

Catherine Boyen

List of Publications by Year in descending order

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55
papers

3,541
citations

159358

30
h-index

155451

55
g-index

62
all docs

62
docs citations

62
times ranked

3172
citing authors

#	ARTICLE	IF	CITATIONS
1	The Ectocarpus genome and the independent evolution of multicellularity in brown algae. <i>Nature</i> , 2010, 465, 617-621.	13.7	774
2	Genome structure and metabolic features in the red seaweed <i>Chondrus crispus</i> shed light on evolution of the Archaeplastida. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5247-5252.	3.3	307
3	Host-microbe interactions as a driver of acclimation to salinity gradients in brown algal cultures. <i>ISME Journal</i> , 2016, 10, 51-63.	4.4	148
4	Global expression analysis of the brown alga <i>Ectocarpus siliculosus</i> (Phaeophyceae) reveals large-scale reprogramming of the transcriptome in response to abiotic stress. <i>Genome Biology</i> , 2009, 10, R66.	13.9	138
5	Complete Sequence of the Mitochondrial DNA of the Rhodophyte <i>Chondrus crispus</i> (Gigartinales). Gene Content and Genome Organization. <i>Journal of Molecular Biology</i> , 1995, 250, 484-495.	2.0	134
6	Development and physiology of the brown alga <i>Ectocarpus siliculosus</i> : two centuries of research. <i>New Phytologist</i> , 2008, 177, 319-332.	3.5	128
7	Transcriptomic and metabolomic analysis of copper stress acclimation in <i>Ectocarpus siliculosus</i> highlights signaling and tolerance mechanisms in brown algae. <i>BMC Plant Biology</i> , 2014, 14, 116.	1.6	98
8	NADPH oxidases in Eukaryotes: red algae provide new hints!. <i>Current Genetics</i> , 2006, 49, 190-204.	0.8	94
9	Chlorophyll-binding proteins revisited - a multigenic family of light-harvesting and stress proteins from a brown algal perspective. <i>BMC Evolutionary Biology</i> , 2010, 10, 365.	3.2	93
10	Integrative analysis of metabolite and transcript abundance during the short-term response to saline and oxidative stress in the brown alga <i>Ectocarpus siliculosus</i> . <i>Plant, Cell and Environment</i> , 2011, 34, 629-642.	2.8	91
11	Characterization of Mannuronan C-5-Epimerase Genes from the Brown Alga <i>Laminaria digitata</i> . <i>Plant Physiology</i> , 2003, 133, 726-735.	2.3	89
12	IDENTIFICATION OF STRESS GENE TRANSCRIPTS IN LAMINARIA DIGITATA (PHAEOPHYCEAE) PROTOPLAST CULTURES BY EXPRESSED SEQUENCE TAG ANALYSIS. <i>Journal of Phycology</i> , 2005, 41, 1227-1235.	1.0	86
13	Response of the transcriptome of the intertidal red seaweed <i>Chondrus crispus</i> to controlled and natural stresses. <i>New Phytologist</i> , 2007, 176, 45-55.	3.5	86
14	Diurnal oscillations of metabolite abundances and gene analysis provide new insights into central metabolic processes of the brown alga <i>Ectocarpus siliculosus</i> . <i>New Phytologist</i> , 2010, 188, 98-110.	3.5	82
15	Isolation Conditions for High Yields of Protoplasts from <i>Laminaria saccharina</i> and <i>L. digitata</i> (Phaeophyceae). <i>Journal of Experimental Botany</i> , 1989, 40, 1237-1246.	2.4	81
16	Towards deciphering dynamic changes and evolutionary mechanisms involved in the adaptation to low salinities in <i>Ectocarpus</i> (brown algae). <i>Plant Journal</i> , 2012, 71, 366-377.	2.8	67
17	Mannitol metabolism in brown algae involves a new phosphatase family. <i>Journal of Experimental Botany</i> , 2014, 65, 559-570.	2.4	67
18	Characterisation of complementary DNAs from the expressed sequence tag analysis of life cycle stages of <i>Laminaria digitata</i> (Phaeophyceae). <i>Plant Molecular Biology</i> , 2000, 43, 503-513.	2.0	64

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19	Expression profiling of <i>Chondrus crispus</i> (Rhodophyta) after exposure to methyl jasmonate. <i>Journal of Experimental Botany</i> , 2006, 57, 3869-3881.	2.4	55
20	MARINE-EXPRESS: taking advantage of high throughput cloning and expression strategies for the post-genomic analysis of marine organisms. <i>Microbial Cell Factories</i> , 2010, 9, 45.	1.9	55
21	Mannitol-1-phosphate dehydrogenase activity in <i>Ectocarpus siliculosus</i> , a key role for mannitol synthesis in brown algae. <i>Planta</i> , 2011, 233, 261-273.	1.6	52
22	AN EXPRESSED SEQUENCE TAG ANALYSIS OF THALLUS AND REGENERATING PROTOPLASTS OF <i>CHONDRUS CRISPUS</i> (GIGARTINALES, RHODOPHYCEAE)1. <i>Journal of Phycology</i> , 2006, 42, 104-112.	1.0	50
23	Exploring the Cultivable <i>Ectocarpus</i> Microbiome. <i>Frontiers in Microbiology</i> , 2017, 8, 2456.	1.5	48
24	Genome and metabolic network of <i>Candidatus Phaeomarinobacter ectocarpi</i> Ec32, a new candidate genus of Alphaproteobacteria frequently associated with brown algae. <i>Frontiers in Genetics</i> , 2014, 5, 241.	1.1	43
25	Nucleotide sequence of the <i>cox3</i> gene from <i>Chondrus crispus</i> : evidence that UGA encodes tryptophan and evolutionary implications. <i>Nucleic Acids Research</i> , 1994, 22, 1400-1403.	6.5	39
26	The genome-scale metabolic network of <i>Ectocarpus siliculosus</i> (EctoGEM): a resource to study brown algal physiology and beyond. <i>Plant Journal</i> , 2014, 80, 367-381.	2.8	39
27	The cell-wall active mannuronan C5-epimerases in the model brown alga <i>Ectocarpus</i> : From gene context to recombinant protein. <i>Glycobiology</i> , 2016, 26, 973-983.	1.3	38
28	<i>Chondrus crispus</i> – A Present and Historical Model Organism for Red Seaweeds. <i>Advances in Botanical Research</i> , 2014, 71, 53-89.	0.5	37
29	Evidence for oxylipin synthesis and induction of a new polyunsaturated fatty acid hydroxylase activity in <i>Chondrus crispus</i> in response to methyljasmonate. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2007, 1771, 565-575.	1.2	35
30	Photosynthesis in <i>Chondrus crispus</i> : The contribution of energy spill-over in the regulation of excitonic flux. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2013, 1827, 834-842.	0.5	35
31	Genes for two subunits of succinate dehydrogenase form a cluster on the mitochondrial genome of Rhodophyta. <i>Current Genetics</i> , 1996, 29, 199-201.	0.8	29
32	The genome of <i>Ectocarpus subulatus</i> – A highly stress-tolerant brown alga. <i>Marine Genomics</i> , 2020, 52, 100740.	0.4	26
33	EXPRESSION PROFILING OF THE MANNURONAN C5-EPIMERASE MULTIGENIC FAMILY IN THE BROWN ALGA <i>LAMINARIA DIGITATA</i> (PHAEOPHYCEAE) UNDER BIOTIC STRESS CONDITIONS ¹ . <i>Journal of Phycology</i> , 2008, 44, 1250-1256.	1.0	25
34	Metabolic Complementarity Between a Brown Alga and Associated Cultivable Bacteria Provide Indications of Beneficial Interactions. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	25
35	New members of the glutathione transferase family discovered in red and brown algae. <i>Biochemical Journal</i> , 2008, 412, 535-544.	1.7	23
36	Transcription initiation and RNA processing in the mitochondria of the red alga <i>Chondrus crispus</i> : convergence in the evolution of transcription mechanisms in mitochondria. <i>Journal of Molecular Biology</i> , 1998, 283, 549-557.	2.0	19

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37	Microarray estimation of genomic inter-strain variability in the genus <i>Ectocarpus</i> (Phaeophyceae). <i>BMC Molecular Biology</i> , 2011, 12, 2.	3.0	19
38	Whole genome survey of the glutathione transferase family in the brown algal model <i>Ectocarpus siliculosus</i> . <i>Marine Genomics</i> , 2008, 1, 135-148.	0.4	18
39	The <i>Ectocarpus</i> Genome and Brown Algal Genomics. <i>Advances in Botanical Research</i> , 2012, 64, 141-184.	0.5	18
40	STUDIES OF VANDADIUM-BROMOPEROXIDASE USING SURFACE AND CORTICAL PROTOPLASTS OF <i>MACROCYSTIS PYRIEFERA</i> (PHAEOPHYTA)1. <i>Journal of Phycology</i> , 1990, 26, 589-592.	1.0	16
41	Toward Systems Biology in Brown Algae to Explore Acclimation and Adaptation to the Shore Environment. <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 883-892.	1.0	15
42	Molecular and biochemical characterization of mannitol-1-phosphate dehydrogenase from the model brown alga <i>Ectocarpus</i> sp.. <i>Phytochemistry</i> , 2015, 117, 509-520.	1.4	15
43	Inferring Biochemical Reactions and Metabolite Structures to Understand Metabolic Pathway Drift. <i>IScience</i> , 2020, 23, 100849.	1.9	15
44	Mutant swarms of a totivirus-like entities are present in the red macroalga <i>Chondrus crispus</i> and have been partially transferred to the nuclear genome. <i>Journal of Phycology</i> , 2016, 52, 493-504.	1.0	14
45	ISOLATION AND CHARACTERIZATION OF SIX cDNAs INVOLVED IN CARBON METABOLISM IN <i>LAMINARIA DIGITATA</i> (PHAEOPHYCEAE). <i>Journal of Phycology</i> , 1999, 35, 1237-1245.	1.0	13
46	Mannitol in six autotrophic stramenopiles and <i>Micromonas</i> . <i>Plant Signaling and Behavior</i> , 2011, 6, 1237-1239.	1.2	13
47	<i>Gracilaria tenuistipitata</i> (Rhodophyta) tolerance to cadmium and copper exposure observed through gene expression and photosynthesis analyses. <i>Journal of Applied Phycology</i> , 2018, 30, 2129-2141.	1.5	12
48	Organisation of the plastid genome from the rhodophyte <i>Chondrus crispus</i> (Gigartinales); sequence and phylogeny of the 16S rRNA gene. <i>European Journal of Phycology</i> , 1995, 30, 133-140.	0.9	11
49	RT-qPCR Normalization Genes in the Red Alga <i>Chondrus crispus</i> . <i>PLoS ONE</i> , 2014, 9, e86574.	1.1	11
50	Physical map and gene organization of the mitochondrial genome of <i>Chondrus crispus</i> (Rhodophyta). <i>Trends in Microbiology</i> , 2010, 18, 107-114.	2.8	10
51	Revisiting Australian <i>Ectocarpus subulatus</i> (Phaeophyceae) From the Hopkins River: Distribution, Abiotic Environment, and Associated Microbiota. <i>Journal of Phycology</i> , 2020, 56, 719-729.	1.0	9
52	MRNA expression in mitochondria of the red alga <i>Chondrus crispus</i> requires a unique RNA-processing mechanism, internal cleavage of upstream tRNAs at pyrimidine 48 1 1 Edited by M. Yaniv. <i>Journal of Molecular Biology</i> , 1999, 288, 579-584.	2.0	6
53	Effects of sampling and storage procedures on 16S rDNA amplicon sequencing results of kelp microbiomes. <i>Marine Genomics</i> , 2022, 63, 100944.	0.4	6
54	Semi-Quantitative Targeted Gas Chromatography-Mass Spectrometry Profiling Supports a Late Side-Chain Reductase Cycloartenol-to-Cholesterol Biosynthesis Pathway in Brown Algae. <i>Frontiers in Plant Science</i> , 2021, 12, 648426.	1.7	5

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55	Effect of essential oil- and iodine treatments on the bacterial microbiota of the brown alga <i>Ectocarpus siliculosus</i> . <i>Journal of Applied Phycology</i> , 2021, 33, 459-470.	1.5	3