

Simon R 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.

68

papers

35,952

citations

47

h-index

76

g-index

76

ext. papers

40,868

ext. citations

22.8

avg, IF

7.28

L-index

#	Paper	IF	Citations
68	A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010 , 467, 1061-73	50.4	6142
67	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012 , 491, 56-65	50.4	6049
66	The International HapMap Project. <i>Nature</i> , 2003 , 426, 789-96	50.4	5039
65	A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , 2007 , 449, 851-61	50.4	3647
64	A new multipoint method for genome-wide association studies by imputation of genotypes. <i>Nature Genetics</i> , 2007 , 39, 906-13	36.3	2040
63	Genome-wide detection and characterization of positive selection in human populations. <i>Nature</i> , 2007 , 449, 913-8	50.4	1367
62	A fine-scale map of recombination rates and hotspots across the human genome. <i>Science</i> , 2005 , 310, 321-4	33.3	836
61	Mapping copy number variation by population-scale genome sequencing. <i>Nature</i> , 2011 , 470, 59-65	50.4	833
60	The fine-scale structure of recombination rate variation in the human genome. <i>Science</i> , 2004 , 304, 581-433.3	33.3	796
59	Inference of population structure using dense haplotype data. <i>PLoS Genetics</i> , 2012 , 8, e1002453	6	660
58	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. <i>Nature</i> , 2010 , 464, 713-20	50.4	639
57	Great ape genetic diversity and population history. <i>Nature</i> , 2013 , 499, 471-5	50.4	574
56	Multiple regions within 8q24 independently affect risk for prostate cancer. <i>Nature Genetics</i> , 2007 , 39, 638-44	36.3	563
55	A genetic atlas of human admixture history. <i>Science</i> , 2014 , 343, 747-751	33.3	492
54	Diversity of human copy number variation and multicopy genes. <i>Science</i> , 2010 , 330, 641-6	33.3	491
53	Drive against hotspot motifs in primates implicates the PRDM9 gene in meiotic recombination. <i>Science</i> , 2010 , 327, 876-9	33.3	465
52	Demographic history and rare allele sharing among human populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 11983-8	11.5	455

51	Sensitive detection of chromosomal segments of distinct ancestry in admixed populations. <i>PLoS Genetics</i> , 2009 , 5, e1000519	6	393
50	Bayesian refinement of association signals for 14 loci in 3 common diseases. <i>Nature Genetics</i> , 2012 , 44, 1294-301	36.3	347
49	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
48	The fine-scale genetic structure of the British population. <i>Nature</i> , 2015 , 519, 309-314	50.4	298
47	Comparison of fine-scale recombination rates in humans and chimpanzees. <i>Science</i> , 2005 , 308, 107-11	33.3	291
46	Integrative annotation of variants from 1092 humans: application to cancer genomics. <i>Science</i> , 2013 , 342, 1235-587	33.3	281
45	Long-range LD can confound genome scans in admixed populations. <i>American Journal of Human Genetics</i> , 2008 , 83, 132-5; author reply 135-9	11	253
44	The landscape of recombination in African Americans. <i>Nature</i> , 2011 , 476, 170-5	50.4	243
43	A fine-scale chimpanzee genetic map from population sequencing. <i>Science</i> , 2012 , 336, 193-8	33.3	218
42	The influence of recombination on human genetic diversity. <i>PLoS Genetics</i> , 2006 , 2, e148	6	185
41	Human recombination hot spots hidden in regions of strong marker association. <i>Nature Genetics</i> , 2005 , 37, 601-6	36.3	146
40	Bounds on the minimum number of recombination events in a sample history. <i>Genetics</i> , 2003 , 163, 375-94		142
39	A method for genome-wide genealogy estimation for thousands of samples. <i>Nature Genetics</i> , 2019 , 51, 1321-1329	36.3	136
38	Re-engineering the zinc fingers of PRDM9 reverses hybrid sterility in mice. <i>Nature</i> , 2016 , 530, 171-176	50.4	135
37	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
36	Live hot, die young: transmission distortion in recombination hotspots. <i>PLoS Genetics</i> , 2007 , 3, e35	6	89
35	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
34	The distribution and causes of meiotic recombination in the human genome. <i>Biochemical Society Transactions</i> , 2006 , 34, 526-30	5.1	84

33	Can one learn history from the allelic spectrum?. <i>Theoretical Population Biology</i> , 2008 , 73, 342-8	1.2	80
32	Rapid genotype imputation from sequence without reference panels. <i>Nature Genetics</i> , 2016 , 48, 965-969	6.3	79
31	Unravelling the hidden ancestry of American admixed populations. <i>Nature Communications</i> , 2015 , 6, 6596	7.4	78
30	Effects of cis and trans genetic ancestry on gene expression in African Americans. <i>PLoS Genetics</i> , 2008 , 4, e1000294	6	75
29	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
28	Application of coalescent methods to reveal fine-scale rate variation and recombination hotspots. <i>Genetics</i> , 2004 , 167, 2067-81	4	58
27	Non-crossover gene conversions show strong GC bias and unexpected clustering in humans. <i>ELife</i> , 2015 , 4,	8.9	57
26	Unified single-cell analysis of testis gene regulation and pathology in five mouse strains. <i>ELife</i> , 2019 , 8,	8.9	54
25	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
24	Human genomic regions with exceptionally high levels of population differentiation identified from 911 whole-genome sequences. <i>Genome Biology</i> , 2014 , 15, R88	18.3	51
23	A map of human PRDM9 binding provides evidence for novel behaviors of PRDM9 and other zinc-finger proteins in meiosis. <i>ELife</i> , 2017 , 6,	8.9	47
22	Recombination in the human Pseudoautosomal region PAR1. <i>PLoS Genetics</i> , 2014 , 10, e1004503	6	47
21	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
20	Estimating meiotic gene conversion rates from population genetic data. <i>Genetics</i> , 2007 , 177, 881-94	4	45
19	The Role of Recent Admixture in Forming the Contemporary West Eurasian Genomic Landscape. <i>Current Biology</i> , 2015 , 25, 2518-26	6.3	42
18	A high-resolution map of non-crossover events reveals impacts of genetic diversity on mammalian meiotic recombination. <i>Nature Communications</i> , 2019 , 10, 3900	17.4	35
17	Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula. <i>Nature Communications</i> , 2019 , 10, 551	17.4	34
16	Fine-Scale Inference of Ancestry Segments Without Prior Knowledge of Admixing Groups. <i>Genetics</i> , 2019 , 212, 869-889	4	24

15	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. <i>American Journal of Human Genetics</i> , 2016 , 98, 857-868	11	14
14	ZCWPW1 is recruited to recombination hotspots by PRDM9 and is essential for meiotic double strand break repair. <i>ELife</i> , 2020 , 9,	8.9	10
13	A method for genome-wide genealogy estimation for thousands of samples		10
12	Inferring Population Histories for Ancient Genomes Using Genome-Wide Genealogies. <i>Molecular Biology and Evolution</i> , 2021 , 38, 3497-3511	8.3	10
11	A model-based approach to capture genetic variation for future association studies. <i>Genome Research</i> , 2007 , 17, 88-95	9.7	9
10	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. <i>Nature Genetics</i> , 2022 ,	36.3	7
9	Rapid genotype imputation from sequence with reference panels. <i>Nature Genetics</i> , 2021 , 53, 1104-1111	36.3	6
8	The Kalash Genetic Isolate? The Evidence for Recent Admixture. <i>American Journal of Human Genetics</i> , 2016 , 98, 396-7	11	5
7	A high-resolution map of non-crossover events reveals impacts of genetic diversity on mammalian meiotic recombination		5
6	Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula		4
5	Unified single-cell analysis of testis gene regulation and pathology in 5 mouse strains		4
4	ZCWPW1 is recruited to recombination hotspots by PRDM9, and is essential for meiotic double strand break repair		3
3	Inferring population histories for ancient genomes using genome-wide genealogies		3
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