Supplementary Material

**Supplementary Table 4.** Differential abundance for the statistically significant proteins found in the SWATH-MS proteomics analysis between *O. vulgaris* 20 days post-hatching paralarvae (PL20) fed on mixed diet (M) and *Artemi*a-based diet (A).

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| UniProt accession | UniProt protein name/species | NCBI accession | NCBI protein name/species | Fold-change(M *vs* A) | p-values Mann-Whitney | Change | Biological process/GO\_ID | Molecular function/ GO\_ID |
| E9GLZ0 | Chymotrypsin-like protein/*Daphnia pulex* | gi|321468619gb|EFX79603.1 | Chymotrypsin-like protein/*Daphnia pulex* | 6.89 | 2.2E-03 | ↑ | Proteolysis/ GO:0006508 | Serine-type endopeptidase activity / GO: 0004252Peptidase activity/GO:0008233Serine-type peptidase activity/GO:0008236Hydrolase activity/GO:0016787 |
| V3ZTE3 | Uncharacterized protein/*Lottia gigantea* | gi|676490520XP\_009065297.1 | Hypothetical protein LOTGIDRAFT\_203267/*Lottia gigantea* | 3.67 | 8.7E-03 | ↑ | Vacuolar transport/ GO:0007034 | \_ |
| \*A0A6P7SI33  | LIM and SH3 domain protein F42H10.3 isoform X18/ *Octopus vulgaris* | gi|871250970XP\_012941291.1 | LIM and SH3 domain protein 1/ *Aplysia californica* | 2.77 | 8.7E-03 | ↑ |  | Metal ion binding/ GO:0046872 |
| \*A0A6P7SUE8 | Misshapen-like kinase 1 isoform X4/ *Octopus vulgaris* | gi|755981826XP\_011309716.1 | PREDICTED: serine/threonine-protein kinase mig-15 isoform X10/*Fopius arisanus* | 2.55 | 4.3E-03 | ↑ | Proteinphosphorylation/GO:0006468Phosphorylation / GO:0016310 | ATP binding /GO:0005524Protein kinase activityGO:004672Kinase activityGO:0016301Nucleotide binding/GO:0000166 |
| \*A0A7E6FHL6 | Titin-like isoform X6/ *Octopus vulgaris*  | gi|762129940XP\_011448097.1 | PREDICTED: titin-like isoform X6/*Crassostrea gigas* | 2.22 | 2.2E-03 | ↑ | \_ | \_ |
| V4BCR7 | UBA domain-containing protein/*Lottia gigantea* | gi|676423133 XP\_009044061.1 | Hypothetical proteinLOTGIDRAFT\_228067/*Lottia gigantea* | 2.14 | 8.7E-03 | ↑ | \_ | \_ |
| A0A6P3URJ4 | SAFB-like transcription modulator isoform X1/ *Bombus impatiens* | gi|815907918XP\_012239672.1 | PREDICTED: SAFB-like transcription modulator isoform X1/*Bombus impatiens* | 2.12 | 4.3E-03 | **↑** | **\_** | RNA binding / GO:0003723Nucleic acid binding / GO:0003676 |
| A0A093GAN7 | Phosvitin/ *Picoides pubescens* | gi|678200283gb|KFV67265.1 | Vitellogenin-2, partial/*Picoides pubescens* | 2.11 | 4.3E-03 | ↑ | Lipid transport / GO:0006869 | Nutrient reservoir activity/GO:0045735Lipid transporter activity / GO:0005319 |
| K1RD19 | RNA-binding protein 4/*Crassostrea gigas* | gi|405974565EKC39200.1 | RNA-binding protein 4/*Crassostrea gigas* | 2.07 | 8.7E-03 | ↑ | \_ | Nucleic acid binding / GO:0003676Zinc ion binding/GO:0008270RNA binding / GO:0003723 |
| V4B4B3 | Uncharacterized protein/*Lottia gigantea* | gi|676492747XP\_009066021.1 | Hypothetical protein LOTGIDRAFT\_133731/*Lottia gigantea* | 2.06 | 4.3E-03 | ↑ | RNA processing / GO:0006396 | RNA binding / GO:0003723Adenosine deaminase activity / GO:0004000   |
| \_ |  | gi|762106002XP\_011435580.1 | PREDICTED: uncharacterized protein LOC105334014 isoform X3 / *Crassostrea gigas* | 2.02 | 2.16E-03 | ↑ | \_ | \_ |
| Q9IBG7 | Kielin/chordin-like protein/ *Xenopus laevis* | sp|Q9IBG7 | Kielin/chordin-like protein/ *Xenopus laevis* | 2.00 | 4.3E-03 | ↑ | \_ | \_ |
| V3ZM47 | Uncharacterized protein/ *Lottia gigantea* | gi|676464632XP\_009056983.1 | Hypothetical protein LOTGIDRAFT\_162734 / *Lottia gigantea* | 0.50 | 4.3E-03 | ↓ | Negative regulation of nucleic acid-templated transcription /GO:0045892 | Transcription corepressor activity / GO:0003714  |
| I6XSF1 | Caspase 3 / *Cynops orientalis* | gi|395395171gb|AFN55260.1 | Caspase 3 / *Cynops orientalis* | 0.50 | 4.3E-03 | ↓ | Proteolysis / GO:000650Apoptotic process / GO:0006915  | Cysteine-type peptidase activity /GO:0008234Cysteine-type endopeptidase activity/GO:0004197Peptidase activity /GO:0008233Hydrolase activity / GO:0016787 |
| A0A6P7T833 | 3-oxoacyl-[acyl-carrier-protein] reductase FabG/ *Octopus vulgaris* | gi|1697406406XP\_029646407.1 | 3-oxoacyl-[acyl-carrier-protein] reductase FabG/*Octopus sinensis* | 0.49 | 2.2E-03 | ↓ | \_ | Oxidoreductase activity /GO:0016491 |
| A0A6P7TI21 | Delta-1-pyrroline-5-carboxylate synthase /*Octopus vulgaris* | gi|1697419816XP\_029649427.1 | Delta-1-pyrroline-5-carboxylate synthase /*Octopus sinensis*  | 0.49 | 4.3E-03 | ↓ | Proline biosynthetic process / GO:0006561L-proline biosynthetic process/ GO:0055129Phosphorylation/ GO:0016310Cellular amino acid biosynthetic process/ GO:0008652Metabolic process /GO:0008152 | Glutamate 5-kinase activity/ GO:0004349Glutamate-5-semialdehyde dehydrogenase activity/GO:0004350Oxidoreductase activity /GO:0016491Oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor/ GO:0016620Catalytic activity/ GO:0003824ATP binding/ GO:0005524Kinase activity/ GO:0016301Transferase activity/GO:0016740Nucleotide binding/GO:0000166 |
| M1VBI1 | Carbonic anhydrase / *Crassostrea gigas* | gi|456359321 dbj|BAM93475 | Carbonic anhydrase / *Crassostrea gigas* | 0.49 | 4.3E-03 | ↓ | \_ | Carbonate dehydratase activity / GO:0004089Zinc ion binding / GO:0008270Lyase activity/ GO:0016829Metal ion binding / GO:0046872  |
| V4ARC8 | Glyco\_18 domain-containing protein/ *Lottia gigantea* | gi|676452477XP\_009053044.1 | Hypothetical protein LOTGIDRAFT\_94382, partial*/ Lottia gigantea* | 0.49 | 4.3E-03 | ↓ | Carbohydrate metabolic process / GO:0005975Metabolic process/ GO:0008152 | Chitin binding / GO:0008061Hydrolase activity / GO:0016787Hydrolase activity, acting on glycosyl bonds/ GO:0016798Hydrolase activity, hydrolyzing O-glycosyl compounds /GO:0004553 |
|  \*\*K1QYG7 | Glutamine--fructose-6-phosphate transaminase (isomerizing)/ *Crassostrea gigas* | gi|762127166XP\_011446658.1 | Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 isoform X5/*Crassostrea gigas* | 0.48 | 2.2E-03 | ↓ | Carbohydrate derivative metabolic process / GO:1901135Glutamine metabolic process / GO:0006541 | Carbohydrate derivative binding, / GO:0097367Transferase activity / GO:0016740Glutamine-fructose-6-phosphate transaminase (isomerizing) activity / GO:0004360Transaminase activity, GO:0008483 |
| V4ABP3 | NTP\_transferase domain-containing protein/ *Lottia gigantea* | gi|676469579XP\_009058578.1 | Hypothetical protein LOTGIDRAFT\_227532 / *Lottia gigantea* | 0.47 | 2.2E-03 | ↓ | Biosynthetic process / GO:0009058 | Transferase activity / GO:0016740Nucleotidyltransferase activity / GO:0016779 |
| K1PJC1 | Adipophilin / *Crassostrea gigas* | gi|405954235 gb|EKC21733.1 | Adipophilin / *Crassostrea gigas* | 0.47 | 4.3E-03 | ↓ | Negative regulation of transcription, DNA-templated/ GO:0045892 | Transcription corepressor activity / GO:0003714 |
| K1QT65 | Collagen alpha-3(VI) chain/ *Crassostrea gigas*  | gi|405966888gb|EKC32120.1 | Collagen alpha-3(VI) chain */ Crassostrea gigas* | 0.47 | 2.2E-03 | ↓ | \_ |  |
| D2KX87 | Serine protease 1/ *Heterololigo bleekeri* | gi|283837550dbj|BAI66447.1 | Serine protease 1 / *Heterololigo bleekeri* | 0.46 | 4.3E-03 | ↓ | Proteolysis / GO:0006508 | Serine-type endopeptidase activity / GO:0004252Hydrolase activity/ GO:0016787Peptidase activity/ GO:0008233Serine-type peptidase activity/GO:0008236 |
| \*\*A0A6P7TL40  | Calcium load-activated calcium channel/ *Octopus vulgaris* | gi|871252834XP\_012941615.1 | Calcium load-activated calcium channel/ *Aplysia californica* | 0.45 | 2.2E-03 | ↓ | Calcium ion transport/ GO:0006816Ion transport/GO:0006811Calcium ion transmembrane transport / GO:0070588Endoplasmic reticulum calcium ion homeostasis / GO:0032469  | Calcium channel activity / GO:0005262  |
| A0A0H5ANU0 | Beta arrestin */ Idiosepius paradoxus* | gi|827883539dbj|BAR90777.1 | Beta arrestin */ Idiosepius paradoxus* | 0.44 | 8.7E-03 | ↓ | Signal transduction / GO:0007165 | \_ |
| V4B2N8 | Derlin/ *Lottia gigantean* | gi|676494434XP\_009066562.1 | Hypothetical protein LOTGIDRAFT\_205920 / *Lottia gigantean* | 0.44 | 4.3E-03 | ↓ | \_ | \_ |
|  \*A0A6P7SKG2 | Glutamine--fructose-6-phosphate transaminase (isomerizing)/ *Octopus vulgaris* | gi|762127168XP\_011446659.1 | Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 isoform X6 / *Crassostrea gigas*  | 0.42 | 8.7E-03 | ↓ | UDP-N-acetylglucosamine biosynthetic process / GO:0006048Carbohydrate derivative biosynthetic process / GO:1901137Carbohydrate derivative metabolic process / GO:1901135Glutamine metabolic process / GO:0006541 | Carbohydrate derivative binding / GO:0097367Transaminase activity / GO:0008483Transferase activity /GO:0016740Glutamine-fructose-6-phosphate transaminase (isomerizing) activity / GO:0004360 |
|  A0A6P7SU44 | Cartilage matrix protein-like/ *Octopus vulgaris* | gi|1697453666XP\_029641815.1 | Cartilage matrix protein-like/*Octopus sinensis* | 0.42 | 4.3E-03 | ↓ | \_ | \_ |
| \*\*A0A7E6FKQ8 | Collagen alpha-4(VI) chain-like/ *Octopus vulgaris* | gi|762116501XP\_011441088.1 | PREDICTED: collagen alpha-4(VI) chain-like / *Crassostrea gigas* | 0.40 | 4.3E-03 | ↓ | \_ | \_ |
| A0A6P7TZN0 | UPF0462 protein C4orf33 homolog isoform X3 /*Octopus vulgaris* | gi|1697376434XP\_029657914.1 | UPF0462 protein C4orf33 homolog isoform X3 /*Octopus sinensis* | 0.38 | 2.2E-03 | ↓ | \_ | \_ |
| W5M2B7 | Tyrosine--tRNA ligas/ *Lepisosteus oculatus*  | gi|573887259XP\_006631409.1 | PREDICTED: tyrosine--tRNA ligase, cytoplasmic-like / *Lepisosteus oculatus* | 0.36 | 2.2E-03 | ↓ | Tyrosyl-tRNA aminoacylation / GO:0006437RNA aminoacylation for protein translation / GO:0006418Translation / GO:0006412 | Tyrosine-tRNA ligase activity / GO:0004831ATP binding/ GO: GO:0005524Aminoacyl-tRNA ligase activity /GO:0004812Ligase / GO:0016874 tRNA binding /GO:0000049Nucleotide binding / GO:0000166RNA binding / GO:0003723 |
| A0A6P7TFX6 | Golgi-associated plant pathogenesis-related protein 1-like/*Octopus vulgaris* | gi|1697419007XP\_029649150.1 | Golgi-associated plant pathogenesis-related protein 1 /*Octopus sinensis* | 0.33 | 4.3E-03 | ↓ | \_ | \_ |
| Q7QIX6 | Nucleoside diphosphate kinase/*Anopheles gambiae* | gi|158286242XP\_308641.4 | AGAP007120-PA / *Anopheles gambiae* str. PEST | 0.31 | 8.7E-03 | ↓ | CTP biosynthetic process / GO:0006241UTP biosynthetic process /GO:0006228GTP biosynthetic process / GO:0006183Nucleoside diphosphate phosphorylation / GO:0006165Phosphorylation / GO:0016310 | Nucleoside diphosphate kinase activity/GO:0004550Kinase activity /GO:0016301ATP binding/GO:0005524Transferase activity/GO:0016740Nucleotide binding /GO:0000166 |
| V3ZYP8 | Uncharacterized protein/*Lottia gigantea* | gi|676479144XP\_009061653.1 | Hypothetical protein LOTGIDRAFT\_127363*/Lottia gigantea* | 0.28 | 2.2E-03 | ↓ | Carboxylic acid metabolic process / GO:0019752 | Pyridoxal phosphate binding / GO:0030170Carbon-carbon lyase activity/ GO:0016830Carboxy-lyase activity / GO:0016831Catalytic activity/GO:0003824Lyase activity /GO:0016829 |
| V3ZV16 | Uncharacterized protein*/Lottia gigantea* | gi|676488352XP\_009064588.1 | Hypothetical protein LOTGIDRAFT\_168464 /*Lottia gigantea* | 0.26 | 2.2E-03 | ↓ | Inorganic anion transport / GO:0015698 Transmembrane transport / GO:0055085Anion transmembrane transport / GO:0098656 | Voltage-gated anion channel activity / GO:0008308 Porin activity/GO:0015288 |
| \*\*A0A6P7SNY5  | Sulfotransferase 6B1/*Octopus vulgaris* | gi|871245287XP\_005102442.2 | Sulfotransferase 6B1-like, partial/*Aplysia californica* | 0.26 | 2.2E-03 | ↓ | \_ | Sulfotransferase activity / GO:0008146Transferase activity/GO:0016740 |
| U5YCS3 | Actin/*Rapana venosa* | gi|557132944gb|AGZ87937.1 | Actin/*Rapana venosa* | 0.20 | 2.2E-03 | ↓ | \_ | \_ |
| E9FS40 | Uncharacterized protein/*Daphnia pulex* | gi|321479428gb|EFX90384.1 | Hypothetical protein DAPPUDRAFT\_309644 /*Daphnia pulex* | 0.18 | 8.7E-03 | ↓ | Extracellular matrix organization / GO:0030198Cell adhesion / GO:0007155 | Cell adhesion molecule binding / GO:0050839 |
| D6WHD6 | Protein disulfide-isomerase/ *Tribolium castaneum* | gi|642916360XP\_008190988.1 | PREDICTED: protein disulfide-isomerase / *Tribolium castaneum* | 0.18 | 8.7E-03 | ↓ | Response to endoplasmic reticulum stress / GO:0034976Protein folding / GO:0006457 | Isomerase activity / GO:0016853Protein disulfide isomerase activity / GO:0003756 |
| Q06268 | Omega-crystallin / *Enteroctopus dofleini* | gi|159741gb|AAA16613.1 | Omega-crystallin / *Enteroctopus dofleini* | 0.16 | 2.2E-03 | ↓ | \_ | \_ |
| A7RPG9 | Homogentisate 1,2-dioxygenase/ *Nematostella vectensis* | gi|156400021XP\_001638799.1 | Predicted protein /*Nematostella vectensis* | 0.16 | 2.2E-03 | ↓ | L-phenylalanine catabolic process / GO:0006559Tyrosine metabolic process / GO:0006570 | Homogentisate 1,2-dioxygenase activity / GO:0004411Metal ion binding /GO:0046872 |
| E9GAM4 | 2-phospho-D-glycerate hydro-lyase/*Daphnia pulex* | gi|321472306EFX83276.1 | Enolase/*Daphnia pulex* | 0.14 | 4.3E-03 | ↓ | Glycolytic process / GO:0006096Regulation of vacuole fusion, non-autophagic/GO:0032889 | Phosphopyruvate hydratase activity / GO:0004634 Lyase activity/GO:0016829Magnesium ion binding/GO:0000287 |
| E9HR84 | Calcium-transporting ATPase/ *Daphnia pulex* | gi|321454575gb|EFX65740.1 | Hypothetical proteinDAPPUDRAFT\_65262 / *Daphnia pulex* | 0.13 | 4.3E-03 | ↓ | Calcium ion transport / GO:0006816Ion transport/GO:0006811Proton transmembrane transport/ GO:1902600Cellular calcium ion homeostasis / GO:0006874Calcium ion transmembrane transport / GO:0070588 | P-type calcium transporter activity/GO:0005388ATP binding / GO:0005524Nucleotide binding/GO:0000166ATPase activity/ GO: 0016887P-type proton-exporting transporter activity/ GO:0008553 |

Footnote: GO ID: GO annotations on QuickGO for Biological process and Molecular function. **(\*)** UniProt accession selected by best alignment hit; (\*\*) UniProt accession selected by protein name/species.