Melissa J Hubisz

List of Publications by Year in
Descending Order

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	Genomic islands of differentiation in a rapid avian radiation have been driven by recent selective sweeps. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 30554-30565	11.5	9
16	Mapping gene flow between ancient hominins through demography-aware inference of the ancestral recombination graph. *PLoS Genetics*, **2020**, 16, e1008895	6	27
15	Inference of Ancestral Recombination Graphs Using ARGweaver. *Methods in Molecular Biology*, **2020**, 2090, 231-266	1.4	6
14	Parallel evolution of ancient, pleiotropic enhancers underlies butterfly wing pattern mimicry. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 24174-24183	11.5	53
13	Ancient gene flow from early modern humans into Eastern Neanderthals. *Nature*, **2016**, 530, 429-33	50.4	269
12	SweepFinder2: increased sensitivity, robustness and flexibility. *Bioinformatics*, **2016**, 32, 1895-7	7.2	122
11	A method for calculating probabilities of fitness consequences for point mutations across the human genome. *Nature Genetics*, **2015**, 47, 276-83	36.3	175
10	Exploring the genesis and functions of Human Accelerated Regions sheds light on their role in human evolution. *Current Opinion in Genetics and Development*, **2014**, 29, 15-21	4.9	57
9	Genome-wide inference of ancestral recombination graphs. *PLoS Genetics*, **2014**, 10, e1004342	6	200
8	Bayesian inference of ancient human demography from individual genome sequences. *Nature Genetics*, **2011**, 43, 1031-4	36.3	387
7	Error and error mitigation in low-coverage genome assemblies. *PLoS ONE*, **2011**, 6, e17034	3.7	29
6	PHAST and RPHAST: phylogenetic analysis with space/time models. *Briefings in Bioinformatics*, **2011**, 12, 41-51	13.4	240
5	Detection of nonneutral substitution rates on mammalian phylogenies. *Genome Research*, **2010**, 20, 110-21	9.1	1338
4	Inferring weak population structure with the assistance of sample group information. *Molecular Ecology Resources*, **2009**, 9, 1322-32	8.4	2406
3	Evolutionary genomics: detecting selection needs comparative data. *Nature*, **2005**, 433, E6; discussion E7-8	50.4	16
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

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