Bradley E Bernstein

List of Publications by Year
in descending order

163	104,406	1994 101	6471 157
papers	citations	h-index	g-index

171	171	171	105783
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Model-based Analysis of ChIP-Seq (MACS). Genome Biology, 2008, 9, R137.	9.6	13,517
2	Comprehensive Mapping of Long-Range Interactions Reveals Folding Principles of the Human Genome. Science, 2009, 326, 289-293.	12.6	7,170
3	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	27.8	5,653
4	A Bivalent Chromatin Structure Marks Key Developmental Genes in Embryonic Stem Cells. Cell, 2006, 125, 315-326.	28.9	4,773
5	Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals. Nature, 2009, 458, 223-227.	27.8	3,801
6	Genome-wide maps of chromatin state in pluripotent and lineage-committed cells. Nature, 2007, 448, 553-560.	27.8	3,733
7	Single-cell RNA-seq highlights intratumoral heterogeneity in primary glioblastoma. Science, 2014, 344, 1396-1401.	12.6	3,648
8	Many human large intergenic noncoding RNAs associate with chromatin-modifying complexes and affect gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11667-11672.	7.1	2,709
9	Mapping and analysis of chromatin state dynamics in nine human cell types. Nature, 2011, 473, 43-49.	27.8	2,630
10	In vitro reprogramming of fibroblasts into a pluripotent ES-cell-like state. Nature, 2007, 448, 318-324.	27.8	2,517
11	Genome-scale DNA methylation maps of pluripotent and differentiated cells. Nature, 2008, 454, 766-770.	27.8	2,267
12	The Mammalian Epigenome. Cell, 2007, 128, 669-681.	28.9	1,909
13	Active genes are tri-methylated at K4 of histone H3. Nature, 2002, 419, 407-411.	27.8	1,871
14	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. Genome Research, 2012, 22, 1813-1831.	5.5	1,708
15	The NIH Roadmap Epigenomics Mapping Consortium. Nature Biotechnology, 2010, 28, 1045-1048.	17.5	1,705
16	Genetic and epigenetic fine mapping of causal autoimmune disease variants. Nature, 2015, 518, 337-343.	27.8	1,669
17	Single-Cell Transcriptomic Analysis of Primary and Metastatic Tumor Ecosystems in Head and Neck Cancer. Cell, 2017, 171, 1611-1624.e24.	28.9	1,656
18	Cohesin Loss Eliminates All Loop Domains. Cell, 2017, 171, 305-320.e24.	28.9	1,454

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19	An Integrative Model of Cellular States, Plasticity, and Genetics for Glioblastoma. Cell, 2019, 178, 835-849.e21.	28.9	1,408
20	Genomic Maps and Comparative Analysis of Histone Modifications in Human and Mouse. Cell, 2005, 120, 169-181.	28.9	1,348
21	Dissecting direct reprogramming through integrative genomic analysis. Nature, 2008, 454, 49-55.	27.8	1,344
22	Initial genome sequencing and analysis of multiple myeloma. Nature, 2011, 471, 467-472.	27.8	1,288
23	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	27.8	1,252
24	Charting a dynamic DNA methylation landscape of the human genome. Nature, 2013, 500, 477-481.	27.8	1,168
25	Insulator dysfunction and oncogene activation in IDH mutant gliomas. Nature, 2016, 529, 110-114.	27.8	1,048
26	Charting histone modifications and the functional organization of mammalian genomes. Nature Reviews Genetics, 2011, 12, 7-18.	16.3	1,019
27	Epigenetic plasticity and the hallmarks of cancer. Science, 2017, 357, .	12.6	920
28	Genomewide Analysis of PRC1 and PRC2 Occupancy Identifies Two Classes of Bivalent Domains. PLoS Genetics, 2008, 4, e1000242.	3.5	878
29	Single-cell RNA-seq supports a developmental hierarchy in human oligodendroglioma. Nature, 2016, 539, 309-313.	27.8	875
30	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. Nature Genetics, 2018, 50, 621-629.	21.4	807
31	Alzheimer's disease: early alterations in brain DNA methylation at ANK1, BIN1, RHBDF2 and other loci. Nature Neuroscience, 2014, 17, 1156-1163.	14.8	800
32	Reconstructing and Reprogramming the Tumor-Propagating Potential of Glioblastoma Stem-like Cells. Cell, 2014, 157, 580-594.	28.9	751
33	Single-cell ChIP-seq reveals cell subpopulations defined by chromatin state. Nature Biotechnology, 2015, 33, 1165-1172.	17.5	748
34	Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. Science, 2017, 355, .	12.6	743
35	Methylation of histone H3 Lys 4 in coding regions of active genes. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 8695-8700.	7.1	673
36	Th17 cells transdifferentiate into regulatory T cells during resolution of inflammation. Nature, 2015, 523, 221-225.	27.8	653

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37	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. Nature Biotechnology, 2010, 28, 1097-1105.	17.5	647
38	Single-Cell RNA-Seq Reveals AML Hierarchies Relevant to Disease Progression and Immunity. Cell, 2019, 176, 1265-1281.e24.	28.9	642
39	Defining functional DNA elements in the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6131-6138.	7.1	635
40	Epigenetic Reprogramming in Cancer. Science, 2013, 339, 1567-1570.	12.6	629
41	The Histone Deacetylase SIRT6 Is a Tumor Suppressor that Controls Cancer Metabolism. Cell, 2012, 151, 1185-1199.	28.9	561
42	ASXL1 Mutations Promote Myeloid Transformation through Loss of PRC2-Mediated Gene Repression. Cancer Cell, 2012, 22, 180-193.	16.8	504
43	Unbiased Reconstruction of a Mammalian Transcriptional Network Mediating Pathogen Responses. Science, 2009, 326, 257-263.	12.6	473
44	Genome-wide Chromatin State Transitions Associated with Developmental and Environmental Cues. Cell, 2013, 152, 642-654.	28.9	473
45	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. Science, 2018, 360, 331-335.	12.6	461
46	Jarid2 and PRC2, partners in regulating gene expression. Genes and Development, 2010, 24, 368-380.	5.9	434
47	Targeted DNA demethylation and activation of endogenous genes using programmable TALE-TET1 fusion proteins. Nature Biotechnology, 2013, 31, 1137-1142.	17.5	433
48	Transcriptional and Epigenetic Dynamics during Specification of Human Embryonic Stem Cells. Cell, 2013, 153, 1149-1163.	28.9	419
49	DNA Sequence-Dependent Compartmentalization and Silencing of Chromatin at the Nuclear Lamina. Cell, 2012, 149, 1474-1487.	28.9	405
50	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
51	Adaptive Chromatin Remodeling Drives Glioblastoma Stem Cell Plasticity and Drug Tolerance. Cell Stem Cell, 2017, 20, 233-246.e7.	11.1	387
52	A High-Throughput Chromatin Immunoprecipitation Approach Reveals Principles of Dynamic Gene Regulation in Mammals. Molecular Cell, 2012, 47, 810-822.	9.7	375
53	GC-Rich Sequence Elements Recruit PRC2 in Mammalian ES Cells. PLoS Genetics, 2010, 6, e1001244.	3.5	368
54	Comparative analysis of metazoan chromatin organization. Nature, 2014, 512, 449-452.	27.8	363

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55	A Genetic Variant Associated with Five Vascular Diseases Is a Distal Regulator of Endothelin-1 Gene Expression. Cell, 2017, 170, 522-533.e15.	28.9	356
56	Signaling Network Model of Chromatin. Cell, 2002, 111, 771-778.	28.9	353
57	Reprogramming Factor Expression Initiates Widespread Targeted Chromatin Remodeling. Cell Stem Cell, 2011, 8, 96-105.	11.1	345
58	Genomic Distribution and Inter-Sample Variation of Non-CpG Methylation across Human Cell Types. PLoS Genetics, 2011, 7, e1002389.	3.5	345
59	Unravelling subclonal heterogeneity and aggressive disease states in TNBC through single-cell RNA-seq. Nature Communications, 2018, 9, 3588.	12.8	342
60	Locus-specific editing of histone modifications at endogenous enhancers. Nature Biotechnology, 2013, 31, 1133-1136.	17.5	339
61	EWS-FLI1ÂUtilizes Divergent Chromatin Remodeling Mechanisms to Directly Activate or Repress Enhancer Elements in Ewing Sarcoma. Cancer Cell, 2014, 26, 668-681.	16.8	334
62	An epigenetic mechanism of resistance to targeted therapy in T cell acute lymphoblastic leukemia. Nature Genetics, 2014, 46, 364-370.	21.4	333
63	Heterodimeric JAKâ€“STAT activation as a mechanism of persistence to JAK2 inhibitor therapy. Nature, 2012, 489, 155-159.	27.8	320
64	Genome-wide programmable transcriptional memory by CRISPR-based epigenome editing. Cell, 2021, 184, 2503-2519.e17.	28.9	312
65	Global nucleosome occupancy in yeast. Genome Biology, 2004, 5, R62.	9.6	309
66	Combinatorial Patterning of Chromatin Regulators Uncovered by Genome-wide Location Analysis in Human Cells. Cell, 2011, 147, 1628-1639.	28.9	303
67	Molecular regulation of H3K4 trimethylation by ASH2L, a shared subunit of MLL complexes. Nature Structural and Molecular Biology, 2006, 13, 852-854.	8.2	288
68	Role for Dpy-30 in ES Cell-Fate Specification by Regulation of H3K4 Methylation within Bivalent Domains. Cell, 2011, 144, 513-525.	28.9	282
69	Insights into GATA-1-Mediated Gene Activation versus Repression via Genome-wide Chromatin Occupancy Analysis. Molecular Cell, 2009, 36, 682-695.	9.7	278
70	Deletion of Asxl1 results in myelodysplasia and severe developmental defects in vivo. Journal of Experimental Medicine, 2013, 210, 2641-2659.	8.5	278
71	Resolving medulloblastoma cellular architecture by single-cell genomics. Nature, 2019, 572, 74-79.	27.8	273
72	SAM Domain Polymerization Links Subnuclear Clustering of PRC1 to Gene Silencing. Developmental Cell, 2013, 26, 565-577.	7.0	271

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73	SMARCB1-mediated SWI/SNF complex function is essential for enhancer regulation. Nature Genetics, 2017, 49, 289-295.	21.4	268
74	Evaluation of SARS-CoV-2 serology assays reveals a range of test performance. Nature Biotechnology, 2020, 38, 1174-1183.	17.5	251
75	Methylation of Histone H3 K4 Mediates Association of the Isw1p ATPase with Chromatin. Molecular Cell, 2003, 12, 1325-1332.	9.7	248
76	An Aberrant Transcription Factor Network Essential for Wnt Signaling and Stem Cell Maintenance in Glioblastoma. Cell Reports, 2013, 3, 1567-1579.	6.4	236
77	Transaminase Inhibition by 2-Hydroxyglutarate Impairs Glutamate Biosynthesis and Redox Homeostasis in Glioma. Cell, 2018, 175, 101-116.e25.	28.9	234
78	Histone H2A Mono-Ubiquitination Is a Crucial Step to Mediate PRC1-Dependent Repression of Developmental Genes to Maintain ES Cell Identity. PLoS Genetics, 2012, 8, e1002774.	3.5	233
79	Genome-wide analysis reveals conserved and divergent features of Notch1/RBPJ binding in human and murine T-lymphoblastic leukemia cells. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 14908-14913.	7.1	221
80	An oncogenic MYB feedback loop drives alternate cell fates in adenoid cystic carcinoma. Nature Genetics, 2016, 48, 265-272.	21.4	216
81	Orthologous CRISPRâ€“Cas9 enzymes for combinatorial genetic screens. Nature Biotechnology, 2018, 36, 179-189.	17.5	216
82	Synergistic effects of substrate-induced conformational changes in phosphoglycerate kinase activation. Nature, 1997, 385, 275-278.	27.8	197
83	Widespread RNA binding by chromatin-associated proteins. Genome Biology, 2016, 17, 28.	8.8	197
84	Epigenome-wide study uncovers large-scale changes in histone acetylation driven by tau pathology in aging and Alzheimerâ€™s human brains. Nature Neuroscience, 2019, 22, 37-46.	14.8	188
85	Whole-genome chromatin profiling from limited numbers of cells using nano-ChIP-seq. Nature Protocols, 2011, 6, 1656-1668.	12.0	186
86	Dual Targeting of Oncogenic Activation and Inflammatory Signaling Increases Therapeutic Efficacy in Myeloproliferative Neoplasms. Cancer Cell, 2018, 33, 29-43.e7.	16.8	186
87	Epigenetic silencing by SETDB1 suppresses tumour intrinsic immunogenicity. Nature, 2021, 595, 309-314.	27.8	181
88	Epstein-Barr virus exploits intrinsic B-lymphocyte transcription programs to achieve immortal cell growth. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 14902-14907.	7.1	180
89	Dissecting neural differentiation regulatory networks through epigenetic footprinting. Nature, 2015, 518, 355-359.	27.8	172
90	H2A.Z landscapes and dual modifications in pluripotent and multipotent stem cells underlie complex genome regulatory functions. Genome Biology, 2012, 13, R85.	9.6	166

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91	Altered chromosomal topology drives oncogenic programs in SDH-deficient GISTs. Nature, 2019, 575, 229-233.	27.8	164
92	Neural-specific Sox2 input and differential Gli-binding affinity provide context and positional information in Shh-directed neural patterning. Genes and Development, 2012, 26, 2802-2816.	5.9	158
93	Transcription elongation factors represent in vivo cancer dependencies in glioblastoma. Nature, 2017, 547, 355-359.	27.8	156
94	Genome-wide chromatin maps derived from limited numbers of hematopoietic progenitors. Nature Methods, 2010, 7, 615-618.	19.0	152
95	Long-range enhancer activity determines Myc sensitivity to Notch inhibitors in T cell leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4946-53.	7.1	151
96	Single-cell and single-molecule epigenomics to uncover genome regulation at unprecedented resolution. Nature Genetics, 2019, 51, 19-25.	21.4	151
97	Systematic dissection of genomic features determining transcription factor binding and enhancer function. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1291-E1300.	7.1	150
98	Re-programing Chromatin with a Bifunctional LSD1/HDAC Inhibitor Induces Therapeutic Differentiation in DIPG. Cancer Cell, 2019, 36, 528-544.e10.	16.8	128
99	Large-Scale Topological Changes Restrain Malignant Progression in Colorectal Cancer. Cell, 2020, 182, 1474-1489.e23.	28.9	126
100	Discovery of Biomarkers Predictive of GSI Response in Triple-Negative Breast Cancer and Adenoid Cystic Carcinoma. Cancer Discovery, 2014, 4, 1154-1167.	9.4	123
101	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	27.8	123
102	Enhancer signatures stratify and predict outcomes of non-functional pancreatic neuroendocrine tumors. Nature Medicine, 2019, 25, 1260-1265.	30.7	120
103	Clinical sensitivity and interpretation of PCR and serological COVIDâ€19 diagnostics for patients presenting to the hospital. FASEB Journal, 2020, 34, 13877-13884.	0.5	117
104	Chromatin profiling by directly sequencing small quantities of immunoprecipitated DNA. Nature Methods, 2010, 7, 47-49.	19.0	112
105	Single-molecule decoding of combinatorially modified nucleosomes. Science, 2016, 352, 717-721.	12.6	112
106	A Multiplexed System for Quantitative Comparisons of Chromatin Landscapes. Molecular Cell, 2016, 61, 170-180.	9.7	111
107	EZH2 Codon 641 Mutations are Common in BCL2-Rearranged Germinal Center B Cell Lymphomas. PLoS ONE, 2011, 6, e28585.	2.5	109
108	Detection of Enhancer-Associated Rearrangements Reveals Mechanisms of Oncogene Dysregulation in B-cell Lymphoma. Cancer Discovery, 2015, 5, 1058-1071.	9.4	105

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109	Development and validation of a T7 based linear amplification for genomic DNA. BMC Genomics, 2003, 4, 19.	2.8	102
110	Wilms Tumor Chromatin Profiles Highlight Stem Cell Properties and a Renal Developmental Network. Cell Stem Cell, 2010, 6, 591-602.	11.1	80
111	Chromatin state maps: new technologies, new insights. Current Opinion in Genetics and Development, 2008, 18, 109-115.	3.3	77
112	EHMT1 and EHMT2 inhibition induces fetal hemoglobin expression. Blood, 2015, 126, 1930-1939.	1.4	76
113	Epithelial-to-Mesenchymal Transition Antagonizes Response to Targeted Therapies in Lung Cancer by Suppressing BIM. Clinical Cancer Research, 2018, 24, 197-208.	7.0	74
114	High Seroprevalence of Anti-SARS-CoV-2 Antibodies in Chelsea, Massachusetts. Journal of Infectious Diseases, 2020, 222, 1955-1959.	4.0	72
115	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. Molecular and Cellular Biology, 2011, 31, 351-364.	2.3	68
116	A B Cell Regulome Links Notch to Downstream Oncogenic Pathways in Small B Cell Lymphomas. Cell Reports, 2017, 21, 784-797.	6.4	65
117	Rpd3p Relocation Mediates a Transcriptional Response to Rapamycin in Yeast. Chemistry and Biology, 2004, 11, 295-299.	6.0	64
118	High-Throughput Single-Cell Labeling (Hi-SCL) for RNA-Seq Using Drop-Based Microfluidics. PLoS ONE, 2015, 10, e0116328.	2.5	64
119	Tissue-specific SMARCA4 binding at active and repressed regulatory elements during embryogenesis. Genome Research, 2014, 24, 920-929.	5.5	63
120	Corrupted coordination of epigenetic modifications leads to diverging chromatin states and transcriptional heterogeneity in CLL. Nature Communications, 2019, 10, 1874.	12.8	63
121	Single-cell lineage analysis reveals genetic and epigenetic interplay in glioblastoma drug resistance. Genome Biology, 2020, 21, 174.	8.8	59
122	Digital transcriptome profiling from attomole-level RNA samples. Genome Research, 2010, 20, 519-525.	5.5	56
123	Epigenome editing strategies for the functional annotation of CTCF insulators. Nature Communications, 2019, 10, 4258.	12.8	55
124	RBPJ maintains brain tumorâ€“initiating cells through CDK9-mediated transcriptional elongation. Journal of Clinical Investigation, 2016, 126, 2757-2772.	8.2	52
125	Pluripotent Chromatin State. Science, 2009, 323, 220-221.	12.6	50
126	Genetic Events That Shape the Cancer Epigenome. Science, 2012, 336, 1513-1514.	12.6	50

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127	In silico abstraction of zinc finger nuclease cleavage profiles reveals an expanded landscape of off-target sites. Nucleic Acids Research, 2013, 41, e181-e181.	14.5	47
128	A bisubstrate analog induces unexpected conformational changes in phosphoglycerate kinase from Trypanosoma brucei. Journal of Molecular Biology, 1998, 279, 1137-1148.	4.2	45
129	Data-Driven Polymer Model for Mechanistic Exploration of Diploid Genome Organization. Biophysical Journal, 2020, 119, 1905-1916.	0.5	45
130	Mitochondrial variant enrichment from high-throughput single-cell RNA sequencing resolves clonal populations. Nature Biotechnology, 2022, 40, 1030-1034.	17.5	45
131	Gain-of-Function Genetic Alterations of G9a Drive Oncogenesis. Cancer Discovery, 2020, 10, 980-997.	9.4	44
132	Immunohistochemical quantification of partial-EMT in oral cavity squamous cell carcinoma primary tumors is associated with nodal metastasis. Oral Oncology, 2019, 99, 104458.	1.5	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. Nature Cell Biology, 2019, 21, 1449-1461.	10.3	40
134	The Use of Chromatin Immunoprecipitation Assays in Genome-Wide Analyses of Histone Modifications. Methods in Enzymology, 2003, 376, 349-360.	1.0	37
135	Single-cell RNA-seq reveals developmental plasticity with coexisting oncogenic states and immune evasion programs in ETP-ALL. Blood, 2021, 137, 2463-2480.	1.4	35
136	Genomic views of chromatin. Current Opinion in Genetics and Development, 2005, 15, 476-481.	3.3	32
137	Chromatin accessibility promotes hematopoietic and leukemia stem cell activity. Nature Communications, 2020, 11, 1406.	12.8	32
138	Extended-representation bisulfite sequencing of gene regulatory elements in multiplexed samples and single cells. Nature Biotechnology, 2021, 39, 1086-1094.	17.5	28
139	Reply to Brunet and Doolittle: Both selected effect and causal role elements can influence human biology and disease. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3366.	7.1	25
140	A Blueprint for an International Cancer Epigenome Consortium. A Report from the AACR Cancer Epigenome Task Force. Cancer Research, 2012, 72, 6319-6324.	0.9	22
141	A Tell-Tail Sign of Chromatin: Histone Mutations Drive Pediatric Glioblastoma. Cancer Cell, 2012, 21, 329-331.	16.8	19
142	The importance of dynamic light scattering in obtaining multiple crystal forms of trypanosoma brucei PGK. Protein Science, 1998, 7, 504-507.	7.6	18
143	Global Approaches to Chromatin. Chemistry and Biology, 2002, 9, 1167-1173.	6.0	17
144	Parallel Single-Cell RNA-Seq and Genetic Recording Reveals Lineage Decisions in Developing Embryoid Bodies. Cell Reports, 2020, 33, 108222.	6.4	16

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145	Sequence-Specific DNA Recognition by Cys2, His2Zinc Fingers. Annals of the New York Academy of Sciences, 1994, 726, 92-104.	3.8	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. Leukemia, 2019, 33, 2061-2077.	7.2	13
147	Detecting sample swaps in diverse NGS data types using linkage disequilibrium. Nature Communications, 2020, 11, 3697.	12.8	12
148	Epigenetic Alterations in Keratinocyte Carcinoma. Journal of Investigative Dermatology, 2021, 141, 1207-1218.	0.7	9
149	Systematic detection of m6A-modified transcripts at single-molecule and single-cell resolution. Cell Reports Methods, 2021, 1, 100061.	2.9	8
150	142â€ƒGenetic and Nongenetic Determinants of Cellular Architecture in IDH1-Mutant Oligodendrogliomas and Astrocytomas Using Single-Cell Transcriptome Analysis. Neurosurgery, 2016, 63, 158.	1.1	4
151	ASXL1 Mutations Promote Myeloid Transformation Through Inhibition of PRC2-Mediated Gene Repression. Blood, 2011, 118, 405-405.	1.4	4
152	HOXA9 Is a Novel Therapeutic Target in Multiple Myeloma.. Blood, 2009, 114, 832-832.	1.4	2
153	Notch-Regulated Enhancers in B-Cell Lymphoma Activate MYC and Potentiate B-Cell Receptor Signaling. Blood, 2016, 128, 457-457.	1.4	2
154	Heterodimeric JAK-STAT Activation As a Mechanism of Persistence to JAK2 Inhibitor Therapy. Blood, 2011, 118, 122-122.	1.4	1
155	MBRS-28. SINGLE-CELL TRANSCRIPTOME ANALYSIS OF MEDULLOBLASTOMA. Neuro-Oncology, 2018, 20, i134-i134.	1.2	0
156	GABPÎ²1L Wakes Up TERT. Cancer Cell, 2018, 34, 358-360.	16.8	0
157	Development of ERG-Enhancer Fluorescent Reporter System to Decipher Functional Heterogeneity in Leukemia. Experimental Hematology, 2018, 64, S87.	0.4	0
158	Conditional Deletion of Asxl1 Results in Myelodysplasia. Blood, 2012, 120, 308-308.	1.4	0
159	Alternative Super-Enhancer States Determine MYC Sensitivity to Notch and Brd4 Inhibitors in T Lymphoblastic Leukemia/Lymphoma. Blood, 2014, 124, 863-863.	1.4	0
160	Characterizing Transcriptional and Epigenetic Signatures Induced By FLT3-ITD Activation. Blood, 2014, 124, 2186-2186.	1.4	0
161	Single-Cell RNA-Seq Reveals AML Cellular Hierarchies Relevant to Clinical Outcomes and Immunity. Blood, 2018, 132, 542-542.	1.4	0
162	Single Cell RNA-Seq Reveals Deranged Developmental Hierarchy with Coexisting Oncogenic States and Immune Evasion Programs in ETP T-ALL. Blood, 2019, 134, 3953-3953.	1.4	0

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163	ETMR-17. SINGLE-CELL TRANSCRIPTOME ANALYSIS OF ETMR PATIENT SAMPLES. Neuro-Oncology, 2020, 22, iii326-iii326.	1.2	0