

Christoph Bock

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.

223
papers

21,102
citations

74
h-index

143
g-index

255
ext. papers

26,892
ext. citations

17
avg, IF

6.78
L-index

#	Paper	IF	Citations
223	Somatic mutations of calreticulin in myeloproliferative neoplasms. <i>New England Journal of Medicine</i> , 2013 , 369, 2379-90	59.2	1367
222	Paternally induced transgenerational environmental reprogramming of metabolic gene expression in mammals. <i>Cell</i> , 2010 , 143, 1084-96	56.2	831
221	Reference Maps of human ES and iPS cell variation enable high-throughput characterization of pluripotent cell lines. <i>Cell</i> , 2011 , 144, 439-52	56.2	756
220	Dnmt3a is essential for hematopoietic stem cell differentiation. <i>Nature Genetics</i> , 2011 , 44, 23-31	36.3	737
219	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. <i>Nature Biotechnology</i> , 2010 , 28, 1097-105	44.5	570
218	Preparation of reduced representation bisulfite sequencing libraries for genome-scale DNA methylation profiling. <i>Nature Protocols</i> , 2011 , 6, 468-81	18.8	505
217	BiQ Analyzer: visualization and quality control for DNA methylation data from bisulfite sequencing. <i>Bioinformatics</i> , 2005 , 21, 4067-8	7.2	505
216	Quantitative comparison of genome-wide DNA methylation mapping technologies. <i>Nature Biotechnology</i> , 2010 , 28, 1106-14	44.5	486
215	Toward understanding and exploiting tumor heterogeneity. <i>Nature Medicine</i> , 2015 , 21, 846-53	50.5	441
214	Specification of tissue-resident macrophages during organogenesis. <i>Science</i> , 2016 , 353,	33.3	436
213	Pooled CRISPR screening with single-cell transcriptome readout. <i>Nature Methods</i> , 2017 , 14, 297-301	21.6	435
212	Comprehensive analysis of DNA methylation data with RnBeads. <i>Nature Methods</i> , 2014 , 11, 1138-1140	21.6	416
211	Epigenomic profiling of young and aged HSCs reveals concerted changes during aging that reinforce self-renewal. <i>Cell Stem Cell</i> , 2014 , 14, 673-88	18	399
210	Analysing and interpreting DNA methylation data. <i>Nature Reviews Genetics</i> , 2012 , 13, 705-19	30.1	398
209	DNA methylation signatures link prenatal famine exposure to growth and metabolism. <i>Nature Communications</i> , 2014 , 5, 5592	17.4	368
208	Proliferation-dependent alterations of the DNA methylation landscape underlie hematopoietic stem cell aging. <i>Cell Stem Cell</i> , 2013 , 12, 413-25	18	322
207	Genomic distribution and inter-sample variation of non-CpG methylation across human cell types. <i>PLoS Genetics</i> , 2011 , 7, e1002389	6	295

206	Single-cell DNA methylome sequencing and bioinformatic inference of epigenomic cell-state dynamics. <i>Cell Reports</i> , 2015 , 10, 1386-97	10.6	290
205	Sequential CHIP-bisulfite sequencing enables direct genome-scale investigation of chromatin and DNA methylation cross-talk. <i>Genome Research</i> , 2012 , 22, 1128-38	9.7	277
204	Recommendations for the design and analysis of epigenome-wide association studies. <i>Nature Methods</i> , 2013 , 10, 949-55	21.6	276
203	A DNA methylation fingerprint of 1628 human samples. <i>Genome Research</i> , 2012 , 22, 407-19	9.7	273
202	DNA methylation dynamics during in vivo differentiation of blood and skin stem cells. <i>Molecular Cell</i> , 2012 , 47, 633-47	17.6	271
201	CHIPmentation: fast, robust, low-input CHIP-seq for histones and transcription factors. <i>Nature Methods</i> , 2015 , 12, 963-965	21.6	267
200	BLUEPRINT to decode the epigenetic signature written in blood. <i>Nature Biotechnology</i> , 2012 , 30, 224-6	44.5	261
199	Genome-scale DNA methylation mapping of clinical samples at single-nucleotide resolution. <i>Nature Methods</i> , 2010 , 7, 133-6	21.6	258
198	Erosion of dosage compensation impacts human iPSC disease modeling. <i>Cell Stem Cell</i> , 2012 , 10, 595-609	28	252
197	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016 , 167, 1145-1149	56.2	232
196	Artemisinins Target GABA Receptor Signaling and Impair Cell Identity. <i>Cell</i> , 2017 , 168, 86-100.e15	56.2	228
195	Molecular interrogation of hypothalamic organization reveals distinct dopamine neuronal subtypes. <i>Nature Neuroscience</i> , 2017 , 20, 176-188	25.5	226
194	A prognostic DNA methylation signature for stage I non-small-cell lung cancer. <i>Journal of Clinical Oncology</i> , 2013 , 31, 4140-7	2.2	210
193	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , 2016 , 34, 726-37	44.5	204
192	LOLA: enrichment analysis for genomic region sets and regulatory elements in R and Bioconductor. <i>Bioinformatics</i> , 2016 , 32, 587-9	7.2	194
191	Spatiotemporal structure of cell fate decisions in murine neural crest. <i>Science</i> , 2019 , 364,	33.3	181
190	Whole-exome sequencing identifies novel MPL and JAK2 mutations in triple-negative myeloproliferative neoplasms. <i>Blood</i> , 2016 , 127, 325-32	2.2	176
189	A kinase-independent function of CDK6 links the cell cycle to tumor angiogenesis. <i>Cancer Cell</i> , 2013 , 24, 167-81	24.3	169

188	Optimization of quantitative MGMT promoter methylation analysis using pyrosequencing and combined bisulfite restriction analysis. <i>Journal of Molecular Diagnostics</i> , 2007 , 9, 368-81	5.1	168
187	High-throughput bisulfite sequencing in mammalian genomes. <i>Methods</i> , 2009 , 48, 226-32	4.6	161
186	Pharmacological targeting of the Wdr5-MLL interaction in C/EBP β -terminal leukemia. <i>Nature Chemical Biology</i> , 2015 , 11, 571-578	11.7	159
185	CpG island methylation in human lymphocytes is highly correlated with DNA sequence, repeats, and predicted DNA structure. <i>PLoS Genetics</i> , 2006 , 2, e26	6	153
184	Longitudinal molecular trajectories of diffuse glioma in adults. <i>Nature</i> , 2019 , 576, 112-120	50.4	151
183	Single-cell transcriptomes reveal characteristic features of human pancreatic islet cell types. <i>EMBO Reports</i> , 2016 , 17, 178-87	6.5	148
182	Computational epigenetics. <i>Bioinformatics</i> , 2008 , 24, 1-10	7.2	147
181	Making sense of big data in health research: Towards an EU action plan. <i>Genome Medicine</i> , 2016 , 8, 71	14.4	146
180	DNA Methylation Dynamics of Human Hematopoietic Stem Cell Differentiation. <i>Cell Stem Cell</i> , 2016 , 19, 808-822	18	142
179	CpG island mapping by epigenome prediction. <i>PLoS Computational Biology</i> , 2007 , 3, e110	5	142
178	Managing drug resistance in cancer: lessons from HIV therapy. <i>Nature Reviews Cancer</i> , 2012 , 12, 494-501	31.3	135
177	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, 1082-95	10.6	129
176	DNA methylation heterogeneity defines a disease spectrum in Ewing sarcoma. <i>Nature Medicine</i> , 2017 , 23, 386-395	50.5	128
175	B cells sustain inflammation and predict response to immune checkpoint blockade in human melanoma. <i>Nature Communications</i> , 2019 , 10, 4186	17.4	127
174	DNA methylation analysis of chromosome 21 gene promoters at single base pair and single allele resolution. <i>PLoS Genetics</i> , 2009 , 5, e1000438	6	127
173	DNA methylation biomarkers in cancer: progress towards clinical implementation. <i>Expert Review of Molecular Diagnostics</i> , 2012 , 12, 473-87	3.8	126
172	Inherited DOCK2 Deficiency in Patients with Early-Onset Invasive Infections. <i>New England Journal of Medicine</i> , 2015 , 372, 2409-22	59.2	125
171	The DNA methylation landscape of glioblastoma disease progression shows extensive heterogeneity in time and space. <i>Nature Medicine</i> , 2018 , 24, 1611-1624	50.5	124

170	Structural cells are key regulators of organ-specific immune responses. <i>Nature</i> , 2020 , 583, 296-302	50.4	122
169	Global DNA demethylation during mouse erythropoiesis in vivo. <i>Science</i> , 2011 , 334, 799-802	33.3	116
168	Microbiota-Derived Metabolites Suppress Arthritis by Amplifying Aryl-Hydrocarbon Receptor Activation in Regulatory B Cells. <i>Cell Metabolism</i> , 2020 , 31, 837-851.e10	24.6	113
167	Genomic epidemiology of superspreading events in Austria reveals mutational dynamics and transmission properties of SARS-CoV-2. <i>Science Translational Medicine</i> , 2020 , 12,	17.5	110
166	Inter-individual variation of DNA methylation and its implications for large-scale epigenome mapping. <i>Nucleic Acids Research</i> , 2008 , 36, e55	20.1	109
165	HCV-Induced Epigenetic Changes Associated With Liver Cancer Risk Persist After Sustained Virologic Response. <i>Gastroenterology</i> , 2019 , 156, 2313-2329.e7	13.3	107
164	Lung stem cell self-renewal relies on BMI1-dependent control of expression at imprinted loci. <i>Cell Stem Cell</i> , 2011 , 9, 272-81	18	101
163	BiQ Analyzer HT: locus-specific analysis of DNA methylation by high-throughput bisulfite sequencing. <i>Nucleic Acids Research</i> , 2011 , 39, W551-6	20.1	99
162	Multi-Omics of Single Cells: Strategies and Applications. <i>Trends in Biotechnology</i> , 2016 , 34, 605-608	15.1	99
161	Chromatin accessibility maps of chronic lymphocytic leukaemia identify subtype-specific epigenome signatures and transcription regulatory networks. <i>Nature Communications</i> , 2016 , 7, 11938	17.4	95
160	Epigenetic biomarker development. <i>Epigenomics</i> , 2009 , 1, 99-110	4.4	94
159	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	15.7	89
158	RnBeads 2.0: comprehensive analysis of DNA methylation data. <i>Genome Biology</i> , 2019 , 20, 55	18.3	89
157	Comprehensive genome and epigenome characterization of CHO cells in response to evolutionary pressures and over time. <i>Biotechnology and Bioengineering</i> , 2016 , 113, 2241-53	4.9	88
156	A promoter DNA demethylation landscape of human hematopoietic differentiation. <i>Nucleic Acids Research</i> , 2012 , 40, 116-31	20.1	86
155	High-resolution mapping of h1 linker histone variants in embryonic stem cells. <i>PLoS Genetics</i> , 2013 , 9, e1003417	6	83
154	Disturbed mitochondrial dynamics in CD8 TILs reinforce T cell exhaustion. <i>Nature Immunology</i> , 2020 , 21, 1540-1551	19.1	78
153	Functional Dissection of the Enhancer Repertoire in Human Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2018 , 23, 276-288.e8	18	77

152	A reversible gene trap collection empowers haploid genetics in human cells. <i>Nature Methods</i> , 2013 , 10, 965-71	21.6	76
151	RRBSMAP: a fast, accurate and user-friendly alignment tool for reduced representation bisulfite sequencing. <i>Bioinformatics</i> , 2012 , 28, 430-2	7.2	76
150	Promoter hypermethylation of the phosphatase DUSP22 mediates PKA-dependent TAU phosphorylation and CREB activation in Alzheimer's disease. <i>Hippocampus</i> , 2014 , 24, 363-8	3.5	75
149	KRAS and CREBBP mutations: a relapse-linked malicious liaison in childhood high hyperdiploid acute lymphoblastic leukemia. <i>Leukemia</i> , 2015 , 29, 1656-67	10.7	74
148	Rational discovery of molecular glue degraders via scalable chemical profiling. <i>Nature Chemical Biology</i> , 2020 , 16, 1199-1207	11.7	73
147	Highly efficient derivation of ventricular cardiomyocytes from induced pluripotent stem cells with a distinct epigenetic signature. <i>Cell Research</i> , 2012 , 22, 142-54	24.7	70
146	Mapping the mouse Allelome reveals tissue-specific regulation of allelic expression. <i>ELife</i> , 2017 , 6,	8.9	69
145	Glioma through the looking GLASS: molecular evolution of diffuse gliomas and the Glioma Longitudinal Analysis Consortium. <i>Neuro-Oncology</i> , 2018 , 20, 873-884	1	63
144	EpiExplorer: live exploration and global analysis of large epigenomic datasets. <i>Genome Biology</i> , 2012 , 13, R96	18.3	63
143	Comparative genome-wide DNA methylation analysis of colorectal tumor and matched normal tissues. <i>Epigenetics</i> , 2012 , 7, 1355-67	5.7	62
142	Aryl Hydrocarbon Receptor Contributes to the Transcriptional Program of IL-10-Producing Regulatory B Cells. <i>Cell Reports</i> , 2019 , 29, 1878-1892.e7	10.6	60
141	SARS-CoV-2 mutations in MHC-I-restricted epitopes evade CD8 T cell responses. <i>Science Immunology</i> , 2021 , 6,	28	58
140	LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , 2020 , 587, 377-386	50.4	56
139	Regulation of DNA methylation patterns by CK2-mediated phosphorylation of Dnmt3a. <i>Cell Reports</i> , 2014 , 8, 743-53	10.6	55
138	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	32.3	55
137	Inference of transcription factor binding from cell-free DNA enables tumor subtype prediction and early detection. <i>Nature Communications</i> , 2019 , 10, 4666	17.4	54
136	An ERK-Dependent Feedback Mechanism Prevents Hematopoietic Stem Cell Exhaustion. <i>Cell Stem Cell</i> , 2018 , 22, 879-892.e6	18	53
135	Dissecting the role of aberrant DNA methylation in human leukaemia. <i>Nature Communications</i> , 2015 , 6, 7091	17.4	51

134	Integrative Proteomic Profiling Reveals PRC2-Dependent Epigenetic Crosstalk Maintains Ground-State Pluripotency. <i>Cell Stem Cell</i> , 2019 , 24, 123-137.e8	18	50
133	Notch inhibition allows oncogene-independent generation of iPS cells. <i>Nature Chemical Biology</i> , 2014 , 10, 632-639	11.7	48
132	Systematic characterization of BAF mutations provides insights into intracomplex synthetic lethalties in human cancers. <i>Nature Genetics</i> , 2019 , 51, 1399-1410	36.3	46
131	DeepBlue epigenomic data server: programmatic data retrieval and analysis of epigenome region sets. <i>Nucleic Acids Research</i> , 2016 , 44, W581-6	20.1	45
130	EpiGRAPH: user-friendly software for statistical analysis and prediction of (epi)genomic data. <i>Genome Biology</i> , 2009 , 10, R14	18.3	45
129	Structural conservation versus functional divergence of maternally expressed microRNAs in the Dlk1/Gtl2 imprinting region. <i>BMC Genomics</i> , 2008 , 9, 346	4.5	45
128	Assessment of established techniques to determine developmental and malignant potential of human pluripotent stem cells. <i>Nature Communications</i> , 2018 , 9, 1925	17.4	45
127	Next-generation sequencing identifies major DNA methylation changes during progression of Ph+ chronic myeloid leukemia. <i>Leukemia</i> , 2016 , 30, 1861-8	10.7	44
126	Ageing-associated DNA methylation dynamics are a molecular readout of lifespan variation among mammalian species. <i>Genome Biology</i> , 2018 , 19, 22	18.3	39
125	The human genomic melting map. <i>PLoS Computational Biology</i> , 2007 , 3, e93	5	39
124	MTHFD1 interaction with BRD4 links folate metabolism to transcriptional regulation. <i>Nature Genetics</i> , 2019 , 51, 990-998	36.3	38
123	STAT5BN642H is a driver mutation for T cell neoplasia. <i>Journal of Clinical Investigation</i> , 2018 , 128, 387-401	15.9	38
122	Molecular design of hypothalamus development. <i>Nature</i> , 2020 , 582, 246-252	50.4	37
121	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	11.5	36
120	Circadian rhythm influences induction of trained immunity by BCG vaccination. <i>Journal of Clinical Investigation</i> , 2020 , 130, 5603-5617	15.9	36
119	Genomic and transcriptional landscape of P2RY8-CRLF2-positive childhood acute lymphoblastic leukemia. <i>Leukemia</i> , 2017 , 31, 1491-1501	10.7	35
118	NOTCH1 activation in breast cancer confers sensitivity to inhibition of SUMOylation. <i>Oncogene</i> , 2015 , 34, 3780-90	9.2	35
117	Mutational landscape of the transcriptome offers putative targets for immunotherapy of myeloproliferative neoplasms. <i>Blood</i> , 2019 , 134, 199-210	2.2	34

116	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	4.9	33
115	Single-Cell RNA Sequencing Analysis Reveals a Crucial Role for CTHRC1 (Collagen Triple Helix Repeat Containing 1) Cardiac Fibroblasts After Myocardial Infarction. <i>Circulation</i> , 2020 , 142, 1831-1847	16.7	33
114	Guadecitabine Plus Ipilimumab in Unresectable Melanoma: The NIBIT-M4 Clinical Trial. <i>Clinical Cancer Research</i> , 2019 , 25, 7351-7362	12.9	33
113	Selective Mediator dependence of cell-type-specifying transcription. <i>Nature Genetics</i> , 2020 , 52, 719-727	36.3	32
112	Chromatin mapping and single-cell immune profiling define the temporal dynamics of ibrutinib response in CLL. <i>Nature Communications</i> , 2020 , 11, 577	17.4	32
111	Mapping the chemical chromatin reactivation landscape identifies BRD4-TAF1 cross-talk. <i>Nature Chemical Biology</i> , 2016 , 12, 504-10	11.7	32
110	Functional analysis of a potassium-chloride co-transporter 3 (SLC12A6) promoter polymorphism leading to an additional DNA methylation site. <i>Neuropsychopharmacology</i> , 2009 , 34, 458-67	8.7	31
109	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	13.3	30
108	The Organoid Cell Atlas. <i>Nature Biotechnology</i> , 2021 , 39, 13-17	44.5	30
107	Ultra-high-throughput single-cell RNA sequencing and perturbation screening with combinatorial fluidic indexing. <i>Nature Methods</i> , 2021 , 18, 635-642	21.6	28
106	The ERBB-STAT3 Axis Drives Tasmanian Devil Facial Tumor Disease. <i>Cancer Cell</i> , 2019 , 35, 125-139.e9	24.3	28
105	Targeting clinical epigenetic reprogramming for chemoprevention of metabolic and viral hepatocellular carcinoma. <i>Gut</i> , 2021 , 70, 157-169	19.2	28
104	A combinatorial screen of the CLOUD uncovers a synergy targeting the androgen receptor. <i>Nature Chemical Biology</i> , 2017 , 13, 771-778	11.7	27
103	Acute BAF perturbation causes immediate changes in chromatin accessibility. <i>Nature Genetics</i> , 2021 , 53, 269-278	36.3	27
102	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021 , 53, 1311-1321	36.3	27
101	Malondialdehyde epitopes are sterile mediators of hepatic inflammation in hypercholesterolemic mice. <i>Hepatology</i> , 2017 , 65, 1181-1195	11.2	26
100	A T cell-specific deletion of HDAC1 protects against experimental autoimmune encephalomyelitis. <i>Journal of Autoimmunity</i> , 2018 , 86, 51-61	15.5	26
99	Epigenomics and Single-Cell Sequencing Define a Developmental Hierarchy in Langerhans Cell Histiocytosis. <i>Cancer Discovery</i> , 2019 , 9, 1406-1421	24.4	26

98	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	8	26
97	Emergence of coronavirus disease 2019 (COVID-19) in Austria. <i>Wiener Klinische Wochenschrift</i> , 2020 , 132, 645-652	2.3	25
96	Colocalization analyses of genomic elements: approaches, recommendations and challenges. <i>Bioinformatics</i> , 2019 , 35, 1615-1624	7.2	24
95	CDK6 coordinates mutant MPN via NF- κ B and apoptotic networks. <i>Blood</i> , 2019 , 133, 1677-1690	2.2	23
94	Combined chemosensitivity and chromatin profiling prioritizes drug combinations in CLL. <i>Nature Chemical Biology</i> , 2019 , 15, 232-240	11.7	21
93	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	10.6	21
92	Relationship between genome and epigenome--challenges and requirements for future research. <i>BMC Genomics</i> , 2014 , 15, 487	4.5	21
91	Differential DNA Methylation Analysis without a Reference Genome. <i>Cell Reports</i> , 2015 , 13, 2621-2633	10.6	21
90	Chromatin accessibility profiling methods. <i>Nature Reviews Methods Primers</i> , 2021 , 1,		21
89	The cytoskeletal regulator HEM1 governs B cell development and prevents autoimmunity. <i>Science Immunology</i> , 2020 , 5,	28	20
88	MethMarker: user-friendly design and optimization of gene-specific DNA methylation assays. <i>Genome Biology</i> , 2009 , 10, R105	18.3	20
87	Chromatin-Based Classification of Genetically Heterogeneous AMLs into Two Distinct Subtypes with Diverse Stemness Phenotypes. <i>Cell Reports</i> , 2019 , 26, 1059-1069.e6	10.6	19
86	Aberrant DNA methylation reprogramming during induced pluripotent stem cell generation is dependent on the choice of reprogramming factors. <i>Cell Regeneration</i> , 2014 , 3, 4	2.5	19
85	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, W501-7	20.1	19
84	RANK links thymic regulatory T cells to fetal loss and gestational diabetes in pregnancy. <i>Nature</i> , 2021 , 589, 442-447	50.4	19
83	VCF.Filter: interactive prioritization of disease-linked genetic variants from sequencing data. <i>Nucleic Acids Research</i> , 2017 , 45, W567-W572	20.1	18
82	Persistence of mature dendritic cells, T2A, and Tc2 cells characterize clinically resolved atopic dermatitis under IL-4R α blockade. <i>Science Immunology</i> , 2021 , 6,	28	18
81	Hyperglycemia Induces Trained Immunity in Macrophages and Their Precursors and Promotes Atherosclerosis. <i>Circulation</i> , 2021 , 144, 961-982	16.7	18

80	Proposed Terminology and Classification of Pre-Malignant Neoplastic Conditions: A Consensus Proposal. <i>EBioMedicine</i> , 2017 , 26, 17-24	8.8	17
79	Knowledge-primed neural networks enable biologically interpretable deep learning on single-cell sequencing data. <i>Genome Biology</i> , 2020 , 21, 190	18.3	17
78	Multimodal analysis of cell-free DNA whole-genome sequencing for pediatric cancers with low mutational burden. <i>Nature Communications</i> , 2021 , 12, 3230	17.4	17
77	Parallel genome-wide screens identify synthetic viable interactions between the BLM helicase complex and Fanconi anemia. <i>Nature Communications</i> , 2017 , 8, 1238	17.4	16
76	Familial early-onset dementia with complex neuropathologic phenotype and genomic background. <i>Neurobiology of Aging</i> , 2016 , 42, 199-204	5.6	16
75	A discrete subset of epigenetically primed human NK cells mediates antigen-specific immune responses. <i>Science Immunology</i> , 2020 , 5,	28	15
74	Temporal dissection of an enhancer cluster reveals distinct temporal and functional contributions of individual elements. <i>Molecular Cell</i> , 2021 , 81, 969-982.e13	17.6	15
73	Quantitative comparison of within-sample heterogeneity scores for DNA methylation data. <i>Nucleic Acids Research</i> , 2020 , 48, e46	20.1	14
72	Life-long epigenetic programming of cortical architecture by maternal Western diet during pregnancy. <i>Molecular Psychiatry</i> , 2020 , 25, 22-36	15.1	14
71	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	18.3	13
70	Coloc-stats: a unified web interface to perform colocalization analysis of genomic features. <i>Nucleic Acids Research</i> , 2018 , 46, W186-W193	20.1	13
69	Histone deacetylases 1 and 2 restrain CD4+ cytotoxic T lymphocyte differentiation. <i>JCI Insight</i> , 2020 , 5,	9.9	13
68	Cell-Type Specificity of Genomic Imprinting in Cerebral Cortex. <i>Neuron</i> , 2020 , 107, 1160-1179.e9	13.9	12
67	MIRA: an R package for DNA methylation-based inference of regulatory activity. <i>Bioinformatics</i> , 2018 , 34, 2649-2650	7.2	11
66	Ultra-high throughput single-cell RNA sequencing by combinatorial fluidic indexing		11
65	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,	17.5	11
64	Parallel reverse genetic screening in mutant human cells using transcriptomics. <i>Molecular Systems Biology</i> , 2016 , 12, 879	12.2	11
63	High-content CRISPR screening. <i>Nature Reviews Methods Primers</i> , 2022 , 2,		10

62	Web-based analysis of (Epi-) genome data using EpiGRAPH and Galaxy. <i>Methods in Molecular Biology</i> , 2010 , 628, 275-96	1.4	10
61	DNA methylation QTL analysis identifies new regulators of human longevity. <i>Human Molecular Genetics</i> , 2020 , 29, 1154-1167	5.6	9
60	Genome-scale CRISPR screens are efficient in non-homologous end-joining deficient cells. <i>Scientific Reports</i> , 2019 , 9, 15751	4.9	9
59	Targeted mutation screening of 292 candidate genes in 38 children with inborn haematological cytopenias efficiently identifies novel disease-causing mutations. <i>British Journal of Haematology</i> , 2018 , 182, 251-258	4.5	9
58	Single-cell analysis reveals innate lymphoid cell lineage infidelity in atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2021 ,	11.5	9
57	The Transcription Factor MAZR/PATZ1 Regulates the Development of FOXP3 Regulatory T Cells. <i>Cell Reports</i> , 2019 , 29, 4447-4459.e6	10.6	8
56	STAT3 promotes melanoma metastasis by CEBP-induced repression of the MITF pathway. <i>Oncogene</i> , 2021 , 40, 1091-1105	9.2	8
55	Complex patterns of chromosome 11 aberrations in myeloid malignancies target CBL, MLL, DDB1 and LMO2. <i>PLoS ONE</i> , 2013 , 8, e77819	3.7	7
54	Mutational dynamics and transmission properties of SARS-CoV-2 superspreading events in Austria		7
53	Life-long impairment of glucose homeostasis upon prenatal exposure to psychostimulants. <i>EMBO Journal</i> , 2020 , 39, e100882	13	7
52	DeepBlueR: large-scale epigenomic analysis in R. <i>Bioinformatics</i> , 2017 , 33, 2063-2064	7.2	6
51	NK Cells Require Cell-Extrinsic and -Intrinsic TYK2 for Full Functionality in Tumor Surveillance and Antibacterial Immunity. <i>Journal of Immunology</i> , 2019 , 202, 1724-1734	5.3	6
50	Imprinted expression in cystic embryoid bodies shows an embryonic and not an extra-embryonic pattern. <i>Developmental Biology</i> , 2015 , 402, 291-305	3.1	6
49	SARS-CoV-2 escapes CD8 T cell surveillance via mutations in MHC-I restricted epitopes		6
48	Distributed changes of the functional connectome in patients with glioblastoma. <i>Scientific Reports</i> , 2020 , 10, 18312	4.9	6
47	Genomic imprinting in mouse blastocysts is predominantly associated with H3K27me3. <i>Nature Communications</i> , 2021 , 12, 3804	17.4	6
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45	Notch-mediated expansion of cord blood progenitors: maintenance of transcriptional and epigenetic fidelity. <i>Leukemia</i> , 2015 , 29, 1948-51	10.7	5

44	NCOR1 Orchestrates Transcriptional Landscapes and Effector Functions of CD4 T Cells. <i>Frontiers in Immunology</i> , 2020 , 11, 579	8.4	5
43	Precision Medicine in Hematology 2021: Definitions, Tools, Perspectives, and Open Questions. <i>HemaSphere</i> , 2021 , 5, e536	0.3	5
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41	Rapid neutrophil mobilisation by VCAM-1+ endothelial extracellular vesicles.. <i>Cardiovascular Research</i> , 2022 ,	9.9	4
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39	Spontaneously Resolved Atopic Dermatitis Shows Melanocyte and Immune Cell Activation Distinct From Healthy Control Skin. <i>Frontiers in Immunology</i> , 2021 , 12, 630892	8.4	4
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36	Functional dissection of the enhancer repertoire in human embryonic stem cells		3
35	Inference of tumor cell-specific transcription factor binding from cell-free DNA enables tumor subtype prediction and early detection of cancer		3
34	Tumor mutational burden and immune infiltrates in renal cell carcinoma and matched brain metastases. <i>ESMO Open</i> , 2021 , 6, 100057	6	3
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32	Curation and expansion of Human Phenotype Ontology for defined groups of inborn errors of immunity. <i>Journal of Allergy and Clinical Immunology</i> , 2021 ,	11.5	3
31	Synergy and competition between cancer genome sequencing and epigenome mapping projects. <i>Genome Medicine</i> , 2014 , 6, 41	14.4	2
30	Forecasting electricity market prices: a neural network based approach		2
29	Abstract CT059: Epigenetic tumor remodelling to improve the efficacy of immune checkpoint blockade: the NIBIT-M4 clinical trial 2018 ,		2
28	Human resident memory T cells exit the skin and mediate systemic Th2-driven inflammation. <i>Journal of Experimental Medicine</i> , 2021 , 218,	16.6	2
27	Pooled CRISPR screening with single-cell transcriptome read-out		2

26	Detailed temporal dissection of an enhancer cluster reveals two distinct roles for individual elements		2
25	Comparative analysis of neutrophil and monocyte epigenomes		2
24	Chromatin mapping and single-cell immune profiling define the temporal dynamics of ibrutinib drug response in chronic lymphocytic leukemia		2
23	Knowledge-primed neural networks enable biologically interpretable deep learning on single-cell sequencing data		2
22	Hematopoietic expression of a chimeric murine-human CALR oncoprotein allows the assessment of anti-CALR antibody immunotherapies in vivo. <i>American Journal of Hematology</i> , 2021 , 96, 698-707	7.1	2
21	High-throughput Mutational Surveillance of the SARS-CoV-2 Spike Gene		2
20	Anti-Apoptotic Molecule BCL2 Is a Therapeutic Target in Steroid-Refractory Graft-Versus-Host Disease. <i>Journal of Investigative Dermatology</i> , 2020 , 140, 2188-2198	4.3	2
19	DNA methylation: a matter of culture. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 249-51	17.6	1
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17	National-scale surveillance of emerging SARS-CoV-2 variants in wastewater		1
16	Epigenome-based prediction of gene expression across species		1
15	Model-Based Whole-Genome Analysis of DNA Methylation Fidelity. <i>Lecture Notes in Computer Science</i> , 2015 , 141-155	0.9	1
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