

Gildas Le CorguillÃ©

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

1,274
citations

471509

17
h-index

610901

24
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24
all docs

24
docs citations

24
times ranked

2331
citing authors

#	ARTICLE	IF	CITATIONS
1	Cyanorak v2.1: a scalable information system dedicated to the visualization and expert curation of marine and brackish picocyanobacteria genomes. <i>Nucleic Acids Research</i> , 2021, 49, D667-D676.	14.5	38
2	Synergic Effects of Temperature and Irradiance on the Physiology of the Marine <i>Synechococcus</i> Strain WH7803. <i>Frontiers in Microbiology</i> , 2020, 11, 1707.	3.5	18
3	Evolutionary Mechanisms of Long-Term Genome Diversification Associated With Niche Partitioning in Marine Picocyanobacteria. <i>Frontiers in Microbiology</i> , 2020, 11, 567431.	3.5	37
4	Crustacean cardioactive peptides: Expression, localization, structure, and a possible involvement in regulation of egg-laying in the cuttlefish <i>Sepia officinalis</i> . <i>General and Comparative Endocrinology</i> , 2018, 260, 67-79.	1.8	10
5	Dietary aquaculture by-product hydrolysates: impact on the transcriptomic response of the intestinal mucosa of European seabass (<i>Dicentrarchus labrax</i>) fed low fish meal diets. <i>BMC Genomics</i> , 2018, 19, 396.	2.8	47
6	Design of antimicrobial peptides from a cuttlefish database. <i>Amino Acids</i> , 2018, 50, 1573-1582.	2.7	16
7	Create, run, share, publish, and reference your LC-MS, FIA-MS, GC-MS, and NMR data analysis workflows with the Workflow4Metabolomics 3.0 Galaxy online infrastructure for metabolomics. <i>International Journal of Biochemistry and Cell Biology</i> , 2017, 93, 89-101.	2.8	99
8	The future of metabolomics in ELIXIR. <i>F1000Research</i> , 2017, 6, 1649.	1.6	19
9	The future of metabolomics in ELIXIR. <i>F1000Research</i> , 2017, 6, 1649.	1.6	11
10	Neuropeptidome of the Cephalopod <i>Sepia officinalis</i> : Identification, Tissue Mapping, and Expression Pattern of Neuropeptides and Neurohormones during Egg Laying. <i>Journal of Proteome Research</i> , 2016, 15, 48-67.	3.7	49
11	How Egg Case Proteins Can Protect Cuttlefish Offspring?. <i>PLoS ONE</i> , 2015, 10, e0132836.	2.5	17
12	Workflow4Metabolomics: a collaborative research infrastructure for computational metabolomics. <i>Bioinformatics</i> , 2015, 31, 1493-1495.	4.1	333
13	Molecular characterization of peptide fractions of a <i>Tilapia</i> (<i>Oreochromis niloticus</i>) by-product hydrolysate and in vitro evaluation of antibacterial activity. <i>Process Biochemistry</i> , 2015, 50, 487-492.	3.7	57
14	The Toll/NF- κ B pathway in cuttlefish symbiotic accessory nidamental gland. <i>Developmental and Comparative Immunology</i> , 2015, 53, 42-46.	2.3	14
15	Transcriptomic and peptidomic analysis of protein hydrolysates from the white shrimp (<i>L. vannamei</i>). <i>Journal of Biotechnology</i> , 2014, 186, 30-37.	3.8	33
16	Dual role of the cuttlefish salivary proteome in defense and predation. <i>Journal of Proteomics</i> , 2014, 108, 209-222.	2.4	41
17	The <i>Ectocarpus</i> Genome and Brown Algal Genomics. <i>Advances in Botanical Research</i> , 2012, 64, 141-184.	1.1	18
18	<i>Prochlorococcus</i> and <i>Synechococcus</i> have Evolved Different Adaptive Mechanisms to Cope with Light and UV Stress. <i>Frontiers in Microbiology</i> , 2012, 3, 285.	3.5	100

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19	Genetic regulation of life cycle transitions in the brown alga <i>Ectocarpus</i> . <i>Plant Signaling and Behavior</i> , 2011, 6, 1858-1860.	2.4	11
20	<i>OUROBOROS</i> is a master regulator of the gametophyte to sporophyte life cycle transition in the brown alga <i>Ectocarpus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11518-11523.	7.1	88
21	Light History Influences the Response of the Marine Cyanobacterium <i>Synechococcus</i> sp. WH7803 to Oxidative Stress. <i>Plant Physiology</i> , 2011, 156, 1934-1954.	4.8	54
22	Ultraviolet stress delays chromosome replication in light/dark synchronized cells of the marine cyanobacterium <i>Prochlorococcus marinus</i> PCC9511. <i>BMC Microbiology</i> , 2010, 10, 204.	3.3	28
23	A sequence-tagged genetic map for the brown alga <i>Ectocarpus siliculosus</i> provides large-scale assembly of the genome sequence. <i>New Phytologist</i> , 2010, 188, 42-51.	7.3	59
24	Plastid genomes of two brown algae, <i>Ectocarpus siliculosus</i> and <i>Fucus vesiculosus</i> : further insights on the evolution of red-algal derived plastids. <i>BMC Evolutionary Biology</i> , 2009, 9, 253.	3.2	77