

Bradley E Bernstein

List of Publications by Year in descending order

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163
papers

104,406
citations

1994

101
h-index

6471

157
g-index

171
all docs

171
docs citations

171
times ranked

105783
citing authors

#	ARTICLE	IF	CITATIONS
1	Mitochondrial variant enrichment from high-throughput single-cell RNA sequencing resolves clonal populations. <i>Nature Biotechnology</i> , 2022, 40, 1030-1034.	17.5	45
2	Epigenetic Alterations in Keratinocyte Carcinoma. <i>Journal of Investigative Dermatology</i> , 2021, 141, 1207-1218.	0.7	9
3	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.	1.4	35
4	Genome-wide programmable transcriptional memory by CRISPR-based epigenome editing. <i>Cell</i> , 2021, 184, 2503-2519.e17.	28.9	312
5	Extended-representation bisulfite sequencing of gene regulatory elements in multiplexed samples and single cells. <i>Nature Biotechnology</i> , 2021, 39, 1086-1094.	17.5	28
6	Epigenetic silencing by SETDB1 suppresses tumour intrinsic immunogenicity. <i>Nature</i> , 2021, 595, 309-314.	27.8	181
7	Systematic detection of m6A-modified transcripts at single-molecule and single-cell resolution. <i>Cell Reports Methods</i> , 2021, 1, 100061.	2.9	8
8	Parallel Single-Cell RNA-Seq and Genetic Recording Reveals Lineage Decisions in Developing Embryoid Bodies. <i>Cell Reports</i> , 2020, 33, 108222.	6.4	16
9	Single-cell lineage analysis reveals genetic and epigenetic interplay in glioblastoma drug resistance. <i>Genome Biology</i> , 2020, 21, 174.	8.8	59
10	Detecting sample swaps in diverse NGS data types using linkage disequilibrium. <i>Nature Communications</i> , 2020, 11, 3697.	12.8	12
11	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	27.8	123
12	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	27.8	1,252
13	Large-Scale Topological Changes Restrain Malignant Progression in Colorectal Cancer. <i>Cell</i> , 2020, 182, 1474-1489.e23.	28.9	126
14	Evaluation of SARS-CoV-2 serology assays reveals a range of test performance. <i>Nature Biotechnology</i> , 2020, 38, 1174-1183.	17.5	251
15	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.	0.5	117
16	High Seroprevalence of Anti-SARS-CoV-2 Antibodies in Chelsea, Massachusetts. <i>Journal of Infectious Diseases</i> , 2020, 222, 1955-1959.	4.0	72
17	Data-Driven Polymer Model for Mechanistic Exploration of Diploid Genome Organization. <i>Biophysical Journal</i> , 2020, 119, 1905-1916.	0.5	45
18	Chromatin accessibility promotes hematopoietic and leukemia stem cell activity. <i>Nature Communications</i> , 2020, 11, 1406.	12.8	32

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19	Gain-of-Function Genetic Alterations of G9a Drive Oncogenesis. <i>Cancer Discovery</i> , 2020, 10, 980-997.	9.4	44
20	ETMR-17. SINGLE-CELL TRANSCRIPTOME ANALYSIS OF ETMR PATIENT SAMPLES. <i>Neuro-Oncology</i> , 2020, 22, iii326-iii326.	1.2	0
21	An Integrative Model of Cellular States, Plasticity, and Genetics for Glioblastoma. <i>Cell</i> , 2019, 178, 835-849.e21.	28.9	1,408
22	Resolving medulloblastoma cellular architecture by single-cell genomics. <i>Nature</i> , 2019, 572, 74-79.	27.8	273
23	Enhancer signatures stratify and predict outcomes of non-functional pancreatic neuroendocrine tumors. <i>Nature Medicine</i> , 2019, 25, 1260-1265.	30.7	120
24	Re-programing Chromatin with a Bifunctional LSD1/HDAC Inhibitor Induces Therapeutic Differentiation in DIPG. <i>Cancer Cell</i> , 2019, 36, 528-544.e10.	16.8	128
25	Altered chromosomal topology drives oncogenic programs in SDH-deficient GISTs. <i>Nature</i> , 2019, 575, 229-233.	27.8	164
26	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.	1.5	43
27	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.	10.3	40
28	Epigenome editing strategies for the functional annotation of CTCF insulators. <i>Nature Communications</i> , 2019, 10, 4258.	12.8	55
29	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.	7.2	13
30	Corrupted coordination of epigenetic modifications leads to diverging chromatin states and transcriptional heterogeneity in CLL. <i>Nature Communications</i> , 2019, 10, 1874.	12.8	63
31	Single-Cell RNA-Seq Reveals AML Hierarchies Relevant to Disease Progression and Immunity. <i>Cell</i> , 2019, 176, 1265-1281.e24.	28.9	642
32	Single-cell and single-molecule epigenomics to uncover genome regulation at unprecedented resolution. <i>Nature Genetics</i> , 2019, 51, 19-25.	21.4	151
33	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.	14.8	188
34	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.	1.4	0
35	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. <i>Science</i> , 2018, 360, 331-335.	12.6	461
36	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. <i>Nature Genetics</i> , 2018, 50, 621-629.	21.4	807

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37	Orthologous CRISPR-Cas9 enzymes for combinatorial genetic screens. <i>Nature Biotechnology</i> , 2018, 36, 179-189.	17.5	216
38	Epithelial-to-Mesenchymal Transition Antagonizes Response to Targeted Therapies in Lung Cancer by Suppressing BIM. <i>Clinical Cancer Research</i> , 2018, 24, 197-208.	7.0	74
39	Dual Targeting of Oncogenic Activation and Inflammatory Signaling Increases Therapeutic Efficacy in Myeloproliferative Neoplasms. <i>Cancer Cell</i> , 2018, 33, 29-43.e7.	16.8	186
40	Transaminase Inhibition by 2-Hydroxyglutarate Impairs Glutamate Biosynthesis and Redox Homeostasis in Glioma. <i>Cell</i> , 2018, 175, 101-116.e25.	28.9	234
41	MBRS-28. SINGLE-CELL TRANSCRIPTOME ANALYSIS OF MEDULLOBLASTOMA. <i>Neuro-Oncology</i> , 2018, 20, i134-i134.	1.2	0
42	GABP ² L Wakes Up TERT. <i>Cancer Cell</i> , 2018, 34, 358-360.	16.8	0
43	Development of ERG-Enhancer Fluorescent Reporter System to Decipher Functional Heterogeneity in Leukemia. <i>Experimental Hematology</i> , 2018, 64, S87.	0.4	0
44	Unravelling subclonal heterogeneity and aggressive disease states in TNBC through single-cell RNA-seq. <i>Nature Communications</i> , 2018, 9, 3588.	12.8	342
45	Single-Cell RNA-Seq Reveals AML Cellular Hierarchies Relevant to Clinical Outcomes and Immunity. <i>Blood</i> , 2018, 132, 542-542.	1.4	0
46	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.	7.1	150
47	Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. <i>Science</i> , 2017, 355, .	12.6	743
48	SMARCB1-mediated SWI/SNF complex function is essential for enhancer regulation. <i>Nature Genetics</i> , 2017, 49, 289-295.	21.4	268
49	Adaptive Chromatin Remodeling Drives Glioblastoma Stem Cell Plasticity and Drug Tolerance. <i>Cell Stem Cell</i> , 2017, 20, 233-246.e7.	11.1	387
50	Cohesin Loss Eliminates All Loop Domains. <i>Cell</i> , 2017, 171, 305-320.e24.	28.9	1,454
51	A B Cell Regulome Links Notch to Downstream Oncogenic Pathways in Small B Cell Lymphomas. <i>Cell Reports</i> , 2017, 21, 784-797.	6.4	65
52	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.	28.9	356
53	Epigenetic plasticity and the hallmarks of cancer. <i>Science</i> , 2017, 357, .	12.6	920
54	Single-Cell Transcriptomic Analysis of Primary and Metastatic Tumor Ecosystems in Head and Neck Cancer. <i>Cell</i> , 2017, 171, 1611-1624.e24.	28.9	1,656

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55	Transcription elongation factors represent in vivo cancer dependencies in glioblastoma. <i>Nature</i> , 2017, 547, 355-359.	27.8	156
56	Single-molecule decoding of combinatorially modified nucleosomes. <i>Science</i> , 2016, 352, 717-721.	12.6	112
57	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	28.9	404
58	Single-cell RNA-seq supports a developmental hierarchy in human oligodendrogloma. <i>Nature</i> , 2016, 539, 309-313.	27.8	875
59	142 Genetic and Nongenetic Determinants of Cellular Architecture in IDH1-Mutant Oligodendrogliomas and Astrocytomas Using Single-Cell Transcriptome Analysis. <i>Neurosurgery</i> , 2016, 63, 158.	1.1	4
60	Widespread RNA binding by chromatin-associated proteins. <i>Genome Biology</i> , 2016, 17, 28.	8.8	197
61	A Multiplexed System for Quantitative Comparisons of Chromatin Landscapes. <i>Molecular Cell</i> , 2016, 61, 170-180.	9.7	111
62	An oncogenic MYB feedback loop drives alternate cell fates in adenoid cystic carcinoma. <i>Nature Genetics</i> , 2016, 48, 265-272.	21.4	216
63	Insulator dysfunction and oncogene activation in IDH mutant gliomas. <i>Nature</i> , 2016, 529, 110-114.	27.8	1,048
64	RBPJ maintains brain tumor-initiating cells through CDK9-mediated transcriptional elongation. <i>Journal of Clinical Investigation</i> , 2016, 126, 2757-2772.	8.2	52
65	Notch-Regulated Enhancers in B-Cell Lymphoma Activate MYC and Potentiate B-Cell Receptor Signaling. <i>Blood</i> , 2016, 128, 457-457.	1.4	2
66	EHMT1 and EHMT2 inhibition induces fetal hemoglobin expression. <i>Blood</i> , 2015, 126, 1930-1939.	1.4	76
67	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	27.8	5,653
68	Th17 cells transdifferentiate into regulatory T cells during resolution of inflammation. <i>Nature</i> , 2015, 523, 221-225.	27.8	653
69	Detection of Enhancer-Associated Rearrangements Reveals Mechanisms of Oncogene Dysregulation in B-cell Lymphoma. <i>Cancer Discovery</i> , 2015, 5, 1058-1071.	9.4	105
70	Single-cell ChIP-seq reveals cell subpopulations defined by chromatin state. <i>Nature Biotechnology</i> , 2015, 33, 1165-1172.	17.5	748
71	Dissecting neural differentiation regulatory networks through epigenetic footprinting. <i>Nature</i> , 2015, 518, 355-359.	27.8	172
72	Genetic and epigenetic fine mapping of causal autoimmune disease variants. <i>Nature</i> , 2015, 518, 337-343.	27.8	1,669

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73	High-Throughput Single-Cell Labeling (Hi-SCL) for RNA-Seq Using Drop-Based Microfluidics. <i>PLoS ONE</i> , 2015, 10, e0116328.	2.5	64
74	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.	7.1	635
75	An epigenetic mechanism of resistance to targeted therapy in T cell acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2014, 46, 364-370.	21.4	333
76	Tissue-specific SMARCA4 binding at active and repressed regulatory elements during embryogenesis. <i>Genome Research</i> , 2014, 24, 920-929.	5.5	63
77	Reconstructing and Reprogramming the Tumor-Propagating Potential of Glioblastoma Stem-like Cells. <i>Cell</i> , 2014, 157, 580-594.	28.9	751
78	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.	7.1	151
79	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.	16.8	334
80	Comparative analysis of metazoan chromatin organization. <i>Nature</i> , 2014, 512, 449-452.	27.8	363
81	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.	7.1	25
82	Alzheimer's disease: early alterations in brain DNA methylation at ANK1, BIN1, RHBDF2 and other loci. <i>Nature Neuroscience</i> , 2014, 17, 1156-1163.	14.8	800
83	Discovery of Biomarkers Predictive of GSI Response in Triple-Negative Breast Cancer and Adenoid Cystic Carcinoma. <i>Cancer Discovery</i> , 2014, 4, 1154-1167.	9.4	123
84	Single-cell RNA-seq highlights intratumoral heterogeneity in primary glioblastoma. <i>Science</i> , 2014, 344, 1396-1401.	12.6	3,648
85	Alternative Super-Enhancer States Determine MYC Sensitivity to Notch and Brd4 Inhibitors in T Lymphoblastic Leukemia/Lymphoma. <i>Blood</i> , 2014, 124, 863-863.	1.4	0
86	Characterizing Transcriptional and Epigenetic Signatures Induced By FLT3-ITD Activation. <i>Blood</i> , 2014, 124, 2186-2186.	1.4	0
87	Charting a dynamic DNA methylation landscape of the human genome. <i>Nature</i> , 2013, 500, 477-481.	27.8	1,168
88	An Aberrant Transcription Factor Network Essential for Wnt Signaling and Stem Cell Maintenance in Glioblastoma. <i>Cell Reports</i> , 2013, 3, 1567-1579.	6.4	236
89	SAM Domain Polymerization Links Subnuclear Clustering of PRC1 to Gene Silencing. <i>Developmental Cell</i> , 2013, 26, 565-577.	7.0	271
90	Targeted DNA demethylation and activation of endogenous genes using programmable TALE-TET1 fusion proteins. <i>Nature Biotechnology</i> , 2013, 31, 1137-1142.	17.5	433

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91	Epigenetic Reprogramming in Cancer. <i>Science</i> , 2013, 339, 1567-1570.	12.6	629
92	Locus-specific editing of histone modifications at endogenous enhancers. <i>Nature Biotechnology</i> , 2013, 31, 1133-1136.	17.5	339
93	Genome-wide Chromatin State Transitions Associated with Developmental and Environmental Cues. <i>Cell</i> , 2013, 152, 642-654.	28.9	473
94	Transcriptional and Epigenetic Dynamics during Specification of Human Embryonic Stem Cells. <i>Cell</i> , 2013, 153, 1149-1163.	28.9	419
95	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.	14.5	47
96	Deletion of <i>Asx1</i> results in myelodysplasia and severe developmental defects in vivo. <i>Journal of Experimental Medicine</i> , 2013, 210, 2641-2659.	8.5	278
97	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.	3.5	233
98	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.	0.9	22
99	ASXL1 Mutations Promote Myeloid Transformation through Loss of PRC2-Mediated Gene Repression. <i>Cancer Cell</i> , 2012, 22, 180-193.	16.8	504
100	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.	5.9	158
101	The Histone Deacetylase SIRT6 Is a Tumor Suppressor that Controls Cancer Metabolism. <i>Cell</i> , 2012, 151, 1185-1199.	28.9	561
102	H2A.Z landscapes and dual modifications in pluripotent and multipotent stem cells underlie complex genome regulatory functions. <i>Genome Biology</i> , 2012, 13, R85.	9.6	166
103	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , 2012, 22, 1813-1831.	5.5	1,708
104	A High-Throughput Chromatin Immunoprecipitation Approach Reveals Principles of Dynamic Gene Regulation in Mammals. <i>Molecular Cell</i> , 2012, 47, 810-822.	9.7	375
105	DNA Sequence-Dependent Compartmentalization and Silencing of Chromatin at the Nuclear Lamina. <i>Cell</i> , 2012, 149, 1474-1487.	28.9	405
106	Heterodimeric JAK-STAT activation as a mechanism of persistence to JAK2 inhibitor therapy. <i>Nature</i> , 2012, 489, 155-159.	27.8	320
107	Genetic Events That Shape the Cancer Epigenome. <i>Science</i> , 2012, 336, 1513-1514.	12.6	50
108	A Tell-Tail Sign of Chromatin: Histone Mutations Drive Pediatric Glioblastoma. <i>Cancer Cell</i> , 2012, 21, 329-331.	16.8	19

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109	Conditional Deletion of <i>Asx1</i> Results in Myelodysplasia. <i>Blood</i> , 2012, 120, 308-308.	1.4	0
110	Role for Dpy-30 in ES Cell-Fate Specification by Regulation of H3K4 Methylation within Bivalent Domains. <i>Cell</i> , 2011, 144, 513-525.	28.9	282
111	Combinatorial Patterning of Chromatin Regulators Uncovered by Genome-wide Location Analysis in Human Cells. <i>Cell</i> , 2011, 147, 1628-1639.	28.9	303
112	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.	7.1	180
113	Reprogramming Factor Expression Initiates Widespread Targeted Chromatin Remodeling. <i>Cell Stem Cell</i> , 2011, 8, 96-105.	11.1	345
114	Charting histone modifications and the functional organization of mammalian genomes. <i>Nature Reviews Genetics</i> , 2011, 12, 7-18.	16.3	1,019
115	Initial genome sequencing and analysis of multiple myeloma. <i>Nature</i> , 2011, 471, 467-472.	27.8	1,288
116	Mapping and analysis of chromatin state dynamics in nine human cell types. <i>Nature</i> , 2011, 473, 43-49.	27.8	2,630
117	Whole-genome chromatin profiling from limited numbers of cells using nano-ChIP-seq. <i>Nature Protocols</i> , 2011, 6, 1656-1668.	12.0	186
118	Genomic Distribution and Inter-Sample Variation of Non-CpG Methylation across Human Cell Types. <i>PLoS Genetics</i> , 2011, 7, e1002389.	3.5	345
119	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. <i>Molecular and Cellular Biology</i> , 2011, 31, 351-364.	2.3	68
120	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.	7.1	221
121	Heterodimeric JAK-STAT Activation As a Mechanism of Persistence to JAK2 Inhibitor Therapy. <i>Blood</i> , 2011, 118, 122-122.	1.4	1
122	ASXL1 Mutations Promote Myeloid Transformation Through Inhibition of PRC2-Mediated Gene Repression. <i>Blood</i> , 2011, 118, 405-405.	1.4	4
123	EZH2 Codon 641 Mutations are Common in BCL2-Rearranged Germinal Center B Cell Lymphomas. <i>PLoS ONE</i> , 2011, 6, e28585.	2.5	109
124	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. <i>Nature Biotechnology</i> , 2010, 28, 1097-1105.	17.5	647
125	The NIH Roadmap Epigenomics Mapping Consortium. <i>Nature Biotechnology</i> , 2010, 28, 1045-1048.	17.5	1,705
126	Chromatin profiling by directly sequencing small quantities of immunoprecipitated DNA. <i>Nature Methods</i> , 2010, 7, 47-49.	19.0	112

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127	Genome-wide chromatin maps derived from limited numbers of hematopoietic progenitors. <i>Nature Methods</i> , 2010, 7, 615-618.	19.0	152
128	Jarid2 and PRC2, partners in regulating gene expression. <i>Genes and Development</i> , 2010, 24, 368-380.	5.9	434
129	Digital transcriptome profiling from attomole-level RNA samples. <i>Genome Research</i> , 2010, 20, 519-525.	5.5	56
130	GC-Rich Sequence Elements Recruit PRC2 in Mammalian ES Cells. <i>PLoS Genetics</i> , 2010, 6, e1001244.	3.5	368
131	Wilms Tumor Chromatin Profiles Highlight Stem Cell Properties and a Renal Developmental Network. <i>Cell Stem Cell</i> , 2010, 6, 591-602.	11.1	80
132	Unbiased Reconstruction of a Mammalian Transcriptional Network Mediating Pathogen Responses. <i>Science</i> , 2009, 326, 257-263.	12.6	473
133	Pluripotent Chromatin State. <i>Science</i> , 2009, 323, 220-221.	12.6	50
134	Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals. <i>Nature</i> , 2009, 458, 223-227.	27.8	3,801
135	Comprehensive Mapping of Long-Range Interactions Reveals Folding Principles of the Human Genome. <i>Science</i> , 2009, 326, 289-293.	12.6	7,170
136	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.	7.1	2,709
137	Insights into GATA-1-Mediated Gene Activation versus Repression via Genome-wide Chromatin Occupancy Analysis. <i>Molecular Cell</i> , 2009, 36, 682-695.	9.7	278
138	HOXA9 Is a Novel Therapeutic Target in Multiple Myeloma.. <i>Blood</i> , 2009, 114, 832-832.	1.4	2
139	Dissecting direct reprogramming through integrative genomic analysis. <i>Nature</i> , 2008, 454, 49-55.	27.8	1,344
140	Genome-scale DNA methylation maps of pluripotent and differentiated cells. <i>Nature</i> , 2008, 454, 766-770.	27.8	2,267
141	Model-based Analysis of ChIP-Seq (MACS). <i>Genome Biology</i> , 2008, 9, R137.	9.6	13,517
142	Chromatin state maps: new technologies, new insights. <i>Current Opinion in Genetics and Development</i> , 2008, 18, 109-115.	3.3	77
143	Genomewide Analysis of PRC1 and PRC2 Occupancy Identifies Two Classes of Bivalent Domains. <i>PLoS Genetics</i> , 2008, 4, e1000242.	3.5	878
144	The Mammalian Epigenome. <i>Cell</i> , 2007, 128, 669-681.	28.9	1,909

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145	In vitro reprogramming of fibroblasts into a pluripotent ES-cell-like state. <i>Nature</i> , 2007, 448, 318-324.	27.8	2,517
146	Genome-wide maps of chromatin state in pluripotent and lineage-committed cells. <i>Nature</i> , 2007, 448, 553-560.	27.8	3,733
147	A Bivalent Chromatin Structure Marks Key Developmental Genes in Embryonic Stem Cells. <i>Cell</i> , 2006, 125, 315-326.	28.9	4,773
148	Molecular regulation of H3K4 trimethylation by ASH2L, a shared subunit of MLL complexes. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 852-854.	8.2	288
149	Genomic views of chromatin. <i>Current Opinion in Genetics and Development</i> , 2005, 15, 476-481.	3.3	32
150	Genomic Maps and Comparative Analysis of Histone Modifications in Human and Mouse. <i>Cell</i> , 2005, 120, 169-181.	28.9	1,348
151	Rpd3p Relocation Mediates a Transcriptional Response to Rapamycin in Yeast. <i>Chemistry and Biology</i> , 2004, 11, 295-299.	6.0	64
152	Global nucleosome occupancy in yeast. <i>Genome Biology</i> , 2004, 5, R62.	9.6	309
153	Development and validation of a T7 based linear amplification for genomic DNA. <i>BMC Genomics</i> , 2003, 4, 19.	2.8	102
154	The Use of Chromatin Immunoprecipitation Assays in Genome-Wide Analyses of Histone Modifications. <i>Methods in Enzymology</i> , 2003, 376, 349-360.	1.0	37
155	Methylation of Histone H3 K4 Mediates Association of the Isw1p ATPase with Chromatin. <i>Molecular Cell</i> , 2003, 12, 1325-1332.	9.7	248
156	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.	7.1	673
157	Signaling Network Model of Chromatin. <i>Cell</i> , 2002, 111, 771-778.	28.9	353
158	Active genes are tri-methylated at K4 of histone H3. <i>Nature</i> , 2002, 419, 407-411.	27.8	1,871
159	Global Approaches to Chromatin. <i>Chemistry and Biology</i> , 2002, 9, 1167-1173.	6.0	17
160	The importance of dynamic light scattering in obtaining multiple crystal forms of trypanosoma brucei PGK. <i>Protein Science</i> , 1998, 7, 504-507.	7.6	18
161	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.	4.2	45
162	Synergistic effects of substrate-induced conformational changes in phosphoglycerate kinase activation. <i>Nature</i> , 1997, 385, 275-278.	27.8	197

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163	Sequence-Specific DNA Recognition by Cys2, His2Zinc Fingers. Annals of the New York Academy of Sciences, 1994, 726, 92-104.	3.8	13