

Nikhath Zafar

List of Publications by Year in descending order

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Version: 2024-02-01

14
papers

2,504
citations

759233

12
h-index

1125743

13
g-index

14
all docs

14
docs citations

14
times ranked

3296
citing authors

#	ARTICLE	IF	CITATIONS
1	The complete genome sequence of the <i>Arabidopsis</i> and tomato pathogen <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 10181-10186.	7.1	785
2	Comparative Genomics of Emerging Human Ehrlichiosis Agents. PLoS Genetics, 2006, 2, e21.	3.5	423
3	Whole-Genome Sequence Analysis of <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> 1448A Reveals Divergence among Pathovars in Genes Involved in Virulence and Transposition. Journal of Bacteriology, 2005, 187, 6488-6498.	2.2	301
4	The comprehensive microbial resource. Nucleic Acids Research, 2010, 38, D340-D345.	14.5	241
5	Mobile elements and mitochondrial genome expansion in the soil fungus and potato pathogen <i>Rhizoctonia solani</i> AG-3. FEMS Microbiology Letters, 2014, 352, 165-173.	1.8	143
6	Sequencing of mitochondrial genomes of nine <i>Aspergillus</i> and <i>Penicillium</i> species identifies mobile introns and accessory genes as main sources of genome size variability. BMC Genomics, 2012, 13, 698.	2.8	131
7	Structure of the germline genome of <i>Tetrahymena thermophila</i> and relationship to the massively rearranged somatic genome. ELife, 2016, 5, .	6.0	130
8	CoreGenes: a computational tool for identifying and cataloging "core" genes in a set of small genomes. BMC Bioinformatics, 2002, 3, 12.	2.6	123
9	Genome Properties: a system for the investigation of prokaryotic genetic content for microbiology, genome annotation and comparative genomics. Bioinformatics, 2005, 21, 293-306.	4.1	72
10	Comparative Genomic Evidence for a Close Relationship between the Dimorphic Prosthecate Bacteria <i>Hyphomonas neptunium</i> and <i>Caulobacter crescentus</i> . Journal of Bacteriology, 2006, 188, 6841-6850.	2.2	57
11	The JCVI standard operating procedure for annotating prokaryotic metagenomic shotgun sequencing data. Standards in Genomic Sciences, 2010, 2, 229-237.	1.5	55
12	Hidden genomic evolution in a morphospecies—The landscape of rapidly evolving genes in <i>Tetrahymena</i> . PLoS Biology, 2019, 17, e3000294.	5.6	31
13	Comparisons of gene colinearity in genomes using GeneOrder2.0. Trends in Biochemical Sciences, 2001, 26, 514-516.	7.5	12
14	Application of global computational tools GeneOrder and CoreGenes to the comparative analyses of chordopoxvirus genomes. Information Sciences, 2002, 146, 127-135.	6.9	0