

# Christoph Bock

## List of Publications by Year in descending order

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221  
papers

31,097  
citations

5430

85  
h-index

6177

164  
g-index

257  
all docs

257  
docs citations

257  
times ranked

53507  
citing authors

#	ARTICLE	IF	CITATIONS
1	Somatic Mutations of Calreticulin in Myeloproliferative Neoplasms. <i>New England Journal of Medicine</i> , 2013, 369, 2379-2390.	13.9	1,698
2	Paternally Induced Transgenerational Environmental Reprogramming of Metabolic Gene Expression in Mammals. <i>Cell</i> , 2010, 143, 1084-1096.	13.5	990
3	Dnmt3a is essential for hematopoietic stem cell differentiation. <i>Nature Genetics</i> , 2012, 44, 23-31.	9.4	916
4	Reference Maps of Human ES and iPS Cell Variation Enable High-Throughput Characterization of Pluripotent Cell Lines. <i>Cell</i> , 2011, 144, 439-452.	13.5	899
5	Pooled CRISPR screening with single-cell transcriptome readout. <i>Nature Methods</i> , 2017, 14, 297-301.	9.0	749
6	Preparation of reduced representation bisulfite sequencing libraries for genome-scale DNA methylation profiling. <i>Nature Protocols</i> , 2011, 6, 468-481.	5.5	667
7	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. <i>Nature Biotechnology</i> , 2010, 28, 1097-1105.	9.4	647
8	Specification of tissue-resident macrophages during organogenesis. <i>Science</i> , 2016, 353, .	6.0	609
9	Toward understanding and exploiting tumor heterogeneity. <i>Nature Medicine</i> , 2015, 21, 846-853.	15.2	604
10	Comprehensive analysis of DNA methylation data with RnBeads. <i>Nature Methods</i> , 2014, 11, 1138-1140.	9.0	565
11	BiQ Analyzer: visualization and quality control for DNA methylation data from bisulfite sequencing. <i>Bioinformatics</i> , 2005, 21, 4067-4068.	1.8	554
12	Quantitative comparison of genome-wide DNA methylation mapping technologies. <i>Nature Biotechnology</i> , 2010, 28, 1106-1114.	9.4	534
13	Epigenomic Profiling of Young and Aged HSCs Reveals Concerted Changes during Aging that Reinforce Self-Renewal. <i>Cell Stem Cell</i> , 2014, 14, 673-688.	5.2	524
14	Analysing and interpreting DNA methylation data. <i>Nature Reviews Genetics</i> , 2012, 13, 705-719.	7.7	504
15	DNA methylation signatures link prenatal famine exposure to growth and metabolism. <i>Nature Communications</i> , 2014, 5, 5592.	5.8	494
16	ChIPmentation: fast, robust, low-input ChIP-seq for histones and transcription factors. <i>Nature Methods</i> , 2015, 12, 963-965.	9.0	417
17	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	13.5	404
18	Proliferation-Dependent Alterations of the DNA Methylation Landscape Underlie Hematopoietic Stem Cell Aging. <i>Cell Stem Cell</i> , 2013, 12, 413-425.	5.2	401

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19	Molecular interrogation of hypothalamic organization reveals distinct dopamine neuronal subtypes. <i>Nature Neuroscience</i> , 2017, 20, 176-188.	7.1	384
20	Single-Cell DNA Methylome Sequencing and Bioinformatic Inference of Epigenomic Cell-State Dynamics. <i>Cell Reports</i> , 2015, 10, 1386-1397.	2.9	378
21	LOLA: enrichment analysis for genomic region sets and regulatory elements in R and Bioconductor. <i>Bioinformatics</i> , 2016, 32, 587-589.	1.8	375
22	Genomic Distribution and Inter-Sample Variation of Non-CpG Methylation across Human Cell Types. <i>PLoS Genetics</i> , 2011, 7, e1002389.	1.5	345
23	Recommendations for the design and analysis of epigenome-wide association studies. <i>Nature Methods</i> , 2013, 10, 949-955.	9.0	345
24	Spatiotemporal structure of cell fate decisions in murine neural crest. <i>Science</i> , 2019, 364, .	6.0	345
25	Sequential ChIP-bisulfite sequencing enables direct genome-scale investigation of chromatin and DNA methylation cross-talk. <i>Genome Research</i> , 2012, 22, 1128-1138.	2.4	344
26	A DNA methylation fingerprint of 1628 human samples. <i>Genome Research</i> , 2012, 22, 407-419.	2.4	341
27	DNA Methylation Dynamics during InÂVivo Differentiation of Blood and Skin Stem Cells. <i>Molecular Cell</i> , 2012, 47, 633-647.	4.5	338
28	Artemisinins Target GABAA Receptor Signaling and Impair $\hat{\pm}$ Cell Identity. <i>Cell</i> , 2017, 168, 86-100.e15.	13.5	330
29	BLUEPRINT to decode the epigenetic signature written in blood. <i>Nature Biotechnology</i> , 2012, 30, 224-226.	9.4	323
30	Longitudinal molecular trajectories of diffuse glioma in adults. <i>Nature</i> , 2019, 576, 112-120.	13.7	320
31	Erosion of Dosage Compensation Impacts Human iPSC Disease Modeling. <i>Cell Stem Cell</i> , 2012, 10, 595-609.	5.2	314
32	Genome-scale DNA methylation mapping of clinical samples at single-nucleotide resolution. <i>Nature Methods</i> , 2010, 7, 133-136.	9.0	302
33	Structural cells are key regulators of organ-specific immune responses. <i>Nature</i> , 2020, 583, 296-302.	13.7	292
34	Microbiota-Derived Metabolites Suppress Arthritis by Amplifying Aryl-Hydrocarbon Receptor Activation in Regulatory B Cells. <i>Cell Metabolism</i> , 2020, 31, 837-851.e10.	7.2	290
35	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , 2016, 34, 726-737.	9.4	270
36	Disturbed mitochondrial dynamics in CD8+ TILs reinforce T cell exhaustion. <i>Nature Immunology</i> , 2020, 21, 1540-1551.	7.0	252

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37	A Prognostic DNA Methylation Signature for Stage I Non-Small-Cell Lung Cancer. <i>Journal of Clinical Oncology</i> , 2013, 31, 4140-4147.	0.8	250
38	A Kinase-Independent Function of CDK6 Links the Cell Cycle to Tumor Angiogenesis. <i>Cancer Cell</i> , 2013, 24, 167-181.	7.7	244
39	B cells sustain inflammation and predict response to immune checkpoint blockade in human melanoma. <i>Nature Communications</i> , 2019, 10, 4186.	5.8	236
40	The DNA methylation landscape of glioblastoma disease progression shows extensive heterogeneity in time and space. <i>Nature Medicine</i> , 2018, 24, 1611-1624.	15.2	229
41	Whole-exome sequencing identifies novel MPL and JAK2 mutations in triple-negative myeloproliferative neoplasms. <i>Blood</i> , 2016, 127, 325-332.	0.6	228
42	Pharmacological targeting of the Wdr5-MLL interaction in C/EBP $\beta$ N-terminal leukemia. <i>Nature Chemical Biology</i> , 2015, 11, 571-578.	3.9	227
43	RnBeads 2.0: comprehensive analysis of DNA methylation data. <i>Genome Biology</i> , 2019, 20, 55.	3.8	223
44	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	9.4	218
45	DNA Methylation Dynamics of Human Hematopoietic Stem Cell Differentiation. <i>Cell Stem Cell</i> , 2016, 19, 808-822.	5.2	216
46	Single-cell transcriptomes reveal characteristic features of human pancreatic islet cell types. <i>EMBO Reports</i> , 2016, 17, 178-187.	2.0	206
47	Genomic epidemiology of superspreading events in Austria reveals mutational dynamics and transmission properties of SARS-CoV-2. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	203
48	Rational discovery of molecular glue degraders via scalable chemical profiling. <i>Nature Chemical Biology</i> , 2020, 16, 1199-1207.	3.9	197
49	Optimization of Quantitative MGMT Promoter Methylation Analysis Using Pyrosequencing and Combined Bisulfite Restriction Analysis. <i>Journal of Molecular Diagnostics</i> , 2007, 9, 368-381.	1.2	194
50	DNA methylation heterogeneity defines a disease spectrum in Ewing sarcoma. <i>Nature Medicine</i> , 2017, 23, 386-395.	15.2	193
51	High-throughput bisulfite sequencing in mammalian genomes. <i>Methods</i> , 2009, 48, 226-232.	1.9	191
52	Making sense of big data in health research: Towards an EU action plan. <i>Genome Medicine</i> , 2016, 8, 71.	3.6	190
53	HCV-Induced Epigenetic Changes Associated With Liver Cancer Risk Persist After Sustained Virologic Response. <i>Gastroenterology</i> , 2019, 156, 2313-2329.e7.	0.6	184
54	CpG Island Methylation in Human Lymphocytes Is Highly Correlated with DNA Sequence, Repeats, and Predicted DNA Structure. <i>PLoS Genetics</i> , 2006, 2, e26.	1.5	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. <i>Cell Reports</i> , 2015, 10, 1082-1095.	2.9	183
56	Computational epigenetics. <i>Bioinformatics</i> , 2008, 24, 1-10.	1.8	180
57	Mitochondria Are a Subset of Extracellular Vesicles Released by Activated Monocytes and Induce Type I IFN and TNF Responses in Endothelial Cells. <i>Circulation Research</i> , 2019, 125, 43-52.	2.0	177
58	Inherited DOCK2 Deficiency in Patients with Early-Onset Invasive Infections. <i>New England Journal of Medicine</i> , 2015, 372, 2409-2422.	13.9	169
59	Glioma progression is shaped by genetic evolution and microenvironment interactions. <i>Cell</i> , 2022, 185, 2184-2199.e16.	13.5	163
60	CpG Island Mapping by Epigenome Prediction. <i>PLoS Computational Biology</i> , 2007, 3, e110.	1.5	162
61	High-content CRISPR screening. <i>Nature Reviews Methods Primers</i> , 2022, 2, .	11.8	155
62	Functional Dissection of the Enhancer Repertoire in Human Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2018, 23, 276-288.e8.	5.2	151
63	Managing drug resistance in cancer: lessons from HIV therapy. <i>Nature Reviews Cancer</i> , 2012, 12, 494-501.	12.8	150
64	DNA methylation biomarkers in cancer: progress towards clinical implementation. <i>Expert Review of Molecular Diagnostics</i> , 2012, 12, 473-487.	1.5	146
65	Inference of transcription factor binding from cell-free DNA enables tumor subtype prediction and early detection. <i>Nature Communications</i> , 2019, 10, 4666.	5.8	146
66	DNA Methylation Analysis of Chromosome 21 Gene Promoters at Single Base Pair and Single Allele Resolution. <i>PLoS Genetics</i> , 2009, 5, e1000438.	1.5	143
67	SARS-CoV-2 mutations in MHC-I-restricted epitopes evade CD8 <sup>+</sup> T cell responses. <i>Science Immunology</i> , 2021, 6, .	5.6	143
68	Global DNA Demethylation During Mouse Erythropoiesis in Vivo. <i>Science</i> , 2011, 334, 799-802.	6.0	142
69	Precursors for Nonlymphoid-Tissue Treg Cells Reside in Secondary Lymphoid Organs and Are Programmed by the Transcription Factor BATF. <i>Immunity</i> , 2020, 52, 295-312.e11.	6.6	140
70	Single-Cell RNA Sequencing Analysis Reveals a Crucial Role for CTHRC1 (Collagen Triple Helix Repeat) Tj ETQq0 0 0 rBT /Overlock 10 Tf	1.6	132
71	Chromatin accessibility maps of chronic lymphocytic leukaemia identify subtype-specific epigenome signatures and transcription regulatory networks. <i>Nature Communications</i> , 2016, 7, 11938.	5.8	131
72	Ultra-high-throughput single-cell RNA sequencing and perturbation screening with combinatorial fluidic indexing. <i>Nature Methods</i> , 2021, 18, 635-642.	9.0	129

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73	Inter-individual variation of DNA methylation and its implications for large-scale epigenome mapping. <i>Nucleic Acids Research</i> , 2008, 36, e55-e55.	6.5	127
74	Multi-Omics of Single Cells: Strategies and Applications. <i>Trends in Biotechnology</i> , 2016, 34, 605-608.	4.9	125
75	Mapping the mouse Allelome reveals tissue-specific regulation of allelic expression. <i>ELife</i> , 2017, 6, .	2.8	120
76	Lung Stem Cell Self-Renewal Relies on BMI1-Dependent Control of Expression at Imprinted Loci. <i>Cell Stem Cell</i> , 2011, 9, 272-281.	5.2	119
77	Glioma through the looking GLASS: molecular evolution of diffuse gliomas and the Glioma Longitudinal Analysis Consortium. <i>Neuro-Oncology</i> , 2018, 20, 873-884.	0.6	119
78	BiQ Analyzer HT: locus-specific analysis of DNA methylation by high-throughput bisulfite sequencing. <i>Nucleic Acids Research</i> , 2011, 39, W551-W556.	6.5	114
79	Single-cell transcriptomics combined with interstitial fluid proteomics defines cell type-specific immune regulation in atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 146, 1056-1069.	1.5	114
80	Epigenetic biomarker development. <i>Epigenomics</i> , 2009, 1, 99-110.	1.0	112
81	Comprehensive genome and epigenome characterization of CHO cells in response to evolutionary pressures and over time. <i>Biotechnology and Bioengineering</i> , 2016, 113, 2241-2253.	1.7	112
82	Hyperglycemia Induces Trained Immunity in Macrophages and Their Precursors and Promotes Atherosclerosis. <i>Circulation</i> , 2021, 144, 961-982.	1.6	109
83	LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , 2020, 587, 377-386.	13.7	108
84	Aryl Hydrocarbon Receptor Contributes to the Transcriptional Program of IL-10-Producing Regulatory B Cells. <i>Cell Reports</i> , 2019, 29, 1878-1892.e7.	2.9	107
85	High-Resolution Mapping of H1 Linker Histone Variants in Embryonic Stem Cells. <i>PLoS Genetics</i> , 2013, 9, e1003417.	1.5	106
86	Molecular design of hypothalamus development. <i>Nature</i> , 2020, 582, 246-252.	13.7	105
87	Acute BAF perturbation causes immediate changes in chromatin accessibility. <i>Nature Genetics</i> , 2021, 53, 269-278.	9.4	103
88	Promoter hypermethylation of the phosphatase DUSP22 mediates PKA-dependent TAU phosphorylation and CREB activation in Alzheimer's disease. <i>Hippocampus</i> , 2014, 24, 363-368.	0.9	98
89	A promoter DNA demethylation landscape of human hematopoietic differentiation. <i>Nucleic Acids Research</i> , 2012, 40, 116-131.	6.5	97
90	The Organoid Cell Atlas. <i>Nature Biotechnology</i> , 2021, 39, 13-17.	9.4	96

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91	Multimodal analysis of cell-free DNA whole-genome sequencing for pediatric cancers with low mutational burden. <i>Nature Communications</i> , 2021, 12, 3230.	5.8	95
92	Chromatin accessibility profiling methods. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	95
93	Circadian rhythm influences induction of trained immunity by BCG vaccination. <i>Journal of Clinical Investigation</i> , 2020, 130, 5603-5617.	3.9	95
94	Systematic characterization of BAF mutations provides insights into intracomplex synthetic lethalties in human cancers. <i>Nature Genetics</i> , 2019, 51, 1399-1410.	9.4	92
95	A reversible gene trap collection empowers haploid genetics in human cells. <i>Nature Methods</i> , 2013, 10, 965-971.	9.0	90
96	KRAS and CREBBP mutations: a relapse-linked malicious liaison in childhood high hyperdiploid acute lymphoblastic leukemia. <i>Leukemia</i> , 2015, 29, 1656-1667.	3.3	90
97	Integrative Proteomic Profiling Reveals PRC2-Dependent Epigenetic Crosstalk Maintains Ground-State Pluripotency. <i>Cell Stem Cell</i> , 2019, 24, 123-137.e8.	5.2	90
98	RRBSMAP: a fast, accurate and user-friendly alignment tool for reduced representation bisulfite sequencing. <i>Bioinformatics</i> , 2012, 28, 430-432.	1.8	85
99	An ERK-Dependent Feedback Mechanism Prevents Hematopoietic Stem Cell Exhaustion. <i>Cell Stem Cell</i> , 2018, 22, 879-892.e6.	5.2	84
100	Selective Mediator dependence of cell-type-specifying transcription. <i>Nature Genetics</i> , 2020, 52, 719-727.	9.4	84
101	Viral variant-resolved wastewater surveillance of SARS-CoV-2 at national scale. <i>Nature Biotechnology</i> , 2022, 40, 1814-1822.	9.4	82
102	Highly efficient derivation of ventricular cardiomyocytes from induced pluripotent stem cells with a distinct epigenetic signature. <i>Cell Research</i> , 2012, 22, 142-154.	5.7	77
103	Assessment of established techniques to determine developmental and malignant potential of human pluripotent stem cells. <i>Nature Communications</i> , 2018, 9, 1925.	5.8	76
104	Persistence of mature dendritic cells, T <sub>H</sub> 2A, and Tc2 cells characterize clinically resolved atopic dermatitis under IL-4R $\alpha$ blockade. <i>Science Immunology</i> , 2021, 6, .	5.6	76
105	EpiExplorer: live exploration and global analysis of large epigenomic datasets. <i>Genome Biology</i> , 2012, 13, R96.	13.9	72
106	Chromatin mapping and single-cell immune profiling define the temporal dynamics of ibrutinib response in CLL. <i>Nature Communications</i> , 2020, 11, 577.	5.8	69
107	Comparative genome-wide DNA methylation analysis of colorectal tumor and matched normal tissues. <i>Epigenetics</i> , 2012, 7, 1355-1367.	1.3	67
108	Knowledge-primed neural networks enable biologically interpretable deep learning on single-cell sequencing data. <i>Genome Biology</i> , 2020, 21, 190.	3.8	67

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109	Regulation of DNA Methylation Patterns by CK2-Mediated Phosphorylation of Dnmt3a. <i>Cell Reports</i> , 2014, 8, 743-753.	2.9	66
110	Notch inhibition allows oncogene-independent generation of iPS cells. <i>Nature Chemical Biology</i> , 2014, 10, 632-639.	3.9	64
111	Dissecting the role of aberrant DNA methylation in human leukaemia. <i>Nature Communications</i> , 2015, 6, 7091.	5.8	62
112	Ageing-associated DNA methylation dynamics are a molecular readout of lifespan variation among mammalian species. <i>Genome Biology</i> , 2018, 19, 22.	3.8	62
113	MTHFD1 interaction with BRD4 links folate metabolism to transcriptional regulation. <i>Nature Genetics</i> , 2019, 51, 990-998.	9.4	61
114	Guadecitabine Plus Ipilimumab in Unresectable Melanoma: The NIBIT-M4 Clinical Trial. <i>Clinical Cancer Research</i> , 2019, 25, 7351-7362.	3.2	61
115	DeepBlue epigenomic data server: programmatic data retrieval and analysis of epigenome region sets. <i>Nucleic Acids Research</i> , 2016, 44, W581-W586.	6.5	60
116	STAT5BN642H is a driver mutation for T cell neoplasia. <i>Journal of Clinical Investigation</i> , 2017, 128, 387-401.	3.9	57
117	Long-term skin-resident memory T cells proliferate in situ and are involved in human graft-versus-host disease. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	57
118	Targeting clinical epigenetic reprogramming for chemoprevention of metabolic and viral hepatocellular carcinoma. <i>Gut</i> , 2021, 70, 157-169.	6.1	57
119	Mutational landscape of the transcriptome offers putative targets for immunotherapy of myeloproliferative neoplasms. <i>Blood</i> , 2019, 134, 199-210.	0.6	54
120	Malondialdehyde epitopes are sterile mediators of hepatic inflammation in hypercholesterolemic mice. <i>Hepatology</i> , 2017, 65, 1181-1195.	3.6	53
121	Colocalization analyses of genomic elements: approaches, recommendations and challenges. <i>Bioinformatics</i> , 2019, 35, 1615-1624.	1.8	53
122	RANK links thymic regulatory T cells to fetal loss and gestational diabetes in pregnancy. <i>Nature</i> , 2021, 589, 442-447.	13.7	52
123	Parental micronutrient deficiency distorts liver DNA methylation and expression of lipid genes associated with a fatty-liver-like phenotype in offspring. <i>Scientific Reports</i> , 2018, 8, 3055.	1.6	50
124	Structural conservation versus functional divergence of maternally expressed microRNAs in the Dlk1/Gtl2 imprinting region. <i>BMC Genomics</i> , 2008, 9, 346.	1.2	49
125	Next-generation sequencing identifies major DNA methylation changes during progression of Ph+ chronic myeloid leukemia. <i>Leukemia</i> , 2016, 30, 1861-1868.	3.3	49
126	EpiGRAPH: user-friendly software for statistical analysis and prediction of (epi)genomic data. <i>Genome Biology</i> , 2009, 10, R14.	13.9	48



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127	Single-cell analysis reveals innate lymphoid cell lineage infidelity in atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 149, 624-639.	1.5	48
128	Temporal dissection of an enhancer cluster reveals distinct temporal and functional contributions of individual elements. <i>Molecular Cell</i> , 2021, 81, 969-982.e13.	4.5	47
129	Emergence of coronavirus disease 2019 (COVID-19) in Austria. <i>Wiener Klinische Wochenschrift</i> , 2020, 132, 645-652.	1.0	46
130	Genomic and transcriptional landscape of P2RY8-CRLF2-positive childhood acute lymphoblastic leukemia. <i>Leukemia</i> , 2017, 31, 1491-1501.	3.3	45
131	Quantitative comparison of within-sample heterogeneity scores for DNA methylation data. <i>Nucleic Acids Research</i> , 2020, 48, e46-e46.	6.5	45
132	The Human Genomic Melting Map. <i>PLoS Computational Biology</i> , 2007, 3, e93.	1.5	44
133	Mapping the chemical chromatin reactivation landscape identifies BRD4-TAF1 cross-talk. <i>Nature Chemical Biology</i> , 2016, 12, 504-510.	3.9	43
134	The ERBB-STAT3 Axis Drives Tasmanian Devil Facial Tumor Disease. <i>Cancer Cell</i> , 2019, 35, 125-139.e9.	7.7	43
135	Epigenomics and Single-Cell Sequencing Define a Developmental Hierarchy in Langerhans Cell Histiocytosis. <i>Cancer Discovery</i> , 2019, 9, 1406-1421.	7.7	42
136	STAT3 promotes melanoma metastasis by CEBP-induced repression of the MITF pathway. <i>Oncogene</i> , 2021, 40, 1091-1105.	2.6	42
137	Epigenetic Homogeneity Within Colorectal Tumors Predicts Shorter Relapse-Free and Overall Survival Times for Patients With Locoregional Cancer. <i>Gastroenterology</i> , 2016, 151, 961-972.	0.6	41
138	NOTCH1 activation in breast cancer confers sensitivity to inhibition of SUMOylation. <i>Oncogene</i> , 2015, 34, 3780-3790.	2.6	40
139	A combinatorial screen of the CLOUD uncovers a synergy targeting the androgen receptor. <i>Nature Chemical Biology</i> , 2017, 13, 771-778.	3.9	39
140	A T cell-specific deletion of HDAC1 protects against experimental autoimmune encephalomyelitis. <i>Journal of Autoimmunity</i> , 2018, 86, 51-61.	3.0	39
141	A discrete subset of epigenetically primed human NK cells mediates antigen-specific immune responses. <i>Science Immunology</i> , 2020, 5, .	5.6	38
142	VCF.Filter: interactive prioritization of disease-linked genetic variants from sequencing data. <i>Nucleic Acids Research</i> , 2017, 45, W567-W572.	6.5	37
143	The cytoskeletal regulator HEM1 governs B cell development and prevents autoimmunity. <i>Science Immunology</i> , 2020, 5, .	5.6	37
144	Functional Analysis of a Potassium-Chloride Co-Transporter 3 (SLC12A6) Promoter Polymorphism Leading to an Additional DNA Methylation Site. <i>Neuropsychopharmacology</i> , 2009, 34, 458-467.	2.8	36

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145	Differential DNA Methylation Analysis without a Reference Genome. <i>Cell Reports</i> , 2015, 13, 2621-2633.	2.9	34
146	Combined chemosensitivity and chromatin profiling prioritizes drug combinations in CLL. <i>Nature Chemical Biology</i> , 2019, 15, 232-240.	3.9	34
147	Chromatin-Based Classification of Genetically Heterogeneous AMLs into Two Distinct Subtypes with Diverse Stemness Phenotypes. <i>Cell Reports</i> , 2019, 26, 1059-1069.e6.	2.9	33
148	Cell-Type Specificity of Genomic Imprinting in Cerebral Cortex. <i>Neuron</i> , 2020, 107, 1160-1179.e9.	3.8	33
149	Human resident memory T cells exit the skin and mediate systemic Th2-driven inflammation. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	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. <i>Genome Biology</i> , 2020, 21, 106.	3.8	30
152	Genomic imprinting in mouse blastocysts is predominantly associated with H3K27me3. <i>Nature Communications</i> , 2021, 12, 3804.	5.8	30
153	A Comprehensive Analysis of the Dynamic Response to Aphidicolin-Mediated Replication Stress Uncovers Targets for ATM and ATMIN. <i>Cell Reports</i> , 2016, 15, 893-908.	2.9	29
154	CDK6 coordinates JAK2V617F mutant MPN via NF- $\kappa$ B and apoptotic networks. <i>Blood</i> , 2019, 133, 1677-1690.	0.6	29
155	Life-long epigenetic programming of cortical architecture by maternal "Western" diet during pregnancy. <i>Molecular Psychiatry</i> , 2020, 25, 22-36.	4.1	28
156	Identification of Novel Imprinted Differentially Methylated Regions by Global Analysis of Human-Parthenogenetic-Induced Pluripotent Stem Cells. <i>Stem Cell Reports</i> , 2013, 1, 79-89.	2.3	27
157	MethMarker: user-friendly design and optimization of gene-specific DNA methylation assays. <i>Genome Biology</i> , 2009, 10, R105.	13.9	25
158	Parallel genome-wide screens identify synthetic viable interactions between the BLM helicase complex and Fanconi anemia. <i>Nature Communications</i> , 2017, 8, 1238.	5.8	25
159	Relationship between genome and epigenome - challenges and requirements for future research. <i>BMC Genomics</i> , 2014, 15, 487.	1.2	24
160	Proposed Terminology and Classification of Pre-Malignant Neoplastic Conditions: A Consensus Proposal. <i>EBioMedicine</i> , 2017, 26, 17-24.	2.7	24
161	Coloc-stats: a unified web interface to perform colocalization analysis of genomic features. <i>Nucleic Acids Research</i> , 2018, 46, W186-W193.	6.5	23
162	Histone deacetylases 1 and 2 restrain CD4+ cytotoxic T lymphocyte differentiation. <i>JCI Insight</i> , 2020, 5, .	2.3	23

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163	Aberrant DNA methylation reprogramming during induced pluripotent stem cell generation is dependent on the choice of reprogramming factors. <i>Cell Regeneration</i> , 2014, 3, 3:4.	1.1	22
164	Rapid neutrophil mobilization by VCAM-1+ endothelial cell-derived extracellular vesicles. <i>Cardiovascular Research</i> , 2023, 119, 236-251.	1.8	22
165	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.	6.5	21
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