

Simon Myers

List of Publications by Citations

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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.

32
papers

12,440
citations

25
h-index

33
g-index

33
ext. papers

14,411
ext. citations

21.5
avg, IF

5.6
L-index

#	Paper	IF	Citations
32	A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , 2007 , 449, 851-61	50.4	3647
31	A new multipoint method for genome-wide association studies by imputation of genotypes. <i>Nature Genetics</i> , 2007 , 39, 906-13	36.3	2040
30	Genome-wide detection and characterization of positive selection in human populations. <i>Nature</i> , 2007 , 449, 913-8	50.4	1367
29	A fine-scale map of recombination rates and hotspots across the human genome. <i>Science</i> , 2005 , 310, 321-4	33.3	836
28	Inference of population structure using dense haplotype data. <i>PLoS Genetics</i> , 2012 , 8, e1002453	6	660
27	Great ape genetic diversity and population history. <i>Nature</i> , 2013 , 499, 471-5	50.4	574
26	A genetic atlas of human admixture history. <i>Science</i> , 2014 , 343, 747-751	33.3	492
25	Drive against hotspot motifs in primates implicates the PRDM9 gene in meiotic recombination. <i>Science</i> , 2010 , 327, 876-9	33.3	465
24	Sensitive detection of chromosomal segments of distinct ancestry in admixed populations. <i>PLoS Genetics</i> , 2009 , 5, e1000519	6	393
23	A common sequence motif associated with recombination hot spots and genome instability in humans. <i>Nature Genetics</i> , 2008 , 40, 1124-9	36.3	335
22	The fine-scale genetic structure of the British population. <i>Nature</i> , 2015 , 519, 309-314	50.4	298
21	A fine-scale chimpanzee genetic map from population sequencing. <i>Science</i> , 2012 , 336, 193-8	33.3	218
20	The influence of recombination on human genetic diversity. <i>PLoS Genetics</i> , 2006 , 2, e148	6	185
19	Human recombination hot spots hidden in regions of strong marker association. <i>Nature Genetics</i> , 2005 , 37, 601-6	36.3	146
18	Evidence for a Common Origin of Blacksmiths and Cultivators in the Ethiopian Ari within the Last 4500 Years: Lessons for Clustering-Based Inference. <i>PLoS Genetics</i> , 2015 , 11, e1005397	6	104
17	Enhanced statistical tests for GWAS in admixed populations: assessment using African Americans from CARE and a Breast Cancer Consortium. <i>PLoS Genetics</i> , 2011 , 7, e1001371	6	86
16	Rapid genotype imputation from sequence without reference panels. <i>Nature Genetics</i> , 2016 , 48, 965-969	36.3	79

15	Unravelling the hidden ancestry of American admixed populations. <i>Nature Communications</i> , 2015 , 6, 6596-67.4	78
14	Effects of cis and trans genetic ancestry on gene expression in African Americans. <i>PLoS Genetics</i> , 2008 , 4, e1000294	6 75
13	Genome-wide comparison of African-ancestry populations from CARE and other cohorts reveals signals of natural selection. <i>American Journal of Human Genetics</i> , 2011 , 89, 368-81	11 63
12	Application of coalescent methods to reveal fine-scale rate variation and recombination hotspots. <i>Genetics</i> , 2004 , 167, 2067-81	4 58
11	Extreme selective sweeps independently targeted the X chromosomes of the great apes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 6413-8	11.5 52
10	Genomic tools for evolution and conservation in the chimpanzee: <i>Pan troglodytes ellioti</i> is a genetically distinct population. <i>PLoS Genetics</i> , 2012 , 8, e1002504	6 45
9	The Role of Recent Admixture in Forming the Contemporary West Eurasian Genomic Landscape. <i>Current Biology</i> , 2015 , 25, 2518-26	6.3 42
8	Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula. <i>Nature Communications</i> , 2019 , 10, 551	17.4 34
7	Fine-Scale Inference of Ancestry Segments Without Prior Knowledge of Admixing Groups. <i>Genetics</i> , 2019 , 212, 869-889	4 24
6	A model-based approach to capture genetic variation for future association studies. <i>Genome Research</i> , 2007 , 17, 88-95	9.7 9
5	Rapid genotype imputation from sequence with reference panels. <i>Nature Genetics</i> , 2021 , 53, 1104-1111	36.3 6
4	The Kalash Genetic Isolate? The Evidence for Recent Admixture. <i>American Journal of Human Genetics</i> , 2016 , 98, 396-7	11 5
3	Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula	4
2	Fine-scale Inference of Ancestry Segments without Prior Knowledge of Admixing Groups	2
1	Altering the Binding Properties of PRDM9 Partially Restores Fertility across the Species Boundary. <i>Molecular Biology and Evolution</i> , 2021 , 38, 5555-5562	8.3 0