphogluconate dehydrogenase C-terminal domain-like, IPR029154*3-hydroxy

ase, editing domain

*Lipocalin/cytosolic fatty-acid binding domain, IPR022271*Lipocalin, ApoD type

inding domain, IPR018164*Alanyl-tRNA synthetase, class IIc, N-terminal

, IPR013087*Zinc finger C2H2-type

nding site

H2- zinc finger protein family subset

lutathione S-transferase, C-terminal-like *dUTPase, trimeric

omain 2

main, IPR016181*Acyl-CoA N-acyltransferase smembrane domain, IPR006201*Neurotransmitter-gated ion-channel

Phosphatidylinositol-4-phosphate 5-kinase, N-terminal domain

R006091*Acyl-CoA oxidase/dehydrogenase, central domain

IM-barrel domain

5816*Vitellinogen, beta-sheet N-terminal, IPR011030*Vitellinogen, superhelical ctamase-inhibitor protein II

hromo shadow domain, IPR016197*Chromo domain-like, IPR014001*Helicase superfamily 1/2, ATP-

hate-dependent transferase, subdomain 2, IPR000192*Aminotransferase class V domain

sandwich domain

enase, N-terminal

tricopeptide-like helical domain, IPR009071*High mobility group box domain, IPR019787*Zinc finger

debranching enzyme, glucanotransferase domain, IPR006421*Glycogen debranching enzyme, meta

1, transmembrane domain, IPR003593*AAA+ ATPase domain sandwich domain

S1A, chymotrypsin family

ɔR027417*P-loop containing nucleoside triphosphate hydrolase

ɔrotein, ASH domain, IPR029955*Abnormal spindle-like microcephaly-associated protein, IPR00004ɛ

C-terminal subdomain, IPR013037*Clathrin adaptor, beta-adaptin, appendage, Ig-like subdomain, IPI

cific endonuclease, IPR001223*Glycoside hydrolase family 18, catalytic domain, IPR011583*Chitina

ɔmodomain, IPR003101*Coactivator CBP, KIX domain olase superfamily

erminal domain, IPR001650*Helicase, C-terminal, IPR014001*Helicase superfamily 1/2, ATP-binding

ycine receptor alpha, IPR006201*Neurotransmitter-gated ion-channel

IPR001723*Nuclear hormone receptor

subtype 2, IPR003599*Immunoglobulin subtype pair

015680*Glutamate-Gated Chloride Channel, IPR006028*Gamma-aminobutyric acid A receptor/Glycir

2 domain, IPR001965*Zinc finger, PHD-type

IM-barrel domain

ubunit, iron-sulphur binding domain, IPR019554*Soluble ligand binding domain

trin repeat, IPR001605*Pleckstrin homology domain, spectrin-type

T-associated domain

IM-barrel domain

30*Growth factor receptor cysteine-rich domain, IPR001881*EGF-like calcium-binding domain

3439*ABC transporter-like, IPR003593*AAA+ ATPase domain

dependent L-type calcium channel, IQ-associated domain, IPR011992*EF-hand domain pair

006176*3-hydroxyacyl-CoA dehydrogenase, NAD binding, IPR016040*NAD(P)-binding domain

alin A-like lectin/glucanase domain, IPR011993*PH domain-like, IPR017986*WD40-repeat-containin nal domain

fold, IPR011009*Protein kinase-like domain

316*Vitellinogen, beta-sheet N-terminal, IPR001747*Lipid transport protein, N-terminal

aminase-like fold

07696*DNA mismatch repair protein MutS, core, IPR017261*DNA mismatch repair protein MutS/MSI

23780*Chromo domain, IPR000330*SNF2-related, N-terminal domain, IPR000953*Chromo/chromo s

n homology domain, IPR021816*Dedicator of cytokinesis C/D, N-terminal

'53*FAD/NAD(P)-binding domain

*Dynein heavy chain, AAA module D4, IPR013602*Dynein heavy chain, domain-2, IPR026983*Dyne

HD-type

amily 3, nine cysteines domain, IPR001828*Receptor, ligand binding region

nerin, IPR032471*GAIN domain, N-terminal, IPR001881*EGF-like calcium-binding domain, IPR0008

PR030247*Canalicular multispecific organic anion transporter 1

33317*Transcription-associated protein 1, IPR011009*Protein kinase-like domain

ol-specific phospholipase C, X domain, IPR000159*Ras-associating (RA) domain, IPR017946*PLC-li

nkyrin repeat-containing domain, IPR017438*Inorganic polyphosphate/ATP-NAD kinase, domain 1, I ed, N-terminal domain

PR030247*Canalicular multispecific organic anion transporter 1

in

R013320*Concanavalin A-like lectin/glucanase domain, IPR000233*Cadherin, cytoplasmic domain, IF

mmunoglobulin subtype, IPR013162*CD80-like, immunoglobulin C2-set, IPR013151*Immunoglobulir

)06028*Gamma-aminobutyric acid A receptor/Glycine receptor alpha ic organic anion transporter 1, IPR003439*ABC transporter-like

phosphate synthetase large subunit-like, ATP-binding domain, IPR006275*Carbamoyl-phosphate syn

domain, IPR004179*Sec63 domain, IPR011545*DEAD/DEAH box helicase domain, IPR001650*He

otein L25/Gln-tRNA synthetase, beta-barrel domain, IPR020059*Glutamyl/glutaminyl-tRNA syntheta

n factor E2F4, IPR015633*E2F Family

pha-helical, IPR033925*Rad51/DMC1/RadA, IPR027417*P-loop containing nucleoside triphosphate h

omain

017986*WD40-repeat-containing domain, IPR011989*Armadillo-like helical, IPR015943*WD40/YVTN

olase superfamily

te domain, IPR032171*C-terminal of Roc (COR) domain, IPR015943*WD40/YVTN repeat-like-contain

A/C-terminal, IPR034157*DNA topoisomerase 2, TOPRIM domain, IPR013759*DNA topoisomerase

minal

tor DP

015946*K homology domain-like, alpha/beta

von Willebrand factor, type D domain

tor binding protein-related protein (IGFBP-rP), MAC25, IPR013098*Immunoglobulin I-set, IPR00903C ype fold

domain, IPR033196*Exosome complex component Rrp43

003598*Immunoglobulin subtype 2

g nucleoside triphosphate hydrolase

'R006091*Acyl-CoA oxidase/dehydrogenase, central domain

noline oxidoreductase, N-terminal

ıconate dehydrogenase, domain 2, IPR006108*3-hydroxyacyl-CoA dehydrogenase, C-terminal

n, IPR020338*SMN complex, gem-associated protein 7

ımmalian

sphomevalonate decarboxylase, IPR029765*Diphosphomevalonate decarboxylase, IPR020568*Ribos

R013786*Acyl-CoA dehydrogenase/oxidase, N-terminal, IPR009100*Acyl-CoA dehydrogenase/oxida noline oxidoreductase, C-terminal

l protein L7Ae/L8/Nhp2 family

osomal protein S5, eukaryotic/archaeal, IPR014721*Ribosomal protein S5 domain 2-type fold, subgr

uconate dehydrogenase, domain 2, IPR006108*3-hydroxyacyl-CoA dehydrogenase, C-terminal main

in

Immunoglobulin subtype

5*Vitellinogen, open beta-sheet, IPR015816*Vitellinogen, beta-sheet N-terminal gand binding domain, IPR011537*NADH ubiquinone oxidoreductase, F subunit

ropeller

887*Glycoside hydrolase family 31, N-terminal domain, IPR000519*P-type trefoil domain

5*Saccharopine dehydrogenase, C-terminal, IPR016040*NAD(P)-binding domain, IPR005097*Saccha

)81*Glutathione S-transferase, Mu class

')-binding domain

sphate-binding fold

e

ucleoside triphosphate hydrolase, IPR017456*CTP synthase, N-terminal

some condensation, RCC1

IPR020422*Dual specificity protein phosphatase domain

yl hydrolase family 32, C-terminal, IPR001362*Glycoside hydrolase, family 32

abenosyn, Rab binding domain, IPR013083*Zinc finger, RING/FYVE/PHD-type

ase, family 4, C-terminal, IPR016040*NAD(P)-binding domain, IPR001236*Lactate/malate dehydroge

al

2F transcription factor, CC-MB domain

ydrolase family 30

l protein L7Ae/L8/Nhp2 family

yisobutyrate dehydrogenase, NAD-binding domain, IPR011548*3-hydroxyisobutyrate dehydrogenase

·binding domain, IPR006576*BRK domain

, PHD-finger

azoa, IPR017853*Glycoside hydrolase superfamily, IPR010401*Glycogen debranching enzyme, IPR

3*IQ motif, EF-hand binding site

R009028*Coatomer/calthrin adaptor appendage, C-terminal subdomain, IPR026739*AP complex sul

se II

domain, IPR030088*SWI/SNF complex subunit SMARCA2, IPR029295*Snf2, ATP coupling domain ne receptor alpha

g domain, IPR023362*PH-BEACH domain, IPR015943*WD40/YVTN repeat-like-containing domain

H, IPR007861*DNA mismatch repair protein MutS, clamp shadow domain, IPR006576*BRK domain

ein heavy chain, IPR011704*ATPase, dynein-related, AAA domain, IPR035706*Dynein heavy chain, 32*GPCR, family 2, secretin-like, IPR001879*GPCR, family 2, extracellular hormone receptor domai

ike phosphodiesterase, TIM beta/alpha-barrel domain, IPR028398*1-phosphatidylinositol 4,5-bisphos

IPR016064*NAD kinase/diacylglycerol kinase-like domain

PR009030*Growth factor receptor cysteine-rich domain

n

nthase, large subunit, IPR035686*Carbamoyl-phosphate synthase small subunit, GATase1 domain, I

elicase, C-terminal, IPR014756*Immunoglobulin E-set

se, class Ib, anti-codon binding domain, IPR000738*WHEP-TRS domain, IPR004526*Glutamyl-tRN hydrolase, IPR013632*DNA recombination and repair protein Rad51-like, C-terminal

N repeat-like-containing domain, IPR013320*Concanavalin A-like lectin/glucanase domain, IPR0233

ining domain, IPR002110*Ankyrin repeat, IPR000719*Protein kinase domain, IPR025875*Leucine ric

, type IIA, central domain, IPR013758*DNA topoisomerase, type IIA, subunit A/ C-terminal, alpha-be

)*Growth factor receptor cysteine-rich domain, IPR007110*Immunoglobulin-like domain

osomal protein S5 domain 2-type fold

ase, N-terminal and middle domain

roup

aropine dehydrogenase, NADP binding domain

enase, N-terminal

032790*Glycogen debranching enzyme, C-terminal

bunit beta

1

ATP-binding dynein motor region D5, IPR024743*Dynein heavy chain, coiled coil stalk, IPR035699*

in

sphate phosphodiesterase epsilon-1, IPR015359*Phosphoinositide-specific phospholipase C, EF-har

IPR011607*Methylglyoxal synthase-like domain, IPR016185*Pre-ATP-grasp domain, IPR005480*Ca

A synthetase, archaeal/eukaryotic cytosolic, IPR020061*Glutamyl/glutaminyl-tRNA synthetase, class

62*PH-BEACH domain

ch repeat 4, IPR001611*Leucine-rich repeat, IPR027417*P-loop containing nucleoside triphosphate

ta, IPR013760*DNA topoisomerase, type IIA-like domain, IPR013506*DNA topoisomerase, type IIA,

Dynein heavy chain, hydrolytic ATP-binding dynein motor region D1 nd-like domain, IPR001192*Phosphoinositide phospholipase C family

arbamoyl-phosphate synthetase, large subunit oligomerisation domain, IPR005483*Carbamoyl-phosp

s Ib, alpha-bundle domain, IPR014729*Rossmann-like alpha/beta/alpha sandwich fold, IPR020058*G hydrolase

subunit B, domain 2, IPR020568*Ribosomal protein S5 domain 2-type fold, IPR014721*Ribosomal

phate synthase large subunit, CPSase domain, IPR006274*Carbamoyl-phosphate synthase, small su

Glutamyl/glutaminyl-tRNA synthetase, class Ib, catalytic domain protein S5 domain 2-type fold, subgroup, IPR024946*Arginine repressor C-terminal-like domain, IPR

ubunit

001154*DNA topoisomerase II, eukaryotic-type, IPR003594*Histidine kinase-like ATPase, C-termina

al domain, IPR031660*C-terminal associated domain of TOPRIM

Table S6 - Differentially expressed genes (DEGs) and significantly over/underexpressed genes

Gene ID	$\log_2$FC	description
tetur04g08210	10.53318879	Hypothetical protein
tetur43g00580	10.31965507	Hypothetical protein
tetur03g05020	10.30919827	CYP392D5p Cytochrome P450 - CYP392D5p probable pseudogene
tetur02g07800	10.1573207	Hypothetical protein
tetur19g00350	10.03178697	Leucine-rich repeat; cysteine-containing subtype
tetur31g02000	9.952407101	SSPA6 Small Secreted Protein; family A Hypothetical protein
tetur20g00010	9.949165627	Hypothetical protein
tetur03g07550	9.815301319	E75 nuclear receptor
tetur07g08169	9.732224334	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur09g01060	9.721873236	Cystine-knot cytokine
tetur02g14741	9.425424397	BTB/Kelch-associated
tetur16g02710	9.402219351	mitochondrial carnitine/acylcarnitine carrier protein
tetur14g03960	9.161742244	PREDICTED: hypothetical protein; partial
tetur03g07440	8.940362654	Hypothetical protein
tetur31g02020	8.58579705	Apple-like
tetur01g13130	8.509692786	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur31g00010	8.376430241	Hypothetical protein
tetur07g07660	8.30106373	Triacylglycerol lipase family
tetur12g00740	8.226429373	Hypothetical protein
tetur03g04990	8.163934198	CYP392D2 Cytochrome P450 - CYP392D2
tetur03g05040	8.14675549	Cytochrome P450 - fragment na Cytochrome P450 -
tetur05g07590	8.146059498	cullin-5
tetur24g00750	8.12676491	gigaxonin
tetur14g02050	8.124915735	MDL11 Immunoglobulin E-set Immunoglobulin E-set
tetur05g05050	8.059590752	UGT UDP-glycosyltransferase; teturUGT28 UGT UDP-glycosyltransferase
tetur03g00830	8.011382306	CYP392A12 Cytochrome P450 - CYP392A12
tetur39g90809	7.958922761	hypothetical protein
tetur09g06240	7.947132023	Hypothetical protein
tetur09g92898	7.821552425	hypothetical protein
tetur01g13110	7.694944053	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur07g01450	7.646487831	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur01g13120	7.640570229	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur02g14731	7.633898665	BTB/Kelch-associated BTB/Kelch-associated
tetur01g11850	7.38088871	LZY1;2 Conserved zygote-specific protein homologue LZY1;2 Conserved zy
tetur06g06630	7.372531307	TuCPI-20 Cystatin hypothetical protein
tetur14g04178	7.286133749	
tetur04g07480	7.283548187	H/ACA ribonucleoprotein complex subunit 3 H/ACA ribonucleoprotein comple
tetur24g00740	7.22390786	BTB/POZ-like
tetur05g05610	7.059100501	HESP1 Highly expressed secreted protein family HESP1 Highly expressed s
tetur06g04530	7.054565003	Hypothetical protein
tetur07g02420	7.012006519	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur14g03770	6.956028396	Golgi-associated plant pathogenesis-related protein 1
tetur01g13100	6.917087302	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur05g05060	6.907994362	UGT UDP-glycosyltransferase; teturUGT29 UGT UDP-glycosyltransferase

tetur06g03010	6.898304341	PLATp2 PLAT/LH2 domain PLAT/LH2 domain
tetur615g00020	6.840353285	PREDICTED: similar to PMP1 protein
tetur24g00820	6.828212464	BTB/POZ-like
tetur06g03050	6.685614713	PLAT14 PLAT/LH2 domain PLAT/LH2 domain PLAT/LH2 domain
tetur03g02710	6.684417014	Scramblase
tetur05g05640	6.608679592	HESP3 Highly Expressed Secreted Protein Family Hypothetical protein
tetur14g03810	6.554603091	Concanavalin A-like lectin/glucanase
tetur06g04580	6.540537707	Hypothetical protein
tetur14g03800	6.48265506	PREDICTED: similar to PMP1 protein
tetur56g90039	6.478997954	hypothetical protein
tetur19g02850	6.452565271	Hypothetical protein
tetur06g04980	6.444115161	short-chain dehydrogenase/reductase SDR
tetur05g04170	6.333472197	RNA 3'-terminal phosphate cyclase-like protein
tetur01g13090	6.332331924	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur06g04970	6.305349971	3-oxoacyl-acyl-carrier-protein reductase
tetur24g00680	6.299190556	kelch-like 18
tetur06g04940	6.296538148	3-oxoacyl-acyl-carrier-protein reductase
tetur24g00720	6.245030453	PREDICTED: similar to zinc finger protein; putative
tetur03g05100	6.233224727	CYP392Dn Cytochrome P450, conserved site CYP Cytochrome P450, conse
tetur07g07890	6.217537732	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur39g00110	6.21423518	PREDICTED: lysophospholipase 3
tetur02g12230	6.181020785	Hypothetical protein
tetur34g00160	6.173058558	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur01g11290	6.168467413	Hypothetical protein
tetur14g03970	6.091456294	ACYPI009414
tetur06g04550	6.074992303	Hypothetical protein
tetur16g03490	6.063868643	antigen B membrane protein
tetur24g00690	6.0437316	BTB/POZ-like
tetur03g05070	5.967400503	CYP392D8 Cytochrome P450 - CYP392D8
tetur02g03040	5.874910622	Hypothetical protein
tetur24g00770	5.808664922	BTB/POZ-like
tetur02g90713	5.784263014	hypothetical protein
tetur24g00800	5.701109666	BTB/POZ-like
tetur02g14721	5.623869754	BTB/Kelch-associated
tetur03g10103	5.582330882	SSPX Single Copy Small Secreted Protein of Unknown Function hypothetic
tetur04g01470	5.546439518	Hypothetical protein
tetur01g01520	5.497329353	Apolipoprotein D precursor; putative
tetur07g02290	5.419089715	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur01g10740	5.38519089	TuCCE03 Carboxyl/cholinesterase TuCCE-03 Carboxyl/cholinesterase
tetur06g04960	5.385133738	short-chain dehydrogenase/reductase SDR
tetur14g03820	5.368218467	PREDICTED: similar to PMP1 protein
tetur14g03760	5.293622033	PREDICTED: hypothetical protein; partial
tetur171g00020	5.287841165	Nucleophile aminohydrolases, N-terminal
tetur03g02760	5.285631551	Scramblase
tetur02g01120	5.039708079	Hypothetical protein
tetur13g04550	4.962006399	Intradiol ring-cleavage dioxygenase, core Intradiol ring-cleavage dioxygenas
tetur17g03400	4.927817537	DDM9-16 Domain of unknown function DUF3421 Domain of unknown functi

tetur05g04580	4.896125569	WTSP10 Wannes-Thomas Secreted Protein 10 Hypothetical protein
tetur283g00010	4.832596239	fructose-1;6-bisphosphatase
tetur30g01490	4.823597419	adenylate cyclase
tetur05g05020	4.794446566	UGT UDP-glycosyltransferase; teturUGT26 UGT UDP-glycosyltransferase
tetur16g02700	4.748784596	mitochondrial carnitine/acylcarnitine carrier protein
tetur16g03200	4.747517274	PREDICTED: similar to adenylate cyclase
tetur29g00990	4.745904161	CCEincTu18 Carboxyl/cholinesterase; incomplete esterase
tetur27g00220	4.701550279	CYP probable pse Cytochrome P450 probable pseudogene
tetur47g00220	4.695304247	Hypothetical protein
tetur14g93002	4.672364781	hypothetical protein
tetur24g00670	4.654848411	GTP-binding protein Rit1
tetur16g03190	4.624904049	SPH3 Serine protease homologue SPH Serine protease homologue
tetur06g02590	4.593246836	SPH43 Serine protease homologue
tetur01g00610	4.571693807	Hypothetical protein
tetur04g00870	4.424486222	Hypothetical protein
tetur03g06980	4.41279154	Apple-like
tetur47g00170	4.390591894	Hypothetical protein
tetur03g00970	4.378573776	CYP392A11 Cytochrome P450 - CYP392A11 CYP392A11v2 Cytochrome P
tetur47g00140	4.28419499	Hypothetical protein
tetur11g00830	4.268567409	NYN domain, limkain-b1-type
tetur03g05110	4.230121884	CYP392D10p Cytochrome P450 - CYP392D10p probable pseudogene
tetur02g12190	4.188797197	Hypothetical protein
tetur04g09459	4.175244854	SSPF2 Small Secreted Protein; Family F hypothetical protein
tetur05g00080	4.130702852	UGT UDP-glycosyltransferase; teturUGT22 UGT UDP-glycosyltransferase
tetur11g05770	4.099070694	TuCCE35 Carboxyl/cholinesterase TuCCE35 Carboxylesterase; type B TuC
tetur16g01880	4.066944177	integrin alpha 2
tetur06g02400	4.064949737	CYP392E2 Cytochrome P450 - CYP392E2
tetur12g00580	4.029972597	Hypothetical protein
tetur20g00700	3.961957245	Hypothetical protein
tetur01g01500	3.914963142	Apolipoprotein D precursor; putative PREDICTED: apolipoprotein D-like; par
tetur17g03440	3.910054353	DDM9-13 Domain of unknown function DUF3421 Domain of unknown functi
tetur05g02210	3.908953592	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur31g01860	3.875709469	Hypothetical protein
tetur03g00800	3.846871051	CYP-pseudogene Cytochrome P450 - probable pseudogene
tetur05g00090	3.823225686	UGT UDP-glycosyltransferase; teturUGT23 UGT UDP-glycosyltransferase
tetur496g00010	3.791652133	dimethyladenosine transferase
tetur355g00010	3.785184835	Solute carrier family 35 member F3/F4
tetur02g01850	3.76153829	adenylyltransferase and sulfurtransferase MOCS3
tetur08g06580	3.741505637	RING finger protein 146
tetur17g02240	3.717300561	Hypothetical protein
tetur31g00830	3.699966585	methyl-accepting chemotaxis sensory transducer
tetur07g07920	3.698843018	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur13g04350	3.683358723	PREDICTED: similar to F55A4.8a
tetur07g05940	3.671939351	intradiol ring-cleavage dioxygenase
tetur02g01760	3.65148695	Hypothetical protein
tetur33g01430	3.650452804	TPAN-53 PAN/Apple domain PAN/Apple domain
tetur02g12210	3.634309418	Hypothetical protein

tetur04g90885	3.608450817	hypothetical protein
tetur05g01700	3.537308976	lipase 1 precursor
tetur19g02860	3.533939729	CPR X cuticle protein; putative CP X cuticle protein; putative cuticle protein
tetur02g14310	3.473623263	Hypothetical protein
tetur28g02600	3.464657033	Hypothetical protein
tetur06g04920	3.443857476	3-oxoacyl-acyl-carrier-protein reductase
tetur14g02720	3.425121963	Hypothetical protein
tetur29g00930	3.413524735	TuCCE58 Carboxyl/cholinesterase TuCCE-49 Carboxyl/cholinesterase
tetur21g03140	3.406491452	CuffL3 Cutoff-like protein HPA1c Hypothetical Protein of Unknown Function
tetur184g00040	3.387135747	PREDICTED: UDP glucuronosyltransferase 2B10 isoform 1
tetur16g01180	3.384703502	Hypothetical protein
tetur13g02160	3.358230437	Hypothetical protein
tetur02g09600	3.293726459	Hypothetical protein
tetur02g12220	3.285726165	Hypothetical protein
tetur02g12500	3.282781751	BTB/Kelch-associated BTB/Kelch-associated
tetur02g07980	3.278168602	Hypothetical protein
tetur05g06600	3.272993545	CYP389C9 Cytochrome P450 - CYP389C9
tetur06g04520	3.193547088	CYP392A16 Cytochrome P450 - CYP392A16
tetur19g02300	3.168162341	intradiol ring-cleavage dioxygenase
tetur02g09830	3.157565278	UGT UDP-glycosyltransferase; teturUGT10 UGT UDP-glycosyltransferase
tetur19g02710	3.15415592	PREDICTED: similar to KIAA1919
tetur06g91354	3.152447161	hypothetical protein
tetur11g05400	3.077012808	excision repair cross-complementing rodent repair deficiency; complementatio
tetur34g00330	3.076583491	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur21g01410	3.043779555	Hypothetical protein
tetur06g01100	3.038735458	Hypothetical protein
tetur12g00120	3.010853749	C-factor
tetur05g07580	2.925735251	cullin-5
tetur17g92134	2.919463563	hypothetical protein
tetur13g04170	2.911960554	GE26306
tetur05g04560	2.907876683	WTSP8 Wannes-Thomas Secreted Protein 8 Hypothetical protein
tetur03g05000	2.904975261	CYP392D3 Cytochrome P450 - CYP392D3
tetur03g91623	2.878114636	hypothetical protein
tetur12g00230	2.850209492	Hypothetical protein
tetur02g09850	2.847312547	UGT UDP-glycosyltransferase; teturUGT11 UGT UDP-glycosyltransferase
tetur13g00540	2.84515034	MZT2a MOZART2 family MZT2a MOZART2 family MOZART2 family
tetur33g01450	2.838563997	TPAN-52 3-Pan modules Cell Surface Protein; Antigen-B homolog Apple-lik
tetur33g01640	2.81688308	Hypothetical protein
tetur02g13950	2.798416844	Hypothetical protein
tetur24g00900	2.784367607	Kelch-type beta propeller
tetur29g00670	2.765063942	Hypothetical protein
tetur08g08040	2.755025615	lethal
tetur35g00800	2.741763651	Hypothetical protein
tetur28g01750	2.733381724	Hypothetical protein
tetur02g07030	2.718125793	Hypothetical protein
tetur10g92745	2.710889756	hypothetical protein
tetur02g14280	2.655621939	Hypothetical protein

tetur12g00590	2.651401946	C-factor
tetur19g02880	2.636625462	Hypothetical protein
tetur05g05290	2.614115595	TuGSTm11 Glutathione S-transferase; class mu
tetur17g02290	2.604879923	Hypothetical protein
tetur06g04890	2.596125768	3-oxoacyl-acyl-carrier-protein reductase
tetur15g03500	2.594848323	ephrin
tetur11g00860	2.590578267	Hypothetical protein
tetur01g06760	2.583131201	TuLeg-21 Legumain-like; pseudogen
tetur02g03550	2.573234002	GK24782
tetur06g01080	2.564360969	PREDICTED: similar to DnaJ
tetur03g00130	2.552932917	lethal
tetur07g05050	2.544654586	Hypothetical protein
tetur18g01120	2.542207296	sin3 histone deacetylase corepressor complex component SDS3
tetur05g07900	2.535946675	TRAF-like
tetur05g04690	2.535254968	UGT UDP-glycosyltransferase; teturUGT25 UGT UDP-glycosyltransferase
tetur17g03530	2.532302989	Epididymal secretory protein E1 precursor
tetur05g09040	2.523131583	biphenyl hydrolase-like
tetur208g00020	2.494575691	Mitochondrial substrate/solute carrier
tetur16g03210	2.470715264	Hypothetical protein
tetur06g02910	2.469767909	p21-activated protein kinase-interacting protein 1-like
tetur21g03020	2.468875225	Hypothetical protein
tetur19g01760	2.451248394	CD63 antigen
tetur31g01960	2.447908642	Hypothetical protein
tetur02g12830	2.443782967	Hypothetical protein
tetur08g05780	2.443326404	Metal-dependent protein hydrolase
tetur07g03040	2.42505974	Hypothetical protein
tetur25g01950	2.401185498	sorbitol dehydrogenase sorbitol dehydrogenase
tetur16g01170	2.391003091	Hypothetical protein
tetur28g01250	2.386396026	intradiol ring-cleavage dioxygenase
tetur04g09479	2.361664624	SSPF3 Small Secreted Protein; Family F hypothetical protein
tetur233g00040	2.353262359	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur66g00070	2.350398105	SP45 Serine protease
tetur18g01530	2.345270635	TuENaC119 Putative Degenerin/Epithelial Sodium Channel DEG/ENaC Tu_E
tetur12g00570	2.320338311	C-signal
tetur05g00070	2.31399452	UGT UDP-glycosyltransferase; teturUGT21 UGT UDP-glycosyltransferase
tetur04g09150	2.3015273	Hypothetical protein
tetur06g05640	2.2967825	Hypothetical protein
tetur128g00060	2.281469861	serpin 3 inhibitory serine protease inhibitor
tetur11g05760	2.279051712	TuCCE34 Carboxyl/cholinesterase TuCCE33 Carboxyl/cholinesterase TuCC
tetur04g06400	2.278714074	Nematode AStacin protease family member
tetur18g01260	2.276890275	cathepsin A
tetur21g02400	2.272949027	NCSP2 Novel Cell surface protein Hypothetical protein
tetur466g00020	2.272014808	Phosphatidic acid phosphatase type 2/haloperoxidase
tetur468g00020	2.260308341	50S ribosomal protein L14
tetur02g15365	2.259724095	hypothetical protein
tetur22g01050	2.243610411	Mitochondrial import inner membrane translocase subunit Tim13
tetur571g00020	2.239664884	PREDICTED: similar to poly

tetur04g05430	2.231255721	Protein of unknown function DUF3743
tetur02g09250	2.225514259	Hypothetical protein
tetur26g00560	2.221381363	PREDICTED: similar to Low-density lipoprotein receptor-related protein 1B pr
tetur01g11070	2.219627248	PREDICTED: similar to KIAA0556 protein
tetur128g00050	2.216262285	Leukocyte elastase inhibitor
tetur12g00610	2.211592089	short-chain dehydrogenase/reductase SDR
tetur20g03250	2.200678207	TuCCE50 Carboxyl/cholinesterase TuCCE-42 Carboxyl/cholinesterase
tetur02g14390	2.199221381	Hypothetical protein
tetur24g00220	2.192460803	Hypothetical protein
tetur41g00100	2.188845363	translation initiation factor IF-3
tetur07g05930	2.181857478	intradiol ring-cleavage dioxygenase
tetur06g91351	2.17381813	hypothetical protein
tetur06g00450	2.171704206	intradiol ring-cleavage dioxygenase
tetur04g00770	2.160865617	SSPF1 Small Secreted Protein; Family F transporter; AcrB/AcrD/AcrF family
tetur02g04830	2.155415491	Hypothetical protein
tetur21g03250	2.152382274	Hypothetical protein
tetur657g00010	2.151753832	lambda-crystallin homolog
tetur01g00490	2.144294808	intradiol ring-cleavage dioxygenase
tetur01g07900	2.140936504	Type-II Transmembrane Protein Hypothetical protein
tetur16g01910	2.127125205	Integrin alpha beta-propellor
tetur12g03950	2.116998461	SP29 Serine protease SP45_3 Serine protease SP29 Serine protease
tetur28g01360	2.114451125	WTSP2 Wannes-Thomas Secreted Protein 2 Hypothetical protein
tetur11g05520	2.114305618	CYP385C4 Cytochrome P450 - CYP385C4
tetur17g02250	2.108049898	PREDICTED: membrane-associated ring finger
tetur29g00940	2.107029521	TuCCE50 Carboxyl/cholinesterase TuCCE-50 Carboxyl/cholinesterase
tetur05g04040	2.101695959	Hypothetical protein
tetur27g00350	2.10040933	CYP392E8 Cytochrome P450 - CYP392E8
tetur11g05740	2.097068604	PLAT9 Lipase/lipooxygenase; PLAT/LH2 Lipase/lipooxygenase; PLAT/LH2
tetur02g03960	2.076187113	Hypothetical protein
tetur29g00220	2.042620825	TuGSTd14 Glutathione S-transferase; class delta
tetur180g00020	2.035143663	Domain of unknown function DUF3421
tetur08g05010	2.032591359	TuPap-11 Cathepsin B
tetur22g01200	2.015426859	SP63/C Serine proteases, trypsin family, histidine active site SP63 Serine pr
tetur17g03420	2.01364256	DDM9-11 Domain of unknown function DUF3421 Domain of unknown functi
tetur06g04880	2.008218493	short-chain dehydrogenase/reductase SDR short-chain dehydrogenase/redu
tetur30g02120	2.005197423	Hypothetical protein
tetur17g92128	2.00403864	hypothetical protein
tetur03g04820	1.994136699	Rtf1; Paf1/RNA polymerase II complex component; homolog
tetur07g03790	1.993971503	BolA-2 BolA-like protein BolA-like protein
tetur02g06640	1.988976954	CYP pseudogene Cytochrome P450 - CYP probable pseudogene
tetur05g05900	1.976932391	frataxin
tetur10g04020	1.976588203	beta-tubulin
tetur20g02800	1.976023099	SPUF5 Plant self-incompatibility S1 Plant self-incompatibility S1
tetur20g02620	1.975596111	Galactose-binding domain-like
tetur04g02490	1.974427173	Hypothetical protein
tetur547g00010	1.971717681	variable lymphocyte receptor A
tetur27g00570	1.962588991	Vsx2 Homeobox, conserved site Homeobox Homeobox, conserved site

tetur04g06360	1.959411175	beta-tubulin
tetur183g00040	1.954678682	clathrin light chain
tetur29g00820	1.944333093	TuCCE57 Carboxyl/cholinesterase TuCCE-48 Carboxyl/cholinesterase
tetur02g03690	1.933639242	Hypothetical protein
tetur15g03650	1.928558798	Hypothetical protein
tetur30g01820	1.917534131	Hypothetical protein
tetur03g05540	1.917534026	CYP392E1 Cytochrome P450 - CYP392E1
tetur20g03210	1.914822731	PREDICTED: similar to adenylate cyclase
tetur07g01460	1.913049205	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur55g00080	1.911363474	MDL Immunoglobulin E-set Immunoglobulin E-set
tetur12g04200	1.906877547	Hypothetical protein
tetur01g06000	1.905709868	Hypothetical protein
tetur08g01180	1.904235305	Hypothetical protein
tetur31g01060	1.894079574	Armadillo-type fold
tetur11g02270	1.893639028	PREDICTED: similar to ankyrin 2;3/unc44
tetur12g02170	1.888344287	Hypothetical protein
tetur01g09320	1.877325193	Nucleotide-binding; alpha-beta plait
tetur10g05070	1.874246906	SPZ3 protein
tetur01g05480	1.853981122	TuPap-17 Cathepsin B
tetur106g00050	1.845657552	PREDICTED: similar to Y41C4A.8 PREDICTED: similar to Y41C4A.8 PRED
tetur04g07910	1.842919041	TuABCC-15 ABC-transporter; class C;
tetur31g00970	1.841393553	synMuvL2 NF-kappa-B-activating protein/UPF0396 NF-kappa-B-activating p
tetur25g00300	1.824306118	NijA homologue of insect Ninjurin A ninjurin a
tetur09g03740	1.823468017	WTTMP1 Wannes-Thomas type-I single-pass transmembrane protein type-I
tetur04g07100	1.81958781	Hypothetical protein
tetur36g00170	1.818485909	hypothetical protein
tetur16g03340	1.813348531	TPAN-1 3-Pan modules Cell Surface Protein; antigen-2 PANR-1 Pan module
tetur27g01730	1.811841502	conserved hypothetical protein
tetur03g06370	1.809562168	TWiK family of potassium channels family member
tetur10g04780	1.803380573	Protease inhibitor I4; serpin
tetur05g07490	1.796341011	unnamed protein product
tetur02g11020	1.770265959	Tu_12344.2 cys-loop ligand-gated ion channel Tu_12344.2 ligand-gated ion
tetur20g01190	1.75453948	UNC93-like protein MFSD11
tetur18g00150	1.753713477	MUscle Attachment abnormal family member
tetur12g00560	1.753662835	putative oxidoreductase protein
tetur09g00550	1.729839386	DDM9-6 Domain of unknown function DUF3421 Domain of unknown functio
tetur11g00740	1.727500262	PREDICTED: similar to limkain b1
tetur05g03540	1.721933447	Rpf2p Brix domain Brix domain
tetur17g03390	1.719828067	DDM9-17 Domain of unknown function DUF3421 Domain of unknown functi
tetur04g02590	1.718520543	PREDICTED: similar to High-affinity cationic amino acid transporter-1
tetur16g01140	1.718059528	Hypothetical protein
tetur08g08070	1.715181546	Hypothetical protein
tetur25g01000	1.708496406	gamma-glutamyl hydrolase precursor
tetur03g00370	1.704385387	Hypothetical protein
tetur10g02410	1.698925468	lambda-crystallin homolog
tetur12g04671	1.68755356	Intradiol ring-cleavage dioxygenase, C-terminal Intradiol ring-cleavage dioxy
tetur21g02530	1.683768732	NADH dehydrogenase 1 alpha subcomplex subunit 13

tetur03g00400	1.682486579	Hypothetical protein
tetur20g01570	1.669876698	Hypothetical protein
tetur02g13650	1.661742969	Conserved hypothetical protein CHP02464
tetur136g00040	1.66010077	Hypothetical protein
tetur08g05990	1.656946689	Rhodopsin-like receptor
tetur03g00040	1.648558478	Hypothetical protein
tetur04g04300	1.644960297	UGT UDP-glycosyltransferase; teturUGT14 UGT UDP-glycosyltransferase
tetur01g03880	1.632649775	Methyltransferase type 11
tetur21g91223	1.630737792	hypothetical protein
tetur01g02520	1.625074104	calcium-binding protein p22
tetur01g10750	1.622883464	TuCCE04 Carboxyl/cholinesterase TuCCE-04 Carboxyl/cholinesterase
tetur01g17304	1.621234683	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur05g02680	1.614795001	PREDICTED: UTP6; small subunit
tetur02g02930	1.614612321	Hypothetical protein
tetur03g10037	1.614234565	
tetur04g07780	1.612236302	UGT UDP-glycosyltransferase; teturUGT19 UGT UDP-glycosyltransferase
tetur31g01980	1.611192243	Nucleotide-binding; alpha-beta plait
tetur35g00180	1.611072179	CCEincTu13 Carboxyl/cholinesterase; incomplete CCEincTu15 Carboxyl/ch
tetur44g00260	1.609994257	LMPT Zinc finger, LIM-type Zinc finger, LIM-type
tetur26g00550	1.608840938	UNCoordinated family member
tetur01g05690	1.607953255	UGT UDP-glycosyltransferase; teturUGT02 UGT UDP-glycosyltransferase
tetur09g06220	1.604599007	Hypothetical protein
tetur08g07940	1.597799307	lethal
tetur04g92226	1.597548049	hypothetical protein
tetur13g03880	1.59746081	Hypothetical protein
tetur07g02450	1.596029779	COX17 Cytochrome c oxidase copper chaperone Cytochrome c oxidase co
tetur18g03640	1.590711809	S-adenosyl-L-methionine-dependent methyltransferase
tetur06g04250	1.588420908	Sec1-like protein
tetur02g05220	1.587617234	secreted protein; putative
tetur03g01730	1.584620168	Histone H4
tetur01g02900	1.581525772	Shisa family
tetur05g04460	1.575929237	vesicular glutamate transporter 1
tetur15g03690	1.569956727	adiponectin receptor protein 2
tetur21g91232	1.56655754	hypothetical protein
tetur07g07980	1.565450573	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur04g06440	1.559527214	Hypothetical protein
tetur13g03510	1.555792549	E3 ubiquitin-protein ligase MARCH5
tetur01g08670	1.554126707	PREDICTED: similar to inorganic phosphate cotransporter; putative
tetur24g01310	1.553084747	TuCCE44 Carboxyl/cholinesterase TuCCE-44 Carboxyl/cholinesterase
tetur15g02770	1.548950399	S-adenosyl-L-methionine-dependent methyltransferase
tetur15g01050	1.546681751	adenylate cyclase
tetur04g02190	1.54369775	Hypothetical protein
tetur06g02820	1.543393201	CYP392E3 Cytochrome P450 - CYP392E3
tetur13g04450	1.540519367	short-chain dehydrogenase/reductase SDR
tetur03g03600	1.538742566	putative gut cathepsin L-like cysteine protease
tetur17g02610	1.536147159	Hypothetical protein
tetur22g00080	1.53283001	Seven cysteines

tetur07g02690	1.53255555	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur07g91887	1.531921703	hypothetical protein
tetur13g02680	1.525826575	GnRH-R2 G-protein coupled neuropeptide receptor.
tetur10g04770	1.524167183	Leukocyte elastase inhibitor
tetur26g00640	1.517399265	Hypothetical protein
tetur03g08810	1.512832919	SSPB1 Small Secreted Protein; Family B Hypothetical protein
tetur05g06390	1.511580763	Hypothetical protein
tetur01g11460	1.511400176	Ato1 Protein atonal/lin-32 Atoh1a Protein atonal/lin-32 HLH Protein atonal/li
tetur32g01970	1.504200259	CutC family protein
tetur41g00400	1.503699711	Hypothetical protein
tetur09g02110	1.501483182	PREDICTED: similar to Neurensin-1
tetur08g00470	1.500851248	PREDICTED: similar to adenylate cyclase
tetur12g01230	1.500019732	conserved hypothetical protein
tetur02g05170	1.483021538	TeturLY6_UPAR4 LY6_UPAR protein Three finger domain protein TFD Pr
tetur05g07690	1.482914484	Hypothetical protein
tetur20g02730	1.481931157	eukaryotic translation initiation factor 3 subunit L
tetur26g01490	1.478252616	TuGSTd11 Glutathione S-transferase; class delta TuGSTd11 Glutathione S-
tetur03g00940	1.472008142	sodium-dependent multivitamin transporter
tetur03g00200	1.471734636	lethal
tetur01g08260	1.471011765	Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L do
tetur16g03430	1.466561212	beta-mannosidase
tetur08g03570	1.465425253	Glutaredoxin-1
tetur02g10980	1.463755923	Hypothetical protein
tetur11g00760	1.463722877	Hypothetical protein
tetur29g00830	1.451773478	Coatomer subunit zeta-1
tetur40g00320	1.445729594	Hypothetical protein
tetur09g92852	1.443686115	hypothetical protein
tetur13g03270	1.436610091	Hypothetical protein
tetur16g90562	1.433662902	hypothetical protein
tetur11g01040	1.433005518	Hypothetical protein
tetur10g04820	1.429987895	Protease inhibitor I4; serpin
tetur19g01700	1.423055769	Tetraspanin/Peripherin
tetur17g03910	1.4223553	peptidase M28
tetur11g05410	1.420087371	PREDICTED: similar to adenylate cyclase
tetur02g00930	1.413373748	Hypothetical protein
tetur01g06610	1.412917844	TuLeg-17 Legumain
tetur71g00010	1.409376542	Hypothetical protein
tetur24g00920	1.407951247	BBS7 Bardet-Biedl syndrome 7 protein; Ciliogenesis BBSome subunit. PRE
tetur26g01500	1.405234506	TuGSTd12 Glutathione S-transferase; class delta
tetur06g04900	1.403712865	3-oxoacyl-acyl-carrier-protein reductase
tetur18g01440	1.401731493	Peptidase M16; core
tetur03g05430	1.400337694	protein XRP2
tetur01g05730	1.398156682	ApoD28 Apolipoprotein D precursor apolipoprotein D
tetur04g03390	1.397713046	Hypothetical protein
tetur06g06170	1.394237922	Hypothetical protein
tetur467g00010	1.390913017	multidrug resistance-associated protein 1
tetur06g01300	1.37945194	Hypothetical protein

tetur08g04770	1.37544273	PREDICTED: similar to n-acetylgalactosaminyltransferase
tetur11g06400	1.373996812	hypothetical protein
tetur11g05700	1.3739261	Hypothetical protein
tetur02g04730	1.36304519	Hypothetical protein
tetur01g01010	1.362310818	OSP1a Orphan Secreted protein OSP1 Orphan Secreted protein Hypotheti
tetur03g08560	1.362272512	hypothetical protein
tetur34g00850	1.362070472	Hypothetical protein
tetur04g05880	1.362002334	regucalcin
tetur02g01210	1.361613005	Hypothetical protein
tetur13g04678	1.357837544	
tetur26g01810	1.356138317	serine/threonine protein phosphatase
tetur540g00010	1.355503767	puromycin-sensitive aminopeptidase
tetur03g08730	1.354972624	MLX max-like protein X isoform gamma
tetur17g02340	1.342857887	Hypothetical protein
tetur27g02480	1.341308935	AN1-type zinc finger protein 2B
tetur06g00460	1.333464875	intradiol ring-cleavage dioxygenase
tetur10g01000	1.33211387	mitochondrial ribosomal protein S17 mitochondrial ribosomal protein S17
tetur01g11120	1.327878417	Hypothetical protein
tetur04g08750	1.322197015	Hypothetical protein
tetur06g06659	1.308778654	
tetur07g00470	1.307144654	Alpha-ketoglutarate-dependent dioxygenase alkB homologue 7
tetur12g02180	1.296378202	Protein-tyrosine phosphatase-like
tetur24g00270	1.292667852	TuPap-21 Cathepsin B
tetur01g02880	1.291093104	Hypothetical protein
tetur02g13390	1.289613918	Hypothetical protein
tetur12g03940	1.285255774	SP28 Serine protease
tetur04g04320	1.282673932	Hypothetical protein
tetur08g02290	1.281403208	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur20g01650	1.276914289	tubulin gamma-1 chain
tetur07g00410	1.272562987	Hypothetical protein
tetur140g00020	1.271907885	Der f 2 allergen
tetur03g07450	1.271062233	TPAN-8 Apple-like Apple-like
tetur30g02410	1.26886246	kynureninase kynureninase
tetur19g01720	1.266313125	CD63 antigen
tetur22g01100	1.262279874	nucleoprotein
tetur21g03100	1.260999136	CuffL6 Cutoff-like protein Hypothetical protein
tetur01g09370	1.259086642	catalase
tetur15g00280	1.249553219	L-galactose dehydrogenase
tetur02g14561	1.246963048	Diacylglycerol/phorbol-ester binding Diacylglycerol/phorbol-ester binding
tetur09g04550	1.245076114	PREDICTED: similar to oxidase/peroxidase PREDICTED: similar to oxidase/
tetur28g00660	1.24350238	PLC-like phosphodiesterase, TIM beta/alpha-barrel domain
tetur27g02598	1.239897166	CYP392E4 Cytochrome P450, E-class, group I CYP392E4 Cytochrome P45
tetur09g04040	1.239808647	LYSC1 C-type Lysozyme precursor LYSC1 C-type Lysozyme precursor LYS
tetur21g00210	1.238281476	CHKB3 Choline/ethanolamine kinase; putative
tetur01g14180	1.2379946	TuCCE12 Carboxyl/cholinesterase TuCCE-12 Carboxyl/cholinesterase
tetur05g02220	1.237588514	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur11g06170	1.231486304	Hypothetical protein

tetur27g00340	1.228128152	CYP392E7 Cytochrome P450 - CYP392E7
tetur01g11400	1.22420621	Ato2 Protein atonal/lin-32 Atoh1a Protein atonal/lin-32 HLH Protein atonal/li
tetur05g05700	1.223986125	ALS similar to Acid labile subunit leucine-rich transmembrane protein; putati
tetur06g03850	1.222531975	Hypothetical protein
tetur04g08520	1.219635724	Hypothetical protein
tetur468g00030	1.219223296	SJCHGC06741 protein
tetur27g02060	1.216708933	Vesicle transport protein; SFT2-like
tetur10g04270	1.213928419	Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L do
tetur05g92688	1.213106942	hypothetical protein
tetur02g01310	1.212037197	UGT UDP-glycosyltransferase; teturUGT06 UGT UDP-glycosyltransferase
tetur24g01940	1.210081548	Hypothetical protein
tetur04g04560	1.209056415	SSPE1 Small Secreted Protein; Family E SSPE1 Hypothetical protein Hyp
tetur05g92646	1.204452609	hypothetical protein
tetur08g06440	1.202564428	Hypothetical protein
tetur187g00020	1.202227045	PREDICTED: similar to Glucosylceramidase precursor PREDICTED: similar
tetur03g00210	1.198765284	lethal
tetur03g09750	1.196898982	PREDICTED: Cdt1 protein-like
tetur26g01450	1.19623852	TuGSTd07 Glutathione S-transferase; class delta
tetur16g03480	1.1960345	TuABCC-35 ABC-transporter; class C TuABCC-34 ABC-transporter; class C
tetur03g09961	1.195653347	CYP392D7 Cytochrome P450, conserved site Cytochrome P450, conserve
tetur10g04430	1.195227772	SP22 Serine protease
tetur09g05830	1.194009931	PHYTOCHROME C
tetur30g00740	1.191555951	PAN/Apple domain
tetur16g03790	1.18551865	CYP392A10 Cytochrome P450 - CYP392A10
tetur02g14000	1.182809521	Hypothetical protein
tetur14g00850	1.182031256	NUDIX hydrolase
tetur09g01590	1.181142232	Hypothetical protein
tetur22g01250	1.179576635	Hypothetical protein
tetur16g01160	1.179295582	Hypothetical protein
tetur15g02550	1.177436251	transmembrane protein 41A precursor
tetur09g04420	1.176846354	TuPap-50 Cathepsin L
tetur06g05090	1.173817342	short chain dehydrogenase
tetur05g06440	1.173257958	Tudor domain
tetur07g03810	1.172864027	Leucine-rich repeat domain, L domain-like
tetur04g05990	1.170915472	innexin; putative
tetur01g01770	1.170044237	Hypothetical protein
tetur07g03880	1.1698874	Nuclear receptor coactivator; interlocking
tetur10g04790	1.167117116	serpin 3 inhibitory serine protease inhibitor
tetur01g09920	1.165928694	OTU domain-containing protein 5/Otubain-like deubiquitinase 1
tetur07g00310	1.164875581	RNA-binding protein 40
tetur04g07710	1.163282309	UGT UDP-glycosyltransferase; teturUGT17p UGT UDP-glycosyltransferase;
tetur91g00020	1.161489424	calmodulin
tetur05g07320	1.159367818	histone H2A
tetur53g00040	1.158316549	lipase 1
tetur02g13070	1.158165171	antigen B membrane protein
tetur05g07290	1.155365935	SAMT2 S-adenosylmethionine-dependent methyltransferase
tetur02g01230	1.145994319	Hypothetical protein

tetur11g00960	1.143799929	Hypothetical protein
tetur23g02150	1.140296402	Hypothetical protein
tetur05g09545	1.140275506	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur03g00110	1.136192853	lethal
tetur01g17294	1.133560995	Leucine-rich repeat domain, L domain-like
tetur08g06800	1.132543963	Hypothetical protein
tetur07g01860	1.129256587	PREDICTED: similar to glucose dehydrogenase
tetur24g00510	1.12828996	Hypothetical protein
tetur02g00720	1.124392616	Hypothetical protein
tetur36g00680	1.122960534	PREDICTED: similar to quiescin Q6-like 1
tetur01g03200	1.119670226	trichoplein; keratin filament binding
tetur29g00070	1.118034464	sialin
tetur17g02830	1.117664209	MAM
tetur01g11110	1.117543778	Hypothetical protein
tetur04g06010	1.116591479	ApoD15 Apolipoprotein D precursor outer membrane lipoprotein Blc
tetur02g12720	1.116464873	Hypothetical protein
tetur08g02700	1.115502716	ADP-ribosylation factor related protein 1
tetur01g11780	1.112759687	Hypothetical protein
tetur07g07400	1.112647053	Homeobox, conserved site
tetur13g00680	1.10911664	transmembrane protein 189
tetur09g01960	1.109104247	TuABCG-12 ABC-transporter; class G TuABCG-10 ABC-transporter; class G
tetur05g02160	1.109078926	Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L dor
tetur14g00880	1.109004676	NUDIX hydrolase
tetur10g00710	1.108684273	Hypothetical protein
tetur13g01630	1.106734328	Growth factor; receptor
tetur06g00570	1.106680267	gem-associated protein; putative
tetur09g01950	1.104778654	TuABCG-11 ABC-transporter; class G TuABCG-09 ABC-transporter; class G
tetur33g00810	1.103573921	alcohol dehydrogenase
tetur423g00010	1.10042058	DnaJ
tetur09g04200	1.098113297	Zinc finger, C2H2 Zinc finger, C2H2
tetur21g01420	1.096855631	Hypothetical protein
tetur08g03680	1.092712975	metaxin-2
tetur02g90633	1.092382335	hypothetical protein
tetur31g01390	1.090764731	TuGSTd16 Glutathione S-transferase; class delta
tetur02g08210	1.090480653	RecName: Full
tetur03g05010	1.088558519	CYP392D4 Cytochrome P450 - CYP392D4
tetur02g04170	1.087621254	MIPP1a multiple inositol polyphosphate phosphatase 1
tetur04g02870	1.085516569	MTAP S-methyl-5-thioadenosine phosphorylase
tetur03g01190	1.084372457	voltage-dependent anion-selective channel protein 2
tetur09g05200	1.083355048	Hypothetical protein
tetur36g00830	1.08296798	Hypothetical protein
tetur12g03720	1.081677054	Hypothetical protein
tetur24g00200	1.079513704	Apple-like
tetur11g03090	1.079492345	sialin
tetur33g90843	1.076709249	hypothetical protein
tetur28g92005	1.074417823	hypothetical protein
tetur05g05190	1.073113445	TuGSTm03 Glutathione S-transferase; class mu

tetur30g01680	1.071032875	Hypothetical protein
tetur02g03090	1.069360259	SP41 Serine protease
tetur13g03900	1.066772063	PREDICTED: similar to retinol dehydrogenase 11
tetur21g01590	1.06590037	lysosomal acid lipase/cholesteryl ester hydrolase
tetur17g03430	1.065075133	cathepsin A
tetur16g03240	1.06361062	PAN/Apple domain
tetur02g13830	1.06159557	Hypothetical protein
tetur17g03220	1.059613186	scarf3b
tetur06g03160	1.056697564	Hypothetical protein
tetur26g02390	1.05511663	PREDICTED: iron/zinc purple acid phosphatase-like protein-like
tetur01g09940	1.054827332	Major facilitator superfamily; general substrate transporter
tetur22g00160	1.05405115	40S ribosomal protein S17
tetur01g08300	1.052431103	DEAD
tetur11g03760	1.052367402	TuCCE33 Carboxyl/cholinesterase TuCCE32 Carboxyl/cholinesterase TuCC
tetur07g04380	1.051563523	Hypothetical protein
tetur06g03180	1.051163276	AP-1 complex subunit sigma-2
tetur06g02350	1.049719318	Diacylglycerol/phorbol-ester binding
tetur22g01870	1.049561206	Hypothetical protein
tetur04g00850	1.048511106	Armadillo-type fold
tetur20g90770	1.04789539	hypothetical protein
tetur06g01040	1.045072678	GPCR158 Probable G-protein coupled receptor 158 precursor PREDICTED
tetur04g01730	1.042465765	methionyl-tRNA formyltransferase methionyl-tRNA formyltransferase
tetur71g00060	1.042311676	antigen B membrane protein
tetur08g04020	1.041934585	IQ calmodulin-binding region
tetur19g02570	1.038953521	PHYH
tetur507g00010	1.036953541	aldo/keto reductase aldo/keto reductase
tetur16g01560	1.036736731	Hypothetical protein
tetur05g01730	1.034634481	Csp1a conserved secreted protein 1 Hypothetical protein
tetur04g01570	1.034213468	NP-R2 G-protein coupled neuropeptide receptor.
tetur01g00890	1.033247013	MIER1 Mesoderm induction early response protein mesoderm induction ear
tetur02g11170	1.028563311	Tu_12344.3 cys-loop ligand-gated ion channel glycine receptor subunit beta
tetur32g02070	1.02709687	Hypothetical protein
tetur26g02831	1.026262686	
tetur04g03910	1.025215564	SSPG2 Small secreted protein; Family G Hypothetical protein
tetur01g09460	1.024619591	PREDICTED: similar to ETHE1 protein
tetur20g00290	1.024125919	CYP392B3 Cytochrome P450 - CYP392B3
tetur16g03460	1.023469796	ApoD9 Apolipoprotein D precursor apolipoprotein D precursor
tetur21g02960	1.021520945	Hypothetical protein
tetur19g00900	1.02091016	Alpha/beta hydrolase fold-5
tetur27g00380	1.02032148	Hypothetical protein
tetur688g00010	1.019374005	retinal rod rhodopsin-sensitive cGMP 3';5'-cyclic phosphodiesterase subunit d
tetur07g06560	1.014132163	Intradiol ring-cleavage dioxygenase, core Intradiol ring-cleavage dioxygenas
tetur03g05030	1.013494288	CYP392D6 Cytochrome P450 - CYP392D6 na Cytochrome P450 -
tetur25g01600	1.012391631	Hypothetical protein
tetur89g00020	1.011299785	Hypothetical protein
tetur01g12910	1.010812557	CDK5 and ABL1 enzyme substrate 1/2 CDK5 and ABL1 enzyme substrate 1
tetur01g08170	1.010146661	Leucine-rich repeat domain, L domain-like

tetur04g03350	1.00821461	Hypothetical protein
tetur11g05590	1.008135671	Hypothetical protein
tetur30g90539	1.007674489	hypothetical protein
tetur03g10063	1.005253877	SSPB3 Small Secreted Protein; Family B hypothetical protein
tetur18g02150	1.002907469	Globin
tetur18g03080	1.00225112	GCN5-related N-acetyltransferase
tetur07g04410	-1.00017372	TuABCC-22 ABC-transporter; class C;
tetur01g13160	-1.0017186	BEAT-R3 Immunoglobulin-like fold Immunoglobulin-like fold Immunoglobul
tetur04g02040	-1.00236087	Hypothetical protein
tetur11g00550	-1.00254559	GG23423
tetur38g00210	-1.00417329	Hypothetical protein
tetur15g00530	-1.00447727	Hypothetical protein
tetur26g01940	-1.00483498	Hypothetical protein
tetur03g07890	-1.00563079	Insulin-like growth factor binding protein, N-terminal Insulin-like growth factor
tetur02g05500	-1.00709669	BAGPCR3 G-protein coupled receptor
tetur05g06480	-1.00721436	Outer membrane chaperone Skp OmpH
tetur23g00350	-1.00843337	Hypothetical protein
tetur19g00810	-1.01944091	Hypothetical protein
tetur18g03020	-1.01980795	Hypothetical protein
tetur08g00460	-1.02008207	adenylate cyclase
tetur06g02510	-1.02047623	Hypothetical protein
tetur01g01200	-1.02096906	ubiquitin-like fusion protein
tetur08g07130	-1.02272791	dynein heavy chain
tetur29g00470	-1.02459755	Regulator of chromosome condensation; RCC1
tetur15g03220	-1.02572018	Low density lipoprotein-receptor; class A cysteine-rich repeat
tetur15g02320	-1.03012882	Hypothetical protein
tetur19g01960	-1.03377963	FOXF1 Winged helix-turn-helix DNA-binding domain Winged helix-turn-helix
tetur22g02250	-1.0358361	Hypothetical protein
tetur05g05870	-1.0392618	Hypothetical protein
tetur08g04450	-1.04007333	secreted salivary gland peptide; putative secreted salivary gland peptide; put
tetur02g01650	-1.04007968	Immunoglobulin-like fold
tetur02g07860	-1.04131831	Chitin binding domain
tetur07g04940	-1.0413242	Hypothetical protein
tetur18g03030	-1.04420713	TEP1
tetur03g91580	-1.04511561	hypothetical protein
tetur04g00310	-1.0476248	PREDICTED: similar to RE60058p
tetur26g00020	-1.04992968	GPCR; family 3
tetur13g02150	-1.04996891	candidate tumor suppressor protein
tetur02g07950	-1.05073463	spectrin; alpha; non-erythrocytic 1
tetur17g01360	-1.05142152	Hypothetical protein
tetur07g07970	-1.05353739	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur20g00830	-1.05385455	CYP407A1 Cytochrome P450 - CYP407A1 CYP- Cytochrome P450 - CYP t
tetur16g04149	-1.05395956	hypothetical protein
tetur10g05240	-1.0557834	Hypothetical protein
tetur36g01110	-1.06176215	GRSP12 Glycine-rich secreted protein GYGSP3 Secreted protein with GYG
tetur19g00240	-1.06206011	CPAP 6 cuticular protein analogous to peritrophins 1-A
tetur02g09200	-1.06245971	Hypothetical protein

tetur36g00940	-1.06380931	TLR1LB
tetur11g03260	-1.06639864	LRR-GPCR3 Leucine Rich Repeat G-protein coupled receptor
tetur02g00420	-1.06743649	Hypothetical protein
tetur09g00600	-1.06932953	TuPap-4 Cathepsin B
tetur04g02440	-1.07090982	PREDICTED: similar to adenylate cyclase
tetur13g00920	-1.07270925	long chain fatty acyl CoA synthetase
tetur02g08770	-1.07363157	RNA-dependent RNA polymerase, eukaryotic-type
tetur06g01390	-1.07648071	Hypothetical protein
tetur13g01920	-1.07798258	PREDICTED: similar to fragile site-associated protein PREDICTED: similar t
tetur06g02560	-1.08144423	Hypothetical protein
tetur10g00320	-1.08234033	PREDICTED: rCG19957-like
tetur21g01490	-1.0850832	probable rRNA-processing protein EBP2 probable rRNA-processing protein
tetur29g00610	-1.08688494	Short-chain dehydrogenase/reductase SDR
tetur03g00430	-1.08968259	Hypothetical protein
tetur03g09880	-1.08985125	TuABCC-11 ABC-transporter; class C;
tetur32g00470	-1.09142053	transmembrane protein 135
tetur20g03290	-1.09367187	Dve dve; Ortholog of Drosophila melanogaster defective proventriculus dve
tetur03g02410	-1.09537762	zf zinc finger protein
tetur16g02020	-1.09573421	zf-C2H2 zinc finger protein zf-C2H2 Zinc finger; C2H2 type
tetur05g01930	-1.09664837	carbonic anhydrase
tetur24g01530	-1.09800543	Dachsous; Adherin precursor dachsous
tetur19g03250	-1.09957344	Homeodomain-like
tetur01g00850	-1.10037933	MIER1 Mesoderm induction early response protein mesoderm induction ear
tetur36g01090	-1.10457453	Endoglin/CD105 antigen
tetur01g04370	-1.10473302	Hypothetical protein
tetur01g03940	-1.10481976	CPR 29 cuticle protein
tetur10g03690	-1.10499504	pan pangolin transcription factor 7-like 2
tetur22g02550	-1.10568169	Insect antifreeze protein
tetur04g00620	-1.10601961	Hypothetical protein
tetur06g05570	-1.10780378	NRT1 RNA binding
tetur01g02990	-1.10864917	SP14/2P Serine protease; polyserase
tetur27g01110	-1.11744463	conserved hypothetical protein
tetur07g03590	-1.11980204	Mediator complex, subunit Med13, N-terminal, metazoa/fungi
tetur15g00870	-1.12336543	voltage-gated ion channel; putative
tetur20g02690	-1.12470935	splicing factor 1 isoform 2
tetur02g03160	-1.12571218	calnexin
tetur09g00510	-1.12868353	DDM9-5 Domain of unknown function DUF3421 Domain of unknown functio
tetur04g03730	-1.13082491	ATPase; P-type; K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter
tetur19g02370	-1.13412142	axotactin
tetur32g00400	-1.13607841	inositol monophosphatase 1
tetur27g00290	-1.13717556	Hypothetical protein
tetur01g00090	-1.13792993	Hypothetical protein
tetur05g05850	-1.14346679	phenylalanyl-tRNA synthetase alpha subunit
tetur95g00060	-1.14461979	PREDICTED: similar to ECM 18 PREDICTED: similar to ECM 18
tetur18g02180	-1.1464128	Hypothetical protein
tetur02g06900	-1.14750229	inositol monophosphatase 3 inositol monophosphatase 3
tetur20g01140	-1.14858665	MD-2-related lipid-recognition domain

tetur17g01120	-1.14863285	Band 7 protein
tetur187g00010	-1.15016119	Glycoside hydrolase; family 30
tetur13g02200	-1.15023099	Hypothetical protein
tetur02g00120	-1.15364986	hypothetical protein
tetur01g08910	-1.15734815	arylsulfatase B precursor; putative
tetur01g06570	-1.15920722	sodium-dependent glucose transporter 1
tetur18g01800	-1.15970553	still life; putative
tetur13g00620	-1.16023385	Hypothetical protein
tetur01g16270	-1.16498388	Hypothetical protein
tetur13g01890	-1.16529267	Nose resistant-to-fluoxetine protein; N-terminal
tetur01g08680	-1.16646364	TuCCE01 Carboxyl/cholinesterase TuCCE-01 Carboxyl/cholinesterase
tetur38g00060	-1.16654619	Chitin binding protein; peritrophin-A
tetur08g06360	-1.16793929	sialin; putative
tetur31g01320	-1.17047815	GNS1/SUR4 membrane protein
tetur29g00920	-1.17166124	MFS transporter protein MFS transporter protein
tetur04g02680	-1.17364576	aquaporin; putative
tetur08g06170	-1.18069624	CYP387A1 Cytochrome P450 - CYP387A1
tetur77g90074	-1.18452735	hypothetical protein
tetur02g01540	-1.18580227	Hypothetical protein
tetur154g00010	-1.18592977	Hypothetical protein
tetur01g12980	-1.18750901	Hypothetical protein
tetur05g01060	-1.18758962	ankyrin repeat protein
tetur32g02170	-1.19137702	PREDICTED: tripartite motif protein 2-like
tetur01g02500	-1.1947001	TuGSTd04 Glutathione S-transferase; class delta
tetur38g00510	-1.19672281	Hypothetical protein
tetur13g00460	-1.19857772	Hypothetical protein
tetur18g01940	-1.20235347	Kelch motif family protein
tetur08g00340	-1.20333958	Mitochondrial inner membrane protein Mitofilin
tetur01g12620	-1.20462633	WTSP15 Wannes-Thomas Secreted Protein 1 Hypothetical protein
tetur23g00070	-1.20526338	Hypothetical protein
tetur18g02050	-1.20733785	GE13940
tetur06g06610	-1.20832895	TuCPI21 Cystatin Cystatin
tetur02g12290	-1.21080007	Transmembrane amino acid transporter protein; similar to slimfast cationic a
tetur01g02460	-1.21409869	DGK1 DiacylGlycerol Kinase DiacylGlycerol Kinase family member
tetur01g92860	-1.21743231	hypothetical protein
tetur13g04520	-1.21855217	Hypothetical protein
tetur07g00690	-1.21932075	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur23g00760	-1.22097508	Hypothetical protein
tetur08g06930	-1.22223683	Nuclear hormone receptor; ligand-binding
tetur17g01380	-1.22304597	Alpha/Beta hydrolase fold
tetur27g01800	-1.22314262	Hypothetical protein
tetur03g02430	-1.23029236	Lipopolysaccharide-modifying protein
tetur17g02900	-1.23519915	Phytanoyl-CoA dioxygenase
tetur31g01970	-1.23855462	PREDICTED: dedicator of cytokinesis 2
tetur04g00480	-1.23979166	TuiGluR11 AMPA/RII glutamate receptor 2 isoform 1 precursor
tetur18g00390	-1.23994218	potassium channel subfamily T member 1
tetur02g14841	-1.2401598	BTB/Kelch-associated

tetur08g02990	-1.24042854	Hypothetical protein
tetur07g00400	-1.24519368	roboL Immunoglobulin subtype 2 roboL Immunoglobulin subtype 2 robo Imm
tetur14g02010	-1.2484381	Alk Transmembrane receptor protein tyrosine kinase activity
tetur19g00820	-1.24945274	Homeodomain-like
tetur01g03010	-1.24960789	HEY2 hairy/enhancer-of-split related with YRPW motif 2
tetur11g00820	-1.24972075	PREDICTED: similar to limkain b1
tetur30g00890	-1.2518451	TuABCH-19 ABC-transporter; class H pABC-29 ABC-transporter; putative;
tetur04g01820	-1.25458905	tetratricopeptide TPR_2
tetur01g09880	-1.25537042	Hypothetical protein
tetur169g00020	-1.25617281	TuENaC123 Na+ channel, amiloride-sensitive Tu_ENaC123 Na+ channel, a
tetur03g04460	-1.25618735	Fibronectin; type III-like fold
tetur20g02380	-1.26374357	SET domain
tetur03g03170	-1.26411286	PREDICTED: similar to Brg1
tetur40g00220	-1.269294	Hypothetical protein
tetur23g01220	-1.27310532	dentin sialophosphoprotein precursor dentin sialophosphoprotein precursor
tetur05g01630	-1.27416889	aminopeptidase N
tetur43g00080	-1.2757326	Vg1 vitellogenin; partial sequence Vit vitellogenin; partial sequence vitelloge
tetur01g07060	-1.27711871	UGT UDP-glucuronosyl/UDP-glucosyltransferase UGT UDP-glucuronosyl/U
tetur15g00340	-1.27888538	UGT UDP-glycosyltransferase; teturUGT55 UGT UDP-glycosyltransferase
tetur71g00050	-1.28317055	Apple-like
tetur20g01230	-1.28336459	vitellogenin vitellogenin
tetur283g00030	-1.28379479	Insect antifreeze protein
tetur16g01230	-1.28912093	blood vessel epicardial substance blood vessel epicardial substance
tetur31g01740	-1.28915528	Hypothetical protein
tetur10g03090	-1.29414001	Tu_GluCl3 cys-loop ligand-gated ion channel TuGluCl-03 glutamate-gated cl
tetur33g01420	-1.30103809	tight junction protein tama; putative
tetur29g00680	-1.30390754	croc Winged helix-turn-helix DNA-binding domain fox Winged helix-turn-helix
tetur34g00370	-1.30450293	brefeldin A-inhibited guanine nucleotide-exchange protein 3 brefeldin A-inhib
tetur25g00090	-1.30865398	polycomb polycomb complex protein BMI-1 polycomb complex protein BMI-
tetur18g02450	-1.30941497	Hypothetical protein
tetur23g00240	-1.31265895	UNCoordinated family member
tetur11g02710	-1.31410346	Gas3p
tetur22g02640	-1.31460713	Insect antifreeze protein
tetur19g00360	-1.31789216	modifier of mdg4
tetur03g08110	-1.32217351	CPAP 13 cuticular protein analogous to peritrophins 1-A
tetur05g02980	-1.32472335	SAC3/GANP/THP3
tetur03g10143	-1.32496787	Fibroin hypothetical protein
tetur05g02310	-1.32593836	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur10g05590	-1.33100365	HNTX-XIV-3.2 precursor
tetur576g00010	-1.33102232	pterin-4-alpha-carbinolamine dehydratase
tetur27g01030	-1.3371739	CYP392E10 Cytochrome P450 - CYP392E10
tetur03g06730	-1.33805478	Armadillo-type fold
tetur16g01760	-1.34161535	AMP-dependent synthetase and ligase
tetur24g00160	-1.34240747	Hypothetical protein
tetur02g03530	-1.34490916	GK24782
tetur26g02600	-1.3476098	protein kinase C binding protein 1
tetur47g00090	-1.35306532	CYP392A9 Cytochrome P450 - CYP392A9

tetur04g03930	-1.35436058	PrtA Chitin binding protein; peritrophin-A Chitin binding protein; peritrophin-
tetur04g03270	-1.35556822	guanine nucleotide-binding protein G
tetur18g01090	-1.36034053	Rfx4 Winged helix-turn-helix DNA-binding domain RFX_DNA_binding Winge
tetur149g00010	-1.36291669	UNCoordinated family member
tetur02g08970	-1.37175423	Hypothetical protein
tetur17g03500	-1.3809299	Tetraspanin/Peripherin
tetur30g90541	-1.38132592	hypothetical protein
tetur11g00950	-1.38857335	Hypothetical protein
tetur06g02690	-1.39077994	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur11g01830	-1.39817279	UGT UDP-glycosyltransferase; teturUGT52 UGT UDP-glycosyltransferase
tetur05g06420	-1.39949503	Hypothetical protein
tetur27g00050	-1.4031057	26S proteasome regulatory complex, non-ATPase subcomplex, Rpn1 subunit
tetur11g00720	-1.40312172	PREDICTED: similar to limkain b1
tetur28g01030	-1.40356186	Fibroin Hypothetical protein
tetur10g02360	-1.40427418	sialin
tetur05g06570	-1.41485475	CYP389C11 Cytochrome P450 - CYP389C11
tetur03g03680	-1.41719502	RE19971p RE19971p
tetur20g00200	-1.42205047	SERP Secreted Protein with 8aa repeat structure Hypothetical protein
tetur13g01570	-1.44050193	Hypothetical protein
tetur37g00460	-1.4439669	DNA topoisomerase 2-alpha
tetur04g03680	-1.44751006	Sterile alpha motif homology
tetur05g02140	-1.45045465	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur08g06210	-1.45182762	TuENaC118 Na+ channel, amiloride-sensitive Tu_ENaC118 Na+ channel, a
tetur20g00130	-1.45775952	Hypothetical protein
tetur55g00130	-1.46271257	TuPap-10 Cathepsin B
tetur08g06700	-1.46381714	Hypothetical protein
tetur12g01380	-1.4642104	S-formylglutathione hydrolase
tetur13g03320	-1.464557	Zinc finger, RING/FYVE/PHD-type Zinc finger, RING/FYVE/PHD-type
tetur309g00020	-1.47194173	TuCCE71 Carboxylesterase type B, active site CCEinc-27a Carboxylesteras
tetur17g01370	-1.47252641	Hypothetical protein
tetur01g03440	-1.47365169	Hypothetical protein
tetur01g03820	-1.47857306	UGT UDP-glycosyltransferase; teturUGT01 UGT UDP-glycosyltransferase
tetur05g00460	-1.48018177	four-jointed
tetur22g01720	-1.48149059	Domain of unknown function DUF1619 Domain of unknown function DUF16
tetur06g05880	-1.49080328	Hypothetical protein
tetur09g03880	-1.49471874	SP48 Serine protease
tetur08g02630	-1.49830003	SSPC3 Small Secreted Protein; family C Hypothetical protein
tetur27g02556	-1.49938861	SLCP1 secreted low complexity protein; putative
tetur06g02530	-1.50092025	PREDICTED: similar to CG14446-PA PREDICTED: similar to CG14446-PA
tetur09g05700	-1.50095857	Alkaline phosphatase-like, alpha/beta/alpha
tetur40g00200	-1.50688816	PREDICTED: similar to ECM 18
tetur03g03700	-1.5095941	RE19971p RE19971p
tetur12g02810	-1.51172905	ovo ovo ovo Zinc finger; C2H2 type
tetur18g01000	-1.51202511	Cadherin conserved site
tetur18g01870	-1.5215778	hypothetical protein IscW_ISCW010909 hypothetical protein IscW_ISCW01
tetur03g91512	-1.52523292	hypothetical protein
tetur41g00430	-1.52672046	NKX6 NK6 transcription factor

tetur02g12620	-1.53156532	hydroxymethylglutaryl-CoA lyase
tetur23g01610	-1.53673686	Hypothetical protein
tetur14g03250	-1.53791003	Hypothetical protein
tetur04g03720	-1.5410224	Lklf krueppel-like factor 2
tetur11g04930	-1.54477141	TuGR49 Chemosensory Receptor; Gustatory receptor family Hypothetical p
tetur04g01610	-1.54946613	CPR 51 Cuticle secreted protein; putative CPR1 Cuticle secreted protein; pu
tetur18g02960	-1.55206422	Hemopexin-like domain
tetur21g00410	-1.55520844	sodium-dependent glucose transporter 1
tetur02g03000	-1.55532132	Hypothetical protein
tetur277g00020	-1.55613426	Hypothetical protein
tetur03g07240	-1.56127321	Apple-like
tetur07g00060	-1.56755522	DNA topoisomerase 2-alpha DNA topoisomerase 2-alpha
tetur568g00010	-1.57873481	BTB
tetur05g04930	-1.58158724	PREDICTED: solute carrier family 10
tetur36g00700	-1.58493091	ninein
tetur29g01220	-1.59215775	sNPF-R G-protein coupled receptor
tetur05g04060	-1.5963293	secreted salivary gland peptide; putative
tetur04g04140	-1.59685246	Hypothetical protein
tetur10g04040	-1.59788705	SLP1 Pheromone/general odorant binding protein; PBP/GOBP Pheromone/
tetur01g11890	-1.61491413	LZY1;4 Conserved zygote-specific protein homologue LZY1;4 Conserved zy
tetur12g00140	-1.61562774	Fibroin Fibrion Hypothetical protein
tetur180g00010	-1.61653878	Hypothetical protein
tetur16g02990	-1.61911206	XCAM14 Novel Hypothetical Cell Adhesion Molecule DSCAM14 Down Synd
tetur04g07590	-1.62880784	RabGAP/TBC
tetur22g01790	-1.63814567	Hypothetical protein
tetur18g00970	-1.65946223	Major facilitator superfamily; general substrate transporter
tetur06g03440	-1.6672826	ApoD4 Apolipoprotein D chlorophyllide A binding protein precursor
tetur11g03440	-1.67104791	CHT12 chitinase chitinase
tetur28g01420	-1.67807448	TuPap-22 Cathepsin B-like
tetur10g05410	-1.68322004	Hypothetical protein
tetur01g03720	-1.69165256	Hypothetical protein
tetur19g03391	-1.6970056	TuENaC12 Na+ channel, amiloride-sensitive ENaC12 Na+ channel, amilorid
tetur07g04840	-1.70679964	neuron navigator 1
tetur04g01580	-1.70779124	HCP1 Hypothetical Cuticular Protein HPR1 Hypothetical Cuticular Protein
tetur21g01730	-1.70881048	Hypothetical protein
tetur28g00620	-1.71172932	phosphatidylinositol-4-phosphate 5-kinase; type I; alpha phosphatidylinositol
tetur22g02610	-1.72202528	Hypothetical protein
tetur01g02010	-1.72334376	Hypothetical protein
tetur03g01500	-1.72662587	hypothetical protein IscW_ISCW007834
tetur24g02210	-1.72857841	TLDc
tetur24g02580	-1.72928838	CCEincTu10 Carboxyl/cholinesterase; incomplete CCEincTu10 Carboxyleste
tetur01g11830	-1.74033229	LZY1;5 Conserved zygote-specific protein homologue LZY1;5 Conserved zy
tetur01g14770	-1.74624382	myo-inositol 2-dehydrogenase
tetur29g00720	-1.74651789	Hypothetical protein
tetur02g05310	-1.75465756	Hypothetical protein
tetur20g00430	-1.75601129	Nose resistant-to-fluoxetine protein, N-terminal
tetur21g03420	-1.75929445	CuffL1 Cutoff-like protein HPA1b Hypothetical Protein of Unknown Function

tetur21g01230	-1.77541665	Hypothetical protein
tetur35g00280	-1.77577156	GRSP16 Glycine-rich secreted protein Hypothetical protein
tetur43g00010	-1.77577268	Vg5 Vitellogenin 5
tetur03g07900	-1.77839552	Nose resistant-to-fluoxetine protein; N-terminal
tetur09g00410	-1.78726179	ADAMX4 Peptidase M12B, ADAM/reprolysin Peptidase M12B, ADAM/repro
tetur02g08430	-1.7972105	elongation of very long chain fatty acids protein 1
tetur32g00990	-1.80045841	PREDICTED: similar to Kuzbanian-like CG1964-PA
tetur32g00960	-1.80810317	Hypothetical protein
tetur04g01060	-1.81948237	Fatty acyl-CoA reductase
tetur32g00940	-1.82720783	Conserved hypothetical protein CHP02464
tetur07g04290	-1.83663796	TuABCC-21 ABC-transporter; class C;
tetur09g01730	-1.83751012	puromycin-sensitive aminopeptidase
tetur17g00080	-1.83865594	TuCCE44 Carboxyl/cholinesterase TuCCE-38 Carboxyl/cholinesterase
tetur07g03980	-1.84292977	Peptidase M14; carboxypeptidase A
tetur05g09280	-1.84849682	Zinc finger, DksA/TraR C4-type conserved site
tetur08g06330	-1.84949638	sialin
tetur26g02450	-1.85571092	pre-mRNA-splicing factor SLU7 pre-mRNA-splicing factor SLU7
tetur11g01900	-1.87965314	PREDICTED: similar to Solute carrier family 12; member 1 PREDICTED: sin
tetur17g02390	-1.88288991	Concanavalin A-like lectin/glucanase
tetur05g04710	-1.88799803	TuLeg-8 Legumain
tetur32g02090	-1.89902987	CPR 2 cuticle protein
tetur07g01950	-1.90104603	SPH9/6C Serine proteases, trypsin family, histidine active site
tetur14g03670	-1.90146867	PREDICTED: similar to shavenoid CG13209-PA
tetur20g02030	-1.91692754	Hypothetical protein
tetur31g00770	-1.91814761	Hypothetical protein
tetur11g04990	-1.92710853	Nuclear hormone receptor, ligand-binding domain
tetur02g09670	-1.92719871	ADSL2 adenylosuccinate lyase adenylosuccinate lyase
tetur18g03905	-1.92812818	Acyl-CoA N-acyltransferase
tetur18g02200	-1.93277313	Hypothetical protein
tetur01g12890	-1.93319543	Hypothetical protein
tetur01g00860	-1.94468723	ribosomal protein S12
tetur13g01930	-1.94951712	PREDICTED: similar to fragile site-associated protein PREDICTED: similar t
tetur19g00760	-1.95354533	CPR G Putative cuticle protein
tetur09g00650	-1.95534903	Cyclic nucleotide-gated channel, C-terminal leucine zipper domain
tetur11g04260	-1.96941154	Chitin binding protein; peritrophin-A
tetur24g00340	-1.98865321	XPA binding protein 2 XPA binding protein 2
tetur07g04060	-1.99391031	Zinc finger, MYND-type
tetur17g02920	-2.00302334	Phytanoyl-CoA dioxygenase
tetur06g02330	-2.03216083	Hypothetical protein
tetur30g01780	-2.035328	Hypothetical protein
tetur31g00280	-2.04294589	CSPCA1 CUB domain CUB domain
tetur13g02090	-2.05241265	TeturLY6_UPAR23 LY6_UPAR protein Hypothetical protein
tetur30g90547	-2.05677411	hypothetical protein
tetur13g04996	-2.06024479	hypothetical protein
tetur37g00650	-2.06110034	alpha-glucosidase
tetur08g06370	-2.0678319	sialin
tetur01g10770	-2.07142267	Tualpha3 cys-loop ligand-gated ion channel; nicotinic acetylcholine receptor s

tetur01g09910	-2.07768507	D-3-phosphoglycerate dehydrogenase
tetur43g00190	-2.07933634	SPRE Secreted Protein related to Elafins omega secalin
tetur30g01760	-2.08631321	sensory box protein/histidinol phosphate phosphatase family protein
tetur46g00010	-2.09282487	PLAT7 Lipase/lipooxygenase; PLAT/LH2 Lipase/lipooxygenase; PLAT/LH2
tetur02g01550	-2.10138855	Hypothetical protein
tetur23g00050	-2.10246608	TuPap-29 Cathepsin L
tetur04g06900	-2.11640507	Bbs4 protein Bbs4 protein
tetur27g01840	-2.11685107	Hypothetical protein
tetur02g08200	-2.11708732	Concanavalin A-like lectin/glucanase
tetur19g00440	-2.1206843	UGT UDP-glycosyltransferase; teturUGT57 UGT UDP-glycosyltransferase
tetur24g00870	-2.13641228	Galactose oxidase/kelch; beta-propeller
tetur20g02680	-2.1364858	Armadillo-type fold
tetur03g03730	-2.15610168	PE-PGRS family protein
tetur04g07990	-2.17089639	Socs Suppressor of cytokine signaling 6 suppressor of cytokine signaling 6
tetur26g00510	-2.20099196	Six-bladed beta-propeller; TolB-like
tetur34g00240	-2.21020531	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur37g00940	-2.21200982	PREDICTED: apolipoprotein D-like
tetur18g01290	-2.21996314	retinal rod rhodopsin-sensitive cGMP 3';5'-cyclic phosphodiesterase subunit d
tetur01g11500	-2.22354646	Hypothetical protein
tetur17g00350	-2.24345228	TuCCE46 Carboxyl/cholinesterase CCEinc-14 Carboxyl/cholinesterase; inco
tetur486g00030	-2.25478921	Nse4
tetur17g00740	-2.25733269	Hypothetical protein
tetur257g90189	-2.25769978	hypothetical protein
tetur01g10810	-2.26149836	TuCCE07 Carboxyl/cholinesterase TuCCE-07 Carboxyl/cholinesterase
tetur16g02410	-2.26317394	TuCCE42 Carboxyl/cholinesterase TuCCE42 Carboxyl/cholinesterase; incon
tetur02g01740	-2.2672126	Leucine-rich repeat; ribonuclease inhibitor subtype
tetur14g03430	-2.26802098	Hypothetical protein
tetur01g15250	-2.26885273	CPR 54 cuticle secreted protein; putative cuticle protein; putative Fibroin
tetur03g01600	-2.27661279	ss PAS fold-3 HLH PAS fold-3
tetur412g00010	-2.29384345	Hypothetical protein
tetur43g90791	-2.29977874	hypothetical protein
tetur17g00300	-2.30202986	TuCCE45 Carboxyl/cholinesterase TuCCE-39 Carboxyl/cholinesterase
tetur21g00330	-2.30561766	Transmembrane BAX inhibitor motif-containing protein 1
tetur09g92864	-2.30716145	hypothetical protein
tetur16g01790	-2.31925408	peptidase E
tetur13g04070	-2.32735502	Hypothetical protein
tetur03g10083	-2.33788077	hypothetical protein
tetur05g07920	-2.33827216	cullin-5
tetur17g00650	-2.34272184	Dopey, N-terminal
tetur01g08720	-2.36826111	Zinc finger, C4H2-type
tetur02g07780	-2.38519329	glucosylceramidase precursor
tetur03g02880	-2.4017502	PREDICTED: similar to adenylate cyclase
tetur49g00020	-2.42146596	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur09g05220	-2.42505134	Hypothetical protein
tetur23g00260	-2.43452401	CYP392D1 Cytochrome P450 - CYP392D1
tetur17g03540	-2.43541233	Hypothetical protein
tetur09g02470	-2.45111586	PREDICTED: similar to CG3825 CG3825-PA

tetur32g02180	-2.45379989	CBR1p Carbonyl reductase [NADPH] 1; pseudo gene carbonyl reductase
tetur34g00220	-2.4619713	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur07g02600	-2.46216617	RNI Leucine-rich repeat domain, L domain-like HYP1a Leucine-rich repeat d
tetur01g14780	-2.48971848	Spz3 Cystine-knot cytokine
tetur65g00010	-2.49663545	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur07g02380	-2.50657454	RAB40L hypothetical small GTP-binding protein Rab40-like ras-related prot
tetur540g00020	-2.58694566	puromycin-sensitive aminopeptidase puromycin-sensitive aminopeptidase
tetur10g05570	-2.59338313	Hypothetical protein
tetur01g12840	-2.65343724	CPR 26 cuticle protein
tetur16g02420	-2.66755269	TuCCE43 Carboxyl/cholinesterase TuCCE43 Carboxyl/cholinesterase; incon
tetur07g01350	-2.67990661	GE10168
tetur01g02480	-2.68536421	TuGSTd03 Glutathione S-transferase; class delta
tetur15g00230	-2.68719635	Hypothetical protein
tetur02g01710	-2.69027759	GRSP4 Glycine-rich secreted protein SSPD2 Small secreted peptide Hypot
tetur05g02790	-2.69067516	CPR 25 cuticle protein
tetur04g07050	-2.70357298	sorbitol dehydrogenase
tetur11g01180	-2.72228957	PREDICTED: similar to limkain b1 PREDICTED: similar to limkain b1
tetur07g07960	-2.72288608	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur21g02540	-2.73022871	steroid dehydrogenase
tetur02g08740	-2.73680663	Hypothetical protein
tetur01g05230	-2.74954561	TuPap-20 Cathepsin B
tetur18g02430	-2.75819613	CPR 13 cuticle protein
tetur08g07590	-2.7639682	Agrin NtA
tetur05g92629	-2.83869113	hypothetical protein
tetur02g05830	-2.84026324	GRSP1 Glycine-rich secreted protein Hypothetical protein
tetur13g04230	-2.84236656	Hypothetical protein
tetur06g04510	-2.84327963	Hypothetical protein
tetur13g04130	-2.85197967	Hypothetical protein
tetur22g02090	-2.86484381	Major facilitator superfamily; general substrate transporter
tetur26g01230	-2.9185023	phosphatidylethanolamine-binding protein
tetur18g02370	-2.91928396	Hypothetical protein
tetur56g90046	-2.98519093	hypothetical protein
tetur03g05660	-2.99174376	PREDICTED: similar to ENSANGP00000012602
tetur13g01210	-2.99241133	Hypothetical protein
tetur03g03690	-3.00666187	Hypothetical protein
tetur01g09190	-3.00782232	Hypothetical protein
tetur19g01450	-3.01977789	Hypothetical protein
tetur02g14701	-3.02681758	BTB/Kelch-associated BTB/Kelch-associated
tetur03g05650	-3.03910672	Hypothetical protein
tetur06g04450	-3.06141651	GRSP7 Glycine-rich secreted protein GRSP7 Glycine-rich secreted protein
tetur01g15540	-3.11711171	Hypothetical protein
tetur17g00580	-3.14906176	PREDICTED: similar to lysosomal acid lipase; putative
tetur14g03240	-3.14981299	Hypothetical protein
tetur11g05720	-3.19023265	PLAT10 Lipase/lipooxygenase; PLAT/LH2 Lipase/lipooxygenase; PLAT/LH
tetur01g07720	-3.19208505	atrial natriuretic peptide receptor 2 precursor
tetur06g02030	-3.21291521	SLIT-ROBO Rho GTPase activating protein 2
tetur12g04390	-3.22924775	no-mechanoreceptor potential A; putative

tetur11g05220	-3.23042362	SP39 Serine protease
tetur02g14811	-3.26474959	BTB/Kelch-associated BTB/Kelch-associated
tetur08g04180	-3.26619804	Hypothetical protein
tetur03g91617	-3.27671971	hypothetical protein
tetur02g07240	-3.37376007	epithelial cell transforming sequence 2 oncogene
tetur05g07750	-3.38745768	autophagy-related protein 101
tetur174g00050	-3.39394633	apolipoprotein D
tetur01g06580	-3.39594596	PREDICTED: rCG19957-like
tetur207g00010	-3.4324202	TuCCE70 Carboxyl/cholinesterase TuCCE-60 Carboxyl/cholinesterase
tetur486g00010	-3.44460273	DNA replication factor Cdt1, C-terminal
tetur26g01220	-3.45248584	phosphatidylethanolamine-binding protein
tetur34g00090	-3.45938396	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur16g01780	-3.47019153	Longitudinals lacking protein-like
tetur05g09325	-3.48573233	UGT UDP-glucuronosyl/UDP-glucosyltransferase UGT UDP-glucuronosyl/U
tetur13g04160	-3.49839063	Hypothetical protein
tetur07g04870	-3.52589432	Hypothetical protein
tetur11g04810	-3.52700664	phytoene dehydrogenase
tetur03g05730	-3.53137892	PREDICTED: similar to kelch-like 12
tetur29g01670	-3.53881911	isoamyl acetate-hydrolyzing esterase 1 homolog
tetur01g12820	-3.54509206	CPR 28 cuticle protein
tetur01g12320	-3.55935444	PSP; proline-rich
tetur03g09490	-3.56805252	Vitellinogen, open beta-sheet, subdomain 1
tetur24g01070	-3.57375756	Hypothetical protein
tetur02g04900	-3.63583813	PREDICTED: similar to Bsdc1 protein
tetur07g91855	-3.68757548	hypothetical protein
tetur01g13600	-3.72593858	solute carrier family 35 member B1 solute carrier family 35 member B1
tetur17g02440	-3.75956828	PREDICTED: similar to neprilysin; partial
tetur02g14691	-3.76672458	eggshell Glycine-rich secreted protein; shows structural similarity to flatworm
tetur97g00050	-3.82574468	DnaJ
tetur17g00660	-3.86500082	protein Red
tetur33g00510	-3.94254735	PREDICTED: similar to AGAP003567-PA
tetur25g00280	-3.9442871	Reeler domain
tetur20g00710	-4.08603595	Hypothetical protein
tetur02g15081	-4.16523045	BTB/Kelch-associated
tetur28g01330	-4.16652607	WTSP1a Wannes-Thomas Secreted Protein 1 WTSP1b Wannes-Thomas S
tetur17g00750	-4.25613279	TuCCE48 Carboxyl/cholinesterase TuCCE-62 Carboxyl/cholinesterase CCE
tetur30g01800	-4.28642237	Hypothetical protein
tetur22g00420	-4.33599977	UGT UDP-glycosyltransferase; teturUGT65 UGT UDP-glycosyltransferase
tetur21g03190	-4.35510386	ApoDR8 Calycin-like Calycin-like
tetur16g03760	-4.36273338	Hypothetical protein
tetur02g15061	-4.37461068	BTB/Kelch-associated
tetur58g00110	-4.39202721	Hypothetical protein
tetur04g06070	-4.40955297	Hypothetical protein
tetur21g03160	-4.48246065	ApoDR10 Calycin-like Calycin-like
tetur31g00820	-4.52199754	Hypothetical protein
tetur01g03900	-4.55649713	Methyltransferase type 11
tetur17g01790	-4.56543218	HLH hypoxia-inducible factor 1 alpha

tetur30g01150	-4.66088854	Hypothetical protein
tetur557g00020	-4.66445882	methylenetetrahydrofolate dehydrogenase methylenetetrahydrofolate dehydı
tetur01g13610	-4.68818154	IAP Proteinase inhibitor I32; inhibitor of apoptosis IAP Proteinase inhibitor I3
tetur432g00010	-4.70101054	Hypothetical protein
tetur07g91894	-4.76189024	Leucine-rich repeat domain, L domain-like
tetur649g00010	-4.79850665	Hypothetical protein
tetur06g01680	-4.7994502	CPR 24 cuticle protein
tetur01g11880	-4.81774991	LZY1;3 conserved zygote-specific protein homologue LZY1;3 conserved zyg
tetur01g02660	-4.81817355	MDL6 Immunoglobulin E-set Immunoglobulin E-set
tetur30g01120	-4.82955064	Plexin domain-containing protein
tetur22g00690	-4.84482068	minor tail protein gp26-like
tetur02g15051	-4.84613389	BTB/Kelch-associated
tetur66g00060	-5.00046602	SP45_2 Serine protease SP47 Serine protease
tetur03g07950	-5.13150587	TuPap-14 Cathepsin B
tetur20g00100	-5.13562388	Hypothetical protein
tetur08g08251	-5.16105909	
tetur20g02780	-5.16353009	cuticular protein similar to Bombyx Hypothetical protein
tetur08g07790	-5.30241136	Hypothetical protein
tetur02g12050	-5.32936642	Hypothetical protein
tetur25g01840	-5.32945068	Hypothetical protein
tetur30g01790	-5.4556715	hypothetical protein
tetur04g07630	-5.59358131	UGT UDP-glycosyltransferase; teturUGT16 UGT UDP-glycosyltransferase M
tetur20g01850	-5.61763501	Hypothetical protein
tetur11g01170	-5.6209667	Hypothetical protein
tetur32g90860	-5.63206333	hypothetical protein
tetur03g08010	-5.65793868	TuPap-26 Cathepsin B
tetur07g00730	-5.67455949	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur03g05060	-5.73813236	Cytochrome P450 - probable pseudogene na Cytochrome P450 -
tetur03g10033	-5.74626244	
tetur02g02560	-5.7781557	BCCIP homolog
tetur03g00740	-5.97036578	nhr-48 Nuclear hormone receptor; ligand-binding Nuclear hormone receptor
tetur25g01710	-5.98661645	thiopurine S-methyltransferase
tetur24g02090	-5.9978283	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur06g02280	-6.01035174	Zinc finger; C2H2-type
tetur01g08240	-6.01822732	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur08g07170	-6.05810249	Helix-loop-helix DNA-binding
tetur03g08300	-6.0591761	HCP2 Hypothetical Cuticular Protein Hypothetical protein
tetur151g00010	-6.16991207	Hypothetical protein
tetur02g09530	-6.17462416	CPR 52 Cuticle secreted protein; putative CPR 52 Cuticle secreted protein; p
tetur24g00860	-6.19566047	kelch-like 18
tetur03g07930	-6.20127707	TuPap-15 Cathepsin B
tetur05g06320	-6.28094712	Hypothetical protein
tetur11g01150	-6.28861378	PREDICTED: similar to limkain b1
tetur24g02150	-6.29652947	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur16g01840	-6.38781956	DDM9-20 Domain of unknown function DUF3421 Domain of unknown functi
tetur11g00880	-6.40258228	PIN domain-like
tetur11g00890	-6.47275314	PREDICTED: similar to limkain b1

tetur437g00010	-6.65633794	Hypothetical protein
tetur03g91543	-6.79371849	hypothetical protein
tetur87g00030	-6.81607583	Hypothetical protein
tetur14g03170	-6.83863729	Hypothetical protein
tetur01g07920	-6.89570473	Leucine-rich repeat domain, L domain-like
tetur16g01800	-6.96404771	short-chain dehydrogenase/reductase SDR
tetur01g08700	-6.96936944	DEAD
tetur09g06230	-7.06497388	CPR 22 cuticle protein
tetur02g07590	-7.08860059	AkrE2 Aldo-keto reductase family E; member 2; likely a pseudogene aldo-ke
tetur641g00010	-7.23538134	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur03g00710	-7.27858164	nhr-48 Nuclear hormone receptor, ligand-binding domain Nuclear hormone
tetur03g00730	-7.34471601	nhr-48 Nuclear hormone receptor, ligand-binding domain Nuclear hormone
tetur20g00030	-7.39221764	Hypothetical protein
tetur20g01860	-7.40597618	Hypothetical protein
tetur16g01860	-7.46770804	DDM9-22 Domain of unknown function DUF3421 Domain of unknown functi
tetur38g00230	-7.63877336	Collagen IV; non-collagenous
tetur21g01510	-7.81346273	GTP1/OBG
tetur14g02600	-7.83142075	Hypothetical protein
tetur26g01920	-7.98043839	Hypothetical protein
tetur01g08030	-8.11933197	RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain,
tetur31g00920	-8.32533074	ApoD24 Apolipoprotein D precursor apolipoprotein D precursor
tetur11g90924	-8.39638471	hypothetical protein
tetur20g02760	-8.46191592	PREDICTED: similar to Fasciclin-1 precursor
tetur148g00040	-8.8861848	Hypothetical protein
tetur30g90545	-8.90114883	hypothetical protein
tetur26g01930	-9.26320838	alanine aminotransferase
tetur40g00150	-9.92128841	Hypothetical protein
tetur148g00010	-10.7961693	Hypothetical protein

between three resistant

ES1 vs IT3	
P.Value	adj.P.Val
3.22E-14	9.02E-11
1.64E-08	5.88E-07
3.24E-10	2.62E-08
9.44E-12	1.81E-09
3.19E-11	4.46E-09
6.37E-12	1.42E-09
1.04E-07	2.68E-06
1.49E-13	1.81E-10
2.68E-13	2.44E-10
7.26E-12	1.49E-09
1.49E-12	5.76E-10
6.15E-12	1.40E-09
5.45E-11	6.83E-09
1.27E-08	4.73E-07
8.49E-13	4.74E-10
5.07E-13	3.46E-10
5.98E-11	7.41E-09
1.53E-12	5.76E-10
1.91E-11	3.21E-09
5.34E-09	2.34E-07
6.40E-09	2.66E-07
9.13E-13	4.74E-10
1.35E-12	5.66E-10
5.71E-13	3.46E-10
3.61E-08	1.13E-06
6.51E-10	4.33E-08
1.34E-10	1.33E-08
1.16E-11	2.11E-09
8.79E-12	1.74E-09
2.03E-12	6.52E-10
3.30E-12	9.47E-10
4.05E-12	1.08E-09
7.08E-12	1.49E-09
1.51E-08	5.45E-07
2.08E-11	3.28E-09
3.06E-09	1.52E-07
4.44E-09	2.01E-07
5.34E-12	1.24E-09
7.28E-11	8.58E-09
3.91E-12	1.07E-09
8.99E-11	1.01E-08
1.07E-11	1.99E-09
1.18E-09	6.97E-08
4.62E-08	1.37E-06

6.86E-11	8.22E-09
7.71E-10	4.92E-08
8.97E-11	1.01E-08
3.85E-10	3.02E-08
3.63E-09	1.71E-07
5.03E-08	1.48E-06
2.63E-11	3.92E-09
1.44E-11	2.49E-09
1.62E-10	1.57E-08
6.08E-11	7.46E-09
1.17E-10	1.18E-08
2.75E-10	2.31E-08
3.25E-09	1.60E-07
4.93E-10	3.59E-08
2.99E-09	1.49E-07
8.82E-11	1.01E-08
1.59E-08	5.71E-07
2.72E-11	4.01E-09
1.01E-07	2.61E-06
1.71E-08	6.08E-07
2.46E-10	2.13E-08
8.19E-10	5.13E-08
3.32E-09	1.61E-07
4.45E-10	3.40E-08
9.73E-11	1.04E-08
1.56E-09	8.69E-08
2.37E-07	5.17E-06
9.64E-11	1.04E-08
4.01E-13	3.37E-10
5.97E-10	4.13E-08
2.38E-10	2.08E-08
2.94E-10	2.41E-08
1.76E-10	1.67E-08
2.52E-10	2.16E-08
5.93E-09	2.51E-07
6.62E-10	4.38E-08
3.56E-10	2.85E-08
2.88E-10	2.38E-08
1.65E-12	5.80E-10
1.67E-09	8.99E-08
4.12E-10	3.21E-08
9.04E-08	2.36E-06
8.89E-08	2.34E-06
1.43E-07	3.43E-06
4.22E-07	8.27E-06
1.27E-12	5.52E-10
2.24E-10	2.02E-08

2.38E-11	3.61E-09
5.60E-08	1.61E-06
4.03E-07	7.93E-06
5.06E-09	2.24E-07
1.50E-10	1.47E-08
1.04E-06	1.72E-05
4.99E-11	6.44E-09
4.96E-14	9.02E-11
1.26E-10	1.26E-08
5.68E-09	2.41E-07
3.63E-10	2.87E-08
1.60E-09	8.81E-08
3.67E-08	1.15E-06
1.85E-09	9.70E-08
1.79E-08	6.24E-07
2.27E-07	5.01E-06
1.07E-06	1.75E-05
1.01E-11	1.90E-09
7.55E-09	3.05E-07
2.07E-07	4.64E-06
9.08E-09	3.59E-07
1.21E-07	3.04E-06
6.83E-12	1.49E-09
7.15E-08	1.97E-06
5.74E-10	4.04E-08
1.24E-05	0.0001311
2.03E-10	1.85E-08
3.81E-09	1.78E-07
6.86E-10	4.46E-08
1.74E-10	1.67E-08
3.50E-09	1.67E-07
4.08E-09	1.88E-07
5.57E-09	2.38E-07
1.00E-10	1.06E-08
1.29E-09	7.30E-08
6.07E-06	7.33E-05
1.34E-06	2.09E-05
9.24E-15	5.24E-11
5.95E-09	2.51E-07
5.45E-09	2.34E-07
8.27E-06	9.39E-05
4.59E-08	1.37E-06
7.32E-11	8.58E-09
3.54E-08	1.11E-06
1.23E-11	2.20E-09
2.32E-08	7.74E-07
9.47E-06	0.0001045

3.99E-09	1.85E-07
1.22E-05	0.0001291
6.87E-06	8.11E-05
5.59E-08	1.61E-06
8.95E-05	0.0006505
6.89E-08	1.92E-06
1.20E-06	1.91E-05
1.47E-09	8.28E-08
1.74E-08	6.16E-07
6.86E-06	8.11E-05
2.88E-07	6.03E-06
1.39E-07	3.39E-06
3.50E-09	1.67E-07
1.17E-07	2.95E-06
1.32E-06	2.07E-05
9.49E-05	0.0006807
1.29E-06	2.03E-05
9.55E-14	1.49E-10
7.00E-06	8.21E-05
1.19E-09	6.99E-08
1.71E-06	2.57E-05
1.61E-07	3.77E-06
4.11E-11	5.58E-09
4.11E-08	1.25E-06
2.73E-12	8.29E-10
1.41E-06	2.18E-05
9.79E-07	1.63E-05
7.32E-07	1.30E-05
3.49E-08	1.10E-06
1.26E-09	7.25E-08
1.85E-12	6.13E-10
4.47E-13	3.46E-10
1.62E-07	3.79E-06
8.95E-08	2.35E-06
1.59E-12	5.77E-10
8.81E-07	1.51E-05
1.93E-08	6.64E-07
2.90E-07	6.06E-06
1.45E-06	2.24E-05
6.50E-07	1.18E-05
7.50E-06	8.65E-05
2.00E-07	4.51E-06
2.42E-06	3.43E-05
2.01E-06	2.94E-05
6.45E-10	4.32E-08
5.16E-09	2.27E-07
3.57E-09	1.69E-07

2.15E-07	4.81E-06
1.63E-05	0.0001655
1.86E-07	4.30E-06
7.57E-08	2.06E-06
4.49E-07	8.63E-06
5.95E-07	1.10E-05
9.04E-06	0.0001008
2.22E-06	3.20E-05
2.43E-08	7.99E-07
9.48E-10	5.78E-08
1.93E-06	2.86E-05
8.60E-07	1.48E-05
4.14E-11	5.58E-09
1.89E-06	2.81E-05
5.07E-11	6.44E-09
2.56E-10	2.18E-08
0.0001212	0.0008221
1.00E-06	1.66E-05
1.75E-09	9.34E-08
3.38E-09	1.63E-07
1.06E-05	0.0001154
5.67E-08	1.62E-06
3.80E-06	5.00E-05
1.00E-05	0.0001098
2.74E-07	5.81E-06
4.99E-09	2.21E-07
7.25E-07	1.29E-05
7.57E-09	3.05E-07
5.45E-10	3.86E-08
1.47E-05	0.0001513
1.33E-09	7.51E-08
0.0007445	0.003412
2.25E-06	3.23E-05
5.13E-06	6.40E-05
5.71E-07	1.06E-05
1.40E-05	0.0001454
1.02E-12	5.08E-10
3.76E-07	7.54E-06
1.27E-09	7.28E-08
5.34E-07	1.00E-05
4.50E-12	1.17E-09
1.33E-06	2.08E-05
2.41E-05	0.0002298
6.09E-05	0.0004792
3.33E-05	0.0002961
3.27E-07	6.68E-06
6.59E-05	0.0005075

9.50E-08	2.46E-06
2.03E-06	2.97E-05
7.01E-08	1.94E-06
0.0001048	0.0007329
1.24E-07	3.10E-06
4.58E-08	1.37E-06
1.23E-12	5.52E-10
1.23E-08	4.65E-07
1.48E-06	2.27E-05
3.03E-06	4.16E-05
7.49E-07	1.32E-05
2.98E-07	6.17E-06
1.48E-06	2.27E-05
7.42E-09	3.01E-07
9.14E-07	1.55E-05
1.16E-07	2.92E-06
8.53E-06	9.64E-05
5.83E-10	4.08E-08
9.76E-11	1.04E-08
5.41E-09	2.34E-07
7.31E-05	0.0005513
7.34E-07	1.31E-05
4.12E-06	5.36E-05
1.31E-06	2.06E-05
5.94E-10	4.13E-08
1.66E-09	8.99E-08
2.25E-09	1.16E-07
2.73E-08	8.87E-07
1.05E-05	0.0001147
2.01E-06	2.94E-05
1.90E-05	0.0001869
1.44E-07	3.45E-06
1.88E-06	2.80E-05
2.12E-06	3.07E-05
7.16E-08	1.97E-06
2.61E-07	5.57E-06
5.14E-05	0.0004193
1.53E-06	2.33E-05
2.18E-06	3.15E-05
3.64E-05	0.0003194
4.05E-08	1.25E-06
1.84E-08	6.40E-07
4.23E-10	3.27E-08
3.94E-07	7.81E-06
1.61E-05	0.0001641
5.49E-07	1.03E-05
4.63E-09	2.07E-07

7.24E-07	1.29E-05
3.75E-07	7.52E-06
5.03E-12	1.19E-09
6.41E-05	0.0004967
6.78E-06	8.05E-05
5.40E-09	2.34E-07
1.07E-08	4.14E-07
3.88E-06	5.09E-05
0.0001798	0.0011305
5.30E-07	9.97E-06
4.64E-07	8.86E-06
3.31E-09	1.61E-07
1.46E-06	2.25E-05
4.79E-10	3.55E-08
1.23E-06	1.96E-05
3.61E-06	4.81E-05
2.38E-05	0.0002275
9.42E-08	2.45E-06
1.58E-09	8.78E-08
2.88E-05	0.0002633
4.23E-09	1.93E-07
1.28E-06	2.02E-05
3.06E-07	6.31E-06
2.75E-08	8.91E-07
1.19E-07	2.98E-06
4.37E-06	5.62E-05
8.78E-09	3.50E-07
7.26E-05	0.0005483
1.35E-06	2.10E-05
2.55E-05	0.0002413
5.33E-05	0.0004312
0.0020808	0.0076013
1.74E-05	0.0001741
1.57E-06	2.39E-05
1.23E-05	0.0001304
1.17E-08	4.46E-07
9.99E-06	0.0001098
3.89E-05	0.0003367
1.10E-06	1.79E-05
5.36E-05	0.0004329
1.07E-08	4.14E-07
2.55E-07	5.49E-06
2.42E-09	1.24E-07
6.49E-05	0.0005023
4.90E-10	3.59E-08
0.0009351	0.0040619
6.30E-10	4.24E-08

9.52E-05	0.0006819
1.69E-07	3.95E-06
9.01E-05	0.0006533
2.16E-07	4.83E-06
1.98E-07	4.50E-06
3.16E-06	4.31E-05
2.02E-05	0.0001971
4.49E-07	8.63E-06
1.04E-08	4.05E-07
1.04E-09	6.27E-08
5.33E-05	0.0004312
0.0002361	0.0014017
1.81E-05	0.0001804
0.0003179	0.0017754
0.0002964	0.0016821
1.34E-07	3.29E-06
0.0002312	0.0013763
4.24E-06	5.48E-05
3.04E-07	6.29E-06
8.40E-09	3.36E-07
8.99E-07	1.53E-05
2.23E-08	7.53E-07
3.95E-07	7.82E-06
0.0010942	0.004596
2.94E-06	4.08E-05
1.36E-06	2.11E-05
5.95E-06	7.22E-05
3.38E-06	4.57E-05
0.0005896	0.0028491
4.82E-10	3.55E-08
1.41E-07	3.41E-06
0.0015255	0.0059679
6.85E-07	1.23E-05
2.69E-07	5.71E-06
2.15E-06	3.12E-05
0.0001227	0.0008299
6.82E-09	2.80E-07
1.32E-08	4.90E-07
1.07E-06	1.75E-05
1.16E-07	2.92E-06
2.43E-08	7.99E-07
0.0002258	0.0013523
2.97E-07	6.16E-06
9.77E-07	1.63E-05
5.79E-07	1.07E-05
4.71E-05	0.0003924
1.52E-07	3.61E-06

2.80E-06	3.91E-05
2.93E-06	4.07E-05
5.31E-10	3.79E-08
3.02E-06	4.15E-05
2.60E-05	0.0002449
7.26E-09	2.96E-07
8.89E-07	1.52E-05
1.82E-05	0.0001812
5.45E-09	2.34E-07
2.93E-05	0.0002675
1.35E-08	4.95E-07
6.25E-07	1.14E-05
0.0001313	0.0008736
0.0020424	0.0074915
8.90E-05	0.0006471
4.02E-05	0.0003446
8.38E-08	2.24E-06
0.0003822	0.0020415
0.000533	0.002633
7.12E-09	2.91E-07
1.73E-05	0.0001741
0.0001059	0.0007374
0.000206	0.0012627
0.0001447	0.0009483
8.17E-10	5.13E-08
1.61E-05	0.0001641
6.35E-05	0.0004935
2.72E-06	3.81E-05
3.39E-06	4.57E-05
1.11E-05	0.0001192
6.62E-07	1.19E-05
3.78E-05	0.0003285
1.37E-07	3.34E-06
0.0006388	0.0030403
7.59E-08	2.06E-06
1.87E-06	2.78E-05
4.43E-06	5.68E-05
1.28E-06	2.02E-05
4.43E-08	1.33E-06
1.74E-05	0.0001741
5.39E-06	6.65E-05
7.20E-05	0.0005448
4.31E-07	8.39E-06
0.0004486	0.0023091
5.07E-05	0.0004152
6.13E-05	0.0004817
1.47E-07	3.51E-06

3.13E-06	4.28E-05
1.11E-08	4.27E-07
5.17E-06	6.43E-05
7.84E-05	0.0005853
2.23E-08	7.53E-07
0.0002312	0.0013763
1.47E-08	5.30E-07
4.55E-09	2.04E-07
4.04E-05	0.0003457
0.000222	0.0013334
3.44E-09	1.65E-07
1.76E-08	6.21E-07
1.98E-10	1.83E-08
6.59E-07	1.19E-05
3.76E-06	4.97E-05
2.03E-07	4.57E-06
4.99E-05	0.0004109
0.0001295	0.0008635
4.78E-05	0.0003966
0.0001532	0.0009903
8.92E-09	3.54E-07
1.64E-05	0.0001667
7.71E-07	1.35E-05
2.46E-05	0.0002339
9.60E-05	0.0006854
0.0012217	0.0050137
2.73E-05	0.0002534
1.63E-06	2.45E-05
5.50E-05	0.0004409
6.71E-05	0.0005149
1.20E-06	1.91E-05
4.05E-06	5.28E-05
1.35E-06	2.10E-05
2.29E-07	5.03E-06
3.45E-07	7.01E-06
0.0008413	0.0037348
0.0005573	0.0027256
1.98E-08	6.76E-07
4.59E-05	0.0003837
7.92E-06	9.05E-05
0.0003259	0.0018059
4.71E-06	5.98E-05
8.43E-05	0.0006186
0.0002019	0.001242
1.14E-05	0.0001223
1.60E-07	3.75E-06
8.91E-07	1.52E-05

5.68E-08	1.62E-06
2.42E-06	3.43E-05
3.72E-05	0.0003239
0.0008406	0.0037348
0.0035598	0.0115849
0.0001788	0.0011259
2.88E-08	9.30E-07
1.46E-08	5.29E-07
2.55E-05	0.0002411
7.05E-05	0.0005365
9.20E-06	0.0001022
7.77E-08	2.10E-06
7.79E-06	8.95E-05
0.0001697	0.001081
1.99E-07	4.50E-06
0.0007433	0.0034094
3.87E-05	0.0003348
7.11E-06	8.29E-05
2.87E-07	6.03E-06
0.0005622	0.0027423
7.33E-06	8.49E-05
0.0007665	0.0034908
1.25E-05	0.0001318
2.33E-07	5.09E-06
2.10E-05	0.0002034
3.25E-05	0.0002906
1.73E-05	0.0001741
0.0003588	0.001946
2.37E-10	2.08E-08
0.0003568	0.0019394
4.25E-09	1.93E-07
0.0003109	0.0017454
4.87E-06	6.15E-05
5.99E-08	1.69E-06
6.11E-07	1.12E-05
9.62E-05	0.0006863
1.71E-07	3.97E-06
1.88E-07	4.32E-06
0.0007397	0.0033987
2.02E-05	0.0001971
1.93E-05	0.0001896
2.90E-05	0.0002656
6.30E-07	1.15E-05
1.25E-06	1.98E-05
4.64E-06	5.90E-05
2.95E-06	4.08E-05
0.0004578	0.0023467

3.78E-05	0.0003285
0.0001928	0.0011952
0.0001508	0.0009782
1.06E-07	2.70E-06
2.14E-06	3.10E-05
0.0001288	0.0008611
6.10E-05	0.0004794
0.0004866	0.0024567
0.0002392	0.0014167
1.06E-07	2.71E-06
4.75E-06	6.02E-05
0.0002598	0.0015117
0.0001193	0.0008121
0.0099173	0.0258894
5.80E-06	7.09E-05
2.43E-05	0.0002315
0.0006233	0.002986
0.0003743	0.0020069
9.26E-06	0.0001028
0.000224	0.0013428
2.88E-07	6.03E-06
0.0001032	0.0007231
3.49E-06	4.68E-05
0.0014103	0.0056206
4.46E-07	8.61E-06
1.37E-08	5.02E-07
0.0023223	0.0082716
4.28E-07	8.36E-06
0.0001336	0.0008876
2.66E-05	0.0002491
0.0001548	0.0009976
1.85E-08	6.40E-07
0.0005422	0.0026685
1.68E-06	2.53E-05
7.13E-05	0.00054
4.10E-06	5.34E-05
1.90E-07	4.35E-06
5.70E-08	1.63E-06
1.35E-08	4.95E-07
0.0029363	0.0099668
0.0005134	0.0025579
3.68E-06	4.89E-05
7.20E-05	0.0005448
0.000723	0.0033527
6.81E-05	0.0005219
1.82E-06	2.71E-05
2.81E-06	3.91E-05

0.0010394	0.0044185
0.0013707	0.0054829
8.52E-07	1.47E-05
0.0012256	0.0050239
6.64E-07	1.19E-05
0.0035944	0.0116664
2.35E-05	0.0002249
4.20E-06	5.44E-05
0.0002576	0.0015007
9.16E-06	0.0001019
4.44E-05	0.0003737
1.79E-07	4.16E-06
2.87E-09	1.45E-07
6.60E-09	2.72E-07
9.38E-05	0.0006736
6.90E-06	8.13E-05
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0.0033032	0.0109189
1.51E-06	2.31E-05
4.44E-05	0.0003737
0.0002678	0.0015522
7.31E-08	2.00E-06
5.93E-06	7.21E-05
0.0007244	0.0033579
2.63E-05	0.0002472
5.62E-05	0.000448
1.11E-05	0.000119
5.93E-07	1.10E-05
8.48E-08	2.26E-06
1.90E-05	0.0001874
0.0011704	0.004845
0.0004366	0.0022565
8.38E-05	0.0006155
0.0024245	0.0085786
4.93E-08	1.45E-06
0.0001008	0.0007113
1.71E-05	0.0001724
0.0002734	0.0015811
1.26E-08	4.73E-07
3.96E-05	0.0003415
0.0001291	0.0008614
7.06E-05	0.0005365
0.0012365	0.0050555
0.0005365	0.0026467
1.47E-06	2.25E-05
0.0007409	0.0034014
0.000251	0.0014713

0.002703	0.0093192
0.0038702	0.0123375
7.11E-05	0.0005392
0.0020914	0.0076376
5.19E-07	9.77E-06
0.0013793	0.0055133
1.35E-06	2.10E-05
5.30E-06	6.56E-05
0.0047987	0.0146225
9.45E-05	0.0006782
0.0001503	0.0009782
0.0005706	0.0027745
9.66E-07	1.61E-05
1.48E-07	3.53E-06
3.67E-05	0.0003204
0.0024668	0.0086858
0.0012581	0.0051276
3.32E-06	4.50E-05
0.0013607	0.0054528
0.0007867	0.0035532
0.0001974	0.0012182
0.000243	0.0014339
0.0025905	0.0090167
4.52E-07	8.65E-06
0.001491	0.0058716
0.0002356	0.0013998
0.0007755	0.0035185
0.0025596	0.008935
0.0001364	0.0009016
0.0017779	0.0067408
1.04E-05	0.0001139
0.0001905	0.0011839
1.53E-07	3.62E-06
0.0007083	0.0033003
0.0001447	0.0009483
3.32E-06	4.50E-05
3.29E-05	0.0002932
0.0010562	0.0044654
0.0001471	0.0009623
0.000213	0.001293
0.0041728	0.0130995
0.0003205	0.0017837
4.35E-05	0.0003679
0.0018523	0.0069459
8.43E-07	1.46E-05
1.01E-06	1.67E-05
3.23E-07	6.61E-06

9.43E-07	1.59E-05
0.0004097	0.0021557
0.0001013	0.0007138
8.56E-05	0.0006274
0.0210124	0.0467839
0.0003361	0.0018542
0.0075847	0.0210542
0.000586	0.0028369
0.0003133	0.0017552
0.0006389	0.0030403
0.0003005	0.0016966
9.06E-06	0.0001009
0.0001236	0.000834
0.0020469	0.0075013
1.21E-05	0.000129
0.0003607	0.0019541
0.0001363	0.0009016
2.21E-05	0.0002136
9.89E-05	0.0007017
1.38E-05	0.0001435
0.0002729	0.0015792
1.05E-06	1.73E-05
6.29E-05	0.0004911
0.0003348	0.0018479
1.87E-07	4.30E-06
0.0112621	0.0285908
0.0022046	0.0079525
0.0029795	0.0100656
5.22E-05	0.0004245
5.52E-07	1.03E-05
1.50E-07	3.56E-06
4.37E-06	5.62E-05
3.98E-05	0.0003418
9.92E-07	1.64E-05
3.60E-08	1.13E-06
4.00E-05	0.0003435
7.89E-05	0.0005874
5.18E-07	9.77E-06
4.64E-05	0.0003867
6.42E-06	7.68E-05
8.51E-07	1.47E-05
2.40E-07	5.21E-06
1.25E-07	3.10E-06
1.37E-05	0.0001427
1.46E-06	2.25E-05
7.93E-05	0.0005895
2.78E-05	0.0002571

1.95E-07	4.45E-06
0.0001856	0.0011608
1.15E-07	2.91E-06
1.67E-05	0.0001693
0.0001575	0.0010129
7.23E-07	1.29E-05
5.26E-05	0.000427
2.14E-05	0.0002074
0.0003518	0.0019165
4.52E-05	0.0003795
0.0157538	0.0371849
0.0001876	0.00117
0.0001426	0.0009373
0.0092233	0.0245175
1.36E-07	3.33E-06
0.0002867	0.0016344
0.0007491	0.0034317
0.0001328	0.0008824
7.86E-06	9.02E-05
0.0092312	0.0245325
0.0009022	0.0039441
2.37E-05	0.0002269
0.0083924	0.022766
1.58E-06	2.39E-05
5.06E-05	0.0004152
8.36E-05	0.0006141
8.68E-08	2.30E-06
8.01E-10	5.08E-08
0.0001665	0.0010633
0.000428	0.002228
2.26E-08	7.58E-07
9.44E-11	1.04E-08
2.33E-08	7.76E-07
8.95E-06	0.0001001
3.02E-05	0.0002729
6.31E-07	1.15E-05
5.18E-06	6.44E-05
0.0002816	0.0016124
2.84E-05	0.000261
5.82E-08	1.65E-06
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1.19E-06	1.90E-05
3.02E-06	4.15E-05
4.05E-07	7.95E-06
3.36E-05	0.0002976
6.49E-07	1.18E-05
0.0001703	0.0010845

1.10E-06	1.79E-05
1.39E-07	3.39E-06
3.07E-07	6.31E-06
2.91E-07	6.07E-06
5.30E-05	0.0004297
9.23E-05	0.0006662
1.06E-06	1.73E-05
5.11E-06	6.39E-05
0.0002309	0.0013763
8.65E-06	9.73E-05
3.59E-05	0.0003159
2.65E-05	0.0002488
0.0037437	0.0120398
4.69E-07	8.95E-06
8.31E-06	9.42E-05
2.65E-06	3.73E-05
0.000102	0.0007174
1.59E-06	2.41E-05
2.78E-05	0.0002569
8.14E-05	0.0006007
1.16E-05	0.0001242
0.0009289	0.0040401
0.0007357	0.0033903
9.27E-06	0.0001028
5.67E-07	1.06E-05
4.08E-08	1.25E-06
9.13E-07	1.55E-05
1.95E-05	0.0001911
0.0019262	0.0071444
7.53E-05	0.0005652
0.0003459	0.0018929
1.26E-05	0.0001326
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9.68E-05	0.0006901
9.43E-05	0.0006773
6.13E-07	1.12E-05
7.30E-05	0.0005509
4.05E-05	0.0003469
0.0003488	0.0019059
3.91E-08	1.21E-06
0.0009299	0.0040426
0.0004178	0.0021878
1.24E-06	1.97E-05
2.94E-05	0.0002675
2.51E-07	5.42E-06
2.27E-07	5.01E-06
4.28E-07	8.36E-06

1.99E-05	0.0001954
3.21E-06	4.38E-05
9.51E-07	1.59E-05
8.09E-05	0.0005983
8.85E-05	0.0006456
9.46E-06	0.0001044
8.17E-06	9.29E-05
5.05E-05	0.0004148
0.0001722	0.0010933
2.27E-07	5.01E-06
3.38E-07	6.87E-06
8.89E-05	0.0006471
0.004355	0.0135275
0.0046196	0.0141732
0.0002792	0.0016044
1.72E-06	2.58E-05
2.24E-05	0.0002158
5.63E-05	0.0004484
6.56E-06	7.81E-05
1.49E-05	0.0001534
2.94E-05	0.0002675
5.18E-05	0.000422
1.04E-07	2.68E-06
1.22E-06	1.93E-05
8.51E-08	2.27E-06
0.0002662	0.001544
2.98E-09	1.49E-07
3.55E-06	4.74E-05
2.24E-06	3.23E-05
1.07E-06	1.75E-05
1.25E-09	7.23E-08
0.0004526	0.002324
2.64E-06	3.73E-05
0.0001138	0.0007818
9.74E-05	0.0006939
9.92E-09	3.89E-07
0.0012164	0.0049954
0.0001238	0.0008345
9.23E-08	2.40E-06
7.60E-06	8.75E-05
2.96E-06	4.08E-05
5.11E-08	1.50E-06
1.82E-07	4.22E-06
5.08E-05	0.0004158
4.81E-05	0.0003991
3.08E-07	6.32E-06
4.33E-07	8.40E-06

3.18E-07	6.53E-06
1.72E-06	2.58E-05
7.89E-06	9.03E-05
0.0001433	0.0009406
0.0001791	0.0011273
2.05E-05	0.0001994
1.35E-05	0.0001409
2.46E-05	0.0002338
7.55E-06	8.70E-05
8.94E-06	0.0001001
3.66E-05	0.0003202
1.61E-09	8.81E-08
7.62E-06	8.77E-05
1.18E-05	0.0001258
6.11E-08	1.72E-06
4.31E-07	8.39E-06
5.41E-08	1.57E-06
9.12E-07	1.55E-05
4.58E-06	5.85E-05
1.08E-08	4.14E-07
4.61E-05	0.0003852
5.34E-08	1.56E-06
0.0001028	0.0007212
1.26E-07	3.13E-06
0.0035972	0.0116683
1.78E-08	6.23E-07
2.64E-05	0.0002484
5.23E-06	6.47E-05
3.17E-11	4.46E-09
1.90E-06	2.82E-05
3.28E-05	0.0002928
5.92E-08	1.67E-06
8.32E-08	2.23E-06
1.07E-06	1.75E-05
0.0001838	0.001151
4.74E-07	8.98E-06
2.54E-05	0.0002404
6.67E-06	7.93E-05
1.19E-05	0.0001265
7.53E-08	2.06E-06
1.14E-07	2.90E-06
4.13E-08	1.25E-06
1.85E-09	9.70E-08
4.85E-05	0.0004014
3.94E-08	1.21E-06
1.12E-06	1.82E-05
1.89E-05	0.0001864

7.16E-06	8.32E-05
1.81E-05	0.0001804
1.75E-08	6.17E-07
0.0014587	0.0057567
2.26E-06	3.24E-05
4.02E-09	1.86E-07
4.24E-09	1.93E-07
8.78E-05	0.0006418
0.000814	0.0036479
2.32E-06	3.32E-05
4.00E-07	7.89E-06
3.10E-10	2.52E-08
4.25E-08	1.28E-06
7.01E-06	8.21E-05
1.03E-10	1.07E-08
0.0031203	0.0104157
1.93E-09	1.01E-07
9.51E-06	0.0001048
5.98E-09	2.51E-07
0.0127707	0.0315851
4.44E-05	0.0003737
1.29E-05	0.0001356
8.67E-08	2.30E-06
3.88E-06	5.09E-05
3.59E-06	4.79E-05
4.72E-07	8.98E-06
4.25E-11	5.66E-09
4.46E-07	8.61E-06
4.89E-05	0.0004045
7.93E-08	2.13E-06
2.94E-07	6.12E-06
1.93E-06	2.85E-05
0.0001842	0.0011527
3.51E-08	1.11E-06
0.0015546	0.0060651
6.04E-07	1.11E-05
1.36E-06	2.11E-05
5.11E-06	6.39E-05
7.00E-08	1.94E-06
2.07E-11	3.28E-09
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5.35E-05	0.0004325
1.78E-09	9.45E-08
2.09E-06	3.05E-05
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3.59E-05	0.0003159
4.72E-10	3.55E-08

4.80E-10	3.55E-08
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2.94E-07	6.12E-06
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5.21E-06	6.45E-05
2.57E-07	5.52E-06
6.57E-05	0.0005068
1.64E-07	3.83E-06
1.12E-06	1.82E-05
2.20E-07	4.90E-06
2.17E-07	4.84E-06
6.14E-10	4.16E-08
3.64E-09	1.71E-07
7.23E-06	8.41E-05
3.42E-07	6.95E-06
1.17E-06	1.88E-05
1.03E-08	4.03E-07
1.29E-07	3.18E-06
7.59E-07	1.34E-05
1.91E-07	4.37E-06
3.98E-07	7.86E-06
2.92E-09	1.47E-07
3.33E-06	4.51E-05
8.19E-06	9.31E-05
1.49E-05	0.0001534
3.64E-09	1.71E-07
1.24E-08	4.68E-07
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1.96E-06	2.89E-05
2.19E-08	7.44E-07
1.08E-06	1.76E-05
4.59E-08	1.37E-06
2.63E-09	1.34E-07
2.46E-08	8.01E-07
1.02E-10	1.06E-08
4.61E-05	0.0003852
8.84E-10	5.42E-08
5.03E-11	6.44E-09
2.26E-06	3.24E-05
4.96E-08	1.46E-06
2.15E-09	1.11E-07
5.03E-06	6.32E-05
1.12E-07	2.87E-06
4.00E-07	7.89E-06
1.41E-07	3.41E-06
7.99E-07	1.39E-05
6.66E-10	4.38E-08

3.34E-06	4.52E-05
2.62E-07	5.57E-06
1.32E-08	4.90E-07
1.97E-08	6.76E-07
9.59E-07	1.61E-05
2.31E-07	5.06E-06
1.23E-09	7.16E-08
1.55E-05	0.0001588
5.66E-06	6.94E-05
8.70E-08	2.30E-06
1.84E-07	4.26E-06
4.98E-10	3.60E-08
2.38E-07	5.17E-06
0.0067513	0.019205
2.25E-06	3.24E-05
2.39E-08	7.90E-07
4.98E-06	6.27E-05
7.28E-10	4.70E-08
6.43E-06	7.69E-05
1.50E-07	3.56E-06
2.04E-06	2.98E-05
7.96E-06	9.09E-05
3.13E-11	4.46E-09
7.83E-08	2.11E-06
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7.87E-06	9.02E-05
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0.0001243	0.0008369
1.19E-08	4.52E-07
4.42E-08	1.33E-06
1.22E-07	3.06E-06
6.47E-07	1.18E-05
8.30E-07	1.44E-05
2.45E-08	8.01E-07
3.88E-12	1.07E-09
4.17E-08	1.26E-06
2.06E-08	6.99E-07
1.44E-08	5.23E-07
2.54E-05	0.0002411
7.76E-08	2.10E-06
1.28E-08	4.77E-07
3.20E-08	1.02E-06
2.02E-09	1.05E-07
9.00E-08	2.36E-06
9.97E-10	6.04E-08
1.30E-07	3.20E-06
3.27E-09	1.60E-07

1.40E-12	5.66E-10
1.47E-05	0.0001517
3.38E-05	0.0002988
8.66E-07	1.49E-05
1.28E-09	7.30E-08
1.29E-11	2.28E-09
9.17E-09	3.61E-07
2.95E-06	4.08E-05
3.46E-08	1.10E-06
4.64E-09	2.07E-07
7.66E-09	3.07E-07
6.29E-08	1.76E-06
1.98E-11	3.24E-09
6.12E-09	2.56E-07
0.0058117	0.0170523
3.92E-07	7.78E-06
0.000429	0.0022315
4.52E-10	3.43E-08
8.71E-08	2.30E-06
3.67E-06	4.88E-05
4.50E-07	8.63E-06
3.81E-05	0.0003304
0.0001076	0.0007471
1.91E-08	6.59E-07
1.29E-07	3.18E-06
1.56E-07	3.67E-06
3.38E-08	1.07E-06
0.000143	0.0009394
8.40E-10	5.21E-08
9.17E-11	1.02E-08
5.42E-09	2.34E-07
2.76E-06	3.86E-05
7.69E-07	1.35E-05
5.28E-10	3.79E-08
2.93E-08	9.42E-07
2.00E-08	6.81E-07
2.67E-10	2.26E-08
6.13E-10	4.16E-08
5.95E-07	1.10E-05
2.28E-08	7.63E-07
3.90E-08	1.21E-06
3.57E-07	7.22E-06
3.12E-06	4.27E-05
1.99E-07	4.50E-06
4.73E-14	9.02E-11
5.43E-13	3.46E-10
2.55E-07	5.50E-06

5.41E-08	1.57E-06
2.34E-10	2.08E-08
1.20E-12	5.52E-10
6.36E-07	1.16E-05
2.03E-10	1.85E-08
1.12E-09	6.69E-08
2.39E-05	0.0002284
1.05E-10	1.07E-08
4.35E-10	3.34E-08
2.30E-10	2.06E-08
3.80E-11	5.25E-09
1.78E-11	3.04E-09
2.56E-06	3.62E-05
8.82E-07	1.51E-05
3.67E-07	7.37E-06
7.18E-08	1.97E-06
0.0001126	0.0007743
7.00E-12	1.49E-09
6.74E-08	1.88E-06
8.25E-05	0.0006078
2.98E-08	9.56E-07
3.60E-10	2.87E-08
6.29E-09	2.62E-07
3.81E-08	1.18E-06
5.95E-06	7.22E-05
9.05E-12	1.76E-09
2.38E-08	7.89E-07
5.51E-09	2.36E-07
1.43E-07	3.43E-06
2.44E-08	7.99E-07
4.72E-11	6.21E-09
6.36E-05	0.0004942
1.48E-07	3.54E-06
8.73E-10	5.38E-08
3.50E-07	7.09E-06
1.53E-09	8.55E-08
1.38E-05	0.0001431
2.26E-11	3.52E-09
2.71E-06	3.81E-05
1.19E-09	6.99E-08
9.61E-15	5.24E-11
3.16E-11	4.46E-09
6.07E-10	4.16E-08
4.51E-09	2.03E-07
8.23E-11	9.56E-09
1.97E-10	1.83E-08
6.70E-11	8.12E-09

2.78E-10	2.32E-08
1.73E-09	9.27E-08
4.64E-12	1.17E-09
1.67E-09	8.99E-08
1.90E-10	1.79E-08
2.37E-11	3.61E-09
1.25E-13	1.71E-10
6.79E-06	8.05E-05
1.11E-09	6.68E-08
8.38E-12	1.69E-09
4.73E-12	1.17E-09
1.56E-10	1.52E-08
3.45E-05	0.0003042
1.01E-10	1.06E-08
1.99E-11	3.24E-09
2.43E-12	7.59E-10
5.53E-13	3.46E-10
1.65E-08	5.88E-07
1.78E-12	6.07E-10
8.87E-13	4.74E-10
6.74E-10	4.40E-08
2.27E-13	2.25E-10
7.43E-10	4.77E-08
3.01E-12	8.88E-10
1.96E-13	2.14E-10
3.47E-14	9.02E-11
8.32E-10	5.19E-08
4.87E-12	1.18E-09

populations (IT2, UK6 and ES1) and two susceptible strains (RO1 and IT3) of *T. urticae*

ipr_ALL
NA
NA
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
NA
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain, IPR006553*Leucine
NA
NA
IPR000536*Nuclear hormone receptor, ligand-binding domain
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR029034*Cystine-knot cytokine, IPR032104*Spaetzle
IPR011333*SKP1/BTB/POZ domain, IPR011705*BTB/Kelch-associated
IPR023395*Mitochondrial carrier domain, IPR018108*Mitochondrial substrate/solute carrier
NA
NA
IPR003609*PAN/Apple domain
IPR032675*Leucine-rich repeat domain, L domain-like
NA
IPR013818*Lipase/vitellogenin, IPR000734*Triacylglycerol lipase family, IPR029058*Alpha/Beta hydrol
NA
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR016159*Cullin repeat-like-containing domain, IPR016158*Cullin homology, IPR001373*Cullin, N-ter
IPR000210*BTB/POZ domain, IPR011705*BTB/Kelch-associated, IPR011333*SKP1/BTB/POZ domair
IPR014756*Immunoglobulin E-set, IPR003172*MD-2-related lipid-recognition domain
IPR007235*Glycosyl transferase, family 28, C-terminal
IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
NA
NA
NA
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR011705*BTB/Kelch-associated, IPR011333*SKP1/BTB/POZ domain, IPR011042*Six-bladed beta-p
NA
IPR000010*Cystatin domain
NA
IPR007264*H/ACA ribonucleoprotein complex, subunit Nop10
IPR000210*BTB/POZ domain, IPR011705*BTB/Kelch-associated, IPR011333*SKP1/BTB/POZ domair
NA
NA
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR001283*Cysteine-rich secretory protein, allergen V5/Tpx-1-related, IPR014044*CAP domain, IPR0
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR007235*Glycosyl transferase, family 28, C-terminal, IPR002213*UDP-glucuronosyl/UDP-glucosyltra

NA
NA
IPR011705*BTB/Kelch-associated, IPR000210*BTB/POZ domain, IPR011333*SKP1/BTB/POZ domai
NA
IPR005552*Scramblase
NA
IPR013320*Concanavalin A-like lectin/glucanase domain
NA
NA
IPR011705*BTB/Kelch-associated
NA
IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
IPR016443*RNA 3'-terminal phosphate cyclase type 2, IPR013791*RNA 3'-terminal phosphate cyclase
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
IPR000210*BTB/POZ domain, IPR011333*SKP1/BTB/POZ domain, IPR011705*BTB/Kelch-associate
IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
IPR011705*BTB/Kelch-associated, IPR000210*BTB/POZ domain, IPR011333*SKP1/BTB/POZ domai
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR032675*Leucine-rich repeat domain, L domain-like
IPR003386*Lecithin:cholesterol/phospholipid:diacylglycerol acyltransferase, IPR029058*Alpha/Beta hy
NA
IPR032675*Leucine-rich repeat domain, L domain-like
NA
NA
NA
NA
IPR011043*Galactose oxidase/kelch, beta-propeller, IPR011705*BTB/Kelch-associated, IPR000210*B
IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
NA
IPR011333*SKP1/BTB/POZ domain, IPR000210*BTB/POZ domain, IPR028764*Kelch repeat and BTB
NA
IPR011705*BTB/Kelch-associated, IPR000210*BTB/POZ domain, IPR011333*SKP1/BTB/POZ domai
IPR011705*BTB/Kelch-associated, IPR011333*SKP1/BTB/POZ domain
NA
NA
IPR000566*Lipocalin/cytosolic fatty-acid binding domain, IPR012674*Calycin
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
NA
NA
NA
IPR005552*Scramblase
NA
IPR015889*Intradiol ring-cleavage dioxygenase, core
IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat

NA
IPR000146*Fructose-1,6-bisphosphatase class 1, IPR033391*Fructose-1-6-bisphosphatase class I, N-
IPR020846*Major facilitator superfamily domain
IPR007235*Glycosyl transferase, family 28, C-terminal, IPR002213*UDP-glucuronosyl/UDP-glucosyltra
IPR023395*Mitochondrial carrier domain, IPR018108*Mitochondrial substrate/solute carrier
IPR020846*Major facilitator superfamily domain
NA
IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
NA
NA
IPR001806*Small GTPase superfamily, IPR020849*Small GTPase superfamily, Ras type, IPR027417*
IPR009003*Peptidase S1, PA clan, IPR001254*Serine proteases, trypsin domain
IPR009003*Peptidase S1, PA clan, IPR001254*Serine proteases, trypsin domain
NA
NA
NA
NA
IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
NA
IPR021139*NYN domain, limkain-b1-type
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
NA
NA
IPR006326*UDP-glycosyltransferase, MGT, IPR007235*Glycosyl transferase, family 28, C-terminal
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR032695*Integrin domain, IPR013649*Integrin alpha-2
IPR001128*Cytochrome P450
NA
NA
IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain
IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
NA
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase, IPR006326*UDP-glycosyltransferase, MGT, I
NA
IPR026505*Solute carrier family 35 member F3/F4
IPR000594*THIF-type NAD/FAD binding fold, IPR001763*Rhodanese-like domain
NA
NA
NA
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily, IPR001958*
IPR015889*Intradiol ring-cleavage dioxygenase, core
NA
IPR003609*PAN/Apple domain
NA

IPR003609*PAN/Apple domain
IPR029058*Alpha/Beta hydrolase fold
IPR000618*Insect cuticle protein
NA
NA
IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
NA
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
NA
NA
NA
NA
NA
NA
IPR011333*SKP1/BTB/POZ domain, IPR011705*BTB/Kelch-associated
NA
IPR002403*Cytochrome P450, E-class, group IV, IPR001128*Cytochrome P450
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR015889*Intradiol ring-cleavage dioxygenase, core
IPR006326*UDP-glycosyltransferase, MGT, IPR007235*Glycosyl transferase, family 28, C-terminal, IP
IPR020846*Major facilitator superfamily domain
NA
IPR017986*WD40-repeat-containing domain, IPR015943*WD40/YVTN repeat-like-containing domain
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
NA
NA
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
IPR016159*Cullin repeat-like-containing domain
NA
NA
NA
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
NA
NA
IPR007235*Glycosyl transferase, family 28, C-terminal, IPR002213*UDP-glucuronosyl/UDP-glucosyltra
IPR024332*MOZART2 family
IPR003609*PAN/Apple domain
NA
NA
IPR011705*BTB/Kelch-associated, IPR000210*BTB/POZ domain, IPR015915*Kelch-type beta propelle
NA
IPR008978*HSP20-like chaperone, IPR001436*Alpha crystallin/Heat shock protein, IPR002068*Alpha
NA
NA
NA
IPR000215*Serpin family, IPR023796*Serpin domain
NA

IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
NA
IPR004045*Glutathione S-transferase, N-terminal, IPR012336*Thioredoxin-like fold, IPR004046*Glutat
NA
IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
IPR031328*Ephrin, IPR001799*Ephrin receptor-binding domain, IPR008972*Cupredoxin
NA
IPR001096*Peptidase C13, legumain
NA
IPR001623*DnaJ domain, IPR015399*Domain of unknown function DUF1977, DnaJ-like
IPR008978*HSP20-like chaperone, IPR031107*Small heat shock protein HSP20, IPR001436*Alpha cr
NA
IPR013907*Sds3-like
IPR013083*Zinc finger, RING/FYVE/PHD-type
IPR007235*Glycosyl transferase, family 28, C-terminal, IPR002213*UDP-glucuronosyl/UDP-glucosyltra
IPR014756*Immunoglobulin E-set, IPR003172*MD-2-related lipid-recognition domain
IPR029058*Alpha/Beta hydrolase fold, IPR000073*Alpha/beta hydrolase fold-1
IPR023395*Mitochondrial carrier domain, IPR018108*Mitochondrial substrate/solute carrier, IPR00206
NA
IPR015943*WD40/YVTN repeat-like-containing domain, IPR017986*WD40-repeat-containing domain,
NA
IPR008952*Tetraspanin, EC2 domain, IPR018499*Tetraspanin/Peripherin
NA
NA
IPR003226*Metal-dependent protein hydrolase
NA
IPR013154*Alcohol dehydrogenase, N-terminal, IPR013149*Alcohol dehydrogenase, C-terminal, IPR0
NA
IPR015889*Intradiol ring-cleavage dioxygenase, core, IPR000627*Intradiol ring-cleavage dioxygenase,
IPR012674*Calycin
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR001254*Serine proteases, trypsin domain, IPR001314*Peptidase S1A, chymotrypsin family, IPR00
NA
IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
IPR007235*Glycosyl transferase, family 28, C-terminal, IPR002213*UDP-glucuronosyl/UDP-glucosyltra
NA
NA
IPR023796*Serpin domain, IPR000215*Serpin family
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR001506*Peptidase M12A, IPR024079*Metallopeptidase, catalytic domain, IPR006026*Peptidase, n
IPR029058*Alpha/Beta hydrolase fold, IPR001563*Peptidase S10, serine carboxypeptidase
NA
NA
IPR000218*Ribosomal protein L14P
NA
IPR035427*Tim10/FAM136A-like domain, IPR004217*Tim10-like
IPR012337*Ribonuclease H-like domain, IPR006941*Ribonuclease CAF1

IPR022214*Mitotic-spindle organizing protein 1

NA

IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR011042*Six-bladed beta-propelle

IPR027859*Domain of unknown function DUF4457, IPR026704*Protein KIAA0556, IPR008979*Galact

IPR023796*Serpin domain, IPR000215*Serpin family

IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain

IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B, IPR000997*Cholinestera

NA

NA

NA

IPR015889*Intradiol ring-cleavage dioxygenase, core

NA

IPR015889*Intradiol ring-cleavage dioxygenase, core

IPR012674*Calycin

NA

NA

IPR006176*3-hydroxyacyl-CoA dehydrogenase, NAD binding, IPR016040*NAD(P)-binding domain, IP

IPR015889*Intradiol ring-cleavage dioxygenase, core

NA

IPR032695*Integrin domain, IPR013517*FG-GAP repeat, IPR013649*Integrin alpha-2, IPR013519*Inte

IPR001314*Peptidase S1A, chymotrypsin family, IPR001254*Serine proteases, trypsin domain, IPR00

NA

IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I

IPR011016*Zinc finger, RING-CH-type, IPR033275*E3 ubiquitin-protein ligase MARCH-like, IPR01308

IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B

NA

IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I

NA

NA

IPR004046*Glutathione S-transferase, C-terminal, IPR004045*Glutathione S-transferase, N-terminal, I

IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat

IPR000668*Peptidase C1A, papain C-terminal, IPR012599*Peptidase C1A, propeptide, IPR013128*Pe

IPR001254*Serine proteases, trypsin domain, IPR009003*Peptidase S1, PA clan, IPR001314*Peptidas

IPR024518*Domain of unknown function DUF3421

IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR

NA

NA

NA

IPR002634*BolA protein

IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I

IPR002908*Frataxin/CyaY, IPR017789*Frataxin

IPR003008*Tubulin/FtsZ, GTPase domain, IPR000217*Tubulin, IPR002453*Beta tubulin, IPR008280*

NA

IPR008979*Galactose-binding domain-like

NA

IPR032675*Leucine-rich repeat domain, L domain-like, IPR003591*Leucine-rich repeat, typical subtype

IPR001356*Homeobox domain, IPR009057*Homeobox domain-like

IPR003008*Tubulin/FtsZ, GTPase domain, IPR000217*Tubulin, IPR018316*Tubulin/FtsZ, 2-layer sand
IPR000996*Clathrin light chain
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
NA
NA
NA
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR003172*MD-2-related lipid-recognition domain, IPR014756*Immunoglobulin E-set
NA
NA
NA
IPR016024*Armadillo-type fold
IPR020683*Ankyrin repeat-containing domain, IPR002110*Ankyrin repeat
NA
IPR000504*RNA recognition motif domain, IPR034237*FOX1, RNA recognition motif
IPR029034*Cystine-knot cytokine, IPR032104*Spaetzle
IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A, IPR012599*Peptidase C1
IPR021454*Protein of unknown function DUF3105
IPR003439*ABC transporter-like, IPR027417*P-loop containing nucleoside triphosphate hydrolase, IP
IPR009269*NF-kappa-B-activating protein
IPR007007*Ninjurin
NA
NA
NA
NA
NA
IPR003280*Two pore domain potassium channel, IPR013099*Potassium channel domain
IPR023796*Serpin domain, IPR000215*Serpin family
NA
IPR006202*Neurotransmitter-gated ion-channel ligand-binding domain, IPR006028*Gamma-aminobut
IPR020846*Major facilitator superfamily domain, IPR010291*Ion channel regulatory protein, UNC-93
IPR000082*SEA domain
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat
IPR024768*Meiosis regulator and mRNA stability factor 1
IPR007109*Brix domain
IPR006616*DM9 repeat, IPR024518*Domain of unknown function DUF3421
NA
NA
NA
IPR029062*Class I glutamine amidotransferase-like, IPR015527*Peptidase C26, gamma-glutamyl hyd
NA
IPR013328*6-phosphogluconate dehydrogenase, domain 2, IPR008927*6-phosphogluconate dehydro
IPR015889*Intradiol ring-cleavage dioxygenase, core, IPR000627*Intradiol ring-cleavage dioxygenase
IPR009346*GRIM-19

NA
NA
IPR012816*NADAR
NA
IPR001096*Peptidase C13, legumain
NA
NA
IPR029063*S-adenosyl-L-methionine-dependent methyltransferase, IPR013216*Methyltransferase typ
IPR023753*FAD/NAD(P)-binding domain, IPR020946*Flavin monooxygenase-like, IPR000960*Flavin r
IPR002048*EF-hand domain, IPR011992*EF-hand domain pair
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR011990*Tetratricopeptide-like helical domain, IPR013949*U3 small nucleolar RNA-associated prote
NA
NA
NA
IPR000504*RNA recognition motif domain
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR001781*Zinc finger, LIM-type
IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR011042*Six-bladed beta-propelle
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase, IPR007235*Glycosyl transferase, family 28, C
NA
IPR001436*Alpha crystallin/Heat shock protein, IPR008978*HSP20-like chaperone, IPR031107*Small
NA
NA
IPR007745*Cytochrome c oxidase copper chaperone, IPR009069*Cysteine alpha-hairpin motif superfa
IPR029063*S-adenosyl-L-methionine-dependent methyltransferase
IPR001619*Sec1-like protein
IPR000863*Sulfotransferase domain, IPR027417*P-loop containing nucleoside triphosphate hydrolase
IPR001951*Histone H4, IPR035425*CENP-T/Histone H4, histone fold, IPR009072*Histone-fold
IPR026910*Shisa family
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR004254*AdipoR/Haemolysin-III-related
IPR013881*Pre-mRNA-splicing factor 3, IPR027104*U4/U6 small nuclear ribonucleoprotein Prp3, IPR0
IPR032675*Leucine-rich repeat domain, L domain-like
NA
IPR033275*E3 ubiquitin-protein ligase MARCH-like
IPR011701*Major facilitator superfamily, IPR020846*Major facilitator superfamily domain
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B, IPR000997*Cholinestera
IPR019410*Lysine methyltransferase, IPR029063*S-adenosyl-L-methionine-dependent methyltransfera
IPR020846*Major facilitator superfamily domain
NA
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
IPR013201*Cathepsin propeptide inhibitor domain (I29), IPR013128*Peptidase C1A
NA
IPR011106*Seven cysteines, N-terminal, IPR002172*Low-density lipoprotein (LDL) receptor class A re

IPR032675*Leucine-rich repeat domain, L domain-like

NA

IPR000276*G protein-coupled receptor, rhodopsin-like, IPR017946*PLC-like phosphodiesterase, TIM b

IPR023796*Serpin domain, IPR000215*Serpin family

NA

NA

NA

IPR011598*Myc-type, basic helix-loop-helix (bHLH) domain, IPR032664*Protein atonal/amos/lin-32

IPR023648*Copper homeostasis CutC domain, IPR005627*Copper homeostasis protein CutC

NA

IPR024883*Neurensin

IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily

NA

NA

NA

IPR019382*Translation initiation factor 3 complex subunit L

IPR004045*Glutathione S-transferase, N-terminal, IPR010987*Glutathione S-transferase, C-terminal-li

NA

IPR001436*Alpha crystallin/Heat shock protein, IPR031107*Small heat shock protein HSP20, IPR0089

IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain

IPR013783*Immunoglobulin-like fold, IPR008979*Galactose-binding domain-like, IPR017853*Glycosid

IPR002109*Glutaredoxin, IPR014025*Glutaredoxin subgroup, IPR011899*Glutaredoxin, eukaryotic/viri

NA

NA

IPR011012*Longin-like domain, IPR022775*AP complex, mu/sigma subunit

NA

NA

NA

NA

IPR029060*PIN domain-like

IPR000215*Serpin family, IPR023796*Serpin domain

IPR018499*Tetraspanin/Peripherin, IPR008952*Tetraspanin, EC2 domain

IPR007484*Peptidase M28

IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily

NA

IPR001096*Peptidase C13, legumain

NA

IPR015943*WD40/YVTN repeat-like-containing domain, IPR017986*WD40-repeat-containing domain

IPR004045*Glutathione S-transferase, N-terminal, IPR004046*Glutathione S-transferase, C-terminal, I

IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR

IPR011249*Metalloenzyme, LuxS/M16 peptidase-like, IPR013578*Peptidase M16C associated

IPR034907*Nucleoside diphosphate kinase-like domain

IPR002345*Lipocalin, IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain, IP

NA

NA

NA

NA

IPR003131*Potassium channel tetramerisation-type BTB domain, IPR029044*Nucleotide-diphospho-su
NA
NA
NA
NA
NA
NA
IPR011042*Six-bladed beta-propeller, TolB-like, IPR013658*SMP-30/Gluconolactonase/LRE-like regio
NA
IPR008979*Galactose-binding domain-like
IPR006186*Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase, IPR0290
NA
IPR011598*Myc-type, basic helix-loop-helix (bHLH) domain, IPR032647*Max-like protein X
NA
IPR000058*Zinc finger, AN1-type
IPR015889*Intradiol ring-cleavage dioxygenase, core
IPR000266*Ribosomal protein S17/S11, IPR012340*Nucleic acid-binding, OB-fold
NA
NA
NA
IPR027450*Alpha-ketoglutarate-dependent dioxygenase AlkB-like, IPR032870*Alpha-ketoglutarate-de
IPR029021*Protein-tyrosine phosphatase-like, IPR020417*Atypical dual specificity phosphatase, IPR0
IPR012599*Peptidase C1A, propeptide, IPR013128*Peptidase C1A, IPR000668*Peptidase C1A, papai
NA
NA
IPR001254*Serine proteases, trypsin domain, IPR001314*Peptidase S1A, chymotrypsin family, IPR00
NA
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR000217*Tubulin, IPR008280*Tubulin/FtsZ, C-terminal, IPR002454*Gamma tubulin, IPR003008*Tu
NA
IPR003172*MD-2-related lipid-recognition domain, IPR014756*Immunoglobulin E-set
IPR003609*PAN/Apple domain
IPR015421*Pyridoxal phosphate-dependent transferase, major region, subdomain 1, IPR010111*Kynu
IPR018499*Tetraspanin/Peripherin, IPR008952*Tetraspanin, EC2 domain
IPR023330*Rhabdovirus nucleocapsid, N-terminal, IPR000448*Rhabdovirus nucleocapsid, IPR023331
NA
IPR018028*Catalase, mono-functional, haem-containing, IPR011614*Catalase core domain, IPR02471
IPR023210*NADP-dependent oxidoreductase domain
IPR015727*Protein kinase C mu-related, IPR002219*Protein kinase C-like, phorbol ester/diacylglycerol
IPR019791*Haem peroxidase, animal type, IPR010255*Haem peroxidase
IPR017946*PLC-like phosphodiesterase, TIM beta/alpha-barrel domain
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR001916*Glycoside hydrolase, family 22, IPR000974*Glycoside hydrolase, family 22, lysozyme, IPR
IPR011009*Protein kinase-like domain
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
NA

IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I

IPR011598*Myc-type, basic helix-loop-helix (bHLH) domain, IPR032664*Protein atonal/amos/lin-32

IPR032675*Leucine-rich repeat domain, L domain-like, IPR003591*Leucine-rich repeat, typical subtype

NA

NA

IPR009866*NADH:ubiquinone oxidoreductase, subunit NDUFB4

IPR007305*Vesicle transport protein, Got1/SFT2-like, IPR011691*Vesicle transport protein, SFT2-like

IPR032675*Leucine-rich repeat domain, L domain-like

IPR022214*Mitotic-spindle organizing protein 1

IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase, IPR007235*Glycosyl transferase, family 28, C

NA

NA

NA

NA

IPR001139*Glycoside hydrolase family 30, IPR017853*Glycoside hydrolase superfamily, IPR033452*G

IPR008978*HSP20-like chaperone, IPR001436*Alpha crystallin/Heat shock protein, IPR031107*Small

IPR032054*DNA replication factor Cdt1, C-terminal

IPR004046*Glutathione S-transferase, C-terminal, IPR010987*Glutathione S-transferase, C-terminal-lik

IPR005292*Multi drug resistance-associated protein, IPR011527*ABC transporter type 1, transmembra

IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450

IPR001314*Peptidase S1A, chymotrypsin family, IPR001254*Serine proteases, trypsin domain, IPR00

NA

NA

IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450

NA

IPR003563*7,8-dihydro-8-oxoguanine triphosphatase

NA

NA

NA

NA

IPR000668*Peptidase C1A, papain C-terminal, IPR013201*Cathepsin propeptide inhibitor domain (I29)

IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain

IPR002999*Tudor domain

IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like

IPR000990*Innexin

NA

IPR009110*Nuclear receptor coactivator, interlocking

IPR000215*Serpin family, IPR023796*Serpin domain

IPR031084*OTU domain-containing protein 5/Otubain-like deubiquitinase 1

IPR000504*RNA recognition motif domain

IPR007235*Glycosyl transferase, family 28, C-terminal

IPR002048*EF-hand domain, IPR011992*EF-hand domain pair

IPR007125*Histone H2A/H2B/H3, IPR002119*Histone H2A, IPR009072*Histone-fold, IPR032454*Hist

IPR006693*Partial AB-hydrolase lipase domain, IPR029058*Alpha/Beta hydrolase fold, IPR000073*Alp

NA

IPR019012*RNA cap guanine-N2 methyltransferase, IPR029063*S-adenosyl-L-methionine-dependent

NA

NA

NA

IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like

IPR002068*Alpha crystallin/Hsp20 domain, IPR008978*HSP20-like chaperone, IPR031107*Small heat

IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like

NA

IPR023753*FAD/NAD(P)-binding domain, IPR007867*Glucose-methanol-choline oxidoreductase, C-te

NA

NA

IPR017905*ERV/ALR sulfhydryl oxidase domain, IPR013766*Thioredoxin domain, IPR012336*Thiored

NA

IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily

IPR000998*MAM domain, IPR013320*Concanavalin A-like lectin/glucanase domain, IPR002172*Low-

NA

IPR003057*Invertebrate colouration protein, IPR000566*Lipocalin/cytosolic fatty-acid binding domain, I

NA

IPR006689*Small GTPase superfamily, ARF/SAR type, IPR027417*P-loop containing nucleoside triph

NA

IPR001356*Homeobox domain, IPR009057*Homeobox domain-like

IPR019547*B domain of TMEM189, localisation domain

IPR013525*ABC-2 type transporter, IPR003593*AAA+ ATPase domain, IPR027417*P-loop containing

IPR032675*Leucine-rich repeat domain, L domain-like

IPR003563*7,8-dihydro-8-oxoguanine triphosphatase, IPR000086*NUDIX hydrolase domain, IPR0157

NA

IPR035437*Staphylococcal nuclease (SNase-like), OB-fold/extended TUDOR domain, IPR002999*Tud

NA

IPR003439*ABC transporter-like, IPR003593*AAA+ ATPase domain, IPR027417*P-loop containing nu

IPR011032*GroES-like, IPR013149*Alcohol dehydrogenase, C-terminal, IPR013154*Alcohol dehydrog

IPR008971*HSP40/DnaJ peptide-binding, IPR002939*Chaperone DnaJ, C-terminal

NA

NA

IPR001279*Metallo-beta-lactamase, IPR011084*DNA repair metallo-beta-lactamase

NA

IPR012336*Thioredoxin-like fold, IPR010987*Glutathione S-transferase, C-terminal-like, IPR004046*G

NA

IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I

IPR029033*Histidine phosphatase superfamily, IPR000560*Histidine phosphatase superfamily, clade-

IPR010044*Methylthioadenosine phosphorylase (MTAP), IPR000845*Nucleoside phosphorylase dom

IPR027246*Eukaryotic porin/Tom40, IPR001925*Porin, eukaryotic type

NA

NA

NA

NA

IPR011701*Major facilitator superfamily, IPR020846*Major facilitator superfamily domain

NA

IPR000998*MAM domain, IPR013320*Concanavalin A-like lectin/glucanase domain

IPR010987*Glutathione S-transferase, C-terminal-like, IPR004046*Glutathione S-transferase, C-termin

NA

IPR001314*Peptidase S1A, chymotrypsin family, IPR001254*Serine proteases, trypsin domain, IPR00

IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain

IPR025483*Lipase, eukaryotic, IPR029058*Alpha/Beta hydrolase fold, IPR006693*Partial AB-hydrolas

IPR029058*Alpha/Beta hydrolase fold, IPR001563*Peptidase S10, serine carboxypeptidase

NA

NA

IPR001304*C-type lectin-like, IPR016186*C-type lectin-like/link domain, IPR016187*C-type lectin fold

NA

IPR008963*Purple acid phosphatase-like, N-terminal, IPR029052*Metallo-dependent phosphatase-like

IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily

IPR001210*Ribosomal protein S17e

IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR001650*Helicase, C-terminal, IP

IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B

NA

IPR016635*Adaptor protein complex, sigma subunit, IPR011012*Longin-like domain, IPR022775*AP c

IPR015727*Protein kinase C mu-related, IPR020454*Diacylglycerol/phorbol-ester binding, IPR002219*

NA

IPR011989*Armadillo-like helical, IPR016024*Armadillo-type fold

NA

IPR017978*GPCR family 3, C-terminal

IPR002376*Formyl transferase, N-terminal, IPR005793*Formyl transferase, C-terminal

NA

IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR000048*IQ motif, EF-hand bindin

IPR008775*Phytanoyl-CoA dioxygenase

IPR023210*NADP-dependent oxidoreductase domain

NA

NA

IPR000276*G protein-coupled receptor, rhodopsin-like

IPR000949*ELM2 domain, IPR009057*Homeobox domain-like, IPR001005*SANT/Myb domain

IPR006202*Neurotransmitter-gated ion-channel ligand-binding domain, IPR006029*Neurotransmitter-g

NA

NA

NA

IPR001279*Metallo-beta-lactamase

IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I

IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain, IPR022271*Lipocalin, A

NA

IPR000073*Alpha/beta hydrolase fold-1, IPR029058*Alpha/Beta hydrolase fold

NA

IPR017287*Retinal rod rhodopsin-sensitive cGMP 3', 5'-cyclic phosphodiesterase, delta subunit, IPR00

IPR015889*Intradiol ring-cleavage dioxygenase, core

IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I

NA

NA

NA

IPR032675*Leucine-rich repeat domain, L domain-like

NA
NA
NA
NA
IPR000971*Globin, IPR002336*Erythrocruorin, IPR009050*Globin-like
IPR016181*Acyl-CoA N-acyltransferase, IPR000182*GNAT domain
IPR011527*ABC transporter type 1, transmembrane domain, IPR027417*P-loop containing nucleoside
IPR013783*Immunoglobulin-like fold, IPR007110*Immunoglobulin-like domain
IPR015943*WD40/YVTN repeat-like-containing domain
IPR020846*Major facilitator superfamily domain
NA
NA
NA
IPR009030*Growth factor receptor cysteine-rich domain, IPR026823*Complement Clr-like EGF domai
IPR000276*G protein-coupled receptor, rhodopsin-like, IPR000929*Dopamine receptor family
IPR002999*Tudor domain
NA
NA
NA
IPR011701*Major facilitator superfamily, IPR020846*Major facilitator superfamily domain
NA
IPR000058*Zinc finger, AN1-type, IPR029071*Ubiquitin-related domain, IPR000626*Ubiquitin domain,
IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR013594*Dynein heavy chain, do
IPR000408*Regulator of chromosome condensation, RCC1, IPR009091*Regulator of chromosome co
IPR002172*Low-density lipoprotein (LDL) receptor class A repeat
NA
IPR001766*Fork head domain, IPR011991*Winged helix-turn-helix DNA-binding domain
NA
NA
NA
IPR003961*Fibronectin type III, IPR003599*Immunoglobulin subtype, IPR003598*Immunoglobulin sub
IPR002557*Chitin binding domain
NA
IPR002890*Alpha-2-macroglobulin, N-terminal
NA
NA
IPR001828*Receptor, ligand binding region, IPR000337*GPCR, family 3, IPR017978*GPCR family 3,
IPR008949*Isoprenoid synthase domain
IPR018159*Spectrin/alpha-actinin, IPR002017*Spectrin repeat
NA
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
NA
NA
NA
IPR002557*Chitin binding domain
NA

IPR032675*Leucine-rich repeat domain, L domain-like, IPR000157*Toll/interleukin-1 receptor homolog
IPR001611*Leucine-rich repeat, IPR000276*G protein-coupled receptor, rhodopsin-like, IPR032675*Le
NA
IPR012599*Peptidase C1A, propeptide, IPR013128*Peptidase C1A, IPR000668*Peptidase C1A, papai
IPR020846*Major facilitator superfamily domain
IPR000873*AMP-dependent synthetase/ligase
IPR007855*RNA-dependent RNA polymerase, eukaryotic-type
NA
IPR033616*Protein KIAA1109
NA
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR008610*Eukaryotic rRNA processing
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
NA
IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR030247*Canalicular multispecific
IPR031926*Transmembrane protein 135, N-terminal domain, IPR026749*Transmembrane protein 135
IPR001356*Homeobox domain, IPR009057*Homeobox domain-like, IPR032392*SATB, ubiquitin-like o
IPR013087*Zinc finger C2H2-type
IPR013087*Zinc finger C2H2-type, IPR013083*Zinc finger, RING/FYVE/PHD-type
IPR001148*Alpha carbonic anhydrase, IPR023561*Carbonic anhydrase, alpha-class
IPR015919*Cadherin-like, IPR027397*Catenin binding domain, IPR002126*Cadherin
NA
IPR000949*ELM2 domain, IPR009057*Homeobox domain-like, IPR001005*SANT/Myb domain
IPR001507*Zona pellucida domain
NA
NA
IPR009071*High mobility group box domain, IPR024940*Transcription factor TCF/LEF, IPR027397*Ca
NA
NA
IPR003100*PAZ domain, IPR003165*Piwi domain, IPR012337*Ribonuclease H-like domain
IPR001254*Serine proteases, trypsin domain, IPR009003*Peptidase S1, PA clan, IPR001314*Peptidas
NA
IPR021643*Mediator complex, subunit Med13, N-terminal, metazoa/fungi, IPR009401*Mediator comple
IPR005821*Ion transport domain, IPR028823*Sodium leak channel non-selective protein
IPR001878*Zinc finger, CCHC-type, IPR004088*K Homology domain, type 1, IPR032570*Splicing fact
IPR020067*Frizzled domain, IPR011009*Protein kinase-like domain, IPR013806*Kringle-like fold, IPR
IPR006616*DM9 repeat, IPR024518*Domain of unknown function DUF3421
IPR023299*P-type ATPase, cytoplasmic domain N, IPR023214*HAD-like domain, IPR008250*P-type
IPR013320*Concanavalin A-like lectin/glucanase domain, IPR001791*Laminin G domain, IPR028875*
IPR033942*Inositol monophosphatase, IPR020552*Inositol monophosphatase, Lithium-sensitive, IPR0
NA
NA
IPR005121*Ferrodoxin-fold anticodon-binding domain, IPR004530*Phenylalanyl-tRNA synthetase, clas
IPR002919*Trypsin Inhibitor-like, cysteine rich domain
NA
IPR000760*Inositol monophosphatase-like
IPR003172*MD-2-related lipid-recognition domain, IPR028996*Ganglioside GM2 activator

IPR001107*Band 7 domain, IPR001972*Stomatin family
IPR001139*Glycoside hydrolase family 30
NA
NA
IPR000917*Sulfatase, N-terminal, IPR017850*Alkaline-phosphatase-like, core domain, IPR017849*Alk
IPR011701*Major facilitator superfamily, IPR020846*Major facilitator superfamily domain
IPR011993*PH domain-like, IPR000219*Dbl homology (DH) domain, IPR001478*PDZ domain, IPR001
NA
NA
IPR006621*Nose resistant-to-fluoxetine protein, N-terminal
IPR002018*Carboxylesterase, type B, IPR029058*Alpha/Beta hydrolase fold
IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR011330*Glycoside hydrolase/de
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR002076*ELO family
IPR005828*Major facilitator, sugar transporter-like, IPR020846*Major facilitator superfamily domain
IPR023271*Aquaporin-like, IPR000425*Major intrinsic protein
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR001506*Peptidase M12A, IPR024079*Metallopeptidase, catalytic domain
NA
NA
NA
IPR020683*Ankyrin repeat-containing domain
IPR001841*Zinc finger, RING-type, IPR027370*RING-type zinc-finger, LisH dimerisation motif, IPR013
IPR004045*Glutathione S-transferase, N-terminal, IPR004046*Glutathione S-transferase, C-terminal, I
NA
NA
IPR011705*BTB/Kelch-associated, IPR015915*Kelch-type beta propeller
IPR019133*Mitochondrial inner membrane protein Mitofilin
NA
NA
NA
IPR000010*Cystatin domain, IPR027214*Cystatin
IPR002293*Amino acid/polyamine transporter I, IPR029485*Cationic amino acid transporter, C-termina
IPR029071*Ubiquitin-related domain, IPR002219*Protein kinase C-like, phorbol ester/diacylglycerol-bi
NA
NA
IPR032675*Leucine-rich repeat domain, L domain-like
NA
IPR000536*Nuclear hormone receptor, ligand-binding domain
IPR029058*Alpha/Beta hydrolase fold, IPR025483*Lipase, eukaryotic, IPR006693*Partial AB-hydrolas
NA
IPR006598*Lipopolysaccharide-modifying protein
IPR008775*Phytanoyl-CoA dioxygenase
IPR010703*Dedicator of cytokinesis, C-terminal, IPR000008*C2 domain, IPR026791*Dedicator of cyto
IPR001508*Ionotropic glutamate receptor, metazoa, IPR001828*Receptor, ligand binding region, IPR0
IPR013099*Potassium channel domain, IPR003929*Potassium channel, BK, alpha subunit
IPR011705*BTB/Kelch-associated, IPR028764*Kelch repeat and BTB domain-containing protein 8, IP

NA
IPR003599*Immunoglobulin subtype, IPR032986*Roundabout homologue 1, IPR013098*Immunoglobu
IPR011009*Protein kinase-like domain, IPR020635*Tyrosine-protein kinase, catalytic domain, IPR0133
NA
IPR011598*Myc-type, basic helix-loop-helix (bHLH) domain, IPR003650*Orange domain
IPR024768*Meiosis regulator and mRNA stability factor 1, IPR021139*NYN domain, limkain-b1-type, I
IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR003593*AAA+ ATPase domain, I
IPR011990*Tetratricopeptide-like helical domain, IPR028833*Tetratricopeptide repeat protein 28, IPR0
NA
IPR001873*Epithelial sodium channel
IPR013783*Immunoglobulin-like fold, IPR003961*Fibronectin type III
IPR001214*SET domain
IPR014978*Glutamine-Leucine-Glutamine, QLQ
NA
NA
IPR014782*Peptidase M1, membrane alanine aminopeptidase, N-terminal, IPR024571*ERAP1-like C-
IPR001747*Lipid transport protein, N-terminal, IPR015819*Lipid transport protein, beta-sheet shell, IP
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
NA
IPR015255*Vitellinogen, open beta-sheet, IPR011030*Vitellinogen, superhelical, IPR015819*Lipid tran
NA
IPR014710*RmlC-like jelly roll fold, IPR006916*Popeye protein
NA
IPR006028*Gamma-aminobutyric acid A receptor/Glycine receptor alpha, IPR006201*Neurotransmitte
IPR000906*ZU5 domain, IPR008145*Guanylate kinase/L-type calcium channel beta subunit, IPR0274
IPR001766*Fork head domain, IPR011991*Winged helix-turn-helix DNA-binding domain
IPR015403*Sec7, C-terminal, IPR000904*Sec7 domain, IPR023394*Sec7 domain, alpha orthogonal b
IPR013083*Zinc finger, RING/FYVE/PHD-type
NA
IPR019143*JNK/Rab-associated protein-1, N-terminal
NA
NA
IPR007588*Zinc finger, FLYWCH-type
IPR002557*Chitin binding domain
IPR005062*SAC3/GANP/THP3
NA
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
NA
IPR001533*Transcriptional coactivator/pterin dehydratase
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR024687*MMS19, C-terminal, IPR011989*Armadillo-like helical, IPR016024*Armadillo-type fold
IPR025110*AMP-binding enzyme, C-terminal domain, IPR000873*AMP-dependent synthetase/ligase
NA
NA
IPR000313*PWWP domain, IPR001487*Bromodomain, IPR011011*Zinc finger, FYVE/PHD-type, IPR0
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I

IPR002557*Chitin binding domain

IPR001408*G-protein alpha subunit, group I, IPR011025*G protein alpha subunit, helical insertion, IPR

IPR011991*Winged helix-turn-helix DNA-binding domain, IPR003150*DNA-binding RFX-type winged-h

IPR019143*JNK/Rab-associated protein-1, N-terminal

NA

IPR008952*Tetraspanin, EC2 domain, IPR000301*Tetraspanin, IPR018499*Tetraspanin/Peripherin

NA

NA

IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like

IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase

NA

IPR016643*26S proteasome regulatory complex, non-ATPase subcomplex, Rpn1 subunit

IPR029060*PIN domain-like, IPR024768*Meiosis regulator and mRNA stability factor 1, IPR021139*NY

NA

IPR011701*Major facilitator superfamily, IPR020846*Major facilitator superfamily domain

IPR002403*Cytochrome P450, E-class, group IV, IPR001128*Cytochrome P450

NA

NA

NA

IPR024946*Arginine repressor C-terminal-like domain, IPR003594*Histidine kinase-like ATPase, C-ter

IPR013761*Sterile alpha motif/pointed domain, IPR001660*Sterile alpha motif domain

IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like

IPR001873*Epithelial sodium channel

NA

IPR013128*Peptidase C1A, IPR000668*Peptidase C1A, papain C-terminal

NA

IPR014186*S-formylglutathione hydrolase, IPR029058*Alpha/Beta hydrolase fold, IPR000801*Putative

IPR011011*Zinc finger, FYVE/PHD-type, IPR013083*Zinc finger, RING/FYVE/PHD-type

IPR002018*Carboxylesterase, type B, IPR029058*Alpha/Beta hydrolase fold

NA

NA

IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase

IPR024868*Four-jointed box protein 1/four-jointed protein

IPR011677*Domain of unknown function DUF1619, IPR010796*B9 domain

NA

IPR009003*Peptidase S1, PA clan, IPR001254*Serine proteases, trypsin domain, IPR001314*Peptidas

NA

NA

IPR031436*Transmembrane protein TMEM132, C-terminal, IPR026307*Transmembrane protein 132, I

IPR004245*Protein of unknown function DUF229, IPR017850*Alkaline-phosphatase-like, core domain,

IPR002919*Trypsin Inhibitor-like, cysteine rich domain

NA

IPR013087*Zinc finger C2H2-type, IPR027755*Transcription factor Ovo-like, IPR013083*Zinc finger, R

IPR015919*Cadherin-like, IPR002126*Cadherin

NA

IPR003609*PAN/Apple domain

IPR001356*Homeobox domain, IPR020479*Homeobox domain, metazoa, IPR000047*Helix-turn-helix

IPR000891*Pyruvate carboxyltransferase, IPR013785*Aldolase-type TIM barrel
NA
NA
IPR013087*Zinc finger C2H2-type
NA
NA
IPR000585*Hemopexin-like domain
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
NA
NA
NA
IPR020568*Ribosomal protein S5 domain 2-type fold, IPR002205*DNA topoisomerase, type IIA, subun
IPR011705*BTB/Kelch-associated, IPR011333*SKP1/BTB/POZ domain, IPR012983*PHR, IPR000210
IPR002657*Bile acid:sodium symporter/arsenical resistance protein Acr3, IPR004710*Bile acid:sodium
IPR002048*EF-hand domain, IPR011992*EF-hand domain pair
IPR000276*G protein-coupled receptor, rhodopsin-like, IPR000611*Neuropeptide Y receptor family
NA
NA
IPR006170*Pheromone/general odorant binding protein
NA
NA
NA
IPR007110*Immunoglobulin-like domain, IPR003961*Fibronectin type III, IPR033027*Down syndrome
IPR000195*Rab-GTPase-TBC domain, IPR033185*Rab GTPase-activating protein 1
NA
IPR013057*Amino acid transporter, transmembrane domain
IPR012674*Calycin, IPR022271*Lipocalin, ApoD type, IPR003057*Invertebrate colouration protein, IPR
IPR001223*Glycoside hydrolase family 18, catalytic domain, IPR017853*Glycoside hydrolase superfam
IPR012599*Peptidase C1A, propeptide, IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Pe
NA
NA
NA
IPR015943*WD40/YVTN repeat-like-containing domain
NA
NA
IPR023610*Phosphatidylinositol-4-phosphate 5-kinase, IPR002498*Phosphatidylinositol-4-phosphate 5
NA
NA
NA
IPR006571*TLDc domain
IPR002018*Carboxylesterase, type B, IPR029058*Alpha/Beta hydrolase fold
NA
IPR004104*Oxidoreductase, C-terminal, IPR000683*Oxidoreductase, N-terminal, IPR016040*NAD(P)-
NA
NA
IPR006621*Nose resistant-to-fluoxetine protein, N-terminal
NA

NA
NA
IPR001747*Lipid transport protein, N-terminal, IPR011030*Vitellinogen, superhelical, IPR001846*von
IPR006621*Nose resistant-to-fluoxetine protein, N-terminal
IPR001762*Disintegrin domain, IPR024079*Metallopeptidase, catalytic domain, IPR006586*ADAM, cy
IPR002076*ELO family
NA
NA
IPR026055*Fatty acyl-CoA reductase, IPR016040*NAD(P)-binding domain, IPR033640*Fatty acyl-Co
IPR012816*NADAR
IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR003593*AAA+ ATPase domain, I
IPR014782*Peptidase M1, membrane alanine aminopeptidase, N-terminal, IPR001930*Peptidase M1,
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR000834*Peptidase M14, carboxypeptidase A, IPR034223*Insect gut carboxypeptidase-like, carbox
NA
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR021715*Pre-mRNA splicing Prp18-interacting factor
IPR018491*SLC12A transporter, C-terminal, IPR002445*Solute carrier family 12 member 1, IPR00484
IPR013320*Concanavalin A-like lectin/glucanase domain
IPR001096*Peptidase C13, legumain
IPR000618*Insect cuticle protein
IPR001254*Serine proteases, trypsin domain, IPR009003*Peptidase S1, PA clan, IPR001314*Peptida
NA
NA
NA
IPR000536*Nuclear hormone receptor, ligand-binding domain
IPR024083*Fumarase/histidase, N-terminal, IPR004769*Adenylosuccinate lyase, IPR019468*Adenylos
IPR000182*GNAT domain, IPR016181*Acyl-CoA N-acyltransferase
NA
NA
IPR029064*50S ribosomal protein L30e-like, IPR000530*Ribosomal protein S12e, IPR004038*Ribosor
IPR018863*Fragile site-associated protein, C-terminal, IPR033616*Protein KIAA1109
IPR000618*Insect cuticle protein
IPR018490*Cyclic nucleotide-binding-like, IPR000595*Cyclic nucleotide-binding domain, IPR032406*C
IPR002509*NodB homology domain, IPR002172*Low-density lipoprotein (LDL) receptor class A repea
IPR011990*Tetratricopeptide-like helical domain, IPR003107*HAT (Half-A-TPR) repeat
IPR002893*Zinc finger, MYND-type
IPR008775*Phytanoyl-CoA dioxygenase
NA
NA
IPR000859*CUB domain
NA
NA
NA
IPR031984*Solute carrier family 3 member 2, N-terminal domain
IPR011701*Major facilitator superfamily, IPR020846*Major facilitator superfamily domain
IPR002394*Nicotinic acetylcholine receptor, IPR006202*Neurotransmitter-gated ion-channel ligand-bin

IPR016040*NAD(P)-binding domain, IPR006140*D-isomer specific 2-hydroxyacid dehydrogenase, NA

NA

NA

IPR001024*PLAT/LH2 domain

NA

IPR013201*Cathepsin propeptide inhibitor domain (I29), IPR000668*Peptidase C1A, papain C-termina

IPR011990*Tetratricopeptide-like helical domain

NA

NA

IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase, IPR007235*Glycosyl transferase, family 28, C

IPR015915*Kelch-type beta propeller, IPR000210*BTB/POZ domain, IPR011705*BTB/Kelch-associate

IPR011989*Armadillo-like helical, IPR016024*Armadillo-type fold

NA

NA

IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR011042*Six-bladed beta-propelle

IPR032675*Leucine-rich repeat domain, L domain-like

IPR012674*Calycin, IPR022271*Lipocalin, ApoD type, IPR000566*Lipocalin/cytosolic fatty-acid bindin

IPR017287*Retinal rod rhodopsin-sensitive cGMP 3', 5'-cyclic phosphodiesterase, delta subunit, IPR00

NA

IPR002018*Carboxylesterase, type B, IPR029058*Alpha/Beta hydrolase fold

IPR014854*Non-structural maintenance of chromosome element 4, C-terminal, IPR027786*Nse4/EID f

NA

NA

IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B, IPR000997*Cholinestera

IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B

IPR032675*Leucine-rich repeat domain, L domain-like, IPR000483*Cysteine-rich flanking region, C-ter

NA

IPR000618*Insect cuticle protein

IPR011598*Myc-type, basic helix-loop-helix (bHLH) domain, IPR000014*PAS domain, IPR013767*PA

NA

NA

IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B

IPR006214*Bax inhibitor 1-related

NA

IPR029062*Class I glutamine amidotransferase-like, IPR005320*Peptidase S51

NA

NA

IPR011991*Winged helix-turn-helix DNA-binding domain, IPR016158*Cullin homology, IPR019559*Cu

IPR007249*Dopey, N-terminal, IPR011989*Armadillo-like helical

IPR018482*Zinc finger, C4H2-type

IPR001139*Glycoside hydrolase family 30, IPR033452*Glycosyl hydrolase family 30, beta sandwich d

IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily

IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like

NA

IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I

NA

IPR019523*Protein phosphatase 1, regulatory subunit 15A/B, C-terminal

IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR032104*Spaetzle, IPR029034*Cystine-knot cytokine
IPR032675*Leucine-rich repeat domain, L domain-like
IPR001496*SOCS box domain
IPR034016*Aminopeptidase N-type, IPR014782*Peptidase M1, membrane alanine aminopeptidase, N-
NA
IPR000618*Insect cuticle protein
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
NA
IPR004046*Glutathione S-transferase, C-terminal, IPR004045*Glutathione S-transferase, N-terminal, I
NA
NA
IPR000618*Insect cuticle protein
IPR016040*NAD(P)-binding domain, IPR011032*GroES-like, IPR013149*Alcohol dehydrogenase, C-te
IPR029060*PIN domain-like, IPR021139*NYN domain, limkain-b1-type, IPR000504*RNA recognition m
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
NA
NA
IPR012599*Peptidase C1A, propeptide, IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Pe
IPR000618*Insect cuticle protein
IPR008993*Tissue inhibitor of metalloproteinases-like, OB-fold, IPR004850*NtA (N-terminal agrin) dom
NA
NA
NA
NA
NA
IPR009357*Solute carrier family 52, riboflavin transporter
IPR008914*Phosphatidylethanolamine-binding protein
NA
IPR011333*SKP1/BTB/POZ domain, IPR011705*BTB/Kelch-associated
IPR011705*BTB/Kelch-associated, IPR011333*SKP1/BTB/POZ domain
NA
NA
NA
NA
IPR011333*SKP1/BTB/POZ domain, IPR011705*BTB/Kelch-associated, IPR028764*Kelch repeat and
NA
NA
NA
IPR000996*Clathrin light chain, IPR029058*Alpha/Beta hydrolase fold, IPR006693*Partial AB-hydrolas
NA
NA
IPR001054*Adenylyl cyclase class-3/4/guanylyl cyclase, IPR029787*Nucleotide cyclase
NA
IPR003609*PAN/Apple domain, IPR001507*Zona pellucida domain

IPR001254*Serine proteases, trypsin domain, IPR001314*Peptidase S1A, chymotrypsin family, IPR00
IPR028764*Kelch repeat and BTB domain-containing protein 8, IPR011333*SKP1/BTB/POZ domain, I
NA
IPR000536*Nuclear hormone receptor, ligand-binding domain
IPR001357*BRCT domain
IPR012445*Autophagy-related protein 101
IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR032054*DNA replication factor Cdt1, C-terminal
IPR008914*Phosphatidylethanolamine-binding protein
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR000210*BTB/POZ domain, IPR011333*SKP1/BTB/POZ domain
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
NA
NA
IPR014105*Carotenoid/retinoid oxidoreductase, IPR023753*FAD/NAD(P)-binding domain, IPR002937
IPR011333*SKP1/BTB/POZ domain, IPR000210*BTB/POZ domain, IPR028764*Kelch repeat and BTB
IPR013830*SGNH hydrolase-type esterase domain
IPR000618*Insect cuticle protein
IPR006568*PSP, proline-rich, IPR007180*Domain of unknown function DUF382
IPR011030*Vitellinogen, superhelical, IPR001747*Lipid transport protein, N-terminal, IPR015817*Vitelli
NA
NA
NA
IPR013657*UAA transporter
IPR008753*Peptidase M13, N-terminal domain, IPR000718*Peptidase M13, IPR029736*Endothelin-co
NA
IPR001623*DnaJ domain
IPR012916*RED-like, N-terminal
IPR024135*Ragulator complex protein LAMTOR5
IPR002861*Reeler domain
NA
IPR011705*BTB/Kelch-associated, IPR028764*Kelch repeat and BTB domain-containing protein 8
NA
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
NA
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
IPR012674*Calycin
NA
IPR011705*BTB/Kelch-associated
NA
NA
IPR012674*Calycin
NA
IPR029063*S-adenosyl-L-methionine-dependent methyltransferase, IPR013216*Methyltransferase typ
IPR011598*Myc-type, basic helix-loop-helix (bHLH) domain, IPR000014*PAS domain

NA
IPR016040*NAD(P)-binding domain, IPR020631*Tetrahydrofolate dehydrogenase/cyclohydrolase, NAI
IPR001370*BIR repeat, IPR006568*PSP, proline-rich, IPR007180*Domain of unknown function DUF38
NA
IPR032675*Leucine-rich repeat domain, L domain-like
NA
IPR000618*Insect cuticle protein
NA
IPR014756*Immunoglobulin E-set
IPR031152*Plexin domain-containing protein
NA
IPR011333*SKP1/BTB/POZ domain, IPR011705*BTB/Kelch-associated
IPR001254*Serine proteases, trypsin domain, IPR001314*Peptidase S1A, chymotrypsin family, IPR00
IPR013128*Peptidase C1A, IPR000668*Peptidase C1A, papain C-terminal, IPR012599*Peptidase C1
NA
NA
NA
NA
NA
NA
NA
IPR007235*Glycosyl transferase, family 28, C-terminal
NA
NA
NA
IPR013128*Peptidase C1A, IPR012599*Peptidase C1A, propeptide, IPR000668*Peptidase C1A, papa
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR001128*Cytochrome P450
NA
IPR025602*BCP1 family
IPR000536*Nuclear hormone receptor, ligand-binding domain
IPR008854*TPMT family, IPR025835*Thiopurine S-methyltransferase, IPR029063*S-adenosyl-L-methi
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
NA
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR011598*Myc-type, basic helix-loop-helix (bHLH) domain, IPR015943*WD40/YVTN repeat-like-conta
NA
IPR028996*Ganglioside GM2 activator
NA
IPR000210*BTB/POZ domain, IPR011333*SKP1/BTB/POZ domain
IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A, IPR012599*Peptidase C1
NA
IPR029060*PIN domain-like
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat
NA
IPR021139*NYN domain, limkain-b1-type, IPR029060*PIN domain-like

NA
IPR011705*BTB/Kelch-associated
NA
NA
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
IPR011545*DEAD/DEAH box helicase domain, IPR014001*Helicase superfamily 1/2, ATP-binding dom
IPR000618*Insect cuticle protein
IPR023210*NADP-dependent oxidoreductase domain, IPR020471*Aldo/keto reductase
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR000536*Nuclear hormone receptor, ligand-binding domain
IPR000536*Nuclear hormone receptor, ligand-binding domain
NA
NA
IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat
IPR001442*Collagen IV, non-collagenous, IPR016187*C-type lectin fold
IPR006073*GTP binding domain, IPR023179*GTP-binding protein, orthogonal bundle domain, IPR014
NA
NA
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR012674*Calycin, IPR002345*Lipocalin, IPR003057*Invertebrate colouration protein, IPR022271*Lip
IPR024768*Meiosis regulator and mRNA stability factor 1
IPR000782*FAS1 domain
IPR028996*Ganglioside GM2 activator
NA
NA
IPR028996*Ganglioside GM2 activator
IPR028996*Ganglioside GM2 activator

e-rich repeat, cysteine-containing subtype

olase fold

rminal

n

ropeller, TolB-like

n

034113*Golgi-associated plant pathogenesis-related protein 1, SCP domain

ansferase

n

e, insert domain, IPR023797*RNA 3'-terminal phosphate cyclase domain, IPR000228*RNA 3'-termina

d

n

ydrolase fold

BTB/POZ domain, IPR011333*SKP1/BTB/POZ domain, IPR011042*Six-bladed beta-propeller, TolB-li

B domain-containing protein 8, IPR011705*BTB/Kelch-associated

n

-terminal

ansferase

P-loop containing nucleoside triphosphate hydrolase

PR007235*Glycosyl transferase, family 28, C-terminal

Tetracycline resistance protein TetA/multidrug resistance protein MdtG

'R002213*UDP-glucuronosyl/UDP-glucosyltransferase

ansferase, IPR006326*UDP-glycosyltransferase, MGT

er, IPR011333*SKP1/BTB/POZ domain

crystallin/Hsp20 domain, IPR031107*Small heat shock protein HSP20 thione S-transferase, C-terminal, IPR010987*Glutathione S-transferase, C-terminal-like

ystallin/Heat shock protein, IPR002068*Alpha crystallin/Hsp20 domain

ansferase

7*Mitochondrial carrier protein

IPR001680*WD40 repeat

11032*GroES-like, IPR016040*NAD(P)-binding domain

, C-terminal

9003*Peptidase S1, PA clan

ansferase, IPR006326*UDP-glycosyltransferase, MGT

netallopeptidase

er, TolB-like, IPR000033*LDLR class B repeat

ose-binding domain-like

se

R008927*6-phosphogluconate dehydrogenase C-terminal domain-like, IPR013328*6-phosphoglucon

egrin alpha beta-propellor, IPR000413*Integrin alpha chain

9003*Peptidase S1, PA clan

3*Zinc finger, RING/FYVE/PHD-type

PR010987*Glutathione S-transferase, C-terminal-like, IPR012336*Thioredoxin-like fold

eptidase C1A

se S1A, chymotrypsin family

Tubulin/FtsZ, C-terminal, IPR018316*Tubulin/FtsZ, 2-layer sandwich domain

e, IPR001611*Leucine-rich repeat

dwich domain, IPR002453*Beta tubulin, IPR008280*Tubulin/FtsZ, C-terminal

A, propeptide

R003593*AAA+ ATPase domain, IPR011527*ABC transporter type 1, transmembrane domain

yric acid A receptor/Glycine receptor alpha, IPR006029*Neurotransmitter-gated ion-channel transme

rolase, IPR011697*Peptidase C26

genase C-terminal domain-like, IPR006108*3-hydroxyacyl-CoA dehydrogenase, C-terminal, IPR006

, C-terminal

e 11
monooxygenase FMO

ein 6

er, TolB-like, IPR000033*LDLR class B repeat
C-terminal

heat shock protein HSP20, IPR002068*Alpha crystallin/Hsp20 domain

amily

e

010541*Domain of unknown function DUF1115

ase
ase, IPR029426*FAM86

epeat

ɔeta/alpha-barrel domain

ke, IPR012336*Thioredoxin-like fold, IPR004046*Glutathione S-transferase, C-terminal

978*HSP20-like chaperone, IPR002068*Alpha crystallin/Hsp20 domain

le hydrolase superfamily

ial, IPR012336*Thioredoxin-like fold

PR012336*Thioredoxin-like fold, IPR010987*Glutathione S-transferase, C-terminal-like

PR022271*Lipocalin, ApoD type, IPR003057*Invertebrate colouration protein ugar transferases, IPR028325*Voltage-gated potassium channel, IPR011333*SKP1/BTB/POZ doma

›n, IPR005511*Senescence marker protein-30 (SMP-30)

)52*Metallo-dependent phosphatase-like, IPR004843*Calcineurin-like phosphoesterase domain, Apa

pendent dioxygenase alkB homologue 7

24950*Dual specificity phosphatase, IPR000340*Dual specificity phosphatase, catalytic domain, IPR

ıin C-terminal

9003*Peptidase S1, PA clan

bulin/FtsZ, GTPase domain, IPR018316*Tubulin/FtsZ, 2-layer sandwich domain

ıreninase, IPR015424*Pyridoxal phosphate-dependent transferase, IPR015422*Pyridoxal phosphate

l*Rhabdovirus nucleocapsid, C-terminal

11*Catalase, mono-functional, haem-containing, clades 1 and 3, IPR010582*Catalase immune-respo

ıl-binding domain, IPR020454*Diacylglycerol/phorbol-ester binding

ː023346*Lysozyme-like domain

e, IPR001611*Leucine-rich repeat

-terminal

lycosyl hydrolase family 30, beta sandwich domain, IPR033453*Glycosyl hydrolase family 30, TIM-

heat shock protein HSP20, IPR002068*Alpha crystallin/Hsp20 domain

ke, IPR012336*Thioredoxin-like fold, IPR004045*Glutathione S-transferase, N-terminal

ane domain, IPR030247*Canalicular multispecific organic anion transporter 1, IPR003593*AAA+ AT

9003*Peptidase S1, PA clan

), IPR013128*Peptidase C1A

one H2A, C-terminal domain

pha/beta hydrolase fold-1

methyltransferase

t shock protein HSP20, IPR001436*Alpha crystallin/Heat shock protein

rminal, IPR000172*Glucose-methanol-choline oxidoreductase, N-terminal

doxin-like fold

density lipoprotein (LDL) receptor class A repeat

IPR012674*Calycin, IPR022271*Lipocalin, ApoD type

osphate hydrolase, IPR005225*Small GTP-binding protein domain

nucleoside triphosphate hydrolase, IPR003439*ABC transporter-like

97*NUDIX hydrolase domain-like

dor domain

ucleoside triphosphate hydrolase, IPR013525*ABC-2 type transporter
genase, N-terminal, IPR016040*NAD(P)-binding domain

lutathione S-transferase, C-terminal, IPR004045*Glutathione S-transferase, N-terminal

2, IPR016274*Histidine acid phosphatase, eukaryotic
ain

nal, IPR012336*Thioredoxin-like fold, IPR004045*Glutathione S-transferase, N-terminal

9003*Peptidase S1, PA clan

e lipase domain

e, IPR025733*Iron/zinc purple acid phosphatase-like C-terminal domain, IPR015914*Purple acid pho

R011545*DEAD/DEAH box helicase domain, IPR014001*Helicase superfamily 1/2, ATP-binding dor

complex, mu/sigma subunit

*Protein kinase C-like, phorbol ester/diacylglycerol-binding domain

g site

gated ion-channel transmembrane domain, IPR006028*Gamma-aminobutyric acid A receptor/Glycine

poD type

08015*GMP phosphodiesterase, delta subunit, IPR014756*Immunoglobulin E-set triphosphate hydrolase, IPR003593*AAA+ ATPase domain, IPR003439*ABC transporter-like

n, IPR001881*EGF-like calcium-binding domain, IPR000742*EGF-like domain

IPR019956*Ubiquitin

nain-1, IPR003593*AAA+ ATPase domain, IPR004273*Dynein heavy chain domain, IPR024317*Dyr

ndensation 1/beta-lactamase-inhibitor protein II

type 2, IPR013783*Immunoglobulin-like fold, IPR013106*Immunoglobulin V-set domain, IPR007110

C-terminal, IPR028082*Periplasmic binding protein-like I y (TIR) domain, IPR001611*Leucine-rich repeat

eucine-rich repeat domain, L domain-like, IPR002131*Glycoprotein hormone receptor family, IPR034

in C-terminal

organic anion transporter 1, IPR003439*ABC transporter-like, IPR011527*ABC transporter type 1, tr

ligomerisation domain

tenin binding domain

se S1A, chymotrypsin family

ex, subunit Med13

or 1, helix-hairpin domain, IPR004087*K Homology domain, IPR031150*BBP/SF1 family

001245*Serine-threonine/tyrosine-protein kinase, catalytic domain, IPR000001*Kringle, IPR020635*

ATPase, A domain, IPR032630*P-type ATPase, C-terminal, IPR001757*P-type ATPase, IPR006539

Contactin-associated protein-like 4, IPR000742*EGF-like domain

00760*Inositol monophosphatase-like

ss IIc, mitochondrial, IPR002319*Phenylalanyl-tRNA synthetase kaline phosphatase-like, alpha/beta/alpha

1849*Pleckstrin homology domain

acetylase, beta/alpha-barrel, IPR002509*NodB homology domain, IPR002557*Chitin binding domair

3083*Zinc finger, RING/FYVE/PHD-type

PR010987*Glutathione S-transferase, C-terminal-like, IPR012336*Thioredoxin-like fold

al

nding domain, IPR017438*Inorganic polyphosphate/ATP-NAD kinase, domain 1, IPR000756*Diacylg

e lipase domain

kinesis, IPR011989*Armadillo-like helical, IPR027007*DHR-1 domain

19594*Ionotropic glutamate receptor, L-glutamate and glycine-binding domain, IPR001320*Ionotropi

R011333*SKP1/BTB/POZ domain

ulin I-set, IPR013783*Immunoglobulin-like fold, IPR003598*Immunoglobulin subtype 2, IPR007110*I

320*Concanavalin A-like lectin/glucanase domain, IPR001245*Serine-threonine/tyrosine-protein kina

PR029060*PIN domain-like

PR003439*ABC transporter-like

)19734*Tetratricopeptide repeat

terminal domain, IPR001930*Peptidase M1, alanine aminopeptidase/leukotriene A4 hydrolase, IPR0

R015816*Vitellinogen, beta-sheet N-terminal

ısport protein, beta-sheet shell, IPR001747*Lipid transport protein, N-terminal, IPR015817*Vitellinoge

r-gated ion-channel, IPR006202*Neurotransmitter-gated ion-channel ligand-binding domain, IPR006

17*P-loop containing nucleoside triphosphate hydrolase, IPR011511*Variant SH3 domain, IPR00147

undle

)13083*Zinc finger, RING/FYVE/PHD-type, IPR001965*Zinc finger, PHD-type

R001019*Guanine nucleotide binding protein (G-protein), alpha subunit, IPR027417*P-loop containing

helix domain

YN domain, limkain-b1-type

minal domain, IPR002205*DNA topoisomerase, type IIA, subunit A/C-terminal, IPR034157*DNA topo

e esterase

se S1A, chymotrypsin family

IPR031437*Transmembrane protein family 132, middle domain

, IPR017849*Alkaline phosphatase-like, alpha/beta/alpha

RING/FYVE/PHD-type, IPR027775*C2H2- zinc finger protein family subset

motif, IPR009057*Homeobox domain-like

ıit A/C-terminal, IPR003594*Histidine kinase-like ATPase, C-terminal domain, IPR013758*DNA topoi

)*BTB/POZ domain

ı symporter, IPR030203*Solute carrier family 10 member 6

cell adhesion molecule, IPR013783*Immunoglobulin-like fold, IPR013098*Immunoglobulin I-set, IPR

R000566*Lipocalin/cytosolic fatty-acid binding domain

nily, IPR011583*Chitinase II, IPR029070*Chitinase insertion domain

eptidase C1A

5-kinase, core, IPR027483*Phosphatidylinositol-4-phosphate 5-kinase, C-terminal, IPR027484*Phos

-binding domain

Villebrand factor, type D domain, IPR015819*Lipid transport protein, beta-sheet shell, IPR015255*Vi

steine-rich, IPR001590*Peptidase M12B, ADAM/reprolysin

\ reductase, C-terminal, IPR013120*Male sterility, NAD-binding

PR011527*ABC transporter type 1, transmembrane domain, IPR003439*ABC transporter-like

alanine aminopeptidase/leukotriene A4 hydrolase, IPR024571*ERAP1-like C-terminal domain, IPR0

ypeptidase domain

1*Amino acid permease/ SLC12A domain, IPR013612*Amino acid permease, N-terminal, IPR00484

se S1A, chymotrypsin family

succinate lyase C-terminal, IPR008948*L-Aspartase-like, IPR000362*Fumarate lyase family, IPR022

mal protein L7Ae/L30e/S12e/Gadd45

Cyclic nucleotide-gated channel, C-terminal leucine zipper domain, IPR005821*Ion transport domain,

t, IPR002557*Chitin binding domain, IPR011330*Glycoside hydrolase/deacetylase, beta/alpha-barre

nding domain, IPR006201*Neurotransmitter-gated ion-channel, IPR006029*Neurotransmitter-gated ic

D-binding domain

l, IPR013128*Peptidase C1A

-terminal

ed, IPR011333*SKP1/BTB/POZ domain

er, TolB-like

g domain

08015*GMP phosphodiesterase, delta subunit, IPR014756*Immunoglobulin E-set

family

ase

rminal, IPR001611*Leucine-rich repeat, IPR003591*Leucine-rich repeat, typical subtype

S fold, IPR013655*PAS fold-3

llin protein, neddylation domain, IPR001373*Cullin, N-terminal, IPR016159*Cullin repeat-like-contain

omain, IPR017853*Glycoside hydrolase superfamily, IPR033453*Glycosyl hydrolase family 30, TIM-

-terminal, IPR001930*Peptidase M1, alanine aminopeptidase/leukotriene A4 hydrolase

PR012336*Thioredoxin-like fold, IPR010987*Glutathione S-transferase, C-terminal-like

erminal, IPR013154*Alcohol dehydrogenase, N-terminal, IPR020843*Polyketide synthase, enoylredu
notif domain, IPR024768*Meiosis regulator and mRNA stability factor 1

eptidase C1A

nain, IPR002350*Kazal domain

BTB domain-containing protein 8

se lipase domain

9003*Peptidase S1, PA clan

PR011705*BTB/Kelch-associated

*Amine oxidase

3 domain-containing protein 8, IPR011705*BTB/Kelch-associated

linogen, open beta-sheet, subdomain 1

onverting enzyme-like 1

e 11

D(P)-binding domain, IPR000672*Tetrahydrofolate dehydrogenase/cyclohydrolase

32

9003*Peptidase S1, PA clan

A, propeptide

in C-terminal

ionine-dependent methyltransferase

aining domain

A, propeptide

nain, IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR001650*Helicase, C-term

813*Guanine nucleotide-binding protein-like 3, N-terminal domain, IPR027417*P-loop containing nuc

ocalin, ApoD type, IPR000566*Lipocalin/cytosolic fatty-acid binding domain

al phosphate cyclase, IPR013792*RNA 3'-terminal phosphate cyclase/enolpyruvate transferase, alph

ike

nate dehydrogenase, domain 2, IPR006108*3-hydroxyacyl-CoA dehydrogenase, C-terminal embrane domain, IPR006201*Neurotransmitter-gated ion-channel

176*3-hydroxyacyl-CoA dehydrogenase, NAD binding, IPR016040*NAD(P)-binding domain

ıin, IPR000772*Ricin B, lectin domain, IPR003972*Potassium channel, voltage dependent, Kv1

ıaH type

{020422*Dual specificity protein phosphatase domain

ɛ-dependent transferase, subdomain 2, IPR000192*Aminotransferase class V domain

ɔnsive domain, IPR020835*Catalase-like domain barrel domain

Pase domain, IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR003439*ABC trar

sphatase, N-terminal, IPR003961*Fibronectin type III, IPR004843*Calcineurin-like phosphoesterase

nain

e receptor alpha, IPR006201*Neurotransmitter-gated ion-channel nein heavy chain, AAA module D4, IPR013602*Dynein heavy chain, domain-2, IPR026983*Dynein h

*Immunoglobulin-like domain, IPR002602*Domain of unknown function DB, IPR013098*Immunoglob

298*TSH/LHCG/FSH receptor, IPR002272*Follicle stimulating hormone receptor

ransmembrane domain, IPR003593*AAA+ ATPase domain

Tyrosine-protein kinase, catalytic domain

*P-type ATPase, subfamily IV, IPR023298*P-type ATPase, transmembrane domain, IPR032631*Pı

ɡlycerol kinase, accessory domain, IPR016064*NAD kinase/diacylglycerol kinase-like domain, IPR02

ic glutamate receptor, IPR028082*Periplasmic binding protein-like I mmunoglobulin-like domain

ıse, catalytic domain, IPR008979*Galactose-binding domain-like

)34016*Aminopeptidase N-type

en, open beta-sheet, subdomain 1, IPR009454*Lipid transport, open beta-sheet, IPR015816*Vitellinc

ׅ029*Neurotransmitter-gated ion-channel transmembrane domain, IPR015680*Glutamate-Gated Chlc

'78*PDZ domain, IPR001452*SH3 domain

g nucleoside triphosphate hydrolase

oisomerase 2, TOPRIM domain, IPR020568*Ribosomal protein S5 domain 2-type fold, IPR013757*T isomerase, type IIA, subunit A/ C-terminal, alpha-beta, IPR034157*DNA topoisomerase 2, TOPRIM

R003599*Immunoglobulin subtype, IPR003598*Immunoglobulin subtype 2

sphatidylinositol-4-phosphate 5-kinase, N-terminal domain itellinogen, open beta-sheet, IPR015816*Vitellinogen, beta-sheet N-terminal

)34016*Aminopeptidase N-type

2*SLC12A transporter family

2761*Fumarate lyase, N-terminal

IPR014710*RmlC-like jelly roll fold
el

on-channel transmembrane domain

ning domain

barrel domain

uctase domain

inal

cleoside triphosphate hydrolase

ıa/beta

nsporter-like

domain, ApaH type

eavy chain, IPR011704*ATPase, dynein-related, AAA domain, IPR035706*Dynein heavy chain, ATF

ulin I-set

-type ATPase, N-terminal

20454*Diacylglycerol/phorbol-ester binding, IPR001206*Diacylglycerol kinase, catalytic domain, IPR0 ogen, beta-sheet N-terminal, IPR001846*von Willebrand factor, type D domain

oride Channel

Type IIA DNA topoisomerase subunit A, alpha-helical domain, IPR013506*DNA topoisomerase, type domain, IPR001241*DNA topoisomerase, type IIA, IPR024946*Arginine repressor C-terminal-like do

-binding dynein motor region D5, IPR024743*Dynein heavy chain, coiled coil stalk, IPR035699*Dyn

00159*Ras-associating (RA) domain

IIA, subunit B, domain 2, IPR031660*C-terminal associated domain of TOPRIM, IPR001241*DNA to omain, IPR014721*Ribosomal protein S5 domain 2-type fold, subgroup, IPR001154*DNA topoisomer

ein heavy chain, hydrolytic ATP-binding dynein motor region D1

poisomerase, type IIA, IPR014721*Ribosomal protein S5 domain 2-type fold, subgroup, IPR013758 rase II, eukaryotic-type, IPR013759*DNA topoisomerase, type IIA, central domain, IPR006171*TOPF

*DNA topoisomerase, type IIA, subunit A/ C-terminal, alpha-beta, IPR013759*DNA topoisomerase, ty

RIM domain, IPR013506*DNA topoisomerase, type IIA, subunit B, domain 2, IPR031660*C-terminal

ype IIA, central domain, IPR006171*TOPRIM domain, IPR013760*DNA topoisomerase, type IIA-like associated domain of TOPRIM, IPR013760*DNA topoisomerase, type IIA-like domain, IPR013757*T

e domain, IPR001154*DNA topoisomerase II, eukaryotic-type

Type IIA DNA topoisomerase subunit A, alpha-helical domain

Table S6

Gene ID	$\log_2$FC
tetur03g05070	9.7352501
tetur03g04990	9.2945918
tetur04g09459	8.1995731
tetur04g09479	7.4626854
tetur01g13120	6.6360221
tetur02g14741	6.5624681
tetur03g00970	6.2538698
tetur05g05060	6.1058949
tetur28g92005	6.0753214
tetur04g00770	5.9690992
tetur03g05110	5.9351063
tetur03g05100	5.9213247
tetur03g00830	5.8942479
tetur14g03970	5.7457934
tetur07g02420	5.6812392
tetur13g04550	5.6790329
tetur05g05050	5.5500315
tetur15g01810	5.5140223
tetur01g12400	5.4342848
tetur31g02020	5.4148779
tetur10g02890	5.3259386
tetur11g05770	5.2814578
tetur14g01700	5.0998646
tetur47g00220	5.0973406
tetur651g00010	5.0623174
tetur05g06440	5.0194263
tetur43g00580	5.0181531
tetur20g00010	4.9887479
tetur05g06470	4.8715354
tetur01g16463	4.7455325
tetur13g04170	4.6918834
tetur04g90885	4.6341694
tetur27g00220	4.5621834
tetur283g00010	4.5506963
tetur07g01450	4.5211802
tetur09g92915	4.4939822
tetur03g09040	4.4680277
tetur02g09200	4.4577456
tetur21g00340	4.4306877
tetur24g00770	4.3774088
tetur24g00680	4.3588574
tetur02g11020	4.2927779
tetur09g03740	4.2231467
tetur12g00590	4.2049612

tetur28g92008	4.135133
tetur12g00580	4.1146213
tetur21g01410	4.1046735
tetur28g00660	4.0706883
tetur19g00350	4.0612004
tetur34g00160	4.0176883
tetur02g14731	3.9816121
tetur02g03040	3.9796251
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tetur47g00090	3.8002677
tetur56g90039	3.7456607
tetur02g14330	3.734248
tetur06g04920	3.7287465
tetur28g00670	3.6911622
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tetur16g02710	3.6197439
tetur40g00030	3.6132475
tetur02g05670	3.5521773
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tetur06g04520	3.5083012
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tetur05g02470	3.4664664
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tetur10g02870	3.4209618
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tetur02g09830	3.3825029
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tetur14g02050	3.3161412
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tetur24g00200	3.3060877
tetur06g04530	3.2774976
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tetur14g03760	3.2637212
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tetur11g05740	3.1919959
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tetur12g00570	3.1621394
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tetur17g03530	3.1319616
tetur540g00010	3.1231561

tetur05g06430	3.1107739
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tetur128g00020	3.0425075
tetur06g04550	3.0242129
tetur03g10063	3.0242019
tetur06g01100	3.0098403
tetur08g05010	3.002773
tetur07g02290	2.9453276
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tetur03g02710	2.9388034
tetur06g05060	2.9016382
tetur24g00820	2.8671657
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tetur23g00880	2.8500884
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tetur07g06390	2.8379565
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tetur10g04020	2.7487203
tetur29g00940	2.7341678
tetur06g01310	2.7063736
tetur24g00670	2.7002069
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tetur07g02250	2.6773728
tetur01g01520	2.6602707
tetur01g11780	2.6419566
tetur34g00170	2.6269636
tetur67g00010	2.621252
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tetur02g14280	2.5953172
tetur12g00600	2.5874896
tetur37g00580	2.5861969
tetur24g00690	2.5598774
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tetur07g02390	2.5516423
tetur12g03950	2.540992
tetur106g00050	2.5332562
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tetur05g04170	2.4827609
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tetur26g01510	2.4208899

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tetur03g05030	2.3810149
tetur28g01360	2.3793754
tetur03g10103	2.3527032
tetur28g01750	2.2889734
tetur01g08280	2.287592
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tetur16g03190	2.2837042
tetur03g00780	2.2663261
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tetur02g09850	2.2512811
tetur24g00780	2.246403
tetur03g05000	2.2417016
tetur06g03100	2.2330765
tetur13g04350	2.2288527
tetur03g91623	2.1631154
tetur02g09600	2.1520259
tetur188g00040	2.1498598
tetur02g14400	2.1426497
tetur24g00220	2.1227341
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tetur26g01450	2.0879238
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tetur28g00580	2.0464913
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tetur06g02050	2.029681
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tetur28g02510	2.0161688
tetur17g03400	2.0042347
tetur27g02598	2.0039695
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tetur05g02210	1.9910049
tetur208g00020	1.9771261
tetur90g00030	1.9618463
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tetur12g01260	1.6588912
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tetur12g00610	1.6380037
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tetur01g14350	1.623431
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tetur02g00800	1.5718443
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tetur04g06770	1.5607439
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tetur05g06360	1.5404943
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tetur03g00130	1.5160972
tetur01g11980	1.5124951
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tetur15g01820	1.4680298
tetur13g02160	1.4659934
tetur04g09150	1.4636346
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tetur11g04470	1.4358819
tetur04g06160	1.4259685
tetur08g05780	1.4209205
tetur254g00010	1.4120211
tetur08g06030	1.4096678
tetur18g00150	1.4093929

tetur16g03420	1.3951409
tetur01g05480	1.392366
tetur17g92134	1.3918746
tetur11g02080	1.3859513
tetur28g01730	1.3858367
tetur03g07310	1.3794307
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tetur12g04600	1.372167
tetur28g00020	1.3706041
tetur10g04770	1.3680864
tetur10g02410	1.3654364
tetur01g05730	1.3616771
tetur11g01190	1.3612393
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tetur06g04900	1.3586708
tetur02g13050	1.3524474
tetur21g01420	1.3495237
tetur19g01700	1.3473422
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tetur21g03020	1.3447563
tetur10g04780	1.3428485
tetur30g00090	1.3387318
tetur21g02400	1.336165
tetur09g00550	1.335763
tetur30g01110	1.3342934
tetur26g01500	1.3273991
tetur35g00190	1.3210164
tetur06g01080	1.313125
tetur01g06610	1.310908
tetur22g02010	1.3047662
tetur13g03510	1.3025494
tetur507g00010	1.2969167
tetur08g02010	1.2944398
tetur03g05010	1.2903317
tetur06g01700	1.2894737
tetur06g02910	1.282909
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tetur02g07030	1.2730662
tetur27g01020	1.2696155
tetur01g08260	1.2691603
tetur02g10970	1.2673007
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tetur11g00880	-5.75693
tetur07g91894	-6.146087
tetur36g91078	-6.273955
tetur11g90924	-7.785506

- Differentially expressed genes (DEGs) and significantly over/underexpressed genes between three re

	Multiple-factors model ar
description	P.Value
CYP392D8 Cytochrome P450 - CYP392D8	7.34E-07
CYP392D2 Cytochrome P450 - CYP392D2	7.61E-06
SSPF2 Small Secreted Protein; Family F hypothetical protein	2.53E-08
SSPF3 Small Secreted Protein; Family F hypothetical protein	0.005659
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	2.21E-05
BTB/Kelch-associated	0.0001923
CYP392A11 Cytochrome P450 - CYP392A11 CYP392A11v2 Cytochrome P450 - CYP39	6.02E-10
UGT UDP-glycosyltransferase; teturUGT29 UGT UDP-glycosyltransferase Glycosyltrans	2.63E-08
hypothetical protein	5.28E-06
SSPF1 Small Secreted Protein; Family F transporter; AcrB/AcrD/AcrF family protein tra	1.97E-07
CYP392D10p Cytochrome P450 - CYP392D10p probable pseudogene	1.72E-09
CYP392Dn Cytochrome P450, conserved site CYP Cytochrome P450, conserved site C	0.0029871
CYP392A12 Cytochrome P450 - CYP392A12	1.63E-07
ACYPI009414	2.74E-07
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	7.23E-09
Intradiol ring-cleavage dioxygenase, core Intradiol ring-cleavage dioxygenase, core	2.51E-06
UGT UDP-glycosyltransferase; teturUGT28 UGT UDP-glycosyltransferase Glycosyltrans	0.0027376
partitioning defective 6 homolog beta	0.0006528
Hypothetical protein	0.0028957
Apple-like	1.23E-05
Hypothetical protein	0.0071666
TuCCE35 Carboxyl/cholinesterase TuCCE35 Carboxylesterase; type B TuCCE34 Carbo	1.73E-06
MDL14 Immunoglobulin E-set Immunoglobulin E-set	0.0001788
Hypothetical protein	8.72E-05
ribosomal protein S12	1.78E-05
Tudor domain	1.48E-06
Hypothetical protein	0.0022372
Hypothetical protein	0.0052669
Zinc finger, DksA/TraR C4-type conserved site	0.0077975
TuPap-18 Peptidase C1A, papain C-terminal Peptidase C1A, papain C-terminal	0.0001111
GE26306	1.84E-08
hypothetical protein	3.87E-05
CYP probable pse Cytochrome P450 probable pseudogene	2.75E-16
fructose-1;6-bisphosphatase	1.18E-05
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	0.0002094
hypothetical protein	0.0008176
NAT10 Acyl-CoA N-acyltransferase Acyl-CoA N-acyltransferase	3.97E-05
Hypothetical protein	0.0006456
Hypothetical protein	0.00031
BTB/POZ-like	3.76E-05
kelch-like 18	0.0001247
Tu_12344.2 cys-loop ligand-gated ion channel Tu_12344.2 ligand-gated ion channel gly	0.0058859
WTTMP1 Wannes-Thomas type-I single-pass transmembrane protein type-I single-pass	3.10E-08
C-factor	3.91E-06

hypothetical protein	2.31E-05
Hypothetical protein	3.95E-07
Hypothetical protein	9.58E-15
PLC-like phosphodiesterase, TIM beta/alpha-barrel domain	3.81E-06
Leucine-rich repeat; cysteine-containing subtype	0.0023663
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	6.64E-07
BTB/Kelch-associated BTB/Kelch-associated	0.0022921
Hypothetical protein	0.0004959
Scramblase	1.86E-07
CYP392A9 Cytochrome P450 - CYP392A9	0.0009288
hypothetical protein	6.12E-06
CYP392A9v2 Cytochrome P450 - CYP392A9v2	0.0009471
3-oxoacyl-acyl-carrier-protein reductase	0.0005553
PLC-like phosphodiesterase, TIM beta/alpha-barrel domain	0.0007316
SP18 Serine protease	0.0022018
mitochondrial carnitine/acylcarnitine carrier protein	0.0088022
Major facilitator superfamily; general substrate transporter	0.0063995
GI21111	0.0001402
Hypothetical protein	0.0009282
CYP392A16 Cytochrome P450 - CYP392A16	6.77E-12
Hypothetical protein	0.0001609
CYP392E8 Cytochrome P450 - CYP392E8	3.52E-11
UGT UDP-glycosyltransferase; teturUGT78p UGT UDP-glycosyltransferase; teturUGT78	1.47E-05
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	0.0046312
BTB/POZ-like	0.003693
Hypothetical protein	9.50E-05
UGT UDP-glycosyltransferase; teturUGT21 UGT UDP-glycosyltransferase Glycosyltrans	2.61E-06
TuCCE44 Carboxyl/cholinesterase TuCCE-38 Carboxyl/cholinesterase	0.0020474
UGT UDP-glycosyltransferase; teturUGT10 UGT UDP-glycosyltransferase Glycosyltrans	1.37E-08
Hypothetical protein	0.0022125
Apolipoprotein D precursor; putative PREDICTED: apolipoprotein D-like; partial	3.52E-10
PREDICTED: similar to adenylate cyclase	0.0025156
CYP392D7 Cytochrome P450, conserved site Cytochrome P450, conserved site	5.43E-07
MDL11 Immunoglobulin E-set Immunoglobulin E-set	0.0018851
BTB/POZ-like	0.0003802
Apple-like	0.0003404
Hypothetical protein	0.0010239
UGT UDP-glycosyltransferase; teturUGT26 UGT UDP-glycosyltransferase Glycosyltrans	3.35E-08
PREDICTED: hypothetical protein; partial	0.0004692
short chain dehydrogenase	0.0001383
hypothetical protein	0.0006332
PLAT9 Lipase/lipooxygenase; PLAT/LH2 Lipase/lipooxygenase; PLAT/LH2 Lipase/lipoc	7.72E-07
Hypothetical protein	0.0005943
C-signal	0.0002768
TuCCE58 Carboxyl/cholinesterase TuCCE-49 Carboxyl/cholinesterase	1.90E-08
Epididymal secretory protein E1 precursor	0.0007484
puromycin-sensitive aminopeptidase	3.50E-06

Cytidine deaminase-like	1.99E-05
hypothetical protein	0.0088609
DDM9-13 Domain of unknown function DUF3421 Domain of unknown function DUF3421	1.31E-09
Protease inhibitor I4; serpin	0.0005675
Hypothetical protein	0.0008362
SSPB3 Small Secreted Protein; Family B hypothetical protein	0.0013804
Hypothetical protein	2.85E-07
TuPap-11 Cathepsin B	1.97E-10
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	0.0001424
hypothetical protein	4.10E-06
Scramblase	0.0011446
short-chain dehydrogenase/reductase SDR	0.001996
BTB/POZ-like	0.0014962
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	0.0064929
TuPap-30 Cathepsin L	6.21E-05
hypothetical protein	0.006324
UGT UDP-glycosyltransferase; teturUGT36 UGT UDP-glycosyltransferase Glycosyltrans	0.0041909
TuCCE03 Carboxyl/cholinesterase TuCCE-03 Carboxyl/cholinesterase	1.03E-05
beta-tubulin	6.16E-13
TuCCE50 Carboxyl/cholinesterase TuCCE-50 Carboxyl/cholinesterase	1.52E-06
Hypothetical protein	0.0005831
GTP-binding protein Rit1	3.38E-06
BTB/Kelch-associated	0.0005475
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	0.0073346
Apolipoprotein D precursor; putative	0.0011077
Hypothetical protein	0.0045573
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	0.0012226
Cytochrome P450	0.0111034
Apolipoprotein D precursor; putative Calycin GH10331	0.0003203
UNC93-like protein MFSD11	4.28E-07
hypothetical protein	0.0009223
Hypothetical protein	3.67E-13
C-factor	4.41E-05
4-nitrophenylphosphatase	1.84E-05
BTB/POZ-like	0.0033668
selenophosphate synthetase 1	0.001678
FBXL1 Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain	0.0005386
SP29 Serine protease SP45_3 Serine protease SP29 Serine protease	3.68E-09
PREDICTED: similar to Y41C4A.8 PREDICTED: similar to Y41C4A.8 PREDICTED: sim	4.97E-08
TuGSTm07 Glutathione S-transferase; class mu	0.0002231
Curculin-like mannose-binding lectin	0.0090583
Intradiol ring-cleavage dioxygenase, core Intradiol ring-cleavage dioxygenase, core Intra	0.0012011
RNA 3'-terminal phosphate cyclase-like protein	0.002047
hypothetical protein	0.0002414
PREDICTED: similar to adenylate cyclase	0.0002673
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	0.0013424
TuGSTd13 Glutathione S-transferase; class delta	0.003743

RNI Unknown_Fbox_Gene, truncated RNI Unknown_Fbox_Gene RNI Unknown_Fbox_	5.44E-05
CYP392D6 Cytochrome P450 - CYP392D6 na Cytochrome P450 -	0.0002675
WTSP2 Wannes-Thomas Secreted Protein 2 Hypothetical protein	3.15E-11
SSPX Single Copy Small Secreted Protein of Unknown Function hypothetical protein	0.0012892
Hypothetical protein	4.92E-05
Nuclear hormone receptor, ligand-binding domain	0.0001066
CYP392E2 Cytochrome P450 - CYP392E2	2.20E-06
DDM9-12 Domain of unknown function DUF3421 Domain of unknown function DUF3421	0.0061526
SPH3 Serine protease homologue SPH Serine protease homologue	0.0017859
PREDICTED: similar to adenylate cyclase	0.0044912
FCOL Fibrillar collagen precursor collagen alpha-1	8.04E-05
UGT UDP-glycosyltransferase; teturUGT11 UGT UDP-glycosyltransferase Glycosyltrans	3.06E-10
PREDICTED: similar to KIAA1378 protein	0.0082935
CYP392D3 Cytochrome P450 - CYP392D3	8.13E-09
ApoD3 Apolipoprotein D apolipoprotein D	0.0005314
PREDICTED: similar to F55A4.8a	0.0012952
hypothetical protein	3.26E-07
Hypothetical protein	1.08E-06
Hypothetical protein	0.0002759
CYP392A10v2 Cytochrome P450 - CYP392A10v2	9.42E-06
Hypothetical protein	1.43E-08
Protein of unknown function DUF2362	0.0006164
Peptidase M16; core	3.61E-05
TuGSTd07 Glutathione S-transferase; class delta	8.53E-07
PREDICTED: similar to limkain b1	4.66E-05
Hypothetical protein	6.39E-08
hypothetical protein	0.0009366
Hypothetical protein	2.17E-11
sorbitol dehydrogenase	0.0019502
serpin 3 inhibitory serine protease inhibitor	9.99E-12
Methyltransferase type 11	5.64E-10
phosphatidylinositol-4-phosphate 5-kinase; type I; alpha	0.0002211
PREDICTED: similar to adenylate cyclase	8.25E-10
xol-1 C. elegans homolog of xol-1; a sex determinant gene	0.0015229
cathepsin A	1.51E-10
C-factor	0.0008113
intradiol ring-cleavage dioxygenase	1.34E-08
Aldehyde dehydrogenase; N-terminal	5.77E-07
DDM9-16 Domain of unknown function DUF3421 Domain of unknown function DUF3421	0.0016526
CYP392E4 Cytochrome P450, E-class, group I CYP392E4 Cytochrome P450, E-class, g	4.74E-08
TuPap-56 Cathepsin L	1.63E-05
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	7.11E-05
Mitochondrial substrate/solute carrier	0.0033415
medium-chain specific acyl-CoA dehydrogenase; mitochondrial precursor	2.36E-07
serpin 3 inhibitory serine protease inhibitor	2.29E-06
Hypothetical protein	4.54E-06
TuCCE34 Carboxyl/cholinesterase TuCCE33 Carboxyl/cholinesterase TuCCE-33 Carbo	5.60E-07

SP45 Serine protease	0.0031617
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	3.41E-06
WD40 repeat, conserved site	0.0001614
TuGSTd14 Glutathione S-transferase; class delta	3.73E-07
hypothetical phage protein	0.0064383
Hypothetical protein	2.19E-05
UGT UDP-glycosyltransferase; teturUGT39 UGT UDP-glycosyltransferase Glycosyltrans	0.0002566
Hypothetical protein	0.0001111
mitochondrial carnitine/acylcarnitine carrier protein	0.0016064
TPAN-53 PAN/Apple domain PAN/Apple domain	0.0068288
Kelch-type beta propeller	0.0004259
Hypothetical protein	6.30E-06
WTSP8 Wannes-Thomas Secreted Protein 8 Hypothetical protein	1.14E-07
SP28 Serine protease	5.31E-06
DDM9-11 Domain of unknown function DUF3421 Domain of unknown function DUF3421	0.0001499
Leucine-rich repeat domain, L domain-like	0.0030417
Hypothetical protein	0.0033031
Hypothetical protein	0.0032779
MYL1;2 Myosin regulatory light chain; isoform1 Myosin regulatory light chain 2; smooth n	0.0002318
Hypothetical protein	0.0002319
TuABCC-07 ABC-transporter; class C;	0.0067913
CCEincTu13 Carboxyl/cholinesterase; incomplete CCEincTu15 Carboxyl/cholinesterase;	0.0011461
TPAN-52 3-Pan modules Cell Surface Protein; Antigen-B homolog Apple-like	4.54E-07
UGT UDP-glycosyltransferase; teturUGT23 UGT UDP-glycosyltransferase Glycosyltrans	0.0043431
adenylyltransferase and sulfurtransferase MOCS3	0.0014931
CYP probable pse Cytochrome P450 - probable pseudogene	0.0001681
CuffL3 Cutoff-like protein HPA1c Hypothetical Protein of Unknown Function Conserved in	0.0002485
GBA1 Glycoside hydrolase; subgroup; catalytic core Glycoside hydrolase; subgroup; cat	1.18E-06
chitinase	0.001817
Hypothetical protein	0.0029742
Hypothetical protein	0.0066826
conserved hypothetical protein	0.0002131
Hypothetical protein	0.0083308
Leukocyte elastase inhibitor	1.30E-09
hypothetical protein	3.78E-07
DDM9-17 Domain of unknown function DUF3421 Domain of unknown function DUF3421	5.46E-07
CYP385C4 Cytochrome P450 - CYP385C4	8.05E-07
Sec1-like protein	3.36E-10
Hypothetical protein	0.0007043
BTB/Kelch-associated BTB/Kelch-associated	0.0001637
CYP392E7 Cytochrome P450 - CYP392E7	1.93E-05
mitochondrial sodium/hydrogen exchanger NHA2	0.0050873
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	0.0010909
Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like Le	2.75E-06
intradiol ring-cleavage dioxygenase	0.0008151
Kelch-type beta propeller	0.0001454
UGT UDP-glycosyltransferase; teturUGT06 UGT UDP-glycosyltransferase rhamnosyltra	1.98E-07

UGT UDP-glycosyltransferase; teturUGT25 UGT UDP-glycosyltransferase Glycosyltrans	3.10E-08
lipase 1 precursor	0.0036435
frataxin	5.08E-09
Hypothetical protein	0.0068144
Hypothetical protein	4.49E-06
short-chain dehydrogenase/reductase SDR	9.03E-05
hypothetical protein	0.003846
NAGLT1a Major facilitator superfamily; general substrate transporter Major facilitator sup	0.0006007
PREDICTED: similar to peritrophin 1 PREDICTED: similar to peritrophin 1	1.52E-06
Hypothetical protein	0.0016229
Transcription initiation factor TFIID subunit 10 Transcription initiation factor TFIID subunit	8.30E-05
Diacylglycerol/phorbol-ester binding Diacylglycerol/phorbol-ester binding	3.54E-07
CYP392B3 Cytochrome P450 - CYP392B3	1.80E-09
Hypothetical protein	0.0009526
apoptosis regulator BAX apoptosis regulator BAX	0.0046164
TuABCC-08 ABC-transporter; class C;	0.0093136
glycogen debranching enzyme	5.41E-11
Chibby family	0.0006785
TuCCE25 Carboxyl/cholinesterase TuCCE-25 Carboxyl/cholinesterase	0.0061507
hypothetical protein	3.92E-06
phospholipid scramblase 2	2.90E-05
kynureninase kynureninase	3.32E-06
hypothetical protein	1.51E-07
Tudor domain	1.07E-06
Hypothetical protein	1.80E-05
sin3 histone deacetylase corepressor complex component SDS3	1.86E-07
Hypothetical protein	0.0093921
lethal	2.41E-05
Hypothetical protein	0.0001045
protein kinase protein kinase	3.18E-05
RDRP-2 RNA-directed RNA polymerase 2	1.00E-05
PREDICTED: similar to inorganic phosphate cotransporter; putative	1.85E-09
PREDICTED: similar to adenylate cyclase	4.47E-12
UGT UDP-glycosyltransferase; teturUGT02 UGT UDP-glycosyltransferase Glycosyltrans	2.08E-08
Phosphatidic acid phosphatase type 2/haloperoxidase	0.0070926
TuGSTd09 Glutathione S-transferase, C-terminal TuGSTd09 Glutathione S-transferase, (	0.0002816
DM DM DNA-binding domain	1.21E-07
Hypothetical protein	0.0009044
Hypothetical protein	0.0024282
SP26/M Low-density lipoprotein LDL receptor class A repeat SP26 Low-density lipoprotei	0.0017182
conserved hypothetical protein	0.003522
serum amyloid A protein-like	9.35E-06
bZIP_2 thyrotroph embryonic factor bZIP_2 Basic region leucine zipper	0.0035059
Metal-dependent protein hydrolase	7.88E-05
phosphotyrosyl phosphatase activator phosphotyrosyl phosphatase activator phosphoty	1.55E-06
TuLeg-16 Legumain	0.0019378
MUscle Attachment abnormal family member	4.54E-08

beta-mannosidase beta-mannosidase	2.31E-05
TuPap-17 Cathepsin B	5.32E-07
hypothetical protein	0.0077457
Hypothetical protein	0.0010474
3-oxoacyl-acyl-carrier-protein reductase	9.54E-06
RNA-directed DNA polymerase	0.0104326
adenylate cyclase	0.0001323
FAD-dependent pyridine nucleotide-disulphide oxidoreductase	2.38E-09
TuCCE37 Carboxyl/cholinesterase TuCCE-35 Carboxyl/cholinesterase	7.24E-05
Low-density lipoprotein LDL receptor class A repeat	3.32E-06
Leukocyte elastase inhibitor	2.37E-05
lambda-crystallin homolog	4.88E-10
ApoD28 Apolipoprotein D precursor apolipoprotein D	0.0012505
PREDICTED: similar to limkain b1	0.009121
Hypothetical protein	0.0009288
3-oxoacyl-acyl-carrier-protein reductase	0.0003954
Hypothetical protein	2.85E-06
Hypothetical protein	5.56E-06
Tetraspanin/Peripherin	0.0006677
TPAN-1 3-Pan modules Cell Surface Protein; antigen-2 PANR-1 Pan module-related Cell	2.35E-10
AP complex subunit beta	3.67E-08
Hypothetical protein	0.0009551
Protease inhibitor I4; serpin	0.001961
Hypothetical protein	4.08E-05
NCSP2 Novel Cell surface protein Hypothetical protein	1.03E-05
DDM9-6 Domain of unknown function DUF3421 Domain of unknown function DUF3421	1.46E-05
Hypothetical protein	0.0062871
TuGSTd12 Glutathione S-transferase; class delta	5.40E-08
CCEincTu14 Carboxyl/cholinesterase; incomplete CCEincTu15 Carboxyl/cholinesterase;	0.0004309
PREDICTED: similar to DnaJ	5.23E-05
TuLeg-17 Legumain	8.86E-09
SIFa Neuropeptide precursor	3.17E-07
E3 ubiquitin-protein ligase MARCH5	3.00E-09
aldo/keto reductase aldo/keto reductase	0.0012149
Ubiquitin-fold modifier-conjugating enzyme 1	0.003666
CYP392D4 Cytochrome P450 - CYP392D4	4.55E-07
Glycoside hydrolase; subgroup; catalytic core	7.15E-05
p21-activated protein kinase-interacting protein 1-like	7.30E-05
CYP385C4v2 Cytochrome P450 - CYP385C4v2	0.0086348
Hypothetical protein	0.002438
CYP392E9 Cytochrome P450 - CYP392E9	0.0006594
Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-like	0.0005132
Hypothetical protein	0.0014159
hypothetical protein	0.0008442
Hypothetical protein	2.41E-05
ribosomal protein S7	0.000425
SP63/C Serine proteases, trypsin family, histidine active site SP63 Serine proteases, tryp	5.59E-06

TuCCE65 Carboxyl/cholinesterase TuCCE-55 Carboxyl/cholinesterase	7.78E-05
Hypothetical protein	7.89E-06
Hypothetical protein	2.86E-09
hypothetical protein	0.0003228
CHT5 chitinase chitinase	1.27E-05
Tetratricopeptide repeat	0.0017492
Hypothetical protein	0.0008312
HR96-like h HR96-like nuclear receptor h NR1/3 member Possible NR1 or NR3 member?	9.37E-07
Hypothetical protein	0.0090496
TeturLY6_UPAR18 LY6_UPAR protein Three finger domain protein TFD Hypothetical p	0.0015721
Tu_12344.3 cys-loop ligand-gated ion channel glycine receptor subunit beta precursor	4.49E-07
TLDc	0.0035032
Scv4 scavenger receptor activity	0.0021222
scavenger receptor class B; member 2	1.52E-07
ApoD99 apolipoprotein D apolipoprotein D	0.0071783
Nab NGFI-A-binding protein homolog NGFI-A- homolog NGFI-A-binding protein 1 NGFI	8.24E-07
Hypothetical protein	0.0001883
SSPA1 Small Secreted Protein; family A Hypothetical protein	1.03E-05
50S ribosomal protein L14	0.0032177
BTB/Kelch-associated	0.0001874
SPZ3 protein	2.96E-06
hypothetical protein	0.0051938
N-alpha-acetyltransferase 15; NatA auxiliary subunit N-alpha-acetyltransferase 15; NatA	9.53E-05
CYP385C3 Cytochrome P450 - CYP385C3	0.0003891
TuPap-57 Cathepsin L-like TuPap-57 Cathepsin L-like	1.21E-06
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	5.02E-07
TuCCE50 Carboxyl/cholinesterase TuCCE-42 Carboxyl/cholinesterase	7.58E-05
WTSP1b Wannes-Thomas Secreted Protein 1 WTSP1a Wannes-Thomas Secreted Prote	9.90E-05
Hypothetical protein	0.0006905
Leukocyte elastase inhibitor	1.23E-05
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	0.0062601
TuABCC-15 ABC-transporter; class C;	1.43E-06
antigen B membrane protein	1.63E-07
Hypothetical protein	6.09E-07
Hypothetical protein	3.26E-05
Hypothetical protein	0.0040272
Hypothetical protein	0.0001426
PREDICTED: sodium-dependent glucose transporter 1-like; partial	0.0001232
gamma-glutamyl hydrolase precursor	9.60E-06
Hypothetical protein	0.0030874
lethal	0.004127
lysosomal acid lipase/cholesteryl ester hydrolase	0.0001784
TuCCE49 Acetyl-cholinesterase TuCCE-41-AChE Acetyl-cholinesterase	0.0001748
TuABCC-26 ABC-transporter; class C;	2.85E-05
bromodomain-containing protein 7	0.000195
UGT UDP-glycosyltransferase; teturUGT13 UGT UDP-glycosyltransferase glycosyltrans	0.0066055
SSPB1 Small Secreted Protein; Family B Hypothetical protein	0.0002067

Double-stranded RNA binding	0.0010306
intradiol ring-cleavage dioxygenase	0.0021054
TuGSTd05 Glutathione S-transferase; class delta	0.0013298
excision repair cross-complementing rodent repair deficiency; complementation group 8	0.01008
PREDICTED: similar to adenylate cyclase	8.63E-08
UGT UDP-glycosyltransferase; teturUGT03 UGT UDP-glycosyltransferase Glycosyltrans	9.84E-08
51 kDA subunit c NADH-quinone oxidoreductase; 51 kDa subunit;	7.53E-09
Hypothetical protein	0.0046047
TuCCE08 Carboxyl/cholinesterase TuCCE-08 Carboxyl/cholinesterase	0.004424
Hypothetical protein	0.0001756
Hypothetical protein	0.0105372
solute carrier family 40	0.0003753
Integrin alpha beta-propellor	0.0017271
GF11962	0.0019442
Vg2 Lipid transport protein, beta-sheet shell Lipid transport protein, beta-sheet shell	0.0087382
hypothetical protein	0.0024973
translation initiation factor IF-3	0.000831
CYP389C8 Cytochrome P450 - CYP389C8	2.40E-06
PREDICTED: 3-hydroxybutyrate dehydrogenase; type 1-like	1.31E-07
PREDICTED: UTP6; small subunit PREDICTED: UTP6; small subunit	5.22E-08
nuclear receptor coactivator 6	3.23E-08
Hypothetical protein	5.16E-05
short chain dehydrogenase/reductase family 16C; member 5	1.81E-05
RecName: Full	0.0001719
Hypothetical protein	0.0094573
Hypothetical protein	0.0016659
Nuclear hormone receptor; ligand-binding	4.26E-05
Hypothetical protein	0.0034492
blood vessel epicardial substance blood vessel epicardial substance	0.0010208
U6 snRNA-associated Sm-like protein LSm5	0.0002046
Zinc finger, C4H2-type	0.0046655
Hypothetical protein	2.29E-07
Hypothetical protein	0.0001493
Pleckstrin-homology domain PH domain/Phosphotyrosine-binding domain PTB	0.0065782
hypothetical protein IscW_ISCW007834	0.0001432
Hypothetical protein	0.0002159
Hypothetical protein	2.32E-05
TuENaC123 Na+ channel, amiloride-sensitive Tu_ENaC123 Na+ channel, amiloride-sens	0.0036499
TuENaC122 Na+ channel, amiloride-sensitive Tu_ENaC122 Na+ channel, amiloride-sens	0.0001199
HCSP1a Hypothetical Cell Surface Protein HCSP1 Hypothetical Cell Surface Protein HC	7.05E-08
PREDICTED: similar to Kuzbanian-like CG1964-PA	0.0001917
Fibronectin; type III-like fold	0.0047708
Hypothetical protein	4.15E-06
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	5.94E-06
Hypothetical protein	0.0002614
Transmembrane BAX inhibitor motif-containing protein 1	0.0004242
Hypothetical protein	7.27E-06

Cyclic nucleotide-gated channel, C-terminal leucine zipper domain	1.98E-05
brefeldin A-inhibited guanine nucleotide-exchange protein 3 brefeldin A-inhibited guanine	7.39E-08
Hypothetical protein	0.0026133
UGT UDP-glucuronosyl/UDP-glucosyltransferase UGT UDP-glucuronosyl/UDP-glucosyltr	2.78E-06
puromycin-sensitive aminopeptidase	4.83E-07
Hypothetical protein	0.0010149
GK22478	1.33E-06
RPS7 ribosomal protein S7 ribosomal protein S7	2.42E-05
zf-C2H2 Zinc finger; C2H2 type	0.0005042
51 kDa subunit c NADH-quinone oxidoreductase; 51 kDa subunit	2.64E-08
Hypothetical protein	0.0044508
hypothetical protein	4.70E-09
hypothetical protein	1.04E-05
Bicarbonate transporter; eukaryotic	0.003575
TeturLY6_UPAR23 LY6_UPAR protein Hypothetical protein	0.0008323
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	2.20E-05
zinc finger protein 183 zinc finger protein 183	1.33E-05
Hypothetical protein	2.77E-06
Leucine-rich repeat domain, L domain-like	5.24E-05
S-formylglutathione hydrolase	2.71E-09
HEY2 hairy/enhancer-of-split related with YRPW motif 2	7.30E-07
FUCTCb alpha-1;3-fucosyltransferase C	2.60E-07
PREDICTED: similar to CG3825 CG3825-PA	0.0005361
Hypothetical protein	6.71E-05
PREDICTED: similar to Bardet-Biedl syndrome 7	0.0006412
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	0.0003036
PREDICTED: similar to adenylate cyclase	0.0026403
Hypothetical protein	0.0023441
Concanavalin A-like lectin/glucanase	2.94E-05
NAGLT1b Major facilitator superfamily; general substrate transporter Major facilitator sup	0.0041057
TuCCE07 Carboxyl/cholinesterase TuCCE-07 Carboxyl/cholinesterase	0.0031751
Hypothetical protein	0.0001858
hypothetical protein Y39G10AR.18	0.0001249
Hypothetical protein	0.0006925
DnaJ	0.0003651
Myosin regulatory light chain 2; smooth muscle isoform	8.02E-05
Telomere-binding beta subunit	0.0019642
Fibroin hypothetical protein	0.0018978
Hypothetical protein	0.0055219
Hypothetical protein	0.0062832
galactokinase	3.82E-05
TuGR99 Chemosensory Receptor; Gustatory receptor family Hypothetical protein	0.0001381
hypothetical protein	0.0003233
SRSP1 Serine-rich secreted protein LSPA1 Large secreted protein; family A LSPA1 Larg	0.0017812
cullin-5	7.49E-05
Zinc finger, C2H2-like	0.0026355
T-complex protein 1 subunit zeta T-complex protein 1 subunit zeta	0.009299

mitochondrial intermembrane space import and assembly protein 40	6.41E-05
Hypothetical protein	0.0005855
CBR1p Carbonyl reductase [NADPH] 1; pseudo gene carbonyl reductase	0.0008773
RNI Leucine-rich repeat domain, L domain-like HYP1a Leucine-rich repeat domain, L don	0.0003992
N-acylneuraminate cytidylyltransferase	0.0017496
PREDICTED: similar to CG13913 CG13913-PA	3.27E-05
Galactose-binding domain-like	0.0004127
SSPC3 Small Secreted Protein; family C Hypothetical protein	0.0006486
PREDICTED: filamin B; beta	8.02E-05
GRSP16 Glycine-rich secreted protein Hypothetical protein	0.0001846
M-phase phosphoprotein 8 M-phase phosphoprotein 8	0.0025009
hydroxymethylglutaryl-CoA lyase	3.31E-06
short chain dehydrogenase	5.95E-06
Hypothetical protein	0.0003918
Hypothetical protein	4.96E-10
no-mechanoreceptor potential A; putative	0.0066394
PREDICTED: similar to shavenoid CG13209-PA	1.90E-06
Hypothetical protein	0.0033009
Hypothetical protein	5.52E-07
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	0.0086976
antigen B membrane protein	0.0013105
UGT UDP-glycosyltransferase; teturUGT52 UGT UDP-glycosyltransferase Glycosyltrans	5.33E-10
lipase 1 precursor	6.09E-09
TuENaC118 Na+ channel, amiloride-sensitive Tu_ENaC118 Na+ channel, amiloride-sens	2.30E-07
hypothetical protein	1.13E-05
Hypothetical protein	0.0098638
CuffL1 Cutoff-like protein HPA1b Hypothetical Protein of Unknown Function Conserved ir	0.0001125
hypothetical protein	0.000177
Major facilitator superfamily; general substrate transporter	7.70E-05
chitobiosyldiphosphodolichol beta-mannosyltransferase chitobiosyldiphosphodolichol beta	0.0003879
CPAP 3 cuticular protein analogous to peritrophins 1-A	5.30E-06
lysosomal alpha-glucosidase precursor	0.002779
PrtA Chitin binding protein; peritrophin-A Chitin binding protein; peritrophin-A	1.06E-07
Vg5 Vitellogenin 5	6.79E-07
CPR 6 cuticle protein CPR 6 cuticle protein	0.0035378
zinc carboxypeptidase	2.51E-06
Hypothetical protein	5.27E-06
Carbohydrate-binding-like fold	1.17E-05
galactosyltransferase; putative	0.0014775
Hypothetical protein	0.0015345
ABC transporter; permease/ATP-binding protein	0.003275
paraxis Myc-type, basic helix-loop-helix bHLH domain HLH Myc-type, basic helix-loop-hel	0.0086857
TuCCE42 Carboxyl/cholinesterase TuCCE42 Carboxyl/cholinesterase; incomplete CCEin	0.0039836
Hypothetical protein	0.0063699
BTB/Kelch-associated BTB/Kelch-associated	0.0051491
exostosin-1	0.0005865
Major facilitator superfamily; general substrate transporter	5.47E-07

BTB	3.49E-05
PMS1	0.0002861
Leucine-rich repeat domain, L domain-like	4.09E-05
PREDICTED: similar to Glucosylceramidase precursor	4.73E-05
sensory box protein/histidinol phosphate phosphatase family protein	0.0064992
Hypothetical protein	1.06E-05
Hypothetical protein	0.003641
beta-1;4-galactosyltransferase	0.002431
Phytanoyl-CoA dioxygenase	2.81E-07
Hypothetical protein	1.55E-05
protein kinase	7.09E-07
Hypothetical protein	0.0045465
hypothetical protein	4.19E-06
Hypothetical protein	6.65E-05
WASH complex subunit strumpellin	0.0011846
Hypothetical protein	0.0015272
Protein phosphatase 2C	0.0005377
TuLeg-8 Legumain	0.0003457
Hypothetical protein	0.0022826
short chain dehydrogenase	0.0079305
PREDICTED: similar to lipase 1	3.60E-05
Lklf krueppel-like factor 2	2.66E-06
SERP Secreted Protein with 8aa repeat structure Hypothetical protein	1.91E-05
epithelial cell transforming sequence 2 oncogene	0.0012296
PREDICTED: similar to lysosomal acid lipase; putative	0.0005568
Glycoside hydrolase; subgroup; catalytic core	6.95E-05
GE13940	6.58E-11
alpha-glucosidase	4.85E-05
Alpha/Beta hydrolase fold	0.000132
SSPG1 Small secreted protein; Family G Hypothetical protein	0.0001035
sialin; putative	0.0037991
candidate tumor suppressor protein	3.56E-05
hypothetical protein	0.004955
Agrin NtA	0.0013776
hypothetical protein	0.0065479
hypothetical protein	0.0090415
Six-bladed beta-propeller; TolB-like	0.0050397
Hypothetical protein	5.78E-05
UGT UDP-glycosyltransferase; teturUGT65 UGT UDP-glycosyltransferase RhlB	0.010244
CPR G Putative cuticle protein	9.73E-05
Fibroin Hypothetical protein	0.0009564
vitellogenin1	0.0002961
GE10869	5.70E-05
protein kinase C alpha type	0.0011552
GRSP1 Glycine-rich secreted protein Hypothetical protein	0.0061555
TuCCE43 Carboxyl/cholinesterase TuCCE43 Carboxyl/cholinesterase; incomplete CCEin	1.10E-05
TMCO7 RNA polymerase II assembly factor Rtp1, C-terminal RNA polymerase II assem	1.25E-05

Hypothetical protein	0.0088128
Hypothetical protein	0.0001232
sorbitol dehydrogenase	3.65E-06
ribosomal protein S12	2.46E-06
Hypothetical protein	0.0001093
Hypothetical protein	0.0026092
sialin	0.0063483
DDM9-21 Domain of unknown function DUF3421 Domain of unknown function DUF3421	0.0017903
Csp1f conserved secreted protein 1 Hypothetical protein	6.91E-05
Hypothetical protein	8.10E-06
TuENaC08 Na+ channel, amiloride-sensitive ENaC08 Na+ channel, amiloride-sensitive E	1.05E-05
Hypothetical protein	0.0065098
Hypothetical protein	0.0011353
ApoD23 Apolipoprotein D precursor apolipoprotein D	2.33E-05
alpha	0.0001583
hypothetical protein	0.0027621
TuCCE61 Carboxyl/cholinesterase TuCCE-51 Carboxyl/cholinesterase	4.81E-06
Hypothetical protein	0.0004087
Sodium/calcium exchanger membrane region SPHp5 Sodium/calcium exchanger membra	8.05E-05
BTB/Kelch-associated	6.63E-05
Clusterin-associated protein-1	0.0008259
Hypothetical protein	0.009187
BTB/Kelch-associated BTB/Kelch-associated	3.44E-05
Alkaline phosphatase-like, alpha/beta/alpha	1.03E-09
Uncharacterised protein family UPF0402	0.0064142
S-adenosyl-L-methionine-dependent methyltransferase	0.000376
hkb huckebein zfp zinc finger protein 273 zf-C2H2 Zinc finger; C2H2 type	0.0039926
LKAP32 Limkain-b1;	0.0032146
UNCoordinated family member	0.0029919
Apple-like	2.81E-09
E2f4 E2F transcription factor, CC-MB domain E2F_TDP E2F transcription factor, CC-MB	0.00037
Hypothetical protein	0.005154
Rfx4 Winged helix-turn-helix DNA-binding domain RFX_DNA_binding Winged helix-turn-h	1.81E-10
phosphatidylcholine-sterol acyltransferase	0.0001448
minor tail protein gp26-like	0.0081463
hypothetical protein	3.93E-05
Longitudinals lacking protein-like	6.04E-05
hypothetical protein	6.88E-07
innexin; putative	0.0066179
WD40 repeat	0.0015066
UNCoordinated family member	3.71E-08
Hypothetical protein	0.0105809
HCP1 Hypothetical Cuticular Protein HPR1 Hypothetical Cuticular Protein Hypothetical	6.30E-06
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	0.0009534
isoamyl acetate-hydrolyzing esterase 1 homolog	0.0043809
CPR 51 Cuticle secreted protein; putative CPR1 Cuticle secreted protein; putative CPR1	4.08E-05
GRSP7 Glycine-rich secreted protein GRSP7 Glycine-rich secreted protein Hypothetical	8.20E-06

Hypothetical protein	1.73E-05
Hypothetical protein	8.33E-06
apoptosis regulator BAX	0.0012929
TuLeg-18 Legumain TuLeg-18 Legumain;	0.0008707
phosphatidylethanolamine-binding protein	4.69E-05
Apple-like	0.0035914
Hypothetical protein	0.0008959
PE-PGRS family protein	2.44E-09
Gfi1b growth factor independent protein 1B zf-C2H2 Zinc finger; C2H2 type	4.34E-07
Hypothetical protein	0.0092866
ATP-dependent RNA helicase DDX51 ATP-dependent RNA helicase DDX51	0.0011255
Hypothetical protein	0.0005459
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	0.0075318
hypothetical protein	0.0001187
hypothetical protein	4.09E-11
Bromo adjacent homology BAH domain	4.69E-07
unnamed protein product	3.91E-05
PREDICTED: similar to kelch-like 12	0.0019208
Hypothetical protein	4.22E-07
Vitellinogen, open beta-sheet, subdomain 1	0.0003739
TuPap-20 Cathepsin B	9.57E-06
Nose resistant-to-fluoxetine protein; N-terminal	0.0053843
GRSP5 Glycine-rich secreted protein Hypothetical protein	0.0027972
Hypothetical protein	2.85E-05
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	0.0038451
apolipoprotein D	7.96E-06
Hypothetical protein	0.0001565
PREDICTED: similar to CG3825 CG3825-PA	0.0011989
Hypothetical protein	0.0005143
BTB/Kelch-associated	0.0001979
Trafficking protein particle complex subunit 5 Trafficking protein particle complex subunit	0.0005246
Hypothetical protein	0.0004713
hypothetical protein	2.07E-05
Hypothetical protein	0.0002181
Hypothetical protein	0.0001495
TuCCE70 Carboxyl/cholinesterase TuCCE-60 Carboxyl/cholinesterase	1.43E-05
major facilitator superfamily MFS_1	0.006355
WASH complex subunit strumpellin	0.0098797
Oxidoreductase-like, N-terminal	0.0004258
conserved hypothetical protein	2.93E-06
TuENaC05 Putative amiloride-sensitive sodium channel ENaC05 Putative amiloride-sens	3.71E-06
acylamino-acid-releasing enzyme	0.0001138
Hypothetical protein	0.0008087
TuPap-28 Peptidase C1A, papain C-terminal Peptidase C1A, papain C-terminal	0.0022614
nhr-48 Nuclear hormone receptor; ligand-binding Nuclear hormone receptor; ligand-bindi	0.0049565
hypothetical protein	0.0017245
Hypothetical protein	0.0021148

Hypothetical protein	0.0012473
D13	2.72E-05
Hypothetical protein	6.77E-07
TuLeg-22 Legumain-like; pseudogene	0.0002455
UNCoordinated family member	4.08E-07
Nse4	5.94E-09
5'-nucleotidase	1.84E-05
Hypothetical protein	5.18E-05
hypothetical protein	0.0086067
Hypothetical protein	4.27E-05
IarsP isoleucyl-tRNA synthetase; pseudogene isoleucyl-tRNA synthetase; cytoplasmic	0.0005135
ApoD22 Apolipoprotein D precursor Lipocalin family protein	0.0069235
Hypothetical protein	1.82E-06
Six-bladed beta-propeller; TolB-like	0.0108891
PREDICTED: similar to AGAP003567-PA	8.49E-08
High mobility group; HMG1/HMG2	0.0011406
Hypothetical protein	0.0006045
spectrin; alpha; non-erythrocytic 1	0.0040154
Hypothetical protein	0.0015541
SP39 Serine protease	6.43E-09
Hypothetical protein	5.48E-09
Hypothetical protein	0.0035993
Cytochrome P450 na Cytochrome P450	0.0063207
nhr-48 Nuclear hormone receptor, ligand-binding domain Nuclear hormone receptor, liga	0.0107144
Carboxypeptidase-like, regulatory domain	0.0001832
CPR 26 cuticle protein	6.04E-06
Hypothetical protein	0.0017144
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	0.0043267
Nuclear hormone receptor, ligand-binding domain	0.0003477
Insect antifreeze protein	0.0004726
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	0.005517
TuPap-14 Cathepsin B	0.0004506
DDM9-22 Domain of unknown function DUF3421 Domain of unknown function DUF3421	0.0063954
Reeler domain	7.10E-06
Hypothetical protein	0.0002829
Hypothetical protein	2.76E-06
CCEincTu16 Carboxyl/cholinesterase; incomplete CCEinc-26 Carboxyl/cholinesterase; in	0.0002092
Hypothetical protein	1.14E-09
phospholipase A2 precursor; putative	4.22E-05
ADAMX4 Peptidase M12B, ADAM/reprolysin Peptidase M12B, ADAM/reprolysin	0.00049
alanyl-tRNA synthetase	0.0016947
HLH hypoxia-inducible factor 1 alpha	0.0082606
phytoene dehydrogenase	2.47E-05
Armadillo-type fold	6.26E-05
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	0.0026322
sialin sialin	0.00134
LZY1;3 conserved zygote-specific protein homologue LZY1;3 conserved zygote-specific	1.09E-06

glucose dehydrogenase	0.0019196
short-chain dehydrogenase/reductase SDR	0.0013872
Hypothetical protein	0.0052943
peritrophic membrane chitin binding protein; putative	0.0006122
Hypothetical protein	0.0004904
Zinc finger, RING/FYVE/PHD-type Zinc finger, RING/FYVE/PHD-type	4.84E-06
Protoporphyrinogen oxidase, C-terminal domain	4.27E-06
Hypothetical protein	0.0027014
Hypothetical protein	0.0034027
TuLeg-19 Legumain	8.20E-06
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	5.53E-08
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	5.03E-05
Hypothetical protein	1.85E-08
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	0.0007632
Uncharacterized oxidoreductase yqjQ Uncharacterized oxidoreductase yqjQ	0.0026349
Hypothetical protein	0.0010273
nhr-48 Nuclear hormone receptor, ligand-binding domain Nuclear hormone receptor, liga	0.0013358
Hypothetical protein	0.0047216
Hypothetical protein	0.0023744
adenylosuccinate lyase	0.0011106
DNA replication factor Cdt1, C-terminal	1.14E-09
ApoD24 Apolipoprotein D precursor apolipoprotein D precursor	0.0067691
GRSP15 Glycine-rich secreted protein Hypothetical protein	0.0003886
Hypothetical protein	3.04E-05
SFRS protein kinase 1	7.12E-05
pseudogene of 04g02210 ferrochelatase ferrochelatase	0.0021657
ApoDR10 Calycin-like Calycin-like	4.06E-06
Zinc finger; C2H2-type	4.55E-06
ApoD21 Apolipoprotein D precursor ApoD21 Apolipoprotein precursor Lipocalin family p	0.0003836
CPR 28 cuticle protein	0.0001654
hypothetical protein	0.0005343
GG20998	0.0002627
ADP-ribosylation factor GTPase-activating protein 1	0.0017335
hypothetical protein	0.0028171
Hypothetical protein	0.002695
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	8.32E-05
Hypothetical protein	0.0008643
GTP1/OBG	0.0004075
PSP; proline-rich	5.34E-06
Hypothetical protein	0.0025952
steroid dehydrogenase	1.05E-07
PLAT13 PLAT single domain protein PLAT/LH2 single domain protein; related Hypothe	0.0072151
RNI Leucine-rich repeat domain, L domain-like Leucine-rich repeat domain, L domain-lik	0.0001795
Hypothetical protein	0.000261
IQ calmodulin-binding region	0.0024231
PREDICTED: similar to neprilysin; partial	9.52E-10
hypothetical protein	0.0007668

DEAD	7.78E-05
Hypothetical protein	3.16E-13
hypothetical protein	4.04E-06
Endonuclease/exonuclease/phosphatase	0.0011804
UGT UDP-glycosyltransferase; teturUGT16 UGT UDP-glycosyltransferase MGT4 Glycos	1.91E-05
Leucine-rich repeat domain, L domain-like	2.14E-07
PREDICTED: UDP-Gal:betaGlcNAc beta 1;3-galactosyltransferase 1-like	2.21E-06
ApoD20 Apolipoprotein D precursor PREDICTED: apolipoprotein D-like	7.11E-06
Hypothetical protein	0.0080107
Hypothetical protein	0.0003873
origin recognition complex subunit 2	2.71E-06
HCP2 Hypothetical Cuticular Protein Hypothetical protein	0.0011589
Cysteine peptidase, asparagine active site	8.92E-07
ovo ovo zf-C2H2 Zinc finger; C2H2 type	0.0009362
K Homology domain, type 1	5.33E-05
Phosphoribosyltransferase-like Phosphoribosyltransferase-like	0.0105445
alanine aminotransferase	0.0004469
partitioning defective 6 homolog beta	0.000622
hypothetical protein	6.71E-05
Hypothetical protein	0.0013827
Hypothetical protein	5.48E-06
PLC-like phosphodiesterase, TIM beta/alpha-barrel domain	0.0032895
DnaJ	6.07E-05
Hypothetical protein	0.0104112
Hypothetical protein	9.88E-05
TuGSTinc03 Glutathione-S-transferase; incomplete;	0.0024574
ovo ovo zf-C2H2 Zinc finger; C2H2 type	0.0049042
cathepsin B	0.0077387
Hypothetical protein	6.46E-06
hypothetical protein	0.0033757
dUTPase deoxyuridine 5'-triphosphate nucleotidohydrolase deoxyuridine 5'-triphosphate	0.0083953
AkrE2 Aldo-keto reductase family E; member 2; likely a pseudogene aldo-keto reductase	1.05E-08
Hypothetical protein	9.22E-06
CPR 22 cuticle protein	0.0029641
PREDICTED: similar to limkain b1	1.09E-05
Hypothetical protein	0.0001966
Hypothetical protein	9.77E-05
PIN domain-like	1.74E-05
Leucine-rich repeat domain, L domain-like	5.05E-06
hypothetical protein	5.64E-05
hypothetical protein	5.38E-07

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4.39E-05
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5.87E-06

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4.96E-06
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4.20E-05
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3.26E-05
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0.0011042
3.52E-05

lations (IT2, UK6 and ES1) and two susceptible strains (RO1 and IT3) of *T. urticae*

ipr_ALL
IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
NA
IPR012674*Calycin
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR011333*SKP1/BTB/POZ domain, IPR011705*BTB/Kelch-associated
IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
IPR007235*Glycosyl transferase, family 28, C-terminal, IPR002213*UDP-glucuronosyl/UDP-glucosyltr
IPR000998*MAM domain, IPR013320*Concanavalin A-like lectin/glucanase domain
IPR012674*Calycin
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
NA
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR015889*Intradiol ring-cleavage dioxygenase, core
IPR007235*Glycosyl transferase, family 28, C-terminal
IPR001478*PDZ domain, IPR000270*PB1 domain, IPR034876*Partitioning defective protein 6
NA
IPR003609*PAN/Apple domain
NA
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR003172*MD-2-related lipid-recognition domain, IPR014756*Immunoglobulin E-set
NA
IPR029064*50S ribosomal protein L30e-like, IPR000530*Ribosomal protein S12e, IPR004038*Riboso
IPR002999*Tudor domain
NA
NA
NA
IPR012599*Peptidase C1A, propeptide, IPR000668*Peptidase C1A, papain C-terminal, IPR013128*P
NA
IPR003609*PAN/Apple domain
IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
IPR000146*Fructose-1,6-bisphosphatase class 1, IPR033391*Fructose-1-6-bisphosphatase class I, N
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
NA
IPR007807*Helicase domain, IPR032672*TmcA/NAT10/Kre33, IPR027992*Possible tRNA binding do
NA
NA
IPR011333*SKP1/BTB/POZ domain, IPR000210*BTB/POZ domain, IPR028764*Kelch repeat and BT
IPR000210*BTB/POZ domain, IPR011333*SKP1/BTB/POZ domain, IPR011705*BTB/Kelch-associate
IPR006202*Neurotransmitter-gated ion-channel ligand-binding domain, IPR006028*Gamma-aminobut
NA
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain

NA
NA
NA
IPR017946*PLC-like phosphodiesterase, TIM beta/alpha-barrel domain
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain, IPR006553*Leucin
IPR032675*Leucine-rich repeat domain, L domain-like
IPR011705*BTB/Kelch-associated, IPR011333*SKP1/BTB/POZ domain, IPR011042*Six-bladed beta-
NA
IPR005552*Scramblase
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR011705*BTB/Kelch-associated
IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
IPR017946*PLC-like phosphodiesterase, TIM beta/alpha-barrel domain
IPR001314*Peptidase S1A, chymotrypsin family, IPR009003*Peptidase S1, PA clan, IPR001254*Seri
IPR023395*Mitochondrial carrier domain, IPR018108*Mitochondrial substrate/solute carrier
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR031968*VASt domain
NA
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
NA
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR000210*BTB/POZ domain, IPR011705*BTB/Kelch-associated, IPR011333*SKP1/BTB/POZ domai
NA
IPR007235*Glycosyl transferase, family 28, C-terminal, IPR002213*UDP-glucuronosyl/UDP-glucosyltr
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR006326*UDP-glycosyltransferase, MGT, IPR007235*Glycosyl transferase, family 28, C-terminal, I
NA
IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain
IPR020846*Major facilitator superfamily domain
IPR002401*Cytochrome P450, E-class, group I, IPR001128*Cytochrome P450
IPR014756*Immunoglobulin E-set, IPR003172*MD-2-related lipid-recognition domain
IPR000210*BTB/POZ domain, IPR011705*BTB/Kelch-associated, IPR011333*SKP1/BTB/POZ domai
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NA
IPR007235*Glycosyl transferase, family 28, C-terminal, IPR002213*UDP-glucuronosyl/UDP-glucosyltr
NA
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
IPR024483*Protein of unknown function DUF2700
NA
NA
IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR014756*Immunoglobulin E-set, IPR003172*MD-2-related lipid-recognition domain
NA

NA
NA
IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat
IPR023796*Serpin domain, IPR000215*Serpin family
NA
NA
NA
IPR000668*Peptidase C1A, papain C-terminal, IPR012599*Peptidase C1A, propeptide, IPR013128*P
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
NA
IPR005552*Scramblase
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
IPR011705*BTB/Kelch-associated, IPR000210*BTB/POZ domain, IPR011333*SKP1/BTB/POZ domai
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A, IPR013201*Cathepsin pro
NA
IPR007235*Glycosyl transferase, family 28, C-terminal
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR003008*Tubulin/FtsZ, GTPase domain, IPR000217*Tubulin, IPR002453*Beta tubulin, IPR008280*
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
NA
IPR001806*Small GTPase superfamily, IPR020849*Small GTPase superfamily, Ras type, IPR027417
IPR011705*BTB/Kelch-associated, IPR011333*SKP1/BTB/POZ domain
IPR032675*Leucine-rich repeat domain, L domain-like
IPR000566*Lipocalin/cytosolic fatty-acid binding domain, IPR012674*Calycin
NA
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR001128*Cytochrome P450
IPR012674*Calycin
IPR020846*Major facilitator superfamily domain, IPR010291*Ion channel regulatory protein, UNC-93
IPR003609*PAN/Apple domain
NA
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
IPR023214*HAD-like domain
IPR011043*Galactose oxidase/kelch, beta-propeller, IPR011705*BTB/Kelch-associated, IPR000210*E
NA
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR001314*Peptidase S1A, chymotrypsin family, IPR001254*Serine proteases, trypsin domain, IPR00
IPR021454*Protein of unknown function DUF3105
IPR012336*Thioredoxin-like fold, IPR010987*Glutathione S-transferase, C-terminal-like, IPR004045*C
NA
IPR015889*Intradiol ring-cleavage dioxygenase, core
IPR016443*RNA 3'-terminal phosphate cyclase type 2, IPR013791*RNA 3'-terminal phosphate cyclase
IPR031968*VASt domain
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR010987*Glutathione S-transferase, C-terminal-like, IPR004045*Glutathione S-transferase, N-termi

IPR032675*Leucine-rich repeat domain, L domain-like
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
NA
NA
NA
IPR000536*Nuclear hormone receptor, ligand-binding domain
IPR001128*Cytochrome P450
IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat
IPR009003*Peptidase S1, PA clan, IPR001254*Serine proteases, trypsin domain
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR008160*Collagen triple helix repeat, IPR000885*Fibrillar collagen, C-terminal, IPR014716*Fibrinog
IPR007235*Glycosyl transferase, family 28, C-terminal, IPR002213*UDP-glucuronosyl/UDP-glucosyltr
IPR000210*BTB/POZ domain, IPR011333*SKP1/BTB/POZ domain
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain, IPR022271*Lipocalin, A
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily, IPR001958*
NA
NA
NA
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
NA
IPR019311*Protein of unknown function DUF2362
IPR011249*Metalloenzyme, LuxS/M16 peptidase-like, IPR013578*Peptidase M16C associated
IPR004046*Glutathione S-transferase, C-terminal, IPR010987*Glutathione S-transferase, C-terminal-l
IPR024768*Meiosis regulator and mRNA stability factor 1, IPR021139*NYN domain, limkain-b1-type, I
NA
NA
NA
IPR020843*Polyketide synthase, enoylreductase domain, IPR016040*NAD(P)-binding domain, IPR01
IPR023796*Serpin domain, IPR000215*Serpin family
IPR029063*S-adenosyl-L-methionine-dependent methyltransferase, IPR013216*Methyltransferase typ
IPR002498*Phosphatidylinositol-4-phosphate 5-kinase, core, IPR027483*Phosphatidylinositol-4-phos
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
NA
IPR029058*Alpha/Beta hydrolase fold, IPR001563*Peptidase S10, serine carboxypeptidase
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
IPR015889*Intradiol ring-cleavage dioxygenase, core
IPR016161*Aldehyde/histidinol dehydrogenase, IPR015590*Aldehyde dehydrogenase domain, IPR01
IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR013201*Cathepsin propeptide inhibitor domain (I29), IPR000668*Peptidase C1A, papain C-termina
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR023395*Mitochondrial carrier domain, IPR018108*Mitochondrial substrate/solute carrier, IPR0020
IPR009075*Acyl-CoA dehydrogenase/oxidase C-terminal, IPR013786*Acyl-CoA dehydrogenase/oxida
IPR023796*Serpin domain, IPR000215*Serpin family
NA
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B

IPR001254*Serine proteases, trypsin domain, IPR001314*Peptidase S1A, chymotrypsin family, IPR0
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR015943*WD40/YVTN repeat-like-containing domain, IPR017986*WD40-repeat-containing domain,
IPR004046*Glutathione S-transferase, C-terminal, IPR004045*Glutathione S-transferase, N-terminal,
NA
NA
NA
NA
IPR023395*Mitochondrial carrier domain, IPR018108*Mitochondrial substrate/solute carrier
IPR003609*PAN/Apple domain
IPR006652*Kelch repeat type 1, IPR015915*Kelch-type beta propeller, IPR011498*Kelch repeat type
NA
NA
IPR001254*Serine proteases, trypsin domain, IPR001314*Peptidase S1A, chymotrypsin family, IPR0
IPR024518*Domain of unknown function DUF3421
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
NA
NA
IPR002048*EF-hand domain, IPR011992*EF-hand domain pair
NA
IPR011527*ABC transporter type 1, transmembrane domain, IPR027417*P-loop containing nucleosid
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR003609*PAN/Apple domain
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase, IPR006326*UDP-glycosyltransferase, MGT,
IPR000594*THIF-type NAD/FAD binding fold, IPR001763*Rhodanese-like domain
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
NA
IPR001139*Glycoside hydrolase family 30, IPR017853*Glycoside hydrolase superfamily, IPR033452*
IPR029070*Chitinase insertion domain, IPR001223*Glycoside hydrolase family 18, catalytic domain,
NA
NA
NA
NA
IPR023796*Serpin domain, IPR000215*Serpin family
NA
IPR006616*DM9 repeat, IPR024518*Domain of unknown function DUF3421
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR001619*Sec1-like protein
NA
IPR011333*SKP1/BTB/POZ domain, IPR011705*BTB/Kelch-associated
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR006153*Cation/H+ exchanger
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR032675*Leucine-rich repeat domain, L domain-like
IPR015889*Intradiol ring-cleavage dioxygenase, core
IPR011705*BTB/Kelch-associated, IPR000210*BTB/POZ domain, IPR015915*Kelch-type beta propel
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase, IPR007235*Glycosyl transferase, family 28,

IPR007235*Glycosyl transferase, family 28, C-terminal, IPR002213*UDP-glucuronosyl/UDP-glucosyltr
IPR029058*Alpha/Beta hydrolase fold, IPR025483*Lipase, eukaryotic, IPR006693*Partial AB-hydrolas
IPR002908*Frataxin/CyaY, IPR017789*Frataxin
NA
NA
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
NA
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR002557*Chitin binding domain
NA
NA
IPR015727*Protein kinase C mu-related, IPR002219*Protein kinase C-like, phorbol ester/diacylglycer
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
NA
IPR026298*Blc2 family
IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR011527*ABC transporter type 1,
IPR032788*Glycogen debranching enzyme, central domain, IPR029436*Eukaryotic glycogen debranc
IPR028118*Chibby family
IPR002018*Carboxylesterase, type B, IPR029058*Alpha/Beta hydrolase fold
IPR000215*Serpin family, IPR023796*Serpin domain
IPR005552*Scramblase
IPR015421*Pyridoxal phosphate-dependent transferase, major region, subdomain 1, IPR010111*Kyn
NA
IPR002999*Tudor domain
NA
IPR013907*Sds3-like
NA
IPR008978*HSP20-like chaperone, IPR031107*Small heat shock protein HSP20, IPR001436*Alpha c
NA
IPR000408*Regulator of chromosome condensation, RCC1, IPR000719*Protein kinase domain, IPR0
IPR007855*RNA-dependent RNA polymerase, eukaryotic-type
IPR011701*Major facilitator superfamily, IPR020846*Major facilitator superfamily domain
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase, IPR007235*Glycosyl transferase, family 28,
NA
IPR004045*Glutathione S-transferase, N-terminal, IPR012336*Thioredoxin-like fold, IPR010987*Gluta
IPR001275*DM DNA-binding domain, IPR026607*DMRT/protein doublesex/protein male abnormal 3
NA
NA
IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR001254*Serine proteases, tryps
NA
NA
IPR004827*Basic-leucine zipper domain, IPR007588*Zinc finger, FLYWCH-type
IPR003226*Metal-dependent protein hydrolase
IPR004327*Phosphotyrosyl phosphatase activator, PTPA
IPR001096*Peptidase C13, legumain
IPR000082*SEA domain

IPR008979*Galactose-binding domain-like, IPR013783*Immunoglobulin-like fold, IPR017853*Glycosi
IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A, IPR012599*Peptidase C1
NA
NA
IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
NA
IPR020846*Major facilitator superfamily domain
IPR023753*FAD/NAD(P)-binding domain
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR013320*Concanavalin A-like lectin/glucanase domain, IPR002172*Low-density lipoprotein (LDL) r
IPR023796*Serpin domain, IPR000215*Serpin family
IPR013328*6-phosphogluconate dehydrogenase, domain 2, IPR008927*6-phosphogluconate dehydr
IPR002345*Lipocalin, IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain, I
IPR029060*PIN domain-like, IPR024768*Meiosis regulator and mRNA stability factor 1, IPR021139*N
NA
IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR
NA
NA
IPR018499*Tetraspanin/Peripherin, IPR008952*Tetraspanin, EC2 domain
NA
IPR008152*Clathrin adaptor, alpha/beta/gamma-adaptin, appendage, Ig-like subdomain, IPR013041*
NA
IPR023796*Serpin domain, IPR000215*Serpin family
NA
NA
IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat
NA
IPR004045*Glutathione S-transferase, N-terminal, IPR004046*Glutathione S-transferase, C-terminal,
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR001623*DnaJ domain, IPR015399*Domain of unknown function DUF1977, DnaJ-like
IPR001096*Peptidase C13, legumain
NA
IPR033275*E3 ubiquitin-protein ligase MARCH-like
IPR023210*NADP-dependent oxidoreductase domain
IPR014806*Ubiquitin-fold modifier-conjugating enzyme 1, IPR016135*Ubiquitin-conjugating enzyme/R
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR017853*Glycoside hydrolase superfamily, IPR033453*Glycosyl hydrolase family 30, TIM-barrel do
IPR015943*WD40/YVTN repeat-like-containing domain, IPR017986*WD40-repeat-containing domain,
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
NA
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
NA
NA
NA
IPR000554*Ribosomal protein S7e
IPR001254*Serine proteases, trypsin domain, IPR009003*Peptidase S1, PA clan, IPR001314*Peptida

IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
NA
NA
NA
IPR011583*Chitinase II, IPR029070*Chitinase insertion domain, IPR017853*Glycoside hydrolase sup
IPR011990*Tetratricopeptide-like helical domain, IPR019734*Tetratricopeptide repeat
NA
IPR001628*Zinc finger, nuclear hormone receptor-type, IPR013088*Zinc finger, NHR/GATA-type, IPR
NA
NA
IPR006202*Neurotransmitter-gated ion-channel ligand-binding domain, IPR006029*Neurotransmitter-
IPR006571*TLDc domain
IPR002159*CD36 family
IPR002159*CD36 family
IPR022271*Lipocalin, ApoD type, IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid bindin
IPR006989*NAB co-repressor, domain, IPR006988*Nab, N-terminal
NA
NA
IPR000218*Ribosomal protein L14P
IPR011333*SKP1/BTB/POZ domain, IPR011705*BTB/Kelch-associated
IPR029034*Cystine-knot cytokine, IPR032104*Spaetzle
NA
IPR011990*Tetratricopeptide-like helical domain, IPR021183*N-terminal acetyltransferase A, auxiliary
IPR001128*Cytochrome P450, IPR002401*Cytochrome P450, E-class, group I
IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A, IPR013201*Cathepsin pr
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B, IPR000997*Cholinester
NA
NA
IPR000215*Serpin family, IPR023796*Serpin domain
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR003439*ABC transporter-like, IPR027417*P-loop containing nucleoside triphosphate hydrolase, IP
NA
NA
NA
NA
NA
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
IPR029062*Class I glutamine amidotransferase-like, IPR015527*Peptidase C26, gamma-glutamyl hy
NA
IPR008978*HSP20-like chaperone, IPR001436*Alpha crystallin/Heat shock protein, IPR002068*Alpha
IPR025483*Lipase, eukaryotic, IPR029058*Alpha/Beta hydrolase fold, IPR006693*Partial AB-hydrolas
IPR000997*Cholinesterase, IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, typ
IPR011527*ABC transporter type 1, transmembrane domain, IPR003439*ABC transporter-like, IPR03
NA
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
NA

IPR014720*Double-stranded RNA-binding domain

IPR015889*Intradiol ring-cleavage dioxygenase, core, IPR000627*Intradiol ring-cleavage dioxygenas

IPR004046*Glutathione S-transferase, C-terminal, IPR012336*Thioredoxin-like fold, IPR010987*Gluta

IPR017986*WD40-repeat-containing domain, IPR015943*WD40/YVTN repeat-like-containing domain

IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily

IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase, IPR007235*Glycosyl transferase, family 28,

IPR011538*NADH-ubiquinone oxidoreductase 51kDa subunit, FMN-binding domain, IPR011537*NAD

NA

IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B

NA

NA

IPR009716*Ferroporti-1, IPR020846*Major facilitator superfamily domain

IPR032695*Integrin domain, IPR013517*FG-GAP repeat, IPR013649*Integrin alpha-2, IPR013519*In

IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily

IPR015819*Lipid transport protein, beta-sheet shell, IPR015255*Vitellinogen, open beta-sheet, IPR00

NA

NA

IPR001128*Cytochrome P450, IPR002403*Cytochrome P450, E-class, group IV

IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain

IPR013949*U3 small nucleolar RNA-associated protein 6, IPR011990*Tetratricopeptide-like helical do

IPR032715*Nuclear receptor coactivator 6, putative nucleic acid-binding region, IPR026638*Nuclear r

NA

IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain

NA

NA

NA

IPR000536*Nuclear hormone receptor, ligand-binding domain

NA

IPR014710*RmlC-like jelly roll fold, IPR006916*Popeye protein

IPR010920*LSM domain, IPR033871*Sm-like protein LSm5, IPR001163*LSM domain, eukaryotic/arc

IPR018482*Zinc finger, C4H2-type

NA

NA

IPR017946*PLC-like phosphodiesterase, TIM beta/alpha-barrel domain, IPR000008*C2 domain, IPR0

NA

NA

NA

IPR001873*Epithelial sodium channel

IPR001873*Epithelial sodium channel

NA

NA

IPR013783*Immunoglobulin-like fold, IPR003961*Fibronectin type III

NA

IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like

NA

IPR006214*Bax inhibitor 1-related

NA

IPR018490*Cyclic nucleotide-binding-like, IPR000595*Cyclic nucleotide-binding domain, IPR032406*
IPR015403*Sec7, C-terminal, IPR000904*Sec7 domain, IPR023394*Sec7 domain, alpha orthogonal
NA
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
IPR014782*Peptidase M1, membrane alanine aminopeptidase, N-terminal, IPR001930*Peptidase M1
NA
IPR006621*Nose resistant-to-fluoxetine protein, N-terminal, IPR009075*Acyl-CoA dehydrogenase/oxi
IPR000554*Ribosomal protein S7e
NA
IPR011538*NADH-ubiquinone oxidoreductase 51kDa subunit, FMN-binding domain, IPR019575*NAD
NA
NA
IPR001926*Tryptophan synthase beta subunit-like PLP-dependent enzyme
IPR011531*Bicarbonate transporter, C-terminal, IPR003020*Bicarbonate transporter, eukaryotic
NA
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR000571*Zinc finger, CCCH-type, IPR001841*Zinc finger, RING-type, IPR013083*Zinc finger, RING
NA
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR014186*S-formylglutathione hydrolase, IPR029058*Alpha/Beta hydrolase fold, IPR000801*Putativ
IPR011598*Myc-type, basic helix-loop-helix (bHLH) domain, IPR003650*Orange domain
IPR031481*Fucosyltransferase, N-terminal, IPR001503*Glycosyl transferase family 10
IPR019523*Protein phosphatase 1, regulatory subunit 15A/B, C-terminal
NA
IPR017986*WD40-repeat-containing domain, IPR015943*WD40/YVTN repeat-like-containing domain
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily
NA
NA
NA
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B, IPR000997*Cholinester
NA
NA
NA
IPR001623*DnaJ domain
IPR011992*EF-hand domain pair, IPR002048*EF-hand domain
IPR001452*SH3 domain, IPR011511*Variant SH3 domain
NA
NA
NA
NA
NA
NA
NA
IPR011991*Winged helix-turn-helix DNA-binding domain, IPR016158*Cullin homology, IPR019559*C
IPR013087*Zinc finger C2H2-type
IPR027413*GroEL-like equatorial domain, IPR002423*Chaperonin Cpn60/TCP-1 family

IPR010625*CHCH
NA
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR029044*Nucleotide-diphospho-sugar transferases
IPR016024*Armadillo-type fold, IPR010472*Formin, FH3 domain, IPR010473*Formin, GTPase-bindin
IPR008979*Galactose-binding domain-like
NA
IPR014756*Immunoglobulin E-set, IPR017868*Filamin/ABP280 repeat-like, IPR013783*Immunoglobu
NA
NA
IPR000891*Pyruvate carboxyltransferase, IPR013785*Aldolase-type TIM barrel
IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain
NA
NA
IPR003609*PAN/Apple domain, IPR001507*Zona pellucida domain
NA
NA
NA
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
NA
IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase
IPR029058*Alpha/Beta hydrolase fold, IPR000073*Alpha/beta hydrolase fold-1
IPR001873*Epithelial sodium channel
NA
NA
NA
NA
IPR020846*Major facilitator superfamily domain
IPR026051*Chitobiosyldiphosphodolichol beta-mannosyltransferase ALG1-like, IPR021841*Vacuolar
IPR002557*Chitin binding domain
IPR011013*Galactose mutarotase-like domain, IPR031727*Galactose mutarotase, N-terminal barrel, I
IPR002557*Chitin binding domain
IPR001747*Lipid transport protein, N-terminal, IPR011030*Vitellinogen, superhelical, IPR001846*von
IPR000618*Insect cuticle protein
IPR034223*Insect gut carboxypeptidase-like, carboxypeptidase domain, IPR000834*Peptidase M14,
NA
IPR013784*Carbohydrate-binding-like fold, IPR019008*Domain of unknown function DUF2012
IPR002659*Glycosyl transferase, family 31
NA
NA
IPR032665*Helix-loop-helix protein delilah, IPR011598*Myc-type, basic helix-loop-helix (bHLH) domai
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
NA
IPR028764*Kelch repeat and BTB domain-containing protein 8, IPR011333*SKP1/BTB/POZ domain,
IPR012496*TMC
IPR013057*Amino acid transporter, transmembrane domain

IPR011705*BTB/Kelch-associated, IPR011333*SKP1/BTB/POZ domain, IPR012983*PHR, IPR00021

IPR028831*DNA mismatch repair protein Pms1

IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain

NA

NA

NA

NA

IPR029044*Nucleotide-diphospho-sugar transferases, IPR003859*Beta-1,4-galactosyltransferase, IP

IPR008775*Phytanoyl-CoA dioxygenase

NA

IPR000719*Protein kinase domain, IPR009091*Regulator of chromosome condensation 1/beta-lacta

NA

IPR011333*SKP1/BTB/POZ domain, IPR003131*Potassium channel tetramerisation-type BTB domai

NA

IPR019393*WASH complex, subunit strumpellin

NA

IPR001932*PPM-type phosphatase domain, IPR015655*Protein phosphatase 2C family

IPR001096*Peptidase C13, legumain

NA

IPR016040*NAD(P)-binding domain, IPR002347*Short-chain dehydrogenase/reductase SDR

IPR025483*Lipase, eukaryotic, IPR029058*Alpha/Beta hydrolase fold, IPR006693*Partial AB-hydrola

IPR013087*Zinc finger C2H2-type

NA

IPR001357*BRCT domain

IPR000996*Clathrin light chain, IPR029058*Alpha/Beta hydrolase fold, IPR006693*Partial AB-hydrola

IPR033453*Glycosyl hydrolase family 30, TIM-barrel domain, IPR033452*Glycosyl hydrolase family 3

NA

IPR031984*Solute carrier family 3 member 2, N-terminal domain

IPR029058*Alpha/Beta hydrolase fold

NA

IPR020846*Major facilitator superfamily domain, IPR011701*Major facilitator superfamily

IPR008949*Isoprenoid synthase domain

IPR016186*C-type lectin-like/link domain, IPR001304*C-type lectin-like, IPR016187*C-type lectin fold

IPR008993*Tissue inhibitor of metalloproteinases-like, OB-fold, IPR004850*NtA (N-terminal agrin) do

NA

IPR011333*SKP1/BTB/POZ domain, IPR011705*BTB/Kelch-associated

IPR002172*Low-density lipoprotein (LDL) receptor class A repeat, IPR011042*Six-bladed beta-propel

NA

IPR002213*UDP-glucuronosyl/UDP-glucosyltransferase

IPR000618*Insect cuticle protein

NA

NA

NA

IPR002219*Protein kinase C-like, phorbol ester/diacylglycerol-binding domain, IPR015727*Protein kin

NA

IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B

IPR011989*Armadillo-like helical, IPR016024*Armadillo-type fold, IPR019451*RNA polymerase II ass

NA
NA
IPR016040*NAD(P)-binding domain, IPR011032*GroES-like, IPR013149*Alcohol dehydrogenase, C-t
IPR029064*50S ribosomal protein L30e-like, IPR000530*Ribosomal protein S12e, IPR004038*Riboso
NA
NA
IPR011701*Major facilitator superfamily, IPR020846*Major facilitator superfamily domain
IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat
NA
NA
NA
NA
NA
IPR003057*Invertebrate colouration protein, IPR022271*Lipocalin, ApoD type, IPR000566*Lipocalin/c
IPR001503*Glycosyl transferase family 10
NA
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
NA
IPR004837*Sodium/calcium exchanger membrane region, IPR004481*Sodium/potassium/calcium exc
IPR011333*SKP1/BTB/POZ domain, IPR011705*BTB/Kelch-associated
IPR019366*Clusterin-associated protein-1
NA
IPR011333*SKP1/BTB/POZ domain, IPR011705*BTB/Kelch-associated, IPR028764*Kelch repeat anc
IPR004245*Protein of unknown function DUF229, IPR017850*Alkaline-phosphatase-like, core domain
IPR019320*BLOC-1-related complex subunit 8
IPR029063*S-adenosyl-L-methionine-dependent methyltransferase, IPR025714*Methyltransferase do
IPR013087*Zinc finger C2H2-type
NA
IPR002490*V-type ATPase, V0 complex, 116kDa subunit family
NA
IPR003316*E2F/DP family, winged-helix DNA-binding domain, IPR015633*E2F Family, IPR028312*T
IPR028996*Ganglioside GM2 activator
IPR011991*Winged helix-turn-helix DNA-binding domain, IPR003150*DNA-binding RFX-type winged-
IPR029058*Alpha/Beta hydrolase fold, IPR003386*Lecithin:cholesterol/phospholipid:diacylglycerol acy
NA
IPR000536*Nuclear hormone receptor, ligand-binding domain
IPR000210*BTB/POZ domain, IPR011333*SKP1/BTB/POZ domain
NA
IPR000990*Innexin
IPR017986*WD40-repeat-containing domain, IPR015943*WD40/YVTN repeat-like-containing domain
IPR019143*JNK/Rab-associated protein-1, N-terminal
NA
NA
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR013830*SGNH hydrolase-type esterase domain
NA
NA

NA
NA
IPR026298*Blc2 family
IPR001096*Peptidase C13, legumain
IPR008914*Phosphatidylethanolamine-binding protein
NA
NA
NA
IPR013087*Zinc finger C2H2-type
NA
IPR014001*Helicase superfamily 1/2, ATP-binding domain, IPR027417*P-loop containing nucleoside
NA
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR001506*Peptidase M12A, IPR024079*Metallopeptidase, catalytic domain
IPR003609*PAN/Apple domain
IPR009071*High mobility group box domain, IPR001025*Bromo adjacent homology (BAH) domain
NA
IPR011333*SKP1/BTB/POZ domain, IPR000210*BTB/POZ domain, IPR028764*Kelch repeat and BT
NA
IPR011030*Vitellinogen, superhelical, IPR001747*Lipid transport protein, N-terminal, IPR015817*Vitel
IPR012599*Peptidase C1A, propeptide, IPR000668*Peptidase C1A, papain C-terminal, IPR013128*P
IPR006621*Nose resistant-to-fluoxetine protein, N-terminal, IPR002656*Acyltransferase 3
NA
NA
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain
NA
IPR019523*Protein phosphatase 1, regulatory subunit 15A/B, C-terminal
NA
IPR011705*BTB/Kelch-associated
IPR024096*NO signalling/Golgi transport ligand-binding domain, IPR016696*TRAPP I complex, subu
NA
NA
NA
NA
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
IPR011701*Major facilitator superfamily, IPR020846*Major facilitator superfamily domain
IPR019393*WASH complex, subunit strumpellin
IPR019180*Oxidoreductase-like, N-terminal
NA
NA
IPR029058*Alpha/Beta hydrolase fold, IPR001375*Peptidase S9, prolyl oligopeptidase, catalytic doma
NA
IPR000668*Peptidase C1A, papain C-terminal, IPR013128*Peptidase C1A
IPR000536*Nuclear hormone receptor, ligand-binding domain
NA
NA

NA
IPR000219*Dbl homology (DH) domain
NA
IPR001096*Peptidase C13, legumain
IPR019143*JNK/Rab-associated protein-1, N-terminal
IPR014854*Non-structural maintenance of chromosome element 4, C-terminal, IPR027786*Nse4/EID
IPR006179*5'-Nucleotidase/apyrase, IPR029052*Metallo-dependent phosphatase-like, IPR008334*5'-
NA
NA
NA
IPR002300*Aminoacyl-tRNA synthetase, class Ia, IPR009008*Valyl/Leucyl/Isoleucyl-tRNA synthetase
IPR000566*Lipocalin/cytosolic fatty-acid binding domain, IPR012674*Calycin, IPR002345*Lipocalin, I
NA
IPR011042*Six-bladed beta-propeller, TolB-like, IPR000033*LDLR class B repeat
IPR024135*Ragulator complex protein LAMTOR5
NA
NA
NA
NA
IPR001254*Serine proteases, trypsin domain, IPR001314*Peptidase S1A, chymotrypsin family, IPR0
NA
NA
NA
IPR000536*Nuclear hormone receptor, ligand-binding domain
IPR008969*Carboxypeptidase-like, regulatory domain
IPR000618*Insect cuticle protein
NA
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
IPR000536*Nuclear hormone receptor, ligand-binding domain
NA
IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain
IPR013128*Peptidase C1A, IPR000668*Peptidase C1A, papain C-terminal, IPR012599*Peptidase C1
IPR024518*Domain of unknown function DUF3421, IPR006616*DM9 repeat
IPR002861*Reeler domain
NA
NA
IPR029058*Alpha/Beta hydrolase fold, IPR002018*Carboxylesterase, type B
NA
IPR016090*Phospholipase A2 domain
IPR001762*Disintegrin domain, IPR024079*Metallopeptidase, catalytic domain, IPR006586*ADAM, c
IPR002318*Alanine-tRNA ligase, class IIc, IPR018162*Alanine-tRNA ligase, class IIc, anti-codon-bind
IPR011598*Myc-type, basic helix-loop-helix (bHLH) domain, IPR000014*PAS domain
IPR014105*Carotenoid/retinoid oxidoreductase, IPR023753*FAD/NAD(P)-binding domain, IPR002937
IPR024687*MMS19, C-terminal, IPR011989*Armadillo-like helical, IPR016024*Armadillo-type fold
IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like
NA
NA

IPR007867*Glucose-methanol-choline oxidoreductase, C-terminal, IPR012132*Glucose-methanol-cho

IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain

NA

IPR002509*NodB homology domain, IPR011330*Glycoside hydrolase/deacetylase, beta/alpha-barrel

NA

IPR011011*Zinc finger, FYVE/PHD-type, IPR013083*Zinc finger, RING/FYVE/PHD-type

NA

NA

NA

IPR001096*Peptidase C13, legumain

IPR032675*Leucine-rich repeat domain, L domain-like

IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain

NA

IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain

IPR002347*Short-chain dehydrogenase/reductase SDR, IPR016040*NAD(P)-binding domain

NA

IPR000536*Nuclear hormone receptor, ligand-binding domain

NA

NA

IPR008948*L-Aspartase-like

IPR032054*DNA replication factor Cdt1, C-terminal

IPR012674*Calycin, IPR002345*Lipocalin, IPR003057*Invertebrate colouration protein, IPR022271*Li

NA

NA

IPR011009*Protein kinase-like domain, IPR000719*Protein kinase domain

NA

IPR012674*Calycin

NA

IPR012674*Calycin, IPR000566*Lipocalin/cytosolic fatty-acid binding domain, IPR002345*Lipocalin, IP

IPR000618*Insect cuticle protein

NA

NA

IPR001164*Arf GTPase activating protein, IPR013328*6-phosphogluconate dehydrogenase, domain 2

NA

NA

IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like

NA

IPR006073*GTP binding domain, IPR023179*GTP-binding protein, orthogonal bundle domain, IPR01

IPR006568*PSP, proline-rich, IPR007180*Domain of unknown function DUF382

IPR028996*Ganglioside GM2 activator

NA

NA

IPR032675*Leucine-rich repeat domain, L domain-like, IPR001810*F-box domain

NA

IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR000048*IQ motif, EF-hand bindi

IPR008753*Peptidase M13, N-terminal domain, IPR000718*Peptidase M13, IPR029736*Endothelin-c

NA

IPR011545*DEAD/DEAH box helicase domain, IPR014001*Helicase superfamily 1/2, ATP-binding do

NA

IPR011705*BTB/Kelch-associated

IPR005135*Endonuclease/exonuclease/phosphatase

IPR007235*Glycosyl transferase, family 28, C-terminal

IPR001810*F-box domain, IPR032675*Leucine-rich repeat domain, L domain-like

IPR002659*Glycosyl transferase, family 31

IPR012674*Calycin, IPR002345*Lipocalin, IPR003057*Invertebrate colouration protein, IPR000566*Li

NA

NA

IPR007220*Origin recognition complex, subunit 2

NA

NA

IPR013083*Zinc finger, RING/FYVE/PHD-type, IPR027775*C2H2- zinc finger protein family subset, I

IPR004087*K Homology domain, IPR004088*K Homology domain, type 1

IPR029057*Phosphoribosyltransferase-like, IPR029933*Uridine-cytidine kinase-like 1

NA

IPR001478*PDZ domain, IPR034876*Partitioning defective protein 6, IPR000270*PB1 domain

NA

IPR028996*Ganglioside GM2 activator

NA

IPR017946*PLC-like phosphodiesterase, TIM beta/alpha-barrel domain

IPR001623*DnaJ domain

NA

NA

IPR012336*Thioredoxin-like fold, IPR004045*Glutathione S-transferase, N-terminal, IPR010987*Glut

IPR013087*Zinc finger C2H2-type, IPR013083*Zinc finger, RING/FYVE/PHD-type, IPR027775*C2H2-

IPR000668*Peptidase C1A, papain C-terminal

NA

NA

IPR029054*dUTPase-like, IPR008181*Deoxyuridine triphosphate nucleotidohydrolase, IPR033704*d

IPR023210*NADP-dependent oxidoreductase domain, IPR020471*Aldo/keto reductase

NA

IPR000618*Insect cuticle protein

IPR021139*NYN domain, limkain-b1-type, IPR029060*PIN domain-like

NA

NA

NA

IPR032675*Leucine-rich repeat domain, L domain-like

NA

IPR024768*Meiosis regulator and mRNA stability factor 1

ransferase

omal protein L7Ae/L30e/S12e/Gadd45

eptidase C1A

-terminal

omain, IPR013562*tRNA(Met) cytidine acetyltransferase TmcA, N-terminal, IPR000182*GNAT domai

B domain-containing protein 8, IPR011705*BTB/Kelch-associated

ed

tyric acid A receptor/Glycine receptor alpha, IPR006029*Neurotransmitter-gated ion-channel transme e-rich repeat, cysteine-containing subtype

-propeller, TolB-like

ine proteases, trypsin domain

in

ransferase, IPR006326*UDP-glycosyltransferase, MGT

PR002213*UDP-glucuronosyl/UDP-glucosyltransferase

in

ransferase

'eptidase C1A

in

opeptide inhibitor domain (I29)

*Tubulin/FtsZ, C-terminal, IPR018316*Tubulin/FtsZ, 2-layer sandwich domain

'*P-loop containing nucleoside triphosphate hydrolase

3TB/POZ domain, IPR011333*SKP1/BTB/POZ domain, IPR011042*Six-bladed beta-propeller, TolB-

)9003*Peptidase S1, PA clan

Glutathione S-transferase, N-terminal, IPR004046*Glutathione S-transferase, C-terminal

e, insert domain, IPR023797*RNA 3'-terminal phosphate cyclase domain, IPR000228*RNA 3'-termin

inal, IPR004046*Glutathione S-transferase, C-terminal, IPR012336*Thioredoxin-like fold gen, alpha/beta/gamma chain, C-terminal globular, subdomain 1, IPR001007*VWFC domain

ransferase, IPR006326*UDP-glycosyltransferase, MGT

ApoD type

*Tetracycline resistance protein TetA/multidrug resistance protein MdtG

like, IPR012336*Thioredoxin-like fold, IPR004045*Glutathione S-transferase, N-terminal

IPR029060*PIN domain-like

3149*Alcohol dehydrogenase, C-terminal, IPR011032*GroES-like, IPR013154*Alcohol dehydrogena

pe 11

phate 5-kinase, C-terminal, IPR023610*Phosphatidylinositol-4-phosphate 5-kinase

16162*Aldehyde dehydrogenase N-terminal domain

al, IPR013128*Peptidase C1A

67*Mitochondrial carrier protein

ase, N-terminal, IPR009100*Acyl-CoA dehydrogenase/oxidase, N-terminal and middle domain, IPR0

)9003*Peptidase S1, PA clan

, IPR012952*BING4, C-terminal domain

IPR010987*Glutathione S-transferase, C-terminal-like, IPR012336*Thioredoxin-like fold

2

)9003*Peptidase S1, PA clan

e triphosphate hydrolase, IPR003593*AAA+ ATPase domain, IPR030247*Canalicular multispecific o

IPR007235*Glycosyl transferase, family 28, C-terminal

'Glycosyl hydrolase family 30, beta sandwich domain, IPR033453*Glycosyl hydrolase family 30, TIM-

IPR017853*Glycoside hydrolase superfamily

ller, IPR011333*SKP1/BTB/POZ domain

C-terminal

ransferase

se lipase domain

ol-binding domain, IPR020454*Diacylglycerol/phorbol-ester binding

, transmembrane domain, IPR030247*Canalicular multispecific organic anion transporter 1, IPR0034

ching enzyme, N-terminal domain, IPR008928*Six-hairpin glycosidase-like, IPR032792*Glycogen deb

ureninase, IPR015424*Pyridoxal phosphate-dependent transferase, IPR015422*Pyridoxal phosphate

crystallin/Heat shock protein, IPR002068*Alpha crystallin/Hsp20 domain

)11009*Protein kinase-like domain, IPR009091*Regulator of chromosome condensation 1/beta-lacta

C-terminal

athione S-transferase, C-terminal-like, IPR004046*Glutathione S-transferase, C-terminal

sin domain, IPR009003*Peptidase S1, PA clan, IPR000859*CUB domain, IPR001314*Peptidase S1 de hydrolase superfamily

A, propeptide

eceptor class A repeat, IPR000998*MAM domain

ogenase C-terminal domain-like, IPR006108*3-hydroxyacyl-CoA dehydrogenase, C-terminal, IPR006

PR022271*Lipocalin, ApoD type, IPR003057*Invertebrate colouration protein

IYN domain, limkain-b1-type

Coatomer/clathrin adaptor appendage, Ig-like subdomain, IPR015151*Beta-adaptin appendage, C-te

IPR012336*Thioredoxin-like fold, IPR010987*Glutathione S-transferase, C-terminal-like

RWD-like

omain, IPR001139*Glycoside hydrolase family 30, IPR033452*Glycosyl hydrolase family 30, beta san

, IPR001680*WD40 repeat

ase S1A, chymotrypsin family

erfamily, IPR001223*Glycoside hydrolase family 18, catalytic domain

000536*Nuclear hormone receptor, ligand-binding domain

gated ion-channel transmembrane domain, IPR006028*Gamma-aminobutyric acid A receptor/Glycin

g domain, IPR003057*Invertebrate colouration protein

subunit

opeptide inhibitor domain (I29)

ase

R003593*AAA+ ATPase domain, IPR011527*ABC transporter type 1, transmembrane domain

drolase, IPR011697*Peptidase C26

a crystallin/Hsp20 domain, IPR031107*Small heat shock protein HSP20

se lipase domain

e B

0247*Canalicular multispecific organic anion transporter 1, IPR003593*AAA+ ATPase domain, IPR0 e, C-terminal

athione S-transferase, C-terminal-like, IPR004045*Glutathione S-transferase, N-terminal

C-terminal

)H ubiquinone oxidoreductase, F subunit, IPR019575*NADH-ubiquinone oxidoreductase 51kDa subu

tegrin alpha beta-propellor, IPR000413*Integrin alpha chain

1846*von Willebrand factor, type D domain, IPR001747*Lipid transport protein, N-terminal, IPR0158

omain

eceptor coactivator 6

haea-type

)11992*EF-hand domain pair, IPR001192*Phosphoinositide phospholipase C family, IPR011993*PH

Cyclic nucleotide-gated channel, C-terminal leucine zipper domain, IPR005821*Ion transport domain
oundle

, alanine aminopeptidase/leukotriene A4 hydrolase, IPR024571*ERAP1-like C-terminal domain, IPR

dase C-terminal

)H-ubiquinone oxidoreductase 51kDa subunit, iron-sulphur binding domain, IPR019554*Soluble ligan

G/FYVE/PHD-type

'e esterase

'ase

ullin protein, neddylation domain, IPR001373*Cullin, N-terminal, IPR016159*Cullin repeat-like-contai ıg domain, IPR011989*Armadillo-like helical

ılin-like fold, IPR001298*Filamin/ABP280 repeat

protein 14 C-terminal Fig4-binding domain

IPR017853*Glycoside hydrolase superfamily, IPR000322*Glycoside hydrolase family 31, IPR025887

Willebrand factor, type D domain, IPR015819*Lipid transport protein, beta-sheet shell, IPR015255*V

carboxypeptidase A

in

IPR011705*BTB/Kelch-associated

0*BTB/POZ domain

R027995*Galactosyltransferase, N-terminal, IPR027791*Galactosyltransferase, C-terminal

nase-inhibitor protein II, IPR011009*Protein kinase-like domain, IPR000408*Regulator of chromosom

n

se lipase domain

ıse lipase domain

0, beta sandwich domain, IPR017853*Glycoside hydrolase superfamily, IPR001139*Glycoside hydrc

main, IPR002350*Kazal domain

ller, TolB-like

ıase C mu-related, IPR020454*Diacylglycerol/phorbol-ester binding

embly factor Rtp1, C-terminal

terminal, IPR013154*Alcohol dehydrogenase, N-terminal, IPR020843*Polyketide synthase, enoylredu

omal protein L7Ae/L30e/S12e/Gadd45

cytosolic fatty-acid binding domain, IPR012674*Calycin, IPR002345*Lipocalin

changer

d BTB domain-containing protein 8

n, IPR017849*Alkaline phosphatase-like, alpha/beta/alpha

omain

ranscription factor E2F4, IPR011991*Winged helix-turn-helix DNA-binding domain, IPR032198*E2F

-helix domain

yltransferase

triphosphate hydrolase, IPR011545*DEAD/DEAH box helicase domain, IPR023214*HAD-like domai

B domain-containing protein 8, IPR011705*BTB/Kelch-associated

llinogen, open beta-sheet, subdomain 1

eptidase C1A

ınit 5, IPR007194*Transport protein particle (TRAPP) component

ain

family

-Nucleotidase, C-terminal, IPR004843*Calcineurin-like phosphoesterase domain, ApaH type

, editing domain

PR003057*Invertebrate colouration protein, IPR022271*Lipocalin, ApoD type

09003*Peptidase S1, PA clan

A, propeptide

ysteine-rich, IPR001590*Peptidase M12B, ADAM/reprolysin

ling domain, IPR018164*Alanyl-tRNA synthetase, class IIc, N-terminal

7*Amine oxidase

oline oxidoreductase, IPR023753*FAD/NAD(P)-binding domain, IPR000172*Glucose-methanol-cholii

ipocalin, ApoD type, IPR000566*Lipocalin/cytosolic fatty-acid binding domain

PR022271*Lipocalin, ApoD type, IPR003057*Invertebrate colouration protein

2, IPR008927*6-phosphogluconate dehydrogenase C-terminal domain-like, IPR029154*3-hydroxyisc

4813*Guanine nucleotide-binding protein-like 3, N-terminal domain, IPR027417*P-loop containing nu

ng site

onverting enzyme-like 1

main, IPR027417*P-loop containing nucleoside triphosphate hydrolase, IPR001650*Helicase, C-tern

ipocalin/cytosolic fatty-acid binding domain, IPR022271*Lipocalin, ApoD type

PR013087*Zinc finger C2H2-type

athione S-transferase, C-terminal-like

- zinc finger protein family subset

JTPase, trimeric

in, IPR016181*Acyl-CoA N-acyltransferase

embrane domain, IPR006201*Neurotransmitter-gated ion-channel

-like

nal phosphate cyclase, IPR013792*RNA 3'-terminal phosphate cyclase/enolpyruvate transferase, alp ase, N-terminal

)06091*Acyl-CoA oxidase/dehydrogenase, central domain rganic anion transporter 1, IPR003439*ABC transporter-like

-barrel domain

39*ABC transporter-like, IPR003593*AAA+ ATPase domain

branching enzyme, glucanotransferase domain, IPR006421*Glycogen debranching enzyme, metazo

e-dependent transferase, subdomain 2, IPR000192*Aminotransferase class V domain

mase-inhibitor protein II

A, chymotrypsin family

6176*3-hydroxyacyl-CoA dehydrogenase, NAD binding, IPR016040*NAD(P)-binding domain

erminal subdomain, IPR013037*Clathrin adaptor, beta-adaptin, appendage, Ig-like subdomain, IPR0

ndwich domain

ıe receptor alpha, IPR006201*Neurotransmitter-gated ion-channel

)27417*P-loop containing nucleoside triphosphate hydrolase unit, iron-sulphur binding domain, IPR019554*Soluble ligand binding domain

16*Vitellinogen, beta-sheet N-terminal, IPR011030*Vitellinogen, superhelical

domain-like, IPR028391*1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-1, IPR00

, IPR014710*RmlC-like jelly roll fold

034016*Aminopeptidase N-type

d binding domain, IPR011537*NADH ubiquinone oxidoreductase, F subunit

ning domain

7*Glycoside hydrolase family 31, N-terminal domain, IPR000519*P-type trefoil domain

/itellinogen, open beta-sheet, IPR015816*Vitellinogen, beta-sheet N-terminal ne condensation, RCC1

plase family 30

uctase domain

transcription factor, CC-MB domain

n

ne oxidoreductase, N-terminal

obutyrate dehydrogenase, NAD-binding domain, IPR011548*3-hydroxyisobutyrate dehydrogenase

ucleoside triphosphate hydrolase

ninal

ha/beta

a, IPR017853*Glycoside hydrolase superfamily, IPR010401*Glycogen debranching enzyme, IPR03

09028*Coatomer/calthrin adaptor appendage, C-terminal subdomain, IPR026739*AP complex subur

1711*Phospholipase C, phosphatidylinositol-specific, Y domain

2790*Glycogen debranching enzyme, C-terminal nit beta