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List of Publications by Year in descending order

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64 papers	5,761 citations	218677 26 h-index	98798 67 g-index
71 all docs	71 docs citations	71 times ranked	14779 citing authors

#	Article	IF	Citations
1	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	21.4	1,124
2	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. Cell, 2016, 167, 1415-1429.e19.	28.9	1,052
3	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	28.9	573
4	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
5	Genome-wide allele-specific analysis: insights into regulatory variation. Nature Reviews Genetics, 2010, 11, 533-538.	16.3	271
6	Genome-Wide Association Study in BRCA1 Mutation Carriers Identifies Novel Loci Associated with Breast and Ovarian Cancer Risk. PLoS Genetics, 2013, 9, e1003212.	3.5	244
7	H3K27M induces defective chromatin spread of PRC2-mediated repressive H3K27me2/me3 and is essential for glioma tumorigenesis. Nature Communications, 2019, 10, 1262.	12.8	215
8	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. Nature Communications, 2016, 7, 13555.	12.8	142
9	The International Human Epigenome Consortium Data Portal. Cell Systems, 2016, 3, 496-499.e2.	6.2	140
10	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. Genome Biology, 2017, 18, 18.	8.8	97
11	Population whole-genome bisulfite sequencing across two tissues highlights the environment as the principal source of human methylome variation. Genome Biology, 2015, 16, 290.	8.8	90
12	High-dose folic acid supplementation alters the human sperm methylome and is influenced by theMTHFRC677T polymorphism. Human Molecular Genetics, 2015, 24, 6301-6313.	2.9	86
13	Characterization of functional methylomes by next-generation capture sequencing identifies novel disease-associated variants. Nature Communications, 2015, 6, 7211.	12.8	84
14	Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. Genome Biology, 2017, 18, 50.	8.8	71
15	Are Data Sharing and Privacy Protection Mutually Exclusive?. Cell, 2016, 167, 1150-1154.	28.9	50
16	Promoter capture Hi-C-based identification of recurrent noncoding mutations in colorectal cancer. Nature Genetics, 2018, 50, 1375-1380.	21.4	49
17	Mutations in THAP11 cause an inborn error of cobalamin metabolism and developmental abnormalities. Human Molecular Genetics, 2017, 26, 2838-2849.	2.9	47
18	Global miRNA expression and correlation with mRNA levels in primary human bone cells. Rna, 2015, 21, 1433-1443.	3.5	43

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19	TCF12 is mutated in anaplastic oligodendroglioma. Nature Communications, 2015, 6, 7207.	12.8	42
20	Conserved expression of transposon-derived non-coding transcripts in primate stem cells. BMC Genomics, 2017, 18, 214.	2.8	40
21	Genomic answers for children: Dynamic analyses of >1000 pediatric rare disease genomes. Genetics in Medicine, 2022, 24, 1336-1348.	2.4	37
22	Genetic Implication of a Novel Thiamine Transporter in Human Hypertension. Journal of the American College of Cardiology, 2014, 63, 1542-1555.	2.8	36
23	Transient DNMT1 suppression reveals hidden heritable marks in the genome. Nucleic Acids Research, 2015, 43, 1485-1497.	14.5	35
24	Epigenome data release: a participant-centered approach to privacy protection. Genome Biology, 2015, 16, 142.	8.8	34
25	Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. Oncotarget, 2016, 7, 80140-80163.	1.8	31
26	Inborn Error of Cobalamin Metabolism Associated with the Intracellular Accumulation of Transcobalamin-Bound Cobalamin and Mutations inZNF143, Which Codes for a Transcriptional Activator. Human Mutation, 2016, 37, 976-982.	2.5	30
27	High-resolution analyses of human sperm dynamic methylome reveal thousands of novel age-related epigenetic alterations. Clinical Epigenetics, 2020, 12, 192.	4.1	29
28	Personalized and graph genomes reveal missing signal in epigenomic data. Genome Biology, 2020, 21, 124.	8.8	29
29	Optimizing ChIP-seq peak detectors using visual labels and supervised machine learning. Bioinformatics, 2017, 33, 491-499.	4.1	28
30	Points-to-consider on the return of results in epigenetic research. Genome Medicine, 2019, 11, 31.	8.2	27
31	Immunoseq: the identification of functionally relevant variants through targeted capture and sequencing of active regulatory regions in human immune cells. BMC Medical Genomics, 2016, 9, 59.	1.5	26
32	Integrative analysis of vascular endothelial cell genomic features identifies AIDA as a coronary artery disease candidate gene. Genome Biology, 2019, 20, 133.	8.8	26
33	Non-CG methylation and multiple histone profiles associate child abuse with immune and small GTPase dysregulation. Nature Communications, 2021, 12, 1132.	12.8	24
34	funtooNorm: an R package for normalization of DNA methylation data when there are multiple cell or tissue types. Bioinformatics, 2016, 32, 593-595.	4.1	22
35	Pitx1 directly modulates the core limb development program to implement hindlimb identity. Development (Cambridge), 2017, 144, 3325-3335.	2.5	22
36	Allelic expression mapping across cellular lineages to establish impact of nonâ€coding <scp>SNP</scp>s. Molecular Systems Biology, 2014, 10, 754.	7.2	21

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37	Customized MethylC-Capture Sequencing to Evaluate Variation in the Human Sperm DNA Methylome Representative of Altered Folate Metabolism. Environmental Health Perspectives, 2019, 127, 87002.	6.0	20
38	Computational Analysis of HLA-presentation of Non-synonymous Recipient Mismatches Indicates Effect on the Risk of Chronic Graft-vs.-Host Disease After Allogeneic HSCT. Frontiers in Immunology, 2019, 10, 1625.	4.8	20
39	DNA methylome analysis of acute lymphoblastic leukemia cells reveals stochastic de novo DNA methylation in CpG islands. Epigenomics, 2016, 8, 1367-1387.	2.1	19
40	Association of breast cancer risk in BRCA1 and BRCA2 mutation carriers with genetic variants showing differential allelic expression: identification of a modifier of breast cancer risk at locus 11q22.3. Breast Cancer Research and Treatment, 2017, 161, 117-134.	2.5	18
41	Genetic Predisposition to Multiple Myeloma at 5q15 Is Mediated by an ELL2 Enhancer Polymorphism. Cell Reports, 2017, 20, 2556-2564.	6.4	17
42	Genome-wide association study implicates immune dysfunction in the development of Hodgkin lymphoma. Blood, 2018, 132, 2040-2052.	1.4	17
43	Dissecting features of epigenetic variants underlying cardiometabolic risk using full-resolution epigenome profiling in regulatory elements. Nature Communications, 2019, 10, 1209.	12.8	16
44	Immune cell residency in the nasal mucosa may partially explain respiratory disease severity across the age range. Scientific Reports, 2021, 11, 15927.	3.3	16
45	Demonstration of Autosomal Monoallelic Expression in Thyroid Tissue Assessed by Whole-Exome and Bulk RNA Sequencing. Thyroid, 2016, 26, 852-859.	4.5	15
46	Combining omics data to identify genes associated with allergic rhinitis. Clinical Epigenetics, 2017, 9, 3.	4.1	15
47	Exploring rare and low-frequency variants in the Saguenayâ€“Lac-Saint-Jean population identified genes associated with asthma and allergy traits. European Journal of Human Genetics, 2019, 27, 90-101.	2.8	15
48	Eosinophil microRNAs Play a Regulatory Role in Allergic Diseases Included in the Atopic March. International Journal of Molecular Sciences, 2020, 21, 9011.	4.1	15
49	Paired rRNA-depleted and polyA-selected RNA sequencing data and supporting multi-omics data from human T cells. Scientific Data, 2020, 7, 376.	5.3	15
50	Rare Genetic Variants in Immune Genes and Neonatal Herpes Simplex Viral Infections. Pediatrics, 2021, 147, .	2.1	15
51	Risk of re-identification of epigenetic methylation data: a more nuanced response is needed. Clinical Epigenetics, 2015, 7, 45.	4.1	14
52	Rheumatoid arthritis-relevant DNA methylation changes identified in ACPA-positive asymptomatic individuals using methylome capture sequencing. Clinical Epigenetics, 2019, 11, 110.	4.1	14
53	Genetic risk factors for decreased bone mineral accretion in children with asthma receiving multiple oral corticosteroid bursts. Journal of Allergy and Clinical Immunology, 2015, 136, 1240-1246.e8.	2.9	13
54	Evolving data access policy: The Canadian context. Facets, 2017, 1, 138-147.	2.4	13

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55	Very long intergenic non-coding RNA transcripts and expression profiles are associated to specific childhood acute lymphoblastic leukemia subtypes. PLoS ONE, 2018, 13, e0207250.	2.5	12
56	Epimutations in both the TESK2 and MMACHC promoters in the Epi-cblC inherited disorder of intracellular metabolism of vitamin B12. Clinical Epigenetics, 2022, 14, 52.	4.1	10
57	Interrogation of allelic chromatin states in human cells by high-density ChIP-genotyping. Epigenetics, 2014, 9, 1238-1251.	2.7	9
58	A Hidden Markov Model for Identifying Differentially Methylated Sites in Bisulfite Sequencing Data. Biometrics, 2019, 75, 210-221.	1.4	9
59	Asthma-associated polymorphisms in 17q12-21 locus modulate methylation and gene expression of GSDMA in naÃ¯ve CD4+ T cells. Journal of Genetics and Genomics, 2020, 47, 171-174.	3.9	9
60	Single Nucleotide Polymorphisms with Cis-Regulatory Effects on Long Non-Coding Transcripts in Human Primary Monocytes. PLoS ONE, 2014, 9, e102612.	2.5	9
61	Communicating science: epigenetics in the spotlight. Environmental Epigenetics, 2020, 6, dvaa015.	1.8	4
62	Thousands of CpGs Show DNA Methylation Differences in ACPA-Positive Individuals. Genes, 2021, 12, 1349.	2.4	2
63	Massively parallel identification of functionally consequential noncoding genetic variants in undiagnosed rare disease patients. Scientific Reports, 2022, 12, 7576.	3.3	1
64	Differentially methylated CpGs in response to growth hormone administration in children with idiopathic short stature. Clinical Epigenetics, 2022, 14, 65.	4.1	1