

Daniel Barker

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10050544/publications.pdf>

Version: 2024-02-01

17
papers

220
citations

1684188

5
h-index

1058476

14
g-index

19
all docs

19
docs citations

19
times ranked

408
citing authors

#	ARTICLE	IF	CITATIONS
1	Design, delivery and evaluation of a bioinformatics education workshop for 13-16-year-olds. <i>Journal of Biological Education</i> , 2022, 56, 570-580.	1.5	4
2	Bringing bioinformatics to schools with the 4273pi project. <i>PLoS Computational Biology</i> , 2022, 18, e1009705.	3.2	2
3	Genomic insights into the biosynthesis and physiology of the cyanobacterial neurotoxin 3-N-methyl-2,3-diaminopropanoic acid (BMAA). <i>Phytochemistry</i> , 2022, 200, 113198.	2.9	5
4	DNA sonification for public engagement in bioinformatics. <i>BMC Research Notes</i> , 2021, 14, 273.	1.4	5
5	Using sound to understand protein sequence data: new sonification algorithms for protein sequences and multiple sequence alignments. <i>BMC Bioinformatics</i> , 2021, 22, 456.	2.6	7
6	Genomic insights into the biosynthesis and physiology of the cyanobacterial neurotoxin 2,4-diaminobutanoic acid (2,4-DAB). <i>Phytochemistry</i> , 2021, 192, 112953.	2.9	5
7	Xenolog classification. <i>Bioinformatics</i> , 2017, 33, 640-649.	4.1	42
8	Comparison of the protein-coding genomes of three deep-sea, sulfur-oxidising bacteria: <i>Candidatus Ruthia magnifica</i> , <i>Candidatus Vesicomysosocius okutani</i> and <i>Thiomicrospira crunogena</i> . <i>BMC Research Notes</i> , 2017, 10, 296.	1.4	5
9	Cluster Analysis of p53 Binding Site Sequences Reveals Subsets with Different Functions. <i>Cancer Informatics</i> , 2016, 15, CIN.S39968.	1.9	1
10	Bringing computational science to the public. <i>SpringerPlus</i> , 2016, 5, 259.	1.2	2
11	On simulated annealing phase transitions in phylogeny reconstruction. <i>Molecular Phylogenetics and Evolution</i> , 2016, 101, 46-55.	2.7	11
12	Comparison of the protein-coding gene content of <i>Chlamydia trachomatis</i> and <i>Protochlamydia amoebophila</i> using a Raspberry Pi computer. <i>BMC Research Notes</i> , 2015, 8, 561.	1.4	4
13	A comparison of the protein-coding genomes of two green sulphur bacteria, <i>Chlorobium tepidum</i> TLS and <i>Pelodictyon phaeoclathratiforme</i> BU-1. <i>BMC Research Notes</i> , 2015, 8, 565.	1.4	2
14	Seeing the wood for the trees: philosophical aspects of classical, Bayesian and likelihood approaches in statistical inference and some implications for phylogenetic analysis. <i>Biology and Philosophy</i> , 2015, 30, 505-525.	1.4	6
15	4273π: Bioinformatics education on low cost ARM hardware. <i>BMC Bioinformatics</i> , 2013, 14, 243.	2.6	19
16	A tribute to Peter Sneath. <i>Taxon</i> , 2012, 61, 481-483.	0.7	0
17	Constrained models of evolution lead to improved prediction of functional linkage from correlated gain and loss of genes. <i>Bioinformatics</i> , 2007, 23, 14-20.	4.1	94