

Vinita Joardar

List of Publications by Year in descending order

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11
papers

2,449
citations

840776

11
h-index

1281871

11
g-index

11
all docs

11
docs citations

11
times ranked

3324
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	Genome sequencing and analysis of the filamentous fungus <i>Penicillium chrysogenum</i> . Nature Biotechnology, 2008, 26, 1161-1168.	17.5	427
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	Identification of <i>Pseudomonas syringae</i> pv. <i>tomato</i> genes induced during infection of <i>Arabidopsis thaliana</i> . Molecular Microbiology, 2002, 44, 73-88.	2.5	180
5	A <i>Rickettsia</i> Genome Overrun by Mobile Genetic Elements Provides Insight into the Acquisition of Genes Characteristic of an Obligate Intracellular Lifestyle. Journal of Bacteriology, 2012, 194, 376-394.	2.2	152
6	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
7	Identification of novel <i>hrp</i> -regulated genes through functional genomic analysis of the <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000 genome. Molecular Microbiology, 2002, 45, 1207-1218.	2.5	138
8	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
9	Consensus coding sequence (CCDS) database: a standardized set of human and mouse protein-coding regions supported by expert curation. Nucleic Acids Research, 2018, 46, D221-D228.	14.5	97
10	Bioinformatics-Enabled Identification of the HrpL Regulon and Type III Secretion System Effector Proteins of <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> 1448A. Molecular Plant-Microbe Interactions, 2006, 19, 1193-1206.	2.6	81
11	Lineage-specific regions in <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000. Molecular Plant Pathology, 2005, 6, 53-64.	4.2	14