Melissa J Hubisz

List of Publications by Year
in descending order

15 papers	7,338 citations	623734 14 h-index	996975 15 g-index
17 all docs	17 docs citations	17 times ranked	15893 citing authors

#	Article	IF	Citations
1	Inferring weak population structure with the assistance of sample group information. Molecular Ecology Resources, 2009, 9, 1322-1332.	4.8	2,931
2	Detection of nonneutral substitution rates on mammalian phylogenies. Genome Research, 2010, 20, 110-121.	5.5	1,878
3	Bayesian inference of ancient human demography from individual genome sequences. Nature Genetics, 2011, 43, 1031-1034.	21.4	526
4	PHAST and RPHAST: phylogenetic analysis with space/time models. Briefings in Bioinformatics, 2011, 12, 41-51.	6.5	396
5	Ancient gene flow from early modern humans into Eastern Neanderthals. Nature, 2016, 530, 429-433.	27.8	392
6	Genome-Wide Inference of Ancestral Recombination Graphs. PLoS Genetics, 2014, 10, e1004342.	3.5	323
7	A method for calculating probabilities of fitness consequences for point mutations across the human genome. Nature Genetics, 2015, 47, 276-283.	21.4	247
8	SweepFinder2: increased sensitivity, robustness and flexibility. Bioinformatics, 2016, 32, 1895-1897.	4.1	238
9	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.	3.3	108
10	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.	7.1	102
11	Mapping gene flow between ancient hominins through demography-aware inference of the ancestral recombination graph. PLoS Genetics, 2020, 16, e1008895.	3.5	76
12	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.	7.1	40
13	Error and Error Mitigation in Low-Coverage Genome Assemblies. PLoS ONE, 2011, 6, e17034.	2.5	33
14	Inference of Ancestral Recombination Graphs Using ARGweaver. Methods in Molecular Biology, 2020, 2090, 231-266.	0.9	27
15	Detecting selection needs comparative data. Nature, 2005, 433, E6-E6.	27.8	17