

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.

102 papers	34,396 citations	30 h-index	115 g-index
115 ext. papers	41,441 ext. citations	8.7 avg, IF	6.38 L-index

#	Paper	IF	Citations
102	A global reference for human genetic variation. <i>Nature</i> , 2015 , 526, 68-74	50.4	8599
101	A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010 , 467, 1061-73	50.4	6142
100	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012 , 491, 56-65	50.4	6049
99	Strong association of de novo copy number mutations with autism. <i>Science</i> , 2007 , 316, 445-9	33.3	2126
98	Large-scale copy number polymorphism in the human genome. <i>Science</i> , 2004 , 305, 525-8	33.3	2016
97	The contribution of de novo coding mutations to autism spectrum disorder. <i>Nature</i> , 2014 , 515, 216-21	50.4	1470
96	Pindel: a pattern growth approach to detect break points of large deletions and medium sized insertions from paired-end short reads. <i>Bioinformatics</i> , 2009 , 25, 2865-71	7.2	1423
95	De novo gene disruptions in children on the autistic spectrum. <i>Neuron</i> , 2012 , 74, 285-99	13.9	1052
94	A systematic survey of loss-of-function variants in human protein-coding genes. <i>Science</i> , 2012 , 335, 823-833	33.3	880
93	Mapping copy number variation by population-scale genome sequencing. <i>Nature</i> , 2011 , 470, 59-65	50.4	833
92	Rare de novo and transmitted copy-number variation in autistic spectrum disorders. <i>Neuron</i> , 2011 , 70, 886-97	13.9	526
91	Sensitive and accurate detection of copy number variants using read depth of coverage. <i>Genome Research</i> , 2009 , 19, 1586-92	9.7	422
90	Comparative isoschizomer profiling of cytosine methylation: the HELP assay. <i>Genome Research</i> , 2006 , 16, 1046-55	9.7	330
89	Representational oligonucleotide microarray analysis: a high-resolution method to detect genome copy number variation. <i>Genome Research</i> , 2003 , 13, 2291-305	9.7	317
88	Novel patterns of genome rearrangement and their association with survival in breast cancer. <i>Genome Research</i> , 2006 , 16, 1465-79	9.7	256
87	A unified genetic theory for sporadic and inherited autism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 12831-6	11.5	244
86	High definition profiling of mammalian DNA methylation by array capture and single molecule bisulfite sequencing. <i>Genome Research</i> , 2009 , 19, 1593-605	9.7	183

85	The BCL6 transcriptional program features repression of multiple oncogenes in primary B cells and is deregulated in DLBCL. <i>Blood</i> , 2009 , 113, 5536-48	2.2	179
84	Transcriptional signature with differential expression of BCL6 target genes accurately identifies BCL6-dependent diffuse large B cell lymphomas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 3207-12	11.5	115
83	A meta-analysis of genome-wide association studies identifies multiple longevity genes. <i>Nature Communications</i> , 2019 , 10, 3669	17.4	102
82	Low load for disruptive mutations in autism genes and their biased transmission. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E5600-7	11.5	96
81	Buffering mechanisms in aging: a systems approach toward uncovering the genetic component of aging. <i>PLoS Computational Biology</i> , 2007 , 3, e170	5	93
80	Genome-wide analysis of DNA binding and transcriptional regulation by the mammalian Doublesex homolog DMRT1 in the juvenile testis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 13360-5	11.5	79
79	The Hypothalamic-Pituitary-Testicular Axis in Exceptionally Old Men. <i>Journal of the Endocrine Society</i> , 2021 , 5, A727-A727	0.4	78
78	An integrative genomic and epigenomic approach for the study of transcriptional regulation. <i>PLoS ONE</i> , 2008 , 3, e1882	3.7	72
77	Structure and function of neonatal social communication in a genetic mouse model of autism. <i>Molecular Psychiatry</i> , 2016 , 21, 1208-14	15.1	54
76	Common genetic variants regulating ADD3 gene expression alter biliary atresia risk. <i>Journal of Hepatology</i> , 2013 , 59, 1285-91	13.4	53
75	Effective DNA/RNA co-extraction for analysis of microRNAs, mRNAs, and genomic DNA from formalin-fixed paraffin-embedded specimens. <i>PLoS ONE</i> , 2012 , 7, e34683	3.7	52
74	Lower-extremity Arterial Thrombosis Associated with COVID-19 Is Characterized by Greater Thrombus Burden and Increased Rate of Amputation and Death. <i>Radiology</i> , 2020 , 297, E263-E269	20.5	42
73	A partial least-square approach for modeling gene-gene and gene-environment interactions when multiple markers are genotyped. <i>Genetic Epidemiology</i> , 2009 , 33, 6-15	2.6	37
72	Uncertainty Quantification for Multiscale Simulations1. <i>Journal of Fluids Engineering, Transactions of the ASME</i> , 2002 , 124, 29-41	2.1	30
71	Multi-modal neuroimaging of dual-task walking: Structural MRI and fNIRS analysis reveals prefrontal grey matter volume moderation of brain activation in older adults. <i>NeuroImage</i> , 2019 , 189, 745-754	7.9	28
70	Positive association of schizophrenia to JARID2 gene. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2007 , 144B, 45-51	3.5	28
69	Distinguishing between longevity and buffered-deleterious genotypes for exceptional human longevity: the case of the MTP gene. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2012 , 67, 1153-60	6.4	22
68	Resequencing of pooled DNA for detecting disease associations with rare variants. <i>Genetic Epidemiology</i> , 2010 , 34, 492-501	2.6	21

67	The effect of fear of falling on prefrontal cortex activation and efficiency during walking in older adults. <i>GeroScience</i> , 2019 , 41, 89-100	8.9	20
66	Association between lifestyle, menstrual/reproductive history, and histological factors and risk of breast cancer in women biopsied for benign breast disease. <i>Breast Cancer Research and Treatment</i> , 2017 , 165, 623-631	4.4	19
65	Model discrimination—another perspective on model-robust designs. <i>Journal of Statistical Planning and Inference</i> , 2007 , 137, 1576-1583	0.8	19
64	Gene size matters. <i>PLoS ONE</i> , 2012 , 7, e49093	3.7	18
63	Meta-analysis of microarray studies reveals a novel hematopoietic progenitor cell signature and demonstrates feasibility of inter-platform data integration. <i>PLoS ONE</i> , 2008 , 3, e2965	3.7	18
62	The nutritional environment determines which and how intestinal stem cells contribute to homeostasis and tumorigenesis. <i>Carcinogenesis</i> , 2019 , 40, 937-946	4.6	17
61	Diffusion Tensor Imaging of the Evolving Response to Mild Traumatic Brain Injury in Rats. <i>Journal of Experimental Neuroscience</i> , 2019 , 13, 1179069519858627	3.6	15
60	Model-robust supersaturated and partially supersaturated designs. <i>Journal of Statistical Planning and Inference</i> , 2009 , 139, 45-53	0.8	15
59	Copy number elevation of 22q11.2 genes arrests the developmental maturation of working memory capacity and adult hippocampal neurogenesis. <i>Molecular Psychiatry</i> , 2018 , 23, 985-992	15.1	14
58	Computing power and sample size for case-control association studies with copy number polymorphism: application of mixture-based likelihood ratio test. <i>PLoS ONE</i> , 2008 , 3, e3475	3.7	12
57	Evaluation of Hair Density in Different Ethnicities in a Healthy American Population Using Quantitative Trichoscopic Analysis. <i>Skin Appendage Disorders</i> , 2018 , 4, 304-307	1.4	12
56	Genetic Variants Associated with FDNY WTC-Related Sarcoidosis. <i>International Journal of Environmental Research and Public Health</i> , 2019 , 16,	4.6	11
55	Ultra-High-Frequency Reprogramming of Individual Long-Term Hematopoietic Stem Cells Yields Low Somatic Variant Induced Pluripotent Stem Cells. <i>Cell Reports</i> , 2019 , 26, 2580-2592.e7	10.6	10
54	Detecting dispersed duplications in high-throughput sequencing data using a database-free approach. <i>Bioinformatics</i> , 2016 , 32, 505-10	7.2	10
53	Evaluation and Adaptation of a Laboratory-Based cDNA Library Preparation Protocol for Retrospective Sequencing of Archived MicroRNAs from up to 35-Year-Old Clinical FFPE Specimens. <i>International Journal of Molecular Sciences</i> , 2017 , 18,	6.3	10
52	Reducing system noise in copy number data using principal components of self-self hybridizations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, E103-10	11.5	7
51	Estimating allele frequency from next-generation sequencing of pooled mitochondrial DNA samples. <i>Frontiers in Genetics</i> , 2011 , 2, 51	4.5	7
50	Non-operative Management for Acute Appendicitis During the COVID-19 Pandemic Does Not Increase the Rate of Complications. <i>Journal of Gastrointestinal Surgery</i> , 2021 , 25, 1327-1329	3.3	7

49	Sources of uncertainty and error in the simulation of flow in porous media. <i>Computational and Applied Mathematics</i> , 2004 , 23,		6
48	Extracellular Vesicle Capture by AnTibody of CHoice and Enzymatic Release (EV-CATCHER): A customizable purification assay designed for small-RNA biomarker identification and evaluation of circulating small-EVs. <i>Journal of Extracellular Vesicles</i> , 2021 , 10, e12110	16.4	6
47	Computational Analysis of Neonatal Mouse Ultrasonic Vocalization. <i>Current Protocols in Mouse Biology</i> , 2018 , 8, e46	1.1	5
46	Bayesian detection of embryonic gene expression onset in <i>C. elegans</i> . <i>Annals of Applied Statistics</i> , 2015 , 9,	2.1	5
45	MicroRNA expression in benign breast tissue and risk of subsequent invasive breast cancer. <i>PLoS ONE</i> , 2018 , 13, e0191814	3.7	5
44	Molecular Histochemistry Identifies Peptidomic Organization and Reorganization Along Striatal Projection Units. <i>Biological Psychiatry</i> , 2016 , 79, 415-420	7.9	5
43	Improved Dose-Response Relationship of (+)-Discodermolide-Taxol Hybrid Congeners. <i>Journal of Natural Products</i> , 2018 , 81, 607-615	4.9	4
42	Measuring shared variants in cohorts of discordant siblings with applications to autism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 7073-7076	11.5	4
41	Detecting multiple causal rare variants in exome sequence data. <i>Genetic Epidemiology</i> , 2011 , 35 Suppl 1, S18-21	2.6	4
40	Design and Statistical Analysis of Pooled Next Generation Sequencing for Rare Variants. <i>Journal of Probability and Statistics</i> , 2012 , 2012, 1-19	0.6	4
39	The Utility of 18FDG PET/CT Versus Bone Scan for Identification of Bone Metastases in a Pediatric Sarcoma Population and a Review of the Literature. <i>Journal of Pediatric Hematology/Oncology</i> , 2021 , 43, 52-58	1.2	4
38	Rare genetic coding variants associated with human longevity and protection against age-related diseases. <i>Nature Aging</i> , 2021 , 1, 783-794		4
37	Structural Refinement of the Tubulin Ligand (+)-Discodermolide to Attenuate Chemotherapy-Mediated Senescence. <i>Molecular Pharmacology</i> , 2020 , 98, 156-167	4.3	3
36	Genome-wide analysis of mitochondrial DNA copy number reveals loci implicated in nucleotide metabolism, platelet activation, and megakaryocyte proliferation. <i>Human Genetics</i> , 2021 , 1	6.3	3
35	Diagnostic yield of head CT in pediatric emergency department patients with acute psychosis or hallucinations. <i>Pediatric Radiology</i> , 2019 , 49, 240-244	2.8	3
34	Framing potential for adverse effects of repetitive subconcussive impacts in soccer in the context of athlete and non-athlete controls. <i>Brain Imaging and Behavior</i> , 2021 , 15, 882-895	4.1	3
33	Adjustment for covariates using summary statistics of genome-wide association studies. <i>Genetic Epidemiology</i> , 2018 , 42, 812-825	2.6	3
32	Detecting, quantifying, and discriminating the mechanism of mosaic chromosomal aneuploidies using MAD-seq. <i>Genome Research</i> , 2018 , 28, 1039-1052	9.7	3

31	Single-cell analysis of somatic mutations in human bronchial epithelial cells in relation to aging and smoking.. <i>Nature Genetics</i> , 2022 ,	36.3	3
30	Effects of Diet Choice on Stem Cell Function Necessitate Clarity in Selection and Reporting. <i>Cell Stem Cell</i> , 2020 , 27, 11-12	18	2
29	A High Resolution Epigenomic Map of Myelofibrosis Reveals Multiple Chromosomal Deletions and Amplifications Accompanied by a High Level of Functionally Important Methylation.. <i>Blood</i> , 2006 , 108, 2684-2684	2.2	2
28	Global DNA Methylation Profiling Demonstrates That Idiopathic Myelofibrosis Is Characterized by a Distinct Epigenetic Signature with Aberrant Methylation Changes in Genes Involved in Inflammation and Hematopoiesis. <i>Blood</i> , 2007 , 110, 1536-1536	2.2	2
27	Optimal Orthogonal Three-Level Factorial Designs for Factor Screening and Response Surface Exploration 2007 , 221-228		2
26	Diagnostic significance of the CT rim sign in cases of gangrenous cholecystitis. <i>Clinical Imaging</i> , 2021 , 73, 53-56	2.7	2
25	P1.11-11 Initial Discovery of Exhaled Small Polar Energetics-Related Metabolites by GC-MS for Lung Cancer Risk Assessment. <i>Journal of Thoracic Oncology</i> , 2019 , 14, S519	8.9	2
24	Ventricular Arterial Coupling: A Novel Echocardiographic Risk Factor for Disease Progression in Pediatric Dilated Cardiomyopathy. <i>Pediatric Cardiology</i> , 2019 , 40, 330-338	2.1	2
23	Survival Disparities in Black Patients With EGFR-mutated Non-small-cell Lung Cancer. <i>Clinical Lung Cancer</i> , 2020 , 21, 177-185	4.9	2
22	Near-Term Decrease in Brain Volume following Mild Traumatic Injury Is Detectible in the Context of Preinjury Volumetric Stability: Neurobiologic Insights from Analysis of Historical Imaging Examinations. <i>American Journal of Neuroradiology</i> , 2018 , 39, 1821-1826	4.4	2
21	The antagonistic pleiotropy of insulin-like growth factor 1. <i>Aging Cell</i> , 2021 , 20, e13443	9.9	2
20	Identification of genes and variants associated with quantitative traits using Bayesian factor screening. <i>BMC Proceedings</i> , 2011 , 5 Suppl 9, S4	2.3	1
19	Genotype copy number variations using Gaussian mixture models: theory and algorithms. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2012 , 11, 5	1.2	1
18	Buffering Mechanisms in Aging: A systems approach towards uncovering the genetic component of aging. <i>PLoS Computational Biology</i> , 2005 , preprint, e170	5	1
17	Computational identification of variables in neonatal vocalizations predictive for postpubertal social behaviors in a mouse model of 16p11.2 deletion. <i>Molecular Psychiatry</i> , 2021 ,	15.1	1
16	Cellular viability and death biomarkers enables the evaluation of ocular irritation using the bovine corneal opacity and permeability assay. <i>Toxicology Letters</i> , 2021 , 340, 52-57	4.4	1
15	Experience with a perfusion-only screening protocol for evaluation of pulmonary embolism during the COVID-19 pandemic surge. <i>Journal of Nuclear Medicine</i> , 2021 ,	8.9	1
14	Epidemiology, Risk Factors and Outcomes of Pneumomediastinum in Patients with Coronavirus Disease 2019: A Case-Control Study. <i>Journal of Intensive Care Medicine</i> , 2022 , 37, 12-20	3.3	1

13	Impact of Patient-Centered Care on the Patient Experience in Nuclear Medicine. <i>Current Problems in Diagnostic Radiology</i> , 2020 , 49, 326-332	1.6	o
12	Emerging Adaptive Strategies Under Temperature Fluctuations in a Laboratory Evolution Experiment of. <i>Frontiers in Microbiology</i> , 2021 , 12, 724982	5.7	o
11	Safety and efficacy of image-guided retrocalcaneal bursa corticosteroid injection for the treatment of retrocalcaneal bursitis. <i>Skeletal Radiology</i> , 2021 , 50, 2471-2482	2.7	o
10	Prognostic Factors for North American Adult T Cell Leukemia Lymphoma: Defining Risk Groups Using a Four-Point Score Prognostic System. <i>Blood</i> , 2020 , 136, 38-39	2.2	
9	High Resolution Epigenomic Mapping of Myelodysplastic Syndrome Reveals a High Level of Functionally Important Methylation.. <i>Blood</i> , 2006 , 108, 2637-2637	2.2	
8	Meta-Transcriptome of Bone Marrow Stem Cells Demonstrates Platform and Lab Dependant Variability in Gene Expression and Reveals a Novel Set of Enriched Genes.. <i>Blood</i> , 2006 , 108, 4189-4189	2.2	
7	Epigenetic Signatures Accurately Distinguish Leukemia Subtypes and Provide a More Comprehensive Representation of Differentially Regulated Genes Than Gene Expression Profiling.. <i>Blood</i> , 2006 , 108, 735-735	2.2	
6	A Comprehensive Genomic Approach Using Gain of Function and Loss of Function Cell Models and ChIP-on-Chip Technology Identifies Novel Promyelocytic Zinc Finger Protein Target Genes.. <i>Blood</i> , 2006 , 108, 1407-1407	2.2	
5	A BCL6 Target Gene Signature Predicts the Biological Behavior and Classification of Diffuse Large B-Cell Lymphoma.. <i>Blood</i> , 2006 , 108, 616-616	2.2	
4	Data Mining of Hematopoietic Stem Cell Microarray Studies Reveals a Novel Stem Cell Gene Expression Signature and Demonstrates Feasibility of Integrating Data from Different Labs and Different Microarray Platforms.. <i>Blood</i> , 2007 , 110, 4073-4073	2.2	
3	Integrated Epigenomic Profiling Reveals Aberrant DNA Hypomethylation in LGL and Demonstrates That a Combination of Genetic and Epigenetic Events Results in Leukemic Evolution in Model of Large Granular Lymphocytic Leukemia.. <i>Blood</i> , 2007 , 110, 2129-2129	2.2	
2	Global Epigenomic Profiling Demonstrates That Myelodysplasia Is Characterized by a Distinct Epigenetic Signature with Aberrant DNA Methylation Changes Involving Various Malignant and Hematopoietic Pathways.. <i>Blood</i> , 2007 , 110, 2436-2436	2.2	
1	Behavioral and Genetic Factors Associated with Successful Long-Term Cessation in Persons with HIV Who Smoke Cigarettes.. <i>Journal of Smoking Cessation</i> , 2021 , 2021, 1894160	0.5	