

# Nikhath Zafar

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11230808/publications.pdf>

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