

Fabio Pardi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1477639/publications.pdf>

Version: 2024-02-01

19
papers

5,428
citations

840776

11
h-index

888059

17
g-index

19
all docs

19
docs citations

19
times ranked

9512
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	27.8	4,709
2	Meta-analysis of genome scans of age-related macular degeneration. <i>Human Molecular Genetics</i> , 2005, 14, 2257-2264.	2.9	224
3	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. <i>Genome Research</i> , 2007, 17, 760-774.	5.5	184
4	Reconstructible Phylogenetic Networks: Do Not Distinguish the Indistinguishable. <i>PLoS Computational Biology</i> , 2015, 11, e1004135.	3.2	65
5	Species Choice for Comparative Genomics: Being Greedy Works. <i>PLoS Genetics</i> , 2005, 1, e71.	3.5	60
6	Resource-Aware Taxon Selection for Maximizing Phylogenetic Diversity. <i>Systematic Biology</i> , 2007, 56, 431-444.	5.6	35
7	Rapid alignment-free phylogenetic identification of metagenomic sequences. <i>Bioinformatics</i> , 2019, 35, 3303-3312.	4.1	35
8	Distribution of phylogenetic diversity under random extinction. <i>Journal of Theoretical Biology</i> , 2008, 251, 286-296.	1.7	26
9	Fast and accurate branch lengths estimation for phylogenomic trees. <i>BMC Bioinformatics</i> , 2016, 17, 23.	2.6	23
10	Robustness of Phylogenetic Inference Based on Minimum Evolution. <i>Bulletin of Mathematical Biology</i> , 2010, 72, 1820-1839.	1.9	15
11	Rearrangement moves on rooted phylogenetic networks. <i>PLoS Computational Biology</i> , 2017, 13, e1005611.	3.2	15
12	Combinatorics of distance-based tree inference. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 16443-16448.	7.1	13
13	On the inference of complex phylogenetic networks by Markov Chain Monte-Carlo. <i>PLoS Computational Biology</i> , 2021, 17, e1008380.	3.2	12
14	Do Branch Lengths Help to Locate a Tree in a Phylogenetic Network?. <i>Bulletin of Mathematical Biology</i> , 2016, 78, 1773-1795.	1.9	8
15	Rapid screening and detection of inter-type viral recombinants using phylo- <i>k</i> -mers. <i>Bioinformatics</i> , 2021, 36, 5351-5360.	4.1	2
16	Finding a most parsimonious or likely tree in a network with respect to an alignment. <i>Journal of Mathematical Biology</i> , 2019, 78, 527-547.	1.9	1
17	Computing the probability of gene trees concordant with the species tree in the multispecies coalescent. <i>Theoretical Population Biology</i> , 2021, 137, 22-31.	1.1	1
18	Distance-Based Phylogeny Reconstruction: Safety and Edge Radius. , 2015, , 1-6.		0

#	ARTICLE	IF	CITATIONS
19	Distance-Based Phylogeny Reconstruction: Safety and Edge Radius. , 2016, , 567-571.		0