Jonathan Marchini

List of Publications by Year in Descending Order

99 papers	31,758 citations	51 h-index	111 g-index
111 ext. papers	39,300 ext. citations	19.7 avg, IF	7 L-index

#	Paper	IF	Citations
99	Genome-wide analysis provides genetic evidence that ACE2 influences COVID-19 risk and yields risk scores associated with severe disease.. *Nature Genetics*, **2022**,	36.3	9
98	Exome sequencing and analysis of 454,787 UK Biobank participants. *Nature*, **2021**, 599, 628-634	50.4	34
97	Computationally efficient whole-genome regression for quantitative and binary traits. *Nature Genetics*, **2021**, 53, 1097-1103	36.3	51
96	Pan-ancestry exome-wide association analyses of COVID-19 outcomes in 586,157 individuals. *American Journal of Human Genetics*, **2021**, 108, 1350-1355	11	25
95	Sequencing of 640,000 exomes identifies variants associated with protection from obesity. *Science*, **2021**, 373,	33.3	22
94	False discovery rate control in genome-wide association studies with population structure. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	4
93	Common Genetic Variation Indicates Separate Causes for Periventricular and Deep White Matter Hyperintensities. *Stroke*, **2020**, 51, 2111-2121	6.7	23
92	Genome-wide gene-environment analyses of major depressive disorder and reported lifetime traumatic experiences in UK Biobank. *Molecular Psychiatry*, **2020**, 25, 1430-1446	15.1	47
91	Genotype imputation using the Positional Burrows Wheeler Transform. *PLoS Genetics*, **2020**, 16, e1009049	5.6	18
90	A non-linear regression method for estimation of gene-environment heritability. *Bioinformatics*, **2020**,	7.2	3
89	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. *Biological Psychiatry*, **2020**, 88, 169-184	7.9	57
88	Exome sequencing and characterization of 49,960 individuals in the UK Biobank. *Nature*, **2020**, 586, 749-756	50.4	122
87	Inferring Gene-by-Environment Interactions with a Bayesian Whole-Genome Regression Model. *American Journal of Human Genetics*, **2020**, 107, 698-713	11	9
86	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. *Biological Psychiatry*, **2020**, 87, 419-430	7.9	9
85	Retraction Note: 11,670 whole-genome sequences representative of the Han Chinese population from the CONVERGE project. *Scientific Data*, **2020**, 7, 123	8.2	1
84	Handedness, language areas and neuropsychiatric diseases: insights from brain imaging and genetics. *Brain*, **2019**, 142, 2938-2947	11.2	67
83	Unified single-cell analysis of testis gene regulation and pathology in five mouse strains. *ELife*, **2019**, 8,	8.9	54

82	The spatial correspondence and genetic influence of interhemispheric connectivity with white matter microstructure. *Nature Neuroscience*, **2019**, 22, 809-819	25.5	31
81	Haplotype Estimation and Genotype Imputation **2019**, 87-114		6
80	Association of Whole-Genome and NETRIN1 Signaling Pathway-Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. *Biological Psychiatry: Cognitive Neuroscience and Neuroimaging*, **2019**, 4, 91-100	3.4	12
79	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics*, **2018**, 50, 559-571	36.3	221
78	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. *Nature Genetics*, **2018**, 50, 1505-1513	36.3	675
77	Genome-wide association studies of brain imaging phenotypes in UK Biobank. *Nature*, **2018**, 562, 210-216	50.4	282
76	The UK Biobank resource with deep phenotyping and genomic data. *Nature*, **2018**, 562, 203-209	50.4	2108
75	An imputation platform to enhance integration of rice genetic resources. *Nature Communications*, **2018**, 9, 3519	17.4	39
74	11,670 whole-genome sequences representative of the Han Chinese population from the CONVERGE project. *Scientific Data*, **2017**, 4, 170011	8.2	29
73	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. *Nature Communications*, **2017**, 8, 14977	17.4	105
72	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. *Cancer Epidemiology Biomarkers and Prevention*, **2017**, 26, 126-135	4	183
71	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. *Cell*, **2016**, 167, 1415-1429.e19	56.2	637
70	Haplotype estimation for biobank-scale data sets. *Nature Genetics*, **2016**, 48, 817-20	36.3	121
69	Phasing for medical sequencing using rare variants and large haplotype reference panels. *Bioinformatics*, **2016**, 32, 1974-80	7.2	15
68	A multiple-phenotype imputation method for genetic studies. *Nature Genetics*, **2016**, 48, 466-72	36.3	52
67	Cystatin C and Cardiovascular Disease: A Mendelian Randomization Study. *Journal of the American College of Cardiology*, **2016**, 68, 934-45	15.1	65
66	Tensor decomposition for multiple-tissue gene expression experiments. *Nature Genetics*, **2016**, 48, 1094-1100	36.3	87
65	Novel insights into the genetics of smoking behaviour, lung function, and chronic obstructive pulmonary disease (UK BiLEVE): a genetic association study in UK Biobank. *Lancet Respiratory Medicine,the*, **2015**, 3, 769-81	35.1	245

64	Multicohort analysis of the maternal age effect on recombination. *Nature Communications*, **2015**, 6, 7846	17.4	21
63	The UK10K project identifies rare variants in health and disease. *Nature*, **2015**, 526, 82-90	50.4	776
62	Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. *Nature Communications*, **2015**, 6, 8111	17.4	186
61	Molecular signatures of major depression. *Current Biology*, **2015**, 25, 1146-56	6.3	162
60	Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. *Nature Communications*, **2014**, 5, 3934	17.4	253
59	A general approach for haplotype phasing across the full spectrum of relatedness. *PLoS Genetics*, **2014**, 10, e1004234	6	377
58	Haplotype estimation using sequencing reads. *American Journal of Human Genetics*, **2013**, 93, 687-96	11	254
57	Improved whole-chromosome phasing for disease and population genetic studies. *Nature Methods*, **2013**, 10, 5-6	21.6	868
56	Multiway admixture deconvolution using phased or unphased ancestral panels. *Genetic Epidemiology*, **2013**, 37, 1-12	2.6	44
55	The origin, evolution, and functional impact of short insertion-deletion variants identified in 179 human genomes. *Genome Research*, **2013**, 23, 749-61	9.7	150
54	Genotype calling and phasing using next-generation sequencing reads and a haplotype scaffold. *Bioinformatics*, **2013**, 29, 84-91	7.2	39
53	Distinct loci in the CHRNA5/CHRNA3/CHRNB4 gene cluster are associated with onset of regular smoking. *Genetic Epidemiology*, **2013**, 37, 846-59	2.6	26
52	Fast and accurate genotype imputation in genome-wide association studies through pre-phasing. *Nature Genetics*, **2012**, 44, 955-9	36.3	1292
51	Joint genotype calling with array and sequence data. *Genetic Epidemiology*, **2012**, 36, 527-37	2.6	5
50	Genome-wide joint meta-analysis of SNP and SNP-by-smoking interaction identifies novel loci for pulmonary function. *PLoS Genetics*, **2012**, 8, e1003098	6	108
49	Increased genetic vulnerability to smoking at CHRNA5 in early-onset smokers. *Archives of General Psychiatry*, **2012**, 69, 854-60		65
48	A linear complexity phasing method for thousands of genomes. *Nature Methods*, **2011**, 9, 179-81	21.6	1228
47	Genotype Imputation **2011**, 157-175		

46	Modeling interactions with known risk loci-a Bayesian model averaging approach. *Annals of Human Genetics*, **2011**, 75, 1-9	2.2	16
45	The effect of genome-wide association scan quality control on imputation outcome for common variants. *European Journal of Human Genetics*, **2011**, 19, 610-4	5.3	25
44	Bayesian hierarchical mixture modeling to assign copy number from a targeted CNV array. *Genetic Epidemiology*, **2011**, 35, 536-48	2.6	15
43	Effect of five genetic variants associated with lung function on the risk of chronic obstructive lung disease, and their joint effects on lung function. *American Journal of Respiratory and Critical Care Medicine*, **2011**, 184, 786-95	10.2	112
42	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. *Nature Genetics*, **2011**, 43, 1082-90	36.3	313
41	HAPGEN2: simulation of multiple disease SNPs. *Bioinformatics*, **2011**, 27, 2304-5	7.2	197
40	Genotype imputation with thousands of genomes. *G3: Genes, Genomes, Genetics*, **2011**, 1, 457-70	3.2	719
39	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. *Nature Genetics*, **2010**, 42, 436-40	36.3	521
38	Genotype imputation for genome-wide association studies. *Nature Reviews Genetics*, **2010**, 11, 499-511	30.1	1134
37	Introduction to the Special Issue: Genome-Wide Association Studies. *Statistical Science*, **2009**, 24,	2.4	2
36	A Bayesian Method for Detecting and Characterizing Allelic Heterogeneity and Boosting Signals in Genome-Wide Association Studies. *Statistical Science*, **2009**, 24,	2.4	17
35	A flexible and accurate genotype imputation method for the next generation of genome-wide association studies. *PLoS Genetics*, **2009**, 5, e1000529	6	2866
34	Designing genome-wide association studies: sample size, power, imputation, and the choice of genotyping chip. *PLoS Genetics*, **2009**, 5, e1000477	6	417
33	Genome-wide and fine-resolution association analysis of malaria in West Africa. *Nature Genetics*, **2009**, 41, 657-65	36.3	297
32	Common variants at five new loci associated with early-onset inflammatory bowel disease. *Nature Genetics*, **2009**, 41, 1335-40	36.3	389
31	Common variants near MC4R are associated with fat mass, weight and risk of obesity. *Nature Genetics*, **2008**, 40, 768-75	36.3	1048
30	Genome-wide association defines more than 30 distinct susceptibility loci for Crohn's disease. *Nature Genetics*, **2008**, 40, 955-62	36.3	2092
29	A robust statistical method for case-control association testing with copy number variation. *Nature Genetics*, **2008**, 40, 1245-52	36.3	143

28	Comparing algorithms for genotype imputation. *American Journal of Human Genetics*, **2008**, 83, 535-9; author reply 539-40	11	35
27	A new multipoint method for genome-wide association studies by imputation of genotypes. *Nature Genetics*, **2007**, 39, 906-13	36.3	2040
26	Genome-wide detection and characterization of positive selection in human populations. *Nature*, **2007**, 449, 913-8	50.4	1367
25	A second generation human haplotype map of over 3.1 million SNPs. *Nature*, **2007**, 449, 851-61	50.4	3647
24	A model-based approach to capture genetic variation for future association studies. *Genome Research*, **2007**, 17, 88-95	9.7	9
23	Independent Component Analysis of Functional Magnetic Resonance Imaging Data Using Wavelet Dictionaries **2007**, 625-632		1
22	Two-stage two-locus models in genome-wide association. *PLoS Genetics*, **2006**, 2, e157	6	173
21	A comparison of phasing algorithms for trios and unrelated individuals. *American Journal of Human Genetics*, **2006**, 78, 437-50	11	267
20	A high-resolution HLA and SNP haplotype map for disease association studies in the extended human MHC. *Nature Genetics*, **2006**, 38, 1166-72	36.3	618
19	Genome-wide strategies for detecting multiple loci that influence complex diseases. *Nature Genetics*, **2005**, 37, 413-7	36.3	730
18	Reply to "Genomic Control to the extreme". *Nature Genetics*, **2004**, 36, 1131-1131	36.3	6
17	The effects of human population structure on large genetic association studies. *Nature Genetics*, **2004**, 36, 512-7	36.3	686
16	Comparing methods of analyzing fMRI statistical parametric maps. *NeuroImage*, **2004**, 22, 1203-13	7.9	49
15	Gene-environment interactions using a Bayesian whole genome regression model		3
14	Improved whole-chromosome phasing for disease and population genetic studies		1
13	A reference panel of 64,976 haplotypes for genotype imputation		15
12	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes		4
11	Genome-wide genetic data on ~500,000 UK Biobank participants		320

List of Publications

10	Genome-wide association studies of brain structure and function in the UK Biobank	9
9	Computationally efficient whole genome regression for quantitative and binary traits	18
8	FDR control in GWAS with population structure	2
7	Fine-mapping of an expanded set of type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps	18
6	BGEN: a binary file format for imputed genotype and haplotype data	22
5	Unified single-cell analysis of testis gene regulation and pathology in 5 mouse strains	4
4	Integrative haplotype estimation with sub-linear complexity	4
3	Whole exome sequencing and characterization of coding variation in 49,960 individuals in the UK Biobank	56
2	Universal latent axes capturing Parkinson's patient deep phenotypic variation reveals patients with a high genetic risk for Alzheimer's disease are more likely to develop a more aggressive form of Parkinson's	1
1	Genotype imputation using the Positional Burrows Wheeler Transform	6