Fabio Pardi

List of Publications by Year
in descending order

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	Computing the probability of gene trees concordant with the species tree in the multispecies coalescent. Theoretical Population Biology, 2021, 137, 22-31.	1.1	1
2	Rapid screening and detection of inter-type viral recombinants using phylo-*k*-mers. Bioinformatics, 2021, 36, 5351-5360.	4.1	2
3	On the inference of complex phylogenetic networks by Markov Chain Monte-Carlo. PLoS Computational Biology, 2021, 17, e1008380.	3.2	12
4	Rapid alignment-free phylogenetic identification of metagenomic sequences. Bioinformatics, 2019, 35, 3303-3312.	4.1	35
5	Finding a most parsimonious or likely tree in a network with respect to an alignment. Journal of Mathematical Biology, 2019, 78, 527-547.	1.9	1
6	Rearrangement moves on rooted phylogenetic networks. PLoS Computational Biology, 2017, 13, e1005611.	3.2	15
7	Do Branch Lengths Help to Locate a Tree in a Phylogenetic Network?. Bulletin of Mathematical Biology, 2016, 78, 1773-1795.	1.9	8
8	Fast and accurate branch lengths estimation for phylogenomic trees. BMC Bioinformatics, 2016, 17, 23.	2.6	23
9	Distance-Based Phylogeny Reconstruction: Safety and Edge Radius. , 2016, , 567-571.		0
10	Reconstructible Phylogenetic Networks: Do Not Distinguish the Indistinguishable. PLoS Computational Biology, 2015, 11, e1004135.	3.2	65
11	Distance-Based Phylogeny Reconstruction: Safety and Edge Radius. , 2015, , 1-6.		0
12	Combinatorics of distance-based tree inference. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16443-16448.	7.1	13
13	Robustness of Phylogenetic Inference Based on Minimum Evolution. Bulletin of Mathematical Biology, 2010, 72, 1820-1839.	1.9	15
14	Distribution of phylogenetic diversity under random extinction. Journal of Theoretical Biology, 2008, 251, 286-296.	1.7	26
15	Resource-Aware Taxon Selection for Maximizing Phylogenetic Diversity. Systematic Biology, 2007, 56, 431-444.	5.6	35
16	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. Genome Research, 2007, 17, 760-774.	5.5	184
17	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
18	Species Choice for Comparative Genomics: Being Greedy Works. PLoS Genetics, 2005, 1, e71.	3.5	60

#	Article	IF	Citations
19	Meta-analysis of genome scans of age-related macular degeneration. Human Molecular Genetics, 2005, 14, 2257-2264.	2.9	224