

Bradley E Bernstein

List of Publications by Year in descending order

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163
papers

104,406
citations

2309

101
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7427

157
g-index

171
all docs

171
docs citations

171
times ranked

116425
citing authors

#	ARTICLE	IF	CITATIONS
1	Model-based Analysis of ChIP-Seq (MACS). <i>Genome Biology</i> , 2008, 9, R137.	13.9	13,517
2	Comprehensive Mapping of Long-Range Interactions Reveals Folding Principles of the Human Genome. <i>Science</i> , 2009, 326, 289-293.	6.0	7,170
3	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	13.7	5,653
4	A Bivalent Chromatin Structure Marks Key Developmental Genes in Embryonic Stem Cells. <i>Cell</i> , 2006, 125, 315-326.	13.5	4,773
5	Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals. <i>Nature</i> , 2009, 458, 223-227.	13.7	3,801
6	Genome-wide maps of chromatin state in pluripotent and lineage-committed cells. <i>Nature</i> , 2007, 448, 553-560.	13.7	3,733
7	Single-cell RNA-seq highlights intratumoral heterogeneity in primary glioblastoma. <i>Science</i> , 2014, 344, 1396-1401.	6.0	3,648
8	Many human large intergenic noncoding RNAs associate with chromatin-modifying complexes and affect gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11667-11672.	3.3	2,709
9	Mapping and analysis of chromatin state dynamics in nine human cell types. <i>Nature</i> , 2011, 473, 43-49.	13.7	2,630
10	In vitro reprogramming of fibroblasts into a pluripotent ES-cell-like state. <i>Nature</i> , 2007, 448, 318-324.	13.7	2,517
11	Genome-scale DNA methylation maps of pluripotent and differentiated cells. <i>Nature</i> , 2008, 454, 766-770.	13.7	2,267
12	The Mammalian Epigenome. <i>Cell</i> , 2007, 128, 669-681.	13.5	1,909
13	Active genes are tri-methylated at K4 of histone H3. <i>Nature</i> , 2002, 419, 407-411.	13.7	1,871
14	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , 2012, 22, 1813-1831.	2.4	1,708
15	The NIH Roadmap Epigenomics Mapping Consortium. <i>Nature Biotechnology</i> , 2010, 28, 1045-1048.	9.4	1,705
16	Genetic and epigenetic fine mapping of causal autoimmune disease variants. <i>Nature</i> , 2015, 518, 337-343.	13.7	1,669
17	Single-Cell Transcriptomic Analysis of Primary and Metastatic Tumor Ecosystems in Head and Neck Cancer. <i>Cell</i> , 2017, 171, 1611-1624.e24.	13.5	1,656
18	Cohesin Loss Eliminates All Loop Domains. <i>Cell</i> , 2017, 171, 305-320.e24.	13.5	1,454

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19	An Integrative Model of Cellular States, Plasticity, and Genetics for Glioblastoma. <i>Cell</i> , 2019, 178, 835-849.e21.	13.5	1,408
20	Genomic Maps and Comparative Analysis of Histone Modifications in Human and Mouse. <i>Cell</i> , 2005, 120, 169-181.	13.5	1,348
21	Dissecting direct reprogramming through integrative genomic analysis. <i>Nature</i> , 2008, 454, 49-55.	13.7	1,344
22	Initial genome sequencing and analysis of multiple myeloma. <i>Nature</i> , 2011, 471, 467-472.	13.7	1,288
23	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	13.7	1,252
24	Charting a dynamic DNA methylation landscape of the human genome. <i>Nature</i> , 2013, 500, 477-481.	13.7	1,168
25	Insulator dysfunction and oncogene activation in IDH mutant gliomas. <i>Nature</i> , 2016, 529, 110-114.	13.7	1,048
26	Charting histone modifications and the functional organization of mammalian genomes. <i>Nature Reviews Genetics</i> , 2011, 12, 7-18.	7.7	1,019
27	Epigenetic plasticity and the hallmarks of cancer. <i>Science</i> , 2017, 357, .	6.0	920
28	Genomewide Analysis of PRC1 and PRC2 Occupancy Identifies Two Classes of Bivalent Domains. <i>PLoS Genetics</i> , 2008, 4, e1000242.	1.5	878
29	Single-cell RNA-seq supports a developmental hierarchy in human oligodendroglioma. <i>Nature</i> , 2016, 539, 309-313.	13.7	875
30	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. <i>Nature Genetics</i> , 2018, 50, 621-629.	9.4	807
31	Alzheimer's disease: early alterations in brain DNA methylation at ANK1, BIN1, RHBDF2 and other loci. <i>Nature Neuroscience</i> , 2014, 17, 1156-1163.	7.1	800
32	Reconstructing and Reprogramming the Tumor-Propagating Potential of Glioblastoma Stem-like Cells. <i>Cell</i> , 2014, 157, 580-594.	13.5	751
33	Single-cell ChIP-seq reveals cell subpopulations defined by chromatin state. <i>Nature Biotechnology</i> , 2015, 33, 1165-1172.	9.4	748
34	Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. <i>Science</i> , 2017, 355, .	6.0	743
35	Methylation of histone H3 Lys 4 in coding regions of active genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 8695-8700.	3.3	673
36	Th17 cells transdifferentiate into regulatory T cells during resolution of inflammation. <i>Nature</i> , 2015, 523, 221-225.	13.7	653

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37	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
38	Single-Cell RNA-Seq Reveals AML Hierarchies Relevant to Disease Progression and Immunity. <i>Cell</i> , 2019, 176, 1265-1281.e24.	13.5	642
39	Defining functional DNA elements in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6131-6138.	3.3	635
40	Epigenetic Reprogramming in Cancer. <i>Science</i> , 2013, 339, 1567-1570.	6.0	629
41	The Histone Deacetylase SIRT6 Is a Tumor Suppressor that Controls Cancer Metabolism. <i>Cell</i> , 2012, 151, 1185-1199.	13.5	561
42	ASXL1 Mutations Promote Myeloid Transformation through Loss of PRC2-Mediated Gene Repression. <i>Cancer Cell</i> , 2012, 22, 180-193.	7.7	504
43	Unbiased Reconstruction of a Mammalian Transcriptional Network Mediating Pathogen Responses. <i>Science</i> , 2009, 326, 257-263.	6.0	473
44	Genome-wide Chromatin State Transitions Associated with Developmental and Environmental Cues. <i>Cell</i> , 2013, 152, 642-654.	13.5	473
45	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. <i>Science</i> , 2018, 360, 331-335.	6.0	461
46	Jarid2 and PRC2, partners in regulating gene expression. <i>Genes and Development</i> , 2010, 24, 368-380.	2.7	434
47	Targeted DNA demethylation and activation of endogenous genes using programmable TALE-TET1 fusion proteins. <i>Nature Biotechnology</i> , 2013, 31, 1137-1142.	9.4	433
48	Transcriptional and Epigenetic Dynamics during Specification of Human Embryonic Stem Cells. <i>Cell</i> , 2013, 153, 1149-1163.	13.5	419
49	DNA Sequence-Dependent Compartmentalization and Silencing of Chromatin at the Nuclear Lamina. <i>Cell</i> , 2012, 149, 1474-1487.	13.5	405
50	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	13.5	404
51	Adaptive Chromatin Remodeling Drives Glioblastoma Stem Cell Plasticity and Drug Tolerance. <i>Cell Stem Cell</i> , 2017, 20, 233-246.e7.	5.2	387
52	A High-Throughput Chromatin Immunoprecipitation Approach Reveals Principles of Dynamic Gene Regulation in Mammals. <i>Molecular Cell</i> , 2012, 47, 810-822.	4.5	375
53	GC-Rich Sequence Elements Recruit PRC2 in Mammalian ES Cells. <i>PLoS Genetics</i> , 2010, 6, e1001244.	1.5	368
54	Comparative analysis of metazoan chromatin organization. <i>Nature</i> , 2014, 512, 449-452.	13.7	363

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55	A Genetic Variant Associated with Five Vascular Diseases Is a Distal Regulator of Endothelin-1 Gene Expression. <i>Cell</i> , 2017, 170, 522-533.e15.	13.5	356
56	Signaling Network Model of Chromatin. <i>Cell</i> , 2002, 111, 771-778.	13.5	353
57	Reprogramming Factor Expression Initiates Widespread Targeted Chromatin Remodeling. <i>Cell Stem Cell</i> , 2011, 8, 96-105.	5.2	345
58	Genomic Distribution and Inter-Sample Variation of Non-CpG Methylation across Human Cell Types. <i>PLoS Genetics</i> , 2011, 7, e1002389.	1.5	345
59	Unravelling subclonal heterogeneity and aggressive disease states in TNBC through single-cell RNA-seq. <i>Nature Communications</i> , 2018, 9, 3588.	5.8	342
60	Locus-specific editing of histone modifications at endogenous enhancers. <i>Nature Biotechnology</i> , 2013, 31, 1133-1136.	9.4	339
61	EWS-FLI1 Utilizes Divergent Chromatin Remodeling Mechanisms to Directly Activate or Repress Enhancer Elements in Ewing Sarcoma. <i>Cancer Cell</i> , 2014, 26, 668-681.	7.7	334
62	An epigenetic mechanism of resistance to targeted therapy in T cell acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2014, 46, 364-370.	9.4	333
63	Heterodimeric JAK-STAT activation as a mechanism of persistence to JAK2 inhibitor therapy. <i>Nature</i> , 2012, 489, 155-159.	13.7	320
64	Genome-wide programmable transcriptional memory by CRISPR-based epigenome editing. <i>Cell</i> , 2021, 184, 2503-2519.e17.	13.5	312
65	Global nucleosome occupancy in yeast. <i>Genome Biology</i> , 2004, 5, R62.	13.9	309
66	Combinatorial Patterning of Chromatin Regulators Uncovered by Genome-wide Location Analysis in Human Cells. <i>Cell</i> , 2011, 147, 1628-1639.	13.5	303
67	Molecular regulation of H3K4 trimethylation by ASH2L, a shared subunit of MLL complexes. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 852-854.	3.6	288
68	Role for Dpy-30 in ES Cell-Fate Specification by Regulation of H3K4 Methylation within Bivalent Domains. <i>Cell</i> , 2011, 144, 513-525.	13.5	282
69	Insights into GATA-1-Mediated Gene Activation versus Repression via Genome-wide Chromatin Occupancy Analysis. <i>Molecular Cell</i> , 2009, 36, 682-695.	4.5	278
70	Deletion of Asxl1 results in myelodysplasia and severe developmental defects in vivo. <i>Journal of Experimental Medicine</i> , 2013, 210, 2641-2659.	4.2	278
71	Resolving medulloblastoma cellular architecture by single-cell genomics. <i>Nature</i> , 2019, 572, 74-79.	13.7	273
72	SAM Domain Polymerization Links Subnuclear Clustering of PRC1 to Gene Silencing. <i>Developmental Cell</i> , 2013, 26, 565-577.	3.1	271

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73	SMARCB1-mediated SWI/SNF complex function is essential for enhancer regulation. <i>Nature Genetics</i> , 2017, 49, 289-295.	9.4	268
74	Evaluation of SARS-CoV-2 serology assays reveals a range of test performance. <i>Nature Biotechnology</i> , 2020, 38, 1174-1183.	9.4	251
75	Methylation of Histone H3 K4 Mediates Association of the Isw1p ATPase with Chromatin. <i>Molecular Cell</i> , 2003, 12, 1325-1332.	4.5	248
76	An Aberrant Transcription Factor Network Essential for Wnt Signaling and Stem Cell Maintenance in Glioblastoma. <i>Cell Reports</i> , 2013, 3, 1567-1579.	2.9	236
77	Transaminase Inhibition by 2-Hydroxyglutarate Impairs Glutamate Biosynthesis and Redox Homeostasis in Glioma. <i>Cell</i> , 2018, 175, 101-116.e25.	13.5	234
78	Histone H2A Mono-Ubiquitination Is a Crucial Step to Mediate PRC1-Dependent Repression of Developmental Genes to Maintain ES Cell Identity. <i>PLoS Genetics</i> , 2012, 8, e1002774.	1.5	233
79	Genome-wide analysis reveals conserved and divergent features of Notch1/RBPJ binding in human and murine T-lymphoblastic leukemia cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14908-14913.	3.3	221
80	An oncogenic MYB feedback loop drives alternate cell fates in adenoid cystic carcinoma. <i>Nature Genetics</i> , 2016, 48, 265-272.	9.4	216
81	Orthologous CRISPR-Cas9 enzymes for combinatorial genetic screens. <i>Nature Biotechnology</i> , 2018, 36, 179-189.	9.4	216
82	Synergistic effects of substrate-induced conformational changes in phosphoglycerate kinase activation. <i>Nature</i> , 1997, 385, 275-278.	13.7	197
83	Widespread RNA binding by chromatin-associated proteins. <i>Genome Biology</i> , 2016, 17, 28.	3.8	197
84	Epigenome-wide study uncovers large-scale changes in histone acetylation driven by tau pathology in aging and Alzheimer's human brains. <i>Nature Neuroscience</i> , 2019, 22, 37-46.	7.1	188
85	Whole-genome chromatin profiling from limited numbers of cells using nano-ChIP-seq. <i>Nature Protocols</i> , 2011, 6, 1656-1668.	5.5	186
86	Dual Targeting of Oncogenic Activation and Inflammatory Signaling Increases Therapeutic Efficacy in Myeloproliferative Neoplasms. <i>Cancer Cell</i> , 2018, 33, 29-43.e7.	7.7	186
87	Epigenetic silencing by SETDB1 suppresses tumour intrinsic immunogenicity. <i>Nature</i> , 2021, 595, 309-314.	13.7	181
88	Epstein-Barr virus exploits intrinsic B-lymphocyte transcription programs to achieve immortal cell growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14902-14907.	3.3	180
89	Dissecting neural differentiation regulatory networks through epigenetic footprinting. <i>Nature</i> , 2015, 518, 355-359.	13.7	172
90	H2A.Z landscapes and dual modifications in pluripotent and multipotent stem cells underlie complex genome regulatory functions. <i>Genome Biology</i> , 2012, 13, R85.	13.9	166

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91	Altered chromosomal topology drives oncogenic programs in SDH-deficient GISTs. <i>Nature</i> , 2019, 575, 229-233.	13.7	164
92	Neural-specific Sox2 input and differential Gli-binding affinity provide context and positional information in Shh-directed neural patterning. <i>Genes and Development</i> , 2012, 26, 2802-2816.	2.7	158
93	Transcription elongation factors represent in vivo cancer dependencies in glioblastoma. <i>Nature</i> , 2017, 547, 355-359.	13.7	156
94	Genome-wide chromatin maps derived from limited numbers of hematopoietic progenitors. <i>Nature Methods</i> , 2010, 7, 615-618.	9.0	152
95	Long-range enhancer activity determines <i>Myc</i> sensitivity to Notch inhibitors in T cell leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4946-53.	3.3	151
96	Single-cell and single-molecule epigenomics to uncover genome regulation at unprecedented resolution. <i>Nature Genetics</i> , 2019, 51, 19-25.	9.4	151
97	Systematic dissection of genomic features determining transcription factor binding and enhancer function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1291-E1300.	3.3	150
98	Re-programing Chromatin with a Bifunctional LSD1/HDAC Inhibitor Induces Therapeutic Differentiation in DIPG. <i>Cancer Cell</i> , 2019, 36, 528-544.e10.	7.7	128
99	Large-Scale Topological Changes Restrain Malignant Progression in Colorectal Cancer. <i>Cell</i> , 2020, 182, 1474-1489.e23.	13.5	126
100	Discovery of Biomarkers Predictive of GSI Response in Triple-Negative Breast Cancer and Adenoid Cystic Carcinoma. <i>Cancer Discovery</i> , 2014, 4, 1154-1167.	7.7	123
101	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	13.7	123
102	Enhancer signatures stratify and predict outcomes of non-functional pancreatic neuroendocrine tumors. <i>Nature Medicine</i> , 2019, 25, 1260-1265.	15.2	120
103	Clinical sensitivity and interpretation of PCR and serological COVID-19 diagnostics for patients presenting to the hospital. <i>FASEB Journal</i> , 2020, 34, 13877-13884.	0.2	117
104	Chromatin profiling by directly sequencing small quantities of immunoprecipitated DNA. <i>Nature Methods</i> , 2010, 7, 47-49.	9.0	112
105	Single-molecule decoding of combinatorially modified nucleosomes. <i>Science</i> , 2016, 352, 717-721.	6.0	112
106	A Multiplexed System for Quantitative Comparisons of Chromatin Landscapes. <i>Molecular Cell</i> , 2016, 61, 170-180.	4.5	111
107	EZH2 Codon 641 Mutations are Common in BCL2-Rearranged Germinal Center B Cell Lymphomas. <i>PLoS ONE</i> , 2011, 6, e28585.	1.1	109
108	Detection of Enhancer-Associated Rearrangements Reveals Mechanisms of Oncogene Dysregulation in B-cell Lymphoma. <i>Cancer Discovery</i> , 2015, 5, 1058-1071.	7.7	105

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109	Development and validation of a T7 based linear amplification for genomic DNA. BMC Genomics, 2003, 4, 19.	1.2	102
110	Wilms Tumor Chromatin Profiles Highlight Stem Cell Properties and a Renal Developmental Network. Cell Stem Cell, 2010, 6, 591-602.	5.2	80
111	Chromatin state maps: new technologies, new insights. Current Opinion in Genetics and Development, 2008, 18, 109-115.	1.5	77
112	EHMT1 and EHMT2 inhibition induces fetal hemoglobin expression. Blood, 2015, 126, 1930-1939.	0.6	76
113	Epithelial-to-Mesenchymal Transition Antagonizes Response to Targeted Therapies in Lung Cancer by Suppressing BIM. Clinical Cancer Research, 2018, 24, 197-208.	3.2	74
114	High Seroprevalence of Anti-SARS-CoV-2 Antibodies in Chelsea, Massachusetts. Journal of Infectious Diseases, 2020, 222, 1955-1959.	1.9	72
115	Mammalian Polycomb-Like Pcl2/Mtf2 Is a Novel Regulatory Component of PRC2 That Can Differentially Modulate Polycomb Activity both at the <i>Hox</i> Gene Cluster and at <i>Cdkn2a</i> Genes. Molecular and Cellular Biology, 2011, 31, 351-364.	1.1	68
116	A B Cell Regulome Links Notch to Downstream Oncogenic Pathways in Small B Cell Lymphomas. Cell Reports, 2017, 21, 784-797.	2.9	65
117	Rpd3p Relocation Mediates a Transcriptional Response to Rapamycin in Yeast. Chemistry and Biology, 2004, 11, 295-299.	6.2	64
118	High-Throughput Single-Cell Labeling (Hi-SCL) for RNA-Seq Using Drop-Based Microfluidics. PLoS ONE, 2015, 10, e0116328.	1.1	64
119	Tissue-specific SMARCA4 binding at active and repressed regulatory elements during embryogenesis. Genome Research, 2014, 24, 920-929.	2.4	63
120	Corrupted coordination of epigenetic modifications leads to diverging chromatin states and transcriptional heterogeneity in CLL. Nature Communications, 2019, 10, 1874.	5.8	63
121	Single-cell lineage analysis reveals genetic and epigenetic interplay in glioblastoma drug resistance. Genome Biology, 2020, 21, 174.	3.8	59
122	Digital transcriptome profiling from attomole-level RNA samples. Genome Research, 2010, 20, 519-525.	2.4	56
123	Epigenome editing strategies for the functional annotation of CTCF insulators. Nature Communications, 2019, 10, 4258.	5.8	55
124	RBPJ maintains brain tumor-initiating cells through CDK9-mediated transcriptional elongation. Journal of Clinical Investigation, 2016, 126, 2757-2772.	3.9	52
125	Pluripotent Chromatin State. Science, 2009, 323, 220-221.	6.0	50
126	Genetic Events That Shape the Cancer Epigenome. Science, 2012, 336, 1513-1514.	6.0	50

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127	In silico abstraction of zinc finger nuclease cleavage profiles reveals an expanded landscape of off-target sites. <i>Nucleic Acids Research</i> , 2013, 41, e181-e181.	6.5	47
128	A bisubstrate analog induces unexpected conformational changes in phosphoglycerate kinase from <i>Trypanosoma brucei</i> . <i>Journal of Molecular Biology</i> , 1998, 279, 1137-1148.	2.0	45
129	Data-Driven Polymer Model for Mechanistic Exploration of Diploid Genome Organization. <i>Biophysical Journal</i> , 2020, 119, 1905-1916.	0.2	45
130	Mitochondrial variant enrichment from high-throughput single-cell RNA sequencing resolves clonal populations. <i>Nature Biotechnology</i> , 2022, 40, 1030-1034.	9.4	45
131	Gain-of-Function Genetic Alterations of G9a Drive Oncogenesis. <i>Cancer Discovery</i> , 2020, 10, 980-997.	7.7	44
132	Immunohistochemical quantification of partial-EMT in oral cavity squamous cell carcinoma primary tumors is associated with nodal metastasis. <i>Oral Oncology</i> , 2019, 99, 104458.	0.8	43
133	Inducible histone K-to-M mutations are dynamic tools to probe the physiological role of site-specific histone methylation in vitro and in vivo. <i>Nature Cell Biology</i> , 2019, 21, 1449-1461.	4.6	40
134	The Use of Chromatin Immunoprecipitation Assays in Genome-Wide Analyses of Histone Modifications. <i>Methods in Enzymology</i> , 2003, 376, 349-360.	0.4	37
135	Single-cell RNA-seq reveals developmental plasticity with coexisting oncogenic states and immune evasion programs in ETP-ALL. <i>Blood</i> , 2021, 137, 2463-2480.	0.6	35
136	Genomic views of chromatin. <i>Current Opinion in Genetics and Development</i> , 2005, 15, 476-481.	1.5	32
137	Chromatin accessibility promotes hematopoietic and leukemia stem cell activity. <i>Nature Communications</i> , 2020, 11, 1406.	5.8	32
138	Extended-representation bisulfite sequencing of gene regulatory elements in multiplexed samples and single cells. <i>Nature Biotechnology</i> , 2021, 39, 1086-1094.	9.4	28
139	Reply to Brunet and Doolittle: Both selected effect and causal role elements can influence human biology and disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3366.	3.3	25
140	A Blueprint for an International Cancer Epigenome Consortium. A Report from the AACR Cancer Epigenome Task Force. <i>Cancer Research</i> , 2012, 72, 6319-6324.	0.4	22
141	A Tell-Tail Sign of Chromatin: Histone Mutations Drive Pediatric Glioblastoma. <i>Cancer Cell</i> , 2012, 21, 329-331.	7.7	19
142	The importance of dynamic light scattering in obtaining multiple crystal forms of trypanosoma brucei PGK. <i>Protein Science</i> , 1998, 7, 504-507.	3.1	18
143	Global Approaches to Chromatin. <i>Chemistry and Biology</i> , 2002, 9, 1167-1173.	6.2	17
144	Parallel Single-Cell RNA-Seq and Genetic Recording Reveals Lineage Decisions in Developing Embryoid Bodies. <i>Cell Reports</i> , 2020, 33, 108222.	2.9	16

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145	Sequence-Specific DNA Recognition by Cys2, His2Zinc Fingers. <i>Annals of the New York Academy of Sciences</i> , 1994, 726, 92-104.	1.8	13
146	A novel method for detecting the cellular stemness state in normal and leukemic human hematopoietic cells can predict disease outcome and drug sensitivity. <i>Leukemia</i> , 2019, 33, 2061-2077.	3.3	13
147	Detecting sample swaps in diverse NGS data types using linkage disequilibrium. <i>Nature Communications</i> , 2020, 11, 3697.	5.8	12
148	Epigenetic Alterations in Keratinocyte Carcinoma. <i>Journal of Investigative Dermatology</i> , 2021, 141, 1207-1218.	0.3	9
149	Systematic detection of m6A-modified transcripts at single-molecule and single-cell resolution. <i>Cell Reports Methods</i> , 2021, 1, 100061.	1.4	8
150	Genetic and Nongenetic Determinants of Cellular Architecture in IDH1-Mutant Oligodendrogliomas and Astrocytomas Using Single-Cell Transcriptome Analysis. <i>Neurosurgery</i> , 2016, 63, 158.	0.6	4
151	ASXL1 Mutations Promote Myeloid Transformation Through Inhibition of PRC2-Mediated Gene Repression. <i>Blood</i> , 2011, 118, 405-405.	0.6	4
152	HOXA9 Is a Novel Therapeutic Target in Multiple Myeloma. <i>Blood</i> , 2009, 114, 832-832.	0.6	2
153	Notch-Regulated Enhancers in B-Cell Lymphoma Activate MYC and Potentiate B-Cell Receptor Signaling. <i>Blood</i> , 2016, 128, 457-457.	0.6	2
154	Heterodimeric JAK-STAT Activation As a Mechanism of Persistence to JAK2 Inhibitor Therapy. <i>Blood</i> , 2011, 118, 122-122.	0.6	1
155	MBRS-28. SINGLE-CELL TRANSCRIPTOME ANALYSIS OF MEDULLOBLASTOMA. <i>Neuro-Oncology</i> , 2018, 20, i134-i134.	0.6	0
156	GABP ² 1L Wakes Up TERT. <i>Cancer Cell</i> , 2018, 34, 358-360.	7.7	0
157	Development of ERG-Enhancer Fluorescent Reporter System to Decipher Functional Heterogeneity in Leukemia. <i>Experimental Hematology</i> , 2018, 64, S87.	0.2	0
158	Conditional Deletion of Asxl1 Results in Myelodysplasia. <i>Blood</i> , 2012, 120, 308-308.	0.6	0
159	Alternative Super-Enhancer States Determine MYC Sensitivity to Notch and Brd4 Inhibitors in T Lymphoblastic Leukemia/Lymphoma. <i>Blood</i> , 2014, 124, 863-863.	0.6	0
160	Characterizing Transcriptional and Epigenetic Signatures Induced By FLT3-ITD Activation. <i>Blood</i> , 2014, 124, 2186-2186.	0.6	0
161	Single-Cell RNA-Seq Reveals AML Cellular Hierarchies Relevant to Clinical Outcomes and Immunity. <i>Blood</i> , 2018, 132, 542-542.	0.6	0
162	Single Cell RNA-Seq Reveals Deranged Developmental Hierarchy with Coexisting Oncogenic States and Immune Evasion Programs in ETP T-ALL. <i>Blood</i> , 2019, 134, 3953-3953.	0.6	0

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163	ETMR-17. SINGLE-CELL TRANSCRIPTOME ANALYSIS OF ETMR PATIENT SAMPLES. <i>Neuro-Oncology</i> , 2020, 22, iii326-iii326.	0.6	0