Xiaoquanwilliam Wen

List of Publications by Year
in descending order

57 papers	19,824 citations	109321 35 h-index	144013 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. Nature Communications, 2022, 13, 1644.	12.8	63
2	Analyzing and reconciling colocalization and transcriptome-wide association studies from the perspective of inferential reproducibility. American Journal of Human Genetics, 2022, 109, 825-837.	6.2	17
3	Structural factor equation models for causal network construction via directed acyclic mixed graphs. Biometrics, 2021, 77, 573-586.	1.4	4
4	Probabilistic colocalization of genetic variants from complex and molecular traits: promise and limitations. American Journal of Human Genetics, 2021, 108, 25-35.	6.2	67
5	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. Genome Biology, 2021, 22, 49.	8.8	150
6	Revisiting the genome-wide significance threshold for common variant GWAS. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	59
7	Functional dynamic genetic effects on gene regulation are specific to particular cell types and environmental conditions. ELife, 2021, 10, .	6.0	41
8	Psychosocial experiences modulate asthma-associated genes through gene-environment interactions. ELife, 2021, 10, .	6.0	15
9	Interspecies variation in hominid gut microbiota controls host gene regulation. Cell Reports, 2021, 37, 110057.	6.4	9
10	BAGSE: a Bayesian hierarchical model approach for gene set enrichment analysis. Bioinformatics, 2020, 36, 1689-1695.	4.1	7
11	Fineâ€mapping and QTL tissueâ€sharing information improves the reliability of causal gene identification. Genetic Epidemiology, 2020, 44, 854-867.	1.3	28
12	Quantify and control reproducibility in high-throughput experiments. Nature Methods, 2020, 17, 1207-1213.	19.0	11
13	A Quantitative Proteome Map of the Human Body. Cell, 2020, 183, 269-283.e19.	28.9	243
14	Cell typeâ€“specific genetic regulation of gene expression across human tissues. Science, 2020, 369, .	12.6	210
15	PTWAS: investigating tissue-relevant causal molecular mechanisms of complex traits using probabilistic TWAS analysis. Genome Biology, 2020, 21, 232.	8.8	46
16	PhenomeXcan: Mapping the genome to the phenome through the transcriptome. Science Advances, 2020, 6, .	10.3	83
17	Impact of admixture and ancestry on eQTL analysis and GWAS colocalization in GTEx. Genome Biology, 2020, 21, 233.	8.8	64
18	Integrating comprehensive functional annotations to boost power and accuracy in gene-based association analysis. PLoS Genetics, 2020, 16, e1009060.	3.5	11

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19	Interpreting Coronary Artery Disease Risk Through Geneâ€“Environment Interactions in Gene Regulation. Genetics, 2019, 213, 651-663.	2.9	20
20	QuASAR-MPRA: accurate allele-specific analysis for massively parallel reporter assays. Bioinformatics, 2018, 34, 787-794.	4.1	28
21	High-throughput characterization of genetic effects on DNAâ€“protein binding and gene transcription. Genome Research, 2018, 28, 1701-1708.	5.5	34
22	Genetic signature to provide robust risk assessment of psoriatic arthritis development in psoriasis patients. Nature Communications, 2018, 9, 4178.	12.8	95
23	Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. Nature Genetics, 2018, 50, 956-967.	21.4	389
24	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. Nature Genetics, 2018, 50, 1234-1239.	21.4	547
25	An eQTL Landscape of Kidney Tissue in Human Nephrotic Syndrome. American Journal of Human Genetics, 2018, 103, 232-244.	6.2	147
26	Robust Bayesian FDR Control Using Bayes Factors, with Applications to Multi-tissue eQTL Discovery. Statistics in Biosciences, 2017, 9, 28-49.	1.2	10
27	Large scale meta-analysis characterizes genetic architecture for common psoriasis associated variants. Nature Communications, 2017, 8, 15382.	12.8	251
28	Environmental perturbations lead to extensive directional shifts in RNA processing. PLoS Genetics, 2017, 13, e1006995.	3.5	25
29	Integrating molecular QTL data into genome-wide genetic association analysis: Probabilistic assessment of enrichment and colocalization. PLoS Genetics, 2017, 13, e1006646.	3.5	205
30	Which Genetics Variants in DNase-Seq Footprints Are More Likely to Alter Binding?. PLoS Genetics, 2016, 12, e1005875.	3.5	56
31	Molecular QTL discovery incorporating genomic annotations using Bayesian false discovery rate control. Annals of Applied Statistics, 2016, 10, .	1.1	54
32	The genetic regulatory signature of type 2 diabetes in human skeletal muscle. Nature Communications, 2016, 7, 11764.	12.8	114
33	Efficient Integrative Multi-SNP Association Analysis via Deterministic Approximation of Posteriors. American Journal of Human Genetics, 2016, 98, 1114-1129.	6.2	147
34	High-throughput allele-specific expression across 250 environmental conditions. Genome Research, 2016, 26, 1627-1638.	5.5	138
35	Cross-Population Joint Analysis of eQTLs: Fine Mapping and Functional Annotation. PLoS Genetics, 2015, 11, e1005176.	3.5	93
36	Bayesian model comparison in genetic association analysis: linear mixed modeling and SNP set testing. Biostatistics, 2015, 16, 701-712.	1.5	5

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37	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	12.6	4,659
38	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	12.6	252
39	Genome-wide Association Analysis of Psoriatic Arthritis and Cutaneous Psoriasis Reveals Differences in Their Genetic Architecture. American Journal of Human Genetics, 2015, 97, 816-836.	6.2	245
40	QuASAR: quantitative allele-specific analysis of reads. Bioinformatics, 2015, 31, 1235-1242.	4.1	70
41	Bayesian methods for genetic association analysis with heterogeneous subgroups: From meta-analyses to geneâ€“environment interactions. Annals of Applied Statistics, 2014, 8, 176-203.	1.1	52
42	The Role of Environmental Heterogeneity in Meta-Analysis of Gene-Environment Interactions With Quantitative Traits. Genetic Epidemiology, 2014, 38, 416-429.	1.3	12
43	Bayesian model selection in complex linear systems, as illustrated in genetic association studies. Biometrics, 2014, 70, 73-83.	1.4	26
44	A Statistical Framework for Joint eQTL Analysis in Multiple Tissues. PLoS Genetics, 2013, 9, e1003486.	3.5	226
45	The Genotype-Tissue Expression (GTEx) project. Nature Genetics, 2013, 45, 580-585.	21.4	6,815
46	Interactions between Glucocorticoid Treatment and Cis-Regulatory Polymorphisms Contribute to Cellular Response Phenotypes. PLoS Genetics, 2011, 7, e1002162.	3.5	103
47	Gene, region and pathway level analyses in wholeâ€genome studies. Genetic Epidemiology, 2010, 34, 222-231.	1.3	46
48	Using linear predictors to impute allele frequencies from summary or pooled genotype data. Annals of Applied Statistics, 2010, 4, 1158-1182.	1.1	74
49	Broad-Scale Recombination Patterns Underlying Proper Disjunction in Humans. PLoS Genetics, 2009, 5, e1000658.	3.5	107
50	High-Resolution Mapping of Crossovers Reveals Extensive Variation in Fine-Scale Recombination Patterns Among Humans. Science, 2008, 319, 1395-1398.	12.6	340
51	Association studies for untyped markers with TUNA. Bioinformatics, 2008, 24, 435-437.	4.1	13
52	A worldwide survey of haplotype variation and linkage disequilibrium in the human genome. Nature Genetics, 2006, 38, 1251-1260.	21.4	474
53	A Map of Recent Positive Selection in the Human Genome. PLoS Biology, 2006, 4, e72.	5.6	2,329
54	Coverage and Characteristics of the Affymetrix GeneChip Human Mapping 100K SNP Set. PLoS Genetics, 2006, 2, e67.	3.5	38

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55	Association mapping and fine mapping with TreeLD. Bioinformatics, 2005, 21, 3168-3170.	4.1	12
56	Coverage and Characteristics of the The Affymetrix GeneChip Â® Human Mapping 100K SNP Set. PLoS Genetics, 2005, preprint, e67.	3.5	0
57	Evidence for Extensive Transmission Distortion in the Human Genome. American Journal of Human Genetics, 2004, 74, 62-72.	6.2	111