

# Bradley E Bernstein

## List of Publications by Citations

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163  
papers

76,761  
citations

94  
h-index

170  
g-index

170  
ext. papers

94,162  
ext. citations

26.4  
avg, IF

7.42  
L-index

#	Paper	IF	Citations
163	Model-based analysis of ChIP-Seq (MACS). <i>Genome Biology</i> , <b>2008</b> , 9, R137	18.3	8406
162	Comprehensive mapping of long-range interactions reveals folding principles of the human genome. <i>Science</i> , <b>2009</b> , 326, 289-93	33.3	4993
161	A bivalent chromatin structure marks key developmental genes in embryonic stem cells. <i>Cell</i> , <b>2006</b> , 125, 315-26	56.2	4097
160	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , <b>2015</b> , 518, 317-30	50.4	3849
159	Genome-wide maps of chromatin state in pluripotent and lineage-committed cells. <i>Nature</i> , <b>2007</b> , 448, 553-60	50.4	3296
158	Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals. <i>Nature</i> , <b>2009</b> , 458, 223-7	50.4	3230
157	Single-cell RNA-seq highlights intratumoral heterogeneity in primary glioblastoma. <i>Science</i> , <b>2014</b> , 344, 1396-401	33.3	2401
156	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> , <b>2009</b> , 106, 11667-72	11.5	2331
155	In vitro reprogramming of fibroblasts into a pluripotent ES-cell-like state. <i>Nature</i> , <b>2007</b> , 448, 318-24	50.4	2247
154	Mapping and analysis of chromatin state dynamics in nine human cell types. <i>Nature</i> , <b>2011</b> , 473, 43-9	50.4	2153
153	Genome-scale DNA methylation maps of pluripotent and differentiated cells. <i>Nature</i> , <b>2008</b> , 454, 766-70	50.4	1999
152	The mammalian epigenome. <i>Cell</i> , <b>2007</b> , 128, 669-81	56.2	1661
151	Active genes are tri-methylated at K4 of histone H3. <i>Nature</i> , <b>2002</b> , 419, 407-11	50.4	1606
150	The NIH Roadmap Epigenomics Mapping Consortium. <i>Nature Biotechnology</i> , <b>2010</b> , 28, 1045-8	44.5	1284
149	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , <b>2012</b> , 22, 1813-31	9.7	1211
148	Dissecting direct reprogramming through integrative genomic analysis. <i>Nature</i> , <b>2008</b> , 454, 49-55	50.4	1205
147	Genetic and epigenetic fine mapping of causal autoimmune disease variants. <i>Nature</i> , <b>2015</b> , 518, 337-43	50.4	1199

146	Genomic maps and comparative analysis of histone modifications in human and mouse. <i>Cell</i> , <b>2005</b> , 120, 169-81	56.2	1198
145	Initial genome sequencing and analysis of multiple myeloma. <i>Nature</i> , <b>2011</b> , 471, 467-72	50.4	1117
144	Charting a dynamic DNA methylation landscape of the human genome. <i>Nature</i> , <b>2013</b> , 500, 477-81	50.4	932
143	Single-Cell Transcriptomic Analysis of Primary and Metastatic Tumor Ecosystems in Head and Neck Cancer. <i>Cell</i> , <b>2017</b> , 171, 1611-1624.e24	56.2	883
142	Cohesin Loss Eliminates All Loop Domains. <i>Cell</i> , <b>2017</b> , 171, 305-320.e24	56.2	878
141	Charting histone modifications and the functional organization of mammalian genomes. <i>Nature Reviews Genetics</i> , <b>2011</b> , 12, 7-18	30.1	852
140	Insulator dysfunction and oncogene activation in IDH mutant gliomas. <i>Nature</i> , <b>2016</b> , 529, 110-4	50.4	759
139	Genomewide analysis of PRC1 and PRC2 occupancy identifies two classes of bivalent domains. <i>PLoS Genetics</i> , <b>2008</b> , 4, e1000242	6	746
138	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> , <b>2002</b> , 99, 8695-700	11.5	593
137	Alzheimer's disease: early alterations in brain DNA methylation at ANK1, BIN1, RHBDF2 and other loci. <i>Nature Neuroscience</i> , <b>2014</b> , 17, 1156-63	25.5	579
136	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. <i>Nature Biotechnology</i> , <b>2010</b> , 28, 1097-105	44.5	570
135	Single-cell RNA-seq supports a developmental hierarchy in human oligodendrogloma. <i>Nature</i> , <b>2016</b> , 539, 309-313	50.4	561
134	An Integrative Model of Cellular States, Plasticity, and Genetics for Glioblastoma. <i>Cell</i> , <b>2019</b> , 178, 835-849.e21	56.2	556
133	Single-cell ChIP-seq reveals cell subpopulations defined by chromatin state. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 1165-72	44.5	551
132	Epigenetic plasticity and the hallmarks of cancer. <i>Science</i> , <b>2017</b> , 357,	33.3	551
131	Reconstructing and reprogramming the tumor-propagating potential of glioblastoma stem-like cells. <i>Cell</i> , <b>2014</b> , 157, 580-94	56.2	549
130	Epigenetic reprogramming in cancer. <i>Science</i> , <b>2013</b> , 339, 1567-70	33.3	518
129	Th17 cells transdifferentiate into regulatory T cells during resolution of inflammation. <i>Nature</i> , <b>2015</b> , 523, 221-5	50.4	505

128	Defining functional DNA elements in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 6131-8	11.5	490
127	The histone deacetylase SIRT6 is a tumor suppressor that controls cancer metabolism. <i>Cell</i> , <b>2012</b> , 151, 1185-99	56.2	476
126	Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. <i>Science</i> , <b>2017</b> , 355,	33.3	455
125	ASXL1 mutations promote myeloid transformation through loss of PRC2-mediated gene repression. <i>Cancer Cell</i> , <b>2012</b> , 22, 180-93	24.3	416
124	Unbiased reconstruction of a mammalian transcriptional network mediating pathogen responses. <i>Science</i> , <b>2009</b> , 326, 257-63	33.3	411
123	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. <i>Nature Genetics</i> , <b>2018</b> , 50, 621-629	36.3	400
122	Genome-wide chromatin state transitions associated with developmental and environmental cues. <i>Cell</i> , <b>2013</b> , 152, 642-54	56.2	400
121	Jarid2 and PRC2, partners in regulating gene expression. <i>Genes and Development</i> , <b>2010</b> , 24, 368-80	12.6	384
120	Targeted DNA demethylation and activation of endogenous genes using programmable TALE-TET1 fusion proteins. <i>Nature Biotechnology</i> , <b>2013</b> , 31, 1137-42	44.5	368
119	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , <b>2020</b> , 583, 699-710	30.4	360
118	DNA sequence-dependent compartmentalization and silencing of chromatin at the nuclear lamina. <i>Cell</i> , <b>2012</b> , 149, 1474-87	56.2	337
117	Transcriptional and epigenetic dynamics during specification of human embryonic stem cells. <i>Cell</i> , <b>2013</b> , 153, 1149-63	56.2	332
116	Signaling network model of chromatin. <i>Cell</i> , <b>2002</b> , 111, 771-8	56.2	319
115	GC-rich sequence elements recruit PRC2 in mammalian ES cells. <i>PLoS Genetics</i> , <b>2010</b> , 6, e1001244	6	314
114	A high-throughput chromatin immunoprecipitation approach reveals principles of dynamic gene regulation in mammals. <i>Molecular Cell</i> , <b>2012</b> , 47, 810-22	17.6	299
113	Locus-specific editing of histone modifications at endogenous enhancers. <i>Nature Biotechnology</i> , <b>2013</b> , 31, 1133-6	44.5	295
112	Reprogramming factor expression initiates widespread targeted chromatin remodeling. <i>Cell Stem Cell</i> , <b>2011</b> , 8, 96-105	18	295
111	Genomic distribution and inter-sample variation of non-CpG methylation across human cell types. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002389	6	295

110	Single-Cell RNA-Seq Reveals AML Hierarchies Relevant to Disease Progression and Immunity. <i>Cell</i> , <b>2019</b> , 176, 1265-1281.e24	56.2	293
109	Global nucleosome occupancy in yeast. <i>Genome Biology</i> , <b>2004</b> , 5, R62	18.3	283
108	Comparative analysis of metazoan chromatin organization. <i>Nature</i> , <b>2014</b> , 512, 449-52	50.4	265
107	Combinatorial patterning of chromatin regulators uncovered by genome-wide location analysis in human cells. <i>Cell</i> , <b>2011</b> , 147, 1628-39	56.2	265
106	An epigenetic mechanism of resistance to targeted therapy in T cell acute lymphoblastic leukemia. <i>Nature Genetics</i> , <b>2014</b> , 46, 364-70	36.3	263
105	Heterodimeric JAK-STAT activation as a mechanism of persistence to JAK2 inhibitor therapy. <i>Nature</i> , <b>2012</b> , 489, 155-9	50.4	260
104	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. <i>Science</i> , <b>2018</b> , 360, 331-335	33.3	255
103	Molecular regulation of H3K4 trimethylation by ASH2L, a shared subunit of MLL complexes. <i>Nature Structural and Molecular Biology</i> , <b>2006</b> , 13, 852-4	17.6	246
102	A Genetic Variant Associated with Five Vascular Diseases Is a Distal Regulator of Endothelin-1 Gene Expression. <i>Cell</i> , <b>2017</b> , 170, 522-533.e15	56.2	236
101	Adaptive Chromatin Remodeling Drives Glioblastoma Stem Cell Plasticity and Drug Tolerance. <i>Cell Stem Cell</i> , <b>2017</b> , 20, 233-246.e7	18	235
100	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , <b>2016</b> , 167, 1145-1149	56.2	232
99	Insights into GATA-1-mediated gene activation versus repression via genome-wide chromatin occupancy analysis. <i>Molecular Cell</i> , <b>2009</b> , 36, 682-95	17.6	232
98	EWS-FLI1 utilizes divergent chromatin remodeling mechanisms to directly activate or repress enhancer elements in Ewing sarcoma. <i>Cancer Cell</i> , <b>2014</b> , 26, 668-681	24.3	223
97	Deletion of Asxl1 results in myelodysplasia and severe developmental defects in vivo. <i>Journal of Experimental Medicine</i> , <b>2013</b> , 210, 2641-59	16.6	220
96	Methylation of histone H3 K4 mediates association of the Isw1p ATPase with chromatin. <i>Molecular Cell</i> , <b>2003</b> , 12, 1325-32	17.6	218
95	Role for Dpy-30 in ES cell-fate specification by regulation of H3K4 methylation within bivalent domains. <i>Cell</i> , <b>2011</b> , 144, 513-25	56.2	214
94	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> , <b>2012</b> , 8, e1002774	6	193
93	SAM domain polymerization links subnuclear clustering of PRC1 to gene silencing. <i>Developmental Cell</i> , <b>2013</b> , 26, 565-77	10.2	190

92	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> , <b>2011</b> , 108, 14908-13	11.5	190
91	An aberrant transcription factor network essential for Wnt signaling and stem cell maintenance in glioblastoma. <i>Cell Reports</i> , <b>2013</b> , 3, 1567-79	10.6	187
90	Unravelling subclonal heterogeneity and aggressive disease states in TNBC through single-cell RNA-seq. <i>Nature Communications</i> , <b>2018</b> , 9, 3588	17.4	187
89	SMARCB1-mediated SWI/SNF complex function is essential for enhancer regulation. <i>Nature Genetics</i> , <b>2017</b> , 49, 289-295	36.3	172
88	Synergistic effects of substrate-induced conformational changes in phosphoglycerate kinase activation. <i>Nature</i> , <b>1997</b> , 385, 275-8	50.4	169
87	Evaluation of SARS-CoV-2 serology assays reveals a range of test performance. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 1174-1183	44.5	166
86	An oncogenic MYB feedback loop drives alternate cell fates in adenoid cystic carcinoma. <i>Nature Genetics</i> , <b>2016</b> , 48, 265-72	36.3	152
85	Whole-genome chromatin profiling from limited numbers of cells using nano-ChIP-seq. <i>Nature Protocols</i> , <b>2011</b> , 6, 1656-68	18.8	148
84	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> , <b>2011</b> , 108, 14902-7	11.5	146
83	Orthologous CRISPR-Cas9 enzymes for combinatorial genetic screens. <i>Nature Biotechnology</i> , <b>2018</b> , 36, 179-189	44.5	144
82	Widespread RNA binding by chromatin-associated proteins. <i>Genome Biology</i> , <b>2016</b> , 17, 28	18.3	143
81	Dissecting neural differentiation regulatory networks through epigenetic footprinting. <i>Nature</i> , <b>2015</b> , 518, 355-359	50.4	140
80	Transaminase Inhibition by 2-Hydroxyglutarate Impairs Glutamate Biosynthesis and Redox Homeostasis in Glioma. <i>Cell</i> , <b>2018</b> , 175, 101-116.e25	56.2	140
79	Genome-wide chromatin maps derived from limited numbers of hematopoietic progenitors. <i>Nature Methods</i> , <b>2010</b> , 7, 615-8	21.6	134
78	Resolving medulloblastoma cellular architecture by single-cell genomics. <i>Nature</i> , <b>2019</b> , 572, 74-79	50.4	133
77	Long-range enhancer activity determines Myc sensitivity to Notch inhibitors in T cell leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, E4946-53	11.5	125
76	H2A.Z landscapes and dual modifications in pluripotent and multipotent stem cells underlie complex genome regulatory functions. <i>Genome Biology</i> , <b>2012</b> , 13, R85	18.3	125
75	Neural-specific Sox2 input and differential Gli-binding affinity provide context and positional information in Shh-directed neural patterning. <i>Genes and Development</i> , <b>2012</b> , 26, 2802-16	12.6	124

74	Dual Targeting of Oncogenic Activation and Inflammatory Signaling Increases Therapeutic Efficacy in Myeloproliferative Neoplasms. <i>Cancer Cell</i> , <b>2018</b> , 33, 29-43.e7	24.3	113
73	Transcription elongation factors represent in vivo cancer dependencies in glioblastoma. <i>Nature</i> , <b>2017</b> , 547, 355-359	50.4	109
72	Chromatin profiling by directly sequencing small quantities of immunoprecipitated DNA. <i>Nature Methods</i> , <b>2010</b> , 7, 47-9	21.6	104
71	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> , <b>2019</b> , 22, 37-46	25.5	99
70	EZH2 codon 641 mutations are common in BCL2-rearranged germinal center B cell lymphomas. <i>PLoS ONE</i> , <b>2011</b> , 6, e28585	3.7	98
69	Development and validation of a T7 based linear amplification for genomic DNA. <i>BMC Genomics</i> , <b>2003</b> , 4, 19	4.5	94
68	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> , <b>2017</b> , 114, E1291-E1300	11.5	93
67	Discovery of biomarkers predictive of GSI response in triple-negative breast cancer and adenoid cystic carcinoma. <i>Cancer Discovery</i> , <b>2014</b> , 4, 1154-67	24.4	92
66	Single-cell and single-molecule epigenomics to uncover genome regulation at unprecedented resolution. <i>Nature Genetics</i> , <b>2019</b> , 51, 19-25	36.3	87
65	Altered chromosomal topology drives oncogenic programs in SDH-deficient GISTs. <i>Nature</i> , <b>2019</b> , 575, 229-233	50.4	81
64	Genome-wide programmable transcriptional memory by CRISPR-based epigenome editing. <i>Cell</i> , <b>2021</b> , 184, 2503-2519.e17	56.2	80
63	Single-molecule decoding of combinatorially modified nucleosomes. <i>Science</i> , <b>2016</b> , 352, 717-21	33.3	80
62	Detection of Enhancer-Associated Rearrangements Reveals Mechanisms of Oncogene Dysregulation in B-cell Lymphoma. <i>Cancer Discovery</i> , <b>2015</b> , 5, 1058-71	24.4	78
61	ETMR-17. SINGLE-CELL TRANSCRIPTOME ANALYSIS OF ETMR PATIENT SAMPLES. <i>Neuro-Oncology</i> , <b>2020</b> , 22, iii326-iii326	1	78
60	MBRS-28. SINGLE-CELL TRANSCRIPTOME ANALYSIS OF MEDULLOBLASTOMA. <i>Neuro-Oncology</i> , <b>2018</b> , 20, i134-i134	1	78
59	A Multiplexed System for Quantitative Comparisons of Chromatin Landscapes. <i>Molecular Cell</i> , <b>2016</b> , 61, 170-80	17.6	74
58	Enhancer signatures stratify and predict outcomes of non-functional pancreatic neuroendocrine tumors. <i>Nature Medicine</i> , <b>2019</b> , 25, 1260-1265	50.5	74
57	Clinical sensitivity and interpretation of PCR and serological COVID-19 diagnostics for patients presenting to the hospital. <i>FASEB Journal</i> , <b>2020</b> , 34, 13877-13884	0.9	71

56	Wilms tumor chromatin profiles highlight stem cell properties and a renal developmental network. <i>Cell Stem Cell</i> , <b>2010</b> , 6, 591-602	18	68
55	Re-programing Chromatin with a Bifunctional LSD1/HDAC Inhibitor Induces Therapeutic Differentiation in DIPG. <i>Cancer Cell</i> , <b>2019</b> , 36, 528-544.e10	24.3	66
54	EHMT1 and EHMT2 inhibition induces fetal hemoglobin expression. <i>Blood</i> , <b>2015</b> , 126, 1930-9	2.2	64
53	Chromatin state maps: new technologies, new insights. <i>Current Opinion in Genetics and Development</i> , <b>2008</b> , 18, 109-15	4.9	63
52	Perspectives on ENCODE. <i>Nature</i> , <b>2020</b> , 583, 693-698	50.4	61
51	Rpd3p relocation mediates a transcriptional response to rapamycin in yeast. <i>Chemistry and Biology</i> , <b>2004</b> , 11, 295-9		57
50	Mammalian polycomb-like Pcl2/Mtf2 is a novel regulatory component of PRC2 that can differentially modulate polycomb activity both at the Hox gene cluster and at Cdkn2a genes. <i>Molecular and Cellular Biology</i> , <b>2011</b> , 31, 351-64	4.8	56
49	High-Throughput Single-Cell Labeling (Hi-SCL) for RNA-Seq Using Drop-Based Microfluidics. <i>PLoS ONE</i> , <b>2015</b> , 10, e0116328	3.7	53
48	Epithelial-to-Mesenchymal Transition Antagonizes Response to Targeted Therapies in Lung Cancer by Suppressing BIM. <i>Clinical Cancer Research</i> , <b>2018</b> , 24, 197-208	12.9	50
47	Digital transcriptome profiling from attomole-level RNA samples. <i>Genome Research</i> , <b>2010</b> , 20, 519-25	9.7	49
46	Tissue-specific SMARCA4 binding at active and repressed regulatory elements during embryogenesis. <i>Genome Research</i> , <b>2014</b> , 24, 920-9	9.7	47
45	Developmental biology. Pluripotent chromatin state. <i>Science</i> , <b>2009</b> , 323, 220-1	33.3	47
44	A B Cell Regulome Links Notch to Downstream Oncogenic Pathways in Small B Cell Lymphomas. <i>Cell Reports</i> , <b>2017</b> , 21, 784-797	10.6	45
43	Molecular biology. Genetic events that shape the cancer epigenome. <i>Science</i> , <b>2012</b> , 336, 1513-4	33.3	45
42	In silico abstraction of zinc finger nuclease cleavage profiles reveals an expanded landscape of off-target sites. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, e181	20.1	43
41	Large-Scale Topological Changes Restrain Malignant Progression in Colorectal Cancer. <i>Cell</i> , <b>2020</b> , 182, 1474-1489.e23	56.2	41
40	A bisubstrate analog induces unexpected conformational changes in phosphoglycerate kinase from <i>Trypanosoma brucei</i> . <i>Journal of Molecular Biology</i> , <b>1998</b> , 279, 1137-48	6.5	40
39	High Seroprevalence of Anti-SARS-CoV-2 Antibodies in Chelsea, Massachusetts. <i>Journal of Infectious Diseases</i> , <b>2020</b> , 222, 1955-1959	7	39



38	Corrupted coordination of epigenetic modifications leads to diverging chromatin states and transcriptional heterogeneity in CLL. <i>Nature Communications</i> , <b>2019</b> , 10, 1874	17.4	38
37	Epigenetic silencing by SETDB1 suppresses tumour intrinsic immunogenicity. <i>Nature</i> , <b>2021</b> , 595, 309-314	50.4	37
36	The use of chromatin immunoprecipitation assays in genome-wide analyses of histone modifications. <i>Methods in Enzymology</i> , <b>2004</b> , 376, 349-60	1.7	36
35	RBPJ maintains brain tumor-initiating cells through CDK9-mediated transcriptional elongation. <i>Journal of Clinical Investigation</i> , <b>2016</b> , 126, 2757-72	15.9	35
34	Epigenome editing strategies for the functional annotation of CTCF insulators. <i>Nature Communications</i> , <b>2019</b> , 10, 4258	17.4	31
33	Genomic views of chromatin. <i>Current Opinion in Genetics and Development</i> , <b>2005</b> , 15, 476-81	4.9	29
32	Immunohistochemical quantification of partial-EMT in oral cavity squamous cell carcinoma primary tumors is associated with nodal metastasis. <i>Oral Oncology</i> , <b>2019</b> , 99, 104458	4.4	25
31	Single-cell lineage analysis reveals genetic and epigenetic interplay in glioblastoma drug resistance. <i>Genome Biology</i> , <b>2020</b> , 21, 174	18.3	23
30	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> , <b>2014</b> , 111, E3366	11.5	22
29	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> , <b>2019</b> , 21, 1449-1461	23.4	21
28	A blueprint for an international cancer epigenome consortium. A report from the AACR Cancer Epigenome Task Force. <i>Cancer Research</i> , <b>2012</b> , 72, 6319-24	10.1	21
27	Data-Driven Polymer Model for Mechanistic Exploration of Diploid Genome Organization. <i>Biophysical Journal</i> , <b>2020</b> , 119, 1905-1916	2.9	19
26	A tell-tail sign of chromatin: histone mutations drive pediatric glioblastoma. <i>Cancer Cell</i> , <b>2012</b> , 21, 329-31	14.3	17
25	Gain-of-Function Genetic Alterations of G9a Drive Oncogenesis. <i>Cancer Discovery</i> , <b>2020</b> , 10, 980-997	24.4	17
24	The importance of dynamic light scattering in obtaining multiple crystal forms of Trypanosoma brucei PGK. <i>Protein Science</i> , <b>1998</b> , 7, 504-7	6.3	16
23	Global approaches to chromatin. <i>Chemistry and Biology</i> , <b>2002</b> , 9, 1167-73		16
22	Chromatin accessibility promotes hematopoietic and leukemia stem cell activity. <i>Nature Communications</i> , <b>2020</b> , 11, 1406	17.4	15
21	Single-cell RNA-seq reveals developmental plasticity with coexisting oncogenic states and immune evasion programs in ETP-ALL. <i>Blood</i> , <b>2021</b> , 137, 2463-2480	2.2	12

20	Sequence-specific DNA recognition by Cys2, His2 zinc fingers. <i>Annals of the New York Academy of Sciences</i> , <b>1994</b> , 726, 92-102; discussion 102-4	6.5	10
19	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> , <b>2019</b> , 33, 2061-2077	10.7	8
18	Parallel Single-Cell RNA-Seq and Genetic Recording Reveals Lineage Decisions in Developing Embryoid Bodies. <i>Cell Reports</i> , <b>2020</b> , 33, 108222	10.6	5
17	Mitochondrial variant enrichment from high-throughput single-cell RNA-seq resolves clonal populations		5
16	Extended-representation bisulfite sequencing of gene regulatory elements in multiplexed samples and single cells. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 1086-1094	44.5	4
15	Epigenetic Alterations in Keratinocyte Carcinoma. <i>Journal of Investigative Dermatology</i> , <b>2021</b> , 141, 1207-1218	43.18	4
14	142 Genetic and Nongenetic Determinants of Cellular Architecture in IDH1-Mutant Oligodendrogliomas and Astrocytomas Using Single-Cell Transcriptome Analysis. <i>Neurosurgery</i> , <b>2016</b> , 63, 158	3.2	3
13	ASXL1 Mutations Promote Myeloid Transformation Through Inhibition of PRC2-Mediated Gene Repression. <i>Blood</i> , <b>2011</b> , 118, 405-405	2.2	3
12	HOXA9 Is a Novel Therapeutic Target in Multiple Myeloma.. <i>Blood</i> , <b>2009</b> , 114, 832-832	2.2	2
11	Mitochondrial variant enrichment from high-throughput single-cell RNA sequencing resolves clonal populations.. <i>Nature Biotechnology</i> , <b>2022</b> ,	44.5	2
10	Heterodimeric JAK-STAT Activation As a Mechanism of Persistence to JAK2 Inhibitor Therapy. <i>Blood</i> , <b>2011</b> , 118, 122-122	2.2	1
9	Notch-Regulated Enhancers in B-Cell Lymphoma Activate MYC and Potentiate B-Cell Receptor Signaling. <i>Blood</i> , <b>2016</b> , 128, 457-457	2.2	1
8	Detecting sample swaps in diverse NGS data types using linkage disequilibrium. <i>Nature Communications</i> , <b>2020</b> , 11, 3697	17.4	1
7	Systematic detection of mA-modified transcripts at single-molecule and single-cell resolution. <i>Cell Reports Methods</i> , <b>2021</b> , 1, 100061-100061		1
6	Single-Cell RNA-Seq Reveals AML Cellular Hierarchies Relevant to Clinical Outcomes and Immunity. <i>Blood</i> , <b>2018</b> , 132, 542-542	2.2	
5	Single Cell RNA-Seq Reveals Deranged Developmental Hierarchy with Coexisting Oncogenic States and Immune Evasion Programs in ETP T-ALL. <i>Blood</i> , <b>2019</b> , 134, 3953-3953	2.2	
4	Alternative Super-Enhancer States Determine MYC Sensitivity to Notch and Brd4 Inhibitors in T Lymphoblastic Leukemia/Lymphoma. <i>Blood</i> , <b>2014</b> , 124, 863-863	2.2	
3	Characterizing Transcriptional and Epigenetic Signatures Induced By FLT3-ITD Activation. <i>Blood</i> , <b>2014</b> , 124, 2186-2186	2.2	

- 2 Conditional Deletion of Asxl1 Results in Myelodysplasia. *Blood*, **2012**, 120, 308-308 2.2
- 1 GABP1L Wakes Up TERT. *Cancer Cell*, **2018**, 34, 358-360 24.3