

Liang Liu

List of Publications by Citations

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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	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014 , 346, 1320-31	33.3	1182
55	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
54	A maximum pseudo-likelihood approach for estimating species trees under the coalescent model. <i>BMC Evolutionary Biology</i> , 2010 , 10, 302	3	413
53	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
52	Estimating species phylogenies using coalescence times among sequences. <i>Systematic Biology</i> , 2009 , 58, 468-77	8.4	342
51	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
50	BEST: Bayesian estimation of species trees under the coalescent model. <i>Bioinformatics</i> , 2008 , 24, 2542-37.2		316
49	Coalescent methods for estimating phylogenetic trees. <i>Molecular Phylogenetics and Evolution</i> , 2009 , 53, 320-8	4.1	279
48	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
47	Estimating species trees from unrooted gene trees. <i>Systematic Biology</i> , 2011 , 60, 661-7	8.4	184
46	Estimating species trees using multiple-allele DNA sequence data. <i>Evolution; International Journal of Organic Evolution</i> , 2008 , 62, 2080-91	3.8	177
45	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
44	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
43	Estimating phylogenetic trees from genome-scale data. <i>Annals of the New York Academy of Sciences</i> , 2015 , 1360, 36-53	6.5	122
42	Origin of land plants using the multispecies coalescent model. <i>Trends in Plant Science</i> , 2013 , 18, 492-5	13.1	98
41	STRAW: Species TRee Analysis Web server. <i>Nucleic Acids Research</i> , 2013 , 41, W238-41	20.1	91
40	Phylogenetic analysis in the anomaly zone. <i>Systematic Biology</i> , 2009 , 58, 452-60	8.4	88

39	The Impact of Missing Data on Species Tree Estimation. <i>Molecular Biology and Evolution</i> , 2016 , 33, 838-603	8.3	82
38	Phybase: an R package for species tree analysis. <i>Bioinformatics</i> , 2010 , 26, 962-3	7.2	82
37	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
36	Phylogeny and biogeography of Orobanchaceae. <i>Folia Geobotanica</i> , 2005 , 40, 115-134	1.4	77
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	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
33	Phylogenomic analyses data of the avian phylogenomics project. <i>GigaScience</i> , 2015 , 4, 4	7.6	54
32	Coalescent methods for estimating species trees from phylogenomic data. <i>Journal of Systematics and Evolution</i> , 2015 , 53, 380-390	2.9	53
31	Transcriptome sequencing and annotation for the Jamaican fruit bat (<i>Artibeus jamaicensis</i>). <i>PLoS ONE</i> , 2012 , 7, e48472	3.7	53
30	Maximum tree: a consistent estimator of the species tree. <i>Journal of Mathematical Biology</i> , 2010 , 60, 95-106	2	51
29	Widespread ancient whole-genome duplications in Malpighiales coincide with Eocene global climatic upheaval. <i>New Phytologist</i> , 2019 , 221, 565-576	9.8	43
28	Incomplete lineage sorting rather than hybridization explains the inconsistent phylogeny of the wisent. <i>Communications Biology</i> , 2018 , 1, 169	6.7	40
27	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
26	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
25	Prognostic Nomogram for Thoracic Esophageal Squamous Cell Carcinoma after Radical Esophagectomy. <i>PLoS ONE</i> , 2015 , 10, e0124437	3.7	19
24	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
23	The Multispecies Coalescent Model Outperforms Concatenation Across Diverse Phylogenomic Data Sets. <i>Systematic Biology</i> , 2020 , 69, 795-812	8.4	19
22	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

21	Comment on "Statistical binning enables an accurate coalescent-based estimation of the avian tree". <i>Science</i> , 2015 , 350, 171	33.3	16
20	A Bayesian model for gene family evolution. <i>BMC Bioinformatics</i> , 2011 , 12, 426	3.6	16
19	Chemical Biology Approaches for Investigating the Functions of Lysine Acetyltransferases. <i>Angewandte Chemie - International Edition</i> , 2018 , 57, 1162-1184	16.4	16
18	Modern Phylogenomics: Building Phylogenetic Trees Using the Multispecies Coalescent Model. <i>Methods in Molecular Biology</i> , 2019 , 1910, 211-239	1.4	15
17	Curcumin supplementation increases survival and lifespan in Drosophila under heat stress conditions. <i>BioFactors</i> , 2018 , 44, 577-587	6.1	11
16	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
15	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
14	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
13	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
12	Genome-scale DNA sequence data and the evolutionary history of placental mammals. <i>Data in Brief</i> , 2018 , 18, 1972-1975	1.2	7
11	Regression multiple imputation for missing data analysis. <i>Statistical Methods in Medical Research</i> , 2020 , 29, 2647-2664	2.3	5
10	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
9	A generalized birth and death process for modeling the fates of gene duplication. <i>BMC Evolutionary Biology</i> , 2015 , 15, 275	3	5
8	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
7	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
6	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
5	Protocols for the Molecular Evolutionary Analysis of Membrane Protein Gene Duplicates. <i>Methods in Molecular Biology</i> , 2019 , 1851, 49-62	1.4	3
4	Weighted least-squares method for right-censored data in accelerated failure time model. <i>Biometrics</i> , 2013 , 69, 358-65	1.8	2

- 3 A homoscedasticity test for the accelerated failure time model. *Computational Statistics*, **2019**, 34, 433-446 1
- 2 Untersuchung der epigenetischen Funktionen von Lysin-Acetyltransferasen mit Methoden der chemischen Biologie. *Angewandte Chemie*, **2018**, 130, 1176-1199 3.6 0
- 1 Nomogram predicting long-term survival probability of thoracic esophageal squamous cell carcinoma after radical esophagectomy.. *Journal of Clinical Oncology*, **2013**, 31, 4094-4094 2.2