

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	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
2	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
3	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
4	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
5	Inferring Biochemical Reactions and Metabolite Structures to Understand Metabolic Pathway Drift. <i>IScience</i> , 2020, 23, 100849.	1.9	15
6	The genome of <i>Ectocarpus subulatus</i> – A highly stress-tolerant brown alga. <i>Marine Genomics</i> , 2020, 52, 100740.	0.4	26
7	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
8	<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
9	Exploring the Cultivable <i>Ectocarpus</i> Microbiome. <i>Frontiers in Microbiology</i> , 2017, 8, 2456.	1.5	48
10	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
11	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
12	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
13	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
14	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
15	<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
16	Mannitol metabolism in brown algae involves a new phosphatase family. <i>Journal of Experimental Botany</i> , 2014, 65, 559-570.	2.4	67
17	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
18	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

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19	RT-qPCR Normalization Genes in the Red Alga <i>Chondrus crispus</i> . PLoS ONE, 2014, 9, e86574.	1.1	11
20	Genome structure and metabolic features in the red seaweed <i>Chondrus crispus</i> shed light on evolution of the Archaeplastida. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5247-5252.	3.3	307
21	Photosynthesis in <i>Chondrus crispus</i> : The contribution of energy spill-over in the regulation of excitonic flux. Biochimica Et Biophysica Acta - Bioenergetics, 2013, 1827, 834-842.	0.5	35
22	The Ectocarpus Genome and Brown Algal Genomics. Advances in Botanical Research, 2012, 64, 141-184.	0.5	18
23	Towards deciphering dynamic changes and evolutionary mechanisms involved in the adaptation to low salinities in <i>Ectocarpus</i> (brown algae). Plant Journal, 2012, 71, 366-377.	2.8	67
24	Toward Systems Biology in Brown Algae to Explore Acclimation and Adaptation to the Shore Environment. OMICS A Journal of Integrative Biology, 2011, 15, 883-892.	1.0	15
25	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> . Plant, Cell and Environment, 2011, 34, 629-642.	2.8	91
26	Mannitol-1-phosphate dehydrogenase activity in <i>Ectocarpus siliculosus</i> , a key role for mannitol synthesis in brown algae. Planta, 2011, 233, 261-273.	1.6	52
27	Microarray estimation of genomic inter-strain variability in the genus <i>Ectocarpus</i> (Phaeophyceae). BMC Molecular Biology, 2011, 12, 2.	3.0	19
28	Mannitol in six autotrophic stramenopiles and <i>Micromonas</i> . Plant Signaling and Behavior, 2011, 6, 1237-1239.	1.2	13
29	Chlorophyll-binding proteins revisited - a multigenic family of light-harvesting and stress proteins from a brown algal perspective. BMC Evolutionary Biology, 2010, 10, 365.	3.2	93
30	MARINE-EXPRESS: taking advantage of high throughput cloning and expression strategies for the post-genomic analysis of marine organisms. Microbial Cell Factories, 2010, 9, 45.	1.9	55
31	Diurnal oscillations of metabolite abundances and gene analysis provide new insights into central metabolic processes of the brown alga <i>Ectocarpus siliculosus</i> . New Phytologist, 2010, 188, 98-110.	3.5	82
32	The <i>Ectocarpus</i> genome and the independent evolution of multicellularity in brown algae. Nature, 2010, 465, 617-621.	13.7	774
33	Global expression analysis of the brown alga <i>Ectocarpus siliculosus</i> (Phaeophyceae) reveals large-scale reprogramming of the transcriptome in response to abiotic stress. Genome Biology, 2009, 10, R66.	13.9	138
34	EXPRESSION PROFILING OF THE MANNURONAN C5á€PIMERASE MULTIGENIC FAMILY IN THE BROWN ALGA <i>LAMINARIA DIGITATA</i> (PHAEOPHYCEAE) UNDER BIOTIC STRESS CONDITIONS ¹ . Journal of Phycology, 2008, 44, 1250-1256.	1.0	25
35	Development and physiology of the brown alga <i>Ectocarpus siliculosus</i> : two centuries of research. New Phytologist, 2008, 177, 319-332.	3.5	128
36	Whole genome survey of the glutathione transferase family in the brown algal model <i>Ectocarpus siliculosus</i> . Marine Genomics, 2008, 1, 135-148.	0.4	18

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37	New members of the glutathione transferase family discovered in red and brown algae. <i>Biochemical Journal</i> , 2008, 412, 535-544.	1.7	23
38	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
39	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
40	AN EXPRESSED SEQUENCE TAG ANALYSIS OF THALLUS AND REGENERATING PROTOPLASTS OF CHONDRUS CRISPUS (GIGARTINALES, RHODOPHYCEAE)1. <i>Journal of Phycology</i> , 2006, 42, 104-112.	1.0	50
41	NADPH oxidases in Eukaryotes: red algae provide new hints!. <i>Current Genetics</i> , 2006, 49, 190-204.	0.8	94
42	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
43	IDENTIFICATION OF STRESS GENE TRANSCRIPTS IN LAMINARIA DIGITATA (PHAEOPHYCEAE) PROTOPLAST CULTURES BY EXPRESSED SEQUENCE TAG ANALYSIS1. <i>Journal of Phycology</i> , 2005, 41, 1227-1235.	1.0	86
44	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
45	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
46	ISOLATION AND CHARACTERIZATION OF SIX cDNAs INVOLVED IN CARBON METABOLISM IN LAMINARIA DIGITATA (PHAEOPHYCEAE). <i>Journal of Phycology</i> , 1999, 35, 1237-1245.	1.0	13
47	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
48	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
49	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
50	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
51	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
52	Physical map and gene organization of the mitochondrial genome of <i>Chondrus crispus</i> (Rhodophyta). <i>Journal of Molecular Biology</i> , 1994, 239, 107-116.	2.9	10
53	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
54	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

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55	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