

Zhao Xu

List of Publications by Year in descending order

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Version: 2024-02-01

16
papers

6,285
citations

758635

12
h-index

940134

16
g-index

16
all docs

16
docs citations

16
times ranked

9230
citing authors

#	ARTICLE	IF	CITATIONS
1	A Draft Sequence of the Rice Genome (<i>Oryza sativa</i> L. ssp. indica). <i>Science</i> , 2002, 296, 79-92.	6.0	3,146
2	LTR_FINDER: an efficient tool for the prediction of full-length LTR retrotransposons. <i>Nucleic Acids Research</i> , 2007, 35, W265-W268.	6.5	1,701
3	The Genomes of <i>Oryza sativa</i> : A History of Duplications. <i>PLoS Biology</i> , 2005, 3, e38.	2.6	808
4	A fungal phylogeny based on 82 complete genomes using the composition vector method. <i>BMC Evolutionary Biology</i> , 2009, 9, 195.	3.2	194
5	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
6	Vertebrate gene predictions and the problem of large genes. <i>Nature Reviews Genetics</i> , 2003, 4, 741-749.	7.7	56
7	<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
8	A draft sequence of the rice (<i>Oryza sativa</i> ssp.indica) genome. <i>Science Bulletin</i> , 2001, 46, 1937-1942.	1.7	35
9	Composition vector approach to whole-genome-based prokaryotic phylogeny: Success and foundations. <i>Journal of Biotechnology</i> , 2010, 149, 115-119.	1.9	31
10	Jackknife and Bootstrap Tests of the Composition Vector Trees. <i>Genomics, Proteomics and Bioinformatics</i> , 2010, 8, 262-267.	3.0	26
11	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
12	Test Data Sets and Evaluation of Gene Prediction Programs on the Rice Genome. <i>Journal of Computer Science and Technology</i> , 2005, 20, 446-453.	0.9	14
13	Whole-genome based Archaea phylogeny and taxonomy: A composition vector approach. <i>Science Bulletin</i> , 2010, 55, 2323-2328.	1.7	6
14	LTR retrotransposons reveal recent extensive inter-subspecies nonreciprocal recombination in Asian cultivated rice. <i>BMC Genomics</i> , 2008, 9, 565.	1.2	5
15	LVTree 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
16	Identification of LTR retrotransposons in eukaryotic genomes: supports from structure and evolution. <i>International Journal of Bioinformatics Research and Applications</i> , 2009, 5, 365.	0.1	2