Chris Wallace

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2277101/publications.pdf

Version: 2024-02-01

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	Mendelian randomization. Nature Reviews Methods Primers, 2022, 2, .	11.8	393
2	Probabilistic classification of antiâ€SARSâ€CoVâ€2 antibody responses improves seroprevalence estimates. Clinical and Translational Immunology, 2022, 11, e1379.	1.7	4
3	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
4	Combining evidence from Mendelian randomization and colocalization: Review and comparison of approaches. American Journal of Human Genetics, 2022, 109, 767-782.	2.6	101
5	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
6	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
7	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
8	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
9	Accurate error control in highâ€dimensional association testing using conditional false discovery rates. Biometrical Journal, 2021, 63, 1096-1130.	0.6	11
10	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
11	Comparison of sparse biclustering algorithms for gene expression datasets. Briefings in Bioinformatics, 2021, 22, .	3.2	7
12	RÃ¡pidoPGS: a rapid polygenic score calculator for summary GWAS data without a test dataset. Bioinformatics, 2021, 37, 4444-4450.	1.8	4
13	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
14	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
15	Detecting chromosomal interactions in Capture Hi-C data with CHiCAGO and companion tools. Nature Protocols, 2021, 16, 4144-4176.	5.5	21
16	A more accurate method for colocalisation analysis allowing for multiple causal variants. PLoS Genetics, 2021, 17, e1009440.	1.5	130
17	Multiâ€tissue transcriptomeâ€wide association studies. Genetic Epidemiology, 2021, 45, 324-337.	0.6	8
18	The flashfm approach for fine-mapping multiple quantitative traits. Nature Communications, 2021, 12, 6147.	5.8	14

#	Article	IF	Citations
19	Leveraging auxiliary data from arbitrary distributions to boost GWAS discovery with Flexible cFDR. PLoS Genetics, 2021, 17, e1009853.	1.5	3
20	Genetic feature engineering enables characterisation of shared risk factors in immune-mediated diseases. Genome Medicine, 2020, 12, 106.	3.6	12
21	Fine-mapping genetic associations. Human Molecular Genetics, 2020, 29, R81-R88.	1.4	32
22	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
23	Improving the coverage of credible sets in Bayesian genetic fine-mapping. PLoS Computational Biology, 2020, 16, e1007829.	1.5	31
24	Eliciting priors and relaxing the single causal variant assumption in colocalisation analyses. PLoS Genetics, 2020, 16, e1008720.	1.5	180
25	Resolving mechanisms of immuneâ€mediated disease in primary <scp>CD</scp> 4 T cells. EMBO Molecular Medicine, 2020, 12, e12112.	3.3	30
26	Improving the coverage of credible sets in Bayesian genetic fine-mapping. , 2020, 16, e1007829.		0
27	Improving the coverage of credible sets in Bayesian genetic fine-mapping. , 2020, 16, e1007829.		0
28	Improving the coverage of credible sets in Bayesian genetic fine-mapping. , 2020, 16, e1007829.		0
29	Improving the coverage of credible sets in Bayesian genetic fine-mapping. , 2020, 16, e1007829.		0
30	Eliciting priors and relaxing the single causal variant assumption in colocalisation analyses. , 2020, 16, e1008720.		0
31	Eliciting priors and relaxing the single causal variant assumption in colocalisation analyses. , 2020, 16, e1008720.		0
32	Eliciting priors and relaxing the single causal variant assumption in colocalisation analyses. , 2020, 16, e1008720.		0
33	Eliciting priors and relaxing the single causal variant assumption in colocalisation analyses. , 2020, 16, e1008720.		0
34	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
35	Genome-wide association study of eosinophilic granulomatosis with polyangiitis reveals genomic loci stratified by ANCA status. Nature Communications, 2019, 10, 5120.	5.8	160
36	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

#	Article	IF	Citations
37	Fine mapping chromatin contacts in capture Hi-C data. BMC Genomics, 2019, 20, 77.	1.2	16
38	simGWAS: a fast method for simulation of large scale caseâ€“control GWAS summary statistics. Bioinformatics, 2019, 35, 1901-1906.	1.8	23
39	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
40	Promoter interactome of human embryonic stem cell-derived cardiomyocytes connects GWAS regions to cardiac gene networks. Nature Communications, 2018, 9, 2526.	5.8	48
41	A method for identifying genetic heterogeneity within phenotypically defined disease subgroups. Nature Genetics, 2017, 49, 310-316.	9.4	29
42	Cells with Treg-specific FOXP3 demethylation but low CD25 are prevalent in autoimmunity. Journal of Autoimmunity, 2017, 84, 75-86.	3.0	78
43	Chromosome contacts in activated T cells identify autoimmune disease candidate genes. Genome Biology, 2017, 18, 165.	3.8	68
44	Neonatal and adult recent thymic emigrants produce IL-8 and express complement receptors CR1 and CR2. JCI Insight, 2017, 2, .	2.3	46
45	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
46	O1-11-04: Temporal Clustering Reveals Heterogeneity Of Cognitive Decline In Dementia. , 2016, 12, P203-P203.		0
47	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. Cell, 2016, 167, 1369-1384.e19.	13.5	863
48	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
49	Epigenetic analysis of regulatory T cells using multiplex bisulfite sequencing. European Journal of Immunology, 2015, 45, 3200-3203.	1.6	26
50	Dissection of a Complex Disease Susceptibility Region Using a Bayesian Stochastic Search Approach to Fine Mapping. PLoS Genetics, 2015, 11, e1005272.	1.5	55
51	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
52	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
53	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
54	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

#	Article	IF	Citations
55	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
56	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
57	Widespread seasonal gene expression reveals annual differences in human immunity and physiology. Nature Communications, 2015, 6, 7000.	5.8	367
58	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
59	Dense genotyping of immune-related susceptibility loci reveals new insights into the genetics of psoriatic arthritis. Nature Communications, 2015, 6, 6046.	5.8	149
60	A Genome-Wide Assessment of the Role of Untagged Copy Number Variants in Type 1 Diabetes. PLoS Genetics, 2014, 10, e1004367.	1.5	17
61	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
62	Bayesian Test for Colocalisation between Pairs of Genetic Association Studies Using Summary Statistics. PLoS Genetics, 2014, 10, e1004383.	1.5	2,012
63	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
64	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
65	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
66	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
67	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
68	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
69	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
70	Statistical Testing of Shared Genetic Control for Potentially Related Traits. Genetic Epidemiology, 2013, 37, 802-813.	0.6	81
71	Statistical colocalization of monocyte gene expression and genetic risk variants for type 1 diabetes. Human Molecular Genetics, 2012, 21, 2815-2824.	1.4	103
72	Extra-binomial variation approach for analysis of pooled DNA sequencing data. Bioinformatics, 2012, 28, 2898-2904.	1.8	7

#	Article	IF	Citations
73	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
74	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
75	Seven newly identified loci for autoimmune thyroid disease. Human Molecular Genetics, 2012, 21, 5202-5208.	1.4	143
76	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
77	Dense genotyping identifies and localizes multiple common and rare variant association signals in celiac disease. Nature Genetics, 2011, 43, 1193-1201.	9.4	682
78	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	9.4	501
79	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
80	Blood Pressure Loci Identified with a Gene-Centric Array. American Journal of Human Genetics, 2011, 89, 688-700.	2.6	159
81	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
82	An Allele ofIKZF1(Ikaros) Conferring Susceptibility to Childhood Acute Lymphoblastic Leukemia Protects Against Type 1 Diabetes. Diabetes, 2011, 60, 1041-1044.	0.3	50
83	Inherited Variation in Vitamin D Genes Is Associated With Predisposition to Autoimmune Disease Type 1 Diabetes. Diabetes, 2011, 60, 1624-1631.	0.3	260
84	Pervasive Sharing of Genetic Effects in Autoimmune Disease. PLoS Genetics, 2011, 7, e1002254.	1.5	540
85	Genome-Wide Association Analysis of Autoantibody Positivity in Type 1 Diabetes Cases. PLoS Genetics, 2011, 7, e1002216.	1.5	230
86	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
87	A trans-acting locus regulates an anti-viral expression network and type 1 diabetes risk. Nature, 2010, 467, 460-464.	13.7	271
88	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
89	Genetic loci influencing kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 373-375.	9.4	246
90	Reduced Expression of IFIH1 Is Protective for Type 1 Diabetes. PLoS ONE, 2010, 5, e12646.	1.1	82

#	Article	IF	Citations
91	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	1.5	453
92	Polymorphisms in the WNK1 Gene Are Associated with Blood Pressure Variation and Urinary Potassium Excretion. PLoS ONE, 2009, 4, e5003.	1.1	43
93	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
94	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
95	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	9.4	1,104
96	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
97	Genome-wide association analysis identifies 20 loci that influence adult height. Nature Genetics, 2008, 40, 575-583.	9.4	742
98	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	9.4	1,179
99	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
100	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
101	Glutathione S-transferase variants and hypertension. Journal of Hypertension, 2008, 26, 1343-1352.	0.3	34
102	SLC2A9 Is a High-Capacity Urate Transporter in Humans. PLoS Medicine, 2008, 5, e197.	3.9	305
103	Extreme Clonality in Lymphoblastoid Cell Lines with Implications for Allele Specific Expression Analyses. PLoS ONE, 2008, 3, e2966.	1.1	50
104	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
105	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
106	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
107	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. Nature Genetics, 2007, 39, 1329-1337.	9.4	1,298
108	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

#	Article	IF	Citations
109	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
110	Two-dimensional genome-scan identifies novel epistatic loci for essential hypertension. Human Molecular Genetics, 2006, 15, 1365-1374.	1.4	50
111	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
112	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
113	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
114	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
115	Chromosome 2p Shows Significant Linkage to Antihypertensive Response in the British Genetics of Hypertension Study. Hypertension, 2006, 47, 603-608.	1.3	33
116	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
117	Linkage analysis of susceptibility to leprosy type using an IBD regression method. Genes and Immunity, 2004, 5, 221-225.	2.2	11
118	Estimating the relative recurrence risk ratio using a global cross-ratio model. Genetic Epidemiology, 2003, 25, 293-302.	0.6	8
119	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
120	Estimating the relative recurrence risk ratio for leprosy in Karonga District, Malawi. Leprosy Review, 2003, 74, 133-40.	0.1	5