

List of Publications by Year in descending order

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52
papers

8,874
citations

87888

38
h-index

175258

52
g-index

53
all docs

53
docs citations

53
times ranked

14774
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetically determined NLRP3 inflammasome activation associates with systemic inflammation and cardiovascular mortality. <i>European Heart Journal</i> , 2021, 42, 1742-1756.	2.2	63
2	Epigenetic control of region-specific transcriptional programs in mouse cerebellar and cortical astrocytes. <i>Glia</i> , 2021, 69, 2160-2177.	4.9	13
3	A meta-analysis of epigenome-wide association studies in Alzheimer's disease highlights novel differentially methylated loci across cortex. <i>Nature Communications</i> , 2021, 12, 3517.	12.8	72
4	Lasp1 regulates adherens junction dynamics and fibroblast transformation in destructive arthritis. <i>Nature Communications</i> , 2021, 12, 3624.	12.8	16
5	Dnmt1 has de novo activity targeted to transposable elements. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 594-603.	8.2	83
6	Rapid Base-Specific Calling of SARS-CoV-2 Variants of Concern Using Combined RT-PCR Melting Curve Screening and SIRPH Technology. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofab364.	0.9	6
7	Identification of tissue-specific and common methylation quantitative trait loci in healthy individuals using MAGAR. <i>Epigenetics and Chromatin</i> , 2021, 14, 44.	3.9	3
8	Transmission of trained immunity and heterologous resistance to infections across generations. <i>Nature Immunology</i> , 2021, 22, 1382-1390.	14.5	72
9	Prediction of single-cell gene expression for transcription factor analysis. <i>GigaScience</i> , 2020, 9, .	6.4	11
10	Reference-free deconvolution, visualization and interpretation of complex DNA methylation data using DecompPipeline, MeDeCom and FactorViz. <i>Nature Protocols</i> , 2020, 15, 3240-3263.	12.0	19
11	Quantitative comparison of within-sample heterogeneity scores for DNA methylation data. <i>Nucleic Acids Research</i> , 2020, 48, e46-e46.	14.5	45
12	GeneTrail 3: advanced high-throughput enrichment analysis. <i>Nucleic Acids Research</i> , 2020, 48, W515-W520.	14.5	67
13	Unique and assay specific features of NOMe-, ATAC- and DNase I-seq data. <i>Nucleic Acids Research</i> , 2019, 47, 10580-10596.	14.5	31
14	DNA methylation signatures of monozygotic twins clinically discordant for multiple sclerosis. <i>Nature Communications</i> , 2019, 10, 2094.	12.8	51
15	Peptide-specific recognition of human cytomegalovirus strains controls adaptive natural killer cells. <i>Nature Immunology</i> , 2018, 19, 453-463.	14.5	319
16	Hairpin Bisulfite Sequencing: Synchronous Methylation Analysis on Complementary DNA Strands of Individual Chromosomes. <i>Methods in Molecular Biology</i> , 2018, 1708, 573-586.	0.9	6
17	A comprehensive analysis of 195 DNA methylomes reveals shared and cell-specific features of partially methylated domains. <i>Genome Biology</i> , 2018, 19, 150.	8.8	71
18	DNA methylation analysis on purified neurons and glia dissects age and Alzheimer's disease-specific changes in the human cortex. <i>Epigenetics and Chromatin</i> , 2018, 11, 41.	3.9	173

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19	MeDeCom: discovery and quantification of latent components of heterogeneous methylomes. <i>Genome Biology</i> , 2017, 18, 55.	8.8	75
20	Combining transcription factor binding affinities with open-chromatin data for accurate gene expression prediction. <i>Nucleic Acids Research</i> , 2017, 45, 54-66.	14.5	112
21	The long non-coding RNA H19 suppresses carcinogenesis and chemoresistance in hepatocellular carcinoma. <i>Cell Stress</i> , 2017, 1, 37-54.	3.2	50
22	The Influence of Hydroxylation on Maintaining CpG Methylation Patterns: A Hidden Markov Model Approach. <i>PLoS Computational Biology</i> , 2016, 12, e1004905.	3.2	18
23	Imprinting of Skin/Inflammation Homing in CD4+ T Cells Is Controlled by DNA Methylation within the <i>Fucosyltransferase 7</i> Gene. <i>Journal of Immunology</i> , 2016, 197, 3406-3414.	0.8	16
24	Epigenomic Profiling of Human CD4+ T Cells Supports a Linear Differentiation Model and Highlights Molecular Regulators of Memory Development. <i>Immunity</i> , 2016, 45, 1148-1161.	14.3	174
25	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , 2016, 34, 726-737.	17.5	270
26	Mitochondrial DNA Variation and Heteroplasmy in Monozygotic Twins Clinically Discordant for Multiple Sclerosis. <i>Human Mutation</i> , 2016, 37, 765-775.	2.5	41
27	Selective impairment of methylation maintenance is the major cause of DNA methylation reprogramming in the early embryo. <i>Epigenetics and Chromatin</i> , 2015, 8, 1.	3.9	149
28	Human Cytomegalovirus Drives Epigenetic Imprinting of the IFNG Locus in NKG2Chi Natural Killer Cells. <i>PLoS Pathogens</i> , 2014, 10, e1004441.	4.7	224
29	BiQ Analyzer HiMod: an interactive software tool for high-throughput locus-specific analysis of 5-methylcytosine and its oxidized derivatives. <i>Nucleic Acids Research</i> , 2014, 42, W501-W507.	14.5	21
30	Comprehensive analysis of DNA methylation data with RnBeads. <i>Nature Methods</i> , 2014, 11, 1138-1140.	19.0	565
31	Suv39h-Dependent H3K9me3 Marks Intact Retrotransposons and Silences LINE Elements in Mouse Embryonic Stem Cells. <i>Molecular Cell</i> , 2014, 55, 277-290.	9.7	278
32	Whole-Genome Bisulfite Sequencing of Two Distinct Interconvertible DNA Methylomes of Mouse Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2013, 13, 360-369.	11.1	424
33	The <i>Polycomb</i> group protein <i>MEDEA</i> and the <i>DNA</i> methyltransferase <i>MET1</i> interact to repress autonomous endosperm development in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2013, 73, 776-787.	5.7	49
34	FGF Signaling Inhibition in ESCs Drives Rapid Genome-wide Demethylation to the Epigenetic Ground State of Pluripotency. <i>Cell Stem Cell</i> , 2013, 13, 351-359.	11.1	371
35	Dynamic Readers for 5-(Hydroxy)Methylcytosine and Its Oxidized Derivatives. <i>Cell</i> , 2013, 152, 1146-1159.	28.9	888
36	DNA Methylation Analysis of Mouse Intestinal Adenoma Identifies a Tumour-Specific Signature That Is Partly Conserved in Human Colon Cancer. <i>PLoS Genetics</i> , 2013, 9, e1003250.	3.5	40

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37	Active Demethylation of the <i>Foxp3</i> Locus Leads to the Generation of Stable Regulatory T Cells within the Thymus. <i>Journal of Immunology</i> , 2013, 190, 3180-3188.	0.8	228
38	In Vivo Control of CpG and Non-CpG DNA Methylation by DNA Methyltransferases. <i>PLoS Genetics</i> , 2012, 8, e1002750.	3.5	337
39	The Dynamics of Genome-wide DNA Methylation Reprogramming in Mouse Primordial Germ Cells. <i>Molecular Cell</i> , 2012, 48, 849-862.	9.7	837
40	Identification of a DNA methylation-independent imprinting control region at the <i>Arabidopsis</i> MEDEA locus. <i>Genes and Development</i> , 2012, 26, 1837-1850.	5.9	48
41	BLUEPRINT to decode the epigenetic signature written in blood. <i>Nature Biotechnology</i> , 2012, 30, 224-226.	17.5	323
42	Overexpression of the IGF2-mRNA binding protein p62 in transgenic mice induces a steatotic phenotype. <i>Journal of Hepatology</i> , 2011, 54, 994-1001.	3.7	56
43	An Epigenetic Tet a Tet with Pluripotency. <i>Cell Stem Cell</i> , 2011, 8, 121-122.	11.1	15
44	Next-Generation Sequencing Reveals Regional Differences of the α -Synuclein Methylation State Independent of Lewy Body Disease. <i>NeuroMolecular Medicine</i> , 2011, 13, 310-320.	3.4	61
45	Dynamic link of DNA demethylation, DNA strand breaks and repair in mouse zygotes. <i>EMBO Journal</i> , 2010, 29, 1877-1888.	7.8	221
46	Assisted reproductive technologies do not enhance the variability of DNA methylation imprints in human. <i>Journal of Medical Genetics</i> , 2010, 47, 371-376.	3.2	106
47	DNA Methylation Analysis of Chromosome 21 Gene Promoters at Single Base Pair and Single Allele Resolution. <i>PLoS Genetics</i> , 2009, 5, e1000438.	3.5	143
48	Epigenetic modifications and related mRNA expression during bovine oocyte in vitro maturation. <i>Reproduction, Fertility and Development</i> , 2009, 21, 738.	0.4	50
49	Inter-individual variation of DNA methylation and its implications for large-scale epigenome mapping. <i>Nucleic Acids Research</i> , 2008, 36, e55-e55.	14.5	127
50	CpG Island Mapping by Epigenome Prediction. <i>PLoS Computational Biology</i> , 2007, 3, e110.	3.2	162
51	CpG Island Methylation in Human Lymphocytes Is Highly Correlated with DNA Sequence, Repeats, and Predicted DNA Structure. <i>PLoS Genetics</i> , 2006, 2, e26.	3.5	183
52	Epigenetic reprogramming in mouse primordial germ cells. <i>Mechanisms of Development</i> , 2002, 117, 15-23.	1.7	1,091