Simon R Myers

List of Publications by Year
in descending order

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63 papers	43,984 citations	41258 49 h-index	110170 64 g-index
76 all docs	76 docs citations	76 times ranked	53359 citing authors

#	Article	IF	Citations
1	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250
2	Inferring Population Histories for Ancient Genomes Using Genome-Wide Genealogies. Molecular Biology and Evolution, 2021, 38, 3497-3511.	3.5	33
3	Rapid genotype imputation from sequence with reference panels. Nature Genetics, 2021, 53, 1104-1111.	9.4	47
4	Altering the Binding Properties of PRDM9 Partially Restores Fertility across the Species Boundary. Molecular Biology and Evolution, 2021, 38, 5555-5562.	3.5	9
5	ZCWPW1 is recruited to recombination hotspots by PRDM9 and is essential for meiotic double strand break repair. ELife, 2020, 9, .	2.8	31
6	Unified single-cell analysis of testis gene regulation and pathology in five mouse strains. ELife, 2019, 8, .	2.8	102
7	A method for genome-wide genealogy estimation for thousands of samples. Nature Genetics, 2019, 51, 1321-1329.	9.4	338
8	A high-resolution map of non-crossover events reveals impacts of genetic diversity on mammalian meiotic recombination. Nature Communications, 2019, 10, 3900.	5.8	66
9	Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula. Nature Communications, 2019, 10, 551.	5.8	63
10	Fine-Scale Inference of Ancestry Segments Without Prior Knowledge of Admixing Groups. Genetics, 2019, 212, 869-889.	1.2	54
11	A map of human PRDM9 binding provides evidence for novel behaviors of PRDM9 and other zinc-finger proteins in meiosis. ELife, 2017, 6, .	2.8	80
12	Rapid genotype imputation from sequence without reference panels. Nature Genetics, 2016, 48, 965-969.	9.4	172
13	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. American Journal of Human Genetics, 2016, 98, 857-868.	2.6	21
14	The Kalash Genetic Isolate? The Evidence for Recent Admixture. American Journal of Human Genetics, 2016, 98, 396-397.	2.6	6
15	Re-engineering the zinc fingers of PRDM9 reverses hybrid sterility in mice. Nature, 2016, 530, 171-176.	13.7	194
16	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.	1.5	194
17	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, 6413-6418.	3.3	75
18	The fine-scale genetic structure of the British population. Nature, 2015, 519, 309-314.	13.7	416

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19	Unravelling the hidden ancestry of American admixed populations. Nature Communications, 2015, 6, 6596.	5.8	110
20	The Role of Recent Admixture in Forming the Contemporary West Eurasian Genomic Landscape. Current Biology, 2015, 25, 2518-2526.	1.8	68
21	Non-crossover gene conversions show strong GC bias and unexpected clustering in humans. ELife, 2015, 4, .	2.8	95
22	Recombination in the Human Pseudoautosomal Region PAR1. PLoS Genetics, 2014, 10, e1004503.	1.5	66
23	A Genetic Atlas of Human Admixture History. Science, 2014, 343, 747-751.	6.0	691
24	Human genomic regions with exceptionally high levels of population differentiation identified from 911 whole-genome sequences. Genome Biology, 2014, 15, R88.	13.9	72
25	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	6.0	341
26	Great ape genetic diversity and population history. Nature, 2013, 499, 471-475.	13.7	768
27	Genomic Tools for Evolution and Conservation in the Chimpanzee: Pan troglodytes ellioti Is a Genetically Distinct Population. PLoS Genetics, 2012, 8, e1002504.	1.5	53
28	Inference of Population Structure using Dense Haplotype Data. PLoS Genetics, 2012, 8, e1002453.	1.5	983
29	Bayesian refinement of association signals for 14 loci in 3 common diseases. Nature Genetics, 2012, 44, 1294-1301.	9.4	469
30	A Fine-Scale Chimpanzee Genetic Map from Population Sequencing. Science, 2012, 336, 193-198.	6.0	273
31	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
32	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	13.7	991
33	Genome-wide Comparison of African-Ancestry Populations from CARe and Other Cohorts Reveals Signals of Natural Selection. American Journal of Human Genetics, 2011, 89, 368-381.	2.6	79
34	Demographic history and rare allele sharing among human populations. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11983-11988.	3.3	589
35	The landscape of recombination in African Americans. Nature, 2011, 476, 170-175.	13.7	319
36	Enhanced Statistical Tests for GWAS in Admixed Populations: Assessment using African Americans from CARe and a Breast Cancer Consortium. PLoS Genetics, 2011, 7, e1001371.	1.5	110

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37	Diversity of Human Copy Number Variation and Multicopy Genes. Science, 2010, 330, 641-646.	6.0	609
38	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. Nature, 2010, 464, 713-720.	13.7	737
39	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	13.7	7,209
40	PRDM9 marks the spot. Nature Genetics, 2010, 42, 821-822.	9.4	20
41	Drive Against Hotspot Motifs in Primates Implicates the PRDM9 Gene in Meiotic Recombination. Science, 2010, 327, 876-879.	6.0	607
42	Sensitive Detection of Chromosomal Segments of Distinct Ancestry in Admixed Populations. PLoS Genetics, 2009, 5, e1000519.	1.5	475
43	Long-Range LD Can Confound Genome Scans in Admixed Populations. American Journal of Human Genetics, 2008, 83, 132-135.	2.6	366
44	A common sequence motif associated with recombination hot spots and genome instability in humans. Nature Genetics, 2008, 40, 1124-1129.	9.4	395
45	Can one learn history from the allelic spectrum?. Theoretical Population Biology, 2008, 73, 342-348.	0.5	113
46	Effects of cis and trans Genetic Ancestry on Gene Expression in African Americans. PLoS Genetics, 2008, 4, e1000294.	1.5	91
47	Live Hot, Die Young: Transmission Distortion in Recombination Hotspots. PLoS Genetics, 2007, 3, e35.	1.5	108
48	Estimating Meiotic Gene Conversion Rates From Population Genetic Data. Genetics, 2007, 177, 881-894.	1.2	62
49	Multiple regions within 8q24 independently affect risk for prostate cancer. Nature Genetics, 2007, 39, 638-644.	9.4	621
50	A new multipoint method for genome-wide association studies by imputation of genotypes. Nature Genetics, 2007, 39, 906-913.	9.4	2,407
51	Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918.	13.7	1,788
52	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	13.7	4,137
53	The distribution and causes of meiotic recombination in the human genome. Biochemical Society Transactions, 2006, 34, 526-530.	1.6	106
54	New insights into the biological basis of genomic disorders. Nature Genetics, 2006, 38, 1363-1364.	9.4	12

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55	The Influence of Recombination on Human Genetic Diversity. PLoS Genetics, 2006, 2, e148.	1.5	231
56	A model-based approach to capture genetic variation for future association studies. Genome Research, 2006, 17, 88-95.	2.4	10
57	Human recombination hot spots hidden in regions of strong marker association. Nature Genetics, 2005, 37, 601-606.	9.4	159
58	Comparison of Fine-Scale Recombination Rates in Humans and Chimpanzees. Science, 2005, 308, 107-111.	6.0	335
59	A Fine-Scale Map of Recombination Rates and Hotspots Across the Human Genome. Science, 2005, 310, 321-324.	6.0	989
60	Application of Coalescent Methods to Reveal Fine-Scale Rate Variation and Recombination Hotspots. Genetics, 2004, 167, 2067-2081.	1.2	62
61	The Fine-Scale Structure of Recombination Rate Variation in the Human Genome. Science, 2004, 304, 581-584.	6.0	941
62	The International HapMap Project. Nature, 2003, 426, 789-796.	13.7	5,735
63	Bounds on the Minimum Number of Recombination Events in a Sample History. Genetics, 2003, 163, 375-394.	1.2	163