Olivier Bastien

List of Publications by Year
in descending order

17	757	840776	888059
papers	citations	11	17
		h-index	g-index

17	17	17	1074
all docs	docs citations	times ranked	citing authors

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