Yi-Chieh Wu

List of Publications by Year
in descending order

16 papers	**8,725** citations	840776 **11** h-index	996975 **15** g-index
18 all docs	**18** docs citations	**18** times ranked	**22510** citing authors

#	Article	IF	Citations
1	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	27.8	5,653
2	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	27.8	1,444
3	Extensive introgression in a malaria vector species complex revealed by phylogenomics. Science, 2015, 347, 1258524.	12.6	527
4	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. Science, 2015, 347, 1258522.	12.6	492
5	Comparative analysis of regulatory information and circuits across distant species. Nature, 2014, 512, 453-456.	27.8	184
6	TreeFix: Statistically Informed Gene Tree Error Correction Using Species Trees. Systematic Biology, 2013, 62, 110-120.	5.6	101
7	Most parsimonious reconciliation in the presence of gene duplication, loss, and deep coalescence using labeled coalescent trees. Genome Research, 2014, 24, 475-486.	5.5	69
8	Improved gene tree error correction in the presence of horizontal gene transfer. Bioinformatics, 2015, 31, 1211-1218.	4.1	64
9	Pareto-optimal phylogenetic tree reconciliation. Bioinformatics, 2014, 30, i87-i95.	4.1	59
10	eMPRess: a systematic cophylogeny reconciliation tool. Bioinformatics, 2021, 37, 2481-2482.	4.1	53
11	Evolution at the Subgene Level: Domain Rearrangements in the Drosophila Phylogeny. Molecular Biology and Evolution, 2012, 29, 689-705.	8.9	42
12	Multiple Optimal Reconciliations Under the Duplication-Loss-Coalescence Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2144-2156.	3.0	11
13	Computing the Diameter of the Space of Maximum Parsimony Reconciliations in the Duplication-Transfer-Loss Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 14-22.	3.0	9
14	Reconciliation feasibility in the presence of gene duplication, loss, and coalescence with multiple individuals per species. BMC Bioinformatics, 2017, 18, 292.	2.6	7
15	Inferring Pareto-optimal reconciliations across multiple event costs under the duplication-loss-coalescence model. BMC Bioinformatics, 2019, 20, 639.	2.6	7
16	An Integer Linear Programming Solution for the Most Parsimonious Reconciliation Problem under the Duplication-Loss-Coalescence Model. , 2020, , .		0