

# Simon Myers

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11579086/publications.pdf>

Version: 2024-02-01

31  
papers

15,550  
citations

201385

27  
h-index

433756

31  
g-index

33  
all docs

33  
docs citations

33  
times ranked

24556  
citing authors

#	ARTICLE	IF	CITATIONS
1	A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , 2007, 449, 851-861.	13.7	4,137
2	A new multipoint method for genome-wide association studies by imputation of genotypes. <i>Nature Genetics</i> , 2007, 39, 906-913.	9.4	2,407
3	Genome-wide detection and characterization of positive selection in human populations. <i>Nature</i> , 2007, 449, 913-918.	13.7	1,788
4	A Fine-Scale Map of Recombination Rates and Hotspots Across the Human Genome. <i>Science</i> , 2005, 310, 321-324.	6.0	989
5	Inference of Population Structure using Dense Haplotype Data. <i>PLoS Genetics</i> , 2012, 8, e1002453.	1.5	983
6	Great ape genetic diversity and population history. <i>Nature</i> , 2013, 499, 471-475.	13.7	768
7	A Genetic Atlas of Human Admixture History. <i>Science</i> , 2014, 343, 747-751.	6.0	691
8	Drive Against Hotspot Motifs in Primates Implicates the <i>PRDM9</i> Gene in Meiotic Recombination. <i>Science</i> , 2010, 327, 876-879.	6.0	607
9	Sensitive Detection of Chromosomal Segments of Distinct Ancestry in Admixed Populations. <i>PLoS Genetics</i> , 2009, 5, e1000519.	1.5	475
10	The fine-scale genetic structure of the British population. <i>Nature</i> , 2015, 519, 309-314.	13.7	416
11	A common sequence motif associated with recombination hot spots and genome instability in humans. <i>Nature Genetics</i> , 2008, 40, 1124-1129.	9.4	395
12	A Fine-Scale Chimpanzee Genetic Map from Population Sequencing. <i>Science</i> , 2012, 336, 193-198.	6.0	273
13	The Influence of Recombination on Human Genetic Diversity. <i>PLoS Genetics</i> , 2006, 2, e148.	1.5	231
14	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.	1.5	194
15	Rapid genotype imputation from sequence without reference panels. <i>Nature Genetics</i> , 2016, 48, 965-969.	9.4	172
16	Human recombination hot spots hidden in regions of strong marker association. <i>Nature Genetics</i> , 2005, 37, 601-606.	9.4	159
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.	1.5	110
18	Unravelling the hidden ancestry of American admixed populations. <i>Nature Communications</i> , 2015, 6, 6596.	5.8	110

#	ARTICLE	IF	CITATIONS
19	Effects of cis and trans Genetic Ancestry on Gene Expression in African Americans. PLoS Genetics, 2008, 4, e1000294.	1.5	91
20	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
21	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
22	The Role of Recent Admixture in Forming the Contemporary West Eurasian Genomic Landscape. Current Biology, 2015, 25, 2518-2526.	1.8	68
23	Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula. Nature Communications, 2019, 10, 551.	5.8	63
24	Application of Coalescent Methods to Reveal Fine-Scale Rate Variation and Recombination Hotspots. Genetics, 2004, 167, 2067-2081.	1.2	62
25	Fine-Scale Inference of Ancestry Segments Without Prior Knowledge of Admixing Groups. Genetics, 2019, 212, 869-889.	1.2	54
26	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
27	Rapid genotype imputation from sequence with reference panels. Nature Genetics, 2021, 53, 1104-1111.	9.4	47
28	PRDM9 marks the spot. Nature Genetics, 2010, 42, 821-822.	9.4	20
29	A model-based approach to capture genetic variation for future association studies. Genome Research, 2006, 17, 88-95.	2.4	10
30	Altering the Binding Properties of PRDM9 Partially Restores Fertility across the Species Boundary. Molecular Biology and Evolution, 2021, 38, 5555-5562.	3.5	9
31	The Kalash Genetic Isolate? The Evidence for Recent Admixture. American Journal of Human Genetics, 2016, 98, 396-397.	2.6	6