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RESEARCH REPORT

# A preliminary investigation of immune-related components in the carapace of *Litopenaeus vannamei*

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## Abstract

The carapace of arthropods not only served as a protective exoskeleton, but also performed a wide range of physiological and biochemical functions. In this study, we preliminarily investigated the protein and metabolite components of the carapace of Pacific white shrimp *Litopenaeus vannamei* and their biological functions, focusing on their roles in the process of innate immunity. The structure of the carapace was analyzed by scanning electron microscopy (SEM), while quantitative proteomics and metabolomics were used to investigate its components and functions. A total of 1,108 proteins and 725 metabolites were identified in the carapace of *L. vannamei*, including 69 immune-related proteins and 9 immune-related metabolites. These diverse components are involved in metabolism, environmental responses and immunity, enriched in pathways such as Toll-like receptor, IMD, NOD-like receptor and melanogenesis, demonstrating the shrimp's ability to combat pathogens through both active and passive immune mechanisms. In conclusion, this study demonstrated that shrimp carapace plays an essential role in the innate immune process.

**Key Words**: *Litopenaeus vannamei*; carapace; exoskeleton; innate immune

### Introduction

Shrimp is an economically important aquatic animal. Shrimp farming is the most rapidly developing industry in aquaculture. *Litopenaeus vannamei* is one of the most important farmed shrimp species, and its farmed production accounts for about 80% of the total annual shrimp production. Nevertheless, the expansion of the global scale of shrimp aquaculture has led to an increase in the frequency of various types of epidemics and diseases, which has become a prominent constraint on the development of the industry (Zhang *et al*., 2019; N'Souvi *et al*., 2024).

As a member of the Crustacea, shrimp lacks acquired immune mechanisms and relies on its innate immune system, which comprises both humoral and cellular immunity, to clear invasive pathogens and foreign objects (Li and Xiang 2013a, 2013b; Zhang *et al*., 2019). The humoral defense of shrimp consists of the phenoloxigen activation system, the agglutination of lectins and the production of immune factors such as antimicrobial peptides, lysozyme, and hemolysin, which are synthesized and released in blood cells, and cellular immunity is in turn governed and influenced by humoral factors (Li and Xiang, 2013b; Kulkarni *et al*., 2021). While the carapace covering the entire body surface represents the initial line of defense for the innate immune system of the shrimp. It is often regarded as a physical barrier to the outside world. Several studies have demonstrated that the carapace contains a diverse range of physical, biochemical, and physiological defense components that change in response to pathogen invasion (Thomas and Blanford, 2003; Moret and Moreau, 2012). For instance, the deposition of melanin as a polymer in the carapace can effectively increase its thickness, hardening and cross-linking, thus preventing parasite invasion and increasing the physical defense of the shrimp shell. Melanin also has strong antimicrobial activity. It has also been demonstrated that phenol oxidase forms dark blackened plugs and increases melanin deposition to protect the healing of areas of exoskeletal damage caused by microbial invasion and mechanical injury, as well as the molting process (St. Leger *et al*., 1988; Hajek and St. Leger, 1994). Antimicrobial peptides produced by epidermal cells,

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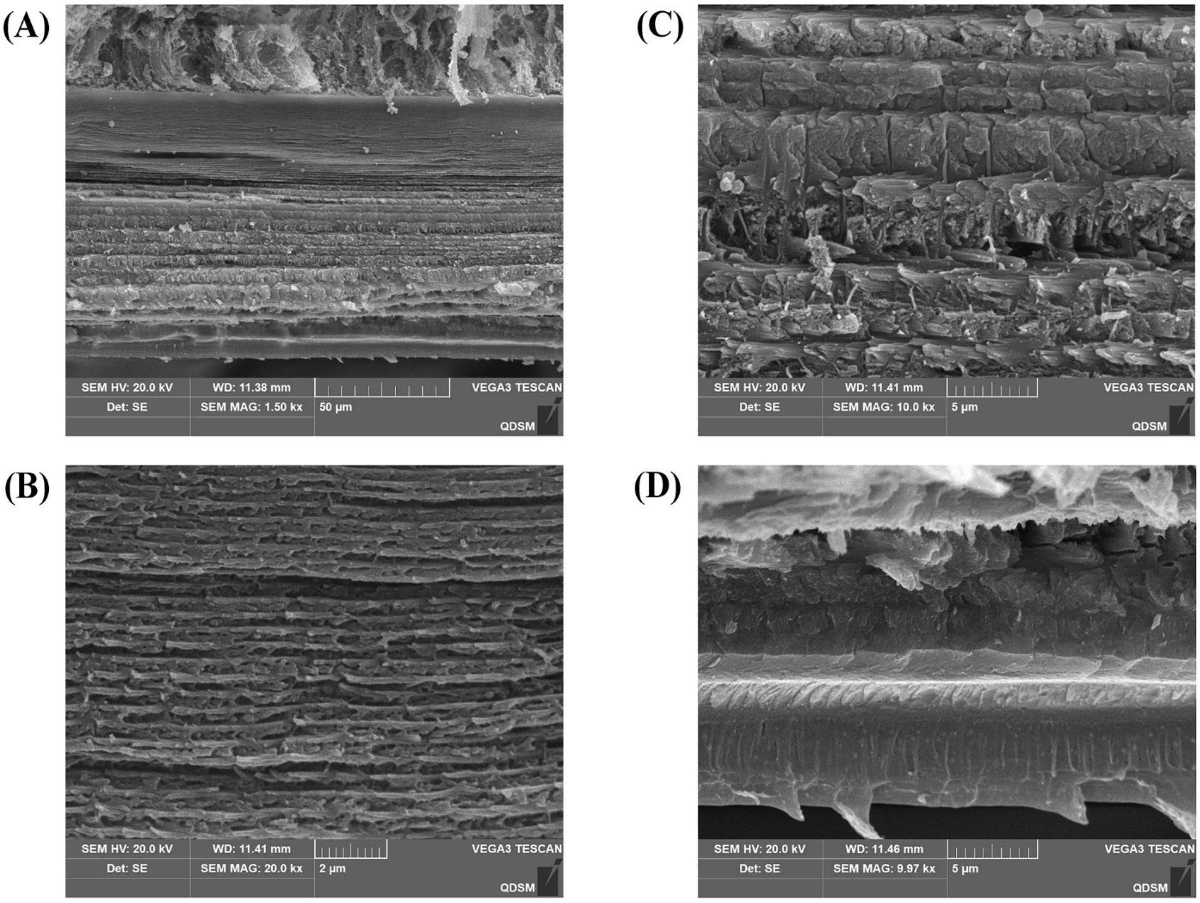

**Fig. 1** Structure of the shrimp carapace. (A) general view; (B) membranous layer; (C) endocuticle; (D) exocuticle and epicuticle (up: exocuticle; down: epicuticle)

such as appendicitis peptides, can enter the carapace during microbial invasion of the damaged cuticle (St. Leger *et al*., 1988). Additionally, chitin, a major component of shrimp shells, has been demonstrated to possess antipathogenic activity. Two main mechanisms have been identified for the inhibition of microorganisms by chitin. Firstly, the polycationic nature of chitin interferes with bacterial metabolism through electrostatic buildup on the bacterial cell surface (Chung *et al*., 2004; Je and Kim, 2006). Secondly, chitin enters the nucleus through osmosis and adsorbs onto the DNA molecule to block the transcription of DNA to RNA (Liu *et al*., 2001). Despite the presence of antimicrobial substances in shrimp carapace, studies on its immune-related components and functions are extremely scarce. Further research is needed to screen immune-related components and elucidate in detail the immune functions of shrimp carapace.

In this study, in order to characterize and further understand the physical barrier function of the shrimp exoskeleton in innate immune process, the three-dimensional structure of the carapace was first observed using SEM and characterized for its immune barrier function. Subsequently, label-free quantitative proteomic and non-targeted metabolomic assays were performed to determine the composition of the *L. vannamei* carapace and to explore its immunologically active functional components. In addition to being rich in essential protective and supportive components, shrimp carapace components are deeply involved in various aspects of metabolic reactions and immune regulation. The present study will contribute significantly to the understanding of the structural composition and innate immune functions of the shrimp carapace, and will provide support for the further discovery of indicators of disease resistance traits in the shrimp.

## Materials and methods

### *Sample collections*

Healthy adult shrimp *L. vannamei*, 45-50 g in weight and 8-12 cm in length, were collected from a market in Qingdao, China, and kept in a ventilated seawater recirculation tank at a temperature of 18-20 °C. The cephalothorax of the shrimp was removed with forceps in an aseptic environment, weighed, and then shredded with scissors and rinsed with aseptic seawater. A minimum of 500 mg

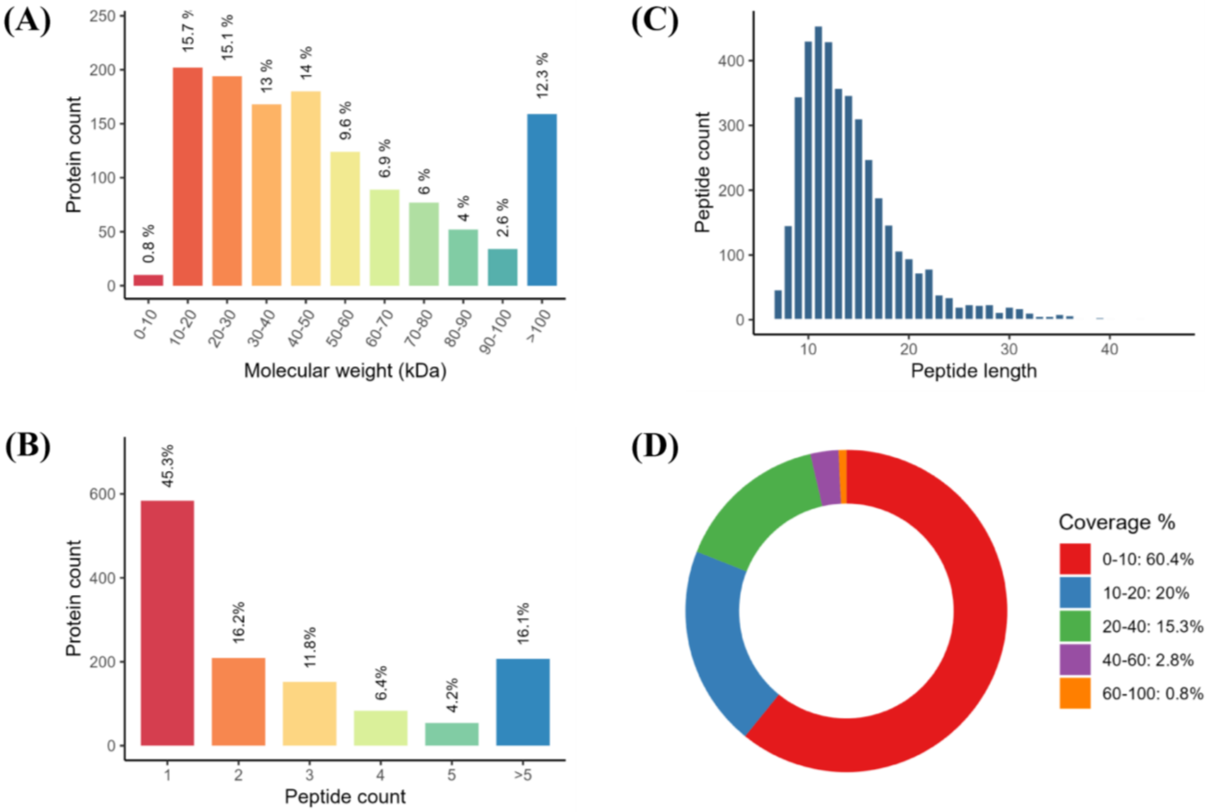

**Fig. 2** Quality control of proteome in shrimp carapace. (A) Mass distribution of protein fractions in shrimp carapace; (B) Distribution of unique peptides in the shrimp carapace proteome; (C) Distribution of peptide lengths of protein fractions; (D) Sequence coverage distribution of protein fractions

of cephalothorax samples was extracted from each shrimp, and different shrimp cephalothorax samples were combined to ensure that each set of samples originated from 3 distinct shrimp individuals. In this study, a total of 27 shrimp were used to prepare 9 parallel samples according to the aforementioned procedure, of which 3 were used for a label-free proteomic assay and 6 for metabolomic assay.

### *Microstructure observation*

The shrimp cephalothorax was stripped, clipped, and washed with 0.1 M phosphate-buffered saline (PBS) buffer for 10 minutes, repeated three times. This was followed by dehydration with ethanol in the order of 30%, 50%, 70%, and 100% by volume for 10 minutes. The samples were then treated with 80%, 90%, and 100% ethanol by volume for 10 minutes each. Following this, the samples were treated with 50% isoamyl acetate-ethanol solution and then subjected to critical point drying and Au-ion sputtering coating under vacuum conditions. Subsequently, the samples were subjected to scanning electron microscope (VEGA3, Tescan, Czech) for photography.

### *Label-free quantitative proteomics*

Shrimp carapace was extracted, quality controlled (QC), and hydrolyzed to peptides by the addition of trypsin at a ratio of 50:1. The peptides were separated in the liquid phase, then ionized with a nano-electrospray ionization source, and analyzed by Orbitrap Exploris 480 mass spectrometer (Thermo Fisher, USA). The data-dependent acquisition (DDA) mode was employed to identify and quantify the proteins in the raw data generated from the mass spectrometry analysis using the MaxQuant 2.1.4.0. The database utilized for the identification was the UniProt library of *L. vannamei*. The identified proteins were subjected to functional annotation using the Gene Ontology (GO), Kyoto Encyclopedia of Genes and Genomes (KEGG), and Evolutionary Genealogy of Genes: Non-supervised Orthologous Groups (eggNOG) databases.

### *Metabolomics*

Following grinding and centrifugation of the shrimp carapace, metabolites were extracted using an ice methanol solution as a medium. Samples were collected by Liquid chromatography-mass spectrometry (LC-MS) system following machine commands. Chromatographic separation was conducted using a Vanquish Flex UPLC ultra-high pressure liquid chromatography system (Thermo Fisher, USA), and reversed-phase separation was performed on an ACQUITY UPLC T3 column (100 mm×2.1 mm, 1.8 µm, Waters, UK). The column temperature was set at 40 degrees Celsius, and the

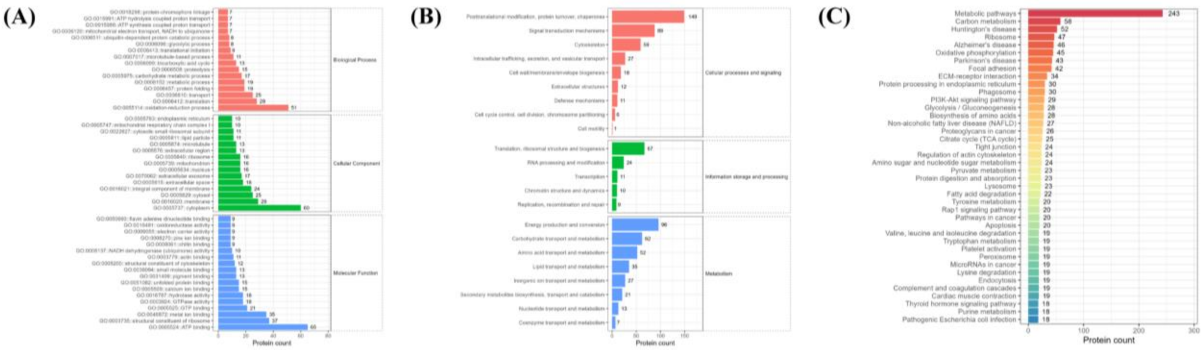

**Fig. 3** Functional annotation and classification of proteins in shrimp carapace. (A) GO terms distribution of proteins in shrimp carapace; (B) EggNOG function classification of proteins in shrimp carapace; (C) Enrichment of KEGG pathway in proteins in shrimp carapace

flow rate was 0.3 mL/min. The mobile phases employed were phase A: water (5 mmol/L ammonium acetate + 5 mmol/L acetic acid); and phase B: acetonitrile (LC-MS acetonitrile). The metabolites eluted from the column were detected using a Q-Exactive high-resolution tandem mass spectrometer (Thermo Scientific, USA) in both positive and negative ion modes. Peak picking, grouping, retention time correction, secondary peak grouping, isotope, and adduct labeling were performed on the acquired mass spectrometry data using XCMS software. The raw LC-MS data were processed with XCMS, CAMERA, and metaX tools. Individual ions were identified in conjunction with retention time (RT) and m/z data, the intensity of each peak was recorded, and a three-dimensional matrix containing arbitrarily assigned peak indices, sample names, and ion intensity information was generated. The metabolites were annotated with the KEGG and Human Metabolome Database (HMDB) databases, with an error threshold of 10 ppm. The metabolite molecular formulae were further identified and verified by isotopic distribution measurements. Finally, the metabolite metabolisms were further validated using an in-house database.

### *Statistical analysis*

Statistical analyses are done in R 4.3.1 software. In the proteomics study, for protein identification using MaxQuant software, it was specified that both graph false positives and protein false positives were less than 0.01. The raw intensity values of proteins were normalized to the median. In metabolomics studies, initially, peaks absent in greater than 50% of the QC samples or in greater than 80% of the actual samples were excluded. Subsequently, missing values were filled using the K-Nearest Neighbours method, Probabilistic Quotient Normalization and QC-robust spline batch correction for data normalization. Subsequently, the corrected data were subjected to further filtration, whereby all ions with coefficients of variation exceeding 30% in the QC samples were removed, thus eliminating any potential interference caused by fluctuations in the experimental process.

## Results

### *Carapace structure*

A cross-section of the carapace of *L. vannamei* was observed using SEM. The carapace of *L. vannamei* shows 4 main horizontal layers at distinct points: exocuticle, epicuticle, endocuticle, and the membranous layer, which is consistent with the basic cuticle structure of crustaceans (Fig. 1).

### *Protein recognition and functional enrichments*

### *Quality control*

Label-free quantitative proteomics analysis of the carapace of *L. vannamei* showed 4218 peptides corresponding to 10476 spectra and 1108 proteins (FDR < 0.01). The top 10 proteins with the highest ion intensity were A0A423TRM8 (Cuticular protein 34), A0A423U9U4 (Pupal cuticle protein 27), A0A3R7NXR2 (Gastrolith protein 30), A0A3R7QJX4 (Single VWC domain protein 1), X2KWE4 (Hemocyanin), A0A423TFA4 (Cuticle protein), A0A423TRF2 (Putative structural constituent of cuticle), A0A423TRP9 (Cuticular protein 34), A0A423SVT7 (Putative elastin a), and A0A3R7M0K6 (Peritrophin A, isoform A). The proteomic data have been deposited in the proteomics identification Database (PRIDE, https://www.ebi.ac.uk/pride/) with the accession number PXD047781. For protein mass distribution, the majority of identified proteins (86.6%) were located in the range of molecular weights 10-70 kDa (67.4%), as well as >100 kDa (12.3%) (Fig. 2a). Among all the proteins identified, 54.7% had two or more unique peptides (Fig. 2b). Each mass spectrometer has a measurement range that limits the length of identified peptides, so the distribution of peptide lengths can reflect the appropriateness of enzyme selection. More than 90% of the shrimp carapace protein fragments were within 30 amino acids in length and were predominantly concentrated between 7 and 15 amino acids (Fig. 2c), suggesting high efficiency in protein hydrolysis. In addition, 39.6% of all proteins had a sequence coverage distribution greater than 10%, and 19.6% had a sequence coverage distribution greater than

**Table 1** *L. vannamei* immune-related proteins

| Uniprot ID | Protein Annotation | Function Description |
|---|---|---|
| A0A423SI55 | Alpha 2 macroglobulin | Shrimp alpha-2-macroglobulin is abundantly expressed in plasma, highly up-regulated in response to microbial infections, and is involved in a variety of immune pathways such as the coagulation system, phagocytosis, and melanization. |
| A0A3R7MMK2 | Alpha2 macroglobulin isoform 2 | |
| A0A423UAM4 | Alpha2 macroglobulin isoform 2 | |
| A0A423U6P8 | Alpha2 macroglobulin isoform 3 | |
| A0A3R7LW48 | Alpha-2-macroglobulin | |
| Q283P7 | Anti-lipopolysaccharide AV-R isoform | Anti-lipopolysaccharide factors are a group of multifunctional broad-spectrum antimicrobial peptides that bind to microbial surface molecules, inhibit crustacean lipopolysaccharide-induced coagulation, and are important components of the shrimp innate immune system. |
| A0A423TC79 | Anti-lipopolysaccharide factor | |
| A0A3R7M6R4 | Cathepsin B | Cathepsin L and B play a major role in lymphoid organ function and may be associated with the degradation of foreign substances isolated in lymphoid organ spheres in *Penaeus monodon*. |
| A0A3R7SR07 | Cathepsin D | |
| A0A3R7PSB0 | Cathepsin F-like cysteine peptidase protein | |
| A0A423SD78 | Cathepsin L | |
| A0A423TKK4 | Chitin binding Peritrophin-A domain | Peritrophin and its analogous proteins can bind chitin and inhibit bacteria, interact with viral proteins, and be induced by pathogens. |
| A0A423SZM6 | Peritrophin | |
| A0A3R7M0K6 | Peritrophin A, isoform A | |
| A0A3R7M838 | Peritrophin-44 | |
| A0A3R7PKN3 | [PUTATIVE] peritrophin-44-like | |
| A0A3R7MSG4 | C-type lectin | C-type lectin and its functional analogs are important pattern recognition receptors (PRRs) that play an important role in the innate immune system of marine invertebrates. |
| A0A423T3D3 | C-type lectin | |
| A0A423TDI9 | C-type lectin | |
| A0A3R7SPH9 | C-type lectin 1 | |
| A0A423TJ07 | C-type lectin protein | |
| A0A423U3B4 | C-type lectin-like protein | |
| A0A3R7MAU7 | C-type lectin domain-containing protein | |
| A0A3R7P3L1 | C-type lectin domain-containing protein | |
| A0A423SP91 | C-type lectin domain-containing protein | |
| A0A423SRW7 | C-type lectin domain-containing protein | |
| A0A423SX67 | C-type lectin domain-containing protein | |
| A0A423U245 | C-type lectin containing domain protein | |
| A0A3R7QRV2 | Mannose-binding protein | |
| A0A423SM49 | Mannose-binding protein | |
| A0A423SY44 | Mannose-binding protein | |
| A0A423THS0 | Mannose-binding protein | |
| A0A423U9P3 | Mutant C-type lectin | |
| A0A3R7PGR8 | [PUTATIVE] C-type lectin-like | |
| A0A3R7SND6 | Crustin-like protein | Shell proteins contain the WAP structural domain, which is also found in many proteins involved in antimicrobial activity, bacterial conditioning, and so on. In decapod crustaceans, shell proteins constitute the largest group of antimicrobial peptides, with more than 50 isoforms, and exhibit antimicrobial activity against both Gram-positive and negative bacteria. |
| A0A3R7N8L8 | Pl-crustin 2 | |
| A0A3R7PLA8 | WAP domain-containing protein | |
| A0A3R7QWD1 | WAP domain-containing protein | |
| A0A423T5D9 | WAP domain-containing protein | |
| Q6GUA8 | Heat shock cognate 70 | Shrimp HSP70 binds to pattern recognition receptor LPS and β-1,3-glucan-binding protein, regulates shrimp innate immunity, and promotes melanogenesis through the phenoloxigen system. |
| A0A423SSL9 | [PUTATIVE] Heat shock protein 70 | |
| A0A3R7M776 | Histone H2A | Histones or histone-derived peptides produced by protein hydrolase cleavage have antimicrobial activity and play a crucial role in the innate immune defense of organisms. |
| A0A423SG35 | Histone H2A | |
| A0A423SY25 | Histone H2A | |
| A0A3R7PJW9 | Histone H2B | |
| A0A3R7Q5C5 | Histone H4 | |
| A0A423SWD4 | Kazal-like domain-containing protein | Most organisms counteract the effects of |

| | | |
|---|---|---|
| A0A423TC23 | Kazal-like domain-containing protein | pathogens and tumor proteases by producing protease inhibitors, which have important roles in modulating host immune defense proteins, inactivating pathogen proteases, coagulation, proPO activation, and antimicrobial activity. Serpin- and Kazal-like protease inhibitors have WAP structural domains, which are essential for their protease inhibition and antimicrobial activity. |
| A0A423TN18 | Kazal-type proteinase inhibitor | |
| A0A423SMH1 | Serine protease inhibitor | |
| A0A3R7N9K2 | Serine proteinase inhibitor | |
| A0A423THL6 | Serine proteinase inhibitor 7 | |
| A0A3R7QAN9 | Serine proteinase inhibitor B3 | |
| A0A3R7QNE7 | [PUTATIVE] serine proteinase inhibitor | |
| A0A3R7QN58 | TNF receptor-associated factor 6 (TRAF6) | TRAF6, as a toll pathway downstream component, activates the promoter of antimicrobial peptide genes in the shrimp and plays a key role in antimicrobial and antiviral responses by regulating AMP gene expression. |
| A0A3R7NEX2 | Prophenoloxidase activating enzyme | Cascades of phenol oxidase proteins (proPO) circulating in arthropod hemolymph defend against pathogens, prevents hemolymph loss, and form clots to block invasion. This process occurs in crustaceans. |
| A0A3R7R002 | Prophenoloxidase activating enzyme | |
| A0A3R7QAY1 | Prophenoloxidase activating enzyme III | |
| A0A3R7PF55 | Prophenoloxidase activating factor | |
| A0A423U5T5 | [PUTATIVE] ensconsin-like isoform X8 | Involved in the Toll and IMD signaling pathway, NF-kappa B signaling pathway |
| A0A423SAB7 | [PUTATIVE] isochorismatase domain-containing protein 2, mitochondrial-like | Involved in the Rap1 signaling pathway, MAPK signaling pathway, Toll and IMD signaling pathway, Toll-like receptor signaling pathway |
| A0A423TXT9 | [PUTATIVE] serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A-like | |
| A0A3R7QAA5 | Protein Spaetzle | Involved in the Toll and IMD signaling pathway |
| A0A3R7MQD9 | Serine protease | |
| A0A3R7PDR4 | Serine protease | |
| A0A3R7PUI1 | Serine protease | |
| A0A3R7QDL3 | Spaetzle domain-containing protein | |
| A0A3R7ML74 | UBC core domain-containing protein | |
| A0A423TBP9 | UBC core domain-containing protein | |

20% (Fig. 2d). The higher peptide coverage reflected the reliability of the identified proteins.

*Function annotation*

Based on GO, eggNOG and KEGG classification and annotation, the potential functions of the identified proteins in the carapace of *L. vannamei* were analyzed.

GO analysis showed that shrimp carapace proteins could be categorized into 16 biological processes (BP), 15 cellular components (CC), and 18 molecular functions (MF) (Fig. 3a). Most of the proteins in the BP categorization were classified into redox processes (51 proteins), translation (28 proteins) and transporter processes (25 proteins). One of the most significantly enriched subgroups in CC classification was cytoplasm (60 proteins), followed by membrane (29 proteins), cytosol (25 proteins) and integral component of membrane (24 proteins) subgroups. For MF classification, the ATP-binding (65 proteins) subgroup was the most abundant, followed by ribosomal structural components (37 proteins) and metal ion binding (35 proteins).

EggNOG analysis showed that, except for 33 proteins that were not annotated or were annotated as “Poorly characterized”, the proteins were classified into three functional categories: Cellular process and signaling, Signal transduction mechanism and Metabolism (Fig. 3b). The most mapped functional categories in the Cellular process and signaling category were Posttranslational modification, protein turnover, chaperones (149 proteins), followed by Signal transduction mechanisms (88 proteins) and Cytoskeleton (59 proteins). The Information storage and processing category was dominated by Translation, ribosomal structure and biogenesis (67 proteins), followed by Energy production and conversion (96 proteins). In the Metabolism category, the most mapped functional class was Energy production and conversion (96 proteins), followed by Carbohydrate transport and metabolism (62 proteins) and Amino acid transport and metabolism (52 proteins).

KEGG analysis showed that 647 proteins were enriched to regulatory pathways in the carapace proteins of *L. vannamei*, with the five most enriched pathways being Metabolic pathways (map01100, 243 proteins), Carbon metabolism (58 proteins), Huntington's disease (52 proteins), Ribosome (47 proteins), Alzheimer's disease (46 proteins) and Oxidative phosphorylation (45 proteins) (Fig. 3c). In addition, a variety of innate immune pathways were identified, such as the NOD-like receptor signaling pathway (map04621), Melanogenesis (map04916),

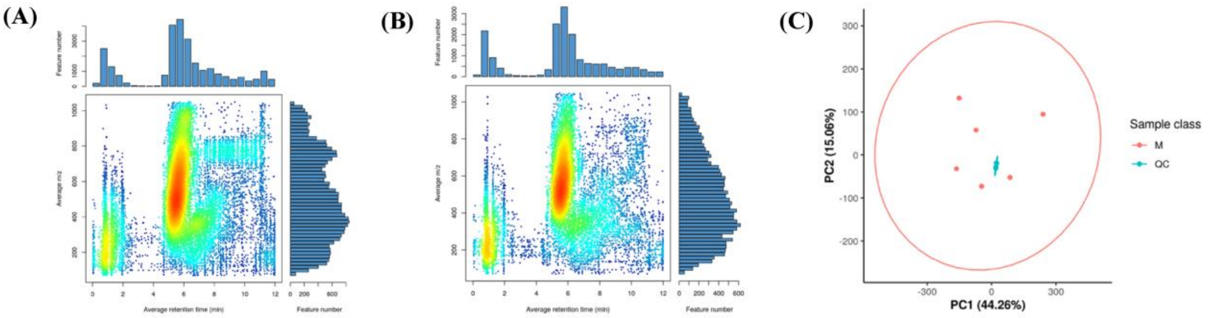

**Fig. 4** Ion distribution and PCA of metabolites in shrimp carapace. (A) Positive ion m/z-rt plot; (B) Negative ion m/z-rt plot; (C) PCA plot

the AMPK signaling pathway (map04152), and the complement and coagulation cascade (map04610), JAK-STAT pathway (map04630), FoxO signaling pathway (map04068), Toll and IMD signaling pathway (map04624), NF-kappa B signaling pathway (map04064), Toll-like receptor signaling pathway (map04620) and MAPK signaling pathway (map04010) (Table S1).

### *Important immune-related proteins*

Based on the functional annotation of the proteins and in conjunction with the research achievements of innate immunity in shrimp, we identified a series of active proteins in the carapace of *L. vannamei* that may have an immune function, including C-type lectin, Alpha-2-macroglobulin, Serpin, Kazal-type protease inhibitor, HSP70 protein, Serine protease, Cathepsin family and Spätzle protein. In addition, we identified 7 proteins related to melanin synthesis, including Hemocyanin and its L2, L3 subunits, Putative calcyphosin-like protein, GTP binding protein alpha subunit Go, Calmodulin, Heterotrimeric GTP-binding protein alpha subunit G-alpha-q. and 6 autophagy-associated proteins, including TNF receptor-associated factor 6 (TRAF6), Cathepsin B, Cathepsin D Cathepsin L, Serine/threonine-protein kinase TOR and Putative Ras-like protein 2 isoform X1, indicating an active innate immune process such as melanin deposition, autophagy and other processes in shrimp carapace (Table 1).

### *Metabolite recognition and functional enrichment of shrimp carapace*

### *Quality control*

The metabolome of the carapace of *L vannamei* was examined in both positive and negative ion modes, and a total of 26217 positive ion spectra and 17327 negative ion spectra were collected, of which 12111 accessions corresponded to the HMDB database and 9773 accessions corresponded to the KEGG database in the positive ion mode, and 6867 accessions corresponded to the HMDB database and 6115 accessions corresponded to the KEGG database in the negative ion mode, 6867 accessions in the positive ion mode and 6115 accessions in the KEGG database. The top 10 metabolites with the highest ion intensity were stearic acid, palmitic acid, betaine, octadecadienoate, trigonelline, oleic acid, eicosapentaenoic acid, docosahexaenoic acid, cis-8,11,14,17-eicosatetraenoic acid and phenylalanine. The metabolomic data obtained in this study have been deposited in the MetaboLights database (https://www.ebi.ac.uk/metabolights/) under the accession number MTBLS9162. For the mass-to-charge ratio and retention time distributions of metabolite ions, positive metabolite ions and negative metabolite ions tended to be concentrated in the average retention time of 4-8 min and the average m/z value between 400 and 800 (Fig. 4a, 4b). The results of the principal component analysis showed that the difference between the quality control samples of metabolites was very small, indicating that the quality control played a good effect (Fig. 4c).

### *Function annotation*

The potential functions of the identified metabolites in the carapace of *L. vannamei* were analyzed based on HMDB and KEGG classification and annotation. For the HMDB classification of primary metabolites, 25 HMDB super classes were enriched in both positive and negative ion modes with similar distribution patterns. Among them, the super classes with the overwhelmingly highest number of features of metabolites were all Lipids and lipid-like molecules, and the more frequent ones were organic heterocyclic compounds, organic acids and derivatives benzenoids, phenylpropanoids and polyketides and organic oxygen compounds (Fig. 5a). For KEGG functional enrichment of primary metabolites, KEGG level1 function was most predominantly enriched in the Metabolism major group and to a lesser extent in Organismal Systems and others, while KEGG level2 function was also predominantly enriched in the degradation-metabolism of amino acids, carbohydrates, lipids, cofactors, and vitamins metabolism as well as in the degradation-metabolism of xenobiotics (Fig. 5b). Finally, the primary metabolites were further compared with the local in-house database to obtain 725 secondary metabolites, and the results of the comparison were enriched into the KEGG database. A total of 578 different compounds were enriched to 174 KEGG pathways, among which the

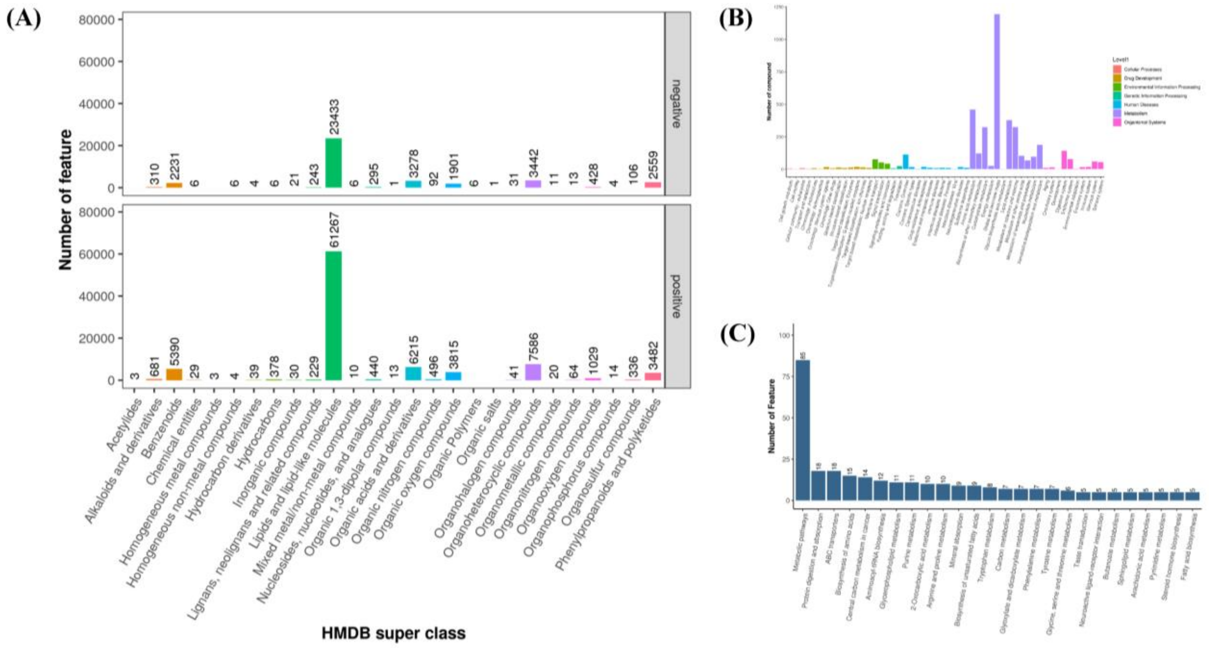

**Fig. 5** Functional annotation of metabolites in shrimp carapace. (A) Enrichment of HMDB pathway for primary metabolites; (B) Enrichment of KEGG pathway for primary metabolites; (C) Enrichment of KEGG pathway for secondary metabolites

most enriched compounds were Metabolic pathways (map01100), followed by Protein digestion and absorption (map04974), ABC transporters (map02010), Biosynthesis of amino acids (map01230), Central carbon metabolism in cancer (map05230), Aminoacyl-tRNA biosynthesis (map00970), and so on (Fig. 5c). Besides, several immune-related signaling pathways were also enriched among others, such as Melanogenesis (map04916), Autophagy-animal (map04140), FoxO signaling pathway (map04068), MAPK signaling pathway (map04010) and Rap1 signaling pathway (map04015) (Table S2).

*Important immune/disease-related metabolites*

Metabolomics studies have also identified several metabolites that may have potential immune functions, including leukotriene E4, lipoxin A4, prostaglandin A1, prostaglandin H1, thromboxane B3, oleic acid, eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA), and all of them act as antimicrobial agents (Table 2). In addition, tyrosine and cyclic adenosine monophosphate (cAMP) are involved in the process of melanogenesis; cAMP is also involved in the MAPK and Rap1 signaling pathways; L-glutamic acid is involved in the FoxO signaling pathway, and all of these pathways have been shown to play an immune function in shrimp. Additionally, 11 phospholipid molecules containing phosphatidylethanolamine heads that are involved in the autophagy process were also been identified (Table 2).

## Discussion

A variety of diseases caused by viruses, bacteria, fungi, and parasitic species pose a significant risk to shrimp at almost all life stages, such as white spot syndrome, which is mainly caused by the white spot syndrome virus (WSSV) (Flegel, 2012), and shrimp infectious hypodermal and hematopoietic necrosis, which is mainly caused by the infectious hypodermal and hematopoietic necrosis virus (IHHNV) (V.M *et al*., 2023). In addition, other diseases affect shrimp, including acute hepatopancreas necrosis disease mainly caused by *Vibrio parahaemolyticus* (AHPND) (Lai *et al*., 2015), and growth retardation in shrimp mainly caused by *Enterocytozoon hepatopenaei* (EHP) (López-Carvallo *et al*., 2022). These diseases not only cause significant losses to the fishery economy, but also seriously hinder the sustainable development of blue agriculture. Further study of the innate immune system can assist in the prevention and control of shrimp disease or the breeding for disease resistance.

Recent studies have confirmed that the crustacean carapace not only play an important role in protecting the body, such as maintaining physiological functions and adapting to the environment, but also perform a variety of physiological and biochemical functions (Brey *et al*., 1993) including resisting parasitic invasion (Moret and Moreau, 2012), antimicrobial (Du *et al*., 2009; Benhabiles *et al*., 2012), antioxidant (Seymour *et al*.,

**Table 2** *L. vannamei* immune-related metabolites

| HMDB ID | Metabolite Annotation | Function Description |
|---|---|---|
| HMDB0002183 | Docosahexaenoic acid (DHA) | EPA and DHA are metabolized to produce lipoxins, resolvins, protectins, and maresins for anti-inflammatory and antibacterial functions. |
| HMDB0001999 | Eicosapentaenoic acid (EPA) | |
| HMDB0000207 | Oleic acid | Oleic acid has antimicrobial effects by promoting the generation of free radicals and increase the formation of microbiotoxic lipid peroxides through direct action on microbial cell membranes. |
| HMDB0004385 | Lipoxin A4 | Lipoxin A4 (LXA4) regulates the inhibition of leukotriene (LT) production to suppress inflammation and modulates immune-related pathways such as NF-κB, PI3K/Akt, JAK-STAT, MAPK, Toll-like receptor, etc. |
| HMDB0002200 | Leukotriene E4 | Leukotrienes (LT), prostaglandins (PG), and Thromboxane B3 (TXB3) play a key role as important pro-inflammatory factors in regulating the quality and strength of the immune response. |
| HMDB0002656 | Prostaglandin A1 | |
| HMDB0013041 | Prostaglandin H1 | |
| HMDB0005099 | Thromboxane B3 | |

1996), and even inhibiting the proliferation of tumor cells (Kannan *et al*., 2011) and so on. However, there is no systematic investigation on the immune-related functions of crustacean carapace. The present study provides the first comprehensive investigation of the carapace components of the shrimp *L. vannamei* to explore its potential immune physiological and biochemical functions. The structural composition of the shrimp carapace was explored by SEM, and the carapace components were systematically analyzed by label-free quantitative proteomics and quantitative metabolomics techniques in a multi-omics approach. We identified many proteins and metabolites from the carapace of *L. vannamei*, which are involved in a wide range of physiological processes, including growth and development, metabolism and biosynthesis of carbohydrates, lipids, amino acids and nucleic acids, cellular signaling and intercellular signaling, immunomodulation, heat shock response, oxidative stress, and melanization response.

SEM observation of *L. vannamei* cuticle showed the same overall consists as other untreated shrimp carapaces for four layers: epicuticle, exocuticle, endocuticle and membranous layer (Fig. 1a) (Rahman and Maniruzzaman, 2023). The epicuticle represents the initial barrier of the shrimp organism against external factors and is characterized by a high concentration of lipids, proteins, and minerals. However, it lacks chitin, which is primarily involved in regulating the organism's osmotic pressure (Fig. 1d) (Lemos and Weissman, 2021). Similar observation has been reported in other literature for the cuticle of the lobster *Homarus americanus* (Sachs *et al*., 2006). The inner three layers are composed of chitin-protein fibers arranged in parallel layers, with the direction between the layers undergoing constant changes (Fig. 1c, 1d). The exocuticle is the primary structural layer of the shrimp exoskeleton, formed prior to molting and began to mineralize and darken in color shortly after molting (Fig. 1d). Fibrous platelets are visible in both the exocuticle and endocuticle of *L. vannamei*. Compared with the cross-section cuticles of the crab and the lobster *H. americanus* viewed by SEM, the endocuticle of *L. vannamei* was denser than the exocuticle. Moreover, *L. vannamei* has an additional membranous layer secreted by the endocuticle connected to the epidermal cells (Naleway *et al*., 2016).

The protein composition of the *L. vannamei* carapace reveals a strong association with oxidative stress defense and metabolic energy production. GO enrichment analysis highlights oxidation-reduction processes as the dominant BP, aligning with the carapace's role as the primary barrier against environmental oxidative damage. Additionally, ATP binding proteins are prevalent within the MF category, which complements the enrichment of energy production and conversion pathways in the eggNOG metabolism group. This suggests that the carapace is rich in proteins that support aerobic respiration, essential for meeting its energy demands, as further evidenced by the significant enrichment of the oxidative phosphorylation pathway in KEGG analysis. Notably, numerous innate immune-related KEGG signaling pathways were enriched, including autophagy, lysosomal, apoptosis, MAPK signaling pathway, C-type lectin receptor signaling pathway, JAK-STAT pathway, NOD-like receptor signaling pathway, Toll and IMD signaling pathways, NF-kappa B signaling pathway, and melanogenesis. These pathways involve two core immune mechanisms in shrimp: the synthesis of antimicrobial peptides and the melanization response. Specifically, shrimp respond to microbial invasion through core immune pathways such as the Toll and IMD signaling pathway and the NF-κB signaling pathway, which modulate the activation of the downstream antimicrobial peptides (AMPs) synthesis pathway as well as the phenol oxidative plasminogen activation cascade-regulated melanization (Tassanakajon *et al*., 2018). Anti-microbial peptides can effectively inhibit microbial activity in the carapace (Aweya *et al*., 2021). In contrast, melanin deposition in the carapace, like the insect 's melanization, effectively enhances the thickness, degree of hardening and cross-linking of the carapace, and possesses a degree of antimicrobial activity (Brey *et al*., 1993; Li and Xiang, 2013a; Zhang *et al*., 2019; Kulkarni *et al*., 2021). Overall, the proteins of *L. vannamei*'s carapace have a diverse composition and perform various biological functions including metabolism, environmental response and immunity. Regarding immune function, the carapace retains two core immune mechanisms in the shrimp, thus enabling active and passive defense against pathogens from physiological and biochemical sources.

For the shrimp carapace metabolome, the composition is highly diverse, with lipids as the major metabolites, alongside notable contributions from heterocyclic organic compounds, organic acids and their derivatives, benzene derivatives, phenylpropanoid compounds, and polyketides. Among these, chitin and chitosan stand out for their dual roles as a structural framework and immune barrier, with additional antibacterial activity demonstrated *in vitro*. Compared to proteins, research on the immune functions of metabolites remains underdeveloped. However, arthropods are known to produce a broad range of endogenous antimicrobial compounds, such as interferons, cytokines, free radicals, and fatty acids (Das, 2018). Phospholipids, in particular, play critical roles in immune processes; for example, phosphatidylserine is involved in apoptosis, while phosphatidylethanolamine plays a role in autophagy. Diets enriched with phospholipids have been shown to enhance the antioxidant capacity and innate immunity of *L. vannamei* (Liang *et al*., 2022). Our findings support the immune relevance of carapace metabolites, as several antimicrobial substances were identified, including leukotrienes, prostaglandins, thromboxanes, and unsaturated fatty acids such as oleic acid, EPA, and DHA. These compounds are central to inflammatory responses and innate immunity, consistent with previous reports (Das, 2018; Majima *et al*., 2023; Suchitha *et al*., 2024). For example, lipoxins limit inflammation while exerting antimicrobial properties (Sasaki and Yokomizo, 2019), and unsaturated fatty acids like EPA and DHA contribute to immunomodulation by targeting microbial membranes and promoting the production of free radicals and lipid peroxides. Furthermore, these fatty acids generate bioactive molecules, including resolvins and protectins, which exhibit anti-inflammatory and antibacterial effects (Santa-María *et al*., 2023). Additionally, tyrosine and cAMP were identified as key compounds linked to melanogenesis, highlighting their role in carapace pigmentation and immunity. Phosphatidylethanolamine derivatives, critical for autophagy, further underscore the functional diversity of carapace metabolites in supporting immune processes.

Overall, these findings highlight the carapace as more than a physical barrier, functioning as a metabolically active and immunologically significant structure. Its complex structure and composition integrates metabolic and immune responses, enabling shrimp to withstand external physiological and biochemical threats effectively.

## Conclusion

In the present study, label-free quantitative proteomics and metabolomics techniques are employed to identify proteins and metabolites in the carapace of *L. vannamei*. The findings demonstrate that, in addition to the protective and supportive components enriched in the shrimp carapace, its components are involved in multiple aspects of environmental stress, metabolic response, and immune response and regulation. It is evident that the shrimp carapace serves a multitude of physiological and biochemical functions beyond mere physical barriers and is intricately linked to innate immune regulation. This is a comprehensive investigation into the protein and metabolite composition of the carapace of *L. vannamei* in general. This study will contribute to the understanding of the exoskeleton of crustaceans and other aquatic invertebrates and provide new insights into the function of marine invertebrate exoskeleton in innate immunity.

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## References

Aweya JJ, Zheng Z, Zheng X, Yao D, Zhang Y. The expanding repertoire of immune-related molecules with antimicrobial activity in penaeid shrimps: a review. Rev. Aquacult. 13(4): 1907-1937, 2021.

Benhabiles MS, Salah R, Lounici H, Drouiche N, Goosen MFA, Mameri N. Antibacterial activity of chitin, chitosan and its oligomers prepared from shrimp shell waste. Food Hydrocoll. 29(1): 48-56, 2012.

Brey PT, Lee WJ, Yamakawa M, Koizumi Y, Perrot S, François M, et al. Role of the integument in insect immunity: epicuticular abrasion and induction of cecropin synthesis in cuticular epithelial cells. Proc. Natl. Acad. Sci. USA. 90(13): 6275-6279, 1993.

Chung YC, Su YP, Chen CC, Jia G, Wang HL, Wu JC, *et al*. Relationship between antibacterial activity of chitosan and surface characteristics of cell wall. Acta. Pharmacol. Sin. 25(7): 932-936, 2004.

Das UN. Antibiotic-like action of essential fatty acids. Can. Med. Assoc. J. 132(12): 1350, 1985.

Das UN. Arachidonic acid and other unsaturated fatty acids and some of their metabolites function as endogenous antimicrobial molecules: A review. J. Adv. Res. 11: 57-66, 2018.

de la Vega E, O'Leary NA, Shockey JE, Robalino J, Payne C, Browdy CL, *et al*. Anti-lipopolysaccharide factor in *Litopenaeus vannamei* (LvALF): A broad spectrum antimicrobial peptide essential for shrimp immunity against bacterial and fungal infection. Mol. Immunol. 45(7): 1916-1925, 2008.

Du Y, Zhao Y, Dai S, Yang B. Preparation of water-soluble chitosan from shrimp shell and its antibacterial activity Innovative. Food. Sci. Emerg. Technol. 10(1): 103-107, 2009.

Flegel TW. Historic emergence, impact and current status of shrimp pathogens in Asia. J. Invertebr. Pathol. 110(2): 166-173, 2012.

Hajek AE, St Leger RJ. Interactions Between Fungal Pathogens and Insect Hosts. Annu. Rev. Entomol. 39: 293-322, 1994.

Je JY, Kim SK. Chitosan Derivatives Killed Bacteria by Disrupting the Outer and Inner Membrane. J. Agric. Food. Chem. 54(18): 6629-6633, 2006.

Junprung W, Supungul P, Sangklai N, Tassanakajon A. Heat Shock Protein 70 Is a Damage-Associated Molecular Pattern That by Binding to Lipopolysaccharide and β-1,3-Glucan–Binding Protein Activates the Prophenoloxidase System in Shrimp. J. Immunol. 209(3): 582-592, 2022.

Kannan A, Hettiarachchy NS, Marshall M, Raghavan S, Kristinsson H. Shrimp shell peptide hydrolysates inhibit human cancer cell proliferation. J. Sci. Food Agric. 91(10): 1920-1924, 2011.

Kulkarni A, Krishnan S, Anand D, Uthaman SK, Otta SK, Karunasagar I, et al. Immune responses and immunoprotection in crustaceans with special reference to shrimp. Rev. Aquacult. 13(1): 431-459, 2021.

Lai HC, Ng TH, Ando M, Lee CT, Chen IT, Chuang JC, et al. Pathogenesis of acute hepatopancreatic necrosis disease (AHPND) in shrimp. Fish Shellfish Immunol. 47(2): 1006-1014, 2015.

Lemos D, Weissman D. Moulting in the grow-out of farmed shrimp: a review. Rev. Aquacult. 13(1): 5-17, 2021.

Li F, Xiang J. Recent advances in researches on the innate immunity of shrimp in China. Dev. Comp. Immunol. 39(1): 11-26, 2013a.

Li F, Xiang J. Signaling pathways regulating innate immune responses in shrimp. Fish Shellfish Immunol. 34(4): 973-980, 2013b.

Liang X, Luo X, Lin H, Han F, Qin JG, Chen L, et al. Growth, Health, and Gut Microbiota of Female Pacific White Shrimp, *Litopenaeus vannamei* Broodstock Fed Different Phospholipid Sources. Antioxidants. 11(6): 1143, 2022.

Liu J, Yu Y, Li F, Zhang X, Xiang J. A new anti-lipopolysaccharide factor (ALF) gene with its SNP polymorphisms related to WSSV-resistance of *Litopenaeus vannamei*. Fish Shellfish Immunol. 39(1): 24-33, 2014.

Liu XF, Guan YL, Yang D, Li Z, Yao K. Antibacterial action of chitosan and carboxymethylated chitosan. J. Appl. Polym. Sci. 79: 1324-1335, 2001.

López-Carvallo JA, Cruz-Flores R, Dhar AK. The emerging pathogen *Enterocytozoon hepatopenaei* drives a degenerative cyclic pattern in the hepatopancreas microbiome of the shrimp (*Penaeus vannamei*). Sci. Rep. 12(1): 14766, 2022.

Majima M, Hosono K, Ito Y, Amano H, Nagashima Y, Matsuda Y, et al. A biologically active lipid, thromboxane, as a regulator of angiogenesis and lymphangiogenesis. Biomed. Pharmacother. 163: 114831, 2023.

Moret Y, Moreau J. The immune role of the arthropod exoskeleton. ISJ-INVERT. SURVIV. J. 9(2): 200-206, 2012.

N'Souvi K, Sun C, Che B, Vodounon A. Shrimp industry in China: overview of the trends in the production, imports and exports during the last two decades, challenges, and outlook. Front. Sustainable Food Syst. 7, 2024.

Naleway SE, Taylor JRA, Porter MM, Meyers MA, McKittrick J. Structure and mechanical properties of selected protective systems in marine organisms. Mater. Sci. Eng. C. 59: 1143-1167, 2016.

Patat SA, Carnegie RB, Kingsbury C, Gross PS, Chapman R, Schey KL. Antimicrobial activity of histones from hemocytes of the Pacific white shrimp. Eur. J. Biochem. 271(23-24): 4825-4833, 2004.

Pongsomboon S, Wongpanya R, Tang S, Chalorsrikul A, Tassanakajon A. Abundantly expressed transcripts in the lymphoid organ of the black tiger shrimp, *Penaeus monodon*, and their implication in immune function. Fish Shellfish Immunol. 25(5): 485-493, 2008.

Ponprateep S, Vatanavicharn T, Lo CF, Tassanakajon A, Rimphanitchayakit V. Alpha-2-macroglobulin is a modulator of prophenoloxidase system in pacific white shrimp *Litopenaeus vannamai*. Fish Shellfish Immunol. 62: 68-74, 2017.

Rahman MM, Maniruzzaman M. A new route of production of the meso-porous chitosan with well-organized honeycomb surface microstructure from shrimp waste without destroying the original structure of native shells: Extraction, modification and characterization study. Results Eng. 19, 101362, 2023.

Sachs C, Fabritius H, Raabe D. Hardness and elastic properties of dehydrated cuticle from the lobster *Homarus americanus* obtained by nanoindentation. J. Mater. Res. 21(8): 1987-1995, 2006.

Santa-María C, López-Enríquez S, Montserrat-de la Paz S, Geniz I, Reyes-Quiroz ME, Moreno M, et al. Update on Anti-Inflammatory Molecular Mechanisms Induced by Oleic Acid. Nutrients. 15(1): 224, 2023.

Sasaki F, Yokomizo T. The leukotriene receptors as therapeutic targets of inflammatory diseases. Int. Immunol. 31(9): 607-615, 2019.

Seymour TA, Li SJ, Morrissey MT. Characterization of a natural antioxidant for shrimp shell waste. J. Agric. Food Chem. 44(3): 682-685, 1996.

Smith VJ, Dyrynda EA. Antimicrobial proteins: From old proteins, new tricks. Mol. Immunol. 68(2, Part B): 383-398, 2015.

St Leger RJ, Cooper RM, Charnley AK. The effect of melanization of *Manduca sexta* cuticle on growth and infection by *Metarhizium anisopliae*. J. Invertebr. Pathol. 52(3): 459-470, 1988.

Suchitha GP, Balaya RDA, Prasad TSK, Dagamajalu S. A signaling network map of Lipoxin (LXA4): an anti-inflammatory molecule. INFLAMM. RES. 73: 1099–1106, 2024.

Tassanakajon A, Rimphanitchayakit V, Visetnan S, Amparyup P, Somboonwiwat K, Charoensapsri W, et al. Shrimp humoral responses against pathogens: antimicrobial peptides and melanization. Dev. Comp. Immunol. 80: 81-93, 2018.

Thomas MB, Blanford S. Thermal biology in insect-parasite interactions. Trends Ecol. Evol. 18(7): 344-350 ,2003.

VM A, Raja B, Kesavan K, Vidya R, Sudhakaran R. Isolation and Identification of Pathogens from Shrimp: IHHNV. In: Thomas J, Amaresan N (eds), Aquaculture Microbiology. Springer Protocols Handbooks, Humana, New York, USA, pp 59-68, 2023.

Wang L, Li F, Wang B, Xiang J. Structure and partial protein profiles of the peritrophic membrane (PM) from the gut of the shrimp *Litopenaeus vannamei*. Fish Shellfish Immunol. 33(6): 1285-1291, 2012.

Wang PH, Wan DH, Gu ZH, Deng XX, Weng SP, Yu XQ, He JG. *Litopenaeus vannamei* tumor necrosis factor receptor-associated factor 6 (TRAF6) responds to *Vibrio alginolyticus* and white spot syndrome virus (WSSV) infection and activates antimicrobial peptide genes. Dev. Comp. Immunol. 35(1): 105-114, 2011.

Wang XW, Wang JX. Diversity and multiple functions of lectins in shrimp immunity. Dev. Comp. Immunol. 39(1): 27-38, 2013.

Zhang X, Yuan J, Sun Y, Li S, Gao Y, Yu Y, et al. Penaeid shrimp genome provides insights into benthic adaptation and frequent molting. Nat. Commun. 10(1): 356, 2019.

Zhang Y, Söderhäll I, Söderhäll K, Jiravanichpaisal P. Expression of immune-related genes in one phase of embryonic development of freshwater crayfish, *Pacifastacus leniusculus.* Fish Shellfish Immunol. 28(4): 649-653, 2010.

**Table S1** Description of the shrimp carapace proteome

| Uniprot ID | Gene name | Description |
|---|---|---|
| A0A076NBT3 | C7M84_022415 | Ubiquitin-60S ribosomal protein L40 |
| A0A0A0RA95 | C7M84_022691 | Mitochondrial cytochrome c oxidase subunit VIa |
| A0A159YJS1 | C7M84_004155 | Flotillin-2 |
| A0A2H4V3C1 | C7M84_012595 | Cardiac muscle actin |
| A0A386R1D6 | C7M84_003844 | Thioredoxin domain-containing protein 17 |
| A0A3G2YPU5 | C7M84_005222 | Heat shock protein 40 |
| A0A3R7LP93 | C7M84_021681 | Ubiquitin carboxyl-terminal hydrolase |
| A0A3R7LQ50 | C7M84_020788 | 14-3-3 epsilon-like transcript variant 1 |
| A0A3R7LQ73 | C7M84_020737 | Neurogenic locus Notch protein |
| A0A3R7LQL8 | C7M84_020405 | Heat shock protein 21 |
| A0A3R7LR38 | C7M84_021806 | Ras-related protein Rab-2A |
| A0A3R7LRD0 | C7M84_019794 | Putative WD repeat-containing protein 65 isoform X2 |
| A0A3R7LRU8 | C7M84_019425 | Thioredoxin |
| A0A3R7LS94 | C7M84_019081 | Putative collagen alpha-2(IV) chain-like |
| A0A3R7LSG6 | C7M84_020426 | Putative proteasome subunit alpha type-6-like |
| A0A3R7LSN5 | C7M84_018726 | Hemocyanin subunit L1 |
| A0A3R7LST6 | C7M84_020172 | Prohibitin |
| A0A3R7LU22 | C7M84_019218 | beta-N-acetylhexosaminidase |
| A0A3R7LU97 | C7M84_018980 | Hemocyte transglutaminase |
| A0A3R7LUE4 | C7M84_018870 | Spectrin alpha chain |
| A0A3R7LW48 | C7M84_021513 | Alpha-2-macroglobulin |
| A0A3R7LW71 | C7M84_015862 | Vegetative cell wall protein gp1-like |
| A0A3R7LWE3 | C7M84_021238 | Microsomal triglyceride transfer protein large subunit |
| A0A3R7LWS7 | C7M84_015390 | Endoribonuclease |
| A0A3R7LWT5 | C7M84_015406 | Venom dipeptidyl peptidase 4 |
| A0A3R7LWZ1 | C7M84_020739 | Neurogenic locus Notch protein |
| A0A3R7LXE7 | C7M84_020359 | Electron transfer flavoprotein-ubiquinone oxidoreductase |
| A0A3R7LXH7 | C7M84_020297 | Malate dehydrogenase, cytoplasmic (Fragment) |
| A0A3R7LXK4 | C7M84_014728 | Heat shock 70 kDa protein 14 |
| A0A3R7LY46 | C7M84_015673 | Transferrin |
| A0A3R7LY50 | C7M84_013057 | Phosphoglycerate mutase |
| A0A3R7LYG3 | C7M84_013980 | Homogentisate 1,2-dioxygenase |
| A0A3R7LYS2 | C7M84_013698 | Myosin heavy chain type 2 |
| A0A3R7LYV0 | C7M84_014984 | Phosphotriesterase-related protein |
| A0A3R7LZ83 | C7M84_019173 | Putative furin-like protease 2-like |
| A0A3R7LZD1 | C7M84_014546 | FAS1 domain-containing protein |
| A0A3R7LZE8 | C7M84_019010 | Farnesyl diphosphate synthase |
| A0A3R7LZM6 | C7M84_014317 | Putative coiled-coil domain-containing protein 27 |
| A0A3R7LZS3 | C7M84_018728 | Hemocyanin subunit L2 |
| A0A3R7M071 | C7M84_018356 | Transmembrane protein |
| A0A3R7M0K6 | C7M84_012112 | Peritrophin A, isoform A |
| A0A3R7M0S1 | C7M84_013298 | Putative dihydropyrimidinase-like isoform X4 |
| A0A3R7M0Z7 | C7M84_011824 | Pupal cuticle protein 27 |
| A0A3R7M105 | C7M84_013034 | 4-hydroxyphenylpyruvate dioxygenase |
| A0A3R7M141 | C7M84_017647 | Crustacyanin subunit C |
| A0A3R7M1D2 | C7M84_017498 | Putative lamin Dm0 |
| A0A3R7M1H0 | C7M84_012594 | Cardiac muscle actin |
| A0A3R7M1N6 | C7M84_011247 | Beta-1,3-glucan-binding protein |
| A0A3R7M1P4 | C7M84_011240 | Tubulin alpha chain |
| A0A3R7M1R2 | C7M84_012388 | 60S ribosomal protein L9 |
| A0A3R7M1U9 | C7M84_017090 | Elongation factor 1-alpha |
| A0A3R7M210 | C7M84_010936 | Dystroglycan 1 (Fragment) |
| A0A3R7M211 | C7M84_016955 | Crustocalcin |
| A0A3R7M266 | C7M84_010818 | Putative titin |
| A0A3R7M2D5 | C7M84_016655 | Putative aminopeptidase W07G4.4 |
| A0A3R7M2G8 | C7M84_010574 | RNA helicase |
| A0A3R7M2N0 | C7M84_016430 | High mobility group protein HMGI-C |
| A0A3R7M363 | C7M84_016021 | Lectin |

| | | |
|---|---|---|
| A0A3R7M382 | C7M84_010014 | isocitrate dehydrogenase (NADP(+)) |
| A0A3R7M3B7 | C7M84_010953 | Putative cuticle protein |
| A0A3R7M410 | C7M84_015328 | GDP-mannose 4,6-dehydratase |
| A0A3R7M413 | C7M84_009329 | Strongly chitin-binding protein-1 |
| A0A3R7M416 | C7M84_010365 | UAP56-interacting factor |
| A0A3R7M475 | C7M84_009168 | Putative N-acetylgalactosamine-6-sulfatase |
| A0A3R7M4E5 | C7M84_009027 | Beta-agarase |
| A0A3R7M4R5 | C7M84_008709 | Slow muscle myosin S1 heavy chain |
| A0A3R7M573 | C7M84_014431 | Hcy-binding domain-containing protein |
| A0A3R7M5H8 | C7M84_008105 | 40S ribosomal protein S20 |
| A0A3R7M5I8 | C7M84_008128 | Hemocyanin_C domain-containing protein |
| A0A3R7M5R5 | C7M84_008810 | Fibrous sheath CABYR-binding protein-like |
| A0A3R7M5U5 | C7M84_008757 | Sodium potassium-transporting ATPase subunit beta |
| A0A3R7M666 | C7M84_008485 | Putative proteasome subunit beta type-2-like |
| A0A3R7M6K0 | C7M84_013349 | Putative regucalcin-like |
| A0A3R7M6R4 | C7M84_006968 | Cathepsin B |
| A0A3R7M6V6 | C7M84_007951 | NADH-cytochrome b5 reductase |
| A0A3R7M776 | C7M84_012863 | Histone H2A |
| A0A3R7M7Y6 | C7M84_006103 | Putative Soluble NSF attachment protein |
| A0A3R7M838 | C7M84_012116 | Peritrophin-44 |
| A0A3R7M839 | C7M84_006862 | Disintegrin domain-containing protein |
| A0A3R7M895 | C7M84_011993 | Sorbitol dehydrogenase |
| A0A3R7M8B1 | C7M84_006686 | Phytanoyl-CoA dioxygenase family protein |
| A0A3R7M8B7 | C7M84_005781 | Derlin |
| A0A3R7M8Q6 | C7M84_011601 | Putative nesprin-1 |
| A0A3R7M8U0 | C7M84_006329 | NAD-dependent deacetylase sirtuin-2 |
| A0A3R7M8V7 | C7M84_006290 | WAP domain-containing protein (Fragment) |
| A0A3R7M921 | C7M84_011327 | Putative DNA/RNA-binding protein KIN17 |
| A0A3R7M947 | C7M84_011274 | Transaldolase |
| A0A3R7M956 | C7M84_011249 | Beta-1,3-glucan-binding protein |
| A0A3R7M9P9 | C7M84_005609 | Transmembrane emp24 domain-containing protein |
| A0A3R7MA32 | C7M84_010512 | Profilin |
| A0A3R7MA69 | C7M84_004185 | Carrier domain-containing protein |
| A0A3R7MA76 | C7M84_005100 | Protein NipSnap |
| A0A3R7MAB0 | C7M84_010383 | Protein kinase domain-containing protein |
| A0A3R7MAR1 | C7M84_003714 | Tricalbin-1 |
| A0A3R7MAU7 | C7M84_009993 | C-type lectin domain-containing protein |
| A0A3R7MB02 | C7M84_003456 | Hemocyanin |
| A0A3R7MB03 | C7M84_004460 | Dihydropteridine reductase |
| A0A3R7MB09 | C7M84_003428 | GDP-L-fucose synthase |
| A0A3R7MBI9 | C7M84_003030 | Isocitrate dehydrogenase [NAD] subunit, mitochondrial |
| A0A3R7MC01 | C7M84_002649 | 26S proteasome regulatory subunit 7 |
| A0A3R7MC29 | C7M84_009035 | ADP/ATP translocase |
| A0A3R7MC33 | C7M84_002578 | Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogena |
| A0A3R7MCL9 | C7M84_002199 | Heat shock protein |
| A0A3R7MD23 | C7M84_001876 | FTP domain-containing protein |
| A0A3R7MD77 | C7M84_008306 | DM5 domain-containing protein |
| A0A3R7MDD5 | C7M84_002427 | Putative fibrinogen-like protein 1 |
| A0A3R7MDX3 | C7M84_002019 | LAM_G_DOMAIN domain-containing protein |
| A0A3R7ME47 | C7M84_007587 | RNA-directed DNA polymerase |
| A0A3R7MEN4 | C7M84_007122 | Fructose-bisphosphate aldolase |
| A0A3R7MF99 | C7M84_000343 | Protein singed |
| A0A3R7MFH7 | C7M84_000101 | Putative 2-oxoglutarate dehydrogenase, mitochondrial isoform X5 |
| A0A3R7MFJ8 | C7M84_006449 | Uncharacterized oxidoreductase |
| A0A3R7MFW0 | C7M84_000677 | Putative sulfite oxidase, mitochondrial (Fragment) |
| A0A3R7MFX0 | C7M84_006221 | Putative urocanate hydratase |
| A0A3R7MFY8 | C7M84_006140 | Tubulin-specific chaperone D |
| A0A3R7MG31 | C7M84_025165 | DUF3421 domain-containing protein |
| A0A3R7MG35 | C7M84_021378 | Galactose mutarotase |
| A0A3R7MG76 | C7M84_000420 | Calcified cuticle protein CP19.0 isoform A |
| A0A3R7MG86 | C7M84_000414 | Putative monocarboxylate transporter 13-like isoform X1 |

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|---|---|---|
| A0A3R7MGW1 | C7M84_020730 | Neurogenic locus Notch protein |
| A0A3R7MGX0 | C7M84_020723 | Tubulin beta-2 chain |
| A0A3R7MH58 | C7M84_004987 | T-complex protein 1 subunit gamma |
| A0A3R7MHG5 | C7M84_020311 | SCP2 domain-containing protein |
| A0A3R7MHH3 | C7M84_024980 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 |
| A0A3R7MHL2 | C7M84_024880 | Basement membrane-specific heparan sulfate proteoglycan core protein |
| A0A3R7MHN6 | C7M84_024016 | peptidylprolyl isomerase |
| A0A3R7MHZ7 | C7M84_024581 | H(+)-transporting two-sector ATPase |
| A0A3R7MIL4 | C7M84_023228 | F-actin-capping protein subunit beta |
| A0A3R7MIM3 | C7M84_019467 | Crustacyanin subunit A |
| A0A3R7MIN0 | C7M84_019484 | Crustacyanin subunit A |
| A0A3R7MIT8 | C7M84_019348 | Fibroin heavy chain-like |
| A0A3R7MIU1 | C7M84_023970 | Saccharopine dehydrogenase-like oxidoreductase |
| A0A3R7MJ56 | C7M84_003263 | Growth and transformation-dependent protein |
| A0A3R7MJ77 | C7M84_022711 | 40S ribosomal protein S23 |
| A0A3R7MJJ9 | C7M84_018768 | GrpE protein homolog 2, mitochondrial |
| A0A3R7MJN5 | C7M84_022334 | NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 |
| A0A3R7MJQ0 | C7M84_023271 | Eukaryotic translation initiation factor 3 subunit H |
| A0A3R7MJV2 | C7M84_002630 | Tyrosine--tRNA ligase |
| A0A3R7MJX1 | C7M84_002597 | 40S ribosomal protein S3a |
| A0A3R7MK72 | C7M84_002401 | Putative RNA-binding protein 4 isoform X2 |
| A0A3R7MK80 | C7M84_022825 | Takeout |
| A0A3R7MKF3 | C7M84_018031 | Eukaryotic peptide chain release factor subunit 1 |
| A0A3R7MKL2 | C7M84_017767 | DNA primase large subunit |
| A0A3R7MKN3 | C7M84_016035 | Clip domain-containing protein (Fragment) |
| A0A3R7MKT2 | C7M84_014327 | fumarate hydratase |
| A0A3R7MKT6 | C7M84_001895 | Cytochrome b-c1 complex subunit 7 |
| A0A3R7MKT9 | C7M84_014050 | Putative sorting nexin-12 isoform X2 |
| A0A3R7MKU8 | C7M84_013680 | Protein quiver |
| A0A3R7MKW0 | C7M84_001848 | Clip domain serine proteinase |
| A0A3R7ML54 | C7M84_022264 | Putative calcium-activated chloride channel regulator 2 |
| A0A3R7ML74 | C7M84_007144 | UBC core domain-containing protein |
| A0A3R7MLJ1 | C7M84_021888 | CARDB domain-containing protein (Fragment) |
| A0A3R7MM06 | C7M84_016830 | Replicase polyprotein 1a |
| A0A3R7MM41 | C7M84_000756 | Putative peroxidase-like protein |
| A0A3R7MM97 | C7M84_013480 | Putative multifunctional protein ADE2-like |
| A0A3R7MMD6 | C7M84_016558 | Glycine cleavage system P protein |
| A0A3R7MME4 | C7M84_016528 | Putative Sarcoplasmic calcium-binding protein |
| A0A3R7MME6 | C7M84_010758 | Protein obstructor-E |
| A0A3R7MMK2 | C7M84_007739 | Alpha2 macroglobulin isoform 2 |
| A0A3R7MMN9 | C7M84_005801 | Putative cytochrome b-c1 complex subunit 2, mitochondrial |
| A0A3R7MN94 | C7M84_016002 | Putative histone-lysine N-methyltransferase ash1-like |
| A0A3R7MNJ3 | C7M84_025025 | Sulfotransferase family cytosolic 1B member 1 |
| A0A3R7MNP1 | C7M84_015694 | 60S ribosomal protein L27a |
| A0A3R7MNV6 | C7M84_015581 | Lysosomal alpha-glucosidase |
| A0A3R7MP37 | C7M84_024610 | 60S ribosomal protein L28 |
| A0A3R7MP64 | C7M84_015402 | Titin-like |
| A0A3R7MPK9 | C7M84_024297 | Probable tRNA(His) guanylyltransferase |
| A0A3R7MPQ8 | C7M84_024205 | D-3-phosphoglycerate dehydrogenase |
| A0A3R7MPR7 | C7M84_014955 | Putative heterogeneous nuclear ribonucleoprotein A1, A2/B1-like isoform X1 |
| A0A3R7MPY8 | C7M84_024003 | Adenosine kinase |
| A0A3R7MQD9 | C7M84_014585 | Serine protease |
| A0A3R7MQJ1 | C7M84_023560 | Secreted protein |
| A0A3R7MQM8 | C7M84_023450 | 60S ribosomal protein L5 |
| A0A3R7MQU7 | C7M84_023302 | Putative myosin heavy chain, non-muscle-like |
| A0A3R7MR04 | C7M84_014184 | ADP-ribosylation factor GTPase-activating protein 2 |
| A0A3R7MRF3 | C7M84_013920 | Carbonic anhydrase |
| A0A3R7MS58 | C7M84_013384 | Tubulin beta chain |
| A0A3R7MS79 | C7M84_013322 | Heat shock protein 60 |
| A0A3R7MSG4 | C7M84_022049 | C-type lectin |
| A0A3R7MSS7 | C7M84_012915 | 40S ribosomal protein S7 |

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|---|---|---|
| A0A3R7MT65 | C7M84_017770 | H+ ATPase |
| A0A3R7MTG0 | C7M84_013488 | Lectin 3 |
| A0A3R7MTH3 | C7M84_012484 | Tetratricopeptide repeat protein 36 |
| A0A3R7MTP4 | C7M84_008895 | UTP--glucose-1-phosphate uridylyltransferase |
| A0A3R7MUX2 | C7M84_011383 | Melanization interactin protein |
| A0A3R7MUZ7 | C7M84_011321 | Gelsolin |
| A0A3R7MV24 | C7M84_011242 | Beta-1,3-glucan-binding protein |
| A0A3R7MVJ7 | C7M84_010897 | Aspartate aminotransferase |
| A0A3R7MW47 | C7M84_010543 | Death-associated protein-like |
| A0A3R7MW78 | C7M84_010492 | ADP-ribosylation factor 1 |
| A0A3R7MXU9 | C7M84_009355 | NodB homology domain-containing protein |
| A0A3R7MXY5 | C7M84_009266 | Cuticle protein AMP3 |
| A0A3R7MY55 | C7M84_009103 | DLGAP1 |
| A0A3R7MYA0 | C7M84_009024 | VWFD domain-containing protein |
| A0A3R7MYQ8 | C7M84_008696 | Putative histidine triad nucleotide-binding protein 2, mitochondrial-like |
| A0A3R7MYS0 | C7M84_008666 | K1109 (Fragment) |
| A0A3R7MZN0 | C7M84_008122 | 40S ribosomal protein S4 |
| A0A3R7MZV2 | C7M84_008017 | Phosphate carrier protein, mitochondrial |
| A0A3R7N1Q9 | C7M84_006594 | Clip domain serine proteinase 1 |
| A0A3R7N1S8 | C7M84_006567 | Metallophos domain-containing protein |
| A0A3R7N2L2 | C7M84_005909 | Ribosomal protein L7 |
| A0A3R7N326 | C7M84_005499 | Thioredoxin-disulfide reductase |
| A0A3R7N3Q3 | C7M84_004924 | Unconventional myosin-6 (Fragment) |
| A0A3R7N4F5 | C7M84_004378 | Putative ubiquitin carboxyl-terminal hydrolase 4 isoform X1 |
| A0A3R7N4N2 | C7M84_004228 | Leucine-rich repeat-containing protein 14 |
| A0A3R7N4Z8 | C7M84_003947 | 40S ribosomal protein S6 |
| A0A3R7N521 | C7M84_003902 | ornithine aminotransferase |
| A0A3R7N5R2 | C7M84_003308 | EH domain-containing protein 1 |
| A0A3R7N6N6 | C7M84_002614 | Rab GDP dissociation inhibitor |
| A0A3R7N738 | C7M84_002314 | Actin-related protein 2/3 complex subunit |
| A0A3R7N799 | C7M84_002150 | Putative ribosome-binding protein 1 isoform X4 (Fragment) |
| A0A3R7N7T1 | C7M84_001761 | 26S proteasome non-ATPase regulatory subunit 2 |
| A0A3R7N7W4 | C7M84_001695 | Ubiquitin-like domain-containing protein |
| A0A3R7N886 | C7M84_001377 | Myosin essential light chain |
| A0A3R7N8L8 | CruIa-6 | Pl-crustin 2 |
| A0A3R7N980 | C7M84_000601 | Peptidyl-prolyl cis-trans isomerase |
| A0A3R7N9B8 | C7M84_000503 | Pro-resilin protein |
| A0A3R7N9H7 | C7M84_000416 | Masquerade-like protein (Fragment) |
| A0A3R7N9K2 | C7M84_000333 | Serine proteinase inhibitor |
| A0A3R7NA33 | C7M84_025409 | RuvB-like helicase |
| A0A3R7NAC3 | C7M84_025144 | Tryptophan 2,3-dioxygenase |
| A0A3R7NAG9 | C7M84_025048 | Lipid storage droplet protein |
| A0A3R7NAP1 | C7M84_024882 | Basement membrane-specific heparan sulfate proteoglycan core protein |
| A0A3R7NBX4 | C7M84_023821 | Peptidyl-prolyl cis-trans isomerase (Fragment) |
| A0A3R7NBY5 | C7M84_023808 | Putative 26S proteasome non-ATPase regulatory subunit 14 |
| A0A3R7NCQ6 | C7M84_023157 | 26S protease regulatory subunit 4 |
| A0A3R7NCZ7 | C7M84_022939 | 60S ribosomal protein L12 |
| A0A3R7ND47 | C7M84_022826 | FAS1 domain-containing protein |
| A0A3R7NDA8 | C7M84_022687 | Tail muscle elongation factor 1 gamma |
| A0A3R7NDF4 | C7M84_022598 | Uncharacterized protein |
| A0A3R7NDT7 | C7M84_022329 | Elongin-C |
| A0A3R7NDX5 | C7M84_022265 | Fibroin heavy chain-like |
| A0A3R7NE38 | C7M84_022082 | Calpain B (Fragment) |
| A0A3R7NEX2 | C7M84_015962 | Prophenoloxidase activating enzyme |
| A0A3R7NNF1 | C7M84_019618 | Transmembrane protein |
| A0A3R7NP30 | C7M84_019198 | Neurofilament heavy polypeptide (Fragment) |
| A0A3R7NP48 | C7M84_019121 | Peptidase S1 domain-containing protein |
| A0A3R7NPL9 | C7M84_018727 | Hemocyanin subunit L2 |
| A0A3R7NPN3 | C7M84_018694 | Superoxide dismutase |
| A0A3R7NRQ6 | C7M84_017089 | Elongation factor 1-alpha |
| A0A3R7NRV9 | C7M84_016985 | NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial |

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| A0A3R7NRW6 | C7M84_016954 | SPARC-related modular calcium-binding protein 2 |
| A0A3R7NS31 | C7M84_016751 | EGF-like domain-containing protein (Fragment) |
| A0A3R7NSG1 | C7M84_016474 | GH18 domain-containing protein |
| A0A3R7NTF9 | C7M84_015718 | MOSC domain-containing protein |
| A0A3R7NTQ3 | C7M84_015514 | Chitin-binding type-2 domain-containing protein |
| A0A3R7NUF2 | C7M84_014948 | Gastrolith protein |
| A0A3R7NUJ0 | C7M84_014845 | Putative rho GDP-dissociation inhibitor 2 (Fragment) |
| A0A3R7NUR5 | C7M84_014673 | Ig-like domain-containing protein |
| A0A3R7NWG1 | C7M84_013216 | Extensin-like |
| A0A3R7NWY8 | C7M84_012785 | MICOS complex subunit |
| A0A3R7NXR2 | C7M84_012114 | Gastrolith protein 30 |
| A0A3R7NXU5 | C7M84_012048 | Laminin subunit gamma-3 |
| A0A3R7NYM0 | C7M84_011273 | NADH-ubiquinone oxidoreductase 39 kDa subunit |
| A0A3R7NYM7 | C7M84_011248 | Beta-1,3-glucan-binding protein |
| A0A3R7NYY6 | C7M84_010969 | 26S protease regulatory subunit 6A |
| A0A3R7NZ48 | C7M84_010820 | Titin |
| A0A3R7NZ83 | C7M84_010754 | Putative eukaryotic peptide chain release factor GTP-binding subur |
| A0A3R7P0W5 | C7M84_009271 | Cuticle protein AM/CP1114 |
| A0A3R7P174 | C7M84_009012 | ANK_REP_REGION domain-containing protein (Fragment) |
| A0A3R7P1C7 | C7M84_008844 | Four and a half LIM domains protein 2 |
| A0A3R7P3F9 | C7M84_007121 | Aminopeptidase |
| A0A3R7P3L1 | C7M84_006993 | C-type lectin domain-containing protein |
| A0A3R7P4C8 | C7M84_006377 | Proteasome subunit beta |
| A0A3R7P4D7 | C7M84_021395 | fructose-bisphosphatase |
| A0A3R7P4H1 | C7M84_006288 | Oplophorus-luciferin 2-monooxygenase non-catalytic subunit |
| A0A3R7P4J3 | C7M84_021247 | Apoptosis-inducing factor 1, mitochondrial |
| A0A3R7P4W6 | C7M84_020923 | T-complex protein 1 subunit epsilon |
| A0A3R7P4Z4 | C7M84_005894 | Separase |
| A0A3R7P543 | C7M84_020736 | Neurogenic locus Notch protein |
| A0A3R7P558 | C7M84_020685 | G-protein coupled receptor 64 |
| A0A3R7P5D9 | C7M84_020533 | Metalloendopeptidase |
| A0A3R7P5Q2 | C7M84_005208 | Putative granulins-like isoform X3 |
| A0A3R7P608 | C7M84_020015 | NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial |
| A0A3R7P657 | C7M84_004822 | Putative serine/threonine-protein phosphatase PP1-beta catalytic subunit-like |
| A0A3R7P6G3 | C7M84_004579 | FAS1 domain-containing protein |
| A0A3R7P6R2 | C7M84_004372 | Putative phosphatidylinositol transfer protein beta isoform isoform X1 |
| A0A3R7P6V3 | C7M84_019469 | Crustacyanin subunit C |
| A0A3R7P724 | C7M84_019389 | Spermatogonial stem-cell renewal factor |
| A0A3R7P7D5 | C7M84_019118 | Putative hemocytin |
| A0A3R7P7M0 | C7M84_018950 | Retinitis pigmentosa 1-like 1 protein |
| A0A3R7P7N6 | C7M84_018903 | Extended synaptotagmin-like protein 2a (Fragment) |
| A0A3R7P8U6 | C7M84_002540 | phosphoserine transaminase |
| A0A3R7P9H1 | C7M84_001986 | Putative dehydrogenase/reductase SDR family member 4-like |
| A0A3R7P9I3 | C7M84_002017 | Ras protein (Fragment) |
| A0A3R7P9X4 | C7M84_017214 | protein disulfide-isomerase |
| A0A3R7PA29 | C7M84_001471 | Ubiquitin carboxyl-terminal hydrolase |
| A0A3R7PA33 | C7M84_017087 | Troponin H |
| A0A3R7PAD7 | C7M84_016871 | ATP citrate synthase (Fragment) |
| A0A3R7PAF4 | C7M84_016834 | Rap1 GTPase-GDP dissociation stimulator 1-B |
| A0A3R7PAJ9 | C7M84_016727 | Polypyrimidine tract-binding protein 1 |
| A0A3R7PAK4 | C7M84_001080 | Reticulon |
| A0A3R7PAL1 | C7M84_001061 | BOWMAN_BIRK domain-containing protein |
| A0A3R7PAP7 | C7M84_016642 | Vigilin |
| A0A3R7PAT7 | C7M84_016573 | Moesin/ezrin/radixin homolog 1 |
| A0A3R7PAZ3 | C7M84_016427 | Glycerol-3-phosphate dehydrogenase [NAD(+)] |
| A0A3R7PBK1 | C7M84_021769 | Protein TANC2 |
| A0A3R7PBR0 | C7M84_015895 | Actin T2 |
| A0A3R7PBU9 | C7M84_021485 | Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial |
| A0A3R7PC66 | C7M84_025262 | 60S acidic ribosomal protein P2 |
| A0A3R7PCD0 | C7M84_020968 | Putative prostatic acid phosphatase |
| A0A3R7PCP7 | C7M84_015129 | Farnesoic acid O-methyltransferase (Fragment) |

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| A0A3R7PCQ1 | C7M84_024778 | Putative antimicrobial peptide |
| A0A3R7PCW4 | C7M84_020447 | Putative hemocyte protein-glutamine gamma-glutamyltransferase |
| A0A3R7PD39 | C7M84_014802 | 10-formyltetrahydrofolate dehydrogenase |
| A0A3R7PDE1 | C7M84_024181 | Putative stathmin isoform X3 |
| A0A3R7PDI4 | C7M84_024081 | Acyl-CoA-binding protein |
| A0A3R7PDR4 | C7M84_023841 | Serine protease |
| A0A3R7PDY2 | C7M84_014112 | Chemosensory protein |
| A0A3R7PE77 | C7M84_019302 | Putative beta-ureidopropionase-like |
| A0A3R7PE80 | C7M84_019277 | Peptidase_M3 domain-containing protein |
| A0A3R7PEB6 | C7M84_019142 | Receptor for activated protein kinase c1 |
| A0A3R7PEF6 | C7M84_013600 | arginine kinase |
| A0A3R7PEG6 | C7M84_023143 | Cuticle protein 6 |
| A0A3R7PEJ3 | C7M84_022967 | Putative calumenin |
| A0A3R7PEN2 | C7M84_018729 | Hemocyanin |
| A0A3R7PEP7 | C7M84_018665 | Ribosomal protein |
| A0A3R7PEQ1 | C7M84_018642 | peptidylprolyl isomerase |
| A0A3R7PF55 | C7M84_022024 | Prophenoloxidase activating factor |
| A0A3R7PF65 | C7M84_012255 | Protein FAM136A |
| A0A3R7PFA1 | C7M84_017607 | Ligase |
| A0A3R7PFF7 | C7M84_016036 | Trypsin-like serine protease |
| A0A3R7PFF9 | C7M84_017359 | Putative 14 kDa phosphohistidine phosphatase-like |
| A0A3R7PFH6 | C7M84_014331 | Putative neurotrypsin-like |
| A0A3R7PFQ9 | C7M84_017022 | Heterogeneous nuclear ribonucleoprotein L |
| A0A3R7PG00 | C7M84_011171 | V-type proton ATPase subunit G |
| A0A3R7PG04 | C7M84_011184 | Putative zinc finger protein ush isoform X2 |
| A0A3R7PG23 | C7M84_011053 | CUB-domain containing protein |
| A0A3R7PG69 | C7M84_016522 | Neuroglian |
| A0A3R7PGB4 | C7M84_010814 | 3-ketoacyl-CoA thiolase, mitochondrial |
| A0A3R7PGD8 | C7M84_016336 | Putative prolyl 4-hydroxylase subunit alpha-1-like isoform X1 |
| A0A3R7PGE6 | C7M84_016311 | Sugar transporter 8 |
| A0A3R7PGN4 | C7M84_016087 | Tubulin beta chain |
| A0A3R7PGP1 | C7M84_010495 | glutamate dehydrogenase [NAD(P)(+)] |
| A0A3R7PGR8 | C7M84_016022 | Putative C-type lectin-like |
| A0A3R7PHF2 | C7M84_009834 | Coatomer subunit beta |
| A0A3R7PHQ6 | C7M84_015080 | Putative alpha-aminoadipic semialdehyde synthase, mitochondrial isoform X1 |
| A0A3R7PHR6 | C7M84_015004 | Calponin-homology (CH) domain-containing protein |
| A0A3R7PHS0 | C7M84_009328 | Strongly chitin-binding protein-1 |
| A0A3R7PHS5 | C7M84_009305 | Ras-associating domain-containing protein |
| A0A3R7PI18 | C7M84_009026 | Beta-1,3-glucan-binding protein |
| A0A3R7PI62 | C7M84_014580 | Pyruvate dehydrogenase E1 component subunit beta |
| A0A3R7PII9 | C7M84_014210 | Putative cytosolic non-specific dipeptidase |
| A0A3R7PIJ5 | C7M84_014191 | Calcified cuticle protein CP19.0 isoform A |
| A0A3R7PIK3 | C7M84_008512 | phospholipase D |
| A0A3R7PIL9 | C7M84_008479 | Beta,beta-carotene 15,15'-monooxygenase |
| A0A3R7PIQ1 | C7M84_014059 | Hyp2 |
| A0A3R7PIV4 | C7M84_013916 | CWF19-like protein 2 |
| A0A3R7PJ66 | C7M84_013640 | NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7 |
| A0A3R7PJ90 | C7M84_007941 | Selenoprotein W2 |
| A0A3R7PJE5 | C7M84_013351 | Regucalcin |
| A0A3R7PJR9 | C7M84_007384 | Vitelline membrane outer layer 1-like protein |
| A0A3R7PJW9 | C7M84_006387 | Histone H2B |
| A0A3R7PK45 | C7M84_012671 | Tubulin alpha chain |
| A0A3R7PKG4 | C7M84_006714 | Beta-1,3-glucan-binding protein |
| A0A3R7PKM8 | C7M84_006569 | inorganic diphosphatase |
| A0A3R7PKN3 | C7M84_012118 | Putative peritrophin-44-like |
| A0A3R7PL10 | C7M84_011817 | alkaline phosphatase (Fragment) |
| A0A3R7PL42 | C7M84_006115 | RNA helicase |
| A0A3R7PL65 | C7M84_011623 | Serine proteinase |
| A0A3R7PLA8 | C7M84_011525 | WAP domain-containing protein |
| A0A3R7PLF1 | C7M84_005780 | Reverse transcriptase domain-containing protein |
| A0A3R7PLU5 | C7M84_011035 | Flotillin-1 |

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|---|---|---|
| A0A3R7PLZ1 | C7M84_005089 | Putative selenium-binding protein 1 |
| A0A3R7PMB6 | C7M84_004819 | Adenylyl cyclase-associated protein |
| A0A3R7PND5 | C7M84_003837 | Rhodanese domain-containing protein |
| A0A3R7PNG1 | C7M84_009489 | Proteasome subunit alpha type |
| A0A3R7PNK0 | C7M84_003641 | Putative collagen alpha-1(IX) chain isoform X9 |
| A0A3R7PNK7 | C7M84_003614 | Malate dehydrogenase |
| A0A3R7PNP1 | C7M84_003492 | Moesin/ezrin/radixin homolog 1 |
| A0A3R7PNZ6 | C7M84_003169 | Outer dense fiber protein 3 |
| A0A3R7PP12 | C7M84_008996 | Putative long-chain-fatty-acid--CoA ligase 4 |
| A0A3R7PP15 | C7M84_003115 | NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3 |
| A0A3R7PP38 | C7M84_003029 | Putative mediator of RNA polymerase II transcription subunit 12-like |
| A0A3R7PPB6 | C7M84_008684 | Sorting nexin-2 |
| A0A3R7PPS2 | CPAP1 | Cuticular protein |
| A0A3R7PPY4 | C7M84_002316 | Tubulin-specific chaperone A |
| A0A3R7PPZ0 | C7M84_008115 | Translation inhibitor L-PSP ribonuclease |
| A0A3R7PR20 | C7M84_007123 | Fructose-bisphosphate aldolase |
| A0A3R7PRC1 | C7M84_001059 | [phosphatase 2A protein]-leucine-carboxy methyltransferase |
| A0A3R7PRD0 | C7M84_001073 | Neutral alpha-glucosidase AB |
| A0A3R7PS73 | C7M84_000351 | Nesprin-1-like |
| A0A3R7PS80 | C7M84_006141 | Cysteine-rich membrane protein 2 |
| A0A3R7PSB0 | C7M84_006040 | Cathepsin F-like cysteine peptidase protein |
| A0A3R7PSD8 | C7M84_005928 | Mucin-19-like |
| A0A3R7PSD9 | C7M84_000113 | Histone H1 |
| A0A3R7PSE6 | C7M84_000100 | Putative 2-oxoglutarate dehydrogenase, mitochondrial |
| A0A3R7PSG3 | C7M84_000069 | Smoothelin domain-containing protein |
| A0A3R7PSX2 | C7M84_005324 | Myosin essential light chain |
| A0A3R7PT21 | C7M84_005137 | ALG-2 interacting protein x |
| A0A3R7PT34 | C7M84_005178 | aldehyde dehydrogenase (NAD(+)) |
| A0A3R7PTA0 | C7M84_024853 | WW domain-binding protein 2 |
| A0A3R7PTG0 | C7M84_004824 | Myosin light chain 2 |
| A0A3R7PU04 | C7M84_024258 | Ig-like domain-containing protein |
| A0A3R7PUI1 | C7M84_023839 | Serine protease |
| A0A3R7PUW0 | C7M84_023547 | SHSP domain-containing protein |
| A0A3R7PUZ2 | C7M84_003479 | Hemocyanin |
| A0A3R7PVP7 | C7M84_021545 | Hemocyanin |
| A0A3R7PVP8 | C7M84_022778 | Chorion peroxidase |
| A0A3R7PVQ7 | C7M84_021515 | glutathione transferase |
| A0A3R7PVV2 | C7M84_022603 | Chitinase-3-like protein 3 |
| A0A3R7PVZ7 | C7M84_022494 | 26S proteasome non-ATPase regulatory subunit 12 |
| A0A3R7PW33 | C7M84_002386 | Putative fibrillin-2-like |
| A0A3R7PW84 | C7M84_002269 | Glyceraldehyde-3-phosphate dehydrogenase |
| A0A3R7PW98 | C7M84_002251 | Glutathione S-transferase 1-like |
| A0A3R7PWQ1 | C7M84_021341 | Putative long-chain-fatty-acid--CoA ligase 4 isoform X1 |
| A0A3R7PWQ4 | C7M84_001798 | 1,4-alpha-glucan branching enzyme |
| A0A3R7PX15 | C7M84_015964 | Serine protease |
| A0A3R7PX93 | C7M84_019801 | Alkaline phosphatase |
| A0A3R7PX94 | C7M84_001281 | Putative hemicentin-1-like |
| A0A3R7PXF2 | C7M84_019694 | Heat shock protein 83 |
| A0A3R7PXW2 | C7M84_011022 | Putative UPF0462 protein C4orf33-like (Fragment) |
| A0A3R7PYG5 | C7M84_018666 | Calreticulin |
| A0A3R7PYH8 | C7M84_000227 | Translocon-associated protein subunit delta |
| A0A3R7PYJ5 | C7M84_000177 | Putative poly(RC)-binding protein 3 isoform X1 |
| A0A3R7PYM6 | C7M84_000080 | Beta-hexosaminidase |
| A0A3R7PYP1 | C7M84_018442 | Putative Thrombospondin-3 |
| A0A3R7PYQ2 | C7M84_025593 | Prothymosin alpha-like |
| A0A3R7PZ26 | C7M84_018064 | 4F2 cell-surface antigen heavy chain |
| A0A3R7Q0J4 | C7M84_016594 | Peroxinectin (Fragment) |
| A0A3R7Q0U8 | C7M84_023770 | Cytochrome c oxidase subunit 5A, mitochondrial |
| A0A3R7Q123 | C7M84_016210 | Hemocyanin |
| A0A3R7Q185 | C7M84_016089 | SCP domain-containing protein |
| A0A3R7Q1P4 | C7M84_023148 | Cuticle protein 6 |

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|---|---|---|
| A0A3R7Q1R0 | C7M84_015760 | phospholipase D |
| A0A3R7Q1X6 | C7M84_022951 | Pupal cuticle protein 27 |
| A0A3R7Q288 | C7M84_015399 | Putative cAMP-dependent protein kinase type II regulatory subunit isoform X2 |
| A0A3R7Q2A6 | C7M84_015332 | Selenoprotein M |
| A0A3R7Q2C8 | C7M84_015285 | Fibulin 2 |
| A0A3R7Q2U0 | C7M84_014872 | Superoxide dismutase [Cu-Zn] |
| A0A3R7Q305 | C7M84_014722 | Cofilin/actin-depolymerizing factor |
| A0A3R7Q373 | C7M84_014564 | Glutathione S-transferase |
| A0A3R7Q393 | C7M84_021889 | Putative filamin-A isoform X4 |
| A0A3R7Q3S1 | C7M84_016817 | Putative mucin-17-like |
| A0A3R7Q420 | C7M84_013897 | Putative glycine--tRNA ligase |
| A0A3R7Q478 | C7M84_008897 | peptidylprolyl isomerase |
| A0A3R7Q4T3 | C7M84_013260 | Extensin-like |
| A0A3R7Q4U6 | C7M84_013231 | JHE-like carboxylesterase 1 |
| A0A3R7Q5C5 | C7M84_012868 | Histone H4 |
| A0A3R7Q635 | C7M84_012261 | NADH dehydrogenase |
| A0A3R7Q691 | C7M84_012119 | Protein obstructor-E |
| A0A3R7Q707 | C7M84_011599 | cGMP-dependent protein kinase |
| A0A3R7Q736 | C7M84_011533 | 60S ribosomal protein L13a |
| A0A3R7Q743 | C7M84_011530 | Putative calcyphosin-like protein |
| A0A3R7Q749 | C7M84_011510 | Ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 |
| A0A3R7Q7P3 | C7M84_011058 | Putative very long-chain specific acyl-CoA dehydrogenase, mitochondrial |
| A0A3R7Q7R8 | C7M84_011002 | Probable imidazolonepropionase |
| A0A3R7Q7T6 | C7M84_010973 | Lamin Dm0 |
| A0A3R7Q8E3 | C7M84_010460 | 3-oxoacyl-[acyl-carrier-protein] reductase |
| A0A3R7Q994 | C7M84_021832 | 40S ribosomal protein S8 |
| A0A3R7Q9D1 | C7M84_021732 | Glycos_transf_1 domain-containing protein |
| A0A3R7Q9V6 | C7M84_021149 | Prefoldin subunit 4 |
| A0A3R7QA34 | C7M84_020853 | Annexin |
| A0A3R7QA79 | C7M84_020724 | Putative tubulin beta-1 chain |
| A0A3R7QAA5 | C7M84_008914 | Protein spaetzle |
| A0A3R7QAG0 | C7M84_008761 | T-complex protein 1 subunit eta (Fragment) |
| A0A3R7QAI3 | C7M84_008714 | Ribosomal protein S13 |
| A0A3R7QAN5 | C7M84_008570 | Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial |
| A0A3R7QAN9 | C7M84_020269 | Serine proteinase inhibitor B3 |
| A0A3R7QAR9 | C7M84_020181 | EGF-like domain-containing protein |
| A0A3R7QAY0 | C7M84_008335 | Putative glycogen debranching enzyme isoform X1 |
| A0A3R7QAY1 | C7M84_020031 | Prophenoloxidase activating enzyme III |
| A0A3R7QAY8 | C7M84_008331 | AHNK |
| A0A3R7QB76 | C7M84_008097 | Polyadenylate-binding protein |
| A0A3R7QBC8 | C7M84_007992 | Acetyl-CoA acetyltransferase, cytosolic |
| A0A3R7QBK5 | C7M84_007756 | Proteasome subunit alpha type |
| A0A3R7QBN0 | C7M84_019457 | Crustacyanin subunit C |
| A0A3R7QBX6 | C7M84_019260 | Peptidase S1 and S6 chymotrypsin/Hap |
| A0A3R7QC40 | C7M84_007343 | Echinoderm microtubule-associated protein-like 1 |
| A0A3R7QC43 | C7M84_019117 | Hemocytin |
| A0A3R7QCC2 | C7M84_007135 | QM protein |
| A0A3R7QCH9 | C7M84_018829 | F-actin-capping protein subunit alpha |
| A0A3R7QCL2 | C7M84_018753 | Uricase |
| A0A3R7QCN8 | C7M84_018722 | Chitin deacetylase 1 |
| A0A3R7QCP1 | C7M84_006921 | Paramyosin |
| A0A3R7QCU3 | C7M84_006787 | Pacifastin heavy chain |
| A0A3R7QDC8 | C7M84_006325 | superoxide dismutase |
| A0A3R7QDE9 | C7M84_006266 | Fibroin heavy chain-like |
| A0A3R7QDG2 | C7M84_018032 | threonine--tRNA ligase |
| A0A3R7QDK6 | C7M84_017909 | Vegetative cell wall protein gp1-like |
| A0A3R7QDL3 | C7M84_006180 | Spaetzle domain-containing protein |
| A0A3R7QDP9 | C7M84_006077 | Dynamin-type G domain-containing protein |
| A0A3R7QDX1 | C7M84_017655 | Calcification-associated peptide-2 |
| A0A3R7QDZ5 | C7M84_017621 | Putative proliferation-associated protein 2G4 |
| A0A3R7QE43 | C7M84_005634 | 40S ribosomal protein S27 |

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|---|---|---|
| A0A3R7QE51 | C7M84_017524 | Lysine--tRNA ligase |
| A0A3R7QE90 | C7M84_005470 | Early cuticle protein 3 |
| A0A3R7QEN7 | EIF6 | Eukaryotic translation initiation factor 6 |
| A0A3R7QEV9 | C7M84_016832 | Filaggrin |
| A0A3R7QF28 | C7M84_016640 | Putative isocitrate dehydrogenase |
| A0A3R7QF35 | C7M84_016595 | Peroxinectin |
| A0A3R7QF51 | C7M84_016563 | Blimp-1 |
| A0A3R7QFC9 | C7M84_004332 | Putative cubilin (Fragment) |
| A0A3R7QFI5 | C7M84_004179 | Putative neural cell adhesion molecule 1 |
| A0A3R7QFL4 | C7M84_004096 | Zinc finger FYVE domain-containing protein 26 |
| A0A3R7QFM7 | C7M84_004054 | Mitochondrial cytochrome c oxidase subunit VIb |
| A0A3R7QFR9 | C7M84_015982 | Serine hydroxymethyltransferase |
| A0A3R7QGA7 | C7M84_015498 | Outer dense fiber protein 3 |
| A0A3R7QGD6 | C7M84_003266 | Protein SOGA2 |
| A0A3R7QGG2 | C7M84_003200 | DJ-1 protein |
| A0A3R7QH39 | C7M84_014726 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 |
| A0A3R7QH50 | C7M84_014707 | DUF4789 domain-containing protein |
| A0A3R7QHA0 | C7M84_014514 | Eukaryotic translation initiation factor 3 subunit M |
| A0A3R7QHC4 | C7M84_002403 | Catalase |
| A0A3R7QHG5 | C7M84_002270 | Mitochondrial 2-oxoglutarate/malate carrier protein |
| A0A3R7QHI2 | C7M84_002203 | Chitin-binding type-2 domain-containing protein |
| A0A3R7QHJ7 | C7M84_002158 | S-formylglutathione hydrolase |
| A0A3R7QHU5 | C7M84_001883 | Dynein light chain |
| A0A3R7QHV0 | C7M84_013937 | RNA helicase |
| A0A3R7QHX6 | C7M84_013855 | Putative cysteine proteinase (Fragment) |
| A0A3R7QIP8 | C7M84_001105 | Fasciclin-2 |
| A0A3R7QIQ8 | C7M84_013054 | Collagen IV NC1 domain-containing protein |
| A0A3R7QIU1 | C7M84_000998 | Putative tenascin-like protein |
| A0A3R7QIX3 | C7M84_000910 | MaoC-like domain-containing protein |
| A0A3R7QJ11 | C7M84_012803 | Putative cyclin-dependent kinase 10 |
| A0A3R7QJW4 | C7M84_000081 | beta-N-acetylhexosaminidase |
| A0A3R7QJX4 | C7M84_000061 | Single VWC domain protein 1 |
| A0A3R7QKV6 | C7M84_024760 | Techylectin-5B |
| A0A3R7QKY1 | C7M84_024677 | ABC transporter |
| A0A3R7QL11 | C7M84_010881 | JHE-like carboxylesterase 1 |
| A0A3R7QL20 | C7M84_024577 | Multifunctional fusion protein (Fragment) |
| A0A3R7QLR9 | C7M84_023805 | Carboxypeptidase |
| A0A3R7QLU2 | C7M84_023720 | LIM domain-containing protein |
| A0A3R7QM12 | C7M84_023455 | proton-translocating NAD(P)(+) transhydrogenase |
| A0A3R7QM52 | C7M84_009833 | Microtubule-associated protein RP/EB family member 3 |
| A0A3R7QMC6 | C7M84_009597 | Putative aminopeptidase N-like |
| A0A3R7QMF7 | C7M84_023051 | Basic proline-rich protein-like |
| A0A3R7QMM9 | C7M84_009267 | Arthrodial cuticle protein AMP16.3 (Fragment) |
| A0A3R7QMR5 | C7M84_009144 | Electron transfer flavoprotein subunit alpha |
| A0A3R7QMW3 | C7M84_009025 | Vitellogenin domain-containing protein |
| A0A3R7QN58 | C7M84_008796 | TNF receptor-associated factor 6 |
| A0A3R7QN99 | C7M84_008674 | Putative MAM domain-containing protein 2-like |
| A0A3R7QNE7 | C7M84_022165 | Putative serine proteinase inhibitor |
| A0A3R7QNI2 | C7M84_008510 | Arthrodial cuticle protein AMP8.1 |
| A0A3R7QP41 | C7M84_008056 | Putative tyrosine/tryptophan monooxygenase (Fragment) |
| A0A3R7QP42 | C7M84_008025 | Protein transport protein Sec61 subunit beta |
| A0A3R7QP72 | C7M84_013490 | Pupal cuticle protein 27 |
| A0A3R7QPD2 | C7M84_009137 | T-complex protein 1 subunit theta |
| A0A3R7QPL5 | C7M84_005193 | FAS1 domain-containing protein |
| A0A3R7QPP9 | C7M84_007466 | Vitellogenin receptor (Fragment) |
| A0A3R7QRC2 | C7M84_006114 | 60S ribosomal protein L8 |
| A0A3R7QRL1 | C7M84_005823 | Lactamase_B domain-containing protein |
| A0A3R7QRM9 | C7M84_005747 | Putative GTP-binding protein SAR1B |
| A0A3R7QRP4 | C7M84_005723 | Muscle LIM protein Mlp84B |
| A0A3R7QRR3 | C7M84_005639 | Heme-binding protein 2 |
| A0A3R7QRV2 | C7M84_005493 | Mannose-binding protein |

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|---|---|---|
| A0A3R7QSN8 | C7M84_004636 | Cytochrome c-1 |
| A0A3R7QSV0 | C7M84_004489 | Lysosomal Pro-X carboxypeptidase |
| A0A3R7QSZ8 | C7M84_004362 | Estrogen sulfotransferase |
| A0A3R7QTG8 | C7M84_003730 | Crustacean calcium-binding protein 23 |
| A0A3R7QTK5 | C7M84_003491 | G protein beta 1 subunit |
| A0A3R7QTN8 | C7M84_003325 | Calcineurin subunit B |
| A0A3R7QTV0 | C7M84_003131 | Intracellular fatty acid binding protein |
| A0A3R7QUA1 | C7M84_002688 | Choline-specific glycerophosphodiester phosphodiesterase |
| A0A3R7QVA7 | C7M84_001747 | Glutathione S-transferase |
| A0A3R7QVL5 | C7M84_001364 | UMP-CMP kinase |
| A0A3R7QVW0 | C7M84_001091 | ATP synthase subunit O, mitochondrial |
| A0A3R7QWD1 | C7M84_000602 | WAP domain-containing protein |
| A0A3R7QWR3 | C7M84_000243 | folate gamma-glutamyl hydrolase |
| A0A3R7QXB9 | C7M84_025145 | Laccase 1 |
| A0A3R7QZ54 | C7M84_022527 | Melanotransferrin |
| A0A3R7QZR3 | C7M84_021358 | Alpha-mannosidase |
| A0A3R7QZU0 | C7M84_020928 | Protein disulfide isomerase 1 |
| A0A3R7R002 | C7M84_015963 | Prophenoloxidase activating enzyme |
| A0A3R7R007 | C7M84_015172 | Cleavage stimulation factor 50 kDa subunit (Fragment) |
| A0A3R7R042 | C7M84_012200 | N(4)-(Beta-N-acetylglucosaminyl)-L-asparaginase |
| A0A3R7R0B0 | C7M84_007743 | Electron transfer flavoprotein subunit beta |
| A0A3R7R0F8 | C7M84_004437 | enoyl-CoA hydratase |
| A0A3R7R0H2 | C7M84_003753 | Putative retinoid-inducible serine carboxypeptidase-like |
| A0A3R7SHH1 | C7M84_020721 | Pupal cuticle protein 27 (Fragment) |
| A0A3R7SHM1 | C7M84_020559 | 40S ribosomal protein S18 |
| A0A3R7SI93 | C7M84_019883 | Putative aldehyde dehydrogenase family 8 member A1-like |
| A0A3R7SIC8 | C7M84_019798 | Putative surface protein bspA-like (Fragment) |
| A0A3R7SIJ9 | C7M84_019638 | Adhesive plaque matrix protein |
| A0A3R7SIP5 | C7M84_019479 | Crustacyanin subunit C |
| A0A3R7SIW3 | C7M84_019181 | Putative serine proteinase inhibitor (Fragment) |
| A0A3R7SJE1 | C7M84_018633 | TGc domain-containing protein |
| A0A3R7SJJ3 | C7M84_018444 | SH2 domain-containing protein |
| A0A3R7SJX7 | C7M84_017918 | M15 protein |
| A0A3R7SK50 | C7M84_017666 | Calcification-associated peptide-2 |
| A0A3R7SKF0 | C7M84_017393 | Translationally-controlled tumor protein homolog |
| A0A3R7SKG8 | C7M84_017349 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial |
| A0A3R7SKK1 | C7M84_017290 | Proteasome subunit beta |
| A0A3R7SL05 | C7M84_016733 | SAPK substrate protein |
| A0A3R7SM43 | C7M84_015333 | Pre-mRNA-processing factor 19 |
| A0A3R7SMA9 | C7M84_015008 | Putative epidermal cell surface receptor isoform X4 |
| A0A3R7SN35 | C7M84_013888 | ATP synthase subunit beta |
| A0A3R7SN98 | C7M84_013646 | Pyruvate carboxylase |
| A0A3R7SND6 | C7M84_013518 | Crustin-like protein |
| A0A3R7SNJ4 | C7M84_013334 | Putative L-xylulose reductase |
| A0A3R7SPH9 | C7M84_012223 | C-type lectin 1 |
| A0A3R7SPI4 | C7M84_012182 | Sarcoplasmic calcium-binding protein |
| A0A3R7SQE6 | C7M84_011007 | Cuticle protein 7 |
| A0A3R7SQF5 | C7M84_011003 | Putative imidazolonepropionase isoform X2 |
| A0A3R7SR07 | C7M84_010375 | Cathepsin D |
| A0A3R7SRB5 | C7M84_009996 | Ubiquitin-conjugating enzyme |
| A0A3R7SRF7 | C7M84_009852 | beta-N-acetylhexosaminidase |
| A0A3R7SRX9 | C7M84_009263 | Cuticle protein AMP4 |
| A0A3R7SS41 | C7M84_009057 | Nicotinic acetylcholine receptor subunit alpha 12 |
| A0A3R7SS49 | C7M84_009022 | Alpha-actinin, sarcomeric |
| A0A3R7SSF0 | C7M84_008615 | 40S ribosomal protein S21 |
| A0A3R7SSF9 | C7M84_008603 | Heterogeneous nuclear ribonucleoprotein Q |
| A0A3R7SSU7 | C7M84_008052 | Putative E3 ubiquitin ligase |
| A0A3R7ST37 | C7M84_007701 | phosphoglucomutase (alpha-D-glucose-1,6-bisphosphate-dependent) |
| A0A3R7STD3 | C7M84_007323 | c-Myc-binding protein |
| A0A3R7STI2 | C7M84_007114 | SMB domain-containing protein |
| A0A3R7STU0 | C7M84_006669 | Mitochondrial-processing peptidase subunit beta |

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|---|---|---|
| A0A3R7STU9 | C7M84_006642 | Thrombospondin |
| A0A3R7SUP0 | C7M84_005496 | Pyruvate dehydrogenase E1 component subunit alpha |
| A0A3R7SUV3 | C7M84_005268 | Putative basement membrane-specific heparan sulfate proteoglycan core protein isoform X11 |
| A0A3R7SV19 | C7M84_004928 | Putative CDGSH iron-sulfur domain-containing protein 3, mitochondrial isoform X1 |
| A0A3R7SVI1 | C7M84_004254 | Beta-hexosaminidase |
| A0A3R7SWG8 | C7M84_002684 | Clathrin light chain |
| A0A3R7SXN5 | C7M84_001049 | Homologous-pairing protein 2 homolog |
| A0A3R7SXR8 | C7M84_000948 | Putative chitinase 10 isoform X1 |
| A0A3R7SY44 | C7M84_000500 | Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial |
| A0A3R7SYF2 | C7M84_025596 | C2H2-type domain-containing protein |
| A0A3R7SYF7 | C7M84_025548 | T-complex protein 1 subunit alpha |
| A0A3R7SYN4 | C7M84_024973 | Carboxypeptidase B |
| A0A3R7SYW9 | C7M84_024465 | Failed axon connections |
| A0A3R7SZH4 | C7M84_023806 | Ribos_L4_asso_C domain-containing protein |
| A0A3R7SZS6 | C7M84_023456 | Isocitrate dehydrogenase [NADP] |
| A0A3R7T009 | C7M84_023241 | Neurofilament heavy polypeptide |
| A0A3R7T0H7 | C7M84_022673 | KH domain-containing protein |
| A0A3R7T0I1 | C7M84_022653 | 60S acidic ribosomal protein P0 |
| A0A3R7T0J2 | C7M84_022613 | MAM domain-containing glycosylphosphatidylinositol anchor protein 1 |
| A0A3R7T1U5 | C7M84_003220 | RNA recognition motif (RRM) |
| A0A423S8R7 | C7M84_021841 | Beta-glucuronidase |
| A0A423S907 | C7M84_021838 | Oxysterol-binding protein |
| A0A423S933 | C7M84_021811 | Tubulin alpha chain (Fragment) |
| A0A423S9H1 | C7M84_021500 | Ribosomal protein S19 |
| A0A423S9R7 | C7M84_021379 | Galactose mutarotase |
| A0A423S9W3 | C7M84_021317 | Nidogen-2 |
| A0A423SA92 | C7M84_021151 | Putative transketolase-like protein 2 isoform X1 |
| A0A423SAB7 | C7M84_021126 | Putative isochorismatase domain-containing protein 2, mitochondrial-like |
| A0A423SB40 | C7M84_020799 | Ribosomal protein S24 |
| A0A423SB71 | C7M84_020770 | Clathrin heavy chain |
| A0A423SB86 | C7M84_020740 | Dumpy |
| A0A423SB92 | C7M84_020731 | Dumpy |
| A0A423SB94 | C7M84_020732 | EGF-like domain-containing protein |
| A0A423SBA6 | C7M84_020741 | Neurogenic locus Notch protein |
| A0A423SBQ1 | C7M84_020557 | PPE domain-containing protein |
| A0A423SBS0 | C7M84_020554 | Secreted protein |
| A0A423SC39 | C7M84_020442 | Choline-specific glycerophosphodiester phosphodiesterase |
| A0A423SCI3 | C7M84_020310 | Hrp65 protein |
| A0A423SCJ5 | C7M84_020299 | NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9 |
| A0A423SCV9 | C7M84_020175 | 3-oxoacyl-[acyl-carrier-protein] reductase |
| A0A423SCY3 | C7M84_020149 | Phosphoglycerate kinase |
| A0A423SD31 | C7M84_020051 | MFS domain-containing protein |
| A0A423SD78 | C7M84_020038 | Cathepsin L |
| A0A423SDB5 | C7M84_020000 | Ig-like domain-containing protein |
| A0A423SDD3 | C7M84_019937 | Chloride intracellular channel |
| A0A423SDH1 | C7M84_019934 | Myosin heavy chain type 1 |
| A0A423SE99 | C7M84_019592 | Chitinase 4 |
| A0A423SEB7 | C7M84_019614 | FreD |
| A0A423SEE9 | C7M84_019583 | Beta-centractin |
| A0A423SEM4 | C7M84_019482 | Crustacyanin subunit A |
| A0A423SEN6 | C7M84_019464 | Crustacyanin subunit C |
| A0A423SEP0 | C7M84_019459 | Crustacyanin subunit C |
| A0A423SEP1 | C7M84_019460 | Crustacyanin subunit A |
| A0A423SEP5 | C7M84_019475 | Crustacyanin subunit A |
| A0A423SER3 | C7M84_019481 | Crustacyanin subunit C |
| A0A423SES2 | C7M84_019462 | Crustacyanin subunit A |
| A0A423SEZ3 | C7M84_019349 | GPI-anchored protein pfl2 (Fragment) |
| A0A423SF76 | C7M84_019258 | GTP binding protein alpha subunit Go |
| A0A423SF93 | C7M84_019285 | TEP isoform 2 (Fragment) |
| A0A423SFA9 | C7M84_019284 | TEP isoform 2 |
| A0A423SFL3 | C7M84_019115 | Putative 40S ribosomal protein S3-like isoform X1 |

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|---|---|---|
| A0A423SFQ4 | C7M84_019072 | Lectin, mannose-binding, 1 |
| A0A423SFZ3 | C7M84_018979 | Type II hemocyte transglutaminase |
| A0A423SG07 | C7M84_018922 | ATP synthase subunit d, mitochondrial |
| A0A423SG23 | C7M84_018983 | Hemocyte transglutaminase |
| A0A423SG35 | C7M84_019013 | Histone H2A |
| A0A423SGM7 | C7M84_018792 | Retinal dehydrogenase 1 |
| A0A423SGQ3 | C7M84_018693 | superoxide dismutase |
| A0A423SGQ4 | C7M84_018759 | Sorbitol dehydrogenase |
| A0A423SGR6 | C7M84_018736 | Hemocyanin subunit L2 |
| A0A423SGR7 | C7M84_018764 | Peroxiredoxin 6 |
| A0A423SGT1 | C7M84_018735 | Hemocyanin subunit L3 |
| A0A423SGT5 | C7M84_018640 | Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial |
| A0A423SGU8 | C7M84_018733 | Hemocyanin subunit L2 |
| A0A423SGV5 | C7M84_018689 | Putative glutaryl-CoA dehydrogenase |
| A0A423SGW3 | C7M84_018710 | Putative NADH dehydrogenase |
| A0A423SGZ6 | C7M84_018673 | Xaa-Pro aminopeptidase 1 |
| A0A423SH09 | C7M84_018690 | Putative glutaryl-CoA dehydrogenase-like |
| A0A423SHB5 | C7M84_018530 | T-complex protein 1 subunit beta |
| A0A423SHU2 | C7M84_018340 | palmitoyl-protein hydrolase |
| A0A423SHW4 | C7M84_018351 | glutaminyl-peptide cyclotransferase |
| A0A423SHX3 | C7M84_018350 | Adenosylhomocysteinase |
| A0A423SI55 | C7M84_018195 | Alpha 2 macroglobulin |
| A0A423SIC8 | C7M84_018174 | Glycine N-methyltransferase |
| A0A423SID4 | C7M84_018077 | Tubulin beta chain |
| A0A423SIX1 | C7M84_017843 | Heat shock protein cognate 5 |
| A0A423SJ04 | C7M84_017919 | M15 protein |
| A0A423SJF6 | C7M84_017722 | Alpha glucosidase |
| A0A423SJK1 | C7M84_017705 | Chorion peroxidase |
| A0A423SJP6 | C7M84_017570 | Serine hydroxymethyltransferase |
| A0A423SJQ9 | C7M84_017658 | Calcification-associated peptide-2 |
| A0A423SJR1 | C7M84_017663 | Calcification-associated peptide-2 |
| A0A423SKE5 | C7M84_017415 | Dihydrolipoyl dehydrogenase |
| A0A423SKL5 | C7M84_017296 | 60S ribosomal protein L14 |
| A0A423SKM7 | C7M84_017350 | Beta,beta-carotene 15,15'-monooxygenase |
| A0A423SKS4 | C7M84_017234 | Elongation factor 2 |
| A0A423SKV4 | C7M84_017177 | Alpha-galactosidase |
| A0A423SKV8 | C7M84_017243 | Vacuolar ATP synthase subunit B K form |
| A0A423SKZ9 | C7M84_017239 | Putative histone H1.0-B-like |
| A0A423SL50 | C7M84_017162 | Carboxylic ester hydrolase |
| A0A423SL52 | C7M84_017174 | Mucin-19-like |
| A0A423SL60 | C7M84_017128 | Talin-1 |
| A0A423SLL0 | C7M84_016912 | Putative myosin regulatory light chain 2 smooth muscle |
| A0A423SLU1 | C7M84_016937 | Bleomycin hydrolase |
| A0A423SLW8 | C7M84_016800 | Putative malate dehydrogenase, cytoplasmic isoform X2 |
| A0A423SLZ6 | C7M84_016866 | Putative eukaryotic translation initiation factor 2 subunit 3 |
| A0A423SM29 | C7M84_016797 | Proteasome subunit alpha type |
| A0A423SM49 | C7M84_016776 | Mannose-binding protein |
| A0A423SMA1 | C7M84_016794 | BRCT domain-containing protein |
| A0A423SMD0 | C7M84_016621 | RNA-directed DNA polymerase |
| A0A423SMD3 | C7M84_016614 | Neurexin-4 |
| A0A423SMD6 | C7M84_016686 | Putative serine/arginine repetitive matrix protein 2 |
| A0A423SMH1 | C7M84_016635 | Serine protease inhibitor |
| A0A423SMN4 | C7M84_016610 | RanBP2-type domain-containing protein |
| A0A423SMP0 | C7M84_016538 | RNA helicase |
| A0A423SMQ8 | C7M84_016559 | Serine/threonine-protein kinase TOR |
| A0A423SMS3 | C7M84_016477 | Tubulin beta chain |
| A0A423SMV5 | C7M84_016475 | Chitinase |
| A0A423SN04 | C7M84_016394 | Putative papilin-like isoform X6 |
| A0A423SN06 | C7M84_016420 | Glucose-6-phosphate isomerase |
| A0A423SN10 | C7M84_016480 | Putative heterogeneous nuclear ribonucleoprotein H2 isoform X2 |
| A0A423SN99 | C7M84_016398 | Lacunin |

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|---|---|---|
| A0A423SNE0 | C7M84_016367 | NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial |
| A0A423SNE1 | C7M84_016268 | Hemolymph clottable protein |
| A0A423SNI6 | C7M84_016261 | T-complex protein 1 subunit delta |
| A0A423SNM5 | C7M84_016193 | Alanine--glyoxylate aminotransferase 2, mitochondrial |
| A0A423SNP0 | C7M84_016267 | Hemolymph clottable protein |
| A0A423SNS5 | C7M84_016142 | Putative Ca2+ sensor |
| A0A423SP21 | C7M84_016044 | Metalloendopeptidase |
| A0A423SP76 | C7M84_016014 | Gastrolith protein 10 |
| A0A423SP91 | C7M84_016023 | C-type lectin domain-containing protein |
| A0A423SQ15 | C7M84_015713 | Strawberry notch homolog 1 |
| A0A423SQ51 | C7M84_015661 | Bip |
| A0A423SR77 | C7M84_015249 | RNA-editing deaminase 1 |
| A0A423SRA7 | C7M84_015213 | Extensin-like |
| A0A423SRW7 | C7M84_015050 | C-type lectin domain-containing protein |
| A0A423SS11 | C7M84_014981 | Endoplasmic reticulum-Golgi intermediate compartment protein 1 |
| A0A423SS33 | C7M84_014945 | ATP synthase-coupling factor 6, mitochondrial |
| A0A423SSC0 | C7M84_014848 | Putative aldehyde dehydrogenase family 8 member A1 isoformX1 |
| A0A423SSF7 | C7M84_014822 | Extensin |
| A0A423SSL4 | C7M84_014790 | maleylacetoacetate isomerase |
| A0A423SSL9 | C7M84_014730 | Putative hypoxia up-regulated protein 1 isoform X2 |
| A0A423SSM5 | C7M84_014729 | Hypoxia up-regulated protein 1 |
| A0A423SSQ2 | C7M84_014701 | PBPe domain-containing protein |
| A0A423SSR6 | C7M84_014680 | Protein SET |
| A0A423SST2 | C7M84_014696 | Delta-aminolevulinic acid dehydratase |
| A0A423STL8 | C7M84_014362 | 26S proteasome non-ATPase regulatory subunit 6 |
| A0A423STM9 | C7M84_014357 | Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial (Fragment) |
| A0A423STZ3 | C7M84_014271 | Chitinase |
| A0A423SU62 | C7M84_014137 | Putative tropinone reductase 2-like (Fragment) |
| A0A423SUD5 | C7M84_014156 | MICOS complex subunit MIC60 |
| A0A423SUJ8 | C7M84_014003 | 2,4-dienoyl-CoA reductase, mitochondrial |
| A0A423SUM6 | C7M84_014007 | NADH dehydrogenase |
| A0A423SUM8 | C7M84_013953 | Fibronectin type-III domain-containing protein |
| A0A423SUS6 | C7M84_013964 | Tubulin alpha chain |
| A0A423SUV4 | C7M84_013889 | Polysialoglycoprotein |
| A0A423SV48 | C7M84_013801 | Putative obg-like ATPase 1 isoform X5 |
| A0A423SVT7 | C7M84_013521 | Putative elastin a |
| A0A423SW39 | C7M84_013419 | Acylamino-acid-releasing enzyme |
| A0A423SWD4 | C7M84_013372 | Agrin |
| A0A423SWH3 | C7M84_013239 | Na+/K+-ATPase alpha subunit |
| A0A423SWM5 | C7M84_013168 | Cuticle protein 6 |
| A0A423SWU6 | C7M84_013161 | Chitin-binding type-2 domain-containing protein |
| A0A423SWU7 | C7M84_013271 | Ankyrin repeat-containing protein |
| A0A423SX22 | C7M84_013113 | 40S ribosomal protein S17 |
| A0A423SX24 | C7M84_013033 | 4-hydroxyphenylpyruvate dioxygenase |
| A0A423SX47 | C7M84_013087 | Vegetative cell wall protein gp1-like |
| A0A423SX67 | C7M84_013011 | C-type lectin domain-containing protein |
| A0A423SXG7 | C7M84_012949 | Trypsinogen 1 |
| A0A423SXS4 | C7M84_012802 | Putative urocanate hydratase |
| A0A423SXZ4 | C7M84_012764 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 |
| A0A423SY07 | C7M84_012695 | 40S ribosomal protein S25 |
| A0A423SY25 | C7M84_012813 | Histone H2A |
| A0A423SY44 | C7M84_012756 | Mannose-binding protein |
| A0A423SYM7 | C7M84_012693 | Citrate synthase |
| A0A423SYQ1 | C7M84_012389 | Prefoldin subunit 3 |
| A0A423SZ32 | C7M84_012313 | Titin (Fragment) |
| A0A423SZG5 | C7M84_012150 | V-type proton ATPase subunit |
| A0A423SZH0 | C7M84_012148 | Pacifastin light chain (Fragment) |
| A0A423SZI5 | C7M84_012117 | Peritrophin (P |
| A0A423SZM6 | C7M84_012113 | Peritrophin |
| A0A423SZR6 | C7M84_012147 | Integrin |

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| A0A423T016 | C7M84_011963 | Putative laminin A chain |
| A0A423T0H6 | C7M84_012003 | Flotillin-1 |
| A0A423T0M6 | C7M84_011721 | AN1-type zinc finger protein 1 |
| A0A423T0R6 | C7M84_011709 | Putative serine protease 44 |
| A0A423T187 | C7M84_011512 | Putative histone-binding protein Caf1 isoform X4 |
| A0A423T189 | C7M84_011497 | PH domain-containing protein |
| A0A423T196 | C7M84_011484 | DUF4585 domain-containing protein |
| A0A423T1K3 | C7M84_011281 | Aldedh domain-containing protein |
| A0A423T1P4 | C7M84_011232 | Fibronectin type-III domain-containing protein |
| A0A423T1V1 | C7M84_011250 | Beta-1,3-glucan binding protein |
| A0A423T1W0 | C7M84_011253 | Beta-1,3-glucan binding protein |
| A0A423T231 | C7M84_011251 | Beta-1,3-glucan-binding protein |
| A0A423T291 | C7M84_011183 | Ligand of Numb protein X 2 |
| A0A423T2H2 | C7M84_010970 | alanine transaminase |
| A0A423T2P8 | C7M84_010919 | Beta-actin |
| A0A423T3D3 | C7M84_010808 | C-type lectin |
| A0A423T3K1 | C7M84_010894 | Adenosylhomocysteinase |
| A0A423T3P0 | C7M84_010623 | Actin-related protein 2 |
| A0A423T3Q5 | C7M84_010552 | Teneurin N-terminal domain-containing protein |
| A0A423T3T2 | C7M84_010782 | Chemosensory protein |
| A0A423T3Z7 | C7M84_010614 | Putative ufm1-specific protease 1-like |
| A0A423T420 | C7M84_010513 | RNA helicase |
| A0A423T425 | C7M84_010387 | Glycine cleavage system H protein, mitochondrial |
| A0A423T4G5 | C7M84_010388 | Putative sulfate transporter |
| A0A423T4K3 | C7M84_010381 | Isocitrate dehydrogenase |
| A0A423T4X7 | C7M84_010148 | S-phase kinase-associated protein 1 |
| A0A423T573 | C7M84_010136 | NADH dehydrogenase |
| A0A423T5A4 | C7M84_009982 | TFIIS-type domain-containing protein |
| A0A423T5D9 | C7M84_009962 | WAP domain-containing protein |
| A0A423T5J3 | C7M84_009863 | Secreted protein (Fragment) |
| A0A423T5P6 | C7M84_009810 | Phosphoacetylglucosamine mutase |
| A0A423T5V2 | C7M84_009761 | Malic enzyme |
| A0A423T5V8 | C7M84_009892 | beta-N-acetylhexosaminidase |
| A0A423T5Y1 | C7M84_009706 | Malate dehydrogenase |
| A0A423T6G9 | C7M84_009529 | Glycine-rich cell wall structural protein |
| A0A423T6N8 | C7M84_009419 | ATP synthase subunit f, mitochondrial |
| A0A423T6N9 | C7M84_009530 | Glycine-rich cell wall structural protein |
| A0A423T6V0 | C7M84_009445 | 40S ribosomal protein S11 |
| A0A423T6Y9 | C7M84_009428 | arginase |
| A0A423T753 | C7M84_009353 | Chitin-binding type-2 domain-containing protein |
| A0A423T763 | C7M84_009332 | Strongly chitin-binding protein-1 |
| A0A423T771 | C7M84_009330 | Early cuticle protein 6 |
| A0A423T7C6 | C7M84_009262 | Cuticle protein AMP4 |
| A0A423T7D0 | C7M84_009268 | Arthrodial cuticle protein AMP8.1 |
| A0A423T7K3 | C7M84_009179 | SCP-like extracellular domain containing protein 1 |
| A0A423T7L7 | C7M84_009195 | Lipoprotein receptor 2A |
| A0A423T7P8 | C7M84_009155 | Putative CD81 protein |
| A0A423T7S3 | C7M84_009096 | Dipeptidyl peptidase 1 |
| A0A423T7X1 | C7M84_009043 | Formimidoyltransferase-cyclodeaminase |
| A0A423T854 | C7M84_008943 | Hemocyanin subunit L2 (Fragment) |
| A0A423T8D0 | C7M84_008875 | LRRCT domain-containing protein |
| A0A423T8V5 | C7M84_008697 | Putative nuclear speckle splicing regulatory protein 1-like |
| A0A423T8Z0 | C7M84_008673 | MAM domain-containing protein |
| A0A423T934 | C7M84_008626 | ATP synthase subunit b |
| A0A423T944 | C7M84_008621 | Putative 4-coumarate--CoA ligase 1 |
| A0A423T968 | C7M84_008599 | Ribosome like protein |
| A0A423T9I1 | C7M84_008469 | Protein phosphatase 1B |
| A0A423T9I4 | C7M84_008446 | Nucleoplasmin isoform 1-like protein |
| A0A423T9M8 | C7M84_008387 | Animal hem peroxidase |
| A0A423T9R6 | C7M84_008333 | Neuroblast differentiation-associated protein AHNAK |
| A0A423T9T3 | C7M84_008384 | Putative basement membrane-specific heparan sulfate proteoglycan core protein isoform X13 |

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| A0A423T9X4 | C7M84_008334 | Neuroblast differentiation-associated protein AHNAK |
| A0A423TA80 | C7M84_008182 | Putative ras-like protein 2 isoform X1 |
| A0A423TAD8 | C7M84_008091 | Staphylococcal nuclease domain-containing protein 1 |
| A0A423TAW0 | C7M84_007955 | Metalloendopeptidase |
| A0A423TAW6 | C7M84_007931 | Putative alpha/beta hydrolase domain-containing protein 14B-like |
| A0A423TB01 | C7M84_007985 | Uncharacterized protein |
| A0A423TB17 | C7M84_007888 | Dehydrogenase/reductase SDR family member 4 |
| A0A423TB59 | C7M84_007914 | Putative methyltransferase-like protein 7A |
| A0A423TB87 | C7M84_007801 | Nucleoside diphosphate kinase |
| A0A423TBB3 | C7M84_007781 | Eukaryotic translation initiation factor 3 subunit I |
| A0A423TBE4 | C7M84_007719 | GATA zinc finger domain-containing protein 14-like |
| A0A423TBK5 | C7M84_007762 | Serine proteinase 1 |
| A0A423TBN1 | C7M84_007646 | Laminin subunit beta-1 |
| A0A423TBN5 | C7M84_007641 | Putative neurofilament heavy polypeptide |
| A0A423TBP9 | C7M84_007616 | UBC core domain-containing protein |
| A0A423TBU1 | C7M84_007633 | ANK_REP_REGION domain-containing protein (Fragment) |
| A0A423TC23 | C7M84_007516 | Kazal-like domain-containing protein |
| A0A423TC32 | C7M84_007498 | Putative cuticle protein |
| A0A423TC50 | C7M84_007448 | Activation factor subunit spp27 |
| A0A423TC54 | C7M84_007473 | Probable methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial |
| A0A423TC66 | C7M84_007533 | Glycine rich superfamily member |
| A0A423TC79 | C7M84_007504 | Anti-lipopolysaccharide factor |
| A0A423TC99 | C7M84_007465 | Vitellogenin domain-containing protein (Fragment) |
| A0A423TCA4 | C7M84_007500 | Glycine-rich cell wall structural protein 1 |
| A0A423TCL3 | C7M84_007321 | Larval cuticle protein LCP-17 |
| A0A423TD62 | C7M84_007052 | Condensation domain-containing protein |
| A0A423TDI9 | C7M84_006994 | C-type lectin |
| A0A423TDL6 | C7M84_007014 | 40S ribosomal protein SA |
| A0A423TDM1 | C7M84_006904 | Putative heterochromatin protein 1-binding protein 3 isoform X8 |
| A0A423TDM7 | C7M84_007005 | Uncharacterized protein |
| A0A423TDQ2 | C7M84_006888 | Crustacyanin-C1 subunit |
| A0A423TE04 | C7M84_006786 | Pacifastin heavy chain |
| A0A423TE44 | C7M84_006818 | Fibril-forming collagen alpha chain-like |
| A0A423TE85 | C7M84_006666 | Uncharacterized protein |
| A0A423TE88 | C7M84_006716 | VWFD domain-containing protein |
| A0A423TEB0 | C7M84_006671 | Peroxiredoxin-5 |
| A0A423TEF3 | C7M84_006650 | Cuticular protein 34 |
| A0A423TEI8 | C7M84_006590 | Lipoprotein |
| A0A423TES1 | C7M84_006548 | Prostaglandin reductase 1 |
| A0A423TET4 | C7M84_006537 | Putative fatty aldehyde dehydrogenase-like |
| A0A423TEU8 | C7M84_006461 | Enoyl-CoA delta isomerase 2 |
| A0A423TEZ4 | C7M84_006448 | cystathionine gamma-lyase |
| A0A423TF87 | C7M84_006352 | Serine protease |
| A0A423TFA4 | C7M84_006298 | Cuticle protein |
| A0A423TFC8 | C7M84_006274 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 |
| A0A423TFE2 | C7M84_006263 | Vegetative cell wall protein gp1-like |
| A0A423TFQ5 | C7M84_006261 | Integrin_alpha2 domain-containing protein |
| A0A423TFU3 | C7M84_006107 | Putative ficolin-1 |
| A0A423TGI1 | C7M84_005885 | Inter-alpha-trypsin inhibitor heavy chain H3 |
| A0A423TH67 | C7M84_005596 | Putative phosphoribosylformylglycinamidine synthase |
| A0A423TH92 | C7M84_005612 | superoxide dismutase |
| A0A423THI6 | C7M84_005505 | 60S ribosomal protein L17 |
| A0A423THJ4 | C7M84_005519 | lactoylglutathione lyase |
| A0A423THL6 | C7M84_005514 | Serine proteinase inhibitor 7 |
| A0A423THN1 | C7M84_005443 | Glyoxylate reductase/hydroxypyruvate reductase |
| A0A423THS0 | C7M84_005492 | Mannose-binding protein |
| A0A423TI28 | C7M84_005287 | Heat shock protein 83 |
| A0A423TI33 | C7M84_005296 | Putative bifunctional purine biosynthesis protein PURH |
| A0A423TI42 | C7M84_005303 | Basic proline-rich protein |
| A0A423TIF1 | C7M84_005182 | Mesencephalic astrocyte-derived neurotrophic factor homolog |
| A0A423TIG4 | C7M84_005134 | Androgenic gland-specific protein |

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| A0A423TII9 | C7M84_005157 | Putative nucleolar transcription factor 1 |
| A0A423TIK6 | C7M84_005126 | Cadherin domain-containing protein (Fragment) |
| A0A423TIL1 | C7M84_005129 | ATP synthase subunit alpha |
| A0A423TIS3 | C7M84_005062 | Heat shock protein |
| A0A423TJ07 | C7M84_004964 | C-type lectin protein |
| A0A423TJ95 | C7M84_004883 | Protein disulfide-isomerase |
| A0A423TJN8 | C7M84_004755 | P-type Cu(+) transporter |
| A0A423TJU0 | C7M84_004686 | Fumarylacetoacetase |
| A0A423TKA1 | C7M84_004512 | VAMP-associated protein |
| A0A423TKA2 | C7M84_004517 | Phosphotransferase |
| A0A423TKF3 | C7M84_004458 | Lissencephaly-1 homolog |
| A0A423TKH1 | C7M84_004492 | Cuticular protein CPR76a |
| A0A423TKK4 | C7M84_004392 | Chitin-binding type-2 domain-containing protein |
| A0A423TKW4 | C7M84_004251 | Aminopeptidase |
| A0A423TKX6 | C7M84_004266 | Myotrophin |
| A0A423TKZ6 | C7M84_004286 | Leucine-rich repeat domain-containing protein |
| A0A423TL37 | C7M84_004182 | Aldo_ket_red domain-containing protein |
| A0A423TL51 | C7M84_004204 | Voltage-dependent anion-selective channel protein 3 |
| A0A423TLB5 | C7M84_004130 | Succinate-semialdehyde dehydrogenase |
| A0A423TLX9 | C7M84_003874 | 60S ribosomal protein L23 |
| A0A423TLY4 | C7M84_003918 | Transgelin |
| A0A423TM80 | C7M84_003807 | PKD_channel domain-containing protein |
| A0A423TMA2 | C7M84_003776 | Cuticle protein 6 |
| A0A423TMW1 | C7M84_003499 | Glutamine synthetase |
| A0A423TN18 | C7M84_003481 | Kazal-type proteinase inhibitor |
| A0A423TN25 | C7M84_003451 | Protein disulfide-isomerase A5 |
| A0A423TN92 | C7M84_003377 | Ribosomal protein L15 |
| A0A423TNI2 | C7M84_003291 | Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial |
| A0A423TNN5 | C7M84_003252 | Disintegrin domain-containing protein |
| A0A423TNY3 | C7M84_003152 | High mobility group nucleosome-binding domain-containing protein 3 |
| A0A423TNZ1 | C7M84_003079 | Tyrosine-protein kinase (Fragment) |
| A0A423TP24 | C7M84_003094 | Ribonuclease E/G |
| A0A423TP90 | C7M84_003065 | Putative cuticle protein |
| A0A423TPE8 | C7M84_002967 | TNFR-Cys domain-containing protein |
| A0A423TPM4 | C7M84_002894 | Peroxiredoxin |
| A0A423TPP0 | C7M84_002897 | vesicle-fusing ATPase |
| A0A423TPQ2 | C7M84_002841 | 6-phosphogluconate dehydrogenase, decarboxylating |
| A0A423TPT8 | C7M84_002802 | Aldedh domain-containing protein |
| A0A423TPU2 | C7M84_002843 | Heat shock protein 67B2 |
| A0A423TPV2 | C7M84_002812 | T-complex protein 1 subunit zeta |
| A0A423TPV3 | C7M84_002803 | Putative aldehyde dehydrogenase 5, mitochondrial-like |
| A0A423TQ14 | C7M84_002779 | Putative articulin p60 |
| A0A423TQC0 | C7M84_002668 | Laminin subunit alpha |
| A0A423TQH5 | C7M84_002575 | Receptor-type tyrosine-protein phosphatase F |
| A0A423TQN2 | C7M84_002517 | Putative kinesin-like protein KIF21A isoform X2 |
| A0A423TQV1 | C7M84_002438 | Pyridoxal-dependent decarboxylase domain-containing protein 1 |
| A0A423TR82 | C7M84_002351 | glutathione transferase |
| A0A423TR93 | C7M84_002318 | Glucosamine-6-phosphate isomerase |
| A0A423TRD3 | C7M84_002271 | Sushi domain-containing protein |
| A0A423TRF2 | C7M84_002255 | Putative structural constituent of cuticle |
| A0A423TRG0 | C7M84_002254 | Cuticle protein |
| A0A423TRH8 | C7M84_002215 | Vegetative cell wall protein gp1-like |
| A0A423TRI4 | C7M84_002217 | Sulfide:quinone oxidoreductase, mitochondrial |
| A0A423TRM5 | C7M84_002169 | Low-density lipoprotein receptor-related protein 2 |
| A0A423TRM8 | C7M84_002176 | Cuticular protein 34 |
| A0A423TRP9 | C7M84_002175 | Cuticular protein 34 |
| A0A423TS60 | C7M84_002009 | Gastrolith protein 10 |
| A0A423TSE4 | C7M84_001927 | Kinesin-like protein |
| A0A423TSI9 | C7M84_001874 | MHD domain-containing protein |
| A0A423TSJ7 | C7M84_001869 | Angiopoietin-related protein 1 |
| A0A423TSK5 | C7M84_001844 | CLIP domain-containing serine protease |

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|---|---|---|
| A0A423TSV6 | C7M84_001734 | Cuticle protein CB5 |
| A0A423TSX5 | C7M84_001720 | U3 small nucleolar RNA-associated protein 15 homolog |
| A0A423TSY3 | C7M84_001688 | Sex-lethal |
| A0A423TTE3 | C7M84_001546 | 40S ribosomal protein S2 |
| A0A423TTK1 | C7M84_001515 | DM5 domain-containing protein |
| A0A423TTQ8 | C7M84_001425 | Putative microtubule-actin cross-linking factor 1 isoform X7 |
| A0A423TTR8 | C7M84_001424 | Spectrin repeat-containing domain protein |
| A0A423TTZ4 | C7M84_001390 | Coatomer subunit epsilon |
| A0A423TUC1 | C7M84_001255 | ATP synthase subunit gamma |
| A0A423TUJ3 | C7M84_001184 | 40S ribosomal protein S13 |
| A0A423TUW0 | C7M84_001038 | Putative host cell factor 1-like |
| A0A423TV72 | C7M84_000925 | Protein arginine N-methyltransferase 8 |
| A0A423TVC2 | C7M84_000893 | Putative chorion peroxidase-like |
| A0A423TVC8 | C7M84_000855 | Putative copine-8 isoform X2 |
| A0A423TVD6 | C7M84_000861 | Putative ankyrin repeat domain-containing protein 1 |
| A0A423TVL8 | C7M84_000730 | ZnF_CDGSH domain-containing protein |
| A0A423TVY7 | C7M84_000625 | Protein hu-li tai shao |
| A0A423TW55 | C7M84_000605 | Kynurenine--oxoglutarate transaminase 3 |
| A0A423TWA1 | C7M84_000506 | Cuticular protein |
| A0A423TWC3 | C7M84_000507 | Pupal cuticle protein C1B |
| A0A423TWD2 | C7M84_000487 | 40S ribosomal protein S12 |
| A0A423TWS3 | C7M84_000350 | KASH domain-containing protein |
| A0A423TWT2 | C7M84_000356 | S10e ribosomal protein |
| A0A423TWV0 | C7M84_000361 | 14-3-3-like protein |
| A0A423TX11 | C7M84_000297 | TAR DNA-binding protein 43 |
| A0A423TX84 | C7M84_000193 | ES1-like protein, mitochondrial |
| A0A423TXE1 | C7M84_000127 | Hypoxanthine phosphoribosyltransferase |
| A0A423TXT9 | C7M84_025569 | Putative serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A-like |
| A0A423TXW1 | C7M84_025574 | Uncharacterized protein |
| A0A423TXX2 | C7M84_000007 | Pyrazinamidase/nicotinamidase |
| A0A423TY67 | C7M84_025430 | KH domain-containing protein (Fragment) |
| A0A423TY88 | C7M84_025422 | Medium-chain specific acyl-CoA dehydrogenase, mitochondrial |
| A0A423TYF6 | C7M84_025336 | 3-hydroxyanthranilate 3,4-dioxygenase |
| A0A423TYK1 | C7M84_025304 | Serine protease-like protein 3 |
| A0A423TYK3 | C7M84_025303 | Serine protease nudel |
| A0A423TYM0 | C7M84_025305 | Mas |
| A0A423TZ62 | C7M84_025106 | Heat shock protein |
| A0A423TZB9 | C7M84_025036 | Vimentin |
| A0A423TZC9 | C7M84_025032 | Bifunctional purine biosynthesis protein ATIC |
| A0A423TZJ9 | C7M84_024997 | 60S ribosomal protein L27 |
| A0A423TZT5 | C7M84_024879 | Putative basement membrane-specific heparan sulfate proteoglycan core protein-like |
| A0A423U039 | C7M84_024785 | ATPase ASNA1 homolog |
| A0A423U069 | C7M84_024776 | Putative antimicrobial peptide |
| A0A423U076 | C7M84_024703 | protein-tyrosine-phosphatase (Fragment) |
| A0A423U084 | C7M84_024723 | DNA topoisomerase (Fragment) |
| A0A423U089 | C7M84_024728 | Spectrin beta chain |
| A0A423U0F0 | C7M84_024651 | Carboxylic ester hydrolase |
| A0A423U0M4 | C7M84_024579 | Putative bifunctional 3 |
| A0A423U0P2 | C7M84_024565 | Olfactory ionotropic receptor IR7 |
| A0A423U0S6 | C7M84_024533 | RNA-binding protein Rsf1 |
| A0A423U164 | C7M84_024403 | DUF3060 domain-containing protein |
| A0A423U1N6 | C7M84_024198 | SEA domain-containing protein |
| A0A423U245 | C7M84_024053 | C type lectin containing domain protein |
| A0A423U2A1 | C7M84_024018 | Hydroxysteroid 17-beta dehydrogenase 10 |
| A0A423U2L6 | C7M84_023887 | Alpha-1,4 glucan phosphorylase |
| A0A423U2M5 | C7M84_023861 | VWFA domain-containing protein |
| A0A423U2Q9 | C7M84_023832 | S-(hydroxymethyl)glutathione dehydrogenase |
| A0A423U2X5 | C7M84_023756 | DM5 domain-containing protein |
| A0A423U2Y2 | C7M84_023744 | Ribosomal_S7 domain-containing protein |
| A0A423U2Y7 | C7M84_023750 | Protein containing Polysaccharide lyase family 8, central |
| A0A423U309 | C7M84_023789 | Eukaryotic translation initiation factor 3 subunit E |

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|---|---|---|
| A0A423U364 | C7M84_023676 | Vinculin |
| A0A423U369 | C7M84_023675 | Vinculin |
| A0A423U3B4 | C7M84_023621 | C-type lectin-like protein |
| A0A423U3D0 | C7M84_023602 | Profilin |
| A0A423U3F7 | C7M84_023577 | Na+/K+/2Cl-cotransporter isoform 1 |
| A0A423U3L4 | C7M84_023513 | Chitinase 6 |
| A0A423U3L9 | C7M84_023578 | Na+/K+/2Cl-cotransporter isoform 1 |
| A0A423U3P0 | C7M84_023496 | Heat shock protein 67B2 |
| A0A423U413 | C7M84_023424 | Integrin beta |
| A0A423U424 | C7M84_023346 | J domain-containing protein |
| A0A423U4B3 | C7M84_023270 | SRCR domain-containing protein |
| A0A423U5E6 | C7M84_022903 | Nascent polypeptide-associated complex subunit alpha, muscle-specific form-like |
| A0A423U5I3 | C7M84_022855 | Protein disulfide-isomerase |
| A0A423U5T5 | C7M84_022776 | Putative ensconsin-like isoform X8 |
| A0A423U5U7 | C7M84_022737 | Putative dynactin subunit 2 |
| A0A423U5W2 | C7M84_022728 | ATP synthase subunit beta |
| A0A423U672 | C7M84_022619 | Beta'-coat protein |
| A0A423U6J3 | C7M84_022506 | Protein SEC13 homolog |
| A0A423U6P8 | C7M84_022437 | Alpha2 macroglobulin isoform 3 |
| A0A423U6S1 | C7M84_022428 | Prolyl endopeptidase |
| A0A423U7E5 | C7M84_022213 | Transmembrane emp24 domain-containing protein 9 |
| A0A423U7E7 | C7M84_022215 | Calmodulin |
| A0A423U7J2 | C7M84_022108 | E1 ubiquitin-activating enzyme |
| A0A423U7J5 | C7M84_022212 | Pyruvate kinase |
| A0A423U7P1 | C7M84_022100 | Putative methenyltetrahydrofolate synthase domain-containing protein isoform X2 |
| A0A423U7P7 | C7M84_022078 | Putative 60S ribosomal protein L18a-like |
| A0A423U7W2 | C7M84_022086 | Putative trifunctional enzyme subunit beta, mitochondrial |
| A0A423U835 | C7M84_021984 | Putative GTP cyclohydrolase 1 type 2 NIF3L1 |
| A0A423U854 | C7M84_021930 | V-type proton ATPase subunit C |
| A0A423U897 | C7M84_021887 | Putative filamin-A isoform X3 |
| A0A423U8F6 | C7M84_021591 | Cytochrome c oxidase subunit 4 |
| A0A423U8J7 | C7M84_021559 | Origin recognition complex subunit 3 |
| A0A423U8L8 | C7M84_021452 | Mitochondrial cytochrome c oxidase subunit Vb |
| A0A423U8M4 | C7M84_021457 | Tubulin alpha chain |
| A0A423U8Q2 | C7M84_021352 | NADH dehydrogenase |
| A0A423U8V3 | C7M84_021315 | Beta-thymosin 3 |
| A0A423U8Y8 | C7M84_020783 | MICOS complex subunit MIC60 (Fragment) |
| A0A423U904 | C7M84_020658 | Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial |
| A0A423U925 | C7M84_020303 | VWFD domain-containing protein |
| A0A423U9I6 | C7M84_015650 | Cuticular protein RR-2 motif 78 |
| A0A423U9K3 | C7M84_015306 | Carboxypeptidase A2-like (Fragment) |
| A0A423U9M1 | C7M84_015015 | ribonuclease H |
| A0A423U9P3 | C7M84_015419 | Mutant C-type lectin |
| A0A423U9T8 | C7M84_013682 | Transgelin |
| A0A423U9U4 | C7M84_013491 | Pupal cuticle protein 27 |
| A0A423U9V4 | C7M84_013492 | Pupal cuticle protein 27 |
| A0A423U9V9 | C7M84_013493 | Pupal cuticle protein 27 |
| A0A423U9Z2 | C7M84_012524 | Succinyl-CoA:3-ketoacid-coenzyme A transferase |
| A0A423UA04 | C7M84_012482 | Putative ribosome-binding protein 1-like isoform X11 |
| A0A423UA78 | C7M84_011290 | Saposin isoform 1 |
| A0A423UA97 | C7M84_009716 | Putative very low-density lipoprotein receptor-like |
| A0A423UAA4 | C7M84_009792 | NK2-3/5 transcription factor |
| A0A423UAG5 | C7M84_009136 | aconitate hydratase |
| A0A423UAI3 | C7M84_008251 | NEDD8 |
| A0A423UAL3 | C7M84_007554 | Phosphoinositide phospholipase C |
| A0A423UAM4 | C7M84_007740 | Alpha2 macroglobulin isoform 2 |
| A0A423UAM6 | C7M84_007425 | 60S ribosomal protein L13 |
| A0A423UAP1 | C7M84_007357 | Ribosomal protein L11 |
| A0A423UAW2 | C7M84_005281 | Translation initiation factor IF-2 |
| A0A423UAZ2 | C7M84_004526 | Signal peptidase complex catalytic subunit SEC11 |
| A0A423UB03 | C7M84_004366 | C-1-tetrahydrofolate synthase, cytoplasmic |

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|---|---|---|
| A0A423UB28 | C7M84_003956 | 26S proteasome non-ATPase regulatory subunit 1 |
| A0A423UBG8 | C7M84_015234 | Acyl-coenzyme A oxidase |
| B7SNI3 | C7M84_013542 | Myosin regulatory light chain 2 |
| D0FH89 | C7M84_012084 | Peroxiredoxin |
| E2IH93 | C7M84_012927 | Fatty-acid binding protein |
| G5D053 | C7M84_014842 | Peptidyl-prolyl cis-trans isomerase |
| H9LFA4 | C7M84_009298 | Mitochondrial ATP synthase delta subunit |
| K0E682 | TIM | Triosephosphate isomerase |
| M9WSX9 | C7M84_016357 | Eukaryotic translation initiation factor 5A |
| Q283P7 | C7M84_024001 | Anti-lipopolysaccharide AV-R isoform |
| Q6GUA8 | HSC70 | Heat shock cognate 70 |
| Q6ITD0 | C7M84_011529 | Heterotrimeric GTP-binding protein alpha subunit G-alpha-q |
| Q9GSP9 | C7M84_010918 | Beta-actin |
| X2KWE4 | C7M84_023278 | Hemocyanin |

**Table S2** KEGG annotation of the shrimp carapace metabolome

| **KEGG Level1** | **KEGG Level2** | **KEGG Level3 (Pathway)** | **ID** | **Count** |
|---|---|---|---|---|
| Metabolism | Global and overview maps | Metabolic pathways | map01100 | 85 |
| Organismal Systems | Digestive system | Protein digestion and absorption | map04974 | 18 |
| Environmental Information Processing | Membrane transport | ABC transporters | map02010 | 18 |
| Metabolism | Global and overview maps | Biosynthesis of amino acids | map01230 | 15 |
| Human Diseases | Cancers: Overview | Central carbon metabolism in cancer | map05230 | 14 |
| Genetic Information Processing | Translation | Aminoacyl-tRNA biosynthesis | map00970 | 12 |
| Metabolism | Lipid metabolism | Glycerophospholipid metabolism | map00564 | 11 |
| Metabolism | Nucleotide metabolism | Purine metabolism | map00230 | 11 |
| Metabolism | Global and overview maps | 2-Oxocarboxylic acid metabolism | map01210 | 10 |
| Metabolism | Amino acid metabolism | Arginine and proline metabolism | map00330 | 10 |
| Organismal Systems | Digestive system | Mineral absorption | map04978 | 9 |
| Metabolism | Lipid metabolism | Biosynthesis of unsaturated fatty acids | map01040 | 9 |
| Metabolism | Amino acid metabolism | Tryptophan metabolism | map00380 | 8 |
| Metabolism | Amino acid metabolism | Phenylalanine metabolism | map00360 | 7 |
| Metabolism | Amino acid metabolism | Tyrosine metabolism | map00350 | 7 |
| Metabolism | Carbohydrate metabolism | Glyoxylate and dicarboxylate metabolism | map00630 | 7 |
| Metabolism | Global and overview maps | Carbon metabolism | map01200 | 7 |
| Metabolism | Amino acid metabolism | Glycine, serine and threonine metabolism | map00260 | 6 |
| Metabolism | Lipid metabolism | Arachidonic acid metabolism | map00590 | 5 |
| Metabolism | Lipid metabolism | Sphingolipid metabolism | map00600 | 5 |
| Environmental Information Processing | Signaling molecules and interaction | Neuroactive ligand-receptor interaction | map04080 | 5 |
| Metabolism | Nucleotide metabolism | Pyrimidine metabolism | map00240 | 5 |
| Metabolism | Carbohydrate metabolism | Butanoate metabolism | map00650 | 5 |
| Metabolism | Lipid metabolism | Fatty acid biosynthesis | map00061 | 5 |
| Organismal Systems | Sensory system | Taste transduction | map04742 | 5 |
| Metabolism | Lipid metabolism | Steroid hormone biosynthesis | map00140 | 5 |
| Human Diseases | Cancers: Overview | Choline metabolism in cancer | map05231 | 4 |
| Organismal Systems | Nervous system | Retrograde endocannabinoid signaling | map04723 | 4 |
| Environmental Information Processing | Signal transduction | Sphingolipid signaling pathway | map04071 | 4 |
| Human Diseases | Neurodegenerative diseases | Parkinson's disease | map05012 | 4 |
| Metabolism | Amino acid metabolism | Phenylalanine, tyrosine and tryptophan biosynthesis | map00400 | 4 |
| Human Diseases | Substance dependence | Alcoholism | map05034 | 4 |
| Metabolism | Energy metabolism | Sulfur metabolism | map00920 | 4 |
| Metabolism | Biosynthesis of other secondary metabolites | Monobactam biosynthesis | map00261 | 4 |
| Metabolism | Metabolism of other amino acids | beta-Alanine metabolism | map00410 | 4 |
| Organismal Systems | Digestive system | Bile secretion | map04976 | 4 |

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|---|---|---|---|---|
| Metabolism | Carbohydrate metabolism | C5-Branched dibasic acid metabolism | map00660 | 4 |
| Metabolism | Amino acid metabolism | Alanine, aspartate and glutamate metabolism | map00250 | 4 |
| Metabolism | Amino acid metabolism | Arginine biosynthesis | map00220 | 4 |
| Metabolism | Amino acid metabolism | Valine, leucine and isoleucine biosynthesis | map00290 | 4 |
| Metabolism | Metabolism of cofactors and vitamins | Nicotinate and nicotinamide metabolism | map00760 | 4 |
| Organismal Systems | Nervous system | Serotonergic synapse | map04726 | 4 |
| Environmental Information Processing | Signal transduction | cAMP signaling pathway | map04024 | 4 |
| Metabolism | Amino acid metabolism | Histidine metabolism | map00340 | 4 |
| Organismal Systems | Digestive system | Vitamin digestion and absorption | map04977 | 4 |
| Organismal Systems | Endocrine system | Glucagon signaling pathway | map04922 | 4 |
| Organismal Systems | Nervous system | GABAergic synapse | map04727 | 4 |
| Human Diseases | Cancers: Overview | Pathways in cancer | map05200 | 4 |
| Human Diseases | Endocrine and metabolic diseases | Insulin resistance | map04931 | 3 |
| Metabolism | Metabolism of other amino acids | Taurine and hypotaurine metabolism | map00430 | 3 |
| Human Diseases | Substance dependence | Amphetamine addiction | map05031 | 3 |
| Human Diseases | Substance dependence | Cocaine addiction | map05030 | 3 |
| Metabolism | Metabolism of cofactors and vitamins | Pantothenate and CoA biosynthesis | map00770 | 3 |
| Metabolism | Amino acid metabolism | Cysteine and methionine metabolism | map00270 | 3 |
| Organismal Systems | Nervous system | Cholinergic synapse | map04725 | 3 |
| Human Diseases | Infectious diseases: Parasitic | Amoebiasis | map05146 | 3 |
| Metabolism | Carbohydrate metabolism | Citrate cycle (TCA cycle) | map00020 | 3 |
| Metabolism | Carbohydrate metabolism | Propanoate metabolism | map00640 | 3 |
| Organismal Systems | Digestive system | Carbohydrate digestion and absorption | map04973 | 3 |
| Organismal Systems | Excretory system | Proximal tubule bicarbonate reclamation | map04964 | 3 |
| Organismal Systems | Nervous system | Glutamatergic synapse | map04724 | 3 |
| Metabolism | Carbohydrate metabolism | Pyruvate metabolism | map00620 | 3 |
| Metabolism | Metabolism of other amino acids | D-Arginine and D-ornithine metabolism | map00472 | 3 |
| Metabolism | Lipid metabolism | alpha-Linolenic acid metabolism | map00592 | 2 |
| Metabolism | Lipid metabolism | Ether lipid metabolism | map00565 | 2 |
| Human Diseases | Infectious diseases: Parasitic | Leishmaniasis | map05140 | 2 |
| Metabolism | Metabolism of cofactors and vitamins | Ubiquinone and other terpenoid-quinone biosynthesis | map00130 | 2 |
| Organismal Systems | Endocrine system | Melanogenesis | map04916 | 2 |
| Organismal Systems | Nervous system | Dopaminergic synapse | map04728 | 2 |
| Metabolism | Energy metabolism | Oxidative phosphorylation | map00190 | 2 |
| Environmental Information Processing | Signal transduction | cGMP-PKG signaling pathway | map04022 | 2 |
| Human Diseases | Infectious diseases: Parasitic | African trypanosomiasis | map05143 | 2 |
| Human Diseases | Substance dependence | Morphine addiction | map05032 | 2 |
| Metabolism | Energy metabolism | Nitrogen metabolism | map00910 | 2 |

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|---|---|---|---|---|
| Metabolism | Metabolism of other amino acids | D-Glutamine and D-glutamate metabolism | map00471 | 2 |
| Metabolism | Metabolism of other amino acids | Glutathione metabolism | map00480 | 2 |
| Organismal Systems | Aging | Longevity regulating pathway - worm | map04212 | 2 |
| Cellular Processes | Cellular community - eukaryotes | Gap junction | map04540 | 2 |
| Organismal Systems | Circulatory system | Vascular smooth muscle contraction | map04270 | 2 |
| Organismal Systems | Endocrine system | Regulation of lipolysis in adipocytes | map04923 | 2 |
| Organismal Systems | Endocrine system | Renin secretion | map04924 | 2 |
| Environmental Information Processing | Signal transduction | Phospholipase D signaling pathway | map04072 | 2 |
| Human Diseases | Drug resistance: Antineoplastic | Endocrine resistance | map01522 | 2 |
| Human Diseases | Infectious diseases: Parasitic | Chagas disease (American trypanosomiasis) | map05142 | 2 |
| Human Diseases | Neurodegenerative diseases | Amyotrophic lateral sclerosis (ALS) | map05014 | 2 |
| Metabolism | Amino acid metabolism | Valine, leucine and isoleucine degradation | map00280 | 2 |
| Metabolism | Biosynthesis of other secondary metabolites | Neomycin, kanamycin and gentamicin biosynthesis | map00524 | 2 |
| Metabolism | Carbohydrate metabolism | Amino sugar and nucleotide sugar metabolism | map00520 | 2 |
| Metabolism | Global and overview maps | Fatty acid metabolism | map01212 | 2 |
| Metabolism | Lipid metabolism | Fatty acid degradation | map00071 | 2 |
| Metabolism | Metabolism of cofactors and vitamins | Porphyrin and chlorophyll metabolism | map00860 | 2 |
| Metabolism | Xenobiotics biodegradation and metabolism | Drug metabolism - cytochrome P450 | map00982 | 2 |
| Organismal Systems | Endocrine system | Ovarian steroidogenesis | map04913 | 2 |
| Organismal Systems | Environmental adaptation | Circadian entrainment | map04713 | 2 |
| Organismal Systems | Nervous system | Long-term potentiation | map04720 | 2 |
| Metabolism | Lipid metabolism | Linoleic acid metabolism | map00591 | 1 |
| Cellular Processes | Transport and catabolism | Autophagy - animal | map04140 | 1 |
| Human Diseases | Infectious diseases: Bacterial | Pathogenic Escherichia coli infection | map05130 | 1 |
| Metabolism | Glycan biosynthesis and metabolism | Glycosylphosphatidylinositol (GPI)-anchor biosynthesis | map00563 | 1 |
| Human Diseases | Endocrine and metabolic diseases | AGE-RAGE signaling pathway in diabetic complications | map04933 | 1 |
| Organismal Systems | Endocrine system | Adipocytokine signaling pathway | map04920 | 1 |
| Organismal Systems | Nervous system | Neurotrophin signaling pathway | map04722 | 1 |
| Metabolism | Lipid metabolism | Primary bile acid biosynthesis | map00120 | 1 |
| Metabolism | Metabolism of cofactors and vitamins | Thiamine metabolism | map00730 | 1 |
| Organismal Systems | Endocrine system | Prolactin signaling pathway | map04917 | 1 |
| Human Diseases | Cancers: Overview | Chemical carcinogenesis | map05204 | 1 |
| Metabolism | Biosynthesis of other secondary metabolites | Caffeine metabolism | map00232 | 1 |
| Human Diseases | Drug resistance: Antineoplastic | Antifolate resistance | map01523 | 1 |
| Human Diseases | Immune diseases | Systemic lupus erythematosus | map05322 | 1 |
| Metabolism | Amino acid metabolism | Lysine degradation | map00310 | 1 |
| Cellular Processes | Cell growth and death | Oocyte meiosis | map04114 | 1 |

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|---|---|---|---|---|
| Drug Development | Target-based classification: Nuclear receptors | Progesterone, androgen and estrogen receptor agonists/antagonists | map07226 | 1 |
| Environmental Information Processing | Signal transduction | Apelin signaling pathway | map04371 | 1 |
| Environmental Information Processing | Signal transduction | Calcium signaling pathway | map04020 | 1 |
| Environmental Information Processing | Signal transduction | FoxO signaling pathway | map04068 | 1 |
| Environmental Information Processing | Signal transduction | Hedgehog signaling pathway | map04340 | 1 |
| Environmental Information Processing | Signal transduction | MAPK signaling pathway | map04010 | 1 |
| Environmental Information Processing | Signal transduction | Rap1 signaling pathway | map04015 | 1 |
| Environmental Information Processing | Signal transduction | Ras signaling pathway | map04014 | 1 |
| Human Diseases | Cancers: Specific types | Non-small cell lung cancer | map05223 | 1 |
| Human Diseases | Cancers: Specific types | Prostate cancer | map05215 | 1 |
| Human Diseases | Cancers: Specific types | Renal cell carcinoma | map05211 | 1 |
| Human Diseases | Cancers: Specific types | Small cell lung cancer | map05222 | 1 |
| Human Diseases | Cardiovascular diseases | Dilated cardiomyopathy | map05414 | 1 |
| Human Diseases | Infectious diseases: Bacterial | Pertussis | map05133 | 1 |
| Human Diseases | Infectious diseases: Bacterial | Salmonella infection | map05132 | 1 |
| Human Diseases | Infectious diseases: Bacterial | Vibrio cholerae infection | map05110 | 1 |
| Human Diseases | Infectious diseases: Parasitic | Toxoplasmosis | map05145 | 1 |
| Human Diseases | Infectious diseases: Viral | HTLV-I infection | map05166 | 1 |
| Human Diseases | Neurodegenerative diseases | Huntington's disease | map05016 | 1 |
| Human Diseases | Neurodegenerative diseases | Prion diseases | map05020 | 1 |
| Human Diseases | Substance dependence | Nicotine addiction | map05033 | 1 |
| Metabolism | Carbohydrate metabolism | Ascorbate and aldarate metabolism | map00053 | 1 |
| Metabolism | Carbohydrate metabolism | Fructose and mannose metabolism | map00051 | 1 |
| Metabolism | Carbohydrate metabolism | Glycolysis / Gluconeogenesis | map00010 | 1 |
| Metabolism | Carbohydrate metabolism | Pentose and glucuronate interconversions | map00040 | 1 |
| Metabolism | Carbohydrate metabolism | Starch and sucrose metabolism | map00500 | 1 |
| Metabolism | Glycan biosynthesis and metabolism | Glycosaminoglycan biosynthesis - heparan sulfate / heparin | map00534 | 1 |
| Metabolism | Lipid metabolism | Fatty acid elongation | map00062 | 1 |
| Metabolism | Metabolism of cofactors and vitamins | Retinol metabolism | map00830 | 1 |
| Metabolism | Metabolism of cofactors and vitamins | Riboflavin metabolism | map00740 | 1 |
| Metabolism | Metabolism of cofactors and vitamins | Vitamin B6 metabolism | map00750 | 1 |
| Metabolism | Metabolism of other amino acids | Phosphonate and phosphinate metabolism | map00440 | 1 |
| Metabolism | Xenobiotics biodegradation and metabolism | Drug metabolism - other enzymes | map00983 | 1 |
| Organismal Systems | Aging | Longevity regulating pathway | map04211 | 1 |
| Organismal Systems | Aging | Longevity regulating pathway - multiple species | map04213 | 1 |

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| Organismal Systems | Circulatory system | Adrenergic signaling in cardiomyocytes | map04261 | 1 |
| Organismal Systems | Digestive system | Gastric acid secretion | map04971 | 1 |
| Organismal Systems | Digestive system | Pancreatic secretion | map04972 | 1 |
| Organismal Systems | Digestive system | Salivary secretion | map04970 | 1 |
| Organismal Systems | Endocrine system | Aldosterone synthesis and secretion | map04925 | 1 |
| Organismal Systems | Endocrine system | Estrogen signaling pathway | map04915 | 1 |
| Organismal Systems | Endocrine system | GnRH signaling pathway | map04912 | 1 |
| Organismal Systems | Endocrine system | Insulin secretion | map04911 | 1 |
| Organismal Systems | Endocrine system | Insulin signaling pathway | map04910 | 1 |
| Organismal Systems | Endocrine system | Oxytocin signaling pathway | map04921 | 1 |
| Organismal Systems | Endocrine system | Progesterone-mediated oocyte maturation | map04914 | 1 |
| Organismal Systems | Endocrine system | Thyroid hormone signaling pathway | map04919 | 1 |
| Organismal Systems | Endocrine system | Thyroid hormone synthesis | map04918 | 1 |
| Organismal Systems | Environmental adaptation | Circadian rhythm | map04710 | 1 |
| Organismal Systems | Excretory system | Aldosterone-regulated sodium reabsorption | map04960 | 1 |
| Organismal Systems | Excretory system | Endocrine and other factor-regulated calcium reabsorption | map04961 | 1 |
| Organismal Systems | Excretory system | Vasopressin-regulated water reabsorption | map04962 | 1 |
| Organismal Systems | Immune system | Chemokine signaling pathway | map04062 | 1 |
| Organismal Systems | Immune system | Fc epsilon RI signaling pathway | map04664 | 1 |
| Organismal Systems | Immune system | Intestinal immune network for IgA production | map04672 | 1 |
| Organismal Systems | Immune system | Leukocyte transendothelial migration | map04670 | 1 |
| Organismal Systems | Immune system | Platelet activation | map04611 | 1 |
| Organismal Systems | Immune system | Th17 cell differentiation | map04659 | 1 |
| Organismal Systems | Nervous system | Long-term depression | map04730 | 1 |
| Organismal Systems | Nervous system | Synaptic vesicle cycle | map04721 | 1 |
| Organismal Systems | Sensory system | Inflammatory mediator regulation of TRP channels | map04750 | 1 |
| Organismal Systems | Sensory system | Olfactory transduction | map04740 | 1 |
| Organismal Systems | Sensory system | Phototransduction - fly | map04745 | 1 |