Chris Bowler

List of Publications by Year
in descending order

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202	33,757	5558 82	4419 172
papers	citations	h-index	g-index

236	236	236	24554
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A robust approach to estimate relative phytoplankton cell abundances from metagenomes. Molecular Ecology Resources, 2023, 23, 16-40.	2.2	29
2	Dynamic Cell Imaging: application to the diatom Phaeodactylum tricornutum under environmental stresses. European Journal of Phycology, 2023, 58, 145-155.	0.9	0
3	Heterotrophic bacterial diazotrophs are more abundant than their cyanobacterial counterparts in metagenomes covering most of the sunlit ocean. ISME Journal, 2022, 16, 927-936.	4.4	41
4	Global marine phytoplankton revealed by the Tara Oceans expedition. , 2022, , 531-561.		2
5	The possible fates of Fragilariopsis cylindrus (polar diatom) cells exposed to prolonged darkness. Journal of Phycology, 2022, 58, 281-296.	1.0	2
6	Cryptic and abundant marine viruses at the evolutionary origins of Earthâ€™s RNA virome. Science, 2022, 376, 156-162.	6.0	124
7	Contribution of genomeâ€scale metabolic modelling to niche theory. Ecology Letters, 2022, 25, 1352-1364.	3.0	11
8	The Ocean Gene Atlas v2.0: online exploration of the biogeography and phylogeny of plankton genes. Nucleic Acids Research, 2022, 50, W516-W526.	6.5	26
9	An Integrated View of Diatom Interactions. , 2022, , 59-86.		1
10	Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. Cell Genomics, 2022, 2, 100123.	3.0	70
11	Coupling Imaging and Omics in Plankton Surveys: State-of-the-Art, Challenges, and Future Directions. Frontiers in Marine Science, 2022, 9, .	1.2	4
12	Biosynthetic potential of the global ocean microbiome. Nature, 2022, 607, 111-118.	13.7	128
13	Diversity and ecological footprint of Global Ocean RNA viruses. Science, 2022, 376, 1202-1208.	6.0	41
14	Priorities for ocean microbiome research. Nature Microbiology, 2022, 7, 937-947.	5.9	27
15	Genome wide natural variation of H3K27me3 selectively marks genes predicted to be important for cell differentiation in Phaeodactylum tricornutum. New Phytologist, 2021, 229, 3208-3220.	3.5	19
16	Phylogenomic fingerprinting of tempo and functions of horizontal gene transfer within ochrophytes. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	37
17	Complex Response of the Chlorarachniophyte Bigelowiella natans to Iron Availability. MSystems, 2021, 6, .	1.7	5
18	Genome-wide analysis of allele-specific expression of genes in the model diatom Phaeodactylum tricornutum. Scientific Reports, 2021, 11, 2954.	1.6	11

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19	Iron metabolism strategies in diatoms. Journal of Experimental Botany, 2021, 72, 2165-2180.	2.4	26
20	Carbon Dioxide Concentration Mechanisms in Natural Populations of Marine Diatoms: Insights From Tara Oceans. Frontiers in Plant Science, 2021, 12, 657821.	1.7	26
21	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. Communications Biology, 2021, 4, 604.	2.0	107
22	Global distribution patterns of marine nitrogen-fixers by imaging and molecular methods. Nature Communications, 2021, 12, 4160.	5.8	58
23	Engineered chlorophyll catabolism conferring predator resistance for microalgal biomass production. Metabolic Engineering, 2021, 66, 79-86.	3.6	7
24	Full-Length Transcriptome of Thalassiosira weissflogii as a Reference Resource and Mining of Chitin-Related Genes. Marine Drugs, 2021, 19, 392.	2.2	9
25	Environmental vulnerability of the global ocean epipelagic plankton community interactome. Science Advances, 2021, 7, .	4.7	54
26	Mitotic recombination between homologous chromosomes drives genomic diversity in diatoms. Current Biology, 2021, 31, 3221-3232.e9.	1.8	29
27	Macroscale patterns of oceanic zooplankton composition and size structure. Scientific Reports, 2021, 11, 15714.	1.6	24
28	Global drivers of eukaryotic plankton biogeography in the sunlit ocean. Science, 2021, 374, 594-599.	6.0	41
29	Compendium of 530 metagenome-assembled bacterial and archaeal genomes from the polar Arctic Ocean. Nature Microbiology, 2021, 6, 1561-1574.	5.9	57
30	Paleo-diatom composition from Santa Barbara Basin deep-sea sediments: a comparison of 18S-V9 and diat-rbcL metabarcoding vs shotgun metagenomics. ISME Communications, 2021, 1, .	1.7	18
31	A genomics approach reveals the global genetic polymorphism, structure, and functional diversity of ten accessions of the marine model diatom Phaeodactylum tricornutum. ISME Journal, 2020, 14, 347-363.	4.4	50
32	Phytoplankton in the Tara Ocean. Annual Review of Marine Science, 2020, 12, 233-265.	5.1	96
33	PhaeoNet: A Holistic RNAseq-Based Portrait of Transcriptional Coordination in the Model Diatom Phaeodactylum tricornutum. Frontiers in Plant Science, 2020, 11, 590949.	1.7	26
34	Large scale patterns of marine diatom richness: Drivers and trends in a changing ocean. Global Ecology and Biogeography, 2020, 29, 1915-1928.	2.7	26
35	Physiological and molecular responses to ocean acidification among strains of a model diatom. Limnology and Oceanography, 2020, 65, 2926-2936.	1.6	7
36	Biogeography of marine giant viruses reveals their interplay with eukaryotes and ecological functions. Nature Ecology and Evolution, 2020, 4, 1639-1649.	3.4	78

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37	Global identification of a marine diatom long noncoding natural antisense transcripts (NATs) and their response to phosphate fluctuations. Scientific Reports, 2020, 10, 14110.	1.6	15
38	Diatoms Are Selective Segregators in Global Ocean Planktonic Communities. MSystems, 2020, 5, .	1.7	38
39	Tara Oceans: towards global ocean ecosystems biology. Nature Reviews Microbiology, 2020, 18, 428-445.	13.6	227
40	Genome-enabled phylogenetic and functional reconstruction of an araphid pennate diatom Plagiostriata sp. CCMP470, previously assigned as a radial centric diatom, and its bacterial commensal. Scientific Reports, 2020, 10, 9449.	1.6	25
41	Probing the Diversity of Polycomb and Trithorax Proteins in Cultured and Environmentally Sampled Microalgae. Frontiers in Marine Science, 2020, 7, .	1.2	26
42	Intraspecific Diversity in the Cold Stress Response of Transposable Elements in the Diatom Leptocylindrus aporus. Genes, 2020, 11, 9.	1.0	16
43	Genetic tool development in marine protists: emerging model organisms for experimental cell biology. Nature Methods, 2020, 17, 481-494.	9.0	97
44	Metabolic Innovations Underpinning the Origin and Diversification of the Diatom Chloroplast. Biomolecules, 2019, 9, 322.	1.8	39
45	Phaeodactylum tricornutum. Trends in Genetics, 2019, 35, 706-707.	2.9	8
46	Meta-Omics Reveals Genetic Flexibility of Diatom Nitrogen Transporters in Response to Environmental Changes. Molecular Biology and Evolution, 2019, 36, 2522-2535.	3.5	23
47	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. Cell, 2019, 179, 1068-1083.e21.	13.5	268
48	Global Trends in Marine Plankton Diversity across Kingdoms of Life. Cell, 2019, 179, 1084-1097.e21.	13.5	271
49	Access to RNA-sequencing data from 1,173 plant species: The 1000 Plant transcriptomes initiative (1KP). GigaScience, 2019, 8, .	3.3	118
50	The Tara Pacific expeditionâ€"A pan-ecosystemic approach of the â€œ-omicsâ€•complexity of coral reef holobionts across the Pacific Ocean. PLoS Biology, 2019, 17, e3000483.	2.6	48
51	Arabidopsis S2Lb links AtCOMPASS-like and SDG2 activity in H3K4me3 independently from histone H2B monoubiquitination. Genome Biology, 2019, 20, 100.	3.8	56
52	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. Cell, 2019, 177, 1109-1123.e14.	13.5	541
53	Communityâ€Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. Global Biogeochemical Cycles, 2019, 33, 391-419.	1.9	76
54	Principles of plastid reductive evolution illuminated by nonphotosynthetic chrysophytes. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 6914-6923.	3.3	96

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55	Marine DNA Viral Macro-and Micro-Diversity From Pole to Pole. SSRN Electronic Journal, 2019, , .	0.4	4
56	Expanding Tara Oceans Protocols for Underway, Ecosystemic Sampling of the Ocean-Atmosphere Interface During Tara Pacific Expedition (2016â€“2018). Frontiers in Marine Science, 2019, 6, .	1.2	42
57	Observational Needs Supporting Marine Ecosystems Modeling and Forecasting: From the Global Ocean to Regional and Coastal Systems. Frontiers in Marine Science, 2019, 6, .	1.2	32
58	Downregulation of mitochondrial alternative oxidase affects chloroplast function, redox status and stress response in a marine diatom. New Phytologist, 2019, 221, 1303-1316.	3.5	51
59	Comparative characterization of putative chitin deacetylases from Phaeodactylum tricornutum and Thalassiosira pseudonana highlights the potential for distinct chitinâ€based metabolic processes in diatoms. New Phytologist, 2019, 221, 1890-1905.	3.5	21
60	The epibiotic life of the cosmopolitan diatom Fragilariopsis doliolus on heterotrophic ciliates in the open ocean. ISME Journal, 2018, 12, 1094-1108.	4.4	26
61	Single-cell genomics of multiple uncultured stramenopiles reveals underestimated functional diversity across oceans. Nature Communications, 2018, 9, 310.	5.8	101
62	A global ocean atlas of eukaryotic genes. Nature Communications, 2018, 9, 373.	5.8	297
63	Neobodonids are dominant kinetoplastids in the global ocean. Environmental Microbiology, 2018, 20, 878-889.	1.8	27
64	Influence of diatom diversity on the ocean biological carbon pump. Nature Geoscience, 2018, 11, 27-37.	5.4	451
65	Integrative analysis of large scale transcriptome data draws a comprehensive landscape of Phaeodactylum tricornutum genome and evolutionary origin of diatoms. Scientific Reports, 2018, 8, 4834.	1.6	131
66	Nanoplanktonic diatoms are globally overlooked but play a role in spring blooms and carbon export. Nature Communications, 2018, 9, 953.	5.8	150
67	Clade-specific diversification dynamics of marine diatoms since the Jurassic. Nature Ecology and Evolution, 2018, 2, 1715-1723.	3.4	40
68	Endocytosis-mediated siderophore uptake as a strategy for Fe acquisition in diatoms. Science Advances, 2018, 4, eaar4536.	4.7	103
69	Competition between Silicifiers and Non-silicifiers in the Past and Present Ocean and Its Evolutionary Impacts. Frontiers in Marine Science, 2018, 5, .	1.2	29
70	Homoeolog expression bias in allopolyploid oleaginous marine diatom Fistulifera solaris. BMC Genomics, 2018, 19, 330.	1.2	41
71	Ubiquitous abundance distribution of non-dominant plankton across the global ocean. Nature Ecology and Evolution, 2018, 2, 1243-1249.	3.4	41
72	A Potential Role for Epigenetic Processes in the Acclimation Response to Elevated pCO2 in the Model Diatom Phaeodactylum tricornutum. Frontiers in Microbiology, 2018, 9, 3342.	1.5	39

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73	DET1-mediated degradation of a SAGA-like deubiquitination module controls H2Bub homeostasis. ELife, 2018, 7, .	2.8	63
74	Evolutionary genomics of the cold-adapted diatom Fragilariopsis cylindrus. Nature, 2017, 541, 536-540.	13.7	332
75	Recent progress in diatom genomics and epigenomics. Current Opinion in Plant Biology, 2017, 36, 46-55.	3.5	33
76	Modelling plankton ecosystems in the meta-omics era. Are we ready?. Marine Genomics, 2017, 32, 1-17.	0.4	29
77	Enhanced NADPH production in the pentose phosphate pathway accelerates lipid accumulation in the oleaginous diatom Fistulifera solaris. Algal Research, 2017, 23, 126-134.	2.4	49
78	The Implications of Eco-Evolutionary Processes for the Emergence of Marine Plankton Community Biogeography. American Naturalist, 2017, 190, 116-130.	1.0	25
79	The evolution of diatoms and their biogeochemical functions. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160397.	1.8	134
80	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. Scientific Data, 2017, 4, 170093.	2.4	147
81	Secondary Plastids of Stramenopiles. Advances in Botanical Research, 2017, 84, 57-103.	0.5	17
82	Differential cellular responses associated with oxidative stress and cell fate decision under nitrate and phosphate limitations in Thalassiosira pseudonana: Comparative proteomics. PLoS ONE, 2017, 12, e0184849.	1.1	16
83	Chimeric origins of ochrophytes and haptophytes revealed through an ancient plastid proteome. ELife, 2017, 6, .	2.8	129
84	Quantitative 3D-imaging for cell biology and ecology of environmental microbial eukaryotes. ELife, 2017, 6, .	2.8	45
85	PhytoCRISP-Ex: a web-based and stand-alone application to find specific target sequences for CRISPR/CAS editing. BMC Bioinformatics, 2016, 17, 261.	1.2	63
86	Diatom Phytochromes Reveal the Existence of Far-Red-Light-Based Sensing in the Ocean. Plant Cell, 2016, 28, 616-628.	3.1	105
87	Insights into global diatom distribution and diversity in the worldâ€™s ocean. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1516-25.	3.3	561
88	Extreme Diversity of Diplonemid Eukaryotes in the Ocean. Current Biology, 2016, 26, 3060-3065.	1.8	105
89	Progressive and Biased Divergent Evolution Underpins the Origin and Diversification of Peridinin Dinoflagellate Plastids. Molecular Biology and Evolution, 2016, 34, msw235.	3.5	13
90	Cyanobacterial symbionts diverged in the late Cretaceous towards lineage-specific nitrogen fixation factories in single-celled phytoplankton. Nature Communications, 2016, 7, 11071.	5.8	72

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91	Ostreococcus tauri is a new model green alga for studying iron metabolism in eukaryotic phytoplankton. BMC Genomics, 2016, 17, 319.	1.2	35
92	Noncoding and coding transcriptome responses of a marine diatom to phosphate fluctuations. New Phytologist, 2016, 210, 497-510.	3.5	118
93	Knockdown of phosphoenolpyruvate carboxykinase increases carbon flux to lipid synthesis in Phaeodactylum tricornutum. Algal Research, 2016, 15, 50-58.	2.4	63
94	Plankton networks driving carbon export in the oligotrophic ocean. Nature, 2016, 532, 465-470.	13.7	670
95	Reverse transcriptase genes are highly abundant and transcriptionally active in marine plankton assemblages. ISME Journal, 2016, 10, 1134-1146.	4.4	35
96	Ultrastructure and Membrane Traffic During Cell Division in the Marine Pennate Diatom Phaeodactylum tricornutum. Protist, 2015, 166, 506-521.	0.6	51
97	An integrative analysis of post-translational histone modifications in the marine diatom Phaeodactylum tricornutum. Genome Biology, 2015, 16, 102.	3.8	107
98	Computational ecoâ€systems biology in <scp>T</scp>ara <scp>O</scp>ceans: translating data into knowledge. Molecular Systems Biology, 2015, 11, 809.	3.2	16
99	Determinants of community structure in the global plankton interactome. Science, 2015, 348, 1262073.	6.0	842
100	Patterns and ecological drivers of ocean viral communities. Science, 2015, 348, 1261498.	6.0	617
101	Structure and function of the global ocean microbiome. Science, 2015, 348, 1261359.	6.0	2,137
102	Eukaryotic plankton diversity in the sunlit ocean. Science, 2015, 348, 1261605.	6.0	1,551
103	Environmental characteristics of Agulhas rings affect interocean plankton transport. Science, 2015, 348, 1261447.	6.0	158
104	Marine microbial biodiversity, bioinformatics and biotechnology (M2B3) data reporting and service standards. Standards in Genomic Sciences, 2015, 10, 20.	1.5	14
105	Central role for ferritin in the day/night regulation of iron homeostasis in marine phytoplankton. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14652-14657.	3.3	57
106	A Novel Protein, Ubiquitous in Marine Phytoplankton, Concentrates Iron at the Cell Surface and Facilitates Uptake. Current Biology, 2015, 25, 364-371.	1.8	90
107	Oil Accumulation by the Oleaginous Diatom Fistulifera solaris as Revealed by the Genome and Transcriptome. Plant Cell, 2015, 27, 162-176.	3.1	149
108	Energetic coupling between plastids and mitochondria drives CO2 assimilation in diatoms. Nature, 2015, 524, 366-369.	13.7	311

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109	Functional characterization of the diatom cyclin-dependent kinase A2 as a mitotic regulator reveals plant-like properties in a non-green lineage. BMC Plant Biology, 2015, 15, 86.	1.6	14
110	Light signaling controls nuclear architecture reorganization during seedling establishment. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E2836-44.	3.3	90
111	Membrane Glycerolipid Remodeling Triggered by Nitrogen and Phosphorus Starvation inPhaeodactylum tricornutum. Plant Physiology, 2015, 167, 118-136.	2.3	286
112	When everything is not everywhere but species evolve: an alternative method to model adaptive properties of marine ecosystems. Journal of Plankton Research, 2015, 37, 28-47.	0.8	20
113	Methylcrotonyl-CoA Carboxylase Regulates Triacylglycerol Accumulation in the Model Diatom Phaeodactylum tricornutum Â Â Â. Plant Cell, 2014, 26, 1681-1697.	3.1	136
114	Evolution of galactoglycerolipid biosynthetic pathways â€“ From cyanobacteria to primary plastids and from primary to secondary plastids. Progress in Lipid Research, 2014, 54, 68-85.	5.3	118
115	Being Selective in the Prochlorococcus Collective. Science, 2014, 344, 366-367.	6.0	3
116	Histone extraction protocol from the two model diatoms Phaeodactylum tricornutum and Thalassiosira pseudonana. Marine Genomics, 2014, 13, 21-25.	0.4	10
117	iTRAQ-Based Proteomic Analysis of the Metabolism Mechanism Associated with Silicon Response in the Marine Diatom Thalassiosira pseudonana. Journal of Proteome Research, 2014, 13, 720-734.	1.8	47
118	Cellular Responses Associated with ROS Production and Cell Fate Decision in Early Stress Response to Iron Limitation in the Diatom Thalassiosira pseudonana. Journal of Proteome Research, 2014, 13, 5510-5523.	1.8	37
119	Adhesion molecules from the diatom Phaeodactylum tricornutum (Bacillariophyceae): genomic identification by aminoâ€acid profiling and in vivo analysis. Journal of Phycology, 2014, 50, 837-849.	1.0	21
120	The molecular life of diatoms. Marine Genomics, 2014, 16, 1-3.	0.4	1
121	Re-print of "Histone extraction protocol from the two model diatoms Phaeodactylum tricornutum and Thalassiosira pseudonana". Marine Genomics, 2014, 16, 67-71.	0.4	1
122	Insights into the role of DNA methylation in diatoms by genome-wide profiling in Phaeodactylum tricornutum. Nature Communications, 2013, 4, 2091.	5.8	113
123	AUREOCHROME1a-Mediated Induction of the Diatom-Specific Cyclin dsCYC2 Controls the Onset of Cell Division in Diatoms (Phaeodactylum tricornutum). Plant Cell, 2013, 25, 215-228.	3.1	136
124	Photomorphogenesis, B-Box Transcription Factors, and the Legacy of Magnus Holm. Plant Cell, 2013, 25, 1192-1195.	3.1	7
125	Bioprospecting Marine Plankton. Marine Drugs, 2013, 11, 4594-4611.	2.2	57
126	Histone H2B Monoubiquitination Facilitates the Rapid Modulation of Gene Expression during Arabidopsis Photomorphogenesis. PLoS Genetics, 2012, 8, e1002825.	1.5	115

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127	Evolution and Functional Diversification of Fructose Bisphosphate Aldolase Genes in Photosynthetic Marine Diatoms. Molecular Biology and Evolution, 2012, 29, 367-379.	3.5	68
128	Chloroplast-mitochondria cross-talk in diatoms. Journal of Experimental Botany, 2012, 63, 1543-1557.	2.4	108
129	Leveraging metabolomics for functional investigations in sequenced marine diatoms. Trends in Plant Science, 2012, 17, 395-403.	4.3	23
130	Protocol: Chromatin immunoprecipitation (ChIP) methodology to investigate histone modifications in two model diatom species. Plant Methods, 2012, 8, 48.	1.9	81
131	The Ectocarpus Genome and Brown Algal Genomics. Advances in Botanical Research, 2012, 64, 141-184.	0.5	18
132	Iron Utilization in Marine Cyanobacteria and Eukaryotic Algae. Frontiers in Microbiology, 2012, 3, 43.	1.5	130
133	Photoantenna in two cryptochromeâ€“photolyase proteins from O. tauri: Presence, nature and ultrafast photoinduced dynamics. Journal of Photochemistry and Photobiology A: Chemistry, 2012, 234, 135-145.	2.0	9
134	Characterisation of alleles of tomato light signalling genes generated by TILLING. Phytochemistry, 2012, 79, 78-86.	1.4	23
135	A Holistic Approach to Marine Eco-Systems Biology. PLoS Biology, 2011, 9, e1001177.	2.6	353
136	Stemming Epigenetics in Marine Stramenopiles. Current Genomics, 2011, 12, 357-370.	0.7	27
137	Decoding algal genomes: tracing back the history of photosynthetic life on Earth. Plant Journal, 2011, 66, 45-57.	2.8	125
138	Integrative epigenomic mapping defines four main chromatin states in Arabidopsis. EMBO Journal, 2011, 30, 1928-1938.	3.5	600
139	The conserved factor DE-ETIOLATED 1 cooperates with CUL4-DDB1DDB2to maintain genome integrity upon UV stress. EMBO Journal, 2011, 30, 1162-1172.	3.5	47
140	Evolution and metabolic significance of the urea cycle in photosynthetic diatoms. Nature, 2011, 473, 203-207.	13.7	453
141	Physiological and Molecular Evidence that Environmental Changes Elicit Morphological Interconversion in the Model Diatom Phaeodactylum tricornutum. Protist, 2011, 162, 462-481.	0.6	84
142	Localization of putative carbonic anhydrases in two marine diatoms, Phaeodactylum tricornutum and Thalassiosira pseudonana. Photosynthesis Research, 2011, 109, 205-221.	1.6	146
143	Diatom cell division in an environmental context. Current Opinion in Plant Biology, 2010, 13, 623-630.	3.5	36
144	Comparative ecophysiology and genomics of the toxic unicellular alga Fibrocapsa japonica. New Phytologist, 2010, 185, 446-458.	3.5	7

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145	Transcription factor families inferred from genome sequences of photosynthetic stramenopiles. New Phytologist, 2010, 188, 52-66.	3.5	126
146	Characterization of two members of the cryptochrome/photolyase family from Ostreococcus tauri provides insights into the origin and evolution of cryptochromes. Plant, Cell and Environment, 2010, 33, 1614-1626.	2.8	108
147	The Ectocarpus genome and the independent evolution of multicellularity in brown algae. Nature, 2010, 465, 617-621.	13.7	774
148	det1-1-induced UV-C hyposensitivity through UVR3 and PHR1 photolyase gene over-expression. Plant Journal, 2010, 63, 392-404.	2.8	41
149	A Gene in the Process of Endosymbiotic Transfer. PLoS ONE, 2010, 5, e13234.	1.1	18
150	An atypical member of the light-harvesting complex stress-related protein family modulates diatom responses to light. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 18214-18219.	3.3	258
151	Integrative Transcript and Metabolite Analysis of Nutritionally Enhanced DE-ETIOLATED1 Downregulated Tomato Fruit. Plant Cell, 2010, 22, 1190-1215.	3.1	160
152	Spectroâ^'Temporal Characterization of the Photoactivation Mechanism of Two New Oxidized Cryptochrome/Photolyase Photoreceptors. Journal of the American Chemical Society, 2010, 132, 4935-4945.	6.6	67
153	Oceanographic and Biogeochemical Insights from Diatom Genomes. Annual Review of Marine Science, 2010, 2, 333-365.	5.1	189
154	Genomic insights into photosynthesis in eukaryotic phytoplankton. Trends in Plant Science, 2010, 15, 565-572.	4.3	44
155	Digital expression profiling of novel diatom transcripts provides insight into their biological functions. Genome Biology, 2010, 11, R85.	13.9	97
156	Genome-wide analysis of the diatom cell cycle unveils a novel type of cyclins involved in environmental signaling. Genome Biology, 2010, 11, R17.	13.9	91
157	Gene silencing in the marine diatom Phaeodactylum tricornutum. Nucleic Acids Research, 2009, 37, e96-e96.	6.5	264
158	Update of the Diatom EST Database: a new tool for digital transcriptomics. Nucleic Acids Research, 2009, 37, D1001-D1005.	6.5	69
159	Potential impact of stress activated retrotransposons on genome evolution in a marine diatom. BMC Genomics, 2009, 10, 624.	1.2	112
160	Mitosis in diatoms: rediscovering an old model for cell division. BioEssays, 2009, 31, 874-884.	1.2	48
161	Diatom PtCPF1 is a new cryptochrome/photolyase family member with DNA repair and transcription regulation activity. EMBO Reports, 2009, 10, 655-661.	2.0	168
162	Microbial oceanography in a sea of opportunity. Nature, 2009, 459, 180-184.	13.7	79

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163	Spectroscopic characterization of a (6-4) photolyase from the green alga Ostreococcus tauri. Journal of Photochemistry and Photobiology B: Biology, 2009, 96, 38-48.	1.7	18
164	Genomic Footprints of a Cryptic Plastid Endosymbiosis in Diatoms. Science, 2009, 324, 1724-1726.	6.0	370
165	Molecular Tools for Discovering the Secrets of Diatoms. BioScience, 2009, 59, 757-765.	2.2	32
166	The Phaeodactylum genome reveals the evolutionary history of diatom genomes. Nature, 2008, 456, 239-244.	13.7	1,458
167	A Diatom Gene Regulating Nitric-Oxide Signaling and Susceptibility to Diatom-Derived Aldehydes. Current Biology, 2008, 18, 895-899.	1.8	126
168	A Model for Carbohydrate Metabolism in the Diatom Phaeodactylum tricornutum Deduced from Comparative Whole Genome Analysis. PLoS ONE, 2008, 3, e1426.	1.1	394
169	A modified Gateway cloning strategy for overexpressing tagged proteins in plants. Plant Methods, 2008, 4, 3.	1.9	54
170	Whole-cell response of the pennate diatom Phaeodactylum tricornutum to iron starvation. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 10438-10443.	3.3	414
171	Evolutionary Origins and Functions of the Carotenoid Biosynthetic Pathway in Marine Diatoms. PLoS ONE, 2008, 3, e2896.	1.1	134
172	The tiny eukaryote Ostreococcus provides genomic insights into the paradox of plankton speciation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7705-7710.	3.3	563
173	Molecular toolbox for studying diatom biology in Phaeodactylum tricornutum. Gene, 2007, 406, 23-35.	1.0	293
174	IDENTIFICATION AND COMPARATIVE GENOMIC ANALYSIS OF SIGNALING AND REGULATORY COMPONENTS IN THE DIATOMTHALASSIOSIRA PSEUDONANA. Journal of Phycology, 2007, 43, 585-604.	1.0	87
175	Genetic and phenotypic characterization of Phaeodactylum tricornutum (Bacillariophyceae) accessions¹. Journal of Phycology, 2007, 43, 992-1009.	1.0	209
176	The Chlamydomonas Genome Reveals the Evolution of Key Animal and Plant Functions. Science, 2007, 318, 245-250.	6.0	2,354
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