

Applied Microbiology and Biotechnology

Supplemental Material

Global omics study of *Tetraselmis chuii* reveals time-related metabolic adaptations upon oxidative stress

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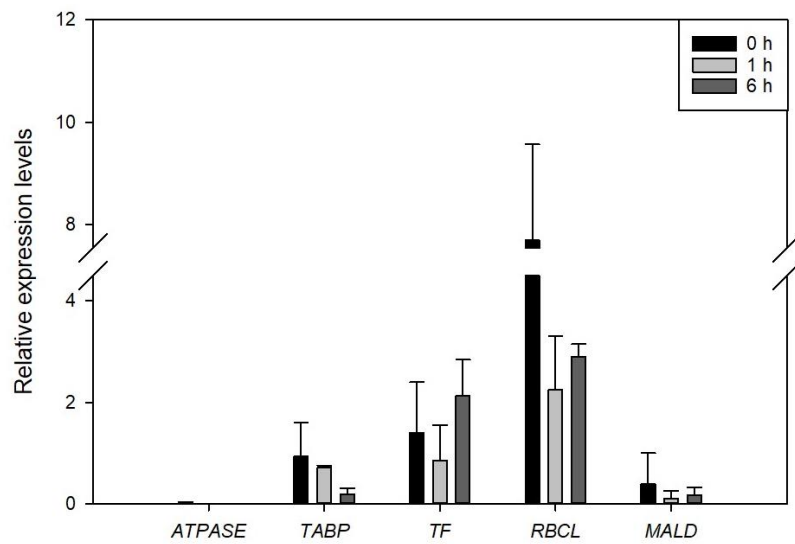


Figure S1: Relative expression levels of genes according to qPCR

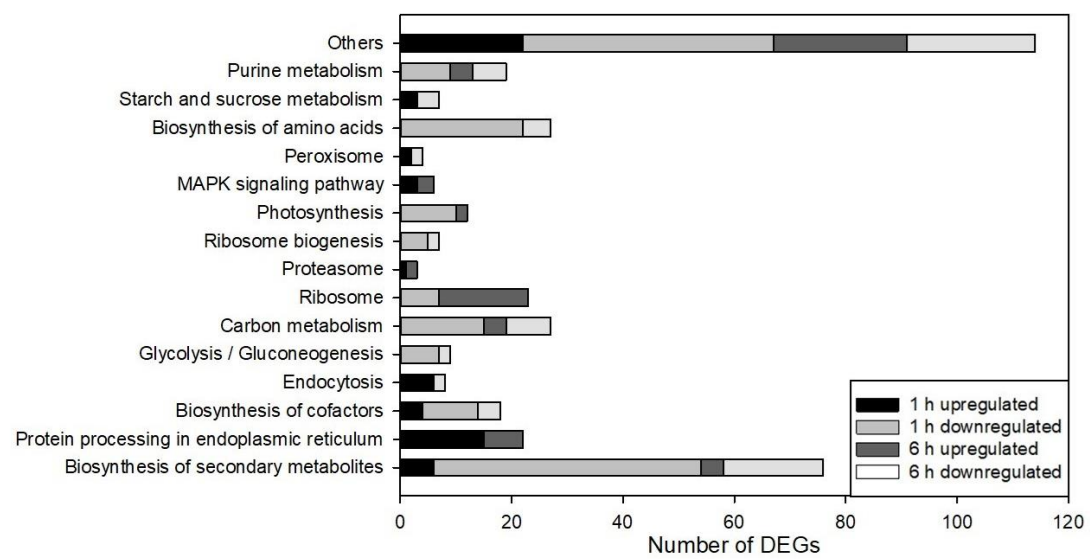


Figure S2: Number of DEGs annotated with KOs and mapped to pathways

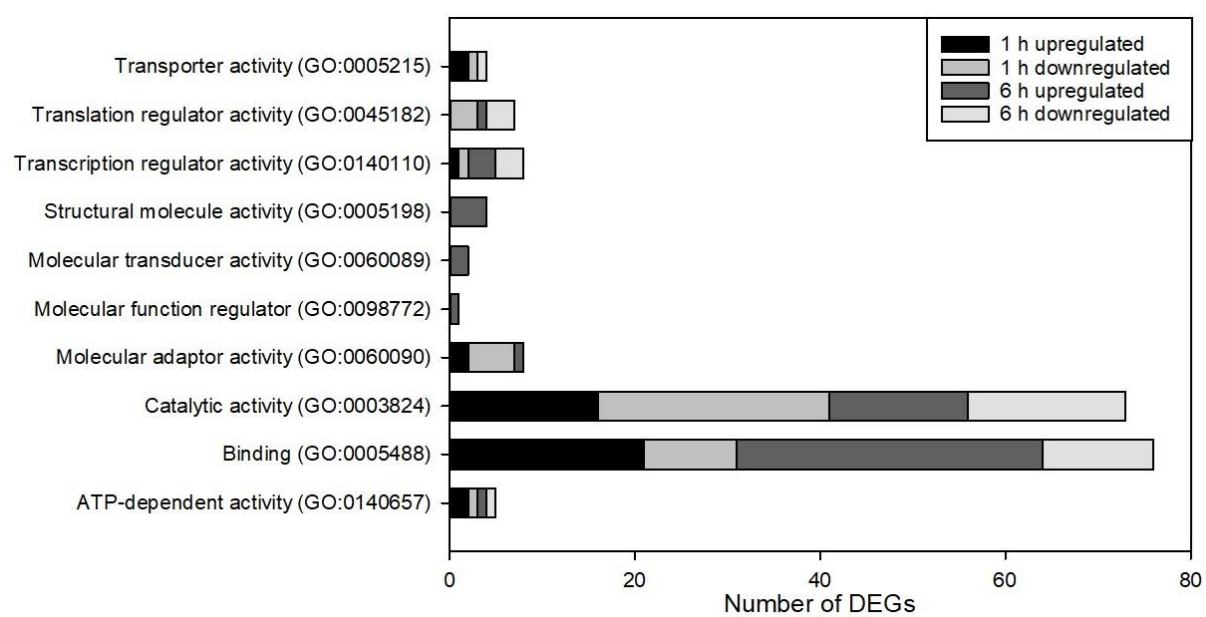


Figure S3: Number of DEGs classified based on GOs

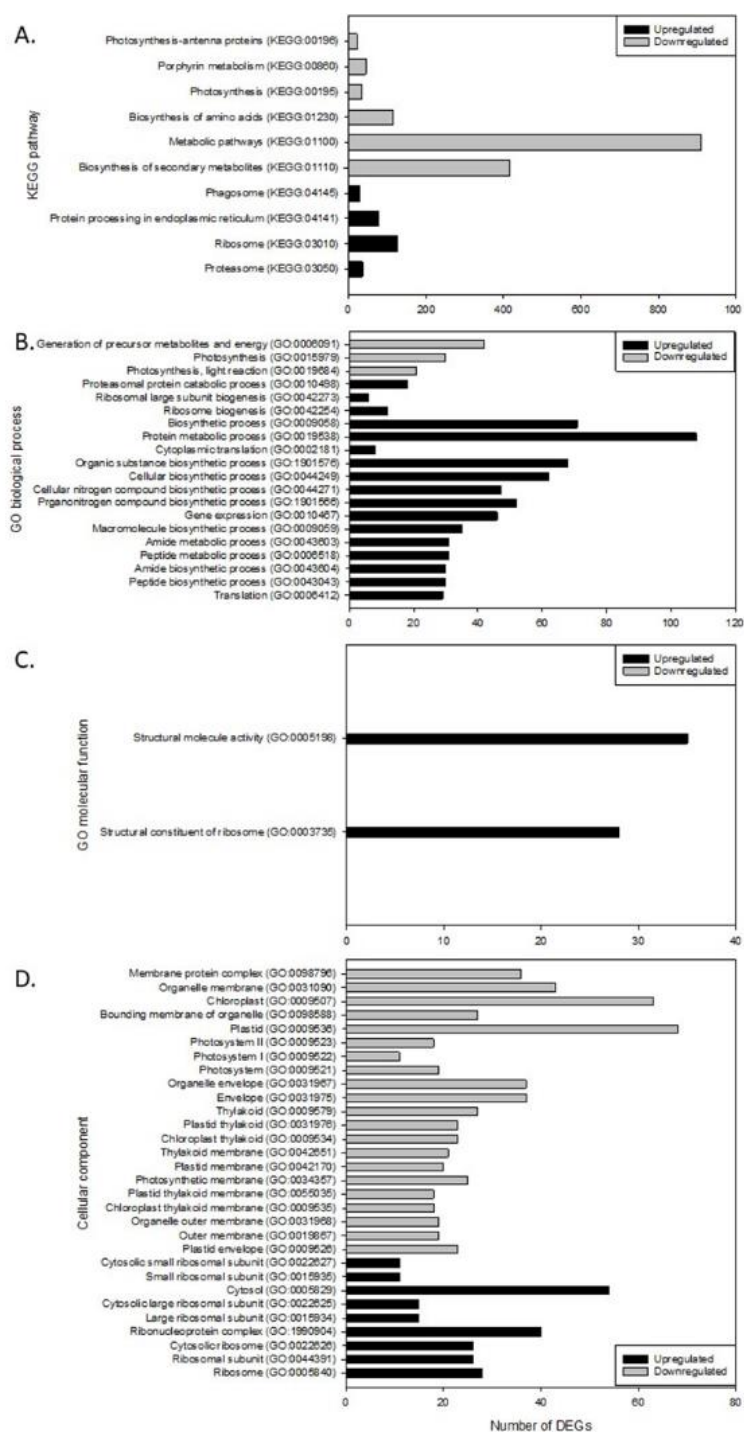


Figure S4: Enrichment analysis of DEGs for 1 h exposure to oxidative stress. A. KEGG pathway, B. GO biological process, C. GO molecular function, D. GO cellular component. The Y-axis shows the annotation terms and the X-axis the number of DEGs.

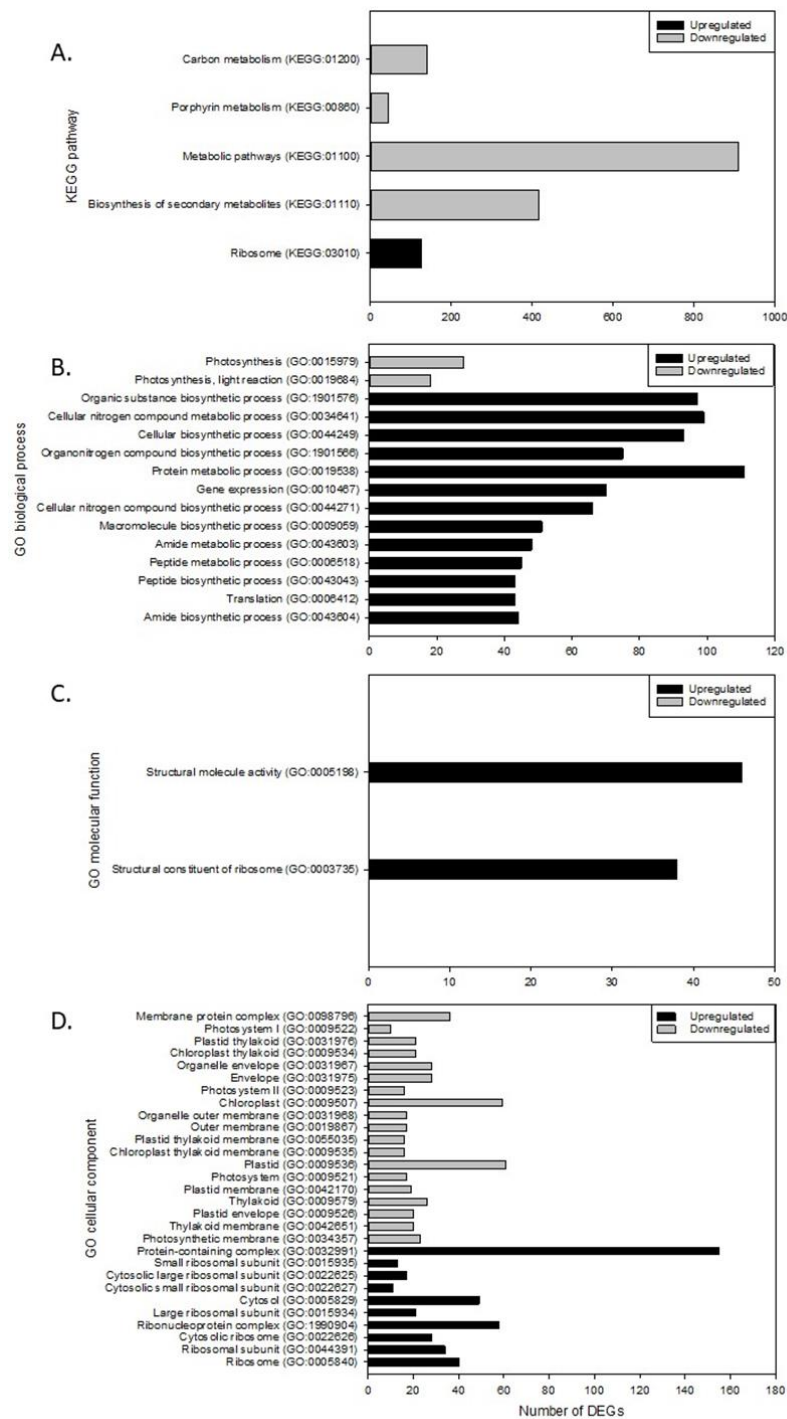


Figure S5: Enrichment analysis of DEGs for 6 h exposure to oxidative stress. A. KEGG pathway, B. GO biological process, C. GO molecular function, D. GO cellular component. The Y-axis shows the annotation terms and the X-axis the number of DEGs.

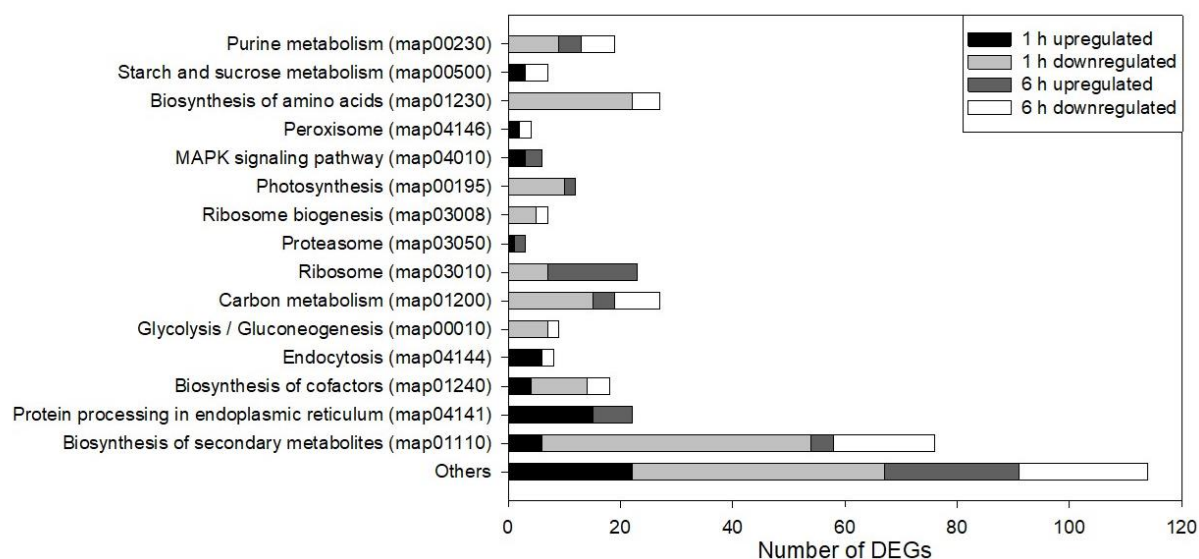


Figure S6. Number of DEGs per pathway being up-regulated and down-regulated in key metabolic pathways after 1 h and 6 h exposure to 0.5 mM H₂O₂.

Table S1: Primers used for RT-qPCR (data provided in excel file)

Table S2: RNAseq data for transcripts with adj.*p* < 0.05 (data provided in excel file)

Table S3: Relative response ratios of identified metabolites with GC/MS (data provided in excel file)