Simon R Myers

List of Publications by Year in Descending Order

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	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. *Nature Genetics*, **2022**,	36.3	7
67	Inferring Population Histories for Ancient Genomes Using Genome-Wide Genealogies. *Molecular Biology and Evolution*, **2021**, 38, 3497-3511	8.3	10
66	Rapid genotype imputation from sequence with reference panels. *Nature Genetics*, **2021**, 53, 1104-1111	36.3	6
65	Altering the Binding Properties of PRDM9 Partially Restores Fertility across the Species Boundary. *Molecular Biology and Evolution*, **2021**, 38, 5555-5562	8.3	0
64	ZCWPW1 is recruited to recombination hotspots by PRDM9 and is essential for meiotic double strand break repair. *ELife*, **2020**, 9,	8.9	10
63	Unified single-cell analysis of testis gene regulation and pathology in five mouse strains. *ELife*, **2019**, 8,	8.9	54
62	A method for genome-wide genealogy estimation for thousands of samples. *Nature Genetics*, **2019**, 51, 1321-1329	36.3	136
61	A high-resolution map of non-crossover events reveals impacts of genetic diversity on mammalian meiotic recombination. *Nature Communications*, **2019**, 10, 3900	17.4	35
60	Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula. *Nature Communications*, **2019**, 10, 551	17.4	34
59	Fine-Scale Inference of Ancestry Segments Without Prior Knowledge of Admixing Groups. *Genetics*, **2019**, 212, 869-889	4	24
58	A map of human PRDM9 binding provides evidence for novel behaviors of PRDM9 and other zinc-finger proteins in meiosis. *ELife*, **2017**, 6,	8.9	47
57	The Kalash Genetic Isolate? The Evidence for Recent Admixture. *American Journal of Human Genetics*, **2016**, 98, 396-7	11	5
56	Re-engineering the zinc fingers of PRDM9 reverses hybrid sterility in mice. *Nature*, **2016**, 530, 171-176	50.4	135
55	Rapid genotype imputation from sequence without reference panels. *Nature Genetics*, **2016**, 48, 965-969	36.3	79
54	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. *American Journal of Human Genetics*, **2016**, 98, 857-868	11	14
53	The fine-scale genetic structure of the British population. *Nature*, **2015**, 519, 309-314	50.4	298
52	Unravelling the hidden ancestry of American admixed populations. *Nature Communications*, **2015**, 6, 6596	17.4	78

51	The Role of Recent Admixture in Forming the Contemporary West Eurasian Genomic Landscape. *Current Biology*, **2015**, 25, 2518-26	6.3	42
50	Evidence for a Common Origin of Blacksmiths and Cultivators in the Ethiopian Ari within the Last 4500 Years: Lessons for Clustering-Based Inference. *PLoS Genetics*, **2015**, 11, e1005397	6	104
49	Extreme selective sweeps independently targeted the X chromosomes of the great apes. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 6413-8	11.5	52
48	Non-crossover gene conversions show strong GC bias and unexpected clustering in humans. *ELife*, **2015**, 4,	8.9	57
47	A genetic atlas of human admixture history. *Science*, **2014**, 343, 747-751	33.3	492
46	Human genomic regions with exceptionally high levels of population differentiation identified from 911 whole-genome sequences. *Genome Biology*, **2014**, 15, R88	18.3	51
45	Recombination in the human Pseudoautosomal region PAR1. *PLoS Genetics*, **2014**, 10, e1004503	6	47
44	Integrative annotation of variants from 1092 humans: application to cancer genomics. *Science*, **2013**, 342, 1235587	33.3	281
43	Great ape genetic diversity and population history. *Nature*, **2013**, 499, 471-5	50.4	574
42	A fine-scale chimpanzee genetic map from population sequencing. *Science*, **2012**, 336, 193-8	33.3	218
41	An integrated map of genetic variation from 1,092 human genomes. *Nature*, **2012**, 491, 56-65	50.4	6049
40	Genomic tools for evolution and conservation in the chimpanzee: Pan troglodytes ellioti is a genetically distinct population. *PLoS Genetics*, **2012**, 8, e1002504	6	45
39	Inference of population structure using dense haplotype data. *PLoS Genetics*, **2012**, 8, e1002453	6	660
38	Bayesian refinement of association signals for 14 loci in 3 common diseases. *Nature Genetics*, **2012**, 44, 1294-301	36.3	347
37	Mapping copy number variation by population-scale genome sequencing. *Nature*, **2011**, 470, 59-65	50.4	833
36	Genome-wide comparison of African-ancestry populations from CARe and other cohorts reveals signals of natural selection. *American Journal of Human Genetics*, **2011**, 89, 368-81	11	63
35	Demographic history and rare allele sharing among human populations. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 11983-8	11.5	455
34	The landscape of recombination in African Americans. *Nature*, **2011**, 476, 170-5	50.4	243

33	Enhanced statistical tests for GWAS in admixed populations: assessment using African Americans from CARe and a Breast Cancer Consortium. *PLoS Genetics*, **2011**, 7, e1001371	6	86
32	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. *Nature*, **2010**, 464, 713-20	50.4	639
31	A map of human genome variation from population-scale sequencing. *Nature*, **2010**, 467, 1061-73	50.4	6142
30	Drive against hotspot motifs in primates implicates the PRDM9 gene in meiotic recombination. *Science*, **2010**, 327, 876-9	33.3	465
29	Diversity of human copy number variation and multicopy genes. *Science*, **2010**, 330, 641-6	33.3	491
28	Sensitive detection of chromosomal segments of distinct ancestry in admixed populations. *PLoS Genetics*, **2009**, 5, e1000519	6	393
27	A common sequence motif associated with recombination hot spots and genome instability in humans. *Nature Genetics*, **2008**, 40, 1124-9	36.3	335
26	Can one learn history from the allelic spectrum?. *Theoretical Population Biology*, **2008**, 73, 342-8	1.2	80
25	Effects of cis and trans genetic ancestry on gene expression in African Americans. *PLoS Genetics*, **2008**, 4, e1000294	6	75
24	Long-range LD can confound genome scans in admixed populations. *American Journal of Human Genetics*, **2008**, 83, 132-5; author reply 135-9	11	253
23	Multiple regions within 8q24 independently affect risk for prostate cancer. *Nature Genetics*, **2007**, 39, 638-44	36.3	563
22	A new multipoint method for genome-wide association studies by imputation of genotypes. *Nature Genetics*, **2007**, 39, 906-13	36.3	2040
21	Genome-wide detection and characterization of positive selection in human populations. *Nature*, **2007**, 449, 913-8	50.4	1367
20	A second generation human haplotype map of over 3.1 million SNPs. *Nature*, **2007**, 449, 851-61	50.4	3647
19	A model-based approach to capture genetic variation for future association studies. *Genome Research*, **2007**, 17, 88-95	9.7	9
18	Live hot, die young: transmission distortion in recombination hotspots. *PLoS Genetics*, **2007**, 3, e35	6	89
17	Estimating meiotic gene conversion rates from population genetic data. *Genetics*, **2007**, 177, 881-94	4	45
16	The influence of recombination on human genetic diversity. *PLoS Genetics*, **2006**, 2, e148	6	185

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15	The distribution and causes of meiotic recombination in the human genome. *Biochemical Society Transactions*, **2006**, 34, 526-30	5.1	84
14	A fine-scale map of recombination rates and hotspots across the human genome. *Science*, **2005**, 310, 321-4	33.3	836
13	Human recombination hot spots hidden in regions of strong marker association. *Nature Genetics*, **2005**, 37, 601-6	36.3	146
12	Comparison of fine-scale recombination rates in humans and chimpanzees. *Science*, **2005**, 308, 107-11	33.3	291
11	Application of coalescent methods to reveal fine-scale rate variation and recombination hotspots. *Genetics*, **2004**, 167, 2067-81	4	58
10	The fine-scale structure of recombination rate variation in the human genome. *Science*, **2004**, 304, 581-4	33.3	796
9	The International HapMap Project. *Nature*, **2003**, 426, 789-96	50.4	5039
8	Bounds on the minimum number of recombination events in a sample history. *Genetics*, **2003**, 163, 375-94	4	142
7	ZCWPW1 is recruited to recombination hotspots by PRDM9, and is essential for meiotic double strand break repair		3
6	Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula		4
5	Fine-scale Inference of Ancestry Segments without Prior Knowledge of Admixing Groups		2
4	Unified single-cell analysis of testis gene regulation and pathology in 5 mouse strains		4
3	A high-resolution map of non-crossover events reveals impacts of genetic diversity on mammalian meiotic recombination		5
2	A method for genome-wide genealogy estimation for thousands of samples		10
1	Inferring population histories for ancient genomes using genome-wide genealogies		3