Gil Mcvean

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/12090342/publications.pdf

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46	24,426	101496	223716
papers	citations	36 h-index	46 g-index

58	58	58	38532
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The UK Biobank resource with deep phenotyping and genomic data. Nature, 2018, 562, 203-209.	13.7	5,221
2	Integrating common and rare genetic variation in diverse human populations. Nature, 2010, 467, 52-58.	13.7	2,625
3	A new multipoint method for genome-wide association studies by imputation of genotypes. Nature Genetics, 2007, 39, 906-913.	9.4	2,407
4	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	13.7	2,400
5	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. Nature Genetics, 2013, 45, 1353-1360.	9.4	1,213
6	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	13.7	991
7	A Fine-Scale Map of Recombination Rates and Hotspots Across the Human Genome. Science, 2005, 310, 321-324.	6.0	989
8	Integrating mapping-, assembly- and haplotype-based approaches for calling variants in clinical sequencing applications. Nature Genetics, 2014, 46, 912-918.	9.4	937
9	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
10	A high-resolution HLA and SNP haplotype map for disease association studies in the extended human MHC. Nature Genetics, 2006, 38, 1166-1172.	9.4	686
11	De novo assembly and genotyping of variants using colored de Bruijn graphs. Nature Genetics, 2012, 44, 226-232.	9.4	564
12	A common sequence motif associated with recombination hot spots and genome instability in humans. Nature Genetics, 2008, 40, 1124-1129.	9.4	395
13	A reference data set of 5.4 million phased human variants validated by genetic inheritance from sequencing a three-generation 17-member pedigree. Genome Research, 2017, 27, 157-164.	2.4	338
14	TNF receptor 1 genetic risk mirrors outcome of anti-TNF therapy in multiple sclerosis. Nature, 2012, 488, 508-511.	13.7	323
15	Arabidopsis meiotic crossover hot spots overlap with H2A.Z nucleosomes at gene promoters. Nature Genetics, 2013, 45, 1327-1336.	9.4	321
16	Class II HLA interactions modulate genetic risk for multiple sclerosis. Nature Genetics, 2015, 47, 1107-1113.	9.4	312
17	A Fine-Scale Chimpanzee Genetic Map from Population Sequencing. Science, 2012, 336, 193-198.	6.0	273
18	The Influence of Recombination on Human Genetic Diversity. PLoS Genetics, 2006, 2, e148.	1.5	231

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19	Recombination rate estimation in the presence of hotspots. Genome Research, 2007, 17, 1219-1227.	2.4	231
20	Clinical whole-genome sequencing in severe early-onset epilepsy reveals new genes and improves molecular diagnosis. Human Molecular Genetics, 2014, 23, 3200-3211.	1.4	222
21	The origin, evolution, and functional impact of short insertionâ€“deletion variants identified in 179 human genomes. Genome Research, 2013, 23, 749-761.	2.4	206
22	Improved genome inference in the MHC using a population reference graph. Nature Genetics, 2015, 47, 682-688.	9.4	197
23	Inferring whole-genome histories in large population datasets. Nature Genetics, 2019, 51, 1330-1338.	9.4	187
24	Resolving TYK2 locus genotype-to-phenotype differences in autoimmunity. Science Translational Medicine, 2016, 8, 363ra149.	5.8	186
25	Indels, structural variation, and recombination drive genomic diversity in Plasmodium falciparum. Genome Research, 2016, 26, 1288-1299.	2.4	180
26	A Statistical Method for Predicting Classical HLA Alleles from SNP Data. American Journal of Human Genetics, 2008, 82, 48-56.	2.6	159
27	Multi-Population Classical HLA Type Imputation. PLoS Computational Biology, 2013, 9, e1002877.	1.5	157
28	HLA*IMPâ€”an integrated framework for imputing classical HLA alleles from SNP genotypes. Bioinformatics, 2011, 27, 968-972.	1.8	151
29	The Structure of Linkage Disequilibrium Around a Selective Sweep. Genetics, 2007, 175, 1395-1406.	1.2	138
30	High-Accuracy HLA Type Inference from Whole-Genome Sequencing Data Using Population Reference Graphs. PLoS Computational Biology, 2016, 12, e1005151.	1.5	87
31	A rare functional cardioprotective APOC3 variant has risen in frequency in distinct population isolates. Nature Communications, 2013, 4, 2872.	5.8	77
32	Imputation of KIR Types from SNP Variation Data. American Journal of Human Genetics, 2015, 97, 593-607.	2.6	73
33	Integrating long-range connectivity information into de Bruijn graphs. Bioinformatics, 2018, 34, 2556-2565.	1.8	61
34	A unified genealogy of modern and ancient genomes. Science, 2022, 375, eabi8264.	6.0	59
35	Bayesian analysis of genetic association across tree-structured routine healthcare data in the UK Biobank. Nature Genetics, 2017, 49, 1311-1318.	9.4	56
36	What drives recombination hotspots to repeat DNA in humans?. Philosophical Transactions of the Royal Society B: Biological Sciences, 2010, 365, 1213-1218.	1.8	54

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37	The impact of age on genetic risk for common diseases. PLoS Genetics, 2021, 17, e1009723.	1.5	53
38	Validation of an Integrated Risk Tool, Including Polygenic Risk Score, for Atherosclerotic Cardiovascular Disease in Multiple Ethnicities and Ancestries. American Journal of Cardiology, 2021, 148, 157-164.	0.7	48
39	A point mutation in the ion conduction pore of AMPA receptor GRIA3 causes dramatically perturbed sleep patterns as well as intellectual disability. Human Molecular Genetics, 2017, 26, 3869-3882.	1.4	35
40	Identifying cross-disease components of genetic risk across hospital data in the UK Biobank. Nature Genetics, 2020, 52, 126-134.	9.4	35
41	Premalignant SOX2 overexpression in the fallopian tubes of ovarian cancer patients: Discovery and validation studies. EBioMedicine, 2016, 10, 137-149.	2.7	34
42	Scanning the human genome for signals of selection. Current Opinion in Genetics and Development, 2006, 16, 624-629.	1.5	29
43	Neuroinflammation â€" using big data to inform clinical practice. Nature Reviews Neurology, 2016, 12, 685-698.	4.9	29
44	Identification of hostâ€"pathogen-disease relationships using a scalable multiplex serology platform in UK Biobank. Nature Communications, 2022, 13, 1818.	5.8	28
45	Estimating Recombination Rates from Genetic Variation in Humans. Methods in Molecular Biology, 2012, 856, 217-237.	0.4	21
46	PRDM9 marks the spot. Nature Genetics, 2010, 42, 821-822.	9.4	20