

# 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

201575

27  
h-index

434063

31  
g-index

33  
all docs

33  
docs citations

33  
times ranked

24556  
citing authors

#	ARTICLE	IF	CITATIONS
1	Rapid genotype imputation from sequence with reference panels. <i>Nature Genetics</i> , 2021, 53, 1104-1111.	9.4	47
2	Altering the Binding Properties of PRDM9 Partially Restores Fertility across the Species Boundary. <i>Molecular Biology and Evolution</i> , 2021, 38, 5555-5562.	3.5	9
3	Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula. <i>Nature Communications</i> , 2019, 10, 551.	5.8	63
4	Fine-Scale Inference of Ancestry Segments Without Prior Knowledge of Admixing Groups. <i>Genetics</i> , 2019, 212, 869-889.	1.2	54
5	Rapid genotype imputation from sequence without reference panels. <i>Nature Genetics</i> , 2016, 48, 965-969.	9.4	172
6	The Kalash Genetic Isolate? The Evidence for Recent Admixture. <i>American Journal of Human Genetics</i> , 2016, 98, 396-397.	2.6	6
7	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
8	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, 6413-6418.	3.3	75
9	The fine-scale genetic structure of the British population. <i>Nature</i> , 2015, 519, 309-314.	13.7	416
10	Unravelling the hidden ancestry of American admixed populations. <i>Nature Communications</i> , 2015, 6, 6596.	5.8	110
11	The Role of Recent Admixture in Forming the Contemporary West Eurasian Genomic Landscape. <i>Current Biology</i> , 2015, 25, 2518-2526.	1.8	68
12	A Genetic Atlas of Human Admixture History. <i>Science</i> , 2014, 343, 747-751.	6.0	691
13	Great ape genetic diversity and population history. <i>Nature</i> , 2013, 499, 471-475.	13.7	768
14	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.	1.5	53
15	Inference of Population Structure using Dense Haplotype Data. <i>PLoS Genetics</i> , 2012, 8, e1002453.	1.5	983
16	A Fine-Scale Chimpanzee Genetic Map from Population Sequencing. <i>Science</i> , 2012, 336, 193-198.	6.0	273
17	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, 368-381.	2.6	79
18	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

#	ARTICLE	IF	CITATIONS
19	PRDM9 marks the spot. <i>Nature Genetics</i> , 2010, 42, 821-822.	9.4	20
20	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
21	Sensitive Detection of Chromosomal Segments of Distinct Ancestry in Admixed Populations. <i>PLoS Genetics</i> , 2009, 5, e1000519.	1.5	475
22	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
23	Effects of cis and trans Genetic Ancestry on Gene Expression in African Americans. <i>PLoS Genetics</i> , 2008, 4, e1000294.	1.5	91
24	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
25	Genome-wide detection and characterization of positive selection in human populations. <i>Nature</i> , 2007, 449, 913-918.	13.7	1,788
26	A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , 2007, 449, 851-861.	13.7	4,137
27	The Influence of Recombination on Human Genetic Diversity. <i>PLoS Genetics</i> , 2006, 2, e148.	1.5	231
28	A model-based approach to capture genetic variation for future association studies. <i>Genome Research</i> , 2006, 17, 88-95.	2.4	10
29	Human recombination hot spots hidden in regions of strong marker association. <i>Nature Genetics</i> , 2005, 37, 601-606.	9.4	159
30	A Fine-Scale Map of Recombination Rates and Hotspots Across the Human Genome. <i>Science</i> , 2005, 310, 321-324.	6.0	989
31	Application of Coalescent Methods to Reveal Fine-Scale Rate Variation and Recombination Hotspots. <i>Genetics</i> , 2004, 167, 2067-2081.	1.2	62