

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	A global reference for human genetic variation. <i>Nature</i> , 2015 , 526, 68-74	50.4	8599
138	A genome-wide association study of global gene expression. <i>Nature Genetics</i> , 2007 , 39, 1202-7	36.3	801
137	Seven new loci associated with age-related macular degeneration. <i>Nature Genetics</i> , 2013 , 45, 433-9, 439e1-2	36.3	577
136	Demographic history and rare allele sharing among human populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 11983-8	11.5	455
135	Genetic variants near TIMP3 and high-density lipoprotein-associated loci influence susceptibility to age-related macular degeneration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 7401-6	11.5	417
134	Variation in genome-wide mutation rates within and between human families. <i>Nature Genetics</i> , 2011 , 43, 712-4	36.3	404
133	A variant of mitochondrial protein LOC387715/ARMS2, not HTRA1, is strongly associated with age-related macular degeneration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 16227-32	11.5	356
132	Control for Population Structure and Relatedness for Binary Traits in Genetic Association Studies via Logistic Mixed Models. <i>American Journal of Human Genetics</i> , 2016 , 98, 653-66	11	207
131	The 1000 Genomes Project: data management and community access. <i>Nature Methods</i> , 2012 , 9, 459-62	21.6	202
130	E2-2 protein and Fuchs' corneal dystrophy. <i>New England Journal of Medicine</i> , 2010 , 363, 1016-24	59.2	197
129	Transcriptome analysis and molecular signature of human retinal pigment epithelium. <i>Human Molecular Genetics</i> , 2010 , 19, 2468-86	5.6	193
128	The functional spectrum of low-frequency coding variation. <i>Genome Biology</i> , 2011 , 12, R84	18.3	161
127	Proliferating SPP1/MERTK-expressing macrophages in idiopathic pulmonary fibrosis. <i>European Respiratory Journal</i> , 2019 , 54,	13.6	156
126	Genetic susceptibility to age-related macular degeneration: a paradigm for dissecting complex disease traits. <i>Human Molecular Genetics</i> , 2007 , 16 Spec No. 2, R174-82	5.6	146
125	Gene expression in skin and lymphoblastoid cells: Refined statistical method reveals extensive overlap in cis-eQTL signals. <i>American Journal of Human Genetics</i> , 2010 , 87, 779-89	11	144
124	Adaptive plasticity of IL-10 and IL-35 T cells cooperatively promotes tumor T cell exhaustion. <i>Nature Immunology</i> , 2019 , 20, 724-735	19.1	143
123	SFRP2/DPP4 and FMO1/LSP1 Define Major Fibroblast Populations in Human Skin. <i>Journal of Investigative Dermatology</i> , 2018 , 138, 802-810	4.3	138

122	Loci influencing blood pressure identified using a cardiovascular gene-centric array. <i>Human Molecular Genetics</i> , 2013 , 22, 1663-78	5.6	119
121	Evidence of association of APOE with age-related macular degeneration: a pooled analysis of 15 studies. <i>Human Mutation</i> , 2011 , 32, 1407-16	4.7	99
120	DNA methylation in nasal epithelium, atopy, and atopic asthma in children: a genome-wide study. <i>Lancet Respiratory Medicine</i> , 2019 , 7, 336-346	35.1	87
119	Genome-wide association study and meta-analysis of intraocular pressure. <i>Human Genetics</i> , 2014 , 133, 41-57	6.3	79
118	IL-17 Receptor Signaling in the Lung Epithelium Is Required for Mucosal Chemokine Gradients and Pulmonary Host Defense against <i>K. pneumoniae</i> . <i>Cell Host and Microbe</i> , 2016 , 20, 596-605	23.4	78
117	The Influence of Age and Sex on Ocular Surface Microbiota in Healthy Adults 2017 , 58, 6030-6037		77
116	Treg Cells Promote the SREBP1-Dependent Metabolic Fitness of Tumor-Promoting Macrophages via Repression of CD8 T Cell-Derived Interferon- γ <i>Immunity</i> , 2019 , 51, 381-397.e6	32.3	76
115	ADCYAP1R1 and asthma in Puerto Rican children. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2013 , 187, 584-8	10.2	75
114	Complement factor D in age-related macular degeneration 2011 , 52, 8828-34		72
113	Stress and Bronchodilator Response in Children with Asthma. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2015 , 192, 47-56	10.2	71
112	Variations in apolipoprotein E frequency with age in a pooled analysis of a large group of older people. <i>American Journal of Epidemiology</i> , 2011 , 173, 1357-64	3.8	67
111	EZH2 and ALDH-1 mark breast epithelium at risk for breast cancer development. <i>Modern Pathology</i> , 2011 , 24, 786-93	9.8	62
110	AIM2 Inflammasome Is Critical for Influenza-Induced Lung Injury and Mortality. <i>Journal of Immunology</i> , 2017 , 198, 4383-4393	5.3	61
109	A likelihood-based framework for variant calling and de novo mutation detection in families. <i>PLoS Genetics</i> , 2012 , 8, e1002944	6	60
108	A Bayesian framework for de novo mutation calling in parents-offspring trios. <i>Bioinformatics</i> , 2015 , 31, 1375-81	7.2	55
107	An epigenome-wide association study of total serum IgE in Hispanic children. <i>Journal of Allergy and Clinical Immunology</i> , 2017 , 140, 571-577	11.5	41
106	PIRs mediate innate myeloid cell memory to nonself MHC molecules. <i>Science</i> , 2020 , 368, 1122-1127	33.3	41
105	A systematic study of normalization methods for Infinium 450K methylation data using whole-genome bisulfite sequencing data. <i>Epigenetics</i> , 2015 , 10, 662-9	5.7	41

104	A 32 kb critical region excluding Y402H in CFH mediates risk for age-related macular degeneration. <i>PLoS ONE</i> , 2011 , 6, e25598	3.7	41
103	Conjunctival Microbiome Changes Associated With Soft Contact Lens and Orthokeratology Lens Wearing 2017 , 58, 128-136		40
102	Genotype calling and haplotyping in parent-offspring trios. <i>Genome Research</i> , 2013 , 23, 142-51	9.7	39
101	Oncological outcome of T1 rectal cancer undergoing standard resection and local excision. <i>Colorectal Disease</i> , 2011 , 13, e14-9	2.1	39
100	Genome-wide analysis of disease progression in age-related macular degeneration. <i>Human Molecular Genetics</i> , 2018 , 27, 929-940	5.6	37
99	Association between CFH Y402H polymorphism and age related macular degeneration in North Indian cohort. <i>PLoS ONE</i> , 2013 , 8, e70193	3.7	37
98	A meta-analysis of genome-wide association studies of asthma in Puerto Ricans. <i>European Respiratory Journal</i> , 2017 , 49,	13.6	36
97	DIMM-SC: a Dirichlet mixture model for clustering droplet-based single cell transcriptomic data. <i>Bioinformatics</i> , 2018 , 34, 139-146	7.2	36
96	A genome-wide association study of chronic obstructive pulmonary disease in Hispanics. <i>Annals of the American Thoracic Society</i> , 2015 , 12, 340-8	4.7	35
95	Deep-learning-based Prediction of Late Age-Related Macular Degeneration Progression. <i>Nature Machine Intelligence</i> , 2020 , 2, 141-150	22.5	35
94	Nasal DNA methylation profiling of asthma and rhinitis. <i>Journal of Allergy and Clinical Immunology</i> , 2020 , 145, 1655-1663	11.5	34
93	Age-related macular degeneration-associated variants at chromosome 10q26 do not significantly alter ARMS2 and HTRA1 transcript levels in the human retina. <i>Molecular Vision</i> , 2010 , 16, 1317-23	2.3	34
92	Cell-deposited matrix improves retinal pigment epithelium survival on aged submacular human Bruch's membrane 2011 , 52, 1345-58		32
91	Bivariate Analysis of Age-Related Macular Degeneration Progression Using Genetic Risk Scores. <i>Genetics</i> , 2017 , 206, 119-133	4	31
90	FastGGM: An Efficient Algorithm for the Inference of Gaussian Graphical Model in Biological Networks. <i>PLoS Computational Biology</i> , 2016 , 12, e1004755	5	31
89	A novel whole blood gene expression signature for asthma, dermatitis, and rhinitis multimorbidity in children and adolescents. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2020 , 75, 3248-3260	9.3	27
88	A Genome-Wide Association Study in Hispanics/Latinos Identifies Novel Signals for Lung Function. The Hispanic Community Health Study/Study of Latinos. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018 , 198, 208-219	10.2	27
87	A Bayesian mixture model for clustering droplet-based single-cell transcriptomic data from population studies. <i>Nature Communications</i> , 2019 , 10, 1649	17.4	25

86	Prognostic analysis for carcinoid tumours of the rectum: a single institutional analysis of 106 patients. <i>Colorectal Disease</i> , 2011 , 13, 150-3	2.1	25
85	Gene Level Meta-Analysis of Quantitative Traits by Functional Linear Models. <i>Genetics</i> , 2015 , 200, 1089-1104	10.4	24
84	SNP@Evolution: a hierarchical database of positive selection on the human genome. <i>BMC Evolutionary Biology</i> , 2009 , 9, 221	3	23
83	Native American ancestry, lung function, and COPD in Costa Ricans. <i>Chest</i> , 2014 , 145, 704-710	5.3	22
82	CXXC finger protein 1 is critical for T-cell intrathymic development through regulating H3K4 trimethylation. <i>Nature Communications</i> , 2016 , 7, 11687	17.4	21
81	SILGGM: An extensive R package for efficient statistical inference in large-scale gene networks. <i>PLoS Computational Biology</i> , 2018 , 14, e1006369	5	18
80	Deficiency in AIM2 induces inflammation and adipogenesis in white adipose tissue leading to obesity and insulin resistance. <i>Diabetologia</i> , 2019 , 62, 2325-2339	10.3	17
79	Long-term outcome of early-stage rectal cancer undergoing standard resection and local excision. <i>Clinical Colorectal Cancer</i> , 2011 , 10, 37-41	3.8	17
78	Genome-wide interaction study of dust mite allergen on lung function in children with asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2017 , 140, 996-1003.e7	11.5	16
77	DISSCO: direct imputation of summary statistics allowing covariates. <i>Bioinformatics</i> , 2015 , 31, 2434-42	7.2	16
76	BREM-SC: a bayesian random effects mixture model for joint clustering single cell multi-omics data. <i>Nucleic Acids Research</i> , 2020 , 48, 5814-5824	20.1	16
75	A Multiomics Approach to Identify Genes Associated with Childhood Asthma Risk and Morbidity. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2017 , 57, 439-447	5.7	15
74	Serum Cadmium and Lead, Current Wheeze, and Lung Function in a Nationwide Study of Adults in the United States. <i>Journal of Allergy and Clinical Immunology: in Practice</i> , 2019 , 7, 2653-2660.e3	5.4	15
73	Single Nucleotide Polymorphism (SNP) Detection and Genotype Calling from Massively Parallel Sequencing (MPS) Data. <i>Statistics in Biosciences</i> , 2013 , 5, 3-25	1.5	14
72	Antiinflammatory effects of bromodomain and extraterminal domain inhibition in cystic fibrosis lung inflammation. <i>JCI Insight</i> , 2016 , 1,	9.9	14
71	Meta-analysis of Complex Diseases at Gene Level with Generalized Functional Linear Models. <i>Genetics</i> , 2016 , 202, 457-70	4	13
70	Single cell RNA sequencing identifies an early monocyte gene signature in acute respiratory distress syndrome. <i>JCI Insight</i> , 2020 , 5,	9.9	13
69	Myofibroblast transcriptome indicates SFRP2 fibroblast progenitors in systemic sclerosis skin. <i>Nature Communications</i> , 2021 , 12, 4384	17.4	13

68	Transcriptomic Responses to Ivacaftor and Prediction of Ivacaftor Clinical Responsiveness. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2019 , 61, 643-652	5.7	12
67	A haplotype-based framework for group-wise transmission/disequilibrium tests for rare variant association analysis. <i>Bioinformatics</i> , 2015 , 31, 1452-9	7.2	12
66	Associating Multivariate Quantitative Phenotypes with Genetic Variants in Family Samples with a Novel Kernel Machine Regression Method. <i>Genetics</i> , 2015 , 201, 1329-39	4	12
65	Geographic Difference Shaped Human Ocular Surface Metagenome of Young Han Chinese From Beijing, Wenzhou, and Guangzhou Cities 2020 , 61, 47		12
64	GMM-Demux: sample demultiplexing, multiplet detection, experiment planning, and novel cell-type verification in single cell sequencing. <i>Genome Biology</i> , 2020 , 21, 188	18.3	12
63	Pancreatic gene expression during recovery after pancreatitis reveals unique transcriptome profiles. <i>Scientific Reports</i> , 2018 , 8, 1406	4.9	11
62	Integration of genetic signature and TNM staging system for predicting the relapse of locally advanced colorectal cancer. <i>International Journal of Colorectal Disease</i> , 2010 , 25, 1277-85	3	11
61	A Genome-Wide Association Study of Post-bronchodilator Lung Function in Children with Asthma. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2015 , 192, 634-7	10.2	10
60	RNA-seq in Pulmonary Medicine: How Much Is Enough?. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2015 , 192, 389-91	10.2	10
59	Gene-Based Association Analysis for Censored Traits Via Fixed Effect Functional Regressions. <i>Genetic Epidemiology</i> , 2016 , 40, 133-43	2.6	10
58	Transcriptomics of atopy and atopic asthma in white blood cells from children and adolescents. <i>European Respiratory Journal</i> , 2019 , 53,	13.6	9
57	Expression Quantitative Trait Methylation Analysis Reveals Methyloomic Associations With Gene Expression in Childhood Asthma. <i>Chest</i> , 2020 , 158, 1841-1856	5.3	9
56	Glycated Hemoglobin A, Lung Function, and Hospitalizations Among Adults with Asthma. <i>Journal of Allergy and Clinical Immunology: in Practice</i> , 2020 , 8, 3409-3415.e1	5.4	9
55	Variants in oxidative stress-related genes affect the chemosensitivity through Nrf2-mediated signaling pathway in biliary tract cancer. <i>EBioMedicine</i> , 2019 , 48, 143-160	8.8	9
54	The genetic variant on chromosome 10p14 is associated with risk of colorectal cancer: results from a case-control study and a meta-analysis. <i>PLoS ONE</i> , 2013 , 8, e64310	3.7	9
53	SNPs identified by GWAS affect asthma risk through DNA methylation and expression of -genes in airway epithelium. <i>European Respiratory Journal</i> , 2020 , 55,	13.6	9
52	High-dimensional profiling clusters asthma severity by lymphoid and non-lymphoid status. <i>Cell Reports</i> , 2021 , 35, 108974	10.6	9
51	The impact of genotype calling errors on family-based studies. <i>Scientific Reports</i> , 2016 , 6, 28323	4.9	8

50	Statistics for X-chromosome associations. <i>Genetic Epidemiology</i> , 2018 , 42, 539-550	2.6	8
49	GWAS GUI: graphical browser for the results of whole-genome association studies with high-dimensional phenotypes. <i>Bioinformatics</i> , 2009 , 25, 284-5	7.2	8
48	Expression quantitative trait loci (eQTL) mapping in Puerto Rican children. <i>PLoS ONE</i> , 2015 , 10, e0122464.	4.7	8
47	Using current data to define new approach in age related macular degeneration: need to accelerate translational research. <i>Current Genomics</i> , 2014 , 15, 266-77	2.6	8
46	Genome-wide association study-based deep learning for survival prediction. <i>Statistics in Medicine</i> , 2020 , 39, 4605-4620	2.3	8
45	Copula-based score test for bivariate time-to-event data, with application to a genetic study of AMD progression. <i>Lifetime Data Analysis</i> , 2019 , 25, 546-568	1.3	8
44	A road map from single-cell transcriptome to patient classification for the immune response to trauma. <i>JCI Insight</i> , 2021 , 6,	9.9	8
43	Bayesian integrative model for multi-omics data with missingness. <i>Bioinformatics</i> , 2018 , 34, 3801-3808	7.2	8
42	Transcriptome-wide and differential expression network analyses of childhood asthma in nasal epithelium. <i>Journal of Allergy and Clinical Immunology</i> , 2020 , 146, 671-675	11.5	7
41	Imputation of missing covariate values in epigenome-wide analysis of DNA methylation data. <i>Epigenetics</i> , 2016 , 11, 132-9	5.7	7
40	Sleep Duration, Current Asthma, and Lung Function in a Nationwide Study of U.S. Adults. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019 , 200, 926-929	10.2	7
39	Rare-Variant Kernel Machine Test for Longitudinal Data from Population and Family Samples. <i>Human Heredity</i> , 2015 , 80, 126-38	1.1	7
38	A computational method for genotype calling in family-based sequencing data. <i>BMC Bioinformatics</i> , 2016 , 17, 37	3.6	6
37	A genome-wide association study of severe asthma exacerbations in Latino children and adolescents. <i>European Respiratory Journal</i> , 2021 , 57,	13.6	6
36	LAIT: a local ancestry inference toolkit. <i>BMC Genetics</i> , 2017 , 18, 83	2.6	5
35	Association of IGFN1 variant with polypoidal choroidal vasculopathy. <i>Journal of Gene Medicine</i> , 2018 , 20, e3007	3.5	5
34	Exposure to violence, chronic stress, nasal DNA methylation, and atopic asthma in children 2020 ,		5
33	A genome-wide association study of asthma hospitalizations in adults. <i>Journal of Allergy and Clinical Immunology</i> , 2021 , 147, 933-940	11.5	5

32	KMgene: a unified R package for gene-based association analysis for complex traits. <i>Bioinformatics</i> , 2018 , 34, 2144-2146	7.2	4
31	Gene-based association analysis for bivariate time-to-event data through functional regression with copula models. <i>Biometrics</i> , 2020 , 76, 619-629	1.8	4
30	Artificial-cell-type aware cell-type classification in CITE-seq. <i>Bioinformatics</i> , 2020 , 36, i542-i550	7.2	4
29	A genome-wide study of DNA methylation in white blood cells and asthma in Latino children and youth. <i>Epigenetics</i> , 2021 , 16, 577-585	5.7	4
28	Genome-Wide Association Studies-Based Machine Learning for Prediction of Age-Related Macular Degeneration Risk. <i>Translational Vision Science and Technology</i> , 2021 , 10, 29	3.3	4
27	A Pipeline for Classifying Relationships Using Dense SNP/SNV Data and Putative Pedigree Information. <i>Genetic Epidemiology</i> , 2016 , 40, 161-71	2.6	3
26	Expression patterns of small numbers of transcripts from functionally-related pathways predict survival in multiple cancers. <i>BMC Cancer</i> , 2019 , 19, 686	4.8	3
25	Meta-analysis of quantitative pleiotropic traits for next-generation sequencing with multivariate functional linear models. <i>European Journal of Human Genetics</i> , 2017 , 25, 350-359	5.3	2
24	An integrative association method for omics data based on a modified Fisher's method with application to childhood asthma. <i>PLoS Genetics</i> , 2019 , 15, e1008142	6	2
23	Clinical utility of ultrahigh fractional exhaled nitric oxide in predicting bronchial hyperresponsiveness in patients with suspected asthma. <i>Postgraduate Medical Journal</i> , 2019 , 95, 541-546	2	2
22	Leveraging Identity-by-Descent for Accurate Genotype Inference in Family Sequencing Data. <i>PLoS Genetics</i> , 2015 , 11, e1005271	6	2
21	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.. <i>EBioMedicine</i> , 2022 , 76, 103860	8.8	2
20	GWAS-based Machine Learning for Prediction of Age-Related Macular Degeneration Risk		2
19	Exposure to violence, chronic stress, nasal DNA methylation, and atopic asthma in children. <i>Pediatric Pulmonology</i> , 2021 , 56, 1896-1905	3.5	2
18	Child maltreatment, anxiety and depression, and asthma among British adults in the UK Biobank.. <i>European Respiratory Journal</i> , 2022 ,	13.6	2
17	Epigenome-wide effects of vitamin D on asthma bronchial epithelial cells. <i>Epigenetics</i> , 2019 , 14, 844-849	5.7	1
16	Under-diagnosis of atopic dermatitis in Puerto Rican children. <i>World Allergy Organization Journal</i> , 2019 , 12, 100003	5.2	1
15	A semiparametric imputation approach for regression with censored covariate with application to an AMD progression study. <i>Statistics in Medicine</i> , 2018 , 37, 3293-3308	2.3	1

14	Expression quantitative trait methylation analysis reveals methylomic associations with gene expression in childhood asthma		1
13	Deep-learning-based Prediction of Late Age-Related Macular Degeneration Progression		1
12	Sample demultiplexing, multiplet detection, experiment planning and novel cell type verification in single cell sequencing		1
11	Myofibroblast transcriptome indicates SFRP2+ fibroblast progenitors in systemic sclerosis skin		1
10	Gene-Based Association Testing of Dichotomous Traits With Generalized Functional Linear Mixed Models Using Extended Pedigrees: Applications to Age-Related Macular Degeneration. <i>Journal of the American Statistical Association</i> , 2021 , 116, 531-545	2.8	1
9	AMD Genetics: Methods and Analyses for Association, Progression, and Prediction. <i>Advances in Experimental Medicine and Biology</i> , 2021 , 1256, 191-200	3.6	1
8	LONGL-Net: temporal correlation structure guided deep learning model to predict longitudinal age-related macular degeneration severity. 2022 , 1, pgab003		1
7	DNA Methylation and Atopic Diseases.. <i>Methods in Molecular Biology</i> , 2022 , 2432, 85-99	1.4	1
6	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. <i>Cytotherapy</i> , 2020 , 22, 149-157	4.8	0
5	A region-based method for causal mediation analysis of DNA methylation data. <i>Epigenetics</i> , 2021 , 1-11	5.7	0
4	Differential gene expression in nasal airway epithelium from overweight or obese youth with asthma.. <i>Pediatric Allergy and Immunology</i> , 2022 , 33, e13776	4.2	0
3	CSMD: a computational subtraction-based microbiome discovery pipeline for species-level characterization of clinical metagenomic samples. <i>Bioinformatics</i> , 2020 , 36, 1577-1583	7.2	
2	Identification and inference for subgroups with differential treatment efficacy from randomized controlled trials with survival outcomes through multiple testing. <i>Statistics in Medicine</i> , 2021 , 40, 6523-6540	2.3	
1	Multi-modal Genotype and Phenotype Mutual Learning to Enhance Single-Modal Input Based Longitudinal Outcome Prediction. <i>Lecture Notes in Computer Science</i> , 2022 , 209-229	0.9	