

Liang Liu

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/7452927/liang-liu-publications-by-year.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

56
papers

6,023
citations

31
h-index

59
g-index

59
ext. papers

7,261
ext. citations

7.2
avg, IF

6
L-index

#	Paper	IF	Citations
56	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	8.4	9
55	Regression multiple imputation for missing data analysis. <i>Statistical Methods in Medical Research</i> , 2020 , 29, 2647-2664	2.3	5
54	Curcumin supplementation improves heat-stress-induced cardiac injury of mice: physiological and molecular mechanisms. <i>Journal of Nutritional Biochemistry</i> , 2020 , 78, 108331	6.3	7
53	The Multispecies Coalescent Model Outperforms Concatenation Across Diverse Phylogenomic Data Sets. <i>Systematic Biology</i> , 2020 , 69, 795-812	8.4	19
52	Widespread ancient whole-genome duplications in Malpighiales coincide with Eocene global climatic upheaval. <i>New Phytologist</i> , 2019 , 221, 565-576	9.8	43
51	Modern Phylogenomics: Building Phylogenetic Trees Using the Multispecies Coalescent Model. <i>Methods in Molecular Biology</i> , 2019 , 1910, 211-239	1.4	15
50	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	5
49	Protocols for the Molecular Evolutionary Analysis of Membrane Protein Gene Duplicates. <i>Methods in Molecular Biology</i> , 2019 , 1851, 49-62	1.4	3
48	A homoscedasticity test for the accelerated failure time model. <i>Computational Statistics</i> , 2019 , 34, 433-446		1
47	Chemical Biology Approaches for Investigating the Functions of Lysine Acetyltransferases. <i>Angewandte Chemie - International Edition</i> , 2018 , 57, 1162-1184	16.4	16
46	Untersuchung der epigenetischen Funktionen von Lysin-Acetyltransferasen mit Methoden der chemischen Biologie. <i>Angewandte Chemie</i> , 2018 , 130, 1176-1199	3.6	0
45	Curcumin supplementation increases survival and lifespan in <i>Drosophila</i> under heat stress conditions. <i>BioFactors</i> , 2018 , 44, 577-587	6.1	11
44	Incomplete lineage sorting rather than hybridization explains the inconsistent phylogeny of the wisent. <i>Communications Biology</i> , 2018 , 1, 169	6.7	40
43	Genome-scale DNA sequence data and the evolutionary history of placental mammals. <i>Data in Brief</i> , 2018 , 18, 1972-1975	1.2	7
42	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	11.5	31
41	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	11.5	78
40	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	18

39	Local admixture of amplified and diversified secreted pathogenesis determinants shapes mosaic <i>Toxoplasma gondii</i> genomes. <i>Nature Communications</i> , 2016 , 7, 10147	17.4	151
38	The Impact of Missing Data on Species Tree Estimation. <i>Molecular Biology and Evolution</i> , 2016 , 33, 838-603	6.3	82
37	Implementing and testing the multispecies coalescent model: A valuable paradigm for phylogenomics. <i>Molecular Phylogenetics and Evolution</i> , 2016 , 94, 447-62	4.1	230
36	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, 5803-12	5.7	36
35	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	4.1	69
34	Phylogenomic analyses data of the avian phylogenomics project. <i>GigaScience</i> , 2015 , 4, 4	7.6	54
33	Comment on "Statistical binning enables an accurate coalescent-based estimation of the avian tree". <i>Science</i> , 2015 , 350, 171	33.3	16
32	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	8.3	57
31	Coalescent methods for estimating species trees from phylogenomic data. <i>Journal of Systematics and Evolution</i> , 2015 , 53, 380-390	2.9	53
30	A generalized birth and death process for modeling the fates of gene duplication. <i>BMC Evolutionary Biology</i> , 2015 , 15, 275	3	5
29	Estimating phylogenetic trees from genome-scale data. <i>Annals of the New York Academy of Sciences</i> , 2015 , 1360, 36-53	6.5	122
28	Prognostic Nomogram for Thoracic Esophageal Squamous Cell Carcinoma after Radical Esophagectomy. <i>PLoS ONE</i> , 2015 , 10, e0124437	3.7	19
27	Coalescent versus concatenation methods and the placement of Amborella as sister to water lilies. <i>Systematic Biology</i> , 2014 , 63, 919-32	8.4	132
26	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	2.2	7
25	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014 , 346, 1320-31	33.3	1182
24	A phylogenetic model for understanding the effect of gene duplication on cancer progression. <i>Nucleic Acids Research</i> , 2014 , 42, 2870-8	20.1	7
23	Investigating the performance of AIC in selecting phylogenetic models. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2014 , 13, 459-75	1.2	5
22	The multispecies coalescent model and land plant origins: a reply to Springer and Gatesy. <i>Trends in Plant Science</i> , 2014 , 19, 270-2	13.1	19

21	Origin of land plants using the multispecies coalescent model. <i>Trends in Plant Science</i> , 2013 , 18, 492-5	13.1	98
20	STRAW: Species TRee Analysis Web server. <i>Nucleic Acids Research</i> , 2013 , 41, W238-41	20.1	91
19	Weighted least-squares method for right-censored data in accelerated failure time model. <i>Biometrics</i> , 2013 , 69, 358-65	1.8	2
18	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	2.2	
17	Transcriptome sequencing and annotation for the Jamaican fruit bat (<i>Artibeus jamaicensis</i>). <i>PLoS ONE</i> , 2012 , 7, e48472	3.7	53
16	Extended quasi-likelihood with fractional polynomials in the frame of the accelerated failure time model. <i>Statistics in Medicine</i> , 2012 , 31, 1369-79	2.3	3
15	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, 14942-7	11.5	328
14	Estimating species trees from unrooted gene trees. <i>Systematic Biology</i> , 2011 , 60, 661-7	8.4	184
13	A Bayesian model for gene family evolution. <i>BMC Bioinformatics</i> , 2011 , 12, 426	3.6	16
12	Phybase: an R package for species tree analysis. <i>Bioinformatics</i> , 2010 , 26, 962-3	7.2	82
11	Maximum tree: a consistent estimator of the species tree. <i>Journal of Mathematical Biology</i> , 2010 , 60, 95-106	2	51
10	A maximum pseudo-likelihood approach for estimating species trees under the coalescent model. <i>BMC Evolutionary Biology</i> , 2010 , 10, 302	3	413
9	Phylogenetic analysis in the anomaly zone. <i>Systematic Biology</i> , 2009 , 58, 452-60	8.4	88
8	Estimating species phylogenies using coalescence times among sequences. <i>Systematic Biology</i> , 2009 , 58, 468-77	8.4	342
7	Coalescent methods for estimating phylogenetic trees. <i>Molecular Phylogenetics and Evolution</i> , 2009 , 53, 320-8	4.1	279
6	Quasi-Likelihood for Right-Censored Data in the Generalized Linear Model. <i>Communications in Statistics - Theory and Methods</i> , 2009 , 38, 2187-2200	0.5	4
5	BEST: Bayesian estimation of species trees under the coalescent model. <i>Bioinformatics</i> , 2008 , 24, 2542-37.2		316
4	Estimating species trees using multiple-allele DNA sequence data. <i>Evolution; International Journal of Organic Evolution</i> , 2008 , 62, 2080-91	3.8	177

3	High-resolution species trees without concatenation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 5936-41	11.5	485
2	Species trees from gene trees: reconstructing Bayesian posterior distributions of a species phylogeny using estimated gene tree distributions. <i>Systematic Biology</i> , 2007 , 56, 504-14	8.4	379
1	Phylogeny and biogeography of Orobanchaceae. <i>Folia Geobotanica</i> , 2005 , 40, 115-134	1.4	77