

Olivier Bastien

List of Publications by Year in descending order

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17
papers

757
citations

840776

11
h-index

888059

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17
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times ranked

1074
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylogeny and Sequence Space: A Combined Approach to Analyze the Evolutionary Trajectories of Homologous Proteins. The Case Study of Aminodeoxychorismate Synthase. <i>Acta Biotheoretica</i> , 2020, 68, 139-156.	1.5	2
2	Diversity and survival of artificial lifeforms under sedimentation and random motion. <i>Theory in Biosciences</i> , 2017, 136, 153-167.	1.4	1
3	New Insights on Thylakoid Biogenesis in Plant Cells. <i>International Review of Cell and Molecular Biology</i> , 2016, 323, 1-30.	3.2	27
4	Glycerolipids in photosynthesis: Composition, synthesis and trafficking. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, 470-480.	1.0	296
5	Evolution of galactoglycerolipid biosynthetic pathways “ From cyanobacteria to primary plastids and from primary to secondary plastids. <i>Progress in Lipid Research</i> , 2014, 54, 68-85.	11.6	118
6	Modeling of regulatory loops controlling galactolipid biosynthesis in the inner envelope membrane of chloroplasts. <i>Journal of Theoretical Biology</i> , 2014, 361, 1-13.	1.7	21
7	Galvestine-1, a novel chemical probe for the study of the glycerolipid homeostasis system in plant cells. <i>Molecular BioSystems</i> , 2012, 8, 2023.	2.9	34
8	How Fitch-Margoliash Algorithm can Benefit from Multi Dimensional Scaling. <i>Evolutionary Bioinformatics</i> , 2011, 7, EBO.S7048.	1.2	4
9	Activation of the Chloroplast Monogalactosyldiacylglycerol Synthase MGD1 by Phosphatidic Acid and Phosphatidylglycerol. <i>Journal of Biological Chemistry</i> , 2010, 285, 6003-6011.	3.4	102
10	Where Does the Alignment Score Distribution Shape Come from?. <i>Evolutionary Bioinformatics</i> , 2010, 6, EBO.S5875.	1.2	7
11	Evolution of biological sequences implies an extreme value distribution of type I for both global and local pairwise alignment scores. <i>BMC Bioinformatics</i> , 2008, 9, 332.	2.6	15
12	A simple derivation of the distribution of pairwise local protein sequence alignment scores. <i>Evolutionary Bioinformatics</i> , 2008, 4, 41-5.	1.2	3
13	The configuration space of homologous proteins: A theoretical and practical framework to reduce the diversity of the protein sequence space after massive all-by-all sequence comparisons. <i>Future Generation Computer Systems</i> , 2007, 23, 410-427.	7.5	6
14	A configuration space of homologous proteins conserving mutual information and allowing a phylogeny inference based on pair-wise Z-score probabilities. <i>BMC Bioinformatics</i> , 2005, 6, 49.	2.6	23
15	Construction of non-symmetric substitution matrices derived from proteomes with biased amino acid distributions. <i>Comptes Rendus - Biologies</i> , 2005, 328, 445-453.	0.2	30
16	Fundamentals of massive automatic pairwise alignments of protein sequences: theoretical significance of Z-value statistics. <i>Bioinformatics</i> , 2004, 20, 534-537.	4.1	33
17	Analysis of the compositional biases in <i>Plasmodium falciparum</i> genome and proteome using <i>Arabidopsis thaliana</i> as a reference. <i>Gene</i> , 2004, 336, 163-173.	2.2	35