

Xiaoquanwilliam Wen

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

19,824
citations

109137

35
h-index

143772

57
g-index

84
all docs

84
docs citations

84
times ranked

37983
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. <i>Nature Communications</i> , 2022, 13, 1644.	5.8	63
2	Analyzing and reconciling colocalization and transcriptome-wide association studies from the perspective of inferential reproducibility. <i>American Journal of Human Genetics</i> , 2022, 109, 825-837.	2.6	17
3	Structural factor equation models for causal network construction via directed acyclic mixed graphs. <i>Biometrics</i> , 2021, 77, 573-586.	0.8	4
4	Probabilistic colocalization of genetic variants from complex and molecular traits: promise and limitations. <i>American Journal of Human Genetics</i> , 2021, 108, 25-35.	2.6	67
5	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. <i>Genome Biology</i> , 2021, 22, 49.	3.8	150
6	Revisiting the genome-wide significance threshold for common variant GWAS. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	59
7	Functional dynamic genetic effects on gene regulation are specific to particular cell types and environmental conditions. <i>ELife</i> , 2021, 10, .	2.8	41
8	Psychosocial experiences modulate asthma-associated genes through gene-environment interactions. <i>ELife</i> , 2021, 10, .	2.8	15
9	Interspecies variation in hominid gut microbiota controls host gene regulation. <i>Cell Reports</i> , 2021, 37, 110057.	2.9	9
10	BAGSE: a Bayesian hierarchical model approach for gene set enrichment analysis. <i>Bioinformatics</i> , 2020, 36, 1689-1695.	1.8	7
11	Fine-mapping and QTL tissue-sharing information improves the reliability of causal gene identification. <i>Genetic Epidemiology</i> , 2020, 44, 854-867.	0.6	28
12	Quantify and control reproducibility in high-throughput experiments. <i>Nature Methods</i> , 2020, 17, 1207-1213.	9.0	11
13	A Quantitative Proteome Map of the Human Body. <i>Cell</i> , 2020, 183, 269-283.e19.	13.5	243
14	Cell type-specific genetic regulation of gene expression across human tissues. <i>Science</i> , 2020, 369, .	6.0	210
15	PTWAS: investigating tissue-relevant causal molecular mechanisms of complex traits using probabilistic TWAS analysis. <i>Genome Biology</i> , 2020, 21, 232.	3.8	46
16	PhenomeXcan: Mapping the genome to the phenome through the transcriptome. <i>Science Advances</i> , 2020, 6, .	4.7	83
17	Impact of admixture and ancestry on eQTL analysis and GWAS colocalization in GTEx. <i>Genome Biology</i> , 2020, 21, 233.	3.8	64
18	Integrating comprehensive functional annotations to boost power and accuracy in gene-based association analysis. <i>PLoS Genetics</i> , 2020, 16, e1009060.	1.5	11

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19	Interpreting Coronary Artery Disease Risk Through Gene-Environment Interactions in Gene Regulation. <i>Genetics</i> , 2019, 213, 651-663.	1.2	20
20	QuASAR-MPRA: accurate allele-specific analysis for massively parallel reporter assays. <i>Bioinformatics</i> , 2018, 34, 787-794.	1.8	28
21	High-throughput characterization of genetic effects on DNA-protein binding and gene transcription. <i>Genome Research</i> , 2018, 28, 1701-1708.	2.4	34
22	Genetic signature to provide robust risk assessment of psoriatic arthritis development in psoriasis patients. <i>Nature Communications</i> , 2018, 9, 4178.	5.8	95
23	Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. <i>Nature Genetics</i> , 2018, 50, 956-967.	9.4	389
24	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. <i>Nature Genetics</i> , 2018, 50, 1234-1239.	9.4	547
25	An eQTL Landscape of Kidney Tissue in Human Nephrotic Syndrome. <i>American Journal of Human Genetics</i> , 2018, 103, 232-244.	2.6	147
26	Robust Bayesian FDR Control Using Bayes Factors, with Applications to Multi-tissue eQTL Discovery. <i>Statistics in Biosciences</i> , 2017, 9, 28-49.	0.6	10
27	Large scale meta-analysis characterizes genetic architecture for common psoriasis associated variants. <i>Nature Communications</i> , 2017, 8, 15382.	5.8	251
28	Environmental perturbations lead to extensive directional shifts in RNA processing. <i>PLoS Genetics</i> , 2017, 13, e1006995.	1.5	25
29	Integrating molecular QTL data into genome-wide genetic association analysis: Probabilistic assessment of enrichment and colocalization. <i>PLoS Genetics</i> , 2017, 13, e1006646.	1.5	205
30	Which Genetics Variants in DNase-Seq Footprints Are More Likely to Alter Binding?. <i>PLoS Genetics</i> , 2016, 12, e1005875.	1.5	56
31	Molecular QTL discovery incorporating genomic annotations using Bayesian false discovery rate control. <i>Annals of Applied Statistics</i> , 2016, 10, .	0.5	54
32	The genetic regulatory signature of type 2 diabetes in human skeletal muscle. <i>Nature Communications</i> , 2016, 7, 11764.	5.8	114
33	Efficient Integrative Multi-SNP Association Analysis via Deterministic Approximation of Posteriors. <i>American Journal of Human Genetics</i> , 2016, 98, 1114-1129.	2.6	147
34	High-throughput allele-specific expression across 250 environmental conditions. <i>Genome Research</i> , 2016, 26, 1627-1638.	2.4	138
35	Cross-Population Joint Analysis of eQTLs: Fine Mapping and Functional Annotation. <i>PLoS Genetics</i> , 2015, 11, e1005176.	1.5	93
36	Bayesian model comparison in genetic association analysis: linear mixed modeling and SNP set testing. <i>Biostatistics</i> , 2015, 16, 701-712.	0.9	5

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37	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. <i>Science</i> , 2015, 348, 648-660.	6.0	4,659
38	Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , 2015, 348, 666-669.	6.0	252
39	Genome-wide Association Analysis of Psoriatic Arthritis and Cutaneous Psoriasis Reveals Differences in Their Genetic Architecture. <i>American Journal of Human Genetics</i> , 2015, 97, 816-836.	2.6	245
40	QuASAR: quantitative allele-specific analysis of reads. <i>Bioinformatics</i> , 2015, 31, 1235-1242.	1.8	70
41	Bayesian methods for genetic association analysis with heterogeneous subgroups: From meta-analyses to gene-environment interactions. <i>Annals of Applied Statistics</i> , 2014, 8, 176-203.	0.5	52
42	The Role of Environmental Heterogeneity in Meta-Analysis of Gene-Environment Interactions With Quantitative Traits. <i>Genetic Epidemiology</i> , 2014, 38, 416-429.	0.6	12
43	Bayesian model selection in complex linear systems, as illustrated in genetic association studies. <i>Biometrics</i> , 2014, 70, 73-83.	0.8	26
44	A Statistical Framework for Joint eQTL Analysis in Multiple Tissues. <i>PLoS Genetics</i> , 2013, 9, e1003486.	1.5	226
45	The Genotype-Tissue Expression (GTEx) project. <i>Nature Genetics</i> , 2013, 45, 580-585.	9.4	6,815
46	Interactions between Glucocorticoid Treatment and Cis-Regulatory Polymorphisms Contribute to Cellular Response Phenotypes. <i>PLoS Genetics</i> , 2011, 7, e1002162.	1.5	103
47	Gene, region and pathway level analyses in whole-genome studies. <i>Genetic Epidemiology</i> , 2010, 34, 222-231.	0.6	46
48	Using linear predictors to impute allele frequencies from summary or pooled genotype data. <i>Annals of Applied Statistics</i> , 2010, 4, 1158-1182.	0.5	74
49	Broad-Scale Recombination Patterns Underlying Proper Disjunction in Humans. <i>PLoS Genetics</i> , 2009, 5, e1000658.	1.5	107
50	High-Resolution Mapping of Crossovers Reveals Extensive Variation in Fine-Scale Recombination Patterns Among Humans. <i>Science</i> , 2008, 319, 1395-1398.	6.0	340
51	Association studies for untyped markers with TUNA. <i>Bioinformatics</i> , 2008, 24, 435-437.	1.8	13
52	A worldwide survey of haplotype variation and linkage disequilibrium in the human genome. <i>Nature Genetics</i> , 2006, 38, 1251-1260.	9.4	474
53	A Map of Recent Positive Selection in the Human Genome. <i>PLoS Biology</i> , 2006, 4, e72.	2.6	2,329
54	Coverage and Characteristics of the Affymetrix GeneChip Human Mapping 100K SNP Set. <i>PLoS Genetics</i> , 2006, 2, e67.	1.5	38

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55	Association mapping and fine mapping with TreeLD. <i>Bioinformatics</i> , 2005, 21, 3168-3170.	1.8	12
56	Coverage and Characteristics of the The Affymetrix GeneChip \hat{A} ® Human Mapping 100K SNP Set. <i>PLoS Genetics</i> , 2005, preprint, e67.	1.5	0
57	Evidence for Extensive Transmission Distortion in the Human Genome. <i>American Journal of Human Genetics</i> , 2004, 74, 62-72.	2.6	111