

## Supplemental Figure Legends

**Figure S1.** Functional category of all the identified proteins expressed during the embryogenesis of honey bee worker (*A.m.ligustica*). Proteins are classified based on the biological process of gene ontology (GO) using Blast2GO (36). Due to proteins usually performing multifunctions, it is therefore a protein may be classified into multiple categories. The percentage of each functional group is obtained on the basis of the number of proteins under each of the functional groups divided by the total number of identified proteins. Color codes represent different protein functional groups.

**Figure S2.** Comparison of the identified proteins by their functional classifications at three developmental stages of the worker bee embryo (*A.m.ligustica*). The percentage of each functional group is obtained on the basis of the number of proteins under each of the functional groups divided by the total number of identified proteins at the corresponding stages. Color codes denote different aged samples.

**Figure S3.** Distribution of exclusive expressed proteins by their functional classification of honey bee workers (*A.m.ligustica*) at 24h, 48h and 72h. Color codes are different aged samples.

**Figure S4.** Protein–protein interaction (PPI) networks of identified proteins in the embryos of honey bee workers (*A.m.ligustica*). Panel A and B are the PPI networks in the embryos at age of 48 h and 72 h, respectively. Panel C is the PPI network of differentially expressed (fold change $\geq$ 2 and  $p$ <0.05) proteins in the embryo of honey bee workers. PPI is predicted using the Interologous Interaction Database (I2D) and visualized by NAViGaTOR software (38, 39). The color symbols represent identified proteins connected in the PPI network with more than ten interaction degrees (Supplemental Table S10, S11 and S14). The regular triangles stand for proteins up-regulated in the embryogenesis of honey bee worker at 24h. Letters from “a” to “p” represent the categories of carbohydrate metabolism/energy, morphogenesis, nucleic acid metabolism, translation, modification, development, cytoskeleton, DNA replication/repairment, cell cycle control/apoptosis, transcription, lipid metabolism,

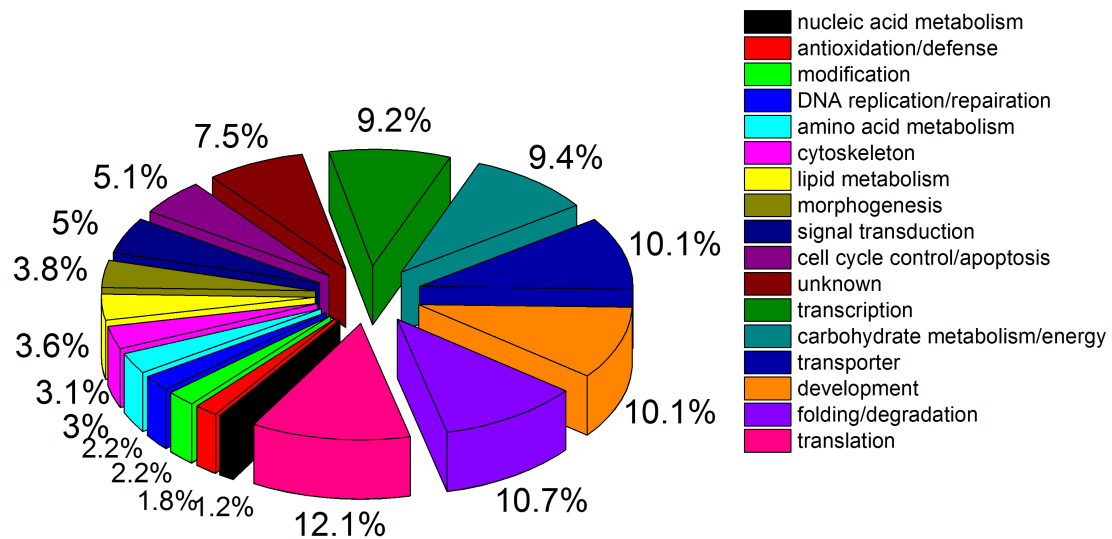
antioxidation/defense, folding/degradation, signal transduction, amino acid metabolism, transporters, respectively. Blue lines indicate interactions between proteins. The intensity of the interaction degree is indicated by a color gradient as noted on the key bar on the down right side of the figure.

**Figure S5.** Comparison of the identified key node proteins in protein–protein interaction networks by their functional classification of the worker bee (*A.m.ligustica*) embryo at age of 24h, 48h, and 72h. Color codes denote different aged samples.

**Figure S6.** Classification of the 544 differentially expressed (fold change $\geq$ 2 and  $p<0.05$ ) proteins across the embryonic development of the honey bee worker (*A.m.ligustica*) at 24h, 48h and 72h.

**Figure S7.** Comparison of the up-regulated proteins in the core proteome by their functional classifications at three developmental stages of the honey bee worker (*A.m.ligustica*) embryo. Color codes denote the three aged samples.

**Figure S1.**



**Figure S2.**

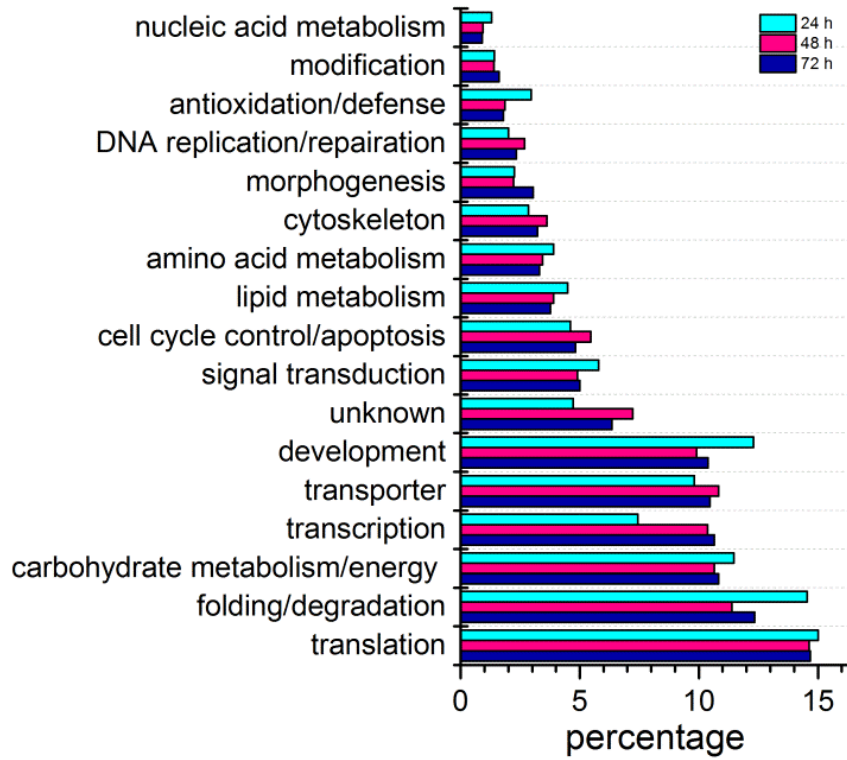


Figure S3.

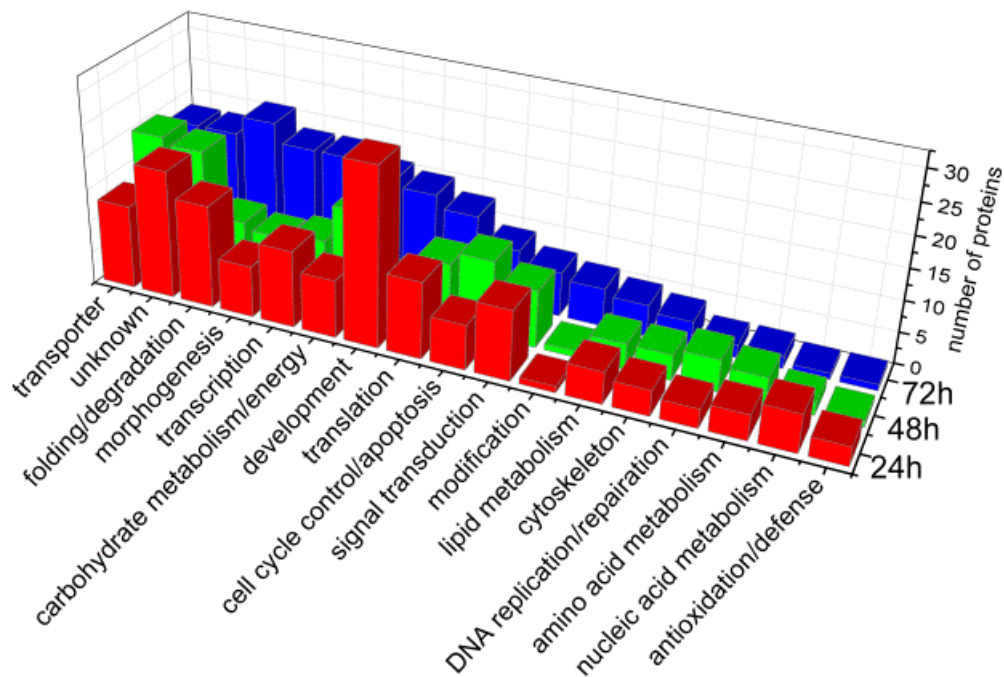


Figure S4.

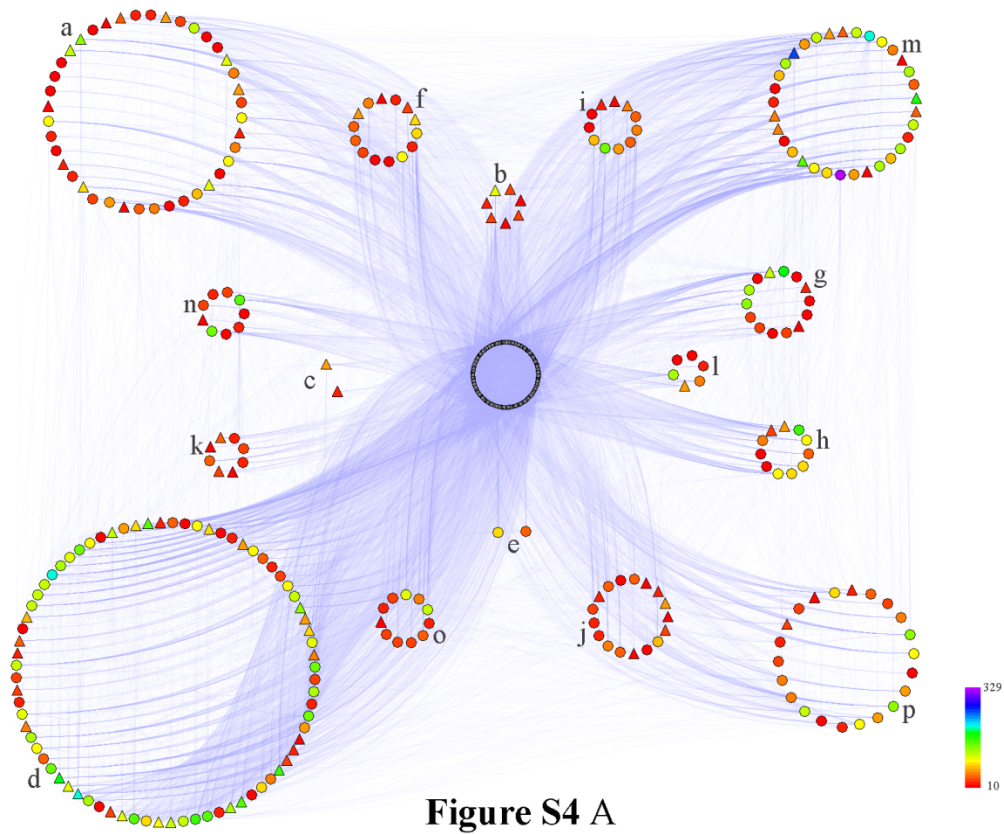


Figure S4 A

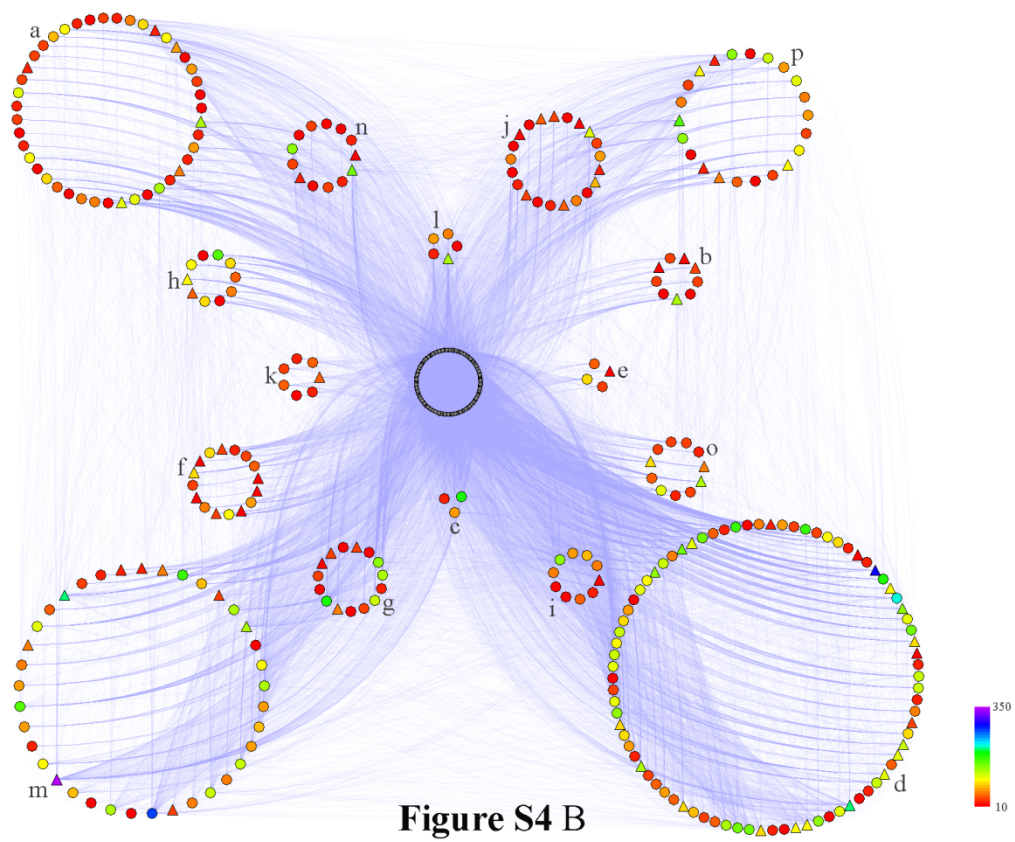


Figure S4 B

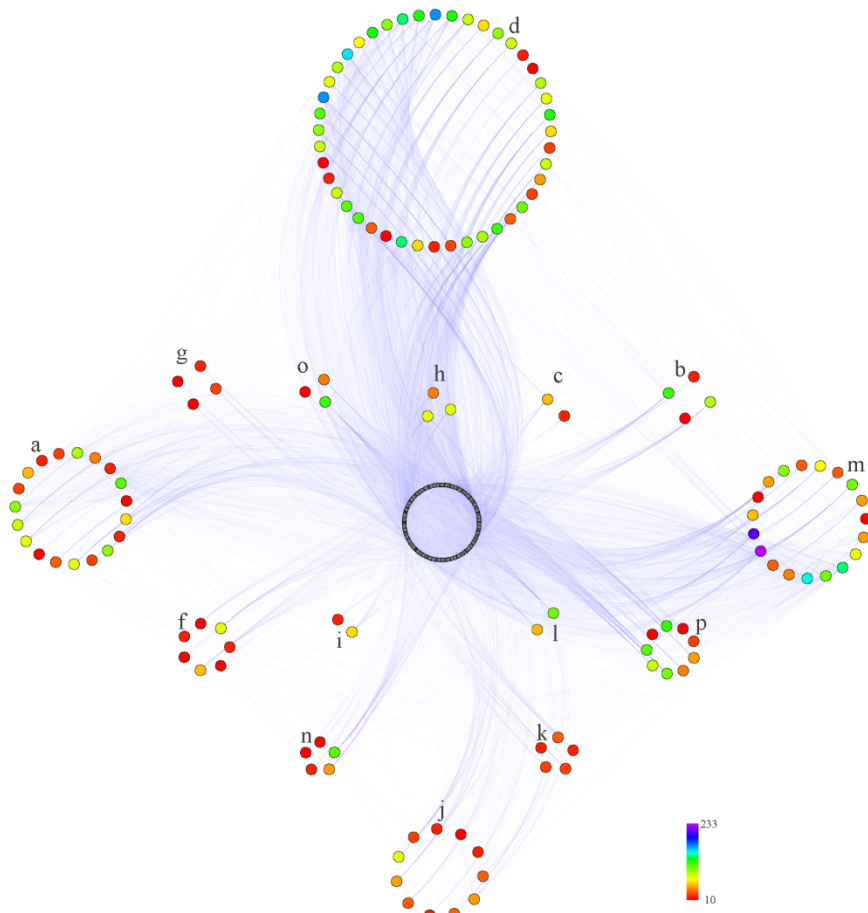
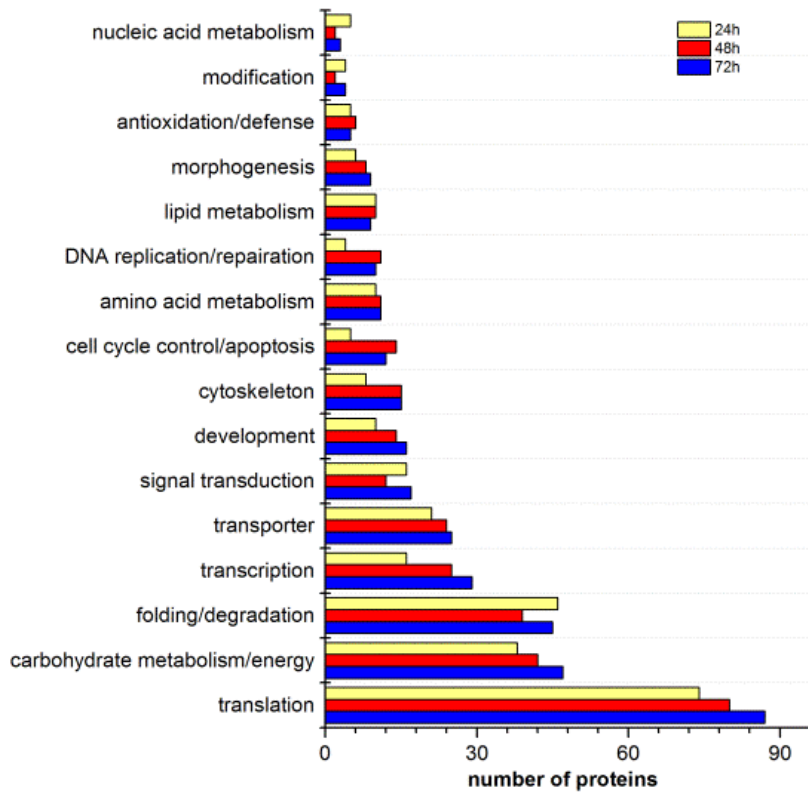
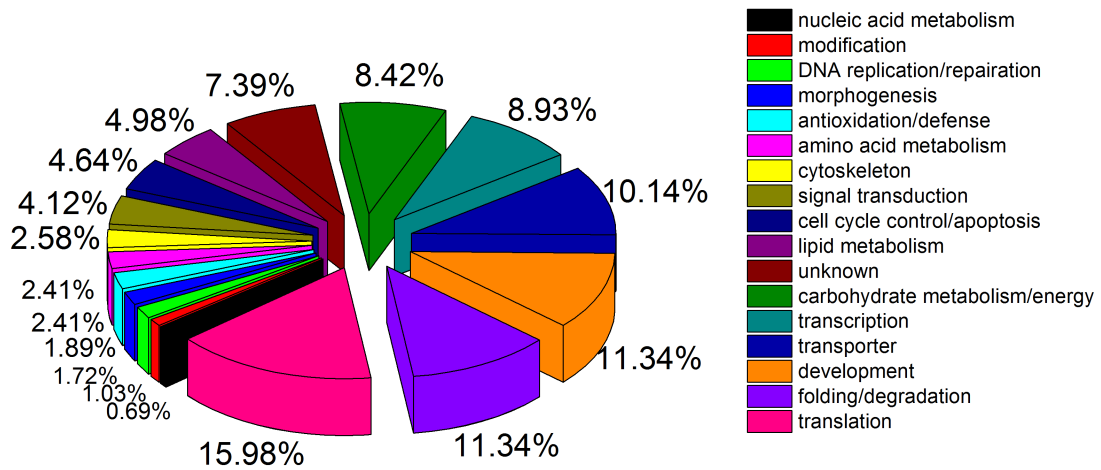


Figure S4 C

Figure S5.



**Figure S6.**



**Figure S7.**

