Wei Chen

List of Publications by Year in Descending Order

139 papers	**15,845** citations	**39** h-index	**125** g-index
151 ext. papers	**21,011** ext. citations	**8.6** avg, IF	**5.36** L-index

#	Paper	IF	Citations
139	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	8.8	2
138	Child maltreatment, anxiety and depression, and asthma among British adults in the UK Biobank.. *European Respiratory Journal*, **2022**,	13.6	2
137	LONGL-Net: temporal correlation structure guided deep learning model to predict longitudinal age-related macular degeneration severity. **2022**, 1, pgab003		1
136	Differential gene expression in nasal airway epithelium from overweight or obese youth with asthma.. *Pediatric Allergy and Immunology*, **2022**, 33, e13776	4.2	0
135	DNA Methylation and Atopic Diseases.. *Methods in Molecular Biology*, **2022**, 2432, 85-99	1.4	1
134	Multi-modal Genotype and Phenotype Mutual Learning to Enhance Single-Modal Input Based Longitudinal Outcome Prediction. *Lecture Notes in Computer Science*, **2022**, 209-229	0.9	
133	Exposure to violence, chronic stress, nasal DNA methylation, and atopic asthma in children. *Pediatric Pulmonology*, **2021**, 56, 1896-1905	3.5	2
132	A region-based method for causal mediation analysis of DNA methylation data. *Epigenetics*, **2021**, 1-11	5.7	0
131	High-dimensional profiling clusters asthma severity by lymphoid and non-lymphoid status. *Cell Reports*, **2021**, 35, 108974	10.6	9
130	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	2.8	1
129	A genome-wide association study of severe asthma exacerbations in Latino children and adolescents. *European Respiratory Journal*, **2021**, 57,	13.6	6
128	A genome-wide study of DNA methylation in white blood cells and asthma in Latino children and youth. *Epigenetics*, **2021**, 16, 577-585	5.7	4
127	A genome-wide association study of asthma hospitalizations in adults. *Journal of Allergy and Clinical Immunology*, **2021**, 147, 933-940	11.5	5
126	A road map from single-cell transcriptome to patient classification for the immune response to trauma. *JCI Insight*, **2021**, 6,	9.9	8
125	Genome-Wide Association Studies-Based Machine Learning for Prediction of Age-Related Macular Degeneration Risk. *Translational Vision Science and Technology*, **2021**, 10, 29	3.3	4
124	Myofibroblast transcriptome indicates SFRP2 fibroblast progenitors in systemic sclerosis skin. *Nature Communications*, **2021**, 12, 4384	17.4	13
123	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	2.2	

122	AMD Genetics: Methods and Analyses for Association, Progression, and Prediction. *Advances in Experimental Medicine and Biology*, **2021**, 1256, 191-200	3.6	1
121	PIRs mediate innate myeloid cell memory to nonself MHC molecules. *Science*, **2020**, 368, 1122-1127	33.3	41
120	BREM-SC: a bayesian random effects mixture model for joint clustering single cell multi-omics data. *Nucleic Acids Research*, **2020**, 48, 5814-5824	20.1	16
119	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	4.8	0
118	Expression Quantitative Trait Methylation Analysis Reveals Methylomic Associations With Gene Expression in Childhood Asthma. *Chest*, **2020**, 158, 1841-1856	5.3	9
117	Glycated Hemoglobin A, Lung Function, and Hospitalizations Among Adults with Asthma. *Journal of Allergy and Clinical Immunology: in Practice*, **2020**, 8, 3409-3415.e1	5.4	9
116	Deep-learning-based Prediction of Late Age-Related Macular Degeneration Progression. *Nature Machine Intelligence*, **2020**, 2, 141-150	22.5	35
115	Transcriptome-wide and differential expression network analyses of childhood asthma in nasal epithelium. *Journal of Allergy and Clinical Immunology*, **2020**, 146, 671-675	11.5	7
114	Geographic Difference Shaped Human Ocular Surface Metagenome of Young Han Chinese From Beijing, Wenzhou, and Guangzhou Cities **2020**, 61, 47		12
113	Nasal DNA methylation profiling of asthma and rhinitis. *Journal of Allergy and Clinical Immunology*, **2020**, 145, 1655-1663	11.5	34
112	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	9.3	27
111	CSMD: a computational subtraction-based microbiome discovery pipeline for species-level characterization of clinical metagenomic samples. *Bioinformatics*, **2020**, 36, 1577-1583	7.2	
110	Single cell RNA sequencing identifies an early monocyte gene signature in acute respiratory distress syndrome. *JCI Insight*, **2020**, 5,	9.9	13
109	Exposure to violence, chronic stress, nasal DNA methylation, and atopic asthma in children **2020**,		5
108	Gene-based association analysis for bivariate time-to-event data through functional regression with copula models. *Biometrics*, **2020**, 76, 619-629	1.8	4
107	SNPs identified by GWAS affect asthma risk through DNA methylation and expression of -genes in airway epithelium. *European Respiratory Journal*, **2020**, 55,	13.6	9
106	Genome-wide association study-based deep learning for survival prediction. *Statistics in Medicine*, **2020**, 39, 4605-4620	2.3	8
105	Artificial-cell-type aware cell-type classification in CITE-seq. *Bioinformatics*, **2020**, 36, i542-i550	7.2	4

104	GMM-Demux: sample demultiplexing, multiplet detection, experiment planning, and novel cell-type verification in single cell sequencing. *Genome Biology*, **2020**, 21, 188	18.3	12
103	Deficiency in AIM2 induces inflammation and adipogenesis in white adipose tissue leading to obesity and insulin resistance. *Diabetologia*, **2019**, 62, 2325-2339	10.3	17
102	Epigenome-wide effects of vitamin D on asthma bronchial epithelial cells. *Epigenetics*, **2019**, 14, 844-849	5.7	1
101	An integrative association method for omics data based on a modified Fisher's method with application to childhood asthma. *PLoS Genetics*, **2019**, 15, e1008142	6	2
100	Transcriptomic Responses to Ivacaftor and Prediction of Ivacaftor Clinical Responsiveness. *American Journal of Respiratory Cell and Molecular Biology*, **2019**, 61, 643-652	5.7	12
99	A Bayesian mixture model for clustering droplet-based single-cell transcriptomic data from population studies. *Nature Communications*, **2019**, 10, 1649	17.4	25
98	Transcriptomics of atopy and atopic asthma in white blood cells from children and adolescents. *European Respiratory Journal*, **2019**, 53,	13.6	9
97	Adaptive plasticity of IL-10 and IL-35 T cells cooperatively promotes tumor T cell exhaustion. *Nature Immunology*, **2019**, 20, 724-735	19.1	143
96	Under-diagnosis of atopic dermatitis in Puerto Rican children. *World Allergy Organization Journal*, **2019**, 12, 100003	5.2	1
95	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	10.2	7
94	Expression patterns of small numbers of transcripts from functionally-related pathways predict survival in multiple cancers. *BMC Cancer*, **2019**, 19, 686	4.8	3
93	Treg Cells Promote the SREBP1-Dependent Metabolic Fitness of Tumor-Promoting Macrophages via Repression of CD8 T Cell-Derived Interferon-□ *Immunity*, **2019**, 51, 381-397.e6	32.3	76
92	Proliferating SPP1/MERTK-expressing macrophages in idiopathic pulmonary fibrosis. *European Respiratory Journal*, **2019**, 54,	13.6	156
91	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	5.4	15
90	Variants in oxidative stress-related genes affect the chemosensitivity through Nrf2-mediated signaling pathway in biliary tract cancer. *EBioMedicine*, **2019**, 48, 143-160	8.8	9
89	Clinical utility of ultrahigh fractional exhaled nitric oxide in predicting bronchial hyperresponsiveness in patients with suspected asthma. *Postgraduate Medical Journal*, **2019**, 95, 541-546	2	2
88	DNA methylation in nasal epithelium, atopy, and atopic asthma in children: a genome-wide study. *Lancet Respiratory Medicine,the*, **2019**, 7, 336-346	35.1	87
87	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	1.3	8

86	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	10.2	27
85	KMgene: a unified R package for gene-based association analysis for complex traits. *Bioinformatics*, **2018**, 34, 2144-2146	7.2	4
84	Association of IGFN1 variant with polypoidal choroidal vasculopathy. *Journal of Gene Medicine*, **2018**, 20, e3007	3.5	5
83	Pancreatic gene expression during recovery after pancreatitis reveals unique transcriptome profiles. *Scientific Reports*, **2018**, 8, 1406	4.9	11
82	Genome-wide analysis of disease progression in age-related macular degeneration. *Human Molecular Genetics*, **2018**, 27, 929-940	5.6	37
81	A semiparametric imputation approach for regression with censored covariate with application to an AMD progression study. *Statistics in Medicine*, **2018**, 37, 3293-3308	2.3	1
80	SILGGM: An extensive R package for efficient statistical inference in large-scale gene networks. *PLoS Computational Biology*, **2018**, 14, e1006369	5	18
79	Statistics for X-chromosome associations. *Genetic Epidemiology*, **2018**, 42, 539-550	2.6	8
78	SFRP2/DPP4 and FMO1/LSP1 Define Major Fibroblast Populations in Human Skin. *Journal of Investigative Dermatology*, **2018**, 138, 802-810	4.3	138
77	DIMM-SC: a Dirichlet mixture model for clustering droplet-based single cell transcriptomic data. *Bioinformatics*, **2018**, 34, 139-146	7.2	36
76	Bayesian integrative model for multi-omics data with missingness. *Bioinformatics*, **2018**, 34, 3801-3808	7.2	8
75	An epigenome-wide association study of total serum IgE in Hispanic children. *Journal of Allergy and Clinical Immunology*, **2017**, 140, 571-577	11.5	41
74	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	11.5	16
73	AIM2 Inflammasome Is Critical for Influenza-Induced Lung Injury and Mortality. *Journal of Immunology*, **2017**, 198, 4383-4393	5.3	61
72	A meta-analysis of genome-wide association studies of asthma in Puerto Ricans. *European Respiratory Journal*, **2017**, 49,	13.6	36
71	Bivariate Analysis of Age-Related Macular Degeneration Progression Using Genetic Risk Scores. *Genetics*, **2017**, 206, 119-133	4	31
70	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	5.7	15
69	Meta-analysis of quantitative pleiotropic traits for next-generation sequencing with multivariate functional linear models. *European Journal of Human Genetics*, **2017**, 25, 350-359	5.3	2

68   The Influence of Age and Sex on Ocular Surface Microbiota in Healthy Adults **2017**, 58, 6030-6037   77

67   LAIT: a local ancestry inference toolkit. *BMC Genetics*, **2017**, 18, 83   2.6   5

66   Conjunctival Microbiome Changes Associated With Soft Contact Lens and Orthokeratology Lens Wearing **2017**, 58, 128-136   40

65   The impact of genotype calling errors on family-based studies. *Scientific Reports*, **2016**, 6, 28323   4.9   8

64   IL-17 Receptor Signaling in the Lung Epithelium Is Required for Mucosal Chemokine Gradients and Pulmonary Host Defense against K. pneumoniae. *Cell Host and Microbe*, **2016**, 20, 596-605   23.4   78

63   CXXC finger protein 1 is critical for T-cell intrathymic development through regulating H3K4 trimethylation. *Nature Communications*, **2016**, 7, 11687   17.4   21

62   A computational method for genotype calling in family-based sequencing data. *BMC Bioinformatics*, **2016**, 17, 37   3.6   6

61   A Pipeline for Classifying Relationships Using Dense SNP/SNV Data and Putative Pedigree Information. *Genetic Epidemiology*, **2016**, 40, 161-71   2.6   3

60   Meta-analysis of Complex Diseases at Gene Level with Generalized Functional Linear Models. *Genetics*, **2016**, 202, 457-70   4   13

59   Imputation of missing covariate values in epigenome-wide analysis of DNA methylation data. *Epigenetics*, **2016**, 11, 132-9   5.7   7

58   Antiinflammatory effects of bromodomain and extraterminal domain inhibition in cystic fibrosis lung inflammation. *JCI Insight*, **2016**, 1,   9.9   14

57   FastGGM: An Efficient Algorithm for the Inference of Gaussian Graphical Model in Biological Networks. *PLoS Computational Biology*, **2016**, 12, e1004755   5   31

56   Gene-Based Association Analysis for Censored Traits Via Fixed Effect Functional Regressions. *Genetic Epidemiology*, **2016**, 40, 133-43   2.6   10

55   Control for Population Structure and Relatedness for Binary Traits in Genetic Association Studies via Logistic Mixed Models. *American Journal of Human Genetics*, **2016**, 98, 653-66   11   207

54   A genome-wide association study of chronic obstructive pulmonary disease in Hispanics. *Annals of the American Thoracic Society*, **2015**, 12, 340-8   4.7   35

53   DISSCO: direct imputation of summary statistics allowing covariates. *Bioinformatics*, **2015**, 31, 2434-42   7.2   16

52   A haplotype-based framework for group-wise transmission/disequilibrium tests for rare variant association analysis. *Bioinformatics*, **2015**, 31, 1452-9   7.2   12

51   A global reference for human genetic variation. *Nature*, **2015**, 526, 68-74   50.4   8599

50	Associating Multivariate Quantitative Phenotypes with Genetic Variants in Family Samples with a Novel Kernel Machine Regression Method. *Genetics*, **2015**, 201, 1329-39	4	12
49	Gene Level Meta-Analysis of Quantitative Traits by Functional Linear Models. *Genetics*, **2015**, 200, 1089-104	4	24
48	A Genome-Wide Association Study of Post-bronchodilator Lung Function in Children with Asthma. *American Journal of Respiratory and Critical Care Medicine*, **2015**, 192, 634-7	10.2	10
47	A Bayesian framework for de novo mutation calling in parents-offspring trios. *Bioinformatics*, **2015**, 31, 1375-81	7.2	55
46	Rare-Variant Kernel Machine Test for Longitudinal Data from Population and Family Samples. *Human Heredity*, **2015**, 80, 126-38	1.1	7
45	Leveraging Identity-by-Descent for Accurate Genotype Inference in Family Sequencing Data. *PLoS Genetics*, **2015**, 11, e1005271	6	2
44	A systematic study of normalization methods for Infinium 450K methylation data using whole-genome bisulfite sequencing data. *Epigenetics*, **2015**, 10, 662-9	5.7	41
43	Stress and Bronchodilator Response in Children with Asthma. *American Journal of Respiratory and Critical Care Medicine*, **2015**, 192, 47-56	10.2	71
42	RNA-seq in Pulmonary Medicine: How Much Is Enough?. *American Journal of Respiratory and Critical Care Medicine*, **2015**, 192, 389-91	10.2	10
41	Expression quantitative trait loci (eQTL) mapping in Puerto Rican children. *PLoS ONE*, **2015**, 10, e0122464	3.7	8
40	Native American ancestry, lung function, and COPD in Costa Ricans. *Chest*, **2014**, 145, 704-710	5.3	22
39	Genome-wide association study and meta-analysis of intraocular pressure. *Human Genetics*, **2014**, 133, 41-57	6.3	79
38	Using current data to define new approach in age related macular degeneration: need to accelerate translational research. *Current Genomics*, **2014**, 15, 266-77	2.6	8
37	Single Nucleotide Polymorphism (SNP) Detection and Genotype Calling from Massively Parallel Sequencing (MPS) Data. *Statistics in Biosciences*, **2013**, 5, 3-25	1.5	14
36	Loci influencing blood pressure identified using a cardiovascular gene-centric array. *Human Molecular Genetics*, **2013**, 22, 1663-78	5.6	119
35	Seven new loci associated with age-related macular degeneration. *Nature Genetics*, **2013**, 45, 433-9, 439e1-2	36.3	577
34	ADCYAP1R1 and asthma in Puerto Rican children. *American Journal of Respiratory and Critical Care Medicine*, **2013**, 187, 584-8	10.2	75
33	Genotype calling and haplotyping in parent-offspring trios. *Genome Research*, **2013**, 23, 142-51	9.7	39

32	Association between CFH Y402H polymorphism and age related macular degeneration in North Indian cohort. *PLoS ONE*, **2013**, 8, e70193	3.7	37
31	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	3.7	9
30	The 1000 Genomes Project: data management and community access. *Nature Methods*, **2012**, 9, 459-62	21.6	202
29	A likelihood-based framework for variant calling and de novo mutation detection in families. *PLoS Genetics*, **2012**, 8, e1002944	6	60
28	Long-term outcome of early-stage rectal cancer undergoing standard resection and local excision. *Clinical Colorectal Cancer*, **2011**, 10, 37-41	3.8	17
27	The functional spectrum of low-frequency coding variation. *Genome Biology*, **2011**, 12, R84	18.3	161
26	Cell-deposited matrix improves retinal pigment epithelium survival on aged submacular human Bruch's membrane **2011**, 52, 1345-58		32
25	A 32 kb critical region excluding Y402H in CFH mediates risk for age-related macular degeneration. *PLoS ONE*, **2011**, 6, e25598	3.7	41
24	Prognostic analysis for carcinoid tumours of the rectum: a single institutional analysis of 106 patients. *Colorectal Disease*, **2011**, 13, 150-3	2.1	25
23	Oncological outcome of T1 rectal cancer undergoing standard resection and local excision. *Colorectal Disease*, **2011**, 13, e14-9	2.1	39
22	Variation in genome-wide mutation rates within and between human families. *Nature Genetics*, **2011**, 43, 712-4	36.3	404
21	Evidence of association of APOE with age-related macular degeneration: a pooled analysis of 15 studies. *Human Mutation*, **2011**, 32, 1407-16	4.7	99
20	EZH2 and ALDH-1 mark breast epithelium at risk for breast cancer development. *Modern Pathology*, **2011**, 24, 786-93	9.8	62
19	Demographic history and rare allele sharing among human populations. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 11983-8	11.5	455
18	Variations in apolipoprotein E frequency with age in a pooled analysis of a large group of older people. *American Journal of Epidemiology*, **2011**, 173, 1357-64	3.8	67
17	Complement factor D in age-related macular degeneration **2011**, 52, 8828-34		72
16	E2-2 protein and Fuchs's corneal dystrophy. *New England Journal of Medicine*, **2010**, 363, 1016-24	59.2	197
15	Transcriptome analysis and molecular signature of human retinal pigment epithelium. *Human Molecular Genetics*, **2010**, 19, 2468-86	5.6	193

List of Publications

14	Genetic variants near TIMP3 and high-density lipoprotein-associated loci influence susceptibility to age-related macular degeneration. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 7401-6	11.5	417
13	Gene expression in skin and lymphoblastoid cells: Refined statistical method reveals extensive overlap in cis-eQTL signals. *American Journal of Human Genetics*, **2010**, 87, 779-89	11	144
12	Integration of genetic signature and TNM staging system for predicting the relapse of locally advanced colorectal cancer. *International Journal of Colorectal Disease*, **2010**, 25, 1277-85	3	11
11	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	2.3	34
10	GWAS GUI: graphical browser for the results of whole-genome association studies with high-dimensional phenotypes. *Bioinformatics*, **2009**, 25, 284-5	7.2	8
9	SNP@Evolution: a hierarchical database of positive selection on the human genome. *BMC Evolutionary Biology*, **2009**, 9, 221	3	23
8	A genome-wide association study of global gene expression. *Nature Genetics*, **2007**, 39, 1202-7	36.3	801
7	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, 16227-32	11.5	356
6	Genetic susceptibility to age-related macular degeneration: a paradigm for dissecting complex disease traits. *Human Molecular Genetics*, **2007**, 16 Spec No. 2, R174-82	5.6	146
5	Expression quantitative trait methylation analysis reveals methylomic associations with gene expression in childhood asthma		1
4	GWAS-based Machine Learning for Prediction of Age-Related Macular Degeneration Risk		2
3	Deep-learning-based Prediction of Late Age-Related Macular Degeneration Progression		1
2	Sample demultiplexing, multiplet detection, experiment planning and novel cell type verification in single cell sequencing		1
1	Myofibroblast transcriptome indicates SFRP2+ fibroblast progenitors in systemic sclerosis skin		1