

Jianying Gu

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

899
citations

687363

13
h-index

580821

25
g-index

31
all docs

31
docs citations

31
times ranked

1403
citing authors

#	ARTICLE	IF	CITATIONS
1	Age distribution of human gene families shows significant roles of both large- and small-scale duplications in vertebrate evolution. <i>Nature Genetics</i> , 2002, 31, 205-209.	21.4	228
2	Induced gene expression in human brain after the split from chimpanzee. <i>Trends in Genetics</i> , 2003, 19, 63-65.	6.7	123
3	Comparative genomics of the pathogenic ciliate <i>Ichthyophthirius multifiliis</i> , its free-living relatives and a host species provide insights into adoption of a parasitic lifestyle and prospects for disease control. <i>Genome Biology</i> , 2011, 12, R100.	9.6	102
4	How much expression divergence after yeast gene duplication could be explained by regulatory motif evolution?. <i>Trends in Genetics</i> , 2004, 20, 403-407.	6.7	77
5	Genome plasticity and systems evolution in <i>Streptomyces</i> . <i>BMC Bioinformatics</i> , 2012, 13, S8.	2.6	61
6	Evolutionary Analysis for Functional Divergence of the Toll-Like Receptor Gene Family and Altered Functional Constraints. <i>Journal of Molecular Evolution</i> , 2007, 65, 119-123.	1.8	43
7	Natural history and functional divergence of protein tyrosine kinases. <i>Gene</i> , 2003, 317, 49-57.	2.2	40
8	Evolutionary Analysis for Functional Divergence of Jak Protein Kinase Domains and Tissue-Specific Genes. <i>Journal of Molecular Evolution</i> , 2002, 54, 725-733.	1.8	35
9	Improved prediction of malaria degradomes by supervised learning with SVM and profile kernel. <i>Genetica</i> , 2009, 136, 189-209.	1.1	31
10	The -omics Era- Toward a Systems-Level Understanding of <i>Streptomyces</i> . <i>Current Genomics</i> , 2011, 12, 404-416.	1.6	24
11	Are GC-rich isochores vanishing in mammals?. <i>Gene</i> , 2006, 385, 50-56.	2.2	22
12	Proteases in Malaria Parasites - A Phylogenomic Perspective. <i>Current Genomics</i> , 2011, 12, 417-427.	1.6	18
13	Genomic and systems evolution in <i>Vibrionaceae</i> species. <i>BMC Genomics</i> , 2009, 10, S11.	2.8	15
14	Comparative genomics of the family <i>Vibrionaceae</i> reveals the wide distribution of genes encoding virulence-associated proteins. <i>BMC Genomics</i> , 2010, 11, 369.	2.8	14
15	Module-based subnetwork alignments reveal novel transcriptional regulators in malaria parasite <i>Plasmodium falciparum</i> . <i>BMC Systems Biology</i> , 2012, 6, S5.	3.0	11
16	A Comparative Genomics, Network-Based Approach to Understanding Virulence in <i>Vibrio cholerae</i> . <i>Journal of Bacteriology</i> , 2009, 191, 6262-6272.	2.2	10
17	Genome evolution and functional divergence in <i>Yersinia</i> . <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2007, 308B, 37-49.	1.3	9
18	Core genome components and lineage specific expansions in malaria parasites <i>Plasmodium</i> . <i>BMC Genomics</i> , 2010, 11, S13.	2.8	8

#	ARTICLE	IF	CITATIONS
19	Comparative Genomics and Systems Biology of Malaria Parasites Plasmodium. Current Bioinformatics, 2012, 7, 478-489.	1.5	8
20	Further statistical analysis for genome-wide expression evolution in primate brain/liver/fibroblast tissue. Human Genomics, 2004, 1, 247.	2.9	6
21	Exploring systems affected by the heat shock response in Plasmodium falciparum via protein association networks. International Journal of Computational Biology and Drug Design, 2014, 7, 369.	0.3	5
22	Editorial: Evolutionary Mechanisms of Infectious Diseases. Frontiers in Microbiology, 2021, 12, 667561.	3.5	4
23	Predicting Type-I (Rate-Shift) Functional Divergence of Protein Sequences and Applications in Functional Genomics. Current Genomics, 2006, 7, 87-96.	1.6	2
24	The Core and Pan-Genome of the Vibrionaceae. , 2009, , .		1
25	Heavy path mining of protein-protein associations in the malaria parasite. Methods, 2015, 83, 63-70.	3.8	1
26	Genome Evolution in Malaria Parasites: I. Core Genome Components. , 2009, , .		0
27	Putative Cell Cycle Related Genes in Plasmodium Falciparum. , 2009, , .		0
28	Prediction of novel systems components in cell cycle regulation in malaria parasite by subnetwork alignments. , 2012, , .		0
29	Network analysis reveals complex interactions in heat shock response in the malaria parasite. , 2013, , .		0
30	Just-in-time expression of influential genes in the cellular networks of the malaria parasite Plasmodium falciparum during the red blood cycle. , 2016, , .		0