

Nicolas Rodrigue

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

1,394
citations

759233

12
h-index

610901

24
g-index

26
all docs

26
docs citations

26
times ranked

2224
citing authors

#	ARTICLE	IF	CITATIONS
1	A Bayesian Mutation-Selection Framework for Detecting Site-Specific Adaptive Evolution in Protein-Coding Genes. <i>Molecular Biology and Evolution</i> , 2021, 38, 1199-1208.	8.9	11
2	Evolution of <i>Carthamus</i> species revealed through sequence analyses of the <i>fad2</i> gene family. <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 419-432.	3.1	3
3	Detecting amino acid preference shifts with codon-level mutation-selection mixture models. <i>BMC Evolutionary Biology</i> , 2019, 19, 62.	3.2	5
4	A Not-So-Long Introduction to Computational Molecular Evolution. <i>Methods in Molecular Biology</i> , 2019, 1910, 71-117.	0.9	5
5	Multiple Factors Confounding Phylogenetic Detection of Selection on Codon Usage. <i>Molecular Biology and Evolution</i> , 2018, 35, 1463-1472.	8.9	10
6	Clonal evolution and genome stability in a 2500-year-old fungal individual. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20182233.	2.6	39
7	Conditional Approximate Bayesian Computation: A New Approach for Across-Site Dependency in High-Dimensional Mutation-Selection Models. <i>Molecular Biology and Evolution</i> , 2018, 35, 2819-2834.	8.9	5
8	COMPASS: the COMPLETELY Arbitrary Sequence Simulator. <i>Bioinformatics</i> , 2017, 33, 3101-3103.	4.1	3
9	Genomics of Compensatory Adaptation in Experimental Populations of <i>Aspergillus nidulans</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 427-436.	1.8	3
10	Detecting Adaptation in Protein-Coding Genes Using a Bayesian Site-Heterogeneous Mutation-Selection Codon Substitution Model. <i>Molecular Biology and Evolution</i> , 2017, 34, 204-214.	8.9	35
11	Whole genome sequencing and comparative genomics of closely related <i>Fusarium</i> Head Blight fungi: <i>Fusarium graminearum</i> , <i>F. meridionale</i> and <i>F. asiaticum</i> . <i>BMC Genomics</i> , 2016, 17, 1014.	2.8	58
12	Grouping substitution types into different relaxed molecular clocks. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150141.	4.0	1
13	Genome-Wide Patterns of Recombination in the Opportunistic Human Pathogen <i>Pseudomonas aeruginosa</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 18-34.	2.5	29
14	Relaxing the Molecular Clock to Different Degrees for Different Substitution Types. <i>Molecular Biology and Evolution</i> , 2015, 32, 1948-1961.	8.9	7
15	The Effect of Selection Environment on the Probability of Parallel Evolution. <i>Molecular Biology and Evolution</i> , 2015, 32, 1436-1448.	8.9	116
16	Site-heterogeneous mutation-selection models within the PhyloBayes-MPI package. <i>Bioinformatics</i> , 2014, 30, 1020-1021.	4.1	61
17	Codon-based phylogenetics introduces novel flagellar gene markers to oomycete systematics. <i>Molecular Phylogenetics and Evolution</i> , 2014, 79, 279-291.	2.7	11
18	PhyloBayes MPI: Phylogenetic Reconstruction with Infinite Mixtures of Profiles in a Parallel Environment. <i>Systematic Biology</i> , 2013, 62, 611-615.	5.6	698

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19	On the Statistical Interpretation of Site-Specific Variables in Phylogeny-Based Substitution Models. <i>Genetics</i> , 2013, 193, 557-564.	2.9	34
20	Codon models as a vehicle for reconciling population genetics with inter-specific sequence data. , 2012, , 97-110.		13
21	Fast Bayesian Choice of Phylogenetic Models: Prospecting Data Augmentationâ€‘Based Thermodynamic Integration. <i>Systematic Biology</i> , 2011, 60, 881-887.	5.6	7
22	Mechanistic revisions of phenomenological modeling strategies in molecular evolution. <i>Trends in Genetics</i> , 2010, 26, 248-252.	6.7	28
23	Mutation-selection models of coding sequence evolution with site-heterogeneous amino acid fitness profiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4629-4634.	7.1	152
24	Computational Methods for Evaluating Phylogenetic Models of Coding Sequence Evolution with Dependence between Codons. <i>Molecular Biology and Evolution</i> , 2009, 26, 1663-1676.	8.9	45
25	Exploring Fast Computational Strategies for Probabilistic Phylogenetic Analysis. <i>Systematic Biology</i> , 2007, 56, 711-726.	5.6	15
26	Jump-Chain Simulation of Markov Substitution Processes Over Phylogenies. <i>Journal of Molecular Evolution</i> , 0, , .	1.8	0