

Richard A Young

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

268
papers

85,396
citations

139
h-index

278
g-index

278
ext. papers

97,916
ext. citations

25.3
avg, IF

7.92
L-index

#	Paper	IF	Citations
268	The nuclear receptor THRB facilitates differentiation of human PSCs into more mature hepatocytes. 2022 ,		1
267	Predicting master transcription factors from pan-cancer expression data. <i>Science Advances</i> , 2021 , 7, eabf6133	11.3	2
266	RNA in formation and regulation of transcriptional condensates. <i>Rna</i> , 2021 ,	5.8	5
265	Retinoic acid rewires the adrenergic core regulatory circuitry of childhood neuroblastoma. <i>Science Advances</i> , 2021 , 7, eabe0834	14.3	2
264	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,	11.5	2
263	Cell-specific transcriptional control of mitochondrial metabolism by TIF1 β drives erythropoiesis. <i>Science</i> , 2021 , 372, 716-721	33.3	8
262	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,	11.5	63
261	STAG2 loss rewires oncogenic and developmental programs to promote metastasis in Ewing sarcoma. <i>Cancer Cell</i> , 2021 , 39, 827-844.e10	24.3	7
260	RNA-Mediated Feedback Control of Transcriptional Condensates. <i>Cell</i> , 2021 , 184, 207-225.e24	56.2	99
259	Targeted brachyury degradation disrupts a highly specific autoregulatory program controlling chordoma cell identity. <i>Cell Reports Medicine</i> , 2021 , 2, 100188	18	4
258	Biomolecular Condensates and Cancer. <i>Cancer Cell</i> , 2021 , 39, 174-192	24.3	38
257	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,	11.5	3
256	Testing the super-enhancer concept. <i>Nature Reviews Genetics</i> , 2021 , 22, 749-755	30.1	11
255	Partitioning of cancer therapeutics in nuclear condensates. <i>Science</i> , 2020 , 368, 1386-1392	33.3	120
254	LIN28B regulates transcription and potentiates MYCN-induced neuroblastoma through binding to ZNF143 at target gene promoters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 16516-16526	11.5	15
253	Cdk1 Controls Global Epigenetic Landscape in Embryonic Stem Cells. <i>Molecular Cell</i> , 2020 , 78, 459-476.e13	13.6	24
252	RNA Regulator of Lipogenesis (RROL) Is a Novel Lncrna Mediating Protein-Protein Interaction at Gene Regulatory Loci Driving Lipogenic Programs in Multiple Myeloma. <i>Blood</i> , 2020 , 136, 20-21	2.2	

251	Targeting MM at the Nexus between Cell Cycle and Transcriptional Regulation Via CDK7 Inhibition. <i>Blood</i> , 2020 , 136, 1-2	2.2	
250	SARS-CoV-2 RNA reverse-transcribed and integrated into the human genome 2020 ,		31
249	MeCP2 links heterochromatin condensates and neurodevelopmental disease. <i>Nature</i> , 2020 , 586, 440-444	50.4	45
248	Biomolecular Condensates in the Nucleus. <i>Trends in Biochemical Sciences</i> , 2020 , 45, 961-977	10.3	103
247	Common variants in signaling transcription-factor-binding sites drive phenotypic variability in red blood cell traits. <i>Nature Genetics</i> , 2020 , 52, 1333-1345	36.3	8
246	CHD7 and Runx1 interaction provides a braking mechanism for hematopoietic differentiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 23626-23635	11.5	8
245	lncRNA DIGIT and BRD3 protein form phase-separated condensates to regulate endoderm differentiation. <i>Nature Cell Biology</i> , 2020 , 22, 1211-1222	23.4	46
244	Mediator Condensates Localize Signaling Factors to Key Cell Identity Genes. <i>Molecular Cell</i> , 2019 , 76, 753-766.e6	17.6	81
243	CDK12 loss in cancer cells affects DNA damage response genes through premature cleavage and polyadenylation. <i>Nature Communications</i> , 2019 , 10, 1757	17.4	84
242	PolIII phosphorylation regulates a switch between transcriptional and splicing condensates. <i>Nature</i> , 2019 , 572, 543-548	50.4	255
241	BORIS promotes chromatin regulatory interactions in treatment-resistant cancer cells. <i>Nature</i> , 2019 , 572, 676-680	50.4	55
240	Enhancer Features that Drive Formation of Transcriptional Condensates. <i>Molecular Cell</i> , 2019 , 75, 549-561.e7	17.6	155
239	Dynamic Enhancer DNA Methylation as Basis for Transcriptional and Cellular Heterogeneity of ESCs. <i>Molecular Cell</i> , 2019 , 75, 905-920.e6	17.6	39
238	ASCL1 is a MYCN- and LMO1-dependent member of the adrenergic neuroblastoma core regulatory circuitry. <i>Nature Communications</i> , 2019 , 10, 5622	17.4	29
237	BET bromodomain proteins regulate enhancer function during adipogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 2144-2149	11.5	45
236	Rescue of Fragile X Syndrome Neurons by DNA Methylation Editing of the FMR1 Gene. <i>Cell</i> , 2018 , 172, 979-992.e6	56.2	239
235	EWS/FLI Confers Tumor Cell Synthetic Lethality to CDK12 Inhibition in Ewing Sarcoma. <i>Cancer Cell</i> , 2018 , 33, 202-216.e6	24.3	75
234	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	24.4	98

233	Pharmacological perturbation of CDK9 using selective CDK9 inhibition or degradation. <i>Nature Chemical Biology</i> , 2018 , 14, 163-170	11.7	243
232	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	4.3	33
231	Suppression of Adaptive Responses to Targeted Cancer Therapy by Transcriptional Repression. <i>Cancer Discovery</i> , 2018 , 8, 59-73	24.4	67
230	Regulation and Dysregulation of Chromosome Structure in Cancer. <i>Annual Review of Cancer Biology</i> , 2018 , 2, 21-40	13.3	19
229	Selective gene dependencies in MYCN-amplified neuroblastoma include the core transcriptional regulatory circuitry. <i>Nature Genetics</i> , 2018 , 50, 1240-1246	36.3	94
228	Transcription Factors Activate Genes through the Phase-Separation Capacity of Their Activation Domains. <i>Cell</i> , 2018 , 175, 1842-1855.e16	56.2	636
227	Non-overlapping Control of Transcriptome by Promoter- and Super-Enhancer-Associated Dependencies in Multiple Myeloma. <i>Cell Reports</i> , 2018 , 25, 3693-3705.e6	10.6	11
226	Coactivator condensation at super-enhancers links phase separation and gene control. <i>Science</i> , 2018 , 361,	33.3	951
225	JDP2: An oncogenic bZIP transcription factor in T cell acute lymphoblastic leukemia. <i>Journal of Experimental Medicine</i> , 2018 , 215, 1929-1945	16.6	11
224	Activation of the oncogene through a somatically acquired neomorphic promoter in T-cell acute lymphoblastic leukemia. <i>Blood</i> , 2017 , 129, 3221-3226	2.2	41
223	Super-Enhancer-Mediated RNA Processing Revealed by Integrative MicroRNA Network Analysis. <i>Cell</i> , 2017 , 168, 1000-1014.e15	56.2	167
222	Transcriptional Addiction in Cancer. <i>Cell</i> , 2017 , 168, 629-643	56.2	491
221	Small genomic insertions form enhancers that misregulate oncogenes. <i>Nature Communications</i> , 2017 , 8, 14385	17.4	46
220	Integrated genomic analyses of de novo pathways underlying atypical meningiomas. <i>Nature Communications</i> , 2017 , 8, 14433	17.4	95
219	The long noncoding RNA controls cardiac fibrosis and remodeling. <i>Science Translational Medicine</i> , 2017 , 9,	17.5	167
218	PHF6 regulates phenotypic plasticity through chromatin organization within lineage-specific genes. <i>Genes and Development</i> , 2017 , 31, 973-989	12.6	27
217	A Phase Separation Model for Transcriptional Control. <i>Cell</i> , 2017 , 169, 13-23	56.2	856
216	A CD47-associated super-enhancer links pro-inflammatory signalling to CD47 upregulation in breast cancer. <i>Nature Communications</i> , 2017 , 8, 14802	17.4	101

215	TOX Regulates Growth, DNA Repair, and Genomic Instability in T-cell Acute Lymphoblastic Leukemia. <i>Cancer Discovery</i> , 2017 , 7, 1336-1353	24.4	30
214	Activation of the p53 Transcriptional Program Sensitizes Cancer Cells to Cdk7 Inhibitors. <i>Cell Reports</i> , 2017 , 21, 467-481	10.6	40
213	New Insights into Genome Structure: Genes of a Feather Stick Together. <i>Molecular Cell</i> , 2017 , 67, 730-731	17.6	7
212	YY1 Is a Structural Regulator of Enhancer-Promoter Loops. <i>Cell</i> , 2017 , 171, 1573-1588.e28	56.2	444
211	Covalent targeting of remote cysteine residues to develop CDK12 and CDK13 inhibitors. <i>Nature Chemical Biology</i> , 2016 , 12, 876-84	11.7	162
210	The rate of protein synthesis in hematopoietic stem cells is limited partly by 4E-BPs. <i>Genes and Development</i> , 2016 , 30, 1698-703	12.6	48
209	Recurrent somatic mutations in POLR2A define a distinct subset of meningiomas. <i>Nature Genetics</i> , 2016 , 48, 1253-9	36.3	173
208	Editing DNA Methylation in the Mammalian Genome. <i>Cell</i> , 2016 , 167, 233-247.e17	56.2	690
207	Insulated Neighborhoods: Structural and Functional Units of Mammalian Gene Control. <i>Cell</i> , 2016 , 167, 1188-1200	56.2	261
206	A zebrafish melanoma model reveals emergence of neural crest identity during melanoma initiation. <i>Science</i> , 2016 , 351, aad2197	33.3	223
205	3D Chromosome Regulatory Landscape of Human Pluripotent Cells. <i>Cell Stem Cell</i> , 2016 , 18, 262-75	18	271
204	Epigenomic analysis detects aberrant super-enhancer DNA methylation in human cancer. <i>Genome Biology</i> , 2016 , 17, 11	18.3	141
203	Activation of proto-oncogenes by disruption of chromosome neighborhoods. <i>Science</i> , 2016 , 351, 1454-1458	35.8	600
202	Models of human core transcriptional regulatory circuitries. <i>Genome Research</i> , 2016 , 26, 385-96	9.7	153
201	Response and resistance to BET bromodomain inhibitors in triple-negative breast cancer. <i>Nature</i> , 2016 , 529, 413-417	50.4	363
200	Activation of the LMO2 Oncogene in T-ALL through a Somatic Acquired Neomorphic Promoter. <i>Blood</i> , 2016 , 128, 733-733	2.2	
199	Stress from Nucleotide Depletion Activates the Transcriptional Regulator HEXIM1 to Suppress Melanoma. <i>Molecular Cell</i> , 2016 , 62, 34-46	17.6	52
198	Parkinson-associated risk variant in distal enhancer of β synuclein modulates target gene expression. <i>Nature</i> , 2016 , 533, 95-9	50.4	360

197	Convergence of developmental and oncogenic signaling pathways at transcriptional super-enhancers. <i>Molecular Cell</i> , 2015 , 58, 362-70	17.6	287
196	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, 3841-6	11.5	86
195	CDK7-dependent transcriptional addiction in triple-negative breast cancer. <i>Cell</i> , 2015 , 163, 174-86	56.2	268
194	Transcription factor trapping by RNA in gene regulatory elements. <i>Science</i> , 2015 , 350, 978-81	33.3	267
193	Genetic predisposition to neuroblastoma mediated by a LMO1 super-enhancer polymorphism. <i>Nature</i> , 2015 , 528, 418-21	50.4	201
192	A Systematic Approach to Identify Candidate Transcription Factors that Control Cell Identity. <i>Stem Cell Reports</i> , 2015 , 5, 763-775	8	93
191	Genome-wide localization of small molecules. <i>Nature Biotechnology</i> , 2014 , 32, 92-6	44.5	138
190	MYC and transcription elongation. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2014 , 4, a020990	5.4	74
189	CDK7 inhibition suppresses super-enhancer-linked oncogenic transcription in MYCN-driven cancer. <i>Cell</i> , 2014 , 159, 1126-1139	56.2	386
188	Oncogene regulation. An oncogenic super-enhancer formed through somatic mutation of a noncoding intergenic element. <i>Science</i> , 2014 , 346, 1373-7	33.3	484
187	Targeting transcription regulation in cancer with a covalent CDK7 inhibitor. <i>Nature</i> , 2014 , 511, 616-20	50.4	507
186	The developmental potential of iPSCs is greatly influenced by reprogramming factor selection. <i>Cell Stem Cell</i> , 2014 , 15, 295-309	18	112
185	D-cyclins repress apoptosis in hematopoietic cells by controlling death receptor Fas and its ligand FasL. <i>Developmental Cell</i> , 2014 , 30, 255-67	10.2	22
184	Control of cell identity genes occurs in insulated neighborhoods in mammalian chromosomes. <i>Cell</i> , 2014 , 159, 374-387	56.2	605
183	Systematic identification of culture conditions for induction and maintenance of naive human pluripotency. <i>Cell Stem Cell</i> , 2014 , 15, 471-487	18	506
182	Small-molecule ROR β antagonists inhibit T helper 17 cell transcriptional network by divergent mechanisms. <i>Immunity</i> , 2014 , 40, 477-89	32.3	207
181	ZFH4 interacts with the NuRD core member CHD4 and regulates the glioblastoma tumor-initiating cell state. <i>Cell Reports</i> , 2014 , 6, 313-24	10.6	77
180	SMC complexes link gene expression and genome architecture. <i>Current Opinion in Genetics and Development</i> , 2014 , 25, 131-7	4.9	13

179	Direct lineage conversion of adult mouse liver cells and B lymphocytes to neural stem cells. <i>Stem Cell Reports</i> , 2014 , 3, 948-56	8	50
178	Targeting transcriptional addictions in small cell lung cancer with a covalent CDK7 inhibitor. <i>Cancer Cell</i> , 2014 , 26, 909-922	24.3	294
177	Saltatory remodeling of Hox chromatin in response to rostrocaudal patterning signals. <i>Nature Neuroscience</i> , 2013 , 16, 1191-1198	25.5	103
176	Global transcriptional and translational repression in human-embryonic-stem-cell-derived Rett syndrome neurons. <i>Cell Stem Cell</i> , 2013 , 13, 446-58	18	217
175	Super-enhancers in the control of cell identity and disease. <i>Cell</i> , 2013 , 155, 934-47	56.2	2053
174	Discovery and characterization of super-enhancer-associated dependencies in diffuse large B cell lymphoma. <i>Cancer Cell</i> , 2013 , 24, 777-90	24.3	491
173	Multiple structural maintenance of chromosome complexes at transcriptional regulatory elements. <i>Stem Cell Reports</i> , 2013 , 1, 371-8	8	86
172	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, 2876-81	11.5	345
171	Transcriptional regulation and its misregulation in disease. <i>Cell</i> , 2013 , 152, 1237-51	56.2	805
170	Master transcription factors and mediator establish super-enhancers at key cell identity genes. <i>Cell</i> , 2013 , 153, 307-19	56.2	2252
169	Selective inhibition of tumor oncogenes by disruption of super-enhancers. <i>Cell</i> , 2013 , 153, 320-34	56.2	1744
168	Poised chromatin at the ZEB1 promoter enables breast cancer cell plasticity and enhances tumorigenicity. <i>Cell</i> , 2013 , 154, 61-74	56.2	608
167	Role of SWI/SNF in acute leukemia maintenance and enhancer-mediated Myc regulation. <i>Genes and Development</i> , 2013 , 27, 2648-62	12.6	300
166	The TAL1 complex targets the FBXW7 tumor suppressor by activating miR-223 in human T cell acute lymphoblastic leukemia. <i>Journal of Experimental Medicine</i> , 2013 , 210, 1545-57	16.6	90
165	Let-7 represses Nr6a1 and a mid-gestation developmental program in adult fibroblasts. <i>Genes and Development</i> , 2013 , 27, 941-54	12.6	34
164	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, 16061-6	11.5	106
163	Core transcriptional regulatory circuit controlled by the TAL1 complex in human T cell acute lymphoblastic leukemia. <i>Cancer Cell</i> , 2012 , 22, 209-21	24.3	202
162	Transcriptional amplification in tumor cells with elevated c-Myc. <i>Cell</i> , 2012 , 151, 56-67	56.2	996

161	Revisiting global gene expression analysis. <i>Cell</i> , 2012 , 151, 476-82	56.2	410
160	Grounded: transcriptional pausing in naive mESCs. <i>Cell Stem Cell</i> , 2012 , 10, 484-5	18	1
159	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, 13004-9	11.5	137
158	CpG island structure and trithorax/polycomb chromatin domains in human cells. <i>Genomics</i> , 2012 , 100, 320-6	4.3	27
157	Functional association of Gdown1 with RNA polymerase II poised on human genes. <i>Molecular Cell</i> , 2012 , 45, 38-50	17.6	99
156	Nanog-like regulates endoderm formation through the Mxtx2-Nodal pathway. <i>Developmental Cell</i> , 2012 , 22, 625-38	10.2	68
155	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, 319-32	18	91
154	Enhancer decommissioning by LSD1 during embryonic stem cell differentiation. <i>Nature</i> , 2012 , 482, 221-5	50.4	436
153	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, 535-40	11.5	139
152	Ligand-dependent dynamics of retinoic acid receptor binding during early neurogenesis. <i>Genome Biology</i> , 2011 , 12, R2	18.3	101
151	Densely interconnected transcriptional circuits control cell states in human hematopoiesis. <i>Cell</i> , 2011 , 144, 296-309	56.2	655
150	BET bromodomain inhibition as a therapeutic strategy to target c-Myc. <i>Cell</i> , 2011 , 146, 904-17	56.2	2045
149	Master transcription factors determine cell-type-specific responses to TGF- β signaling. <i>Cell</i> , 2011 , 147, 565-76	56.2	447
148	Lineage regulators direct BMP and Wnt pathways to cell-specific programs during differentiation and regeneration. <i>Cell</i> , 2011 , 147, 577-89	56.2	234
147	The Msx1 Homeoprotein Recruits Polycomb to the Nuclear Periphery during Development. <i>Developmental Cell</i> , 2011 , 21, 575-88	10.2	70
146	Genome-wide maps of histone modifications unwind in vivo chromatin states of the hair follicle lineage. <i>Cell Stem Cell</i> , 2011 , 9, 219-32	18	159
145	Evidence that gene activation and silencing during stem cell differentiation requires a transcriptionally paused intermediate state. <i>PLoS ONE</i> , 2011 , 6, e22416	3.7	9
144	Gene induction and repression during terminal erythropoiesis are mediated by distinct epigenetic changes. <i>Blood</i> , 2011 , 118, e128-38	2.2	84

143	The histone methyltransferase SETDB1 is recurrently amplified in melanoma and accelerates its onset. <i>Nature</i> , 2011 , 471, 513-7	50.4	405
142	DHODH modulates transcriptional elongation in the neural crest and melanoma. <i>Nature</i> , 2011 , 471, 518-22	32.4	329
141	Control of the embryonic stem cell state. <i>Cell</i> , 2011 , 144, 940-54	56.2	853
140	Embryonic stem cell-based mapping of developmental transcriptional programs. <i>Nature Methods</i> , 2011 , 8, 1056-8	21.6	60
139	Transcriptional role of cyclin D1 in development revealed by a genetic-proteomic screen. <i>Nature</i> , 2010 , 463, 374-8	50.4	217
138	Mediator and cohesin connect gene expression and chromatin architecture. <i>Nature</i> , 2010 , 467, 430-5	50.4	1410
137	Ten years of genetics and genomics: what have we achieved and where are we heading?. <i>Nature Reviews Genetics</i> , 2010 , 11, 723-33	30.1	50
136	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, 1479-84	12.6	84
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, 21931-6	11.5	2453
134	Short RNAs are transcribed from repressed polycomb target genes and interact with polycomb repressive complex-2. <i>Molecular Cell</i> , 2010 , 38, 675-88	17.6	312
133	c-Myc regulates transcriptional pause release. <i>Cell</i> , 2010 , 141, 432-45	56.2	930
132	Derivation of pre-X inactivation human embryonic stem cells under physiological oxygen concentrations. <i>Cell</i> , 2010 , 141, 872-83	56.2	306
131	Global control of motor neuron topography mediated by the repressive actions of a single hox gene. <i>Neuron</i> , 2010 , 67, 781-96	13.9	107
130	Chromatin structure and gene expression programs of human embryonic and induced pluripotent stem cells. <i>Cell Stem Cell</i> , 2010 , 7, 249-57	18	347
129	Transcription. Repressive transcription. <i>Science</i> , 2010 , 329, 150-1	33.3	45
128	SetDB1 contributes to repression of genes encoding developmental regulators and maintenance of ES cell state. <i>Genes and Development</i> , 2009 , 23, 2484-9	12.6	228
127	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, 17876-81	11.5	161
126	Mir-214-dependent regulation of the polycomb protein Ezh2 in skeletal muscle and embryonic stem cells. <i>Molecular Cell</i> , 2009 , 36, 61-74	17.6	285

125	Analysis of the mouse embryonic stem cell regulatory networks obtained by ChIP-chip and CHIP-PET. <i>Genome Biology</i> , 2008 , 9, R126	18.3	47
124	Divergent transcription from active promoters. <i>Science</i> , 2008 , 322, 1849-51	33.3	695
123	Genome-wide analysis of the H3K4 histone demethylase RBP2 reveals a transcriptional program controlling differentiation. <i>Molecular Cell</i> , 2008 , 31, 520-530	17.6	105
122	Wnt signaling promotes reprogramming of somatic cells to pluripotency. <i>Cell Stem Cell</i> , 2008 , 3, 132-5	18	357
121	Stem cells, the molecular circuitry of pluripotency and nuclear reprogramming. <i>Cell</i> , 2008 , 132, 567-82	56.2	1126
120	Connecting microRNA genes to the core transcriptional regulatory circuitry of embryonic stem cells. <i>Cell</i> , 2008 , 134, 521-33	56.2	1228
119	H2AZ is enriched at polycomb complex target genes in ES cells and is necessary for lineage commitment. <i>Cell</i> , 2008 , 135, 649-61	56.2	264
118	Aberrant chromatin at genes encoding stem cell regulators in human mixed-lineage leukemia. <i>Genes and Development</i> , 2008 , 22, 3403-8	12.6	204
117	Tcf3 is an integral component of the core regulatory circuitry of embryonic stem cells. <i>Genes and Development</i> , 2008 , 22, 746-55	12.6	384
116	RNA polymerase stalling at developmental control genes in the <i>Drosophila melanogaster</i> embryo. <i>Nature Genetics</i> , 2007 , 39, 1512-6	36.3	589
115	Foxp3 occupancy and regulation of key target genes during T-cell stimulation. <i>Nature</i> , 2007 , 445, 931-5	50.4	577
114	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, 385-90	12.6	232
113	A chromatin landmark and transcription initiation at most promoters in human cells. <i>Cell</i> , 2007 , 130, 77-88	56.2	1541
112	Cell cycle genes are the evolutionarily conserved targets of the E2F4 transcription factor. <i>PLoS ONE</i> , 2007 , 2, e1061	3.7	49
111	A hypothesis-based approach for identifying the binding specificity of regulatory proteins from chromatin immunoprecipitation data. <i>Bioinformatics</i> , 2006 , 22, 423-9	7.2	70
110	Activated signal transduction kinases frequently occupy target genes. <i>Science</i> , 2006 , 313, 533-6	33.3	208
109	Core transcriptional regulatory circuitry in human hepatocytes. <i>Molecular Systems Biology</i> , 2006 , 2, 2006-0017	10.1	155
108	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, 18261-6	11.5	639

107	Coordinated binding of NF-kappaB 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, 5899-904	11.5	135
106	Zebrafish promoter microarrays identify actively transcribed embryonic genes. <i>Genome Biology</i> , 2006 , 7, R71	18.3	75
105	Control of developmental regulators by Polycomb in human embryonic stem cells. <i>Cell</i> , 2006 , 125, 301-136.2	136.2	1882
104	Transcriptional regulatory networks downstream of TAL1/SCL in T-cell acute lymphoblastic leukemia. <i>Blood</i> , 2006 , 108, 986-92	2.2	58
103	High-resolution computational models of genome binding events. <i>Nature Biotechnology</i> , 2006 , 24, 963-74.5	74.5	74
102	Evidence for an instructive mechanism of de novo methylation in cancer cells. <i>Nature Genetics</i> , 2006 , 38, 149-53	36.3	419
101	Chromatin immunoprecipitation and microarray-based analysis of protein location. <i>Nature Protocols</i> , 2006 , 1, 729-48	18.8	581
100	Polycomb complexes repress developmental regulators in murine embryonic stem cells. <i>Nature</i> , 2006 , 441, 349-53	50.4	2008
99	Global and gene-specific analyses show distinct roles for Myod and Myog at a common set of promoters. <i>EMBO Journal</i> , 2006 , 25, 502-11	13	188
98	Binding of pRB to the PHD protein RBP2 promotes cellular differentiation. <i>Molecular Cell</i> , 2005 , 18, 623-35.6	35.6	187
97	Genome-wide map of nucleosome acetylation and methylation in yeast. <i>Cell</i> , 2005 , 122, 517-27	56.2	1102
96	Core transcriptional regulatory circuitry in human embryonic stem cells. <i>Cell</i> , 2005 , 122, 947-56	56.2	3494
95	Insights into host responses against pathogens from transcriptional profiling. <i>Nature Reviews Microbiology</i> , 2005 , 3, 281-94	22.2	524
94	The core centromere and Sgo1 establish a 50-kb cohesin-protected domain around centromeres during meiosis I. <i>Genes and Development</i> , 2005 , 19, 3017-30	12.6	76
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