Wei Chen

List of Publications by Year
in descending order

136	24,232	61984	13771
papers	citations	43 h-index	129 g-index

151	151	151	45901
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A region-based method for causal mediation analysis of DNA methylation data. Epigenetics, 2022, 17, 286-296.	2.7	4
2	The independent prognostic value of global epigenetic alterations: An analysis of single-cell ATAC-seq of circulating leukocytes from trauma patients followed by validation in whole blood leukocyte transcriptomes across three etiologies of critical illness. EBioMedicine, 2022, 76, 103860.	6.1	7
3	Child maltreatment, anxiety and depression, and asthma among British adults in the UK Biobank. European Respiratory Journal, 2022, 60, 2103160.	6.7	8
4	LONGL-Net: temporal correlation structure guided deep learning model to predict longitudinal age-related macular degeneration severity. , 2022, 1, pgab003.		7
5	Differential gene expression in nasal airway epithelium from overweight or obese youth with asthma. Pediatric Allergy and Immunology, 2022, 33, e13776.	2.6	5
6	Robust and accurate estimation of cellular fraction from tissue omics data via ensemble deconvolution. Bioinformatics, 2022, 38, 3004-3010.	4.1	10
7	DNA Methylation and Atopic Diseases. Methods in Molecular Biology, 2022, 2432, 85-99.	0.9	1
8	Gene-Based Association Testing of Dichotomous Traits With Generalized Functional Linear Mixed Models Using Extended Pedigrees: Applications to Age-Related Macular Degeneration. Journal of the American Statistical Association, 2021, 116, 531-545.	3.1	3
9	A genome-wide association study of severe asthma exacerbations in Latino children and adolescents. European Respiratory Journal, 2021, 57, 2002693.	6.7	15
10	A genome-wide study of DNA methylation in white blood cells and asthma in Latino children and youth. Epigenetics, 2021, 16, 577-585.	2.7	10
11	A genome-wide association study of asthma hospitalizations in adults. Journal of Allergy and Clinical Immunology, 2021, 147, 933-940.	2.9	23
12	A road map from single-cell transcriptome to patient classification for the immune response to trauma. JCI Insight, 2021, 6, .	5.0	29
13	Genome-Wide Association Studies-Based Machine Learning for Prediction of Age-Related Macular Degeneration Risk. Translational Vision Science and Technology, 2021, 10, 29.	2.2	14
14	Exposure to violence, chronic stress, nasal DNA methylation, and atopic asthma in children. Pediatric Pulmonology, 2021, 56, 1896-1905.	2.0	22
15	High-dimensional profiling clusters asthma severity by lymphoid and non-lymphoid status. Cell Reports, 2021, 35, 108974.	6.4	32
16	Inference of large modified Poisson-type graphical models: Application to RNA-seq data in childhood atopic asthma studies. Annals of Applied Statistics, 2021, 15, .	1.1	1
17	CHIT: an allele-specific method for testing the association between molecular quantitative traits and phenotypeâ€“genotype interaction. Bioinformatics, 2021, 37, 4764-4770.	4.1	0
18	Myofibroblast transcriptome indicates SFRP2hi fibroblast progenitors in systemic sclerosis skin. Nature Communications, 2021, 12, 4384.	12.8	101

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19	Identification and inference for subgroups with differential treatment efficacy from randomized controlled trials with survival outcomes through multiple testing. Statistics in Medicine, 2021, 40, 6523-6540.	1.6	2
20	AMD Genetics: Methods and Analyses for Association, Progression, and Prediction. Advances in Experimental Medicine and Biology, 2021, 1256, 191-200.	1.6	6
21	Geneâ€based association analysis for bivariate timeâ€toâ€event data through functional regression with copula models. Biometrics, 2020, 76, 619-629.	1.4	6
22	SNPs identified by GWAS affect asthma risk through DNA methylation and expression of cis-genes in airway epithelium. European Respiratory Journal, 2020, 55, 1902079.	6.7	21
23	Genomeâ€wide association studyâ€based deep learning for survival prediction. Statistics in Medicine, 2020, 39, 4605-4620.	1.6	26
24	Artificial-cell-type aware cell-type classification in CITE-seq. Bioinformatics, 2020, 36, i542-i550.	4.1	10
25	GMM-Demux: sample demultiplexing, multiplet detection, experiment planning, and novel cell-type verification in single cell sequencing. Genome Biology, 2020, 21, 188.	8.8	37
26	PIRs mediate innate myeloid cell memory to nonself MHC molecules. Science, 2020, 368, 1122-1127.	12.6	92
27	BREM-SC: a bayesian random effects mixture model for joint clustering single cell multi-omics data. Nucleic Acids Research, 2020, 48, 5814-5824.	14.5	50
28	Rapid reconstitution of regulatory T-cell subsets is associated with reduced rates of acute graft-versus-host disease and absence of viremia after cord blood transplantation in children with reduced-intensity conditioning using alemtuzumab. Cytotherapy, 2020, 22, 149-157.	0.7	1
29	Expression Quantitative Trait Methylation Analysis Reveals Methylomic Associations With Gene Expression in Childhood Asthma. Chest, 2020, 158, 1841-1856.	0.8	28
30	Glycated Hemoglobin A1c, Lung Function, and Hospitalizations Among Adults with Asthma. Journal of Allergy and Clinical Immunology: in Practice, 2020, 8, 3409-3415.e1.	3.8	26
31	Deep-learning-based prediction of late age-related macular degeneration progression. Nature Machine Intelligence, 2020, 2, 141-150.	16.0	79
32	Transcriptome-wide and differential expression network analyses of childhood asthma in nasal epithelium. Journal of Allergy and Clinical Immunology, 2020, 146, 671-675.	2.9	16
33	Geographic Difference Shaped Human Ocular Surface Metagenome of Young Han Chinese From Beijing, Wenzhou, and Guangzhou Cities. , 2020, 61, 47.		29
34	Nasal DNA methylation profiling of asthma and rhinitis. Journal of Allergy and Clinical Immunology, 2020, 145, 1655-1663.	2.9	56
35	A novel whole blood gene expression signature for asthma, dermatitis, and rhinitis multimorbidity in children and adolescents. Allergy: European Journal of Allergy and Clinical Immunology, 2020, 75, 3248-3260.	5.7	55
36	Single cell RNA sequencing identifies an early monocyte gene signature in acute respiratory distress syndrome. JCI Insight, 2020, 5, .	5.0	39

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37	Sleep Duration, Current Asthma, and Lung Function in a Nationwide Study of U.S. Adults. American Journal of Respiratory and Critical Care Medicine, 2019, 200, 926-929.	5.6	15
38	Expression patterns of small numbers of transcripts from functionally-related pathways predict survival in multiple cancers. BMC Cancer, 2019, 19, 686.	2.6	8
39	Treg Cells Promote the SREBP1-Dependent Metabolic Fitness of Tumor-Promoting Macrophages via Repression of CD8+ T Cell-Derived Interferon-Î³. Immunity, 2019, 51, 381-397.e6.	14.3	186
40	Proliferating SPP1/MERTK-expressing macrophages in idiopathic pulmonary fibrosis. European Respiratory Journal, 2019, 54, 1802441.	6.7	400
41	Serum Cadmium and Lead, Current Wheeze, and Lung Function in a Nationwide Study of Adults in the United States. Journal of Allergy and Clinical Immunology: in Practice, 2019, 7, 2653-2660.e3.	3.8	29
42	CSMD: a computational subtraction-based microbiome discovery pipeline for species-level characterization of clinical metagenomic samples. Bioinformatics, 2019, 36, 1577-1583.	4.1	2
43	Variants in oxidative stress-related genes affect the chemosensitivity through Nrf2-mediated signaling pathway in biliary tract cancer. EBioMedicine, 2019, 48, 143-160.	6.1	20
44	Clinical utility of ultrahigh fractional exhaled nitric oxide in predicting bronchial hyperresponsiveness in patients with suspected asthma. Postgraduate Medical Journal, 2019, 95, 541-546.	1.8	3
45	Deficiency in AIM2 induces inflammation and adipogenesis in white adipose tissue leading to obesity and insulin resistance. Diabetologia, 2019, 62, 2325-2339.	6.3	31
46	Epigenome-wide effects of vitamin D on asthma bronchial epithelial cells. Epigenetics, 2019, 14, 844-849.	2.7	3
47	An integrative association method for omics data based on a modified Fisherâ€™s method with application to childhood asthma. PLoS Genetics, 2019, 15, e1008142.	3.5	3
48	Transcriptomic Responses to Ivacaftor and Prediction of Ivacaftor Clinical Responsiveness. American Journal of Respiratory Cell and Molecular Biology, 2019, 61, 643-652.	2.9	23
49	A Bayesian mixture model for clustering droplet-based single-cell transcriptomic data from population studies. Nature Communications, 2019, 10, 1649.	12.8	56
50	Transcriptomics of atopy and atopic asthma in white blood cells from children and adolescents. European Respiratory Journal, 2019, 53, 1900102.	6.7	20
51	Adaptive plasticity of IL-10+ and IL-35+ Treg cells cooperatively promotes tumor T cell exhaustion. Nature Immunology, 2019, 20, 724-735.	14.5	297
52	Under-diagnosis of atopic dermatitis in Puerto Rican children. World Allergy Organization Journal, 2019, 12, 100003.	3.5	3
53	DNA methylation in nasal epithelium, atopy, and atopic asthma in children: a genome-wide study. Lancet Respiratory Medicine,the, 2019, 7, 336-346.	10.7	147
54	Copula-based score test for bivariate time-to-event data, with application to a genetic study of AMD progression. Lifetime Data Analysis, 2019, 25, 546-568.	0.9	14

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55	A Genome-Wide Association Study in Hispanics/Latinos Identifies Novel Signals for Lung Function. The Hispanic Community Health Study/Study of Latinos. American Journal of Respiratory and Critical Care Medicine, 2018, 198, 208-219.	5.6	37
56	KMgene: a unified R package for gene-based association analysis for complex traits. Bioinformatics, 2018, 34, 2144-2146.	4.1	9
57	Association of IGFN1 variant with polypoidal choroidal vasculopathy. Journal of Gene Medicine, 2018, 20, e3007.	2.8	8
58	Pancreatic gene expression during recovery after pancreatitis reveals unique transcriptome profiles. Scientific Reports, 2018, 8, 1406.	3.3	14
59	Genome-wide analysis of disease progression in age-related macular degeneration. Human Molecular Genetics, 2018, 27, 929-940.	2.9	67
60	SFRP2/DPP4 and FMO1/LSP1 Define Major Fibroblast Populations in Human Skin. Journal of Investigative Dermatology, 2018, 138, 802-810.	0.7	236
61	DIMM-SC: a Dirichlet mixture model for clustering droplet-based single cell transcriptomic data. Bioinformatics, 2018, 34, 139-146.	4.1	68
62	Bayesian integrative model for multi-omics data with missingness. Bioinformatics, 2018, 34, 3801-3808.	4.1	15
63	A semiparametric imputation approach for regression with censored covariate with application to an AMD progression study. Statistics in Medicine, 2018, 37, 3293-3308.	1.6	3
64	SILGGM: An extensive R package for efficient statistical inference in large-scale gene networks. PLoS Computational Biology, 2018, 14, e1006369.	3.2	33
65	Statistics for Xâ€chromosome associations. Genetic Epidemiology, 2018, 42, 539-550.	1.3	16
66	An epigenome-wide association study of total serum IgE in Hispanic children. Journal of Allergy and Clinical Immunology, 2017, 140, 571-577.	2.9	53
67	Genome-wide interaction study of dust mite allergen on lung function in children with asthma. Journal of Allergy and Clinical Immunology, 2017, 140, 996-1003.e7.	2.9	25
68	AIM2 Inflammasome Is Critical for Influenza-Induced Lung Injury and Mortality. Journal of Immunology, 2017, 198, 4383-4393.	0.8	85
69	A meta-analysis of genome-wide association studies of asthma in PuertoÂRicans. European Respiratory Journal, 2017, 49, 1601505.	6.7	51
70	Bivariate Analysis of Age-Related Macular Degeneration Progression Using Genetic Risk Scores. Genetics, 2017, 206, 119-133.	2.9	46
71	A Multiomics Approach to Identify Genes Associated with Childhood Asthma Risk and Morbidity. American Journal of Respiratory Cell and Molecular Biology, 2017, 57, 439-447.	2.9	26
72	Meta-analysis of quantitative pleiotropic traits for next-generation sequencing with multivariate functional linear models. European Journal of Human Genetics, 2017, 25, 350-359.	2.8	4

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73	The Influence of Age and Sex on Ocular Surface Microbiota in Healthy Adults. , 2017, 58, 6030.		107
74	LAIT: a local ancestry inference toolkit. BMC Genetics, 2017, 18, 83.	2.7	5
75	Conjunctival Microbiome Changes Associated With Soft Contact Lens and Orthokeratology Lens Wearing. , 2017, 58, 128.		55
76	Antiinflammatory effects of bromodomain and extraterminal domain inhibition in cystic fibrosis lung inflammation. JCI Insight, 2016, 1, .	5.0	21
77	FastGGM: An Efficient Algorithm for the Inference of Gaussian Graphical Model in Biological Networks. PLoS Computational Biology, 2016, 12, e1004755.	3.2	63
78	Gene-Based Association Analysis for Censored Traits Via Fixed Effect Functional Regressions. Genetic Epidemiology, 2016, 40, 133-143.	1.3	12
79	Control for Population Structure and Relatedness for Binary Traits in Genetic Association Studies via Logistic Mixed Models. American Journal of Human Genetics, 2016, 98, 653-666.	6.2	347
80	The impact of genotype calling errors on family-based studies. Scientific Reports, 2016, 6, 28323.	3.3	12
81	IL-17 Receptor Signaling in the Lung Epithelium Is Required for Mucosal Chemokine Gradients and Pulmonary Host Defense against K.Apneumoniae. Cell Host and Microbe, 2016, 20, 596-605.	11.0	115
82	CXXC finger protein 1 is critical for T-cell intrathymic development through regulating H3K4 trimethylation. Nature Communications, 2016, 7, 11687.	12.8	38
83	A computational method for genotype calling in family-based sequencing data. BMC Bioinformatics, 2016, 17, 37.	2.6	8
84	A Pipeline for Classifying Relationships Using Dense SNP/SNV Data and Putative Pedigree Information. Genetic Epidemiology, 2016, 40, 161-171.	1.3	3
85	Meta-analysis of Complex Diseases at Gene Level with Generalized Functional Linear Models. Genetics, 2016, 202, 457-470.	2.9	18
86	Imputation of missing covariate values in epigenome-wide analysis of DNA methylation data. Epigenetics, 2016, 11, 132-139.	2.7	10
87	Rare-Variant Kernel Machine Test for Longitudinal Data from Population and Family Samples. Human Heredity, 2015, 80, 126-138.	0.8	9
88	Leveraging Identity-by-Descent for Accurate Genotype Inference in Family Sequencing Data. PLoS Genetics, 2015, 11, e1005271.	3.5	3
89	A systematic study of normalization methods for Infinium 450K methylation data using whole-genome bisulfite sequencing data. Epigenetics, 2015, 10, 662-669.	2.7	68
90	Stress and Bronchodilator Response in Children with Asthma. American Journal of Respiratory and Critical Care Medicine, 2015, 192, 47-56.	5.6	99

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91	RNA-seq in Pulmonary Medicine: How Much Is Enough?. American Journal of Respiratory and Critical Care Medicine, 2015, 192, 389-391.	5.6	11
92	A Genome-Wide Association Study of Chronic Obstructive Pulmonary Disease in Hispanics. Annals of the American Thoracic Society, 2015, 12, 340-348.	3.2	41
93	DISSCO: direct imputation of summary statistics allowing covariates. Bioinformatics, 2015, 31, 2434-2442.	4.1	18
94	A haplotype-based framework for group-wise transmission/disequilibrium tests for rare variant association analysis. Bioinformatics, 2015, 31, 1452-1459.	4.1	14
95	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
96	Associating Multivariate Quantitative Phenotypes with Genetic Variants in Family Samples with a Novel Kernel Machine Regression Method. Genetics, 2015, 201, 1329-1339.	2.9	14
97	Gene Level Meta-Analysis of Quantitative Traits by Functional Linear Models. Genetics, 2015, 200, 1089-1104.	2.9	25
98	A Genome-Wide Association Study of Post-bronchodilator Lung Function in Children with Asthma. American Journal of Respiratory and Critical Care Medicine, 2015, 192, 634-637.	5.6	16
99	A Bayesian framework for de novo mutation calling in parents-offspring trios. Bioinformatics, 2015, 31, 1375-1381.	4.1	87
100	Expression Quantitative Trait Loci (eQTL) Mapping in Puerto Rican Children. PLoS ONE, 2015, 10, e0122464.	2.5	10
101	Genome-wide association study and meta-analysis of intraocular pressure. Human Genetics, 2014, 133, 41-57.	3.8	93
102	Native American Ancestry, Lung Function, and COPD in Costa Ricans. Chest, 2014, 145, 704-710.	0.8	23
103	Using Current Data to Define New Approach in Age Related Macular Degeneration: Need to Accelerate Translational Research. Current Genomics, 2014, 15, 266-277.	1.6	10
104	Single Nucleotide Polymorphism (SNP) Detection and Genotype Calling from Massively Parallel Sequencing (MPS) Data. Statistics in Biosciences, 2013, 5, 3-25.	1.2	15
105	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	2.9	141
106	Seven new loci associated with age-related macular degeneration. Nature Genetics, 2013, 45, 433-439.	21.4	687
107	ADCYAP1R1 and Asthma in Puerto Rican Children. American Journal of Respiratory and Critical Care Medicine, 2013, 187, 584-588.	5.6	97
108	Genotype calling and haplotyping in parent-offspring trios. Genome Research, 2013, 23, 142-151.	5.5	46

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109	Association between CFH Y402H Polymorphism and Age Related Macular Degeneration in North Indian Cohort. PLoS ONE, 2013, 8, e70193.	2.5	42
110	The Genetic Variant on Chromosome 10p14 Is Associated with Risk of Colorectal Cancer: Results from a Case-Control Study and a Meta-Analysis. PLoS ONE, 2013, 8, e64310.	2.5	9
111	A Likelihood-Based Framework for Variant Calling and De Novo Mutation Detection in Families. PLoS Genetics, 2012, 8, e1002944.	3.5	71
112	The 1000 Genomes Project: data management and community access. Nature Methods, 2012, 9, 459-462.	19.0	308
113	Long-Term Outcome of Early-Stage Rectal Cancer Undergoing Standard Resection and Local Excision. Clinical Colorectal Cancer, 2011, 10, 37-41.	2.3	23
114	The functional spectrum of low-frequency coding variation. Genome Biology, 2011, 12, R84.	9.6	173
115	Cell-Deposited Matrix Improves Retinal Pigment Epithelium Survival on Aged Submacular Human Bruch's Membrane. , 2011, 52, 1345.		37
116	A 32 kb Critical Region Excluding Y402H in CFH Mediates Risk for Age-Related Macular Degeneration. PLoS ONE, 2011, 6, e25598.	2.5	46
117	Prognostic analysis for carcinoid tumours of the rectum: a single institutional analysis of 106 patients. Colorectal Disease, 2011, 13, 150-153.	1.4	26
118	Oncological outcome of T1 rectal cancer undergoing standard resection and local excision. Colorectal Disease, 2011, 13, e14-e19.	1.4	50
119	Variation in genome-wide mutation rates within and between human families. Nature Genetics, 2011, 43, 712-714.	21.4	525
120	Evidence of association ofAPOEwith age-related macular degeneration - a pooled analysis of 15 studies. Human Mutation, 2011, 32, 1407-1416.	2.5	130
121	EZH2 and ALDH-1 mark breast epithelium at risk for breast cancer development. Modern Pathology, 2011, 24, 786-793.	5.5	66
122	Demographic history and rare allele sharing among human populations. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11983-11988.	7.1	589
123	Variations in Apolipoprotein E Frequency With Age in a Pooled Analysis of a Large Group of Older People. American Journal of Epidemiology, 2011, 173, 1357-1364.	3.4	85
124	Complement Factor D in Age-Related Macular Degeneration. , 2011, 52, 8828.		92
125	Gene Expression in Skin and Lymphoblastoid Cells: Refined Statistical Method Reveals Extensive Overlap in cis-eQTL Signals. American Journal of Human Genetics, 2010, 87, 779-789.	6.2	169
126	Integration of genetic signature and TNM staging system for predicting the relapse of locally advanced colorectal cancer. International Journal of Colorectal Disease, 2010, 25, 1277-1285.	2.2	14

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127	E2-2 Protein and Fuchs's Corneal Dystrophy. New England Journal of Medicine, 2010, 363, 1016-1024.	27.0	247
128	Transcriptome analysis and molecular signature of human retinal pigment epithelium. Human Molecular Genetics, 2010, 19, 2468-2486.	2.9	249
129	Genetic variants near TIMP3 and high-density lipoproteinâ€“associated loci influence susceptibility to age-related macular degeneration. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7401-7406.	7.1	475
130	Age-related macular degeneration-associated variants at chromosome 10q26 do not significantly alter ARMS2 and HTRA1 transcript levels in the human retina. Molecular Vision, 2010, 16, 1317-23.	1.1	40
131	GWAS GUI: graphical browser for the results of whole-genome association studies with high-dimensional phenotypes. Bioinformatics, 2009, 25, 284-285.	4.1	8
132	SNP@Evolution: a hierarchical database of positive selection on the human genome. BMC Evolutionary Biology, 2009, 9, 221.	3.2	26
133	A variant of mitochondrial protein LOC387715/ARMS2, not HTRA1, is strongly associated with age-related macular degeneration. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 16227-16232.	7.1	398
134	Genetic susceptibility to age-related macular degeneration: a paradigm for dissecting complex disease traits. Human Molecular Genetics, 2007, 16, R174-R182.	2.9	168
135	A genome-wide association study of global gene expression. Nature Genetics, 2007, 39, 1202-1207.	21.4	882
136	A Genome-wide Study of DNA Methylation in Nasal Epithelium and Atopy and Atopic Asthma in Children. SSRN Electronic Journal, 0, , .	0.4	0