

# Yi-Chieh Wu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7079200/publications.pdf>

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