

Nicolas Lartillot

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7168493/publications.pdf>

Version: 2024-02-01

65
papers

16,474
citations

94433

37
h-index

106344

65
g-index

76
all docs

76
docs citations

76
times ranked

15735
citing authors

#	ARTICLE	IF	CITATIONS
1	Relative Time Constraints Improve Molecular Dating. <i>Systematic Biology</i> , 2022, 71, 797-809.	5.6	9
2	An Improved Codon Modeling Approach for Accurate Estimation of the Mutation Bias. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	4
3	A Bayesian Mutationâ€“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
4	Inferring the Deep Past from Molecular Data. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	19
5	Long-Lived Species of Bivalves Exhibit Low MT-DNA Substitution Rates. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 626042.	3.5	7
6	Reconstructing the History of Variation in Effective Population Size along Phylogenies. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	13
7	Inferring Long-Term Effective Population Size with Mutationâ€“Selection Models. <i>Molecular Biology and Evolution</i> , 2021, 38, 4573-4587.	8.9	10
8	Scalable Empirical Mixture Models That Account for Across-Site Compositional Heterogeneity. <i>Molecular Biology and Evolution</i> , 2020, 37, 3616-3631.	8.9	32
9	From Inquilines to Gall Inducers: Genomic Signature of a Life-Style Transition in <i>Synergus</i> Gall Wasps. <i>Genome Biology and Evolution</i> , 2020, 12, 2060-2073.	2.5	9
10	IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era. <i>Molecular Biology and Evolution</i> , 2020, 37, 1530-1534.	8.9	5,960
11	Detecting adaptive convergent amino acid evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180234.	4.0	15
12	Life History Traits Impact the Nuclear Rate of Substitution but Not the Mitochondrial Rate in Isopods. <i>Molecular Biology and Evolution</i> , 2018, 35, 2900-2912.	8.9	28
13	Conditional Approximate Bayesian Computation: A New Approach for Across-Site Dependency in High-Dimensional Mutationâ€“Selection Models. <i>Molecular Biology and Evolution</i> , 2018, 35, 2819-2834.	8.9	5
14	Molecular adaptation in Rubisco: Discriminating between convergent evolution and positive selection using mechanistic and classical codon models. <i>PLoS ONE</i> , 2018, 13, e0192697.	2.5	17
15	Improved Modeling of Compositional Heterogeneity Supports Sponges as Sister to All Other Animals. <i>Current Biology</i> , 2017, 27, 3864-3870.e4.	3.9	244
16	The Red Queen model of recombination hot-spot evolution: a theoretical investigation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160463.	4.0	32
17	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
18	RevBayes: Bayesian Phylogenetic Inference Using Graphical Models and an Interactive Model-Specification Language. <i>Systematic Biology</i> , 2016, 65, 726-736.	5.6	538

#	ARTICLE	IF	CITATIONS
19	A mixed relaxed clock model. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150132.	4.0	48
20	Closing the gap between rocks and clocks using total-evidence dating. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150136.	4.0	115
21	Reply to Halanych et al.: Ctenophore misplacement is corroborated by independent datasets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E948-9.	7.1	14
22	Probabilistic models of eukaryotic evolution: time for integration. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140338.	4.0	11
23	Genomic data do not support comb jellies as the sister group to all other animals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15402-15407.	7.1	286
24	The Red Queen Model of Recombination Hotspots Evolution in the Light of Archaic and Modern Human Genomes. <i>PLoS Genetics</i> , 2014, 10, e1004790.	3.5	62
25	Monte Carlo algorithms for Brownian phylogenetic models. <i>Bioinformatics</i> , 2014, 30, 3020-3028.	4.1	13
26	PhyloBayes MPI: Phylogenetic Reconstruction with Infinite Mixtures of Profiles in a Parallel Environment. <i>Systematic Biology</i> , 2013, 62, 611-615.	5.6	698
27	Interaction between Selection and Biased Gene Conversion in Mammalian Protein-Coding Sequence Evolution Revealed by a Phylogenetic Covariance Analysis. <i>Molecular Biology and Evolution</i> , 2013, 30, 356-368.	8.9	33
28	Phylogenetic Patterns of GC-Biased Gene Conversion in Placental Mammals and the Evolutionary Dynamics of Recombination Landscapes. <i>Molecular Biology and Evolution</i> , 2013, 30, 489-502.	8.9	68
29	Serine Codon-Usage Bias in Deep Phylogenomics: Pancrustacean Relationships as a Case Study. <i>Systematic Biology</i> , 2013, 62, 121-133.	5.6	124
30	Lateral Gene Transfer from the Dead. <i>Systematic Biology</i> , 2013, 62, 386-397.	5.6	100
31	An Experimentally Tested Scenario for the Structural Evolution of Eukaryotic Cys2His2 Zinc Fingers from Eubacterial Ros Homologs. <i>Molecular Biology and Evolution</i> , 2013, 30, 1504-1513.	8.9	23
32	Reconstructing the Phylogenetic History of Long-Term Effective Population Size and Life-History Traits Using Patterns of Amino Acid Replacement in Mitochondrial Genomes of Mammals and Birds. <i>Genome Biology and Evolution</i> , 2013, 5, 1273-1290.	2.5	62
33	JOINT RECONSTRUCTION OF DIVERGENCE TIMES AND LIFE-HISTORY EVOLUTION IN PLACENTAL MAMMALS USING A PHYLOGENETIC COVARIANCE MODEL. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 1773-1787.	2.3	71
34	History Can Matter: Non-Markovian Behavior of Ancestral Lineages. <i>Systematic Biology</i> , 2011, 60, 276-290.	5.6	7
35	A Phylogenetic Model for Investigating Correlated Evolution of Substitution Rates and Continuous Phenotypic Characters. <i>Molecular Biology and Evolution</i> , 2011, 28, 729-744.	8.9	193
36	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

#	ARTICLE	IF	CITATIONS
37	A Dirichlet Process Covarion Mixture Model and Its Assessments Using Posterior Predictive Discrepancy Tests. <i>Molecular Biology and Evolution</i> , 2010, 27, 371-384.	8.9	30
38	Statistical Potentials for Improved Structurally Constrained Evolutionary Models. <i>Molecular Biology and Evolution</i> , 2010, 27, 1546-1560.	8.9	49
39	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
40	PhyloBayes 3: a Bayesian software package for phylogenetic reconstruction and molecular dating. <i>Bioinformatics</i> , 2009, 25, 2286-2288.	4.1	1,198
41	Additional molecular support for the new chordate phylogeny. <i>Genesis</i> , 2008, 46, 592-604.	1.6	207
42	Parallel adaptations to high temperatures in the Archaean eon. <i>Nature</i> , 2008, 456, 942-945.	27.8	198
43	A Site- and Time-Heterogeneous Model of Amino Acid Replacement. <i>Molecular Biology and Evolution</i> , 2008, 25, 842-858.	8.9	195
44	Bayesian Comparisons of Codon Substitution Models. <i>Genetics</i> , 2008, 180, 1579-1591.	2.9	22
45	Improvement of molecular phylogenetic inference and the phylogeny of Bilateria. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 1463-1472.	4.0	167
46	Phylogenetic mixture models for proteins. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 3965-3976.	4.0	202
47	Empirical profile mixture models for phylogenetic reconstruction. <i>Bioinformatics</i> , 2008, 24, 2317-2323.	4.1	292
48	Exploring Fast Computational Strategies for Probabilistic Phylogenetic Analysis. <i>Systematic Biology</i> , 2007, 56, 711-726.	5.6	15
49	A General Comparison of Relaxed Molecular Clock Models. <i>Molecular Biology and Evolution</i> , 2007, 24, 2669-2680.	8.9	454
50	Suppression of long-branch attraction artefacts in the animal phylogeny using a site-heterogeneous model. <i>BMC Evolutionary Biology</i> , 2007, 7, S4.	3.2	551
51	Detecting and Overcoming Systematic Errors in Genome-Scale Phylogenies. <i>Systematic Biology</i> , 2007, 56, 389-399.	5.6	288
52	Computing Bayes Factors Using Thermodynamic Integration. <i>Systematic Biology</i> , 2006, 55, 195-207.	5.6	564
53	Multipolar Consensus for Phylogenetic Trees. <i>Systematic Biology</i> , 2006, 55, 837-843.	5.6	14
54	A Bayesian Compound Stochastic Process for Modeling Nonstationary and Nonhomogeneous Sequence Evolution. <i>Molecular Biology and Evolution</i> , 2006, 23, 2058-2071.	8.9	139

#	ARTICLE	IF	CITATIONS
55	Assessing Site-Interdependent Phylogenetic Models of Sequence Evolution. <i>Molecular Biology and Evolution</i> , 2006, 23, 1762-1775.	8.9	66
56	Conjugate Gibbs Sampling for Bayesian Phylogenetic Models. <i>Journal of Computational Biology</i> , 2006, 13, 1701-1722.	1.6	60
57	Multigene Analyses of Bilaterian Animals Corroborate the Monophyly of Ecdysozoa, Lophotrochozoa, and Protostomia. <i>Molecular Biology and Evolution</i> , 2005, 22, 1246-1253.	8.9	517
58	Site interdependence attributed to tertiary structure in amino acid sequence evolution. <i>Gene</i> , 2005, 347, 207-217.	2.2	89
59	Phylogenomics. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2005, 36, 541-562.	8.3	303
60	A Bayesian Mixture Model for Across-Site Heterogeneities in the Amino-Acid Replacement Process. <i>Molecular Biology and Evolution</i> , 2004, 21, 1095-1109.	8.9	1,329
61	The expression of a caudal homologue in a mollusc, <i>Patella vulgata</i> . <i>Gene Expression Patterns</i> , 2003, 3, 35-37.	0.8	27
62	Phylogenetic Analysis of the Wnt Gene Family. <i>Current Biology</i> , 2002, 12, 1395-1400.	3.9	106
63	Expression patterns of fork head and gooseoid homologues in the mollusc <i>Patella vulgata</i> supports the ancestry of the anterior mesendoderm across Bilateria. <i>Development Genes and Evolution</i> , 2002, 212, 551-561.	0.9	65
64	Animal evolution: the end of the intermediate taxa?. <i>Trends in Genetics</i> , 1999, 15, 104-108.	6.7	186
65	Reconstruction of body mass evolution in the Cetartiodactyla and mammals using phylogenomic data. , 0, 1, .		1