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A Taste of Algal Genomes from the Joint Genome Institute

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Algae and the JGI mission

Algae play profound roles in aquatic food chains and the carbon cycle, can impose health and economic costs through toxic blooms, provide models for the study of symbiosis, photosynthesis, and eukaryotic evolution, and are candidate sources for bio-fuels; all of these research areas are part of the mission of DOE’s Joint Genome Institute (JGI). To date JGI has sequenced, assembled, annotated, and released to the public the genomes of 18 species and strains of algae, sampling almost all of the major clades of photosynthetic eukaryotes. With more algal genomes currently undergoing analysis, JGI continues its commitment to driving forward basic and applied algal science. Among these ongoing projects are the pan-genome of the dominant coccolithophore Emiliania huxleyi, the interactions between the 4 genomes in the nucleomorph-containing Bigelowiella natans and Guillardia theta, and the search for symbiosis genes of lichens.

The lichen photobiont Asterochloris sp.

Genomes of the 2 lichen symbionts.

The lichen symbiosis, and its in vitro reconstitution.

Bnatans Gtheta each has 4 genomes.

Enrichment or depletion of Pfams in families clustered from Asterochloris and 10 other species of Chlorophyta.

Abundance of heat shock protein (HSP) genes in the genomes of Asterochloris and other species of Chlorophyta.

Genes of the 2 lichen symbionts.

Enrichment or depletion of Pfams in families clustered from Asterochloris and 10 other species of Chlorophyta.

Abundance of heat shock protein (HSP) genes in the genomes of Asterochloris and other species of Chlorophyta.

Genes of the 2 lichen symbionts.

Depleted families

Enriched families

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