# Simon R Myers

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3633943/publications.pdf

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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 | A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073. | 13.7 | 7,209 |
| 2 | An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65. | 13.7 | 7,199 |
| 3 | The International HapMap Project. Nature, 2003, 426, 789-796. | 13.7 | 5,735 |
| 4 | A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861. | 13.7 | 4,137 |
| 5 | A new multipoint method for genome-wide association studies by imputation of genotypes. Nature Genetics, 2007, 39, 906-913. | 9.4 | 2,407 |
| 6 | Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918. | 13.7 | 1,788 |
| 7 | Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65. | 13.7 | 991 |
| 8 | A Fine-Scale Map of Recombination Rates and Hotspots Across the Human Genome. Science, 2005, 310, 321-324. | 6.0 | 989 |
| 9 | Inference of Population Structure using Dense Haplotype Data. PLoS Genetics, 2012, 8, e1002453. | 1.5 | 983 |
| 10 | The Fine-Scale Structure of Recombination Rate Variation in the Human Genome. Science, 2004, 304, 581-584. | 6.0 | 941 |
| 11 | Great ape genetic diversity and population history. Nature, 2013, 499, 471-475. | 13.7 | 768 |
| 12 | 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 |
| 13 | A Genetic Atlas of Human Admixture History. Science, 2014, 343, 747-751. | 6.0 | 691 |
| 14 | Multiple regions within 8q24 independently affect risk for prostate cancer. Nature Genetics, 2007, 39, 638-644. | 9.4 | 621 |
| 15 | Diversity of Human Copy Number Variation and Multicopy Genes. Science, 2010, 330, 641-646. | 6.0 | 609 |
| 16 | Drive Against Hotspot Motifs in Primates Implicates the PRDM9 Gene in Meiotic Recombination. Science, 2010, 327, 876-879. | 6.0 | 607 |
| 17 | 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 |
| 18 | Sensitive Detection of Chromosomal Segments of Distinct Ancestry in Admixed Populations. PLoS Genetics, 2009, 5, e1000519. | 1.5 | 475 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Bayesian refinement of association signals for 14 loci in 3 common diseases. Nature Genetics, 2012, 44, 1294-1301. | 9.4 | 469 |
| 20 | The fine-scale genetic structure of the British population. Nature, 2015, 519, 309-314. | 13.7 | 416 |
| 21 | A common sequence motif associated with recombination hot spots and genome instability in humans. Nature Genetics, 2008, 40, 1124-1129. | 9.4 | 395 |
| 22 | Long-Range LD Can Confound Genome Scans in Admixed Populations. American Journal of Human Genetics, 2008, 83, 132-135. | 2.6 | 366 |
| 23 | Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587. | 6.0 | 341 |
| 24 | A method for genome-wide genealogy estimation for thousands of samples. Nature Genetics, 2019, 51, 1321-1329. | 9.4 | 338 |
| 25 | Comparison of Fine-Scale Recombination Rates in Humans and Chimpanzees. Science, 2005, 308, 107-111. | 6.0 | 335 |
| 26 | The landscape of recombination in African Americans. Nature, 2011, 476, 170-175. | 13.7 | 319 |
| 27 | A Fine-Scale Chimpanzee Genetic Map from Population Sequencing. Science, 2012, 336, 193-198. | 6.0 | 273 |
| 28 | 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 |
| 29 | The Influence of Recombination on Human Genetic Diversity. PLoS Genetics, 2006, 2, e148. | 1.5 | 231 |
| 30 | 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 |
| 31 | Re-engineering the zinc fingers of PRDM9 reverses hybrid sterility in mice. Nature, 2016, 530, 171-176. | 13.7 | 194 |
| 32 | Rapid genotype imputation from sequence without reference panels. Nature Genetics, 2016, 48, 965-969. | 9.4 | 172 |
| 33 | Bounds on the Minimum Number of Recombination Events in a Sample History. Genetics, 2003, 163, 375-394. | 1.2 | 163 |
| 34 | Human recombination hot spots hidden in regions of strong marker association. Nature Genetics, 2005, 37, 601-606. | 9.4 | 159 |
| 35 | Can one learn history from the allelic spectrum?. Theoretical Population Biology, 2008, 73, 342-348. | 0.5 | 113 |
| 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 | Unravelling the hidden ancestry of American admixed populations. Nature Communications, 2015, 6, 6596. | 5.8 | 110 |
| 38 | Live Hot, Die Young: Transmission Distortion in Recombination Hotspots. PLoS Genetics, 2007, 3, e35. | 1.5 | 108 |
| 39 | The distribution and causes of meiotic recombination in the human genome. Biochemical Society Transactions, 2006, 34, 526-530. | 1.6 | 106 |
| 40 | Unified single-cell analysis of testis gene regulation and pathology in five mouse strains. ELife, 2019, 8, . | 2.8 | 102 |
| 41 | Non-crossover gene conversions show strong GC bias and unexpected clustering in humans. ELife, 2015, 4, . | 2.8 | 95 |
| 42 | Effects of cis and trans Genetic Ancestry on Gene Expression in African Americans. PLoS Genetics, 2008, 4, e1000294. | 1.5 | 91 |
| 43 | 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 |
| 44 | 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 |
| 45 | 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 |
| 46 | Human genomic regions with exceptionally high levels of population differentiation identified from 911 whole-genome sequences. Genome Biology, 2014, 15, R88. | 13.9 | 72 |
| 47 | The Role of Recent Admixture in Forming the Contemporary West Eurasian Genomic Landscape. Current Biology, 2015, 25, 2518-2526. | 1.8 | 68 |
| 48 | Recombination in the Human Pseudoautosomal Region PAR1. PLoS Genetics, 2014, 10, e1004503. | 1.5 | 66 |
| 49 | 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 |
| 50 | Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula. Nature Communications, 2019, 10, 551. | 5.8 | 63 |
| 51 | Application of Coalescent Methods to Reveal Fine-Scale Rate Variation and Recombination Hotspots. Genetics, 2004, 167, 2067-2081. | 1.2 | 62 |
| 52 | Estimating Meiotic Gene Conversion Rates From Population Genetic Data. Genetics, 2007, 177, 881-894. | 1.2 | 62 |
| 53 | Fine-Scale Inference of Ancestry Segments Without Prior Knowledge of Admixing Groups. Genetics, 2019, 212, 869-889. | 1.2 | 54 |
| 54 | 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 |

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|---|---|---|---|
| 55 | Rapid genotype imputation from sequence with reference panels. Nature Genetics, 2021, 53, 1104-1111. | 9.4 | 47 |
| 56 | Inferring Population Histories for Ancient Genomes Using Genome-Wide Genealogies. Molecular Biology and Evolution, 2021, 38, 3497-3511. | 3.5 | 33 |
| 57 | ZCWPW1 is recruited to recombination hotspots by PRDM9 and is essential for meiotic double strand break repair. ELife, 2020, 9, . | 2.8 | 31 |
| 58 | 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 |
| 59 | PRDM9 marks the spot. Nature Genetics, 2010, 42, 821-822. | 9.4 | 20 |
| 60 | New insights into the biological basis of genomic disorders. Nature Genetics, 2006, 38, 1363-1364. | 9.4 | 12 |
| 61 | A model-based approach to capture genetic variation for future association studies. Genome Research, 2006, 17, 88-95. | 2.4 | 10 |
| 62 | Altering the Binding Properties of PRDM9 Partially Restores Fertility across the Species Boundary. Molecular Biology and Evolution, 2021, 38, 5555-5562. | 3.5 | 9 |
| 63 | The Kalash Genetic Isolate? The Evidence for Recent Admixture. American Journal of Human Genetics, 2016, 98, 396-397. | 2.6 | 6 |