

Richard A Young

List of Publications by Year in descending order

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266
papers

106,683
citations

¹⁹⁶
149
h-index

⁵³⁸
265
g-index

278
all docs

278
docs citations

278
times ranked

85399
citing authors

#	ARTICLE	IF	CITATIONS
1	Core Transcriptional Regulatory Circuitry in Human Embryonic Stem Cells. <i>Cell</i> , 2005, 122, 947-956.	13.5	4,000
2	Histone H3K27ac separates active from poised enhancers and predicts developmental state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21931-21936.	3.3	3,446
3	Master Transcription Factors and Mediator Establish Super-Enhancers at Key Cell Identity Genes. <i>Cell</i> , 2013, 153, 307-319.	13.5	3,202
4	Super-Enhancers in the Control of Cell Identity and Disease. <i>Cell</i> , 2013, 155, 934-947.	13.5	2,916
5	Transcriptional Regulatory Networks in <i>Saccharomyces cerevisiae</i> . <i>Science</i> , 2002, 298, 799-804.	6.0	2,706
6	BET Bromodomain Inhibition as a Therapeutic Strategy to Target c-Myc. <i>Cell</i> , 2011, 146, 904-917.	13.5	2,432
7	Selective Inhibition of Tumor Oncogenes by Disruption of Super-Enhancers. <i>Cell</i> , 2013, 153, 320-334.	13.5	2,366
8	Polycomb complexes repress developmental regulators in murine embryonic stem cells. <i>Nature</i> , 2006, 441, 349-353.	13.7	2,273
9	Control of Developmental Regulators by Polycomb in Human Embryonic Stem Cells. <i>Cell</i> , 2006, 125, 301-313.	13.5	2,059
10	Transcriptional regulatory code of a eukaryotic genome. <i>Nature</i> , 2004, 431, 99-104.	13.7	1,969
11	Genome-Wide Location and Function of DNA Binding Proteins. <i>Science</i> , 2000, 290, 2306-2309.	6.0	1,826
12	A Chromatin Landmark and Transcription Initiation at Most Promoters in Human Cells. <i>Cell</i> , 2007, 130, 77-88.	13.5	1,725
13	Dissecting the Regulatory Circuitry of a Eukaryotic Genome. <i>Cell</i> , 1998, 95, 717-728.	13.5	1,722
14	Mediator and cohesin connect gene expression and chromatin architecture. <i>Nature</i> , 2010, 467, 430-435.	13.7	1,707
15	Coactivator condensation at super-enhancers links phase separation and gene control. <i>Science</i> , 2018, 361, .	6.0	1,687
16	A Phase Separation Model for Transcriptional Control. <i>Cell</i> , 2017, 169, 13-23.	13.5	1,341
17	Connecting microRNA Genes to the Core Transcriptional Regulatory Circuitry of Embryonic Stem Cells. <i>Cell</i> , 2008, 134, 521-533.	13.5	1,332
18	Transcriptional Amplification in Tumor Cells with Elevated c-Myc. <i>Cell</i> , 2012, 151, 56-67.	13.5	1,262

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19	Stem Cells, the Molecular Circuitry of Pluripotency and Nuclear Reprogramming. <i>Cell</i> , 2008, 132, 567-582.	13.5	1,251
20	Genome-wide Map of Nucleosome Acetylation and Methylation in Yeast. <i>Cell</i> , 2005, 122, 517-527.	13.5	1,242
21	Remodeling of Yeast Genome Expression in Response to Environmental Changes. <i>Molecular Biology of the Cell</i> , 2001, 12, 323-337.	0.9	1,206
22	Transcriptional Regulation and Its Misregulation in Disease. <i>Cell</i> , 2013, 152, 1237-1251.	13.5	1,205
23	Control of Pancreas and Liver Gene Expression by HNF Transcription Factors. <i>Science</i> , 2004, 303, 1378-1381.	6.0	1,202
24	Transcription Factors Activate Genes through the Phase-Separation Capacity of Their Activation Domains. <i>Cell</i> , 2018, 175, 1842-1855.e16.	13.5	1,195
25	c-Myc Regulates Transcriptional Pause Release. <i>Cell</i> , 2010, 141, 432-445.	13.5	1,104
26	Control of the Embryonic Stem Cell State. <i>Cell</i> , 2011, 144, 940-954.	13.5	1,050
27	E2F integrates cell cycle progression with DNA repair, replication, and G2/M checkpoints. <i>Genes and Development</i> , 2002, 16, 245-256.	2.7	1,002
28	Targeted Recruitment of Set1 Histone Methylase by Elongating Pol II Provides a Localized Mark and Memory of Recent Transcriptional Activity. <i>Molecular Cell</i> , 2003, 11, 709-719.	4.5	961
29	Editing DNA Methylation in the Mammalian Genome. <i>Cell</i> , 2016, 167, 233-247.e17.	13.5	932
30	Activation of proto-oncogenes by disruption of chromosome neighborhoods. <i>Science</i> , 2016, 351, 1454-1458.	6.0	880
31	Genome-wide analysis of cAMP-response element binding protein occupancy, phosphorylation, and target gene activation in human tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4459-4464.	3.3	878
32	Densely Interconnected Transcriptional Circuits Control Cell States in Human Hematopoiesis. <i>Cell</i> , 2011, 144, 296-309.	13.5	843
33	Transcriptional Addiction in Cancer. <i>Cell</i> , 2017, 168, 629-643.	13.5	843
34	Divergent Transcription from Active Promoters. <i>Science</i> , 2008, 322, 1849-1851.	6.0	801
35	Control of Cell Identity Genes Occurs in Insulated Neighborhoods in Mammalian Chromosomes. <i>Cell</i> , 2014, 159, 374-387.	13.5	793
36	Poised Chromatin at the ZEB1 Promoter Enables Breast Cancer Cell Plasticity and Enhances Tumorigenicity. <i>Cell</i> , 2013, 154, 61-74.	13.5	753

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37	YY1 Is a Structural Regulator of Enhancer-Promoter Loops. <i>Cell</i> , 2017, 171, 1573-1588.e28.	13.5	749
38	NOTCH1 directly regulates c-MYC and activates a feed-forward-loop transcriptional network promoting leukemic cell growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 18261-18266.	3.3	745
39	The Plasticity of Dendritic Cell Responses to Pathogens and Their Components. <i>Science</i> , 2001, 294, 870-875.	6.0	730
40	Transcription of Eukaryotic Protein-Coding Genes. <i>Annual Review of Genetics</i> , 2000, 34, 77-137.	3.2	719
41	Systematic Identification of Culture Conditions for Induction and Maintenance of Naive Human Pluripotency. <i>Cell Stem Cell</i> , 2014, 15, 471-487.	5.2	702
42	Targeting transcription regulation in cancer with a covalent CDK7 inhibitor. <i>Nature</i> , 2014, 511, 616-620.	13.7	698
43	Chromatin immunoprecipitation and microarray-based analysis of protein location. <i>Nature Protocols</i> , 2006, 1, 729-748.	5.5	671
44	RNA polymerase stalling at developmental control genes in the <i>Drosophila melanogaster</i> embryo. <i>Nature Genetics</i> , 2007, 39, 1512-1516.	9.4	671
45	An oncogenic super-enhancer formed through somatic mutation of a noncoding intergenic element. <i>Science</i> , 2014, 346, 1373-1377.	6.0	665
46	Foxp3 occupancy and regulation of key target genes during T-cell stimulation. <i>Nature</i> , 2007, 445, 931-935.	13.7	644
47	Human macrophage activation programs induced by bacterial pathogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 1503-1508.	3.3	639
48	Discovery and Characterization of Super-Enhancer-Associated Dependencies in Diffuse Large B Cell Lymphoma. <i>Cancer Cell</i> , 2013, 24, 777-790.	7.7	635
49	Serial Regulation of Transcriptional Regulators in the Yeast Cell Cycle. <i>Cell</i> , 2001, 106, 697-708.	13.5	604
50	An RNA polymerase II holoenzyme responsive to activators. <i>Nature</i> , 1994, 368, 466-469.	13.7	594
51	Insights into host responses against pathogens from transcriptional profiling. <i>Nature Reviews Microbiology</i> , 2005, 3, 281-294.	13.6	581
52	Master Transcription Factors Determine Cell-Type-Specific Responses to TGF- β Signaling. <i>Cell</i> , 2011, 147, 565-576.	13.5	536
53	Computational discovery of gene modules and regulatory networks. <i>Nature Biotechnology</i> , 2003, 21, 1337-1342.	9.4	528
54	Enhancer decommissioning by LSD1 during embryonic stem cell differentiation. <i>Nature</i> , 2012, 482, 221-225.	13.7	527

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55	Revisiting Global Gene Expression Analysis. <i>Cell</i> , 2012, 151, 476-482.	13.5	526
56	[35] Epitope tagging and protein surveillance. <i>Methods in Enzymology</i> , 1991, 194, 508-519.	0.4	514
57	Stress proteins, infection, and immune surveillance. <i>Cell</i> , 1989, 59, 5-8.	13.5	512
58	The histone methyltransferase SETDB1 is recurrently amplified in melanoma and accelerates its onset. <i>Nature</i> , 2011, 471, 513-517.	13.7	506
59	CDK7 Inhibition Suppresses Super-Enhancer-Linked Oncogenic Transcription in MYCN-Driven Cancer. <i>Cell</i> , 2014, 159, 1126-1139.	13.5	498
60	Response and resistance to BET bromodomain inhibitors in triple-negative breast cancer. <i>Nature</i> , 2016, 529, 413-417.	13.7	490
61	RNA Polymerase II. <i>Annual Review of Biochemistry</i> , 1991, 60, 689-715.	5.0	473
62	Stress Proteins and Immunology. <i>Annual Review of Immunology</i> , 1990, 8, 401-420.	9.5	469
63	Parkinson-associated risk variant in distal enhancer of α -synuclein modulates target gene expression. <i>Nature</i> , 2016, 533, 95-99.	13.7	466
64	A multisubunit complex associated with the RNA polymerase II CTD and TATA-binding protein in yeast. <i>Cell</i> , 1993, 73, 1361-1375.	13.5	457
65	Pol II phosphorylation regulates a switch between transcriptional and splicing condensates. <i>Nature</i> , 2019, 572, 543-548.	13.7	457
66	Evidence for an instructive mechanism of de novo methylation in cancer cells. <i>Nature Genetics</i> , 2006, 38, 149-153.	9.4	456
67	Tcf3 is an integral component of the core regulatory circuitry of embryonic stem cells. <i>Genes and Development</i> , 2008, 22, 746-755.	2.7	444
68	BRCA1 is a component of the RNA polymerase II holoenzyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 5605-5610.	3.3	433
69	A kinase-cyclin pair in the RNA polymerase II holoenzyme. <i>Nature</i> , 1995, 374, 193-196.	13.7	411
70	DHODH modulates transcriptional elongation in the neural crest and melanoma. <i>Nature</i> , 2011, 471, 518-522.	13.7	411
71	Divergent transcription of long noncoding RNA/mRNA gene pairs in embryonic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2876-2881.	3.3	409
72	Chromatin Structure and Gene Expression Programs of Human Embryonic and Induced Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2010, 7, 249-257.	5.2	405

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73	Wnt Signaling Promotes Reprogramming of Somatic Cells to Pluripotency. <i>Cell Stem Cell</i> , 2008, 3, 132-135.	5.2	396
74	Role of SWI/SNF in acute leukemia maintenance and enhancer-mediated <i>Myc</i> regulation. <i>Genes and Development</i> , 2013, 27, 2648-2662.	2.7	394
75	Transcription factor trapping by RNA in gene regulatory elements. <i>Science</i> , 2015, 350, 978-981.	6.0	389
76	Genome-Wide Distribution of ORC and MCM Proteins in <i>S. cerevisiae</i> : High-Resolution Mapping of Replication Origins. <i>Science</i> , 2001, 294, 2357-2360.	6.0	385
77	Convergence of Developmental and Oncogenic Signaling Pathways at Transcriptional Super-Enhancers. <i>Molecular Cell</i> , 2015, 58, 362-370.	4.5	382
78	Targeting Transcriptional Addictions in Small Cell Lung Cancer with a Covalent CDK7 Inhibitor. <i>Cancer Cell</i> , 2014, 26, 909-922.	7.7	376
79	Pharmacological perturbation of CDK9 using selective CDK9 inhibition or degradation. <i>Nature Chemical Biology</i> , 2018, 14, 163-170.	3.9	376
80	Insulated Neighborhoods: Structural and Functional Units of Mammalian Gene Control. <i>Cell</i> , 2016, 167, 1188-1200.	13.5	373
81	Dissection of <i>Mycobacterium tuberculosis</i> antigens using recombinant DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1985, 82, 2583-2587.	3.3	372
82	Temporal Regulation of RNA Polymerase II by Srb10 and Kin28 Cyclin-Dependent Kinases. <i>Molecular Cell</i> , 1998, 2, 43-53.	4.5	370
83	3D Chromosome Regulatory Landscape of Human Pluripotent Cells. <i>Cell Stem Cell</i> , 2016, 18, 262-275.	5.2	369
84	RNA Polymerase II Holoenzyme Contains SWI/SNF Regulators Involved in Chromatin Remodeling. <i>Cell</i> , 1996, 84, 235-244.	13.5	367
85	Derivation of Pre-X Inactivation Human Embryonic Stem Cells under Physiological Oxygen Concentrations. <i>Cell</i> , 2010, 141, 872-883.	13.5	367
86	Association of Cdk-activating kinase subunits with transcription factor TFIIF. <i>Nature</i> , 1995, 374, 280-282.	13.7	366
87	Genes for the major protein antigens of the leprosy parasite <i>Mycobacterium leprae</i> . <i>Nature</i> , 1985, 316, 450-452.	13.7	365
88	Chromosomal landscape of nucleosome-dependent gene expression and silencing in yeast. <i>Nature</i> , 1999, 402, 418-421.	13.7	364
89	Rescue of Fragile X Syndrome Neurons by DNA Methylation Editing of the FMR1 Gene. <i>Cell</i> , 2018, 172, 979-992.e6.	13.5	351
90	CDK7-Dependent Transcriptional Addiction in Triple-Negative Breast Cancer. <i>Cell</i> , 2015, 163, 174-186.	13.5	346

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91	Biomedical Discovery with DNA Arrays. <i>Cell</i> , 2000, 102, 9-15.	13.5	342
92	Rapid analysis of the DNA-binding specificities of transcription factors with DNA microarrays. <i>Nature Genetics</i> , 2004, 36, 1331-1339.	9.4	341
93	A zebrafish melanoma model reveals emergence of neural crest identity during melanoma initiation. <i>Science</i> , 2016, 351, aad2197.	6.0	339
94	Short RNAs Are Transcribed from Repressed Polycomb Target Genes and Interact with Polycomb Repressive Complex-2. <i>Molecular Cell</i> , 2010, 38, 675-688.	4.5	338
95	Redundant roles for the TFIID and SAGA complexes in global transcription. <i>Nature</i> , 2000, 405, 701-704.	13.7	330
96	RNA-Mediated Feedback Control of Transcriptional Condensates. <i>Cell</i> , 2021, 184, 207-225.e24.	13.5	324
97	Mir-214-Dependent Regulation of the Polycomb Protein Ezh2 in Skeletal Muscle and Embryonic Stem Cells. <i>Molecular Cell</i> , 2009, 36, 61-74.	4.5	320
98	Functional redundancy and structural polymorphism in the large subunit of RNA polymerase II. <i>Cell</i> , 1987, 50, 909-915.	13.5	317
99	Global and Hox-specific roles for the MLL1 methyltransferase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 8603-8608.	3.3	314
100	H2AZ Is Enriched at Polycomb Complex Target Genes in ES Cells and Is Necessary for Lineage Commitment. <i>Cell</i> , 2008, 135, 649-661.	13.5	307
101	The RNA polymerase II holoenzyme and its implications for gene regulation. <i>Trends in Biochemical Sciences</i> , 1995, 20, 113-116.	3.7	305
102	SetDB1 contributes to repression of genes encoding developmental regulators and maintenance of ES cell state. <i>Genes and Development</i> , 2009, 23, 2484-2489.	2.7	292
103	Enhancer Features that Drive Formation of Transcriptional Condensates. <i>Molecular Cell</i> , 2019, 75, 549-561.e7.	4.5	284
104	Exchange of RNA Polymerase II Initiation and Elongation Factors during Gene Expression In Vivo. <i>Molecular Cell</i> , 2002, 9, 799-809.	4.5	282
105	Partitioning of cancer therapeutics in nuclear condensates. <i>Science</i> , 2020, 368, 1386-1392.	6.0	281
106	Lineage Regulators Direct BMP and Wnt Pathways to Cell-Specific Programs during Differentiation and Regeneration. <i>Cell</i> , 2011, 147, 577-589.	13.5	277
107	Whole-genome ChIP-chip analysis of Dorsal, Twist, and Snail suggests integration of diverse patterning processes in the <i>Drosophila</i> embryo. <i>Genes and Development</i> , 2007, 21, 385-390.	2.7	274
108	Global Transcriptional and Translational Repression in Human-Embryonic-Stem-Cell-Derived Rett Syndrome Neurons. <i>Cell Stem Cell</i> , 2013, 13, 446-458.	5.2	273

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109	Negative regulation of Gcn4 and Msn2 transcription factors by Srb10 cyclin-dependent kinase. <i>Genes and Development</i> , 2001, 15, 1078-1092.	2.7	272
110	Recurrent somatic mutations in POLR2A define a distinct subset of meningiomas. <i>Nature Genetics</i> , 2016, 48, 1253-1259.	9.4	265
111	Genetic predisposition to neuroblastoma mediated by a LMO1 super-enhancer polymorphism. <i>Nature</i> , 2015, 528, 418-421.	13.7	263
112	Core Transcriptional Regulatory Circuit Controlled by the TAL1 Complex in Human T Cell Acute Lymphoblastic Leukemia. <i>Cancer Cell</i> , 2012, 22, 209-221.	7.7	262
113	Biomolecular Condensates in the Nucleus. <i>Trends in Biochemical Sciences</i> , 2020, 45, 961-977.	3.7	259
114	Small-Molecule ROR β Antagonists Inhibit T Helper 17 Cell Transcriptional Network by Divergent Mechanisms. <i>Immunity</i> , 2014, 40, 477-489.	6.6	253
115	Covalent targeting of remote cysteine residues to develop CDK12 and CDK13 inhibitors. <i>Nature Chemical Biology</i> , 2016, 12, 876-884.	3.9	249
116	Transcriptional role of cyclin D1 in development revealed by a genetic-proteomic screen. <i>Nature</i> , 2010, 463, 374-378.	13.7	247
117	Genome-wide location and regulated recruitment of the RSC nucleosome-remodeling complex. <i>Genes and Development</i> , 2002, 16, 806-819.	2.7	239
118	Super-Enhancer-Mediated RNA Processing Revealed by Integrative MicroRNA Network Analysis. <i>Cell</i> , 2017, 168, 1000-1014.e15.	13.5	239
119	Aberrant chromatin at genes encoding stem cell regulators in human mixed-lineage leukemia. <i>Genes and Development</i> , 2008, 22, 3403-3408.	2.7	237
120	Activated Signal Transduction Kinases Frequently Occupy Target Genes. <i>Science</i> , 2006, 313, 533-536.	6.0	235
121	The long noncoding RNA <i>Wisper</i> controls cardiac fibrosis and remodeling. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	232
122	Global and gene-specific analyses show distinct roles for Myod and Myog at a common set of promoters. <i>EMBO Journal</i> , 2006, 25, 502-511.	3.5	227
123	Models of human core transcriptional regulatory circuitries. <i>Genome Research</i> , 2016, 26, 385-396.	2.4	223
124	Binding of pRB to the PHD Protein RBP2 Promotes Cellular Differentiation. <i>Molecular Cell</i> , 2005, 18, 623-635.	4.5	215
125	Global Position and Recruitment of HATs and HDACs in the Yeast Genome. <i>Molecular Cell</i> , 2004, 16, 199-209.	4.5	212
126	Program-Specific Distribution of a Transcription Factor Dependent on Partner Transcription Factor and MAPK Signaling. <i>Cell</i> , 2003, 113, 395-404.	13.5	206

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127	HIV-1 Tat reprograms immature dendritic cells to express chemoattractants for activated T cells and macrophages. <i>Nature Medicine</i> , 2003, 9, 191-197.	15.2	205
128	The ribonuclease III site flanking 23S sequences in the 30S ribosomal precursor RNA of <i>E. coli</i> . <i>Cell</i> , 1980, 19, 393-401.	13.5	202
129	Aire unleashes stalled RNA polymerase to induce ectopic gene expression in thymic epithelial cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 535-540.	3.3	202
130	Selective gene dependencies in MYCN-amplified neuroblastoma include the core transcriptional regulatory circuitry. <i>Nature Genetics</i> , 2018, 50, 1240-1246.	9.4	199
131	The transcription factors T-bet and GATA-3 control alternative pathways of T-cell differentiation through a shared set of target genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17876-17881.	3.3	197
132	An Unusual Eukaryotic Protein Phosphatase Required for Transcription by RNA Polymerase II and CTD Dephosphorylation in <i>S. cerevisiae</i> . <i>Molecular Cell</i> , 1999, 4, 55-62.	4.5	191
133	Mediator Condensates Localize Signaling Factors to Key Cell Identity Genes. <i>Molecular Cell</i> , 2019, 76, 753-766.e6.	4.5	188
134	Human T-cell clones recognize a major <i>M. leprae</i> protein antigen expressed in <i>E. coli</i> . <i>Nature</i> , 1986, 319, 63-66.	13.7	187
135	Genome-wide Maps of Histone Modifications Unwind In Vivo Chromatin States of the Hair Follicle Lineage. <i>Cell Stem Cell</i> , 2011, 9, 219-232.	5.2	187
136	Epigenomic analysis detects aberrant super-enhancer DNA methylation in human cancer. <i>Genome Biology</i> , 2016, 17, 11.	3.8	184
137	An Activator Target in the RNA Polymerase II Holoenzyme. <i>Molecular Cell</i> , 1998, 1, 895-904.	4.5	183
138	RNA polymerase II C-terminal repeat influences response to transcriptional enhancer signals. <i>Nature</i> , 1990, 347, 491-494.	13.7	182
139	RNA Polymerase II Holoenzymes and Subcomplexes. <i>Journal of Biological Chemistry</i> , 1998, 273, 27757-27760.	1.6	180
140	Core transcriptional regulatory circuitry in human hepatocytes. <i>Molecular Systems Biology</i> , 2006, 2, 2006.0017.	3.2	179
141	X-linked H3K27me3 demethylase Utx is required for embryonic development in a sex-specific manner. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13004-13009.	3.3	179
142	A novel transcription factor reveals a functional link between the RNA polymerase II CTD and TFIID. <i>Cell</i> , 1992, 69, 883-894.	13.5	177
143	Reverse-transcribed SARS-CoV-2 RNA can integrate into the genome of cultured human cells and can be expressed in patient-derived tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	175
144	MYC Drives a Subset of High-Risk Pediatric Neuroblastomas and Is Activated through Mechanisms Including Enhancer Hijacking and Focal Enhancer Amplification. <i>Cancer Discovery</i> , 2018, 8, 320-335.	7.7	172

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145	Deciphering gene expression regulatory networks. <i>Current Opinion in Genetics and Development</i> , 2002, 12, 130-136.	1.5	171
146	A CD47-associated super-enhancer links pro-inflammatory signalling to CD47 upregulation in breast cancer. <i>Nature Communications</i> , 2017, 8, 14802.	5.8	168
147	Genome-wide localization of small molecules. <i>Nature Biotechnology</i> , 2014, 32, 92-96.	9.4	165
148	[51] Gene isolation by screening λ gt11 libraries with antibodies. <i>Methods in Enzymology</i> , 1987, 152, 458-469.	0.4	164
149	Identification of the gal4 suppressor Sug1 as a subunit of the yeast 26S proteasome. <i>Nature</i> , 1996, 379, 655-657.	13.7	164
150	[7] λ gt 11: Gene isolation with antibody probes and other applications. <i>Methods in Enzymology</i> , 1987, 154, 107-128.	0.4	161
151	CDK12 loss in cancer cells affects DNA damage response genes through premature cleavage and polyadenylation. <i>Nature Communications</i> , 2019, 10, 1757.	5.8	159
152	Increased Antimycobacterial Immunity in Interleukin-10-Deficient Mice. <i>Infection and Immunity</i> , 1999, 67, 3087-3095.	1.0	158
153	Coordinated binding of NF- κ B family members in the response of human cells to lipopolysaccharide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 5899-5904.	3.3	157
154	Biomolecular Condensates and Cancer. <i>Cancer Cell</i> , 2021, 39, 174-192.	7.7	157
155	Integrated genomic analyses of de novo pathways underlying atypical meningiomas. <i>Nature Communications</i> , 2017, 8, 14433.	5.8	156
156	Tandem promoters direct E. coli ribosomal RNA synthesis. <i>Cell</i> , 1979, 17, 225-234.	13.5	150
157	A Systematic Approach to Identify Candidate Transcription Factors that Control Cell Identity. <i>Stem Cell Reports</i> , 2015, 5, 763-775.	2.3	148
158	A set of genes critical to development is epigenetically poised in mouse germ cells from fetal stages through completion of meiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16061-16066.	3.3	141
159	Saltatory remodeling of Hox chromatin in response to rostrocaudal patterning signals. <i>Nature Neuroscience</i> , 2013, 16, 1191-1198.	7.1	140
160	A mammalian SRB protein associated with an RNA polymerase II holoenzyme. <i>Nature</i> , 1996, 380, 82-85.	13.7	137
161	The Developmental Potential of iPSCs Is Greatly Influenced by Reprogramming Factor Selection. <i>Cell Stem Cell</i> , 2014, 15, 295-309.	5.2	137
162	The Genome-Wide Localization of Rsc9, a Component of the RSC Chromatin-Remodeling Complex, Changes in Response to Stress. <i>Molecular Cell</i> , 2002, 9, 563-573.	4.5	135

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163	A Proposed Mechanism for the Induction of Cytotoxic T Lymphocyte Production by Heat Shock Fusion Proteins. <i>Immunity</i> , 2000, 12, 263-272.	6.6	126
164	Global Control of Motor Neuron Topography Mediated by the Repressive Actions of a Single Hox Gene. <i>Neuron</i> , 2010, 67, 781-796.	3.8	125
165	In Vivo Cytotoxic T Lymphocyte Elicitation by Mycobacterial Heat Shock Protein 70 Fusion Proteins Maps to a Discrete Domain and Is Cd4+ T Cell Independent. <i>Journal of Experimental Medicine</i> , 2000, 191, 403-408.	4.2	123
166	Genome-wide Analysis of the H3K4 Histone Demethylase RBP2 Reveals a Transcriptional Program Controlling Differentiation. <i>Molecular Cell</i> , 2008, 31, 520-530.	4.5	123
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