Danny Reinberg

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	CRISPR and biochemical screens identify MAZ as a cofactor in CTCF-mediated insulation at Hox clusters. Nature Genetics, 2022, 54, 202-212.	9.4	37
2	Inheritance of repressed chromatin domains during S phase requires the histone chaperone NPM1. Science Advances, 2022, 8, eabm3945.	4.7	15
3	Parental nucleosome segregation and the inheritance of cellular identity. Nature Reviews Genetics, 2021, 22, 379-392.	7.7	63
4	Structures of monomeric and dimeric PRC2:EZH1 reveal flexible modules involved in chromatin compaction. Nature Communications, 2021, 12, 714.	5.8	54
5	Early behavioral and molecular events leading to caste switching in the ant <i>Harpegnathos</i> . Genes and Development, 2021, 35, 410-424.	2.7	17
6	Reversible plasticity in brain size, behaviour and physiology characterizes caste transitions in a socially flexible ant (<i>Harpegnathos saltator</i>). Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20210141.	1.2	32
7	The H3K36me2 writer-reader dependency in H3K27M-DIPG. Science Advances, 2021, 7, .	4.7	20
8	A molecular toolkit for superorganisms. Trends in Genetics, 2021, 37, 846-859.	2.9	6
9	The missing link <i>er</i> : emerging trends for H1 variant-specific functions. Genes and Development, 2021, 35, 40-58.	2.7	34
10	NRF1 association with AUTS2-Polycomb mediates specific gene activation in the brain. Molecular Cell, 2021, 81, 4663-4676.e8.	4.5	23
11	Evolution, developmental expression and function of odorant receptors in insects. Journal of Experimental Biology, 2020, 223, .	0.8	67
12	Active and Repressed Chromatin Domains Exhibit Distinct Nucleosome Segregation during DNA Replication. Cell, 2019, 179, 953-963.e11.	13.5	116
13	Automethylation of PRC2 promotes H3K27 methylation and is impaired in H3K27M pediatric glioma. Genes and Development, 2019, 33, 1428-1440.	2.7	75
14	A Method to Study de novo Formation of Chromatin Domains. Journal of Visualized Experiments, 2019, , .	0.2	0
15	Distinct Classes of Chromatin Loops Revealed by Deletion of an RNA-Binding Region in CTCF. Molecular Cell, 2019, 76, 395-411.e13.	4.5	172
16	RNA Interactions Are Essential for CTCF-Mediated Genome Organization. Molecular Cell, 2019, 76, 412-422.e5.	4.5	183
17	LEDGF and HDGF2 relieve the nucleosome-induced barrier to transcription in differentiated cells. Science Advances, 2019, 5, eaay3068.	4.7	61
18	PRC2 is high maintenance. Genes and Development, 2019, 33, 903-935.	2.7	197

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19	Distinct Stimulatory Mechanisms Regulate the Catalytic Activity of Polycomb Repressive Complex 2. Molecular Cell, 2018, 70, 435-448.e5.	4.5	90
20	Allosteric Activation Dictates PRC2 Activity Independent of Its Recruitment to Chromatin. Molecular Cell, 2018, 70, 422-434.e6.	4.5	100
21	Multiple modes of PRC2 inhibition elicit global chromatin alterations in H3K27M pediatric glioma. Science Advances, 2018, 4, eaau5935.	4.7	126
22	Antennal Olfactory Physiology and Behavior of Males of the Ponerine Ant Harpegnathos saltator. Journal of Chemical Ecology, 2018, 44, 999-1007.	0.9	13
23	Recent Advances in Behavioral (Epi)Genetics in Eusocial Insects. Annual Review of Genetics, 2018, 52, 489-510.	3.2	55
24	Chromatin domains rich in inheritance. Science, 2018, 361, 33-34.	6.0	118
25	Functions of FACT in Breaking the Nucleosome and Maintaining Its Integrity at the Single-Nucleosome Level. Molecular Cell, 2018, 71, 284-293.e4.	4.5	87
26	Capturing the Onset of PRC2-Mediated Repressive Domain Formation. Molecular Cell, 2018, 70, 1149-1162.e5.	4.5	222
27	RNA Binding to CBP Stimulates Histone Acetylation and Transcription. Cell, 2017, 168, 135-149.e22.	13.5	298
28	Chemosensory sensitivity reflects reproductive status in the ant Harpegnathos saltator. Scientific Reports, 2017, 7, 3732.	1.6	33
29	Low-Grade Astrocytoma Mutations in IDH1, P53, and ATRX Cooperate to Block Differentiation of Human Neural Stem Cells via Repression of SOX2. Cell Reports, 2017, 21, 1267-1280.	2.9	95
30	Specialized odorant receptors in social insects that detect cuticular hydrocarbon cues and candidate pheromones. Nature Communications, 2017, 8, 297.	5.8	95
31	PR-Set7 deficiency limits uterine epithelial population growth hampering postnatal gland formation in mice. Cell Death and Differentiation, 2017, 24, 2013-2021.	5.0	11
32	Phospho-H1 Decorates the Inter-chromatid Axis and Is Evicted along with Shugoshin by SET during Mitosis. Molecular Cell, 2017, 67, 579-593.e6.	4.5	20
33	An Engineered orco Mutation Produces Aberrant Social Behavior and Defective Neural Development in Ants. Cell, 2017, 170, 736-747.e9.	13.5	188
34	The Neuropeptide Corazonin Controls Social Behavior and Caste Identity in Ants. Cell, 2017, 170, 748-759.e12.	13.5	146
35	Functional characterization of odorant receptors in the ponerine ant, <i>Harpegnathos saltator</i> . Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8586-8591. -	3.3	84
36	The chromatin remodeling factor CHD7 controls cerebellar development by regulating reelin expression. Journal of Clinical Investigation, 2017, 127, 874-887.	3.9	61

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37	CTCF-mediated topological boundaries during development foster appropriate gene regulation. Genes and Development, 2016, 30, 2657-2662.	2.7	161
38	ISL1 and JMJD3 synergistically control cardiac differentiation of embryonic stem cells. Nucleic Acids Research, 2016, 44, 6741-6755.	6.5	40
39	MED12 Regulates HSC-Specific Enhancers Independently of Mediator Kinase Activity to Control Hematopoiesis. Cell Stem Cell, 2016, 19, 784-799.	5.2	88
40	Structural basis of oncogenic histone H3K27M inhibition of human polycomb repressive complex 2. Nature Communications, 2016, 7, 11316.	5.8	326
41	Chromatin Starts to Come Clean. Molecular Cell, 2016, 64, 439-441.	4.5	2
42	Co-repressor CBFA2T2 regulates pluripotency and germline development. Nature, 2016, 534, 387-390.	13.7	61
43	Epigenetic (re)programming of caste-specific behavior in the ant <i>Camponotus floridanus</i> . Science, 2016, 351, aac6633.	6.0	184
44	USP7 Cooperates with SCML2 To Regulate the Activity of PRC1. Molecular and Cellular Biology, 2015, 35, 1157-1168.	1.1	50
45	CTCF establishes discrete functional chromatin domains at the <i>Hox</i> clusters during differentiation. Science, 2015, 347, 1017-1021.	6.0	490
46	Spontaneous development of hepatocellular carcinoma with cancer stem cell properties in <scp>PR</scp> ― <scp>SET</scp> 7â€deficient livers. EMBO Journal, 2015, 34, 430-447.	3.5	39
47	Analysis of the Histone H3.1 Interactome: A Suitable Chaperone for the Right Event. Molecular Cell, 2015, 60, 697-709.	4.5	61
48	Cuticular Hydrocarbon Pheromones for Social Behavior and Their Coding in the Ant Antenna. Cell Reports, 2015, 12, 1261-1271.	2.9	121
49	DNA Methylation in Social Insects: How Epigenetics Can Control Behavior and Longevity. Annual Review of Entomology, 2015, 60, 435-452.	5.7	156
50	An AUTS2–Polycomb complex activates gene expression in the CNS. Nature, 2014, 516, 349-354.	13.7	264
51	Erk1/2 Activity Promotes Chromatin Features and RNAPII Phosphorylation at Developmental Promoters in Mouse ESCs. Cell, 2014, 156, 678-690.	13.5	144
52	CTCF regulates the human p53 gene through direct interaction with its natural antisense transcript, Wrap53. Genes and Development, 2014, 28, 723-734.	2.7	171
53	Selective Methylation of Histone H3 Variant H3.1 Regulates Heterochromatin Replication. Science, 2014, 343, 1249-1253.	6.0	165
54	Interactions between JARID2 and Noncoding RNAs Regulate PRC2 Recruitment to Chromatin. Molecular Cell, 2014, 53, 290-300.	4.5	320

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55	Jarid2 Is Implicated in the Initial Xist-Induced Targeting of PRC2 to the Inactive X Chromosome. Molecular Cell, 2014, 53, 301-316.	4.5	221
56	BRD4 assists elongation of both coding and enhancer RNAs by interacting with acetylated histones. Nature Structural and Molecular Biology, 2014, 21, 1047-1057.	3.6	247
57	Nascent RNA interaction keeps PRC2 activity poised and in check. Genes and Development, 2014, 28, 1983-1988.	2.7	173
58	Eusocial insects as emerging models for behavioural epigenetics. Nature Reviews Genetics, 2014, 15, 677-688.	7.7	186
59	Epigenetic inheritance: histone bookmarks across generations. Trends in Cell Biology, 2014, 24, 664-674.	3.6	136
60	Chromatin features and the epigenetic regulation of pluripotency states in ESCs. Development (Cambridge), 2014, 141, 2376-2390.	1.2	79
61	Interactions with RNA direct the Polycomb group protein SCML2 to chromatin where it represses target genes. ELife, 2014, 3, e02637.	2.8	46
62	PRC2 binds active promoters and contacts nascent RNAs in embryonic stem cells. Nature Structural and Molecular Biology, 2013, 20, 1258-1264.	3.6	281
63	Epigenome editing. Nature Biotechnology, 2013, 31, 1097-1099.	9.4	27
64	Nucleosome-binding activities within JARID2 and EZH1 regulate the function of PRC2 on chromatin. Genes and Development, 2013, 27, 2663-2677.	2.7	149
65	Social insect genomes exhibit dramatic evolution in gene composition and regulation while preserving regulatory features linked to sociality. Genome Research, 2013, 23, 1235-1247.	2.4	205
66	Putting a halt on PRC2 in pediatric glioblastoma. Nature Genetics, 2013, 45, 587-589.	9.4	9
67	SFMBT1 functions with LSD1 to regulate expression of canonical histone genes and chromatin-related factors. Genes and Development, 2013, 27, 749-766.	2.7	73
68	A chromatin link to caste identity in the carpenter ant <i>Camponotus floridanus</i> . Genome Research, 2013, 23, 486-496.	2.4	125
69	Polycomb Protein SCML2 Regulates the Cell Cycle by Binding and Modulating CDK/CYCLIN/p21 Complexes. PLoS Biology, 2013, 11, e1001737.	2.6	28
70	A double take on bivalent promoters. Genes and Development, 2013, 27, 1318-1338.	2.7	699
71	Histone chaperone FACT action during transcription through chromatin by RNA polymerase II. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7654-7659.	3.3	182
72	Deregulated FGF and homeotic gene expression underlies cerebellar vermis hypoplasia in CHARGE syndrome. ELife, 2013, 2, e01305.	2.8	55

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73	Phylogenetic and Transcriptomic Analysis of Chemosensory Receptors in a Pair of Divergent Ant Species Reveals Sex-Specific Signatures of Odor Coding. PLoS Genetics, 2012, 8, e1002930.	1.5	192
74	EZH2 couples pancreatic regeneration to neoplastic progression. Genes and Development, 2012, 26, 439-444.	2.7	103
75	Fcp1 Dephosphorylation of the RNA Polymerase II C-Terminal Domain Is Required for Efficient Transcription of Heat Shock Genes. Molecular and Cellular Biology, 2012, 32, 3428-3437.	1.1	26
76	The role of PR-Set7 in replication licensing depends on Suv4-20h. Genes and Development, 2012, 26, 2580-2589.	2.7	109
77	<i>Trans</i> -tail regulation of MLL4-catalyzed H3K4 methylation by H4R3 symmetric dimethylation is mediated by a tandem PHD of MLL4. Genes and Development, 2012, 26, 2749-2762.	2.7	181
78	PR-Set7 and H4K20me1: at the crossroads of genome integrity, cell cycle, chromosome condensation, and transcription. Genes and Development, 2012, 26, 325-337.	2.7	264
79	SIRT3 Functions in the Nucleus in the Control of Stress-Related Gene Expression. Molecular and Cellular Biology, 2012, 32, 5022-5034.	1.1	170
80	Prdm3 and Prdm16 are H3K9me1 Methyltransferases Required for Mammalian Heterochromatin Integrity. Cell, 2012, 150, 948-960.	13.5	271
81	Asymmetrically Modified Nucleosomes. Cell, 2012, 151, 181-193.	13.5	367
82	PCGF Homologs, CBX Proteins, and RYBP Define Functionally Distinct PRC1 Family Complexes. Molecular Cell, 2012, 45, 344-356.	4.5	741
83	Genome-wide and Caste-Specific DNA Methylomes of the Ants Camponotus floridanus and Harpegnathos saltator. Current Biology, 2012, 22, 1755-1764.	1.8	361
84	Crystal Structure of TDRD3 and Methyl-Arginine Binding Characterization of TDRD3, SMN and SPF30. PLoS ONE, 2012, 7, e30375.	1.1	71
85	BRD4 jump-starts transcription after mitotic silencing. Genome Biology, 2011, 12, 133.	13.9	13
86	Epigenetic inheritance: Uncontested?. Cell Research, 2011, 21, 435-441.	5.7	90
87	Chromatin higher-order structures and gene regulation. Current Opinion in Genetics and Development, 2011, 21, 175-186.	1.5	373
88	L3MBTL2 Protein Acts in Concert with PcG Protein-Mediated Monoubiquitination of H2A to Establish a Repressive Chromatin Structure. Molecular Cell, 2011, 42, 438-450.	4.5	124
89	The C-Terminal Domain of RNA Polymerase II Is Modified by Site-Specific Methylation. Science, 2011, 332, 99-103.	6.0	190
90	The Polycomb complex PRC2 and its mark in life. Nature, 2011, 469, 343-349.	13.7	2,783

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91	Histone Tails: Ideal Motifs for Probing Epigenetics through Chemical Biology Approaches. ChemBioChem, 2011, 12, 236-252.	1.3	33
92	A dual flip-out mechanism for 5mC recognition by the <i>Arabidopsis</i> SUVH5 SRA domain and its impact on DNA methylation and H3K9 dimethylation in vivo. Genes and Development, 2011, 25, 137-152.	2.7	108
93	The Structure of NSD1 Reveals an Autoregulatory Mechanism Underlying Histone H3K36 Methylation. Journal of Biological Chemistry, 2011, 286, 8361-8368.	1.6	157
94	The program for processing newly synthesized histones H3.1 and H4. Nature Structural and Molecular Biology, 2010, 17, 1343-1351.	3.6	214
95	Chromatin structure and the inheritance of epigenetic information. Nature Reviews Genetics, 2010, 11, 285-296.	7.7	642
96	New chaps in the histone chaperone arena. Genes and Development, 2010, 24, 1334-1338.	2.7	36
97	Jarid2 and PRC2, partners in regulating gene expression. Genes and Development, 2010, 24, 368-380.	2.7	434
98	Phosphorylation of the PRC2 component Ezh2 is cell cycle-regulated and up-regulates its binding to ncRNA. Genes and Development, 2010, 24, 2615-2620.	2.7	336
99	Genomic Comparison of the Ants <i>Camponotus floridanus</i> and <i>Harpegnathos saltator</i> . Science, 2010, 329, 1068-1071.	6.0	420
100	G9a and Glp Methylate Lysine 373 in the Tumor Suppressor p53. Journal of Biological Chemistry, 2010, 285, 9636-9641.	1.6	339
101	Molecular Signals of Epigenetic States. Science, 2010, 330, 612-616.	6.0	811
102	Highly Compacted Chromatin Formed In Vitro Reflects the Dynamics of Transcription Activation In Vivo. Molecular Cell, 2010, 38, 41-53.	4.5	85
103	Regulation of the Histone H4 Monomethylase PR-Set7 by CRL4Cdt2-Mediated PCNA-Dependent Degradation during DNA Damage. Molecular Cell, 2010, 40, 364-376.	4.5	213
104	MBT domain proteins in development and disease. Seminars in Cell and Developmental Biology, 2010, 21, 221-230.	2.3	138
105	Monomethylation of Histone H4-Lysine 20 Is Involved in Chromosome Structure and Stability and Is Essential for Mouse Development. Molecular and Cellular Biology, 2009, 29, 2278-2295.	1.1	271
106	Heterogeneous Nuclear Ribonucleoprotein L Is a Subunit of Human KMT3a/Set2 Complex Required for H3 Lys-36 Trimethylation Activity in Vivo. Journal of Biological Chemistry, 2009, 284, 15701-15707.	1.6	97
107	Dynamic Histone H1 Isotype 4 Methylation and Demethylation by Histone Lysine Methyltransferase G9a/KMT1C and the Jumonji Domain-containing JMJD2/KDM4 Proteins. Journal of Biological Chemistry, 2009, 284, 8395-8405.	1.6	171
108	Calorie restriction and the exercise of chromatin. Genes and Development, 2009, 23, 1849-1869.	2.7	130

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109	The Target of the NSD Family of Histone Lysine Methyltransferases Depends on the Nature of the Substrate. Journal of Biological Chemistry, 2009, 284, 34283-34295.	1.6	257
110	Role of the polycomb protein EED in the propagation of repressive histone marks. Nature, 2009, 461, 762-767.	13.7	1,018
111	Escaping fates with open states. Nature, 2009, 460, 802-803.	13.7	9
112	Processing the H3K36me3 signature. Nature Genetics, 2009, 41, 270-271.	9.4	35
113	Histones: Annotating Chromatin. Annual Review of Genetics, 2009, 43, 559-599.	3.2	737
114	A gateway to study protein lysine methylation. Nature Chemical Biology, 2008, 4, 332-334.	3.9	11
115	Is there a code embedded in proteins that is based on post-translational modifications?. Nature Reviews Molecular Cell Biology, 2008, 9, 815-820.	16.1	271
116	Ezh1 and Ezh2 Maintain Repressive Chromatin through Different Mechanisms. Molecular Cell, 2008, 32, 503-518.	4.5	748
117	Ezh2 Requires PHF1 To Efficiently Catalyze H3 Lysine 27 Trimethylation In Vivo. Molecular and Cellular Biology, 2008, 28, 2718-2731.	1.1	257
118	Nonradioactive, ultrasensitive site-specific protein–protein photocrosslinking: interactions of α-helix 2 of TATA-binding protein with general transcription factor TFIIA and transcriptional repressor NC2. Nucleic Acids Research, 2008, 36, 6143-6154.	6.5	5
119	Beyond histone methyl-lysine binding: How malignant brain tumor (MBT) protein L3MBTL1 impacts chromatin structure. Cell Cycle, 2008, 7, 578-585.	1.3	28
120	Methylation-Acetylation Interplay Activates p53 in Response to DNA Damage. Molecular and Cellular Biology, 2007, 27, 6756-6769.	1.1	168
121	SirT3 is a nuclear NAD+-dependent histone deacetylase that translocates to the mitochondria upon cellular stress. Genes and Development, 2007, 21, 920-928.	2.7	409
122	L3MBTL1, a Histone-Methylation-Dependent Chromatin Lock. Cell, 2007, 129, 915-928.	13.5	318
123	New Nomenclature for Chromatin-Modifying Enzymes. Cell, 2007, 131, 633-636.	13.5	849
124	Facultative Heterochromatin: Is There a Distinctive Molecular Signature?. Molecular Cell, 2007, 28, 1-13.	4.5	425
125	Recognition of Trimethylated Histone H3 Lysine 4 Facilitates the Recruitment of Transcription Postinitiation Factors and Pre-mRNA Splicing. Molecular Cell, 2007, 28, 665-676.	4.5	478
126	Demethylation of H3K27 Regulates Polycomb Recruitment and H2A Ubiquitination. Science, 2007, 318, 447-450.	6.0	678

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127	NAD+-dependent deacetylation of H4 lysine 16 by class III HDACs. Oncogene, 2007, 26, 5505-5520.	2.6	259
128	SIRT1 regulates the histone methyl-transferase SUV39H1 during heterochromatin formation. Nature, 2007, 450, 440-444.	13.7	380
129	Histone Lysine Demethylases and Their Impact on Epigenetics. Cell, 2006, 125, 213-217.	13.5	193
130	Histone H2B Monoubiquitination Functions Cooperatively with FACT to Regulate Elongation by RNA Polymerase II. Cell, 2006, 125, 703-717.	13.5	636
131	Methods to identify and functionally analyze factors that specifically recognize histone lysine methylation. Methods, 2006, 40, 331-338.	1.9	10
132	Promoter activation when the ChIPs are down. Nature Structural and Molecular Biology, 2006, 13, 96-97.	3.6	2
133	Histone H3 Lys 4 methylation: caught in a bind?. Genes and Development, 2006, 20, 2779-2786.	2.7	213
134	de FACTo Nucleosome Dynamics*. Journal of Biological Chemistry, 2006, 281, 23297-23301.	1.6	210
135	Drosophila Paf1 Modulates Chromatin Structure at Actively Transcribed Genes. Molecular and Cellular Biology, 2006, 26, 250-260.	1.1	110
136	Suz12 binds to silenced regions of the genomein a cell-type-specific manner. Genome Research, 2006, 16, 890-900.	2.4	276
137	SirT2 is a histone deacetylase with preference for histone H4 Lys 16 during mitosis. Genes and Development, 2006, 20, 1256-1261.	2.7	535
138	The human PAF complex coordinates transcription with events downstream of RNA synthesis. Genes and Development, 2005, 19, 1668-1673.	2.7	192
139	Histone variants meet their match. Nature Reviews Molecular Cell Biology, 2005, 6, 139-149.	16.1	260
140	PR-Set7-dependent methylation of histone H4 Lys 20 functions in repression of gene expression and is essential for mitosis. Genes and Development, 2005, 19, 431-435.	2.7	164
141	Specificity and mechanism of the histone methyltransferase Pr-Set7. Genes and Development, 2005, 19, 1444-1454.	2.7	159
142	Human but Not Yeast CHD1 Binds Directly and Selectively to Histone H3 Methylated at Lysine 4 via Its Tandem Chromodomains. Journal of Biological Chemistry, 2005, 280, 41789-41792.	1.6	338
143	Functional Characterization of Core Promoter Elements: the Downstream Core Element Is Recognized by TAF1. Molecular and Cellular Biology, 2005, 25, 9674-9686.	1.1	92
144	Composition and histone substrates of polycomb repressive group complexes change during cellular differentiation. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1859-1864.	3.3	371

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145	PARP-1 Determines Specificity in a Retinoid Signaling Pathway via Direct Modulation of Mediator. Molecular Cell, 2005, 18, 83-96.	4.5	207
146	Functional Characterization of Core Promoter Elements: DPE-Specific Transcription Requires the Protein Kinase CK2 and the PC4 Coactivator. Molecular Cell, 2005, 18, 471-481.	4.5	63
147	Monoubiquitination of Human Histone H2B: The Factors Involved and Their Roles in HOX Gene Regulation. Molecular Cell, 2005, 20, 601-611.	4.5	439
148	The key to development: interpreting the histone code?. Current Opinion in Genetics and Development, 2005, 15, 163-176.	1.5	666
149	Polycomb Group Protein Ezh2 Controls Actin Polymerization and Cell Signaling. Cell, 2005, 121, 425-436.	13.5	345
150	Silencing of human polycomb target genes is associated with methylation of histone H3 Lys 27. Genes and Development, 2004, 18, 1592-1605.	2.7	447
151	Differential Histone H3 Lys-9 and Lys-27 Methylation Profiles on the X Chromosome. Molecular and Cellular Biology, 2004, 24, 5475-5484.	1.1	194
152	Human Spt6 Stimulates Transcription Elongation by RNA Polymerase II In Vitro. Molecular and Cellular Biology, 2004, 24, 3324-3336.	1.1	106
153	Functional interactions of RNA-capping enzyme with factors that positively and negatively regulate promoter escape by RNA polymerase II. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7572-7577.	3.3	148
154	Elongation by RNA polymerase II: the short and long of it. Genes and Development, 2004, 18, 2437-2468.	2.7	596
155	From chromatin to cancer: a new histone lysine methyltransferase enters the mix. Nature Cell Biology, 2004, 6, 685-687.	4.6	40
156	Regulation of p53 activity through lysine methylation. Nature, 2004, 432, 353-360.	13.7	706
157	Transcription through chromatin: understanding a complex FACT. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2004, 1677, 87-99.	2.4	71
158	Recent highlights of RNA-polymerase-II-mediated transcription. Current Opinion in Cell Biology, 2004, 16, 263-271.	2.6	167
159	Steps Toward Understanding the Inheritance of Repressive Methyl-Lysine Marks in Histones. Cold Spring Harbor Symposia on Quantitative Biology, 2004, 69, 171-182.	2.0	14
160	Facts about FACT and transcript elongation through chromatin. Current Opinion in Genetics and Development, 2004, 14, 139-146.	1.5	111
161	A Unified Nomenclature for Protein Subunits of Mediator Complexes Linking Transcriptional Regulators to RNA Polymerase II. Molecular Cell, 2004, 14, 553-557.	4.5	230
162	Human SirT1 Interacts with Histone H1 and Promotes Formation of Facultative Heterochromatin. Molecular Cell, 2004, 16, 93-105.	4.5	796

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163	Different Ezh2-Containing Complexes Target Methylation of Histone H1 or Nucleosomal Histone H3. Molecular Cell, 2004, 14, 183-193.	4.5	393
164	Epigenetic Dynamics of Imprinted X Inactivation During Early Mouse Development. Science, 2004, 303, 644-649.	6.0	736
165	A silencing pathway to induce H3-K9 and H4-K20 trimethylation at constitutive heterochromatin. Genes and Development, 2004, 18, 1251-1262.	2.7	946
166	Histone lysine methylation: a signature for chromatin function. Trends in Genetics, 2003, 19, 629-639.	2.9	613
167	Tips in Analyzing Antibodies Directed Against Specific Histone Tail Modifications. Methods in Enzymology, 2003, 376, 255-269.	0.4	22
168	Techniques Used to Study Transcription on Chromatin Templates. Methods in Enzymology, 2003, 377, 474-499.	0.4	10
169	FACT Facilitates Transcription-Dependent Nucleosome Alteration. Science, 2003, 301, 1090-1093.	6.0	762
170	Tracking FACT and the RNA Polymerase II Elongation Complex Through Chromatin in Vivo. Science, 2003, 301, 1094-1096.	6.0	261
171	Tails of Intrigue. Cell, 2003, 113, 429-432.	13.5	282
172	Methods and tips for the purification of human histone methyltransferases. Methods, 2003, 31, 49-58.	1.9	57
173	Histone deposition and chromatin assembly by RSF. Methods, 2003, 31, 96-103.	1.9	19
174	ASAP, a Novel Protein Complex Involved in RNA Processing and Apoptosis. Molecular and Cellular Biology, 2003, 23, 2981-2990.	1.1	131
175	Facile synthesis of site-specifically acetylated and methylated histone proteins: Reagents for evaluation of the histone code hypothesis. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 12033-12038.	3.3	109
176	The mediator coactivator complex: functional and physical roles in transcriptional regulation. Journal of Cell Science, 2003, 116, 3667-3675.	1.2	123
177	Functional Analysis of the Subunits of the Chromatin Assembly Factor RSF. Molecular and Cellular Biology, 2003, 23, 6759-6768.	1.1	105
178	The C-terminal domain phosphatase and transcription elongation activities of FCP1 are regulated by phosphorylation. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 2328-2333.	3.3	31
179	The Constantly Changing Face of Chromatin. Science of Aging Knowledge Environment: SAGE KE, 2003, 2003, 4re-4.	0.9	147
180	Human Elongator facilitates RNA polymerase II transcription through chromatin. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 1241-1246.	3.3	149

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181	FCP1, a Phosphatase Specific for the Heptapeptide Repeat of the Largest Subunit of RNA Polymerase II, Stimulates Transcription Elongation. Molecular and Cellular Biology, 2002, 22, 7543-7552.	1.1	62
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