

Bailin Hao

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

1,065
citations

758635

12
h-index

839053

18
g-index

22
all docs

22
docs citations

22
times ranked

1503
citing authors

#	ARTICLE	IF	CITATIONS
1	Polyphyly in 16S rRNA-based LVTre Versus Monophyly in Whole-genome-based CVTree. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 310-319.	3.0	8
2	On monospecific genera in prokaryotic taxonomy. <i>Synthetic and Systems Biotechnology</i> , 2017, 2, 226-235.	1.8	5
3	Whole-Genome-Based Phylogeny and Taxonomy for Prokaryotes. , 2017, , .		1
4	LVTre Viewer: An Interactive Display for the All-Species Living Tree Incorporating Automatic Comparison with Prokaryotic Systematics. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 94-102.	3.0	3
5	Skeleton graph expansion of critical exponents in "cultural revolution" years. , 2016, , 3-27.		0
6	Whole-genome-based phylogeny supports the objections against the reclassification of <i>Eubacterium rectale</i> to <i>Agathobacter rectalis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2451-2451.	0.8	6
7	CVTree3 Web Server for Whole-genome-based and Alignment-free Prokaryotic Phylogeny and Taxonomy. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 321-331.	3.0	185
8	Phylogeny and Taxonomy of Archaea: A Comparison of the Whole-Genome-Based CVTree Approach with 16S rRNA Sequence Analysis. <i>Life</i> , 2015, 5, 949-968.	1.1	26
9	Skeleton graph expansion of critical exponents in "cultural revolution" years. <i>International Journal of Modern Physics B</i> , 2014, 28, 1430008.	1.0	0
10	On K-peptide length in composition vector phylogeny of prokaryotes. <i>Computational Biology and Chemistry</i> , 2014, 53, 166-173.	1.1	16
11	Geographic divergence of "Sulfolobus islandicus" strains assessed by genomic analyses including electronic DNA hybridization confirms they are geovars. <i>Antonie Van Leeuwenhoek</i> , 2014, 105, 431-435.	0.7	6
12	<i>Shigella</i> Strains Are Not Clones of <i>Escherichia Coli</i> but Sister Species in the Genus <i>Escherichia</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 61-65.	3.0	52
13	Whole-genome based Archaea phylogeny and taxonomy: A composition vector approach. <i>Science Bulletin</i> , 2010, 55, 2323-2328.	1.7	6
14	Composition vector approach to whole-genome-based prokaryotic phylogeny: Success and foundations. <i>Journal of Biotechnology</i> , 2010, 149, 115-119.	1.9	31
15	Jackknife and Bootstrap Tests of the Composition Vector Trees. <i>Genomics, Proteomics and Bioinformatics</i> , 2010, 8, 262-267.	3.0	26
16	CVTree update: a newly designed phylogenetic study platform using composition vectors and whole genomes. <i>Nucleic Acids Research</i> , 2009, 37, W174-W178.	6.5	180
17	A fungal phylogeny based on 82 complete genomes using the composition vector method. <i>BMC Evolutionary Biology</i> , 2009, 9, 195.	3.2	194
18	Prokaryote phylogeny meets taxonomy: An exhaustive comparison of composition vector trees with systematic bacteriology. <i>Science in China Series C: Life Sciences</i> , 2007, 50, 587-599.	1.3	22

#	ARTICLE	IF	CITATIONS
19	CVTree: a phylogenetic tree reconstruction tool based on whole genomes. Nucleic Acids Research, 2004, 32, W45-W47.	6.5	202
20	PROKARYOTE PHYLOGENY WITHOUT SEQUENCE ALIGNMENT: FROM AVOIDANCE SIGNATURE TO COMPOSITION DISTANCE. Journal of Bioinformatics and Computational Biology, 2004, 02, 1-19.	0.3	70
21	Molecular phylogeny of coronaviruses including human SARS-CoV. Science Bulletin, 2003, 48, 1170-1174.	1.7	22
22	Factorizable Language: From Dynamics to Biology. , 0, , 147-186.		4