

# Richard A Young

## List of Publications by Year in descending order

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266  
papers

106,683  
citations

<sup>196</sup>  
149  
h-index

<sup>538</sup>  
265  
g-index

278  
all docs

278  
docs citations

278  
times ranked

85399  
citing authors

#	ARTICLE	IF	CITATIONS
1	RNA in formation and regulation of transcriptional condensates. <i>Rna</i> , 2022, 28, 52-57.	1.6	55
2	The nuclear receptor THR $\beta$ facilitates differentiation of human PSCs into more mature hepatocytes. <i>Cell Stem Cell</i> , 2022, 29, 795-809.e11.	5.2	5
3	Learning the chemical grammar of biomolecular condensates. <i>Nature Chemical Biology</i> , 2022, 18, 1298-1306.	3.9	56
4	Genetic variation associated with condensate dysregulation in disease. <i>Developmental Cell</i> , 2022, 57, 1776-1788.e8.	3.1	41
5	RNA-Mediated Feedback Control of Transcriptional Condensates. <i>Cell</i> , 2021, 184, 207-225.e24.	13.5	324
6	Targeted brachyury degradation disrupts a highly specific autoregulatory program controlling chordoma cell identity. <i>Cell Reports Medicine</i> , 2021, 2, 100188.	3.3	15
7	Biomolecular Condensates and Cancer. <i>Cancer Cell</i> , 2021, 39, 174-192.	7.7	157
8	Cell-specific transcriptional control of mitochondrial metabolism by TIF1 $\beta$ drives erythropoiesis. <i>Science</i> , 2021, 372, 716-721.	6.0	25
9	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
10	STAG2 loss rewires oncogenic and developmental programs to promote metastasis in Ewing sarcoma. <i>Cancer Cell</i> , 2021, 39, 827-844.e10.	7.7	49
11	Response to Parry et al.: Strong evidence for genomic integration of SARS-CoV-2 sequences and expression in patient tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	9
12	Testing the super-enhancer concept. <i>Nature Reviews Genetics</i> , 2021, 22, 749-755.	7.7	53
13	Retinoic acid rewires the adrenergic core regulatory circuitry of childhood neuroblastoma. <i>Science Advances</i> , 2021, 7, eabe0834.	4.7	22
14	Reply to Briggs et al.: Genomic integration and expression of SARS-CoV-2 sequences can explain prolonged or recurrent viral RNA detection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	6
15	Predicting master transcription factors from pan-cancer expression data. <i>Science Advances</i> , 2021, 7, eabf6123.	4.7	30
16	MeCP2 links heterochromatin condensates and neurodevelopmental disease. <i>Nature</i> , 2020, 586, 440-444.	13.7	112
17	Biomolecular Condensates in the Nucleus. <i>Trends in Biochemical Sciences</i> , 2020, 45, 961-977.	3.7	259
18	Common variants in signaling transcription-factor-binding sites drive phenotypic variability in red blood cell traits. <i>Nature Genetics</i> , 2020, 52, 1333-1345.	9.4	24

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19	CHD7 and Runx1 interaction provides a braking mechanism for hematopoietic differentiation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 23626-23635.	3.3	18
20	lncRNA DIGIT and BRD3 protein form phase-separated condensates to regulate endoderm differentiation. Nature Cell Biology, 2020, 22, 1211-1222.	4.6	100
21	Partitioning of cancer therapeutics in nuclear condensates. Science, 2020, 368, 1386-1392.	6.0	281
22	LIN28B regulates transcription and potentiates MYCN-induced neuroblastoma through binding to ZNF143 at target gene promoters. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 16516-16526.	3.3	31
23	Cdk1 Controls Global Epigenetic Landscape in Embryonic Stem Cells. Molecular Cell, 2020, 78, 459-476.e13.	4.5	76
24	RNA Regulator of Lipogenesis (RROL) Is a Novel Lncrna Mediating Protein-Protein Interaction at Gene Regulatory Loci Driving Lipogenic Programs in Multiple Myeloma. Blood, 2020, 136, 20-21.	0.6	0
25	Targeting MM at the Nexus between Cell Cycle and Transcriptional Regulation Via CDK7 Inhibition. Blood, 2020, 136, 1-2.	0.6	0
26	Pol <sup>II</sup> phosphorylation regulates a switch between transcriptional and splicing condensates. Nature, 2019, 572, 543-548.	13.7	457
27	BORIS promotes chromatin regulatory interactions in treatment-resistant cancer cells. Nature, 2019, 572, 676-680.	13.7	89
28	Enhancer Features that Drive Formation of Transcriptional Condensates. Molecular Cell, 2019, 75, 549-561.e7.	4.5	284
29	Dynamic Enhancer DNA Methylation as Basis for Transcriptional and Cellular Heterogeneity of ESCs. Molecular Cell, 2019, 75, 905-920.e6.	4.5	73
30	Mediator Condensates Localize Signaling Factors to Key Cell Identity Genes. Molecular Cell, 2019, 76, 753-766.e6.	4.5	188
31	CDK12 loss in cancer cells affects DNA damage response genes through premature cleavage and polyadenylation. Nature Communications, 2019, 10, 1757.	5.8	159
32	ASCL1 is a MYCN- and LMO1-dependent member of the adrenergic neuroblastoma core regulatory circuitry. Nature Communications, 2019, 10, 5622.	5.8	56
33	BET bromodomain proteins regulate enhancer function during adipogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 2144-2149.	3.3	65
34	Rescue of Fragile X Syndrome Neurons by DNA Methylation Editing of the FMR1 Gene. Cell, 2018, 172, 979-992.e6.	13.5	351
35	EWS/FLI Confers Tumor Cell Synthetic Lethality to CDK12 Inhibition in Ewing Sarcoma. Cancer Cell, 2018, 33, 202-216.e6.	7.7	116
36	MYC Drives a Subset of High-Risk Pediatric Neuroblastomas and Is Activated through Mechanisms Including Enhancer Hijacking and Focal Enhancer Amplification. Cancer Discovery, 2018, 8, 320-335.	7.7	172

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37	Pharmacological perturbation of CDK9 using selective CDK9 inhibition or degradation. <i>Nature Chemical Biology</i> , 2018, 14, 163-170.	3.9	376
38	High MITF Expression Is Associated with Super-Enhancers and Suppressed by CDK7 Inhibition in Melanoma. <i>Journal of Investigative Dermatology</i> , 2018, 138, 1582-1590.	0.3	46
39	Suppression of Adaptive Responses to Targeted Cancer Therapy by Transcriptional Repression. <i>Cancer Discovery</i> , 2018, 8, 59-73.	7.7	96
40	Regulation and Dysregulation of Chromosome Structure in Cancer. <i>Annual Review of Cancer Biology</i> , 2018, 2, 21-40.	2.3	26
41	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
42	Non-overlapping Control of Transcriptome by Promoter- and Super-Enhancer-Associated Dependencies in Multiple Myeloma. <i>Cell Reports</i> , 2018, 25, 3693-3705.e6.	2.9	23
43	Coactivator condensation at super-enhancers links phase separation and gene control. <i>Science</i> , 2018, 361, .	6.0	1,687
44	JDP2: An oncogenic bZIP transcription factor in T cell acute lymphoblastic leukemia. <i>Journal of Experimental Medicine</i> , 2018, 215, 1929-1945.	4.2	22
45	Selective gene dependencies in MYCN-amplified neuroblastoma include the core transcriptional regulatory circuitry. <i>Nature Genetics</i> , 2018, 50, 1240-1246.	9.4	199
46	Activation of the LMO2 oncogene through a somatically acquired neomorphic promoter in T-cell acute lymphoblastic leukemia. <i>Blood</i> , 2017, 129, 3221-3226.	0.6	61
47	Super-Enhancer-Mediated RNA Processing Revealed by Integrative MicroRNA Network Analysis. <i>Cell</i> , 2017, 168, 1000-1014.e15.	13.5	239
48	Transcriptional Addiction in Cancer. <i>Cell</i> , 2017, 168, 629-643.	13.5	843
49	Small genomic insertions form enhancers that misregulate oncogenes. <i>Nature Communications</i> , 2017, 8, 14385.	5.8	76
50	Integrated genomic analyses of de novo pathways underlying atypical meningiomas. <i>Nature Communications</i> , 2017, 8, 14433.	5.8	156
51	The long noncoding RNA <i>Wisper</i> controls cardiac fibrosis and remodeling. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	232
52	PHF6 regulates phenotypic plasticity through chromatin organization within lineage-specific genes. <i>Genes and Development</i> , 2017, 31, 973-989.	2.7	50
53	A Phase Separation Model for Transcriptional Control. <i>Cell</i> , 2017, 169, 13-23.	13.5	1,341
54	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

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55	TOX Regulates Growth, DNA Repair, and Genomic Instability in T-cell Acute Lymphoblastic Leukemia. <i>Cancer Discovery</i> , 2017, 7, 1336-1353.	7.7	48
56	Activation of the p53 Transcriptional Program Sensitizes Cancer Cells to Cdk7 Inhibitors. <i>Cell Reports</i> , 2017, 21, 467-481.	2.9	65
57	New Insights into Genome Structure: Genes of a Feather Stick Together. <i>Molecular Cell</i> , 2017, 67, 730-731.	4.5	9
58	YY1 Is a Structural Regulator of Enhancer-Promoter Loops. <i>Cell</i> , 2017, 171, 1573-1588.e28.	13.5	749
59	Stress from Nucleotide Depletion Activates the Transcriptional Regulator HEXIM1 to Suppress Melanoma. <i>Molecular Cell</i> , 2016, 62, 34-46.	4.5	71
60	Parkinson-associated risk variant in distal enhancer of $\alpha$ -synuclein modulates target gene expression. <i>Nature</i> , 2016, 533, 95-99.	13.7	466
61	Covalent targeting of remote cysteine residues to develop CDK12 and CDK13 inhibitors. <i>Nature Chemical Biology</i> , 2016, 12, 876-884.	3.9	249
62	The rate of protein synthesis in hematopoietic stem cells is limited partly by 4E-BPs. <i>Genes and Development</i> , 2016, 30, 1698-1703.	2.7	91
63	Recurrent somatic mutations in POLR2A define a distinct subset of meningiomas. <i>Nature Genetics</i> , 2016, 48, 1253-1259.	9.4	265
64	Editing DNA Methylation in the Mammalian Genome. <i>Cell</i> , 2016, 167, 233-247.e17.	13.5	932
65	Insulated Neighborhoods: Structural and Functional Units of Mammalian Gene Control. <i>Cell</i> , 2016, 167, 1188-1200.	13.5	373
66	A zebrafish melanoma model reveals emergence of neural crest identity during melanoma initiation. <i>Science</i> , 2016, 351, aad2197.	6.0	339
67	3D Chromosome Regulatory Landscape of Human Pluripotent Cells. <i>Cell Stem Cell</i> , 2016, 18, 262-275.	5.2	369
68	Epigenomic analysis detects aberrant super-enhancer DNA methylation in human cancer. <i>Genome Biology</i> , 2016, 17, 11.	3.8	184
69	Activation of proto-oncogenes by disruption of chromosome neighborhoods. <i>Science</i> , 2016, 351, 1454-1458.	6.0	880
70	Models of human core transcriptional regulatory circuitries. <i>Genome Research</i> , 2016, 26, 385-396.	2.4	223
71	Response and resistance to BET bromodomain inhibitors in triple-negative breast cancer. <i>Nature</i> , 2016, 529, 413-417.	13.7	490
72	Activation of the LMO2 Oncogene in T-ALL through a Somatic Acquired Neomorphic Promoter. <i>Blood</i> , 2016, 128, 733-733.	0.6	0

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73	A Systematic Approach to Identify Candidate Transcription Factors that Control Cell Identity. <i>Stem Cell Reports</i> , 2015, 5, 763-775.	2.3	148
74	Convergence of Developmental and Oncogenic Signaling Pathways at Transcriptional Super-Enhancers. <i>Molecular Cell</i> , 2015, 58, 362-370.	4.5	382
75	Chromatin proteomic profiling reveals novel proteins associated with histone-marked genomic regions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3841-3846.	3.3	123
76	CDK7-Dependent Transcriptional Addiction in Triple-Negative Breast Cancer. <i>Cell</i> , 2015, 163, 174-186.	13.5	346
77	Transcription factor trapping by RNA in gene regulatory elements. <i>Science</i> , 2015, 350, 978-981.	6.0	389
78	Genetic predisposition to neuroblastoma mediated by a LMO1 super-enhancer polymorphism. <i>Nature</i> , 2015, 528, 418-421.	13.7	263
79	Direct Lineage Conversion of Adult Mouse Liver Cells and B Lymphocytes to Neural Stem Cells. <i>Stem Cell Reports</i> , 2014, 3, 948-956.	2.3	57
80	Targeting Transcriptional Addictions in Small Cell Lung Cancer with a Covalent CDK7 Inhibitor. <i>Cancer Cell</i> , 2014, 26, 909-922.	7.7	376
81	Genome-wide localization of small molecules. <i>Nature Biotechnology</i> , 2014, 32, 92-96.	9.4	165
82	MYC and Transcription Elongation. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2014, 4, a020990-a020990.	2.9	97
83	CDK7 Inhibition Suppresses Super-Enhancer-Linked Oncogenic Transcription in MYCN-Driven Cancer. <i>Cell</i> , 2014, 159, 1126-1139.	13.5	498
84	An oncogenic super-enhancer formed through somatic mutation of a noncoding intergenic element. <i>Science</i> , 2014, 346, 1373-1377.	6.0	665
85	Targeting transcription regulation in cancer with a covalent CDK7 inhibitor. <i>Nature</i> , 2014, 511, 616-620.	13.7	698
86	The Developmental Potential of iPSCs Is Greatly Influenced by Reprogramming Factor Selection. <i>Cell Stem Cell</i> , 2014, 15, 295-309.	5.2	137
87	D-Cyclins Repress Apoptosis in Hematopoietic Cells by Controlling Death Receptor Fas and Its Ligand FasL. <i>Developmental Cell</i> , 2014, 30, 255-267.	3.1	27
88	Control of Cell Identity Genes Occurs in Insulated Neighborhoods in Mammalian Chromosomes. <i>Cell</i> , 2014, 159, 374-387.	13.5	793
89	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
90	Small-Molecule ROR $\gamma$ t Antagonists Inhibit T Helper 17 Cell Transcriptional Network by Divergent Mechanisms. <i>Immunity</i> , 2014, 40, 477-489.	6.6	253

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91	ZFX4 Interacts with the NuRD Core Member CHD4 and Regulates the Glioblastoma Tumor-Initiating Cell State. <i>Cell Reports</i> , 2014, 6, 313-324.	2.9	106
92	SMC complexes link gene expression and genome architecture. <i>Current Opinion in Genetics and Development</i> , 2014, 25, 131-137.	1.5	20
93	Saltatory remodeling of Hox chromatin in response to rostrocaudal patterning signals. <i>Nature Neuroscience</i> , 2013, 16, 1191-1198.	7.1	140
94	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
95	Super-Enhancers in the Control of Cell Identity and Disease. <i>Cell</i> , 2013, 155, 934-947.	13.5	2,916
96	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
97	Multiple Structural Maintenance of Chromosome Complexes at Transcriptional Regulatory Elements. <i>Stem Cell Reports</i> , 2013, 1, 371-378.	2.3	113
98	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
99	Transcriptional Regulation and Its Misregulation in Disease. <i>Cell</i> , 2013, 152, 1237-1251.	13.5	1,205
100	Master Transcription Factors and Mediator Establish Super-Enhancers at Key Cell Identity Genes. <i>Cell</i> , 2013, 153, 307-319.	13.5	3,202
101	Selective Inhibition of Tumor Oncogenes by Disruption of Super-Enhancers. <i>Cell</i> , 2013, 153, 320-334.	13.5	2,366
102	Poised Chromatin at the ZEB1 Promoter Enables Breast Cancer Cell Plasticity and Enhances Tumorigenicity. <i>Cell</i> , 2013, 154, 61-74.	13.5	753
103	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
104	The TAL1 complex targets the <i>FBXW7</i> tumor suppressor by activating miR-223 in human T cell acute lymphoblastic leukemia. <i>Journal of Experimental Medicine</i> , 2013, 210, 1545-1557.	4.2	107
105	Let-7 represses <i>Nr6a1</i> and a mid-gestation developmental program in adult fibroblasts. <i>Genes and Development</i> , 2013, 27, 941-954.	2.7	44
106	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
107	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
108	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

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109	Transcriptional Amplification in Tumor Cells with Elevated c-Myc. <i>Cell</i> , 2012, 151, 56-67.	13.5	1,262
110	Revisiting Global Gene Expression Analysis. <i>Cell</i> , 2012, 151, 476-482.	13.5	526
111	Grounded: Transcriptional Pausing in Naive mESCs. <i>Cell Stem Cell</i> , 2012, 10, 484-485.	5.2	1
112	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
113	CpG island structure and trithorax/polycomb chromatin domains in human cells. <i>Genomics</i> , 2012, 100, 320-326.	1.3	35
114	Functional Association of Gdown1 with RNA Polymerase II Poised on Human Genes. <i>Molecular Cell</i> , 2012, 45, 38-50.	4.5	114
115	Nanog-like Regulates Endoderm Formation through the Mxtx2-Nodal Pathway. <i>Developmental Cell</i> , 2012, 22, 625-638.	3.1	95
116	The Polycomb Group Protein L3mbtl2 Assembles an Atypical PRC1-Family Complex that Is Essential in Pluripotent Stem Cells and Early Development. <i>Cell Stem Cell</i> , 2012, 11, 319-332.	5.2	118
117	Enhancer decommissioning by LSD1 during embryonic stem cell differentiation. <i>Nature</i> , 2012, 482, 221-225.	13.7	527
118	Ligand-dependent dynamics of retinoic acid receptor binding during early neurogenesis. <i>Genome Biology</i> , 2011, 12, R2.	13.9	117
119	Densely Interconnected Transcriptional Circuits Control Cell States in Human Hematopoiesis. <i>Cell</i> , 2011, 144, 296-309.	13.5	843
120	BET Bromodomain Inhibition as a Therapeutic Strategy to Target c-Myc. <i>Cell</i> , 2011, 146, 904-917.	13.5	2,432
121	Master Transcription Factors Determine Cell-Type-Specific Responses to TGF- $\beta$ Signaling. <i>Cell</i> , 2011, 147, 565-576.	13.5	536
122	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
123	The Msx1 Homeoprotein Recruits Polycomb to the Nuclear Periphery during Development. <i>Developmental Cell</i> , 2011, 21, 575-588.	3.1	82
124	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
125	Evidence That Gene Activation and Silencing during Stem Cell Differentiation Requires a Transcriptionally Paused Intermediate State. <i>PLoS ONE</i> , 2011, 6, e22416.	1.1	12
126	Gene induction and repression during terminal erythropoiesis are mediated by distinct epigenetic changes. <i>Blood</i> , 2011, 118, e128-e138.	0.6	103



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127	The histone methyltransferase SETDB1 is recurrently amplified in melanoma and accelerates its onset. <i>Nature</i> , 2011, 471, 513-517.	13.7	506
128	DHODH modulates transcriptional elongation in the neural crest and melanoma. <i>Nature</i> , 2011, 471, 518-522.	13.7	411
129	Control of the Embryonic Stem Cell State. <i>Cell</i> , 2011, 144, 940-954.	13.5	1,050
130	Embryonic stem cell-based mapping of developmental transcriptional programs. <i>Nature Methods</i> , 2011, 8, 1056-1058.	9.0	71
131	Transcriptional role of cyclin D1 in development revealed by a genetic-proteomic screen. <i>Nature</i> , 2010, 463, 374-378.	13.7	247
132	Mediator and cohesin connect gene expression and chromatin architecture. <i>Nature</i> , 2010, 467, 430-435.	13.7	1,707
133	Ten years of genetics and genomics: what have we achieved and where are we heading?. <i>Nature Reviews Genetics</i> , 2010, 11, 723-733.	7.7	65
134	Ronin/Hcf-1 binds to a hyperconserved enhancer element and regulates genes involved in the growth of embryonic stem cells. <i>Genes and Development</i> , 2010, 24, 1479-1484.	2.7	106
135	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
136	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
137	c-Myc Regulates Transcriptional Pause Release. <i>Cell</i> , 2010, 141, 432-445.	13.5	1,104
138	Derivation of Pre-X Inactivation Human Embryonic Stem Cells under Physiological Oxygen Concentrations. <i>Cell</i> , 2010, 141, 872-883.	13.5	367
139	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
140	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
141	Repressive Transcription. <i>Science</i> , 2010, 329, 150-151.	6.0	47
142	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
143	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
144	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

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145	Analysis of the mouse embryonic stem cell regulatory networks obtained by CHIP-chip and CHIP-PET. <i>Genome Biology</i> , 2008, 9, R126.	13.9	53
146	Divergent Transcription from Active Promoters. <i>Science</i> , 2008, 322, 1849-1851.	6.0	801
147	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
148	Wnt Signaling Promotes Reprogramming of Somatic Cells to Pluripotency. <i>Cell Stem Cell</i> , 2008, 3, 132-135.	5.2	396
149	Stem Cells, the Molecular Circuitry of Pluripotency and Nuclear Reprogramming. <i>Cell</i> , 2008, 132, 567-582.	13.5	1,251
150	Connecting microRNA Genes to the Core Transcriptional Regulatory Circuitry of Embryonic Stem Cells. <i>Cell</i> , 2008, 134, 521-533.	13.5	1,332
151	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
152	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
153	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
154	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
155	A Chromatin Landmark and Transcription Initiation at Most Promoters in Human Cells. <i>Cell</i> , 2007, 130, 77-88.	13.5	1,725
156	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
157	Foxp3 occupancy and regulation of key target genes during T-cell stimulation. <i>Nature</i> , 2007, 445, 931-935.	13.7	644
158	Cell Cycle Genes Are the Evolutionarily Conserved Targets of the E2F4 Transcription Factor. <i>PLoS ONE</i> , 2007, 2, e1061.	1.1	51
159	Zebrafish promoter microarrays identify actively transcribed embryonic genes. <i>Genome Biology</i> , 2006, 7, R71.	13.9	80
160	Control of Developmental Regulators by Polycomb in Human Embryonic Stem Cells. <i>Cell</i> , 2006, 125, 301-313.	13.5	2,059
161	Transcriptional regulatory networks downstream of TAL1/SCL in T-cell acute lymphoblastic leukemia. <i>Blood</i> , 2006, 108, 986-992.	0.6	62
162	High-resolution computational models of genome binding events. <i>Nature Biotechnology</i> , 2006, 24, 963-970.	9.4	82

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163	Evidence for an instructive mechanism of de novo methylation in cancer cells. <i>Nature Genetics</i> , 2006, 38, 149-153.	9.4	456
164	Chromatin immunoprecipitation and microarray-based analysis of protein location. <i>Nature Protocols</i> , 2006, 1, 729-748.	5.5	671
165	Polycomb complexes repress developmental regulators in murine embryonic stem cells. <i>Nature</i> , 2006, 441, 349-353.	13.7	2,273
166	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
167	A hypothesis-based approach for identifying the binding specificity of regulatory proteins from chromatin immunoprecipitation data. <i>Bioinformatics</i> , 2006, 22, 423-429.	1.8	73
168	Activated Signal Transduction Kinases Frequently Occupy Target Genes. <i>Science</i> , 2006, 313, 533-536.	6.0	235
169	Core transcriptional regulatory circuitry in human hepatocytes. <i>Molecular Systems Biology</i> , 2006, 2, 2006.0017.	3.2	179
170	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
171	Coordinated binding of NF- $\kappa$ 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
172	Insights into host responses against pathogens from transcriptional profiling. <i>Nature Reviews Microbiology</i> , 2005, 3, 281-294.	13.6	581
173	The core centromere and Sgo1 establish a 50-kb cohesin-protected domain around centromeres during meiosis I. <i>Genes and Development</i> , 2005, 19, 3017-3030.	2.7	87
174	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
175	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
176	Binding of pRB to the PHD Protein RBP2 Promotes Cellular Differentiation. <i>Molecular Cell</i> , 2005, 18, 623-635.	4.5	215
177	Genome-wide Map of Nucleosome Acetylation and Methylation in Yeast. <i>Cell</i> , 2005, 122, 517-527.	13.5	1,242
178	Core Transcriptional Regulatory Circuitry in Human Embryonic Stem Cells. <i>Cell</i> , 2005, 122, 947-956.	13.5	4,000
179	A Role for Toll-Like Receptor 4 in Dendritic Cell Activation and Cytolytic CD8+ T Cell Differentiation in Response to a Recombinant Heat Shock Fusion Protein. <i>Journal of Immunology</i> , 2004, 172, 2885-2893.	0.4	36
180	Rapid analysis of the DNA-binding specificities of transcription factors with DNA microarrays. <i>Nature Genetics</i> , 2004, 36, 1331-1339.	9.4	341

#	ARTICLE	IF	CITATIONS
181	Transcriptional regulatory code of a eukaryotic genome. <i>Nature</i> , 2004, 431, 99-104.	13.7	1,969
182	Control of Pancreas and Liver Gene Expression by HNF Transcription Factors. <i>Science</i> , 2004, 303, 1378-1381.	6.0	1,202
183	Global Position and Recruitment of HATs and HDACs in the Yeast Genome. <i>Molecular Cell</i> , 2004, 16, 199-209.	4.5	212
184	Systematic analysis of essential yeast TAFs in genome-wide transcription and preinitiation complex assembly. <i>EMBO Journal</i> , 2003, 22, 3395-3402.	3.5	93
185	Computational discovery of gene modules and regulatory networks. <i>Nature Biotechnology</i> , 2003, 21, 1337-1342.	9.4	528
186	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
187	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
188	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
189	Bayesian Estimation of Transcript Levels Using a General Model of Array Measurement Noise. <i>Journal of Computational Biology</i> , 2003, 10, 433-452.	0.8	15
190	Cumulative Toll-Like Receptor Activation in Human Macrophages Treated with Whole Bacteria. <i>Journal of Immunology</i> , 2003, 170, 5203-5209.	0.4	92
191	Transcriptional activating regions target a cyclin-dependent kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 14706-14709.	3.3	51
192	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
193	Genome-wide location and regulated recruitment of the RSC nucleosome-remodeling complex. <i>Genes and Development</i> , 2002, 16, 806-819.	2.7	239
194	A Highly Potent Artificial Transcription Factor. <i>Biochemistry</i> , 2002, 41, 7209-7216.	1.2	38
195	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
196	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
197	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
198	Deciphering gene expression regulatory networks. <i>Current Opinion in Genetics and Development</i> , 2002, 12, 130-136.	1.5	171

#	ARTICLE	IF	CITATIONS
199	Transcriptional Regulatory Networks in <i>Saccharomyces cerevisiae</i> . <i>Science</i> , 2002, 298, 799-804.	6.0	2,706
200	Combining location and expression data for principled discovery of genetic regulatory network models. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2002, , 437-49.	0.7	63
201	The Plasticity of Dendritic Cell Responses to Pathogens and Their Components. <i>Science</i> , 2001, 294, 870-875.	6.0	730
202	Serial Regulation of Transcriptional Regulators in the Yeast Cell Cycle. <i>Cell</i> , 2001, 106, 697-708.	13.5	604
203	Yeast Artificial Chromosome Targeting Technology: An Approach for the Deletion of Genes in the C57BL/6 Mouse. <i>Analytical Biochemistry</i> , 2001, 296, 270-278.	1.1	6
204	Promoter-specific activation defects by a novel yeast TBP mutant compromised for TFIIB interaction. <i>Current Biology</i> , 2001, 11, 1794-1798.	1.8	9
205	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
206	Yeast NC2 Associates with the RNA Polymerase II Preinitiation Complex and Selectively Affects Transcription In Vivo. <i>Molecular and Cellular Biology</i> , 2001, 21, 2736-2742.	1.1	65
207	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
208	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
209	<title>Maximum-likelihood estimation of optimal scaling factors for expression array normalization</title>. , 2001, , .		47
210	Redundant roles for the TFIID and SAGA complexes in global transcription. <i>Nature</i> , 2000, 405, 701-704.	13.7	330
211	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
212	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
213	Biomedical Discovery with DNA Arrays. <i>Cell</i> , 2000, 102, 9-15.	13.5	342
214	Transcription of Eukaryotic Protein-Coding Genes. <i>Annual Review of Genetics</i> , 2000, 34, 77-137.	3.2	719
215	Genome-Wide Location and Function of DNA Binding Proteins. <i>Science</i> , 2000, 290, 2306-2309.	6.0	1,826
216	Transcriptional Regulation of the <i>Schizosaccharomyces pombe</i> Malic Enzyme Gene, <i>mae2</i> . <i>Journal of Biological Chemistry</i> , 1999, 274, 9969-9975.	1.6	11

#	ARTICLE	IF	CITATIONS
217	Chromosomal landscape of nucleosome-dependent gene expression and silencing in yeast. <i>Nature</i> , 1999, 402, 418-421.	13.7	364
218	Genome expression on the World Wide Web. <i>Trends in Genetics</i> , 1999, 15, 202-204.	2.9	13
219	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
220	Increased Antimycobacterial Immunity in Interleukin-10-Deficient Mice. <i>Infection and Immunity</i> , 1999, 67, 3087-3095.	1.0	158
221	Regulatory targets in the RNA polymerase II holoenzyme. <i>Current Opinion in Genetics and Development</i> , 1998, 8, 565-570.	1.5	52
222	An Activator Target in the RNA Polymerase II Holoenzyme. <i>Molecular Cell</i> , 1998, 1, 895-904.	4.5	183
223	Temporal Regulation of RNA Polymerase II by Srb10 and Kin28 Cyclin-Dependent Kinases. <i>Molecular Cell</i> , 1998, 2, 43-53.	4.5	370
224	Broad, but Not Universal, Transcriptional Requirement for yTAFII17, a Histone H3-like TAFII Present in TFIID and SAGA. <i>Molecular Cell</i> , 1998, 2, 653-661.	4.5	94
225	Dissecting the Regulatory Circuitry of a Eukaryotic Genome. <i>Cell</i> , 1998, 95, 717-728.	13.5	1,722
226	RNA Polymerase II Holoenzymes and Subcomplexes. <i>Journal of Biological Chemistry</i> , 1998, 273, 27757-27760.	1.6	180
227	Interplay of Positive and Negative Regulators in Transcription Initiation by RNA Polymerase II Holoenzyme. <i>Molecular and Cellular Biology</i> , 1998, 18, 4455-4462.	1.1	93
228	A Strategy for Rapid, High-Confidence Protein Identification. <i>Analytical Chemistry</i> , 1997, 69, 3995-4001.	3.2	98
229	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
230	Baculoviral Transfer Vectors for Expression of FLAG® Fusion Proteins in Insect Cells. <i>BioTechniques</i> , 1997, 23, 622-627.	0.8	13
231	RNA Polymerase II Holoenzyme Contains SWI/SNF Regulators Involved in Chromatin Remodeling. <i>Cell</i> , 1996, 84, 235-244.	13.5	367
232	[16] Purification of yeast RNA polymerase II holoenzymes. <i>Methods in Enzymology</i> , 1996, 273, 176-184.	0.4	14
233	Identification of the gal4 suppressor Sug1 as a subunit of the yeast 26S proteasome. <i>Nature</i> , 1996, 379, 655-657.	13.7	164
234	A mammalian SRB protein associated with an RNA polymerase II holoenzyme. <i>Nature</i> , 1996, 380, 82-85.	13.7	137

#	ARTICLE	IF	CITATIONS
235	Activation without a vital ingredient. <i>Nature</i> , 1996, 383, 119-120.	13.7	13
236	The RNA polymerase II holoenzyme and its implications for gene regulation. <i>Trends in Biochemical Sciences</i> , 1995, 20, 113-116.	3.7	305
237	Human Stress Protein hsp70: Overexpression in <i>E. coli</i> , Purification and Characterization. <i>Bio/technology</i> , 1995, 13, 1105-1109.	1.9	8
238	A kinase-cyclin pair in the RNA polymerase II holoenzyme. <i>Nature</i> , 1995, 374, 193-196.	13.7	411
239	Association of Cdk-activating kinase subunits with transcription factor TFIIF. <i>Nature</i> , 1995, 374, 280-282.	13.7	366
240	An RNA polymerase II holoenzyme responsive to activators. <i>Nature</i> , 1994, 368, 466-469.	13.7	594
241	RPB7, one of two dissociable subunits of yeast RNA polymerase II, is essential for cell viability. <i>Yeast</i> , 1993, 9, 295-299.	0.8	81
242	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
243	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
244	[35] Epitope tagging and protein surveillance. <i>Methods in Enzymology</i> , 1991, 194, 508-519.	0.4	514
245	RNA Polymerase II. <i>Annual Review of Biochemistry</i> , 1991, 60, 689-715.	5.0	473
246	[15] Gene isolation with $\lambda$ gt11 system. <i>Methods in Enzymology</i> , 1991, 194, 230-238.	0.4	7
247	RNA polymerase II C-terminal repeat influences response to transcriptional enhancer signals. <i>Nature</i> , 1990, 347, 491-494.	13.7	182
248	Development of a BCG Recombinant Vehicle for Candidate AIDS Vaccines. <i>International Reviews of Immunology</i> , 1990, 7, 79-83.	1.5	14
249	RNA polymerase II: subunit structure and function. <i>Trends in Biochemical Sciences</i> , 1990, 15, 347-351.	3.7	92
250	Stress Proteins and Immunology. <i>Annual Review of Immunology</i> , 1990, 8, 401-420.	9.5	469
251	Stress Proteins as Immune Targets in Bacterial and Parasitic Infections. , 1990, , 123-130.		0
252	Identification of Mycobacterial Antigens Recognized by T Lymphocytes. <i>Clinical Infectious Diseases</i> , 1989, 11, S443-S447.	2.9	20

#	ARTICLE	IF	CITATIONS
253	Stress proteins, infection, and immune surveillance. <i>Cell</i> , 1989, 59, 5-8.	13.5	512
254	A gene from <i>Mycobacterium tuberculosis</i> which is homologous to the DnaJ heat shock protein of <i>E. coli</i> . <i>Nucleic Acids Research</i> , 1988, 16, 1636-1636.	6.5	45
255	[51] Gene isolation by screening $\lambda$ gt11 libraries with antibodies. <i>Methods in Enzymology</i> , 1987, 152, 458-469.	0.4	164
256	[40] Cloning cDNA into $\lambda$ gt10 and $\lambda$ gt11. <i>Methods in Enzymology</i> , 1987, 152, 359-371.	0.4	28
257	[7] $\lambda$ gt 11: Gene isolation with antibody probes and other applications. <i>Methods in Enzymology</i> , 1987, 154, 107-128.	0.4	161
258	Functional redundancy and structural polymorphism in the large subunit of RNA polymerase II. <i>Cell</i> , 1987, 50, 909-915.	13.5	317
259	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
260	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
261	Genes for the major protein antigens of the leprosy parasite <i>Mycobacterium leprae</i> . <i>Nature</i> , 1985, 316, 450-452.	13.7	365
262	Genes for the protein antigens of the tuberculosis and leprosy bacilli. <i>Bioscience Reports</i> , 1985, 5, 839-845.	1.1	6
263	Immunoscreening $\lambda$ gtII Recombinant DNA Expression Libraries. , 1985, , 29-41.		17
264	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
265	Tandem promoters direct <i>E. coli</i> ribosomal RNA synthesis. <i>Cell</i> , 1979, 17, 225-234.	13.5	150
266	Host factor for coliphage $\phi$ 2 RNA replication: Presence in procaryotes and association with the 30S ribosomal subunit in <i>Escherichia coli</i> . <i>Molecular Genetics and Genomics</i> , 1977, 153, 39-43.	2.4	12