

Maria Anisimova

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

21,814
citations

230014

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182931

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62
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docs citations

62
times ranked

36287
citing authors

#	ARTICLE	IF	CITATIONS
1	New Algorithms and Methods to Estimate Maximum-Likelihood Phylogenies: Assessing the Performance of PhyML 3.0. <i>Systematic Biology</i> , 2010, 59, 307-321.	2.7	15,166
2	Approximate Likelihood-Ratio Test for Branches: A Fast, Accurate, and Powerful Alternative. <i>Systematic Biology</i> , 2006, 55, 539-552.	2.7	2,426
3	Survey of Branch Support Methods Demonstrates Accuracy, Power, and Robustness of Fast Likelihood-based Approximation Schemes. <i>Systematic Biology</i> , 2011, 60, 685-699.	2.7	912
4	Accuracy and Power of the Likelihood Ratio Test in Detecting Adaptive Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2001, 18, 1585-1592.	3.5	658
5	Accuracy and Power of Bayes Prediction of Amino Acid Sites Under Positive Selection. <i>Molecular Biology and Evolution</i> , 2002, 19, 950-958.	3.5	388
6	Tandem repeats lead to sequence assembly errors and impose multi-level challenges for genome and protein databases. <i>Nucleic Acids Research</i> , 2019, 47, 10994-11006.	6.5	236
7	Repertoire, unified nomenclature and evolution of the Type III effector gene set in the <i>Ralstonia solanacearum</i> species complex. <i>BMC Genomics</i> , 2013, 14, 859.	1.2	206
8	Multiple Hypothesis Testing to Detect Lineages under Positive Selection that Affects Only a Few Sites. <i>Molecular Biology and Evolution</i> , 2007, 24, 1219-1228.	3.5	197
9	Morphometric, Behavioral, and Genomic Evidence for a New Orangutan Species. <i>Current Biology</i> , 2017, 27, 3487-3498.e10.	1.8	192
10	Investigating Protein-Coding Sequence Evolution with Probabilistic Codon Substitution Models. <i>Molecular Biology and Evolution</i> , 2009, 26, 255-271.	3.5	141
11	ALFA: A Simulation Framework for Genome Evolution. <i>Molecular Biology and Evolution</i> , 2012, 29, 1115-1123.	3.5	130
12	CodonPhyML: Fast Maximum Likelihood Phylogeny Estimation under Codon Substitution Models. <i>Molecular Biology and Evolution</i> , 2013, 30, 1270-1280.	3.5	99
13	Functional diversification of the <i>GALAXY</i> type III effector family contributes to <i>Ralstonia solanacearum</i> adaptation on different plant hosts. <i>New Phytologist</i> , 2011, 192, 976-987.	3.5	97
14	Deep Conservation of Human Protein Tandem Repeats within the Eukaryotes. <i>Molecular Biology and Evolution</i> , 2014, 31, 1132-1148.	3.5	62
15	The evolution and function of protein tandem repeats in plants. <i>New Phytologist</i> , 2015, 206, 397-410.	3.5	54
16	State-of the art methodologies dictate new standards for phylogenetic analysis. <i>BMC Evolutionary Biology</i> , 2013, 13, 161.	3.2	51
17	Phylogenomic analysis of natural selection pressure in <i>Streptococcus</i> genomes. <i>BMC Evolutionary Biology</i> , 2007, 7, 154.	3.2	47
18	Repeat or not repeat? Statistical validation of tandem repeat prediction in genomic sequences. <i>Nucleic Acids Research</i> , 2012, 40, 10005-10017.	6.5	47

#	ARTICLE	IF	CITATIONS
19	Origin and Evolution of GALA-LRR, a New Member of the CC-LRR Subfamily: From Plants to Bacteria?. PLoS ONE, 2008, 3, e1694.	1.1	46
20	A New Census of Protein Tandem Repeats and Their Relationship with Intrinsic Disorder. Genes, 2020, 11, 407.	1.0	45
21	Functional assignment to positively selected sites in the core type <scp>III</scp> effector <scp>RipG</scp>7 from <scp><i>R</i></scp><i>alstonia solanacearum</i>. Molecular Plant Pathology, 2016, 17, 553-564.	2.0	39
22	Molecular Evolution of the Hepatitis Delta Virus Antigen Gene: Recombination or Positive Selection?. Journal of Molecular Evolution, 2004, 59, 815-826.	0.8	38
23	Markov Models of Amino Acid Substitution to Study Proteins with Intrinsically Disordered Regions. PLoS ONE, 2011, 6, e20488.	1.1	36
24	Gene copy number variation and its significance in cyanobacterial phylogeny. BMC Microbiology, 2012, 12, 177.	1.3	36
25	Natural Selection on Coding and Noncoding DNA Sequences Is Associated with Virulence Genes in a Plant Pathogenic Fungus. Genome Biology and Evolution, 2014, 6, 2368-2379.	1.1	31
26	Finding the balance between the mathematical and biological optima in multiple sequence alignment. Trends in Evolutionary Biology, 2010, 2, 7.	0.4	30
27	Coevolution of amino acid residues in the key photosynthetic enzyme Rubisco. BMC Evolutionary Biology, 2011, 11, 266.	3.2	28
28	Evolution of cyanobacterial morphotypes. Communicative and Integrative Biology, 2011, 4, 424-427.	0.6	27
29	Selection on the Protein-Coding Genome. Methods in Molecular Biology, 2012, 856, 113-140.	0.4	26
30	Graph-based modeling of tandem repeats improves global multiple sequence alignment. Nucleic Acids Research, 2013, 41, e162-e162.	6.5	25
31	Antibody-Specific Model of Amino Acid Substitution for Immunological Inferences from Alignments of Antibody Sequences. Molecular Biology and Evolution, 2015, 32, 806-819.	3.5	25
32	Enabling semantic queries across federated bioinformatics databases. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	23
33	Parametric models of codon evolution. , 2012, , 12-33.		23
34	Genomic Insights into Evolution of AdpA Family Master Regulators of Morphological Differentiation and Secondary Metabolism in Streptomyces. Journal of Molecular Evolution, 2018, 86, 204-215.	0.8	20
35	Statistical Approaches to Detecting and Analyzing Tandem Repeats in Genomic Sequences. Frontiers in Bioengineering and Biotechnology, 2015, 3, 31.	2.0	19
36	Progressive multiple sequence alignment with indel evolution. BMC Bioinformatics, 2018, 19, 331.	1.2	19

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37	Genomes reveal marked differences in the adaptive evolution between orangutan species. <i>Genome Biology</i> , 2018, 19, 193.	3.8	18
38	Evolutionary Genomics. <i>Methods in Molecular Biology</i> , 2019, , .	0.4	18
39	Unraveling Patterns of Site-to-Site Synonymous Rates Variation and Associated Gene Properties of Protein Domains and Families. <i>PLoS ONE</i> , 2014, 9, e95034.	1.1	17
40	TRAL: tandem repeat annotation library. <i>Bioinformatics</i> , 2015, 31, 3051-3053.	1.8	17
41	Maximum-Likelihood Tree Estimation Using Codon Substitution Models with Multiple Partitions. <i>Molecular Biology and Evolution</i> , 2015, 32, 2208-2216.	3.5	14
42	Evolution of cyanobacterial morphotypes: Taxa required for improved phylogenomic approaches. <i>Communicative and Integrative Biology</i> , 2011, 4, 424-7.	0.6	14
43	Darwin and Fisher meet at biotech: on the potential of computational molecular evolution in industry. <i>BMC Evolutionary Biology</i> , 2015, 15, 76.	3.2	10
44	Positive and Negative Selection in the β -Esterase Gene Cluster of the <i>Drosophila melanogaster</i> Subgroup. <i>Journal of Molecular Evolution</i> , 2006, 62, 496-510.	0.8	9
45	Selection Acting on Genomes. <i>Methods in Molecular Biology</i> , 2019, 1910, 373-397.	0.4	9
46	TRAL 2.0: Tandem Repeat Detection With Circular Profile Hidden Markov Models and Evolutionary Aligner. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	1.0	9
47	Complex Interplay of Evolutionary Forces in the ladybird Homeobox Genes of <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2011, 6, e22613.	1.1	7
48	PANDITplus: toward better integration of evolutionary view on molecular sequences with supplementary bioinformatics resources. <i>Trends in Evolutionary Biology</i> , 2010, 2, 1.	0.4	6
49	ProPIP: a tool for progressive multiple sequence alignment with Poisson Indel Process. <i>BMC Bioinformatics</i> , 2021, 22, 518.	1.2	5
50	DNA polymorphism and selection at the bindin locus in three <i>Strongylocentrotus</i> sp. (Echinoidea). <i>BMC Genetics</i> , 2016, 17, 66.	2.7	4
51	Accounting for Programmed Ribosomal Frameshifting in the Computation of Codon Usage Bias Indices. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3173-3183.	0.8	3
52	Accelerating phylogeny-aware alignment with indel evolution using short time Fourier transform. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa092.	1.5	3
53	The Use of the Rare TTA Codon in <i>Streptomyces</i> Genes: Significance of the Codon Context?. <i>Indian Journal of Microbiology</i> , 2021, 61, 24-30.	1.5	2
54	Impact of Diabetes Mellitus on Voice : A Methodological Commentary. <i>Journal of Voice</i> , 2020, , .	0.6	1

#	ARTICLE	IF	CITATIONS
55	Beyond Microsatellite Instability: Intrinsic Disorder as a Potential Link Between Protein Short Tandem Repeats and Cancer. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	1.0	1