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TRANSCRIPTOMIC PROFILING IN BRINE SHRIMP *ARTEMIA FRANCISCANA*

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The brine shrimp *Artemia franciscana* is a model organism for studying stress tolerance, developmental biology, and aquaculture applications. It plays a vital role in the aquatic food chain, serving as a primary nutritional source for fish larvae in culture systems. However, its omics resources remain limited, necessitating transcriptome-level insights. Here, we present a de novo transcriptome assembly of *A. franciscana* to establish a comprehensive molecular resource for functional and evolutionary studies. Given the emerging relevance of genotoxicity, transcriptomic profiling of *A. franciscana* was performed using next-generation sequencing. The sequencing results yielded a substantial dataset comprising 383,589 transcripts with an N50 value of 2,069. The completeness of the genome assembly was evaluated using BUSCO, which identified 95% conserved genes, ensuring high assembly quality. Functional annotation was conducted using multiple tools, including BLAST and EggNOG, while Gene Ontology (GO) annotation was assigned through GO analysis using blast2GO. Pathway annotation was performed using the Reactome and KEGG databases. This study provides a comprehensive reference dataset, reinforcing *A. franciscana* as a valuable model organism for future research.

Keywords: *Transcriptome assembly, Functional annotation, Artemia franciscana*