

# Melissa J Hubisz

## List of Publications by Citations

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**Version:** 2024-04-10

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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.

17 papers	5,338 citations	13 h-index	17 g-index
17 ext. papers	6,624 ext. citations	16.4 avg, IF	5.77 L-index

#	Paper	IF	Citations
17	Inferring weak population structure with the assistance of sample group information. <i>Molecular Ecology Resources</i> , <b>2009</b> , 9, 1322-32	8.4	2406
16	Detection of nonneutral substitution rates on mammalian phylogenies. <i>Genome Research</i> , <b>2010</b> , 20, 110-17	9.7	1338
15	Bayesian inference of ancient human demography from individual genome sequences. <i>Nature Genetics</i> , <b>2011</b> , 43, 1031-4	36.3	387
14	Ancient gene flow from early modern humans into Eastern Neanderthals. <i>Nature</i> , <b>2016</b> , 530, 429-33	50.4	269
13	PHAST and RPHAST: phylogenetic analysis with space/time models. <i>Briefings in Bioinformatics</i> , <b>2011</b> , 12, 41-51	13.4	240
12	Genome-wide inference of ancestral recombination graphs. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004342	6	200
11	A method for calculating probabilities of fitness consequences for point mutations across the human genome. <i>Nature Genetics</i> , <b>2015</b> , 47, 276-83	36.3	175
10	SweepFinder2: increased sensitivity, robustness and flexibility. <i>Bioinformatics</i> , <b>2016</b> , 32, 1895-7	7.2	122
9	Exploring the genesis and functions of Human Accelerated Regions sheds light on their role in human evolution. <i>Current Opinion in Genetics and Development</i> , <b>2014</b> , 29, 15-21	4.9	57
8	Parallel evolution of ancient, pleiotropic enhancers underlies butterfly wing pattern mimicry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 24174-24183	11.5	53
7	Error and error mitigation in low-coverage genome assemblies. <i>PLoS ONE</i> , <b>2011</b> , 6, e17034	3.7	29
6	Mapping gene flow between ancient hominins through demography-aware inference of the ancestral recombination graph. <i>PLoS Genetics</i> , <b>2020</b> , 16, e1008895	6	27
5	Evolutionary genomics: detecting selection needs comparative data. <i>Nature</i> , <b>2005</b> , 433, E6; discussion E7-8	50.4	16
4	Genomic islands of differentiation in a rapid avian radiation have been driven by recent selective sweeps. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 30554-30563	11.5	28
3	Inference of Ancestral Recombination Graphs Using ARGweaver. <i>Methods in Molecular Biology</i> , <b>2020</b> , 2090, 231-266	1.4	6
2	Probabilities of Fitness Consequences for Point Mutations Across the Human Genome		2
1	Mapping gene flow between ancient hominins through demography-aware inference of the ancestral recombination graph		2

