

# Simon Myers

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

32  
papers

12,440  
citations

25  
h-index

33  
g-index

33  
ext. papers

14,411  
ext. citations

21.5  
avg, IF

5.6  
L-index

| #  | Paper   | IF   | Citations |
|----|---|------|-----------|
| 32 | Rapid genotype imputation from sequence with reference panels. <i>Nature Genetics</i> , <b>2021</b> , 53, 1104-1111   | 36.3 | 6         |
| 31 | Altering the Binding Properties of PRDM9 Partially Restores Fertility across the Species Boundary. <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 5555-5562                                 | 8.3  | 0         |
| 30 | Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula. <i>Nature Communications</i> , <b>2019</b> , 10, 551  | 17.4 | 34        |
| 29 | Fine-Scale Inference of Ancestry Segments Without Prior Knowledge of Admixing Groups. <i>Genetics</i> , <b>2019</b> , 212, 869-889  | 4    | 24        |
| 28 | The Kalash Genetic Isolate? The Evidence for Recent Admixture. <i>American Journal of Human Genetics</i> , <b>2016</b> , 98, 396-7  | 11   | 5         |
| 27 | Rapid genotype imputation from sequence without reference panels. <i>Nature Genetics</i> , <b>2016</b> , 48, 965-969  | 36.3 | 79        |
| 26 | The fine-scale genetic structure of the British population. <i>Nature</i> , <b>2015</b> , 519, 309-314  | 50.4 | 298       |
| 25 | Unravelling the hidden ancestry of American admixed populations. <i>Nature Communications</i> , <b>2015</b> , 6, 6596   | 17.4 | 78        |
| 24 | The Role of Recent Admixture in Forming the Contemporary West Eurasian Genomic Landscape. <i>Current Biology</i> , <b>2015</b> , 25, 2518-26  | 6.3  | 42        |
| 23 | 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> , <b>2015</b> , 11, e1005397  | 6    | 104       |
| 22 | 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> , <b>2015</b> , 112, 6413-8 | 11.5 | 52        |
| 21 | A genetic atlas of human admixture history. <i>Science</i> , <b>2014</b> , 343, 747-751   | 33.3 | 492       |
| 20 | Great ape genetic diversity and population history. <i>Nature</i> , <b>2013</b> , 499, 471-5  | 50.4 | 574       |
| 19 | A fine-scale chimpanzee genetic map from population sequencing. <i>Science</i> , <b>2012</b> , 336, 193-8   | 33.3 | 218       |
| 18 | Genomic tools for evolution and conservation in the chimpanzee: <i>Pan troglodytes ellioti</i> is a genetically distinct population. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002504                   | 6    | 45        |
| 17 | Inference of population structure using dense haplotype data. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002453  | 6    | 660       |
| 16 | Genome-wide comparison of African-ancestry populations from CARE and other cohorts reveals signals of natural selection. <i>American Journal of Human Genetics</i> , <b>2011</b> , 89, 368-81           | 11   | 63        |

|    |   |      |      |
|----|---|------|------|
| 15 | Enhanced statistical tests for GWAS in admixed populations: assessment using African Americans from CARE and a Breast Cancer Consortium. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1001371 | 6    | 86   |
| 14 | Drive against hotspot motifs in primates implicates the PRDM9 gene in meiotic recombination. <i>Science</i> , <b>2010</b> , 327, 876-9  | 33.3 | 465  |
| 13 | Sensitive detection of chromosomal segments of distinct ancestry in admixed populations. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000519   | 6    | 393  |
| 12 | A common sequence motif associated with recombination hot spots and genome instability in humans. <i>Nature Genetics</i> , <b>2008</b> , 40, 1124-9                                       | 36.3 | 335  |
| 11 | Effects of cis and trans genetic ancestry on gene expression in African Americans. <i>PLoS Genetics</i> , <b>2008</b> , 4, e1000294   | 6    | 75   |
| 10 | A new multipoint method for genome-wide association studies by imputation of genotypes. <i>Nature Genetics</i> , <b>2007</b> , 39, 906-13   | 36.3 | 2040 |
| 9  | Genome-wide detection and characterization of positive selection in human populations. <i>Nature</i> , <b>2007</b> , 449, 913-8   | 50.4 | 1367 |
| 8  | A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , <b>2007</b> , 449, 851-61   | 50.4 | 3647 |
| 7  | A model-based approach to capture genetic variation for future association studies. <i>Genome Research</i> , <b>2007</b> , 17, 88-95  | 9.7  | 9    |
| 6  | The influence of recombination on human genetic diversity. <i>PLoS Genetics</i> , <b>2006</b> , 2, e148   | 6    | 185  |
| 5  | A fine-scale map of recombination rates and hotspots across the human genome. <i>Science</i> , <b>2005</b> , 310, 321-4   | 33.3 | 836  |
| 4  | Human recombination hot spots hidden in regions of strong marker association. <i>Nature Genetics</i> , <b>2005</b> , 37, 601-6  | 36.3 | 146  |
| 3  | Application of coalescent methods to reveal fine-scale rate variation and recombination hotspots. <i>Genetics</i> , <b>2004</b> , 167, 2067-81  | 4    | 58   |
| 2  | Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula  |      | 4    |
| 1  | Fine-scale Inference of Ancestry Segments without Prior Knowledge of Admixing Groups  |      | 2    |