Chris Wallace

List of Publications by Year in Descending Order

134 papers	25,924 citations	48 h-index	156 g-index
156 ext. papers	29,908 ext. citations	13.2 avg, IF	7.45 L-index

#	Paper	IF	Citations
134	Mendelian randomization. *Nature Reviews Methods Primers*, **2022**, 2,		10
133	Probabilistic classification of anti-SARS-CoV-2 antibody responses improves seroprevalence estimates.. *Clinical and Translational Immunology*, **2022**, 11, e1379	6.8	1
132	INNODIA Master Protocol for the evaluation of investigational medicinal products in children, adolescents and adults with newly diagnosed type 1 diabetes.. *Trials*, **2022**, 23, 414	2.8	1
131	The flashfm approach for fine-mapping multiple quantitative traits. *Nature Communications*, **2021**, 12, 6147	17.4	0
130	Leveraging auxiliary data from arbitrary distributions to boost GWAS discovery with Flexible cFDR. *PLoS Genetics*, **2021**, 17, e1009853	6	0
129	Accurate error control in high-dimensional association testing using conditional false discovery rates. *Biometrical Journal*, **2021**, 63, 1096-1130	1.5	3
128	Seropositivity in blood donors and pregnant women during the first year of SARS-CoV-2 transmission in Stockholm, Sweden. *Journal of Internal Medicine*, **2021**, 290, 666-676	10.8	14
127	Comparison of sparse biclustering algorithms for gene expression datasets. *Briefings in Bioinformatics*, **2021**, 22,	13.4	1
126	EPISPOT: An epigenome-driven approach for detecting and interpreting hotspots in molecular QTL studies. *American Journal of Human Genetics*, **2021**, 108, 983-1000	11	1
125	Detection of quantitative trait loci from RNA-seq data with or without genotypes using BaseQTL.. *Nature Computational Science*, **2021**, 1, 421-432		1
124	Patient-reported wellbeing and clinical disease measures over time captured by multivariate trajectories of disease activity in individuals with juvenile idiopathic arthritis in the UK: a multicentre prospective longitudinal study. *Lancet Rheumatology, The*, **2021**, 3, e111-e121	14.2	5
123	Identification of susceptibility loci for Takayasu arteritis through a large multi-ancestral genome-wide association study. *American Journal of Human Genetics*, **2021**, 108, 84-99	11	8
122	Detecting chromosomal interactions in Capture Hi-C data with CHiCAGO and companion tools. *Nature Protocols*, **2021**, 16, 4144-4176	18.8	2
121	A more accurate method for colocalisation analysis allowing for multiple causal variants. *PLoS Genetics*, **2021**, 17, e1009440	6	5
120	Multi-tissue transcriptome-wide association studies. *Genetic Epidemiology*, **2021**, 45, 324-337	2.6	2
119	Functional effects of variation in transcription factor binding highlight long-range gene regulation by epromoters. *Nucleic Acids Research*, **2020**, 48, 2866-2879	20.1	11
118	Improving the coverage of credible sets in Bayesian genetic fine-mapping. *PLoS Computational Biology*, **2020**, 16, e1007829	5	16

117	Eliciting priors and relaxing the single causal variant assumption in colocalisation analyses. *PLoS Genetics*, **2020**, 16, e1008720	6	54
116	Resolving mechanisms of immune-mediated disease in primary CD4 T cells. *EMBO Molecular Medicine*, **2020**, 12, e12112	12	14
115	Genetic feature engineering enables characterisation of shared risk factors in immune-mediated diseases. *Genome Medicine*, **2020**, 12, 106	14.4	3
114	Fine-mapping genetic associations. *Human Molecular Genetics*, **2020**, 29, R81-R88	5.6	13
113	Improving the coverage of credible sets in Bayesian genetic fine-mapping **2020**, 16, e1007829		
112	Improving the coverage of credible sets in Bayesian genetic fine-mapping **2020**, 16, e1007829		
111	Improving the coverage of credible sets in Bayesian genetic fine-mapping **2020**, 16, e1007829		
110	Improving the coverage of credible sets in Bayesian genetic fine-mapping **2020**, 16, e1007829		
109	Eliciting priors and relaxing the single causal variant assumption in colocalisation analyses **2020**, 16, e1008720		
108	Eliciting priors and relaxing the single causal variant assumption in colocalisation analyses **2020**, 16, e1008720		
107	Eliciting priors and relaxing the single causal variant assumption in colocalisation analyses **2020**, 16, e1008720		
106	Eliciting priors and relaxing the single causal variant assumption in colocalisation analyses **2020**, 16, e1008720		
105	Fine mapping chromatin contacts in capture Hi-C data. *BMC Genomics*, **2019**, 20, 77	4.5	10
104	Stochastic search and joint fine-mapping increases accuracy and identifies previously unreported associations in immune-mediated diseases. *Nature Communications*, **2019**, 10, 3216	17.4	19
103	Genome-wide association study of eosinophilic granulomatosis with polyangiitis reveals genomic loci stratified by ANCA status. *Nature Communications*, **2019**, 10, 5120	17.4	71
102	Multivariate Genome-wide Association Analysis of a Cytokine Network Reveals Variants with Widespread Immune, Haematological, and Cardiometabolic Pleiotropy. *American Journal of Human Genetics*, **2019**, 105, 1076-1090	11	16
101	simGWAS: a fast method for simulation of large scale case-control GWAS summary statistics. *Bioinformatics*, **2019**, 35, 1901-1906	7.2	9
100	The chromosome 6q22.33 region is associated with age at diagnosis of type 1 diabetes and disease risk in those diagnosed under 5 years of age. *Diabetologia*, **2018**, 61, 147-157	10.3	19

99	Promoter interactome of human embryonic stem cell-derived cardiomyocytes connects GWAS regions to cardiac gene networks. *Nature Communications*, **2018**, 9, 2526	17.4	34
98	A method for identifying genetic heterogeneity within phenotypically defined disease subgroups. *Nature Genetics*, **2017**, 49, 310-316	36.3	17
97	Chromosome contacts in activated T cells identify autoimmune disease candidate genes. *Genome Biology*, **2017**, 18, 165	18.3	41
96	Cells with Treg-specific FOXP3 demethylation but low CD25 are prevalent in autoimmunity. *Journal of Autoimmunity*, **2017**, 84, 75-86	15.5	46
95	Neonatal and adult recent thymic emigrants produce IL-8 and express complement receptors CR1 and CR2. *JCI Insight*, **2017**, 2,	9.9	26
94	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. *Cell*, **2016**, 167, 1369-1384.e19	56.2	556
93	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. *Cell*, **2016**, 167, 1145-1149	56.2	232
92	Regulatory T Cell Responses in Participants with Type 1 Diabetes after a Single Dose of Interleukin-2: A Non-Randomised, Open Label, Adaptive Dose-Finding Trial. *PLoS Medicine*, **2016**, 13, e1002139	11.6	76
91	O1-11-04: Temporal Clustering Reveals Heterogeneity Of Cognitive Decline In Dementia **2016**, 12, P203-P203		
90	A pleiotropy-informed Bayesian false discovery rate adapted to a shared control design finds new disease associations from GWAS summary statistics. *PLoS Genetics*, **2015**, 11, e1004926	6	37
89	Widespread seasonal gene expression reveals annual differences in human immunity and physiology. *Nature Communications*, **2015**, 6, 7000	17.4	268
88	Natural Variation in Interleukin-2 Sensitivity Influences Regulatory T-Cell Frequency and Function in Individuals With Long-standing Type 1 Diabetes. *Diabetes*, **2015**, 64, 3891-902	0.9	34
87	Dense genotyping of immune-related susceptibility loci reveals new insights into the genetics of psoriatic arthritis. *Nature Communications*, **2015**, 6, 6046	17.4	103
86	Epigenetic analysis of regulatory T cells using multiplex bisulfite sequencing. *European Journal of Immunology*, **2015**, 45, 3200-3	6.1	21
85	Dissection of a Complex Disease Susceptibility Region Using a Bayesian Stochastic Search Approach to Fine Mapping. *PLoS Genetics*, **2015**, 11, e1005272	6	42
84	Fine mapping of type 1 diabetes susceptibility loci and evidence for colocalization of causal variants with lymphoid gene enhancers. *Nature Genetics*, **2015**, 47, 381-6	36.3	414
83	Statistical colocalization of genetic risk variants for related autoimmune diseases in the context of common controls. *Nature Genetics*, **2015**, 47, 839-46	36.3	97
82	Integration of disease association and eQTL data using a Bayesian colocalisation approach highlights six candidate causal genes in immune-mediated diseases. *Human Molecular Genetics*, **2015**, 24, 3305-13	5.6	94

81	Capture Hi-C reveals novel candidate genes and complex long-range interactions with related autoimmune risk loci. *Nature Communications*, **2015**, 6, 10069	17.4	121
80	IL-21 production by CD4+ effector T cells and frequency of circulating follicular helper T cells are increased in type 1 diabetes patients. *Diabetologia*, **2015**, 58, 781-90	10.3	86
79	A type I interferon transcriptional signature precedes autoimmunity in children genetically at risk for type 1 diabetes. *Diabetes*, **2014**, 63, 2538-50	0.9	188
78	A method for gene-based pathway analysis using genomewide association study summary statistics reveals nine new type 1 diabetes associations. *Genetic Epidemiology*, **2014**, 38, 661-70	2.6	43
77	Multi-parametric flow cytometric and genetic investigation of the peripheral B cell compartment in human type 1 diabetes. *Clinical and Experimental Immunology*, **2014**, 177, 571-85	6.2	41
76	Effects of long-term averaging of quantitative blood pressure traits on the detection of genetic associations. *American Journal of Human Genetics*, **2014**, 95, 49-65	11	52
75	A hybrid qPCR/SNP array approach allows cost efficient assessment of KIR gene copy numbers in large samples. *BMC Genomics*, **2014**, 15, 274	4.5	12
74	A genome-wide assessment of the role of untagged copy number variants in type 1 diabetes. *PLoS Genetics*, **2014**, 10, e1004367	6	16
73	VSEAMS: a pipeline for variant set enrichment analysis using summary GWAS data identifies IKZF3, BATF and ESRRA as key transcription factors in type 1 diabetes. *Bioinformatics*, **2014**, 30, 3342-8	7.2	12
72	Bayesian test for colocalisation between pairs of genetic association studies using summary statistics. *PLoS Genetics*, **2014**, 10, e1004383	6	868
71	Plasma concentrations of soluble IL-2 receptor α (CD25) are increased in type 1 diabetes and associated with reduced C-peptide levels in young patients. *Diabetologia*, **2014**, 57, 366-72	10.3	21
70	Postthymic expansion in human CD4 naive T cells defined by expression of functional high-affinity IL-2 receptors. *Journal of Immunology*, **2013**, 190, 2554-66	5.3	34
69	Statistical testing of shared genetic control for potentially related traits. *Genetic Epidemiology*, **2013**, 37, 802-13	2.6	53
68	Seven newly identified loci for autoimmune thyroid disease. *Human Molecular Genetics*, **2012**, 21, 5202-8	5.6	120
67	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2012**, 90, 1116-1117	11	78
66	Statistical colocalization of monocyte gene expression and genetic risk variants for type 1 diabetes. *Human Molecular Genetics*, **2012**, 21, 2815-24	5.6	71
65	Extra-binomial variation approach for analysis of pooled DNA sequencing data. *Bioinformatics*, **2012**, 28, 2898-904	7.2	4
64	Long-range DNA looping and gene expression analyses identify DEXI as an autoimmune disease candidate gene. *Human Molecular Genetics*, **2012**, 21, 322-33	5.6	91

63	Comparative analysis of genome-wide association studies signals for lipids, diabetes, and coronary heart disease: Cardiovascular Biomarker Genetics Collaboration. *European Heart Journal*, **2012**, 33, 393-407	9.5	75
62	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. *Nature Genetics*, **2011**, 43, 1131-8	36.3	415
61	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2011**, 88, 6-18	11	103
60	Blood pressure loci identified with a gene-centric array. *American Journal of Human Genetics*, **2011**, 89, 688-700	11	137
59	Genetic association analyses of atopic illness and proinflammatory cytokine genes with type 1 diabetes. *Diabetes/Metabolism Research and Reviews*, **2011**, 27, 838-43	7.5	35
58	Dense genotyping identifies and localizes multiple common and rare variant association signals in celiac disease. *Nature Genetics*, **2011**, 43, 1193-201	36.3	535
57	An allele of IKZF1 (Ikaros) conferring susceptibility to childhood acute lymphoblastic leukemia protects against type 1 diabetes. *Diabetes*, **2011**, 60, 1041-4	0.9	41
56	Inherited variation in vitamin D genes is associated with predisposition to autoimmune disease type 1 diabetes. *Diabetes*, **2011**, 60, 1624-31	0.9	222
55	Pervasive sharing of genetic effects in autoimmune disease. *PLoS Genetics*, **2011**, 7, e1002254	6	413
54	Genome-wide association analysis of autoantibody positivity in type 1 diabetes cases. *PLoS Genetics* , **2011**, 7, e1002216	6	195
53	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. *Nature*, **2010**, 464, 713-20	50.4	639
52	A trans-acting locus regulates an anti-viral expression network and type 1 diabetes risk. *Nature*, **2010**, 467, 460-4	50.4	224
51	The imprinted DLK1-MEG3 gene region on chromosome 14q32.2 alters susceptibility to type 1 diabetes. *Nature Genetics*, **2010**, 42, 68-71	36.3	238
50	Genetic loci influencing kidney function and chronic kidney disease. *Nature Genetics*, **2010**, 42, 373-5	36.3	205
49	Reduced expression of IFIH1 is protective for type 1 diabetes. *PLoS ONE*, **2010**, 5, e12646	3.7	66
48	Genome-wide association scan meta-analysis identifies three Loci influencing adiposity and fat distribution. *PLoS Genetics*, **2009**, 5, e1000508	6	393
47	Polymorphisms in the WNK1 gene are associated with blood pressure variation and urinary potassium excretion. *PLoS ONE*, **2009**, 4, e5003	3.7	36
46	Meta-analysis of 28,141 individuals identifies common variants within five new loci that influence uric acid concentrations. *PLoS Genetics*, **2009**, 5, e1000504	6	495

45	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. *Nature Genetics*, **2009**, 41, 25-34	36.3	1368
44	Genome-wide association study identifies eight loci associated with blood pressure. *Nature Genetics*, **2009**, 41, 666-76	36.3	970
43	Common genetic variation near the phospholamban gene is associated with cardiac repolarisation: meta-analysis of three genome-wide association studies. *PLoS ONE*, **2009**, 4, e6138	3.7	50
42	Genome-wide association analysis identifies 20 loci that influence adult height. *Nature Genetics*, **2008**, 40, 575-83	36.3	654
41	Common variants near MC4R are associated with fat mass, weight and risk of obesity. *Nature Genetics*, **2008**, 40, 768-75	36.3	1048
40	Genome-wide association study identifies genes for biomarkers of cardiovascular disease: serum urate and dyslipidemia. *American Journal of Human Genetics*, **2008**, 82, 139-49	11	361
39	Glutathione S-transferase variants and hypertension. *Journal of Hypertension*, **2008**, 26, 1343-52	1.9	30
38	SLC2A9 is a high-capacity urate transporter in humans. *PLoS Medicine*, **2008**, 5, e197	11.6	254
37	Extreme clonality in lymphoblastoid cell lines with implications for allele specific expression analyses. *PLoS ONE*, **2008**, 3, e2966	3.7	48
36	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. *Nature Genetics*, **2007**, 39, 1329-37	36.3	1130
35	Robust associations of four new chromosome regions from genome-wide analyses of type 1 diabetes. *Nature Genetics*, **2007**, 39, 857-64	36.3	1159
34	Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. *Nature*, **2007**, 447, 661-78	50.4	7801
33	Genetic association analysis of inositol polyphosphate phosphatase-like 1 (INPPL1, SHIP2) variants with essential hypertension. *Journal of Medical Genetics*, **2007**, 44, 603-5	5.8	13
32	Information capture using SNPs from HapMap and whole-genome chips differs in a sample of inflammatory and cardiovascular gene-centric regions from genome-wide estimates. *Genome Research*, **2007**, 17, 1596-602	9.7	7
31	Replication of genome-wide association signals in UK samples reveals risk loci for type 2 diabetes. *Science*, **2007**, 316, 1336-41	33.3	1823
30	Appropriate use of information on family history of disease in recruitment for linkage analysis studies. *Annals of Human Genetics*, **2006**, 70, 360-71	2.2	3
29	Increased support for linkage of a novel locus on chromosome 5q13 for essential hypertension in the British Genetics of Hypertension Study. *Hypertension*, **2006**, 48, 105-11	8.5	21
28	Chromosome 2p shows significant linkage to antihypertensive response in the British Genetics of Hypertension Study. *Hypertension*, **2006**, 47, 603-8	8.5	31

27	Two-dimensional genome-scan identifies novel epistatic loci for essential hypertension. *Human Molecular Genetics*, **2006**, 15, 1365-74	5.6	47
26	Improved power offered by a score test for linkage disequilibrium mapping of quantitative-trait loci by selective genotyping. *American Journal of Human Genetics*, **2006**, 78, 498-504	11	38
25	Linkage analysis using co-phenotypes in the BRIGHT study reveals novel potential susceptibility loci for hypertension. *American Journal of Human Genetics*, **2006**, 79, 323-31	11	20
24	Haplotypes of the beta-2 adrenergic receptor associate with high diastolic blood pressure in the Caerphilly prospective study. *Journal of Hypertension*, **2006**, 24, 471-7	1.9	13
23	Haplotypes of the WNK1 gene associate with blood pressure variation in a severely hypertensive population from the British Genetics of Hypertension study. *Human Molecular Genetics*, **2005**, 14, 1805-14	5.6	82
22	Linkage analysis of susceptibility to leprosy type using an IBD regression method. *Genes and Immunity*, **2004**, 5, 221-5	4.4	8
21	Estimating the relative recurrence risk ratio using a global cross-ratio model. *Genetic Epidemiology*, **2003**, 25, 293-302	2.6	7
20	Trends in drug overdose deaths in England and Wales 1993-98: methadone does not kill more people than heroin. *Addiction*, **2003**, 98, 419-25	4.6	54
19	Estimating the relative recurrence risk ratio for leprosy in Karonga District, Malawi. *Leprosy Review*, **2003**, 74, 133-40	0.6	4
18	Fine mapping chromatin contacts in capture Hi-C data		1
17	Eliciting priors and relaxing the single causal variant assumption in colocalisation analyses		2
16	Statistical Colocalization of Genetic Risk Variants for Related Autoimmune Diseases in the Context of Common Controls		3
15	A method for identifying genetic heterogeneity within phenotypically-defined disease subgroups		1
14	A rare IL2RA haplotype identifies SNP rs61839660 as causal for autoimmunity		2
13	Type 1 diabetes genome-wide association analysis with imputation identifies five new risk regions		8
12	Cells with Treg-specific FOXP3 demethylation but low CD25 are prevalent in autoimmunity		1
11	Informed dimension reduction of clinically-related genome-wide association summary data characterises cross-trait axes of genetic risk		1
10	Probabilistic approaches for classifying highly variable anti-SARS-CoV-2 antibody responses		3

List of Publications

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7	simGWAS: a fast method for simulation of large scale case-control GWAS summarystatistics	1
6	Accurate error control in high dimensional association testing using conditional false discovery rates	4
5	Genetically distinct clinical subsets, and associations with asthma and eosinophil abundance, within Eosinophilic Granulomatosis with Polyangiitis	3
4	Improving the coverage of credible sets in Bayesian genetic fine-mapping	1
3	A Pleiotropy-Informed Bayesian False Discovery Rate adapted to a Shared Control Design Finds New Disease Associations From GWAS Summary Statistics	3
2	Recent thymic emigrants produce antimicrobial IL-8, express complement receptors and are precursors of a tissue-homing Th8 lineage of memory cells	1
1	A more accurate method for colocalisation analysis allowing for multiple causal variants	1