**Dataset S5**. Functional annotations of zebrafish (*Danio rerio*) and Chinook salmon (*Oncorhynchus tshawytscha*) genes showing distant homology to magnetotactic bacteria biomineralization proteins. The complete repertoire of zebrafish (226) and Chinook salmon genes (181) identified as 'universally conserved' in eukaryotes and with matches to zebrafish ZDB-Gene identifiers were functionally annotated in PANTHER, Protein Analysis Through Evolutionary Relationships, applying the built-in Benjamini-Hochberg false discovery rate (FDR P < 0.05) to correct for multiple tests. All categories are listed regardless of significance level. Results are shown for gene ontology (GO) complete categories biological process (BP), molecular function (MF), cellular component (CC), and the reactome pathway (R). Shading is used to depict individual GO category groupings, with sub-category hierarchy (H) indicated using a numeric scale: zero indicates the most specific sub-category, and incrementally higher numbers indicate the next-broader-level within each ontology hierarchy. The number of observed genes (No. Obs.) refers to the number of genes assigned to each GO category, while the number of expected genes (No. Exp.) is modeled by PANTHER using the number of genes in the input file relative to the background contents of the zebrafish genome (No. genes in genome). Fold-enrichment (F-E) is calculated by dividing No. Obs. by No. Exp, based on background genome contents of zebrafish.

| | | | | Zebrafish | | | | | Chinook salmon | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Cat. | H | GO Complete | No. Genes in Genome | No. Obs. | No. Exp. | F-E | Raw P value | FDR | No. Obs. | No. Exp. | F-E | Raw P value | FDR |
| BP | 0 | protein refolding | 23 | 10 | 0.21 | 48.01 | 2.15E-13 | 6.34E-10 | 6 | 0.16 | 36.45 | 4.92E-08 | 1.09E-04 |
| | 1 | protein folding | 125 | 17 | 1.13 | 15.02 | 1.30E-14 | 5.77E-11 | 13 | 0.89 | 14.53 | 2.08E-11 | 9.21E-08 |
| | 0 | zinc ion transport | 20 | 8 | 0.18 | 44.17 | 9.91E-11 | 9.75E-08 | 7 | 0.14 | 48.90 | 6.42E-10 | 1.89E-06 |
| | 1 | transition metal ion transport | 75 | 9 | 0.68 | 13.25 | 6.62E-08 | 3.91E-05 | 7 | 0.54 | 13.04 | 1.98E-06 | 1.94E-03 |
| | 0 | cellular response to heat | 23 | 9 | 0.21 | 43.21 | 7.56E-12 | 9.56E-09 | 5 | 0.16 | 30.37 | 1.48E-06 | 1.63E-03 |
| | 1 | response to heat | 34 | 9 | 0.31 | 29.23 | 1.40E-10 | 1.24E-07 | 5 | 0.24 | 20.55 | 8.12E-06 | 5.99E-03 |
| | 2 | response to temperature stimulus | 57 | 9 | 0.52 | 17.44 | 7.66E-09 | 4.84E-06 | 5 | 0.41 | 12.26 | 7.99E-05 | 3.93E-02 |
| | 0 | response to zinc ion | 13 | 5 | 0.12 | 42.47 | 4.34E-07 | 2.26E-04 | 4 | 0.09 | 42.99 | 5.46E-06 | 4.40E-03 |
| | 0 | chaperone cofactor-dependent protein refolding | 27 | 10 | 0.24 | 40.90 | 7.84E-13 | 1.74E-09 | 6 | 0.19 | 31.05 | 1.12E-07 | 1.98E-04 |
| | 1 | chaperone-mediated protein folding | 34 | 13 | 0.31 | 42.22 | 1.87E-16 | 1.65E-12 | 10 | 0.24 | 41.09 | 5.15E-13 | 4.56E-09 |
| | 1 | 'de novo' posttranslational protein folding | 28 | 10 | 0.25 | 39.44 | 1.06E-12 | 1.87E-09 | 6 | 0.2 | 29.94 | 1.35E-07 | 1.99E-04 |
| | 2 | 'de novo' protein folding | 29 | 10 | 0.26 | 38.08 | 1.41E-12 | 2.08E-09 | 6 | 0.21 | 28.91 | 1.62E-07 | 2.05E-04 |
| | 0 | mesenchyme morphogenesis | 11 | 4 | 0.10 | 40.16 | 7.98E-06 | 3.93E-03 | 3 | 0.08 | 38.10 | 1.21E-04 | 4.88E-02 |
| | 0 | cellular response to unfolded protein | 31 | 9 | 0.28 | 32.06 | 6.92E-11 | 7.66E-08 | 5 | 0.22 | 22.54 | 5.41E-06 | 4.79E-03 |
| | 1 | response to unfolded protein | 37 | 9 | 0.34 | 26.86 | 2.66E-10 | 2.14E-07 | 5 | 0.26 | 18.88 | 1.18E-05 | 8.03E-03 |
| | 2 | response to topologically incorrect protein | 54 | 9 | 0.49 | 18.41 | 5.01E-09 | 3.41E-06 | 5 | 0.39 | 12.94 | 6.29E-05 | 3.28E-02 |
| | 1 | cellular response to topologically incorrect protein | 48 | 9 | 0.43 | 20.71 | 2.00E-09 | 1.47E-06 | 5 | 0.34 | 14.55 | 3.73E-05 | 2.36E-02 |
| | 0 | protein peptidyl-prolyl isomerization | 24 | 4 | 0.22 | 18.41 | 1.09E-04 | 3.33E-02 | 4 | 0.17 | 23.29 | 4.42E-05 | 2.45E-02 |
| MF | 0 | protein folding chaperone | 11 | 9 | 0.1 | 90.35 | 4.97E-14 | 2.64E-11 | 5 | 0.08 | 63.51 | 7.03E-08 | 3.20E-05 |

|  |  |  |  | Zebrafish |  |  |  |  | Chinook salmon |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Cat. | H | GO Complete | No. Genes in Genome | No. Obs. | No. Exp. | F-E | Raw P value | FDR | No. Obs. | No. Exp. | F-E | Raw P value | FDR |
|  | 0 | misfolded protein binding | 14 | 11 | 0.13 | 86.77 | 9.53E-17 | 1.01E-13 | 6 | 0.1 | 59.88 | 4.23E-09 | 3.36E-06 |
|  | 0 | zinc ion transmembrane transporter activity | 20 | 8 | 0.18 | 44.17 | 9.91E-11 | 3.94E-08 | 7 | 0.14 | 48.9 | 6.42E-10 | 6.81E-07 |
|  | 1 | divalent inorganic cation transmembrane transporter activity | 20 | 8 | 0.18 | 44.17 | 9.91E-11 | 4.50E-08 | 7 | 0.14 | 48.90 | 6.42E-10 | 1.02E-06 |
|  | 1 | transition metal ion transmembrane transporter activity | 32 | 8 | 0.29 | 27.61 | 2.24E-09 | 6.47E-07 | 7 | 0.23 | 30.56 | 1.03E-08 | 6.58E-06 |
|  | 0 | Hsp90 protein binding | 12 | 3 | 0.11 | 27.61 | 3.00E-04 | 3.29E-02 | 4 | 0.09 | 46.57 | 4.20E-06 | 1.48E-03 |
|  | 1 | heat shock protein binding | 41 | 14 | 0.37 | 37.71 | 4.63E-17 | 7.37E-14 | 11 | 0.29 | 37.49 | 8.06E-14 | 2.56E-10 |
|  | 0 | peptidyl-prolyl cis-trans isomerase activity | 41 | 7 | 0.37 | 18.85 | 2.30E-07 | 4.89E-05 | 7 | 0.29 | 23.85 | 4.69E-08 | 2.49E-05 |
|  | 1 | cis-trans isomerase activity | 50 | 7 | 0.45 | 15.46 | 7.72E-07 | 1.54E-04 | 7 | 0.36 | 19.56 | 1.60E-07 | 6.35E-05 |
|  | 2 | isomerase activity | 134 | 7 | 1.21 | 5.77 | 2.92E-04 | 3.44E-02 | 7 | 0.96 | 7.30 | 6.92E-05 | 2.00E-02 |
|  | 0 | 4 iron, 4 sulfur cluster binding | 36 | 5 | 0.33 | 15.34 | 3.21E-05 | 4.86E-03 | 4 | 0.26 | 15.52 | 1.85E-04 | 4.52E-02 |
|  | 0 | insulin-like growth factor binding | 32 | 4 | 0.29 | 13.80 | 2.97E-04 | 3.38E-02 | 4 | 0.23 | 17.46 | 1.22E-04 | 3.23E-02 |
|  | 0 | unfolded protein binding | 96 | 12 | 0.87 | 13.80 | 2.67E-10 | 8.50E-08 | 7 | 0.69 | 10.19 | 9.09E-06 | 2.89E-03 |
| CC | 0 | actin-based cell projection | 29 | 5 | 0.26 | 19.04 | 0.000 | 0.017 | 5 | 0.21 | 24.09 | 0.000 | 0.006 |
| R | 0 | Zinc efflux and compartmentalization by the SLC30 family | 4 | 4 | 0.04 | > 100 | 4.30E-07 | 1.68E-04 | 2 | 0.03 | 69.86 | 7.39E-04 | 4.44E-02 |
|  | 0 | c-src mediated regulation of Cx43 function and closure of gap junctions | 4 | 2 | 0.04 | 55.22 | 1.17E-03 | 3.67E-02 | 2 | 0.03 | 69.86 | 7.39E-04 | 4.62E-02 |
|  | 1 | Regulation of gap junction activity | 4 | 2 | 0.04 | 55.22 | 1.17E-03 | 3.74E-02 | 2 | 0.03 | 69.86 | 7.39E-04 | 4.81E-02 |
|  | 2 | Gap junction trafficking and regulation | 20 | 4 | 0.18 | 22.09 | 5.83E-05 | 3.50E-03 | 3 | 0.14 | 20.96 | 5.63E-04 | 4.00E-02 |
|  | 0 | Phosphorylation of the APC/C | 18 | 5 | 0.16 | 30.68 | 1.64E-06 | 3.21E-04 | 4 | 0.13 | 31.05 | 1.63E-05 | 3.19E-03 |
|  | 0 | HSP90 chaperone cycle for steroid hormone receptors (SHR) | 18 | 5 | 0.16 | 30.68 | 1.64E-06 | 2.85E-04 | 4 | 0.13 | 31.05 | 1.63E-05 | 2.83E-03 |
|  | 1 | Cellular responses to stress | 292 | 12 | 2.64 | 4.54 | 2.14E-05 | 1.59E-03 | 9 | 2.09 | 4.31 | 3.18E-04 | 2.76E-02 |
|  | 0 | Inactivation of APC/C via direct inhibition of the APC/C complex | 19 | 5 | 0.17 | 29.06 | 2.06E-06 | 3.22E-04 | 4 | 0.14 | 29.41 | 1.97E-05 | 3.07E-03 |
|  | 1 | Inhibition of the proteolytic activity of APC/C required for the onset of anaphase by mitotic spindle checkpoint components | 19 | 5 | 0.17 | 29.06 | 2.06E-06 | 2.93E-04 | 4 | 0.14 | 29.41 | 1.97E-05 | 2.79E-03 |
|  | 2 | Regulation of APC/C activators between G1/S and early anaphase | 30 | 5 | 0.27 | 18.41 | 1.45E-05 | 1.13E-03 | 4 | 0.21 | 18.63 | 9.68E-05 | 1.01E-02 |
|  | 0 | Conversion from APC/C:Cdc20 to APC/C:Cdh1 in late anaphase | 19 | 5 | 0.17 | 29.06 | 2.06E-06 | 2.68E-04 | 4 | 0.14 | 29.41 | 1.97E-05 | 2.56E-03 |

|  |  |  |  | Zebrafish |  |  |  |  | Chinook salmon |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Cat. | H | GO Complete | No. Genes in Genome | No. Obs. | No. Exp. | F-E | Raw P value | FDR | No. Obs. | No. Exp. | F-E | Raw P value | FDR |
|  | 0 | APC/C:Cdc20 mediated degradation of Cyclin B | 22 | 5 | 0.2 | 25.1 | 3.83E-06 | 4.27E-04 | 4 | 0.16 | 25.40 | 3.26E-05 | 3.92E-03 |
|  | 0 | MET activates PTK2 signaling | 37 | 8 | 0.34 | 23.88 | 6.03E-09 | 9.42E-06 | 6 | 0.26 | 22.66 | 5.81E-07 | 4.54E-04 |
|  | 1 | MET promotes cell motility | 54 | 8 | 0.49 | 16.36 | 8.29E-08 | 4.32E-05 | 6 | 0.39 | 15.52 | 4.32E-06 | 1.69E-03 |
|  | 2 | Signaling by MET | 98 | 9 | 0.89 | 10.14 | 5.40E-07 | 1.69E-04 | 6 | 0.7 | 8.55 | 1.01E-04 | 9.87E-03 |
|  | 3 | Signaling by Receptor Tyrosine Kinases | 449 | 16 | 4.07 | 3.94 | 5.27E-06 | 4.84E-04 | 14 | 3.21 | 4.36 | 6.21E-06 | 1.62E-03 |
|  | 4 | Signal Transduction | 2196 | 36 | 19.89 | 1.81 | 5.63E-04 | 2.15E-02 | 36 | 15.72 | 2.29 | 3.60E-06 | 1.88E-03 |
|  | 0 | APC-Cdc20 mediated degradation of Nek2A | 24 | 5 | 0.22 | 23.01 | 5.55E-06 | 4.82E-04 | 4 | 0.17 | 23.29 | 4.42E-05 | 4.93E-03 |
|  | 0 | Laminin interactions | 34 | 7 | 0.31 | 22.74 | 7.42E-08 | 5.79E-05 | 6 | 0.24 | 24.66 | 3.72E-07 | 5.81E-04 |
|  | 0 | EPHB-mediated forward signaling | 63 | 7 | 0.57 | 12.27 | 3.17E-06 | 3.81E-04 | 5 | 0.45 | 11.09 | 1.24E-04 | 1.14E-02 |
|  | 1 | EPH-Ephrin signaling | 96 | 8 | 0.87 | 9.2 | 4.57E-06 | 4.47E-04 | 5 | 0.69 | 7.28 | 7.83E-04 | 4.53E-02 |
|  | 0 | RHO GTPase Effectors | 269 | 12 | 2.44 | 4.93 | 9.80E-06 | 8.06E-04 | 11 | 1.93 | 5.71 | 5.62E-06 | 1.75E-03 |
|  | 1 | Signaling by Rho GTPases | 418 | 13 | 3.79 | 3.43 | 1.53E-04 | 7.02E-03 | 13 | 2.99 | 4.35 | 1.38E-05 | 3.08E-03 |