

# Liang Liu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7452927/publications.pdf>

Version: 2024-02-01

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	Species Tree Estimation and the Impact of Gene Loss Following Whole-Genome Duplication. <i>Systematic Biology</i> , 2022, 71, 1348-1361.	5.6	10
2	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
3	Regression multiple imputation for missing data analysis. <i>Statistical Methods in Medical Research</i> , 2020, 29, 2647-2664.	1.5	18
4	Curcumin supplementation improves heat-stress-induced cardiac injury of mice: physiological and molecular mechanisms. <i>Journal of Nutritional Biochemistry</i> , 2020, 78, 108331.	4.2	18
5	The Multispecies Coalescent Model Outperforms Concatenation Across Diverse Phylogenomic Data Sets. <i>Systematic Biology</i> , 2020, 69, 795-812.	5.6	47
6	Widespread ancient whole-genome duplications in Malpighiales coincide with Eocene global climatic upheaval. <i>New Phytologist</i> , 2019, 221, 565-576.	7.3	86
7	Modern Phylogenomics: Building Phylogenetic Trees Using the Multispecies Coalescent Model. <i>Methods in Molecular Biology</i> , 2019, 1910, 211-239.	0.9	30
8	The effect of alignment uncertainty, substitution models and priors in building and dating the mammal tree of life. <i>BMC Evolutionary Biology</i> , 2019, 19, 203.	3.2	11
9	Protocols for the Molecular Evolutionary Analysis of Membrane Protein Gene Duplicates. <i>Methods in Molecular Biology</i> , 2019, 1851, 49-62.	0.9	16
10	A homoscedasticity test for the accelerated failure time model. <i>Computational Statistics</i> , 2019, 34, 433-446.	1.5	2
11	Chemical Biology Approaches for Investigating the Functions of Lysine Acetyltransferases. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 1162-1184.	13.8	28
12	Untersuchung der epigenetischen Funktionen von Lysin-Acetyltransferasen mit Methoden der chemischen Biologie. <i>Angewandte Chemie</i> , 2018, 130, 1176-1199.	2.0	3
13	Curcumin supplementation increases survival and lifespan in <i>Drosophila</i> under heat stress conditions. <i>BioFactors</i> , 2018, 44, 577-587.	5.4	21
14	Incomplete lineage sorting rather than hybridization explains the inconsistent phylogeny of the wisent. <i>Communications Biology</i> , 2018, 1, 169.	4.4	84
15	Genome-scale DNA sequence data and the evolutionary history of placental mammals. <i>Data in Brief</i> , 2018, 18, 1972-1975.	1.0	18
16	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
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	The Impact of Missing Data on Species Tree Estimation. <i>Molecular Biology and Evolution</i> , 2016, 33, 838-860.	8.9	134
22	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
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	A generalized birth and death process for modeling the fates of gene duplication. <i>BMC Evolutionary Biology</i> , 2015, 15, 275.	3.2	12
25	Estimating phylogenetic trees from genome-scale data. <i>Annals of the New York Academy of Sciences</i> , 2015, 1360, 36-53.	3.8	165
26	Prognostic Nomogram for Thoracic Esophageal Squamous Cell Carcinoma after Radical Esophagectomy. <i>PLoS ONE</i> , 2015, 10, e0124437.	2.5	24
27	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
28	Phylogenomic analyses data of the avian phylogenomics project. <i>GigaScience</i> , 2015, 4, 4.	6.4	72
29	Comment on "Statistical binning enables an accurate coalescent-based estimation of the avian tree". <i>Science</i> , 2015, 350, 171-171.	12.6	18
30	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
31	On Mechanistic Modeling of Gene Content Evolution: Birth-Death Models and Mechanisms of Gene Birth and Gene Retention. <i>Computation</i> , 2014, 2, 112-130.	2.0	10
32	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
33	A phylogenetic model for understanding the effect of gene duplication on cancer progression. <i>Nucleic Acids Research</i> , 2014, 42, 2870-2878.	14.5	7
34	Investigating the performance of AIC in selecting phylogenetic models. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2014, 13, 459-75.	0.6	10
35	The multispecies coalescent model and land plant origins: a reply to Springer and Gatesy. <i>Trends in Plant Science</i> , 2014, 19, 270-272.	8.8	20
36	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

#	ARTICLE	IF	CITATIONS
37	Origin of land plants using the multispecies coalescent model. <i>Trends in Plant Science</i> , 2013, 18, 492-495.	8.8	109
38	STRAW: Species TRee Analysis Web server. <i>Nucleic Acids Research</i> , 2013, 41, W238-W241.	14.5	93
39	Weighted Least-Squares Method for Right-Censored Data in Accelerated Failure Time Model. <i>Biometrics</i> , 2013, 69, 358-365.	1.4	3
40	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
41	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
42	Transcriptome Sequencing and Annotation for the Jamaican Fruit Bat ( <i>Artibeus jamaicensis</i> ). <i>PLoS ONE</i> , 2012, 7, e48472.	2.5	77
43	Extended quasi-likelihood with fractional polynomials in the frame of the accelerated failure time model. <i>Statistics in Medicine</i> , 2012, 31, 1369-1379.	1.6	5
44	Estimating Species Trees from Unrooted Gene Trees. <i>Systematic Biology</i> , 2011, 60, 661-667.	5.6	243
45	A Bayesian model for gene family evolution. <i>BMC Bioinformatics</i> , 2011, 12, 426.	2.6	24
46	Maximum tree: a consistent estimator of the species tree. <i>Journal of Mathematical Biology</i> , 2010, 60, 95-106.	1.9	74
47	A maximum pseudo-likelihood approach for estimating species trees under the coalescent model. <i>BMC Evolutionary Biology</i> , 2010, 10, 302.	3.2	548
48	Phybase: an R package for species tree analysis. <i>Bioinformatics</i> , 2010, 26, 962-963.	4.1	115
49	Phylogenetic Analysis in the Anomaly Zone. <i>Systematic Biology</i> , 2009, 58, 452-460.	5.6	103
50	Estimating Species Phylogenies Using Coalescence Times among Sequences. <i>Systematic Biology</i> , 2009, 58, 468-477.	5.6	410
51	Coalescent methods for estimating phylogenetic trees. <i>Molecular Phylogenetics and Evolution</i> , 2009, 53, 320-328.	2.7	353
52	Quasi-Likelihood for Right-Censored Data in the Generalized Linear Model. <i>Communications in Statistics - Theory and Methods</i> , 2009, 38, 2187-2200.	1.0	5
53	ESTIMATING SPECIES TREES USING MULTIPLE-ALLELE DNA SEQUENCE DATA. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 2080-2091.	2.3	189
54	BEST: Bayesian estimation of species trees under the coalescent model. <i>Bioinformatics</i> , 2008, 24, 2542-2543.	4.1	367

#	ARTICLE	IF	CITATIONS
55	High-resolution species trees without concatenation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 5936-5941.	7.1	530
56	Species Trees from Gene Trees: Reconstructing Bayesian Posterior Distributions of a Species Phylogeny Using Estimated Gene Tree Distributions. Systematic Biology, 2007, 56, 504-514.	5.6	434
57	Phylogeny and biogeography of Orobanchaceae. Folia Geobotanica, 2005, 40, 115-134.	0.9	95