Shrinivasrao Mane

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The genetic consequences of dog breed formation—Accumulation of deleterious genetic variation and fixation of mutations associated with myxomatous mitral valve disease in cavalier King Charles spaniels. PLoS Genetics, 2021, 17, e1009726.	1.5	12
2	Genome analysis of a major urban malaria vector mosquito, Anopheles stephensi. Genome Biology, 2014, 15, 459.	3.8	119
3	Comparative Phylogenomics and Evolution of the Brucellae Reveal a Path to Virulence. Journal of Bacteriology, 2014, 196, 920-930.	1.0	122
4	Phylogeographic evidence of cognate recognition site patterns and transformation efficiency differences in H. pylori: theory of strain dominance. BMC Microbiology, 2013, 13, 211.	1.3	11
5	Genomic Comparison between a Virulent Type A1 Strain of Francisella tularensis and Its Attenuated O-Antigen Mutant. Journal of Bacteriology, 2012, 194, 2775-2776.	1.0	20
6	Comparative Genomics of Early-Diverging <i>Brucella</i> Strains Reveals a Novel Lipopolysaccharide Biosynthesis Pathway. MBio, 2012, 3, e00246-11.	1.8	33
7	Comparative Genomics of Early-Diverging Brucella Strains Reveals a Novel Lipopolysaccharide Biosynthesis Pathway. MBio, 2012, 3, e00246-12.	1.8	37
8	Contrasting patterns of evolution following whole genome versus tandem duplication events in <i>Populus</i> . Genome Research, 2012, 22, 95-105.	2.4	126
9	Helicobacter pylori Colonization Ameliorates Clucose Homeostasis in Mice through a PPAR γ-Dependent Mechanism. PLoS ONE, 2012, 7, e50069.	1.1	37
10	PATRIC: the Comprehensive Bacterial Bioinformatics Resource with a Focus on Human Pathogenic Species. Infection and Immunity, 2011, 79, 4286-4298.	1.0	252
11	Changes in spinach phylloepiphytic bacteria communities following minimal processing and refrigerated storage described using pyrosequencing of 16S rRNA amplicons. Journal of Applied Microbiology, 2011, 110, 1203-1214.	1.4	141
12	Microbial diversity in saliva of oral squamous cell carcinoma. FEMS Immunology and Medical Microbiology, 2011, 61, 269-277.	2.7	142
13	The genome of woodland strawberry (Fragaria vesca). Nature Genetics, 2011, 43, 109-116.	9.4	1,091
14	Host-Interactive Genes in Amerindian <i>Helicobacter pylori</i> Diverge from Their Old World Homologs and Mediate Inflammatory Responses. Journal of Bacteriology, 2010, 192, 3078-3092.	1.0	50
15	Multi-Platform Next-Generation Sequencing of the Domestic Turkey (Meleagris gallopavo): Genome Assembly and Analysis. PLoS Biology, 2010, 8, e1000475.	2.6	348
16	Transcriptome sequencing of the Microarray Quality Control (MAQC) RNA reference samples using next generation sequencing. BMC Genomics, 2009, 10, 264.	1.2	67
17	Physiological and molecular adaptations to drought in Andean potato genotypes. Journal of Experimental Botany, 2008, 59, 2109-2123.	2.4	175
18	Molecular and physiological adaptation to prolonged drought stress in the leaves of two Andean potato genotypes. Functional Plant Biology, 2008, 35, 669.	1.1	47

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19	Genome Sequence of Brucella abortus Vaccine Strain S19 Compared to Virulent Strains Yields Candidate Virulence Genes. PLoS ONE, 2008, 3, e2193.	1.1	108
20	Targeted Development of Registries of Biological Parts. PLoS ONE, 2008, 3, e2671.	1.1	63
21	Early PLDα-mediated events in response to progressive drought stress in Arabidopsis: a transcriptome analysis. Journal of Experimental Botany, 2007, 58, 241-252.	2.4	67
22	Validation and Estimation of Parameters for a General Probabilistic Model of the PCR Process. Journal of Computational Biology, 2007, 14, 97-112.	0.8	4
23	Effects of chronic ozone exposure on gene expression in Arabidopsis thaliana ecotypes and in Thellungiella halophila. Plant, Cell and Environment, 2006, 29, 854-868.	2.8	69
24	Response diversity of Arabidopsis thaliana ecotypes in elevated [CO2] in the field. Plant Molecular Biology, 2006, 62, 593-609.	2.0	66
25	The statistics of identifying differentially expressed genes in Expresso and TM4: a comparison. BMC Bioinformatics, 2006, 7, 215.	1.2	25