Christoph Bock

List of Publications by Year
in descending order

221 papers	31,097 citations	4658 85 h-index	5394 164 g-index
257 all docs	257 docs citations	257 times ranked	48906 citing authors

#	ARTICLE	IF	CITATIONS
1	Somatic Mutations of Calreticulin in Myeloproliferative Neoplasms. New England Journal of Medicine, 2013, 369, 2379-2390.	27.0	1,698
2	Paternally Induced Transgenerational Environmental Reprogramming of Metabolic Gene Expression in Mammals. Cell, 2010, 143, 1084-1096.	28.9	990
3	Dnmt3a is essential for hematopoietic stem cell differentiation. Nature Genetics, 2012, 44, 23-31.	21.4	916
4	Reference Maps of Human ES and iPS Cell Variation Enable High-Throughput Characterization of Pluripotent Cell Lines. Cell, 2011, 144, 439-452.	28.9	899
5	Pooled CRISPR screening with single-cell transcriptome readout. Nature Methods, 2017, 14, 297-301.	19.0	749
6	Preparation of reduced representation bisulfite sequencing libraries for genome-scale DNA methylation profiling. Nature Protocols, 2011, 6, 468-481.	12.0	667
7	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. Nature Biotechnology, 2010, 28, 1097-1105.	17.5	647
8	Specification of tissue-resident macrophages during organogenesis. Science, 2016, 353, .	12.6	609
9	Toward understanding and exploiting tumor heterogeneity. Nature Medicine, 2015, 21, 846-853.	30.7	604
10	Comprehensive analysis of DNA methylation data with RnBeads. Nature Methods, 2014, 11, 1138-1140.	19.0	565
11	BiQ Analyzer: visualization and quality control for DNA methylation data from bisulfite sequencing. Bioinformatics, 2005, 21, 4067-4068.	4.1	554
12	Quantitative comparison of genome-wide DNA methylation mapping technologies. Nature Biotechnology, 2010, 28, 1106-1114.	17.5	534
13	Epigenomic Profiling of Young and Aged HSCs Reveals Concerted Changes during Aging that Reinforce Self-Renewal. Cell Stem Cell, 2014, 14, 673-688.	11.1	524
14	Analysing and interpreting DNA methylation data. Nature Reviews Genetics, 2012, 13, 705-719.	16.3	504
15	DNA methylation signatures link prenatal famine exposure to growth and metabolism. Nature Communications, 2014, 5, 5592.	12.8	494
16	ChIPmentation: fast, robust, low-input ChIP-seq for histones and transcription factors. Nature Methods, 2015, 12, 963-965.	19.0	417
17	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
18	Proliferation-Dependent Alterations of the DNA Methylation Landscape Underlie Hematopoietic Stem Cell Aging. Cell Stem Cell, 2013, 12, 413-425.	11.1	401

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19	Molecular interrogation of hypothalamic organization reveals distinct dopamine neuronal subtypes. Nature Neuroscience, 2017, 20, 176-188.	14.8	384
20	Single-Cell DNA Methylome Sequencing and Bioinformatic Inference of Epigenomic Cell-State Dynamics. Cell Reports, 2015, 10, 1386-1397.	6.4	378
21	LOLA: enrichment analysis for genomic region sets and regulatory elements in R and Bioconductor. Bioinformatics, 2016, 32, 587-589.	4.1	375
22	Genomic Distribution and Inter-Sample Variation of Non-CpG Methylation across Human Cell Types. PLoS Genetics, 2011, 7, e1002389.	3.5	345
23	Recommendations for the design and analysis of epigenome-wide association studies. Nature Methods, 2013, 10, 949-955.	19.0	345
24	Spatiotemporal structure of cell fate decisions in murine neural crest. Science, 2019, 364, .	12.6	345
25	Sequential ChIP-bisulfite sequencing enables direct genome-scale investigation of chromatin and DNA methylation cross-talk. Genome Research, 2012, 22, 1128-1138.	5.5	344
26	A DNA methylation fingerprint of 1628 human samples. Genome Research, 2012, 22, 407-419.	5.5	341
27	DNA Methylation Dynamics during InÂVivo Differentiation of Blood and Skin Stem Cells. Molecular Cell, 2012, 47, 633-647.	9.7	338
28	Artemisinins Target GABAA Receptor Signaling and Impair Î± Cell Identity. Cell, 2017, 168, 86-100.e15.	28.9	330
29	BLUEPRINT to decode the epigenetic signature written in blood. Nature Biotechnology, 2012, 30, 224-226.	17.5	323
30	Longitudinal molecular trajectories of diffuse glioma in adults. Nature, 2019, 576, 112-120.	27.8	320
31	Erosion of Dosage Compensation Impacts Human iPSC Disease Modeling. Cell Stem Cell, 2012, 10, 595-609.	11.1	314
32	Genome-scale DNA methylation mapping of clinical samples at single-nucleotide resolution. Nature Methods, 2010, 7, 133-136.	19.0	302
33	Structural cells are key regulators of organ-specific immune responses. Nature, 2020, 583, 296-302.	27.8	292
34	Microbiota-Derived Metabolites Suppress Arthritis by Amplifying Aryl-Hydrocarbon Receptor Activation in Regulatory B Cells. Cell Metabolism, 2020, 31, 837-851.e10.	16.2	290
35	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. Nature Biotechnology, 2016, 34, 726-737.	17.5	270
36	Disturbed mitochondrial dynamics in CD8+ TILs reinforce T cell exhaustion. Nature Immunology, 2020, 21, 1540-1551.	14.5	252

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37	A Prognostic DNA Methylation Signature for Stage I Non–Small-Cell Lung Cancer. Journal of Clinical Oncology, 2013, 31, 4140-4147.	1.6	250
38	A Kinase-Independent Function of CDK6 Links the Cell Cycle to Tumor Angiogenesis. Cancer Cell, 2013, 24, 167-181.	16.8	244
39	B cells sustain inflammation and predict response to immune checkpoint blockade in human melanoma. Nature Communications, 2019, 10, 4186.	12.8	236
40	The DNA methylation landscape of glioblastoma disease progression shows extensive heterogeneity in time and space. Nature Medicine, 2018, 24, 1611-1624.	30.7	229
41	Whole-exome sequencing identifies novel MPL and JAK2 mutations in triple-negative myeloproliferative neoplasms. Blood, 2016, 127, 325-332.	1.4	228
42	Pharmacological targeting of the Wdr5-MLL interaction in C/EBPα N-terminal leukemia. Nature Chemical Biology, 2015, 11, 571-578.	8.0	227
43	RnBeads 2.0: comprehensive analysis of DNA methylation data. Genome Biology, 2019, 20, 55.	8.8	223
44	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	21.4	218
45	DNA Methylation Dynamics of Human Hematopoietic Stem Cell Differentiation. Cell Stem Cell, 2016, 19, 808-822.	11.1	216
46	Single-cell transcriptomes reveal characteristic features of human pancreatic islet cell types. EMBO Reports, 2016, 17, 178-187.	4.5	206
47	Genomic epidemiology of superspreading events in Austria reveals mutational dynamics and transmission properties of SARS-CoV-2. Science Translational Medicine, 2020, 12, .	12.4	203
48	Rational discovery of molecular glue degraders via scalable chemical profiling. Nature Chemical Biology, 2020, 16, 1199-1207.	8.0	197
49	Optimization of Quantitative MGMT Promoter Methylation Analysis Using Pyrosequencing and Combined Bisulfite Restriction Analysis. Journal of Molecular Diagnostics, 2007, 9, 368-381.	2.8	194
50	DNA methylation heterogeneity defines a disease spectrum in Ewing sarcoma. Nature Medicine, 2017, 23, 386-395.	30.7	193
51	High-throughput bisulfite sequencing in mammalian genomes. Methods, 2009, 48, 226-232.	3.8	191
52	Making sense of big data in health research: Towards an EU action plan. Genome Medicine, 2016, 8, 71.	8.2	190
53	HCV-Induced Epigenetic Changes Associated With Liver Cancer Risk Persist After Sustained Virologic Response. Gastroenterology, 2019, 156, 2313-2329.e7.	1.3	184
54	CpG Island Methylation in Human Lymphocytes Is Highly Correlated with DNA Sequence, Repeats, and Predicted DNA Structure. PLoS Genetics, 2006, 2, e26.	3.5	183

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55	Epigenome Mapping Reveals Distinct Modes of Gene Regulation and Widespread Enhancer Reprogramming by the Oncogenic Fusion Protein EWS-FLI1. Cell Reports, 2015, 10, 1082-1095.	6.4	183
56	Computational epigenetics. Bioinformatics, 2008, 24, 1-10.	4.1	180
57	Mitochondria Are a Subset of Extracellular Vesicles Released by Activated Monocytes and Induce Type I IFN and TNF Responses in Endothelial Cells. Circulation Research, 2019, 125, 43-52.	4.5	177
58	Inherited DOCK2 Deficiency in Patients with Early-Onset Invasive Infections. New England Journal of Medicine, 2015, 372, 2409-2422.	27.0	169
59	Glioma progression is shaped by genetic evolution and microenvironment interactions. Cell, 2022, 185, 2184-2199.e16.	28.9	163
60	CpG Island Mapping by Epigenome Prediction. PLoS Computational Biology, 2007, 3, e110.	3.2	162
61	High-content CRISPR screening. Nature Reviews Methods Primers, 2022, 2, .	21.2	155
62	Functional Dissection of the Enhancer Repertoire in Human Embryonic Stem Cells. Cell Stem Cell, 2018, 23, 276-288.e8.	11.1	151
63	Managing drug resistance in cancer: lessons from HIV therapy. Nature Reviews Cancer, 2012, 12, 494-501.	28.4	150
64	DNA methylation biomarkers in cancer: progress towards clinical implementation. Expert Review of Molecular Diagnostics, 2012, 12, 473-487.	3.1	146
65	Inference of transcription factor binding from cell-free DNA enables tumor subtype prediction and early detection. Nature Communications, 2019, 10, 4666.	12.8	146
66	DNA Methylation Analysis of Chromosome 21 Gene Promoters at Single Base Pair and Single Allele Resolution. PLoS Genetics, 2009, 5, e1000438.	3.5	143
67	SARS-CoV-2 mutations in MHC-I-restricted epitopes evade CD8 ⁺ T cell responses. Science Immunology, 2021, 6, .	11.9	143
68	Global DNA Demethylation During Mouse Erythropoiesis in Vivo. Science, 2011, 334, 799-802.	12.6	142
69	Precursors for Nonlymphoid-Tissue Treg Cells Reside in Secondary Lymphoid Organs and Are Programmed by the Transcription Factor BATF. Immunity, 2020, 52, 295-312.e11.	14.3	140
70	Single-Cell RNA Sequencing Analysis Reveals a Crucial Role for CTHRC1 (Collagen Triple Helix Repeat) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.6	132
71	Chromatin accessibility maps of chronic lymphocytic leukaemia identify subtype-specific epigenome signatures and transcription regulatory networks. Nature Communications, 2016, 7, 11938.	12.8	131
72	Ultra-high-throughput single-cell RNA sequencing and perturbation screening with combinatorial fluidic indexing. Nature Methods, 2021, 18, 635-642.	19.0	129

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73	Inter-individual variation of DNA methylation and its implications for large-scale epigenome mapping. Nucleic Acids Research, 2008, 36, e55-e55.	14.5	127
74	Multi-Omics of Single Cells: Strategies and Applications. Trends in Biotechnology, 2016, 34, 605-608.	9.3	125
75	Mapping the mouse Allelome reveals tissue-specific regulation of allelic expression. ELife, 2017, 6, .	6.0	120
76	Lung Stem Cell Self-Renewal Relies on BMI1-Dependent Control of Expression at Imprinted Loci. Cell Stem Cell, 2011, 9, 272-281.	11.1	119
77	Glioma through the looking GLASS: molecular evolution of diffuse gliomas and the Glioma Longitudinal Analysis Consortium. Neuro-Oncology, 2018, 20, 873-884.	1.2	119
78	BiQ Analyzer HT: locus-specific analysis of DNA methylation by high-throughput bisulfite sequencing. Nucleic Acids Research, 2011, 39, W551-W556.	14.5	114
79	Single-cell transcriptomics combined with interstitial fluid proteomics defines cell type–specific immune regulation in atopic dermatitis. Journal of Allergy and Clinical Immunology, 2020, 146, 1056-1069.	2.9	114
80	Epigenetic biomarker development. Epigenomics, 2009, 1, 99-110.	2.1	112
81	Comprehensive genome and epigenome characterization of CHO cells in response to evolutionary pressures and over time. Biotechnology and Bioengineering, 2016, 113, 2241-2253.	3.3	112
82	Hyperglycemia Induces Trained Immunity in Macrophages and Their Precursors and Promotes Atherosclerosis. Circulation, 2021, 144, 961-982.	1.6	109
83	LifeTime and improving European healthcare through cell-based interceptive medicine. Nature, 2020, 587, 377-386.	27.8	108
84	Aryl Hydrocarbon Receptor Contributes to the Transcriptional Program of IL-10-Producing Regulatory B Cells. Cell Reports, 2019, 29, 1878-1892.e7.	6.4	107
85	High-Resolution Mapping of H1 Linker Histone Variants in Embryonic Stem Cells. PLoS Genetics, 2013, 9, e1003417.	3.5	106
86	Molecular design of hypothalamus development. Nature, 2020, 582, 246-252.	27.8	105
87	Acute BAF perturbation causes immediate changes in chromatin accessibility. Nature Genetics, 2021, 53, 269-278.	21.4	103
88	Promoter hypermethylation of the phosphatase DUSP22 mediates PKA–dependent TAU phosphorylation and CREB activation in Alzheimer's disease. Hippocampus, 2014, 24, 363-368.	1.9	98
89	A promoter DNA demethylation landscape of human hematopoietic differentiation. Nucleic Acids Research, 2012, 40, 116-131.	14.5	97
90	The Organoid Cell Atlas. Nature Biotechnology, 2021, 39, 13-17.	17.5	96

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91	Multimodal analysis of cell-free DNA whole-genome sequencing for pediatric cancers with low mutational burden. Nature Communications, 2021, 12, 3230.	12.8	95
92	Chromatin accessibility profiling methods. Nature Reviews Methods Primers, 2021, 1, .	21.2	95
93	Circadian rhythm influences induction of trained immunity by BCG vaccination. Journal of Clinical Investigation, 2020, 130, 5603-5617.	8.2	95
94	Systematic characterization of BAF mutations provides insights into intracomplex synthetic lethalities in human cancers. Nature Genetics, 2019, 51, 1399-1410.	21.4	92
95	A reversible gene trap collection empowers haploid genetics in human cells. Nature Methods, 2013, 10, 965-971.	19.0	90
96	KRAS and CREBBP mutations: a relapse-linked malicious liaison in childhood high hyperdiploid acute lymphoblastic leukemia. Leukemia, 2015, 29, 1656-1667.	7.2	90
97	Integrative Proteomic Profiling Reveals PRC2-Dependent Epigenetic Crosstalk Maintains Ground-State Pluripotency. Cell Stem Cell, 2019, 24, 123-137.e8.	11.1	90
98	RRBSMAP: a fast, accurate and user-friendly alignment tool for reduced representation bisulfite sequencing. Bioinformatics, 2012, 28, 430-432.	4.1	85
99	An ERK-Dependent Feedback Mechanism Prevents Hematopoietic Stem Cell Exhaustion. Cell Stem Cell, 2018, 22, 879-892.e6.	11.1	84
100	Selective Mediator dependence of cell-type-specifying transcription. Nature Genetics, 2020, 52, 719-727.	21.4	84
101	Viral variant-resolved wastewater surveillance of SARS-CoV-2 at national scale. Nature Biotechnology, 2022, 40, 1814-1822.	17.5	82
102	Highly efficient derivation of ventricular cardiomyocytes from induced pluripotent stem cells with a distinct epigenetic signature. Cell Research, 2012, 22, 142-154.	12.0	77
103	Assessment of established techniques to determine developmental and malignant potential of human pluripotent stem cells. Nature Communications, 2018, 9, 1925.	12.8	76
104	Persistence of mature dendritic cells, T_H2A, and Tc2 cells characterize clinically resolved atopic dermatitis under IL-4Rα blockade. Science Immunology, 2021, 6, .	11.9	76
105	EpiExplorer: live exploration and global analysis of large epigenomic datasets. Genome Biology, 2012, 13, R96.	9.6	72
106	Chromatin mapping and single-cell immune profiling define the temporal dynamics of ibrutinib response in CLL. Nature Communications, 2020, 11, 577.	12.8	69
107	Comparative genome-wide DNA methylation analysis of colorectal tumor and matched normal tissues. Epigenetics, 2012, 7, 1355-1367.	2.7	67
108	Knowledge-primed neural networks enable biologically interpretable deep learning on single-cell sequencing data. Genome Biology, 2020, 21, 190.	8.8	67

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109	Regulation of DNA Methylation Patterns by CK2-Mediated Phosphorylation of Dnmt3a. Cell Reports, 2014, 8, 743-753.	6.4	66
110	Notch inhibition allows oncogene-independent generation of iPS cells. Nature Chemical Biology, 2014, 10, 632-639.	8.0	64
111	Dissecting the role of aberrant DNA methylation in human leukaemia. Nature Communications, 2015, 6, 7091.	12.8	62
112	Ageing-associated DNA methylation dynamics are a molecular readout of lifespan variation among mammalian species. Genome Biology, 2018, 19, 22.	8.8	62
113	MTHFD1 interaction with BRD4 links folate metabolism to transcriptional regulation. Nature Genetics, 2019, 51, 990-998.	21.4	61
114	Guadecitabine Plus Ipilimumab in Unresectable Melanoma: The NIBIT-M4 Clinical Trial. Clinical Cancer Research, 2019, 25, 7351-7362.	7.0	61
115	DeepBlue epigenomic data server: programmatic data retrieval and analysis of epigenome region sets. Nucleic Acids Research, 2016, 44, W581-W586.	14.5	60
116	STAT5BN642H is a driver mutation for T cell neoplasia. Journal of Clinical Investigation, 2017, 128, 387-401.	8.2	57
117	Long-term skin-resident memory T cells proliferate in situ and are involved in human graft-versus-host disease. Science Translational Medicine, 2020, 12, .	12.4	57
118	Targeting clinical epigenetic reprogramming for chemoprevention of metabolic and viral hepatocellular carcinoma. Gut, 2021, 70, 157-169.	12.1	57
119	Mutational landscape of the transcriptome offers putative targets for immunotherapy of myeloproliferative neoplasms. Blood, 2019, 134, 199-210.	1.4	54
120	Malondialdehyde epitopes are sterile mediators of hepatic inflammation in hypercholesterolemic mice. Hepatology, 2017, 65, 1181-1195.	7.3	53
121	Colocalization analyses of genomic elements: approaches, recommendations and challenges. Bioinformatics, 2019, 35, 1615-1624.	4.1	53
122	RANK links thymic regulatory T cells to fetal loss and gestational diabetes in pregnancy. Nature, 2021, 589, 442-447.	27.8	52
123	Parental micronutrient deficiency distorts liver DNA methylation and expression of lipid genes associated with a fatty-liver-like phenotype in offspring. Scientific Reports, 2018, 8, 3055.	3.3	50
124	Structural conservation versus functional divergence of maternally expressed microRNAs in the Dlk1/Gtl2 imprinting region. BMC Genomics, 2008, 9, 346.	2.8	49
125	Next-generation sequencing identifies major DNA methylation changes during progression of Ph+ chronic myeloid leukemia. Leukemia, 2016, 30, 1861-1868.	7.2	49
126	EpiGRAPH: user-friendly software for statistical analysis and prediction of (epi)genomic data. Genome Biology, 2009, 10, R14.	9.6	48

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127	Single-cell analysis reveals innate lymphoid cell lineage infidelity in atopic dermatitis. Journal of Allergy and Clinical Immunology, 2022, 149, 624-639.	2.9	48
128	Temporal dissection of an enhancer cluster reveals distinct temporal and functional contributions of individual elements. Molecular Cell, 2021, 81, 969-982.e13.	9.7	47
129	Emergence of coronavirus disease 2019 (COVID-19) in Austria. Wiener Klinische Wochenschrift, 2020, 132, 645-652.	1.9	46
130	Genomic and transcriptional landscape of P2RY8-CRLF2-positive childhood acute lymphoblastic leukemia. Leukemia, 2017, 31, 1491-1501.	7.2	45
131	Quantitative comparison of within-sample heterogeneity scores for DNA methylation data. Nucleic Acids Research, 2020, 48, e46-e46.	14.5	45
132	The Human Genomic Melting Map. PLoS Computational Biology, 2007, 3, e93.	3.2	44
133	Mapping the chemical chromatin reactivation landscape identifies BRD4-TAF1 cross-talk. Nature Chemical Biology, 2016, 12, 504-510.	8.0	43
134	The ERBB-STAT3 Axis Drives Tasmanian Devil Facial Tumor Disease. Cancer Cell, 2019, 35, 125-139.e9.	16.8	43
135	Epigenomics and Single-Cell Sequencing Define a Developmental Hierarchy in Langerhans Cell Histiocytosis. Cancer Discovery, 2019, 9, 1406-1421.	9.4	42
136	STAT3 promotes melanoma metastasis by CEBP-induced repression of the MITF pathway. Oncogene, 2021, 40, 1091-1105.	5.9	42
137	Epigenetic Homogeneity Within Colorectal Tumors Predicts Shorter Relapse-Free and Overall Survival Times for Patients With Locoregional Cancer. Gastroenterology, 2016, 151, 961-972.	1.3	41
138	NOTCH1 activation in breast cancer confers sensitivity to inhibition of SUMOylation. Oncogene, 2015, 34, 3780-3790.	5.9	40
139	A combinatorial screen of the CLOUD uncovers a synergy targeting the androgen receptor. Nature Chemical Biology, 2017, 13, 771-778.	8.0	39
140	A T cell-specific deletion of HDAC1 protects against experimental autoimmune encephalomyelitis. Journal of Autoimmunity, 2018, 86, 51-61.	6.5	39
141	A discrete subset of epigenetically primed human NK cells mediates antigen-specific immune responses. Science Immunology, 2020, 5, .	11.9	38
142	VCF.Filter: interactive prioritization of disease-linked genetic variants from sequencing data. Nucleic Acids Research, 2017, 45, W567-W572.	14.5	37
143	The cytoskeletal regulator HEM1 governs B cell development and prevents autoimmunity. Science Immunology, 2020, 5, .	11.9	37
144	Functional Analysis of a Potassium-Chloride Co-Transporter 3 (SLC12A6) Promoter Polymorphism Leading to an Additional DNA Methylation Site. Neuropsychopharmacology, 2009, 34, 458-467.	5.4	36

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145	Differential DNA Methylation Analysis without a Reference Genome. Cell Reports, 2015, 13, 2621-2633.	6.4	34
146	Combined chemosensitivity and chromatin profiling prioritizes drug combinations in CLL. Nature Chemical Biology, 2019, 15, 232-240.	8.0	34
147	Chromatin-Based Classification of Genetically Heterogeneous AMLs into Two Distinct Subtypes with Diverse Stemness Phenotypes. Cell Reports, 2019, 26, 1059-1069.e6.	6.4	33
148	Cell-Type Specificity of Genomic Imprinting in Cerebral Cortex. Neuron, 2020, 107, 1160-1179.e9.	8.1	33
149	Human resident memory T cells exit the skin and mediate systemic Th2-driven inflammation. Journal of Experimental Medicine, 2021, 218, .	8.5	32
150	10. Ein integrierter Ansatz zur Beschreibung und Analyse genetisch-epigenetischer Zellzustände. , 2014, , 135-150.		31
151	Single-cell RNA-seq with spike-in cells enables accurate quantification of cell-specific drug effects in pancreatic islets. Genome Biology, 2020, 21, 106.	8.8	30
152	Genomic imprinting in mouse blastocysts is predominantly associated with H3K27me3. Nature Communications, 2021, 12, 3804.	12.8	30
153	A Comprehensive Analysis of the Dynamic Response to Aphidicolin-Mediated Replication Stress Uncovers Targets for ATM and ATMIN. Cell Reports, 2016, 15, 893-908.	6.4	29
154	CDK6 coordinates JAK2V617F mutant MPN via NF-κB and apoptotic networks. Blood, 2019, 133, 1677-1690.	1.4	29
155	Life-long epigenetic programming of cortical architecture by maternal â€˜Westernâ€™ diet during pregnancy. Molecular Psychiatry, 2020, 25, 22-36.	7.9	28
156	Identification of Novel Imprinted Differentially Methylated Regions by Global Analysis of Human-Parthenogenetic-Induced Pluripotent Stem Cells. Stem Cell Reports, 2013, 1, 79-89.	4.8	27
157	MethMarker: user-friendly design and optimization of gene-specific DNA methylation assays. Genome Biology, 2009, 10, R105.	9.6	25
158	Parallel genome-wide screens identify synthetic viable interactions between the BLM helicase complex and Fanconi anemia. Nature Communications, 2017, 8, 1238.	12.8	25
159	Relationship between genome and epigenome - challenges and requirements for future research. BMC Genomics, 2014, 15, 487.	2.8	24
160	Proposed Terminology and Classification of Pre-Malignant Neoplastic Conditions: A Consensus Proposal. EBioMedicine, 2017, 26, 17-24.	6.1	24
161	Coloc-stats: a unified web interface to perform colocalization analysis of genomic features. Nucleic Acids Research, 2018, 46, W186-W193.	14.5	23
162	Histone deacetylases 1 and 2 restrain CD4+ cytotoxic T lymphocyte differentiation. JCI Insight, 2020, 5, .	5.0	23

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163	Aberrant DNA methylation reprogramming during induced pluripotent stem cell generation is dependent on the choice of reprogramming factors. Cell Regeneration, 2014, 3, 3:4.	2.6	22
164	Rapid neutrophil mobilization by VCAM-1+ endothelial cell-derived extracellular vesicles. Cardiovascular Research, 2023, 119, 236-251.	3.8	22
165	BiQ Analyzer HiMod: an interactive software tool for high-throughput locus-specific analysis of 5-methylcytosine and its oxidized derivatives. Nucleic Acids Research, 2014, 42, W501-W507.	14.5	21
166	Spontaneously Resolved Atopic Dermatitis Shows Melanocyte and Immune Cell Activation Distinct From Healthy Control Skin. Frontiers in Immunology, 2021, 12, 630892.	4.8	21
167	MIRA: an R package for DNA methylation-based inference of regulatory activity. Bioinformatics, 2018, 34, 2649-2650.	4.1	19
168	Distributed changes of the functional connectome in patients with glioblastoma. Scientific Reports, 2020, 10, 18312.	3.3	19
169	αβγδ T cells play a vital role in fetal human skin development and immunity. Journal of Experimental Medicine, 2021, 218, .	8.5	17
170	Emergence of SARS-CoV-2 Alpha lineage and its correlation with quantitative wastewater-based epidemiology data. Water Research, 2022, 215, 118257.	11.3	17
171	Parallel reverse genetic screening in mutant human cells using transcriptomics. Molecular Systems Biology, 2016, 12, 879.	7.2	16
172	Familial early-onset dementia with complex neuropathologic phenotype and genomic background. Neurobiology of Aging, 2016, 42, 199-204.	3.1	16
173	Curation and expansion of Human Phenotype Ontology for defined groups of inborn errors of immunity. Journal of Allergy and Clinical Immunology, 2022, 149, 369-378.	2.9	16
174	DNA methylation QTL analysis identifies new regulators of human longevity. Human Molecular Genetics, 2020, 29, 1154-1167.	2.9	15
175	Response to comment on "Genomic epidemiology of superspreading events in Austria reveals mutational dynamics and transmission properties of SARS-CoV-2". Science Translational Medicine, 2021, 13, eabj3222.	12.4	14
176	Comprehensive Analysis of Nasal Polyps Reveals a More Pronounced Type 2 Transcriptomic Profile of Epithelial Cells and Mast Cells in Aspirin-Exacerbated Respiratory Disease. Frontiers in Immunology, 2022, 13, 850494.	4.8	14
177	NK Cells Require Cell-Extrinsic and -Intrinsic TYK2 for Full Functionality in Tumor Surveillance and Antibacterial Immunity. Journal of Immunology, 2019, 202, 1724-1734.	0.8	13
178	The Transcription Factor MAZR/PATZ1 Regulates the Development of FOXP3+ Regulatory T Cells. Cell Reports, 2019, 29, 4447-4459.e6.	6.4	13
179	NCOR1 Orchestrates Transcriptional Landscapes and Effector Functions of CD4+ T Cells. Frontiers in Immunology, 2020, 11, 579.	4.8	13
180	Tumor mutational burden and immune infiltrates in renal cell carcinoma and matched brain metastases. ESMO Open, 2021, 6, 100057.	4.5	13

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181	Targeted mutation screening of 292 candidate genes in 38 children with inborn haematological cytopenias efficiently identifies novel disease–causing mutations. British Journal of Haematology, 2018, 182, 251-258.	2.5	12
182	An inhibitor-mediated beta-cell dedifferentiation model reveals distinct roles for FoxO1 in glucagon repression and insulin maturation. Molecular Metabolism, 2021, 54, 101329.	6.5	12
183	Genome-scale CRISPR screens are efficient in non-homologous end-joining deficient cells. Scientific Reports, 2019, 9, 15751.	3.3	11
184	Life–long impairment of glucose homeostasis upon prenatal exposure to psychostimulants. EMBO Journal, 2020, 39, e100882.	7.8	11
185	Anti-Apoptotic Molecule BCL2 Is a Therapeutic Target in Steroid-Refractory Graft-Versus-Host Disease. Journal of Investigative Dermatology, 2020, 140, 2188-2198.	0.7	11
186	Precision Medicine in Hematology 2021: Definitions, Tools, Perspectives, and Open Questions. HemaSphere, 2021, 5, e536.	2.7	11
187	Web-Based Analysis of (Epi-) Genome Data Using EpiGRAPH and Galaxy. Methods in Molecular Biology, 2010, 628, 275-296.	0.9	10
188	Notch-mediated expansion of cord blood progenitors: maintenance of transcriptional and epigenetic fidelity. Leukemia, 2015, 29, 1948-1951.	7.2	9
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