

Liang Liu

List of Publications by Year in descending order

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57
papers

7,932
citations

126907

33
h-index

149698

56
g-index

59
all docs

59
docs citations

59
times ranked

7496
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	12.6	1,583
2	A maximum pseudo-likelihood approach for estimating species trees under the coalescent model. <i>BMC Evolutionary Biology</i> , 2010, 10, 302.	3.2	548
3	High-resolution species trees without concatenation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5936-5941.	7.1	530
4	Species Trees from Gene Trees: Reconstructing Bayesian Posterior Distributions of a Species Phylogeny Using Estimated Gene Tree Distributions. <i>Systematic Biology</i> , 2007, 56, 504-514.	5.6	434
5	Estimating Species Phylogenies Using Coalescence Times among Sequences. <i>Systematic Biology</i> , 2009, 58, 468-477.	5.6	410
6	Resolving conflict in eutherian mammal phylogeny using phylogenomics and the multispecies coalescent model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 14942-14947.	7.1	407
7	BEST: Bayesian estimation of species trees under the coalescent model. <i>Bioinformatics</i> , 2008, 24, 2542-2543.	4.1	367
8	Coalescent methods for estimating phylogenetic trees. <i>Molecular Phylogenetics and Evolution</i> , 2009, 53, 320-328.	2.7	353
9	Implementing and testing the multispecies coalescent model: A valuable paradigm for phylogenomics. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 447-462.	2.7	321
10	Estimating Species Trees from Unrooted Gene Trees. <i>Systematic Biology</i> , 2011, 60, 661-667.	5.6	243
11	Local admixture of amplified and diversified secreted pathogenesis determinants shapes mosaic <i>Toxoplasma gondii</i> genomes. <i>Nature Communications</i> , 2016, 7, 10147.	12.8	243
12	ESTIMATING SPECIES TREES USING MULTIPLE-ALLELE DNA SEQUENCE DATA. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 2080-2091.	2.3	189
13	Coalescent versus Concatenation Methods and the Placement of Amborella as Sister to Water Lilies. <i>Systematic Biology</i> , 2014, 63, 919-932.	5.6	166
14	Estimating phylogenetic trees from genome-scale data. <i>Annals of the New York Academy of Sciences</i> , 2015, 1360, 36-53.	3.8	165
15	The Impact of Missing Data on Species Tree Estimation. <i>Molecular Biology and Evolution</i> , 2016, 33, 838-860.	8.9	134
16	Genomic evidence reveals a radiation of placental mammals uninterrupted by the KPg boundary. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7282-E7290.	7.1	119
17	Phybase: an R package for species tree analysis. <i>Bioinformatics</i> , 2010, 26, 962-963.	4.1	115
18	Origin of land plants using the multispecies coalescent model. <i>Trends in Plant Science</i> , 2013, 18, 492-495.	8.8	109

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19	Genes with minimal phylogenetic information are problematic for coalescent analyses when gene tree estimation is biased. <i>Molecular Phylogenetics and Evolution</i> , 2015, 92, 63-71.	2.7	104
20	Phylogenetic Analysis in the Anomaly Zone. <i>Systematic Biology</i> , 2009, 58, 452-460.	5.6	103
21	Phylogeny and biogeography of <i>Orobanchaceae</i> . <i>Folia Geobotanica</i> , 2005, 40, 115-134.	0.9	95
22	STRAW: Species TRee Analysis Web server. <i>Nucleic Acids Research</i> , 2013, 41, W238-W241.	14.5	93
23	Coalescent methods for estimating species trees from phylogenomic data. <i>Journal of Systematics and Evolution</i> , 2015, 53, 380-390.	3.1	89
24	Widespread ancient whole-genome duplications in Malpighiales coincide with Eocene global climatic upheaval. <i>New Phytologist</i> , 2019, 221, 565-576.	7.3	86
25	Incomplete lineage sorting rather than hybridization explains the inconsistent phylogeny of the wisent. <i>Communications Biology</i> , 2018, 1, 169.	4.4	84
26	Transcriptome Sequencing and Annotation for the Jamaican Fruit Bat (<i>Artibeus jamaicensis</i>). <i>PLoS ONE</i> , 2012, 7, e48472.	2.5	77
27	Maximum tree: a consistent estimator of the species tree. <i>Journal of Mathematical Biology</i> , 2010, 60, 95-106.	1.9	74
28	Phylogenomic analyses data of the avian phylogenomics project. <i>GigaScience</i> , 2015, 4, 4.	6.4	72
29	Coalescent Methods Are Robust to the Simultaneous Effects of Long Branches and Incomplete Lineage Sorting. <i>Molecular Biology and Evolution</i> , 2015, 32, 791-805.	8.9	69
30	The Perfect Storm: Gene Tree Estimation Error, Incomplete Lineage Sorting, and Ancient Gene Flow Explain the Most Recalcitrant Ancient Angiosperm Clade, Malpighiales. <i>Systematic Biology</i> , 2021, 70, 491-507.	5.6	61
31	Supplementation with Major Royal-Jelly Proteins Increases Lifespan, Feeding, and Fecundity in <i>Drosophila</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 5803-5812.	5.2	55
32	The Multispecies Coalescent Model Outperforms Concatenation Across Diverse Phylogenomic Data Sets. <i>Systematic Biology</i> , 2020, 69, 795-812.	5.6	47
33	Reply to Gatesy and Springer: Claims of homology errors and zombie lineages do not compromise the dating of placental diversification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9433-E9434.	7.1	37
34	Models for gene duplication when dosage balance works as a transition state to subsequent neo- or sub-functionalization. <i>BMC Evolutionary Biology</i> , 2016, 16, 45.	3.2	35
35	Modern Phylogenomics: Building Phylogenetic Trees Using the Multispecies Coalescent Model. <i>Methods in Molecular Biology</i> , 2019, 1910, 211-239.	0.9	30
36	Chemical Biology Approaches for Investigating the Functions of Lysine Acetyltransferases. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 1162-1184.	13.8	28

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37	A Bayesian model for gene family evolution. BMC Bioinformatics, 2011, 12, 426.	2.6	24
38	Prognostic Nomogram for Thoracic Esophageal Squamous Cell Carcinoma after Radical Esophagectomy. PLoS ONE, 2015, 10, e0124437.	2.5	24
39	Curcumin supplementation increases survival and lifespan in <i>Drosophila</i> under heat stress conditions. BioFactors, 2018, 44, 577-587.	5.4	21
40	The multispecies coalescent model and land plant origins: a reply to Springer and Gatesy. Trends in Plant Science, 2014, 19, 270-272.	8.8	20
41	Comment on "Statistical binning enables an accurate coalescent-based estimation of the avian tree". Science, 2015, 350, 171-171.	12.6	18
42	Genome-scale DNA sequence data and the evolutionary history of placental mammals. Data in Brief, 2018, 18, 1972-1975.	1.0	18
43	Regression multiple imputation for missing data analysis. Statistical Methods in Medical Research, 2020, 29, 2647-2664.	1.5	18
44	Curcumin supplementation improves heat-stress-induced cardiac injury of mice: physiological and molecular mechanisms. Journal of Nutritional Biochemistry, 2020, 78, 108331.	4.2	18
45	Protocols for the Molecular Evolutionary Analysis of Membrane Protein Gene Duplicates. Methods in Molecular Biology, 2019, 1851, 49-62.	0.9	16
46	A generalized birth and death process for modeling the fates of gene duplication. BMC Evolutionary Biology, 2015, 15, 275.	3.2	12
47	The effect of alignment uncertainty, substitution models and priors in building and dating the mammal tree of life. BMC Evolutionary Biology, 2019, 19, 203.	3.2	11
48	On Mechanistic Modeling of Gene Content Evolution: Birth-Death Models and Mechanisms of Gene Birth and Gene Retention. Computation, 2014, 2, 112-130.	2.0	10
49	Investigating the performance of AIC in selecting phylogenetic models. Statistical Applications in Genetics and Molecular Biology, 2014, 13, 459-75.	0.6	10
50	Species Tree Estimation and the Impact of Gene Loss Following Whole-Genome Duplication. Systematic Biology, 2022, 71, 1348-1361.	5.6	10
51	A phylogenetic model for understanding the effect of gene duplication on cancer progression. Nucleic Acids Research, 2014, 42, 2870-2878.	14.5	7
52	Quasi-Likelihood for Right-Censored Data in the Generalized Linear Model. Communications in Statistics - Theory and Methods, 2009, 38, 2187-2200.	1.0	5
53	Extended quasi-likelihood with fractional polynomials in the frame of the accelerated failure time model. Statistics in Medicine, 2012, 31, 1369-1379.	1.6	5
54	Weighted Least Squares Method for Right-Censored Data in Accelerated Failure Time Model. Biometrics, 2013, 69, 358-365.	1.4	3

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55	Untersuchung der epigenetischen Funktionen von Lysin-Acetyltransferasen mit Methoden der chemischen Biologie. <i>Angewandte Chemie</i> , 2018, 130, 1176-1199.	2.0	3
56	A homoscedasticity test for the accelerated failure time model. <i>Computational Statistics</i> , 2019, 34, 433-446.	1.5	2
57	Nomogram predicting long-term survival probability of thoracic esophageal squamous cell carcinoma after radical esophagectomy.. <i>Journal of Clinical Oncology</i> , 2013, 31, 4094-4094.	1.6	0