Chris Wallace

List of Publications by Year
in descending order

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120 papers	32,752 citations	36203 51 h-index	22764 112 g-index
156 all docs	156 docs citations	156 times ranked	38899 citing authors

#	Article	IF	Citations
1	Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. Nature, 2007, 447, 661-678.	13.7	8,895
2	Replication of Genome-Wide Association Signals in UK Samples Reveals Risk Loci for Type 2 Diabetes. Science, 2007, 316, 1336-1341.	6.0	2,040
3	Bayesian Test for Colocalisation between Pairs of Genetic Association Studies Using Summary Statistics. PLoS Genetics, 2014, 10, e1004383.	1.5	2,012
4	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	9.4	1,572
5	Robust associations of four new chromosome regions from genome-wide analyses of type 1 diabetes. Nature Genetics, 2007, 39, 857-864.	9.4	1,324
6	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. Nature Genetics, 2007, 39, 1329-1337.	9.4	1,298
7	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	9.4	1,179
8	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	9.4	1,104
9	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. Cell, 2016, 167, 1369-1384.e19.	13.5	863
10	Genome-wide association analysis identifies 20 loci that influence adult height. Nature Genetics, 2008, 40, 575-583.	9.4	742
11	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
12	Dense genotyping identifies and localizes multiple common and rare variant association signals in celiac disease. Nature Genetics, 2011, 43, 1193-1201.	9.4	682
13	Fine mapping of type 1 diabetes susceptibility loci and evidence for colocalization of causal variants with lymphoid gene enhancers. Nature Genetics, 2015, 47, 381-386.	9.4	589
14	Meta-Analysis of 28,141 Individuals Identifies Common Variants within Five New Loci That Influence Uric Acid Concentrations. PLoS Genetics, 2009, 5, e1000504.	1.5	572
15	Pervasive Sharing of Genetic Effects in Autoimmune Disease. PLoS Genetics, 2011, 7, e1002254.	1.5	540
16	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	9.4	501
17	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	1.5	453
18	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404

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19	Genome-wide Association Study Identifies Genes for Biomarkers of Cardiovascular Disease: Serum Urate and Dyslipidemia. American Journal of Human Genetics, 2008, 82, 139-149.	2.6	397
20	Mendelian randomization. Nature Reviews Methods Primers, 2022, 2, .	11.8	393
21	Widespread seasonal gene expression reveals annual differences in human immunity and physiology. Nature Communications, 2015, 6, 7000.	5.8	367
22	SLC2A9 Is a High-Capacity Urate Transporter in Humans. PLoS Medicine, 2008, 5, e197.	3.9	305
23	The imprinted DLK1-MEG3 gene region on chromosome 14q32.2 alters susceptibility to type 1 diabetes. Nature Genetics, 2010, 42, 68-71.	9.4	281
24	A trans-acting locus regulates an anti-viral expression network and type 1 diabetes risk. Nature, 2010, 467, 460-464.	13.7	271
25	A Type I Interferon Transcriptional Signature Precedes Autoimmunity in Children Genetically at Risk for Type 1 Diabetes. Diabetes, 2014, 63, 2538-2550.	0.3	261
26	Inherited Variation in Vitamin D Genes Is Associated With Predisposition to Autoimmune Disease Type 1 Diabetes. Diabetes, 2011, 60, 1624-1631.	0.3	260
27	Genetic loci influencing kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 373-375.	9.4	246
28	Genome-Wide Association Analysis of Autoantibody Positivity in Type 1 Diabetes Cases. PLoS Genetics, 2011, 7, e1002216.	1.5	230
29	Eliciting priors and relaxing the single causal variant assumption in colocalisation analyses. PLoS Genetics, 2020, 16, e1008720.	1.5	180
30	Capture Hi-C reveals novel candidate genes and complex long-range interactions with related autoimmune risk loci. Nature Communications, 2015, 6, 10069.	5.8	161
31	Genome-wide association study of eosinophilic granulomatosis with polyangiitis reveals genomic loci stratified by ANCA status. Nature Communications, 2019, 10, 5120.	5.8	160
32	Blood Pressure Loci Identified with a Gene-Centric Array. American Journal of Human Genetics, 2011, 89, 688-700.	2.6	159
33	Dense genotyping of immune-related susceptibility loci reveals new insights into the genetics of psoriatic arthritis. Nature Communications, 2015, 6, 6046.	5.8	149
34	Seven newly identified loci for autoimmune thyroid disease. Human Molecular Genetics, 2012, 21, 5202-5208.	1.4	143
35	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, 3305-3313.	1.4	134
36	A more accurate method for colocalisation analysis allowing for multiple causal variants. PLoS Genetics, 2021, 17, e1009440.	1.5	130

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37	Statistical colocalization of genetic risk variants for related autoimmune diseases in the context of common controls. Nature Genetics, 2015, 47, 839-846.	9.4	128
38	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	2.6	122
39	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.	3.9	117
40	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, 781-790.	2.9	116
41	Statistical colocalization of monocyte gene expression and genetic risk variants for type 1 diabetes. Human Molecular Genetics, 2012, 21, 2815-2824.	1.4	103
42	Combining evidence from Mendelian randomization and colocalization: Review and comparison of approaches. American Journal of Human Genetics, 2022, 109, 767-782.	2.6	101
43	Long-range DNA looping and gene expression analyses identify DEXI as an autoimmune disease candidate gene. Human Molecular Genetics, 2012, 21, 322-333.	1.4	100
44	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.	1.0	93
45	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, 1805-1814.	1.4	91
46	Reduced Expression of IFIH1 Is Protective for Type 1 Diabetes. PLoS ONE, 2010, 5, e12646.	1.1	82
47	Statistical Testing of Shared Genetic Control for Potentially Related Traits. Genetic Epidemiology, 2013, 37, 802-813.	0.6	81
48	Cells with Treg-specific FOXP3 demethylation but low CD25 are prevalent in autoimmunity. Journal of Autoimmunity, 2017, 84, 75-86.	3.0	78
49	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.	2.6	73
50	Chromosome contacts in activated T cells identify autoimmune disease candidate genes. Genome Biology, 2017, 18, 165.	3.8	68
51	Trends in drug overdose deaths in England and Wales 1993-98: methadone does not kill more people than heroin. Addiction, 2003, 98, 419-425.	1.7	62
52	Postthymic Expansion in Human CD4 Naive T Cells Defined by Expression of Functional High-Affinity IL-2 Receptors. Journal of Immunology, 2013, 190, 2554-2566.	0.4	60
53	Multi-parametric flow cytometric and genetic investigation of the peripheral B cell compartment in human type 1 diabetes. Clinical and Experimental Immunology, 2014, 177, 571-585.	1.1	55
54	Dissection of a Complex Disease Susceptibility Region Using a Bayesian Stochastic Search Approach to Fine Mapping. PLoS Genetics, 2015, 11, e1005272.	1.5	55

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55	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.	1.5	55
56	A Method for Geneâ€Based Pathway Analysis Using Genomewide Association Study Summary Statistics Reveals Nine New Type 1 Diabetes Associations. Genetic Epidemiology, 2014, 38, 661-670.	0.6	54
57	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.	1.1	53
58	Two-dimensional genome-scan identifies novel epistatic loci for essential hypertension. Human Molecular Genetics, 2006, 15, 1365-1374.	1.4	50
59	An Allele ofIKZF1(Ikaros) Conferring Susceptibility to Childhood Acute Lymphoblastic Leukemia Protects Against Type 1 Diabetes. Diabetes, 2011, 60, 1041-1044.	0.3	50
60	Extreme Clonality in Lymphoblastoid Cell Lines with Implications for Allele Specific Expression Analyses. PLoS ONE, 2008, 3, e2966.	1.1	50
61	Promoter interactome of human embryonic stem cell-derived cardiomyocytes connects GWAS regions to cardiac gene networks. Nature Communications, 2018, 9, 2526.	5.8	48
62	Natural Variation in Interleukin-2 Sensitivity Influences Regulatory T-Cell Frequency and Function in Individuals With Long-standing Type 1 Diabetes. Diabetes, 2015, 64, 3891-3902.	0.3	46
63	Neonatal and adult recent thymic emigrants produce IL-8 and express complement receptors CR1 and CR2. JCI Insight, 2017, 2, .	2.3	46
64	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.	2.6	43
65	Polymorphisms in the WNK1 Gene Are Associated with Blood Pressure Variation and Urinary Potassium Excretion. PLoS ONE, 2009, 4, e5003.	1.1	43
66	Genetic association analyses of atopic illness and proinflammatory cytokine genes with type 1 diabetes. Diabetes/Metabolism Research and Reviews, 2011, 27, 838-843.	1.7	43
67	The chromosome 6q22.33 region is associated with age at diagnosis of type 1 diabetes and disease risk in those diagnosed under 5Âyears of age. Diabetologia, 2018, 61, 147-157.	2.9	37
68	Glutathione S-transferase variants and hypertension. Journal of Hypertension, 2008, 26, 1343-1352.	0.3	34
69	Seropositivity in blood donors and pregnant women during the first year of SARSâ€CoVâ€2 transmission in Stockholm, Sweden. Journal of Internal Medicine, 2021, 290, 666-676.	2.7	34
70	Chromosome 2p Shows Significant Linkage to Antihypertensive Response in the British Genetics of Hypertension Study. Hypertension, 2006, 47, 603-608.	1.3	33
71	Fine-mapping genetic associations. Human Molecular Genetics, 2020, 29, R81-R88.	1.4	32
72	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.	2.6	31

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73	Improving the coverage of credible sets in Bayesian genetic fine-mapping. PLoS Computational Biology, 2020, 16, e1007829.	1.5	31
74	Plasma concentrations of soluble IL-2 receptor Î± (CD25) are increased in type 1 diabetes and associated with reduced C-peptide levels in young patients. Diabetologia, 2014, 57, 366-372.	2.9	30
75	Resolving mechanisms of immuneâ€mediated disease in primary <scp>CD</scp> 4 T cells. EMBO Molecular Medicine, 2020, 12, e12112.	3.3	30
76	A method for identifying genetic heterogeneity within phenotypically defined disease subgroups. Nature Genetics, 2017, 49, 310-316.	9.4	29
77	Epigenetic analysis of regulatory T cells using multiplex bisulfite sequencing. European Journal of Immunology, 2015, 45, 3200-3203.	1.6	26
78	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.	2.6	26
79	Stochastic search and joint fine-mapping increases accuracy and identifies previously unreported associations in immune-mediated diseases. Nature Communications, 2019, 10, 3216.	5.8	24
80	simGWAS: a fast method for simulation of large scale caseâ€“control GWAS summary statistics. Bioinformatics, 2019, 35, 1901-1906.	1.8	23
81	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.	2.2	23
82	Linkage Analysis Using Co-Phenotypes in the BRIGHT Study Reveals Novel Potential Susceptibility Loci for Hypertension. American Journal of Human Genetics, 2006, 79, 323-331.	2.6	22
83	Increased Support for Linkage of a Novel Locus on Chromosome 5q13 for Essential Hypertension in the British Genetics of Hypertension Study. Hypertension, 2006, 48, 105-111.	1.3	22
84	Detecting chromosomal interactions in Capture Hi-C data with CHiCAGO and companion tools. Nature Protocols, 2021, 16, 4144-4176.	5.5	21
85	Genetic association analysis of inositol polyphosphate phosphatase-like 1 (INPPL1, SHIP2) variants with essential hypertension. Journal of Medical Genetics, 2007, 44, 603-605.	1.5	17
86	A Genome-Wide Assessment of the Role of Untagged Copy Number Variants in Type 1 Diabetes. PLoS Genetics, 2014, 10, e1004367.	1.5	17
87	Fine mapping chromatin contacts in capture Hi-C data. BMC Genomics, 2019, 20, 77.	1.2	16
88	Functional effects of variation in transcription factor binding highlight long-range gene regulation by epromoters. Nucleic Acids Research, 2020, 48, 2866-2879.	6.5	15
89	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, 3342-3348.	1.8	14
90	The flashfm approach for fine-mapping multiple quantitative traits. Nature Communications, 2021, 12, 6147.	5.8	14

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91	Haplotypes of the beta-2 adrenergic receptor associate with high diastolic blood pressure in the Caerphilly prospective study. Journal of Hypertension, 2006, 24, 471-477.	0.3	13
92	A hybrid qPCR/SNP array approach allows cost efficient assessment of KIR gene copy numbers in large samples. BMC Genomics, 2014, 15, 274.	1.2	12
93	Genetic feature engineering enables characterisation of shared risk factors in immune-mediated diseases. Genome Medicine, 2020, 12, 106.	3.6	12
94	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.	0.7	12
95	Linkage analysis of susceptibility to leprosy type using an IBD regression method. Genes and Immunity, 2004, 5, 221-225.	2.2	11
96	Accurate error control in highâ€dimensional association testing using conditional false discovery rates. Biometrical Journal, 2021, 63, 1096-1130.	0.6	11
97	Autoimmunity Is a Significant Feature of Idiopathic Pulmonary Arterial Hypertension. American Journal of Respiratory and Critical Care Medicine, 2022, 206, 81-93.	2.5	9
98	Estimating the relative recurrence risk ratio using a global cross-ratio model. Genetic Epidemiology, 2003, 25, 293-302.	0.6	8
99	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, 1596-1602.	2.4	8
100	Detection of quantitative trait loci from RNA-seq data with or without genotypes using BaseQTL. Nature Computational Science, 2021, 1, 421-432.	3.8	8
101	Multiâ€tissue transcriptomeâ€wide association studies. Genetic Epidemiology, 2021, 45, 324-337.	0.6	8
102	Extra-binomial variation approach for analysis of pooled DNA sequencing data. Bioinformatics, 2012, 28, 2898-2904.	1.8	7
103	Comparison of sparse biclustering algorithms for gene expression datasets. Briefings in Bioinformatics, 2021, 22, .	3.2	7
104	EPISPOT: An epigenome-driven approach for detecting and interpreting hotspots in molecular QTL studies. American Journal of Human Genetics, 2021, 108, 983-1000.	2.6	6
105	Estimating the relative recurrence risk ratio for leprosy in Karonga District, Malawi. Leprosy Review, 2003, 74, 133-40.	0.1	5
106	RÃ¡pidoPGS: a rapid polygenic score calculator for summary GWAS data without a test dataset. Bioinformatics, 2021, 37, 4444-4450.	1.8	4
107	Probabilistic classification of antiâ€SARSâ€CoVâ€2 antibody responses improves seroprevalence estimates. Clinical and Translational Immunology, 2022, 11, e1379.	1.7	4
108	Appropriate Use of Information on Family History of Disease in Recruitment for Linkage Analysis Studies. Annals of Human Genetics, 2008, 70, 360-371.	0.3	3

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109	Leveraging auxiliary data from arbitrary distributions to boost GWAS discovery with Flexible cFDR. PLoS Genetics, 2021, 17, e1009853.	1.5	3
110	Use of MRP8/14 in clinical practice as a predictor of outcome after methotrexate withdrawal in patients with juvenile idiopathic arthritis. Clinical Rheumatology, 2022, 41, 2825-2830.	1.0	3
111	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2012, 90, 1116-1117.	2.6	0
112	O1-11-04: Temporal Clustering Reveals Heterogeneity Of Cognitive Decline In Dementia. , 2016, 12, P203-P203.		0
113	Improving the coverage of credible sets in Bayesian genetic fine-mapping. , 2020, 16, e1007829.		0
114	Improving the coverage of credible sets in Bayesian genetic fine-mapping. , 2020, 16, e1007829.		0
115	Improving the coverage of credible sets in Bayesian genetic fine-mapping. , 2020, 16, e1007829.		0
116	Improving the coverage of credible sets in Bayesian genetic fine-mapping. , 2020, 16, e1007829.		0
117	Eliciting priors and relaxing the single causal variant assumption in colocalisation analyses. , 2020, 16, e1008720.		0
118	Eliciting priors and relaxing the single causal variant assumption in colocalisation analyses. , 2020, 16, e1008720.		0
119	Eliciting priors and relaxing the single causal variant assumption in colocalisation analyses. , 2020, 16, e1008720.		0
120	Eliciting priors and relaxing the single causal variant assumption in colocalisation analyses. , 2020, 16, e1008720.		0