Supplementary information

Table S1. List of bioinformatic webtools used in this study

Software	URL	Remark
Amino acid sequence retrieval		
Uniprot	https://www.uniprot.org/	Protein database
Sequence similarity search		
BLAST: Basic Local Alignment Search Tool	https://www.ncbi.nlm.nih.gov/	BLASTp is used to search for similar sequences from microalgal genomes
Protein function prediction		
BLAST: Basic Local Alignment Search Tool	https://www.ncbi.nlm.nih.gov/	Primary function prediction
Final Validation		
InterProScan	http://www.ebi.ac.uk/InterProScan/	Function prediction
SUPERFAMILY 2.0	http://supfam.org	Function prediction
CATH	https://www.cathdb.info/	Function prediction
Pfam	http://pfam.xfam.org/	Function prediction
SignalP 5.0	https://services.healthtech.dtu.dk/service.php?SignalP-5.0	Subcellular localization
Alphafold2	https://github.com/sokrypton/ColabFold	Structure modelling
Modelarchive	https://modelarchive.org/	Structure archive
ProFunc	https://www.hsls.pitt.edu/obrc/index.php?page=URL1125088260	Structure-based annotation