

# Danny Reinberg

## List of Publications by Year in descending order

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277  
papers

65,415  
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263

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794

247  
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301  
docs citations

301  
times ranked

45705  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Polycomb complex PRC2 and its mark in life. <i>Nature</i> , 2011, 469, 343-349.	13.7	2,783
2	Histone methyltransferase activity associated with a human multiprotein complex containing the Enhancer of Zeste protein. <i>Genes and Development</i> , 2002, 16, 2893-2905.	2.7	1,430
3	Transcription regulation by histone methylation: interplay between different covalent modifications of the core histone tails. <i>Genes and Development</i> , 2001, 15, 2343-2360.	2.7	1,316
4	Role of the polycomb protein EED in the propagation of repressive histone marks. <i>Nature</i> , 2009, 461, 762-767.	13.7	1,018
5	Analysis of the NuRD subunits reveals a histone deacetylase core complex and a connection with DNA methylation. <i>Genes and Development</i> , 1999, 13, 1924-1935.	2.7	951
6	A silencing pathway to induce H3-K9 and H4-K20 trimethylation at constitutive heterochromatin. <i>Genes and Development</i> , 2004, 18, 1251-1262.	2.7	946
7	The general transcription factors of RNA polymerase II. <i>Genes and Development</i> , 1996, 10, 2657-2683.	2.7	901
8	New Nomenclature for Chromatin-Modifying Enzymes. <i>Cell</i> , 2007, 131, 633-636.	13.5	849
9	Molecular Signals of Epigenetic States. <i>Science</i> , 2010, 330, 612-616.	6.0	811
10	Human SirT1 Interacts with Histone H1 and Promotes Formation of Facultative Heterochromatin. <i>Molecular Cell</i> , 2004, 16, 93-105.	4.5	796
11	A Unified Theory of Gene Expression. <i>Cell</i> , 2002, 108, 439-451.	13.5	787
12	MBD2 is a transcriptional repressor belonging to the MeCP1 histone deacetylase complex. <i>Nature Genetics</i> , 1999, 23, 58-61.	9.4	783
13	FACT Facilitates Transcription-Dependent Nucleosome Alteration. <i>Science</i> , 2003, 301, 1090-1093.	6.0	762
14	Ezh1 and Ezh2 Maintain Repressive Chromatin through Different Mechanisms. <i>Molecular Cell</i> , 2008, 32, 503-518.	4.5	748
15	The Dermatomyositis-Specific Autoantigen Mi2 Is a Component of a Complex Containing Histone Deacetylase and Nucleosome Remodeling Activities. <i>Cell</i> , 1998, 95, 279-289.	13.5	745
16	PCGF Homologs, CBX Proteins, and RYBP Define Functionally Distinct PRC1 Family Complexes. <i>Molecular Cell</i> , 2012, 45, 344-356.	4.5	741
17	Histones: Annotating Chromatin. <i>Annual Review of Genetics</i> , 2009, 43, 559-599.	3.2	737
18	Epigenetic Dynamics of Imprinted X Inactivation During Early Mouse Development. <i>Science</i> , 2004, 303, 644-649.	6.0	736

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19	Dual role of TFIIH in DNA excision repair and in transcription by RNA polymerase II. <i>Nature</i> , 1994, 368, 769-772.	13.7	725
20	Regulation of p53 activity through lysine methylation. <i>Nature</i> , 2004, 432, 353-360.	13.7	706
21	A double take on bivalent promoters. <i>Genes and Development</i> , 2013, 27, 1318-1338.	2.7	699
22	Demethylation of H3K27 Regulates Polycomb Recruitment and H2A Ubiquitination. <i>Science</i> , 2007, 318, 447-450.	6.0	678
23	The key to development: interpreting the histone code?. <i>Current Opinion in Genetics and Development</i> , 2005, 15, 163-176.	1.5	666
24	Human general transcription factor IIH phosphorylates the C-terminal domain of RNA polymerase II. <i>Nature</i> , 1992, 358, 641-645.	13.7	665
25	Chromatin structure and the inheritance of epigenetic information. <i>Nature Reviews Genetics</i> , 2010, 11, 285-296.	7.7	642
26	Histone H2B Monoubiquitination Functions Cooperatively with FACT to Regulate Elongation by RNA Polymerase II. <i>Cell</i> , 2006, 125, 703-717.	13.5	636
27	Histone lysine methylation: a signature for chromatin function. <i>Trends in Genetics</i> , 2003, 19, 629-639.	2.9	613
28	Elongation by RNA polymerase II: the short and long of it. <i>Genes and Development</i> , 2004, 18, 2437-2468.	2.7	596
29	FACT, a Factor that Facilitates Transcript Elongation through Nucleosomes. <i>Cell</i> , 1998, 92, 105-116.	13.5	587
30	Histone Deacetylases and SAP18, a Novel Polypeptide, Are Components of a Human Sin3 Complex. <i>Cell</i> , 1997, 89, 357-364.	13.5	548
31	SirT2 is a histone deacetylase with preference for histone H4 Lys 16 during mitosis. <i>Genes and Development</i> , 2006, 20, 1256-1261.	2.7	535
32	PR-Set7 Is a Nucleosome-Specific Methyltransferase that Modifies Lysine 20 of Histone H4 and Is Associated with Silent Chromatin. <i>Molecular Cell</i> , 2002, 9, 1201-1213.	4.5	525
33	The chromatin-specific transcription elongation factor FACT comprises human SPT16 and SSRP1 proteins. <i>Nature</i> , 1999, 400, 284-288.	13.7	497
34	CTCF establishes discrete functional chromatin domains at the <i>Hox</i> clusters during differentiation. <i>Science</i> , 2015, 347, 1017-1021.	6.0	490
35	Set9, a novel histone H3 methyltransferase that facilitates transcription by precluding histone tail modifications required for heterochromatin formation. <i>Genes and Development</i> , 2002, 16, 479-489.	2.7	482
36	Recognition of Trimethylated Histone H3 Lysine 4 Facilitates the Recruitment of Transcription Postinitiation Factors and Pre-mRNA Splicing. <i>Molecular Cell</i> , 2007, 28, 665-676.	4.5	478

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37	Common Themes in Assembly and Function of Eukaryotic Transcription Complexes. Annual Review of Biochemistry, 1995, 64, 533-561.	5.0	448
38	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
39	Monoubiquitination of Human Histone H2B: The Factors Involved and Their Roles in HOX Gene Regulation. Molecular Cell, 2005, 20, 601-611.	4.5	439
40	Jarid2 and PRC2, partners in regulating gene expression. Genes and Development, 2010, 24, 368-380.	2.7	434
41	Cdk-activating kinase complex is a component of human transcription factor TFIIH. Nature, 1995, 374, 283-287.	13.7	430
42	Facultative Heterochromatin: Is There a Distinctive Molecular Signature?. Molecular Cell, 2007, 28, 1-13.	4.5	425
43	Transcription by RNA polymerase II: initiator-directed formation of transcription-competent complexes <sup>1</sup>. FASEB Journal, 1992, 6, 3300-3309.	0.2	422
44	Genomic Comparison of the Ants <i>Camponotus floridanus</i> and <i>Harpegnathos saltator</i> . Science, 2010, 329, 1068-1071.	6.0	420
45	Binding of general transcription factor TFIIB to an acidic activating region. Nature, 1991, 353, 569-571.	13.7	416
46	SirT3 is a nuclear NAD <sup>+</sup> -dependent histone deacetylase that translocates to the mitochondria upon cellular stress. Genes and Development, 2007, 21, 920-928.	2.7	409
47	Different Ezh2-Containing Complexes Target Methylation of Histone H1 or Nucleosomal Histone H3. Molecular Cell, 2004, 14, 183-193.	4.5	393
48	Dr1, a TATA-binding protein-associated phosphoprotein and inhibitor of class II gene transcription. Cell, 1992, 70, 477-489.	13.5	389
49	SIRT1 regulates the histone methyl-transferase SUV39H1 during heterochromatin formation. Nature, 2007, 450, 440-444.	13.7	380
50	Chromatin higher-order structures and gene regulation. Current Opinion in Genetics and Development, 2011, 21, 175-186.	1.5	373
51	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
52	Asymmetrically Modified Nucleosomes. Cell, 2012, 151, 181-193.	13.5	367
53	DNA topoisomerase I is involved in both repression and activation of transcription. Nature, 1993, 365, 227-232.	13.7	361
54	Genome-wide and Caste-Specific DNA Methylomes of the Ants <i>Camponotus floridanus</i> and <i>Harpegnathos saltator</i> . Current Biology, 2012, 22, 1755-1764.	1.8	361

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55	Initiation of Transcription by RNA Polymerase II: A Multi-step Process. <i>Progress in Molecular Biology and Translational Science</i> , 1993, 44, 67-108.	1.9	354
56	Polycomb Group Protein Ezh2 Controls Actin Polymerization and Cell Signaling. <i>Cell</i> , 2005, 121, 425-436.	13.5	345
57	A human RNA polymerase II complex associated with SRB and DNA-repair proteins. <i>Nature</i> , 1996, 381, 86-89.	13.7	342
58	TFIIH is negatively regulated by cdk8-containing mediator complexes. <i>Nature</i> , 2000, 407, 102-106.	13.7	341
59	C9a and Glp Methylate Lysine 373 in the Tumor Suppressor p53. <i>Journal of Biological Chemistry</i> , 2010, 285, 9636-9641.	1.6	339
60	Human but Not Yeast CHD1 Binds Directly and Selectively to Histone H3 Methylated at Lysine 4 via Its Tandem Chromodomains. <i>Journal of Biological Chemistry</i> , 2005, 280, 41789-41792.	1.6	338
61	New core promoter element in RNA polymerase II-dependent transcription: sequence-specific DNA binding by transcription factor TFIIB. <i>Genes and Development</i> , 1998, 12, 34-44.	2.7	336
62	Phosphorylation of the PRC2 component Ezh2 is cell cycle-regulated and up-regulates its binding to ncRNA. <i>Genes and Development</i> , 2010, 24, 2615-2620.	2.7	336
63	Structural basis of oncogenic histone H3K27M inhibition of human polycomb repressive complex 2. <i>Nature Communications</i> , 2016, 7, 11316.	5.8	326
64	Interaction of human thyroid hormone receptor beta with transcription factor TFIIB may mediate target gene derepression and activation by thyroid hormone.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993, 90, 8832-8836.	3.3	321
65	Interactions between JARID2 and Noncoding RNAs Regulate PRC2 Recruitment to Chromatin. <i>Molecular Cell</i> , 2014, 53, 290-300.	4.5	320
66	L3MBTL1, a Histone-Methylation-Dependent Chromatin Lock. <i>Cell</i> , 2007, 129, 915-928.	13.5	318
67	The nonphosphorylated form of RNA polymerase II preferentially associates with the preinitiation complex.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991, 88, 10004-10008.	3.3	307
68	Cloning of a human gene encoding the general transcription initiation factor IIB. <i>Nature</i> , 1991, 352, 689-695.	13.7	307
69	RNA Binding to CBP Stimulates Histone Acetylation and Transcription. <i>Cell</i> , 2017, 168, 135-149.e22.	13.5	298
70	Recycling of the general transcription factors during RNA polymerase II transcription.. <i>Genes and Development</i> , 1995, 9, 1479-1490.	2.7	289
71	Tails of Intrigue. <i>Cell</i> , 2003, 113, 429-432.	13.5	282
72	PRC2 binds active promoters and contacts nascent RNAs in embryonic stem cells. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1258-1264.	3.6	281

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73	Direct interaction between adenovirus E1A protein and the TATA box binding transcription factor IID.. Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 5124-5128.	3.3	278
74	Suz12 binds to silenced regions of the genome in a cell-type-specific manner. Genome Research, 2006, 16, 890-900.	2.4	276
75	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
76	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
77	Prdm3 and Prdm16 are H3K9me1 Methyltransferases Required for Mammalian Heterochromatin Integrity. Cell, 2012, 150, 948-960.	13.5	271
78	SAP30, a Novel Protein Conserved between Human and Yeast, Is a Component of a Histone Deacetylase Complex. Molecular Cell, 1998, 1, 1021-1031.	4.5	268
79	A Human RNA Polymerase II Complex Containing Factors That Modify Chromatin Structure. Molecular and Cellular Biology, 1998, 18, 5355-5363.	1.1	266
80	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
81	An AUTS2 Polycomb complex activates gene expression in the CNS. Nature, 2014, 516, 349-354.	13.7	264
82	Tracking FACT and the RNA Polymerase II Elongation Complex Through Chromatin in Vivo. Science, 2003, 301, 1094-1096.	6.0	261
83	Histone variants meet their match. Nature Reviews Molecular Cell Biology, 2005, 6, 139-149.	16.1	260
84	NAD+-dependent deacetylation of H4 lysine 16 by class III HDACs. Oncogene, 2007, 26, 5505-5520.	2.6	259
85	Ezh2 Requires PHF1 To Efficiently Catalyze H3 Lysine 27 Trimethylation In Vivo. Molecular and Cellular Biology, 2008, 28, 2718-2731.	1.1	257
86	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
87	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
88	Interaction between an acidic activator and transcription factor TFIIB is required for transcriptional activation. Nature, 1993, 363, 741-744.	13.7	245
89	Mechanism of ATP-Dependent Promoter Melting by Transcription Factor IIIH. Science, 2000, 288, 1418-1421.	6.0	236
90	Advances in RNA polymerase II transcription. Current Opinion in Cell Biology, 1992, 4, 488-495.	2.6	230

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91	A Unified Nomenclature for Protein Subunits of Mediator Complexes Linking Transcriptional Regulators to RNA Polymerase II. <i>Molecular Cell</i> , 2004, 14, 553-557.	4.5	230
92	RNA polymerase II elongation through chromatin. <i>Nature</i> , 2000, 407, 471-476.	13.7	229
93	Specific interaction between the nonphosphorylated form of RNA polymerase II and the TATA-binding protein. <i>Cell</i> , 1992, 69, 871-881.	13.5	228
94	Multiple functional domains of human transcription factor IIB: distinct interactions with two general transcription factors and RNA polymerase II.. <i>Genes and Development</i> , 1993, 7, 1021-1032.	2.7	222
95	Capturing the Onset of PRC2-Mediated Repressive Domain Formation. <i>Molecular Cell</i> , 2018, 70, 1149-1162.e5.	4.5	222
96	Jarid2 Is Implicated in the Initial Xist-Induced Targeting of PRC2 to the Inactive X Chromosome. <i>Molecular Cell</i> , 2014, 53, 301-316.	4.5	221
97	Mitotic-specific methylation of histone H4 Lys 20 follows increased PR-Set7 expression and its localization to mitotic chromosomes. <i>Genes and Development</i> , 2002, 16, 2225-2230.	2.7	217
98	The program for processing newly synthesized histones H3.1 and H4. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1343-1351.	3.6	214
99	Histone H3 Lys 4 methylation: caught in a bind?. <i>Genes and Development</i> , 2006, 20, 2779-2786.	2.7	213
100	Regulation of the Histone H4 Monomethylase PR-Set7 by CRL4Cdt2-Mediated PCNA-Dependent Degradation during DNA Damage. <i>Molecular Cell</i> , 2010, 40, 364-376.	4.5	213
101	Mammalian capping enzyme complements mutant <i>Saccharomyces cerevisiae</i> lacking mRNA guanylyltransferase and selectively binds the elongating form of RNA polymerase II. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 12898-12903.	3.3	213
102	NAT, a Human Complex Containing Srb Polypeptides that Functions as a Negative Regulator of Activated Transcription. <i>Molecular Cell</i> , 1998, 2, 213-222.	4.5	210
103	de FACTo Nucleosome Dynamics*. <i>Journal of Biological Chemistry</i> , 2006, 281, 23297-23301.	1.6	210
104	Structure and functional properties of human general transcription factor IIE. <i>Nature</i> , 1991, 354, 369-373.	13.7	209
105	Role of the Sin3-Histone Deacetylase Complex in Growth Regulation by the Candidate Tumor Suppressor p33 <sup>ING1</sup> . <i>Molecular and Cellular Biology</i> , 2002, 22, 835-848.	1.1	207
106	PARP-1 Determines Specificity in a Retinoid Signaling Pathway via Direct Modulation of Mediator. <i>Molecular Cell</i> , 2005, 18, 83-96.	4.5	207
107	Social insect genomes exhibit dramatic evolution in gene composition and regulation while preserving regulatory features linked to sociality. <i>Genome Research</i> , 2013, 23, 1235-1247.	2.4	205
108	PRC2 is high maintenance. <i>Genes and Development</i> , 2019, 33, 903-935.	2.7	197

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109	Differential Histone H3 Lys-9 and Lys-27 Methylation Profiles on the X Chromosome. <i>Molecular and Cellular Biology</i> , 2004, 24, 5475-5484.	1.1	194
110	Histone Lysine Demethylases and Their Impact on Epigenetics. <i>Cell</i> , 2006, 125, 213-217.	13.5	193
111	The human PAF complex coordinates transcription with events downstream of RNA synthesis. <i>Genes and Development</i> , 2005, 19, 1668-1673.	2.7	192
112	Phylogenetic and Transcriptomic Analysis of Chemosensory Receptors in a Pair of Divergent Ant Species Reveals Sex-Specific Signatures of Odor Coding. <i>PLoS Genetics</i> , 2012, 8, e1002930.	1.5	192
113	The C-Terminal Domain of RNA Polymerase II Is Modified by Site-Specific Methylation. <i>Science</i> , 2011, 332, 99-103.	6.0	190
114	An Engineered orco Mutation Produces Aberrant Social Behavior and Defective Neural Development in Ants. <i>Cell</i> , 2017, 170, 736-747.e9.	13.5	188
115	Eusocial insects as emerging models for behavioural epigenetics. <i>Nature Reviews Genetics</i> , 2014, 15, 677-688.	7.7	186
116	Epigenetic (re)programming of caste-specific behavior in the ant <i>Camponotus floridanus</i> . <i>Science</i> , 2016, 351, aac6633.	6.0	184
117	RNA Interactions Are Essential for CTCF-Mediated Genome Organization. <i>Molecular Cell</i> , 2019, 76, 412-422.e5.	4.5	183
118	Histone chaperone FACT action during transcription through chromatin by RNA polymerase II. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7654-7659.	3.3	182
119	Transcriptional regulation of MLL4-catalyzed H3K4 methylation by H4R3 symmetric dimethylation is mediated by a tandem PHD of MLL4. <i>Genes and Development</i> , 2012, 26, 2749-2762.	2.7	181
120	RBP1 Recruits the mSIN3-Histone Deacetylase Complex to the Pocket of Retinoblastoma Tumor Suppressor Family Proteins Found in Limited Discrete Regions of the Nucleus at Growth Arrest. <i>Molecular and Cellular Biology</i> , 2001, 21, 2918-2932.	1.1	177
121	The initiator directs the assembly of a transcription factor IID-dependent transcription complex.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991, 88, 8052-8056.	3.3	176
122	Requirement for TFIIF kinase activity in transcription by RNA polymerase II. <i>Nature</i> , 1995, 377, 557-560.	13.7	176
123	RNA polymerase II stalled at a thymine dimer: footprint and effect on excision repair. <i>Nucleic Acids Research</i> , 1997, 25, 787-793.	6.5	174
124	Nascent RNA interaction keeps PRC2 activity poised and in check. <i>Genes and Development</i> , 2014, 28, 1983-1988.	2.7	173
125	A protein phosphatase functions to recycle RNA polymerase II. <i>Genes and Development</i> , 1999, 13, 1540-1552.	2.7	173
126	Distinct Classes of Chromatin Loops Revealed by Deletion of an RNA-Binding Region in CTCF. <i>Molecular Cell</i> , 2019, 76, 395-411.e13.	4.5	172

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127	Dynamic Histone H1 Isotype 4 Methylation and Demethylation by Histone Lysine Methyltransferase G9a/KMT1C and the Jumonji Domain-containing JMJD2/KDM4 Proteins. <i>Journal of Biological Chemistry</i> , 2009, 284, 8395-8405.	1.6	171
128	CTCF regulates the human p53 gene through direct interaction with its natural antisense transcript, Wrap53. <i>Genes and Development</i> , 2014, 28, 723-734.	2.7	171
129	SIRT3 Functions in the Nucleus in the Control of Stress-Related Gene Expression. <i>Molecular and Cellular Biology</i> , 2012, 32, 5022-5034.	1.1	170
130	Where transcription meets repair. <i>Cell</i> , 1994, 77, 9-12.	13.5	169
131	Methylation-Acetylation Interplay Activates p53 in Response to DNA Damage. <i>Molecular and Cellular Biology</i> , 2007, 27, 6756-6769.	1.1	168
132	Recent highlights of RNA-polymerase-II-mediated transcription. <i>Current Opinion in Cell Biology</i> , 2004, 16, 263-271.	2.6	167
133	The small subunit of transcription factor IIF recruits RNA polymerase II into the preinitiation complex.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991, 88, 9999-10003.	3.3	166
134	Selective Methylation of Histone H3 Variant H3.1 Regulates Heterochromatin Replication. <i>Science</i> , 2014, 343, 1249-1253.	6.0	165
135	PR-Set7-dependent methylation of histone H4 Lys 20 functions in repression of gene expression and is essential for mitosis. <i>Genes and Development</i> , 2005, 19, 431-435.	2.7	164
136	CTCF-mediated topological boundaries during development foster appropriate gene regulation. <i>Genes and Development</i> , 2016, 30, 2657-2662.	2.7	161
137	Specificity and mechanism of the histone methyltransferase Pr-Set7. <i>Genes and Development</i> , 2005, 19, 1444-1454.	2.7	159
138	Human cyclin-dependent kinase-activating kinase exists in three distinct complexes.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 6488-6493.	3.3	157
139	The Structure of NSD1 Reveals an Autoregulatory Mechanism Underlying Histone H3K36 Methylation. <i>Journal of Biological Chemistry</i> , 2011, 286, 8361-8368.	1.6	157
140	DNA Methylation in Social Insects: How Epigenetics Can Control Behavior and Longevity. <i>Annual Review of Entomology</i> , 2015, 60, 435-452.	5.7	156
141	RNA polymerase II as a control panel for multiple coactivator complexes. <i>Current Opinion in Genetics and Development</i> , 1999, 9, 132-139.	1.5	155
142	Human Elongator facilitates RNA polymerase II transcription through chromatin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 1241-1246.	3.3	149
143	Nucleosome-binding activities within JARID2 and EZH1 regulate the function of PRC2 on chromatin. <i>Genes and Development</i> , 2013, 27, 2663-2677.	2.7	149
144	Functional interactions of RNA-capping enzyme with factors that positively and negatively regulate promoter escape by RNA polymerase II. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7572-7577.	3.3	148

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145	The Constantly Changing Face of Chromatin. <i>Science of Aging Knowledge Environment: SAGE KE</i> , 2003, 2003, 4re-4.	0.9	147
146	Purification and Characterization of a Human Factor That Assembles and Remodels Chromatin. <i>Journal of Biological Chemistry</i> , 2000, 275, 14787-14790.	1.6	146
147	The Neuropeptide Corazonin Controls Social Behavior and Caste Identity in Ants. <i>Cell</i> , 2017, 170, 748-759.e12.	13.5	146
148	Erk1/2 Activity Promotes Chromatin Features and RNAPII Phosphorylation at Developmental Promoters in Mouse ESCs. <i>Cell</i> , 2014, 156, 678-690.	13.5	144
149	MBT domain proteins in development and disease. <i>Seminars in Cell and Developmental Biology</i> , 2010, 21, 221-230.	2.3	138
150	Epigenetic inheritance: histone bookmarks across generations. <i>Trends in Cell Biology</i> , 2014, 24, 664-674.	3.6	136
151	Solution structure of the c-terminal core domain of human TFIIIB: Similarity to cyclin A and interaction with TATA-binding protein. <i>Cell</i> , 1995, 82, 857-867.	13.5	134
152	ASAP, a Novel Protein Complex Involved in RNA Processing and Apoptosis. <i>Molecular and Cellular Biology</i> , 2003, 23, 2981-2990.	1.1	131
153	Calorie restriction and the exercise of chromatin. <i>Genes and Development</i> , 2009, 23, 1849-1869.	2.7	130
154	Multiple modes of PRC2 inhibition elicit global chromatin alterations in H3K27M pediatric glioma. <i>Science Advances</i> , 2018, 4, eaau5935.	4.7	126
155	A chromatin link to caste identity in the carpenter ant <i>Camponotus floridanus</i> . <i>Genome Research</i> , 2013, 23, 486-496.	2.4	125
156	L3MBTL2 Protein Acts in Concert with PcG Protein-Mediated Monoubiquitination of H2A to Establish a Repressive Chromatin Structure. <i>Molecular Cell</i> , 2011, 42, 438-450.	4.5	124
157	The mediator coactivator complex: functional and physical roles in transcriptional regulation. <i>Journal of Cell Science</i> , 2003, 116, 3667-3675.	1.2	123
158	Requirement of a corepressor for Dr1-mediated repression of transcription.. <i>Genes and Development</i> , 1996, 10, 1033-1048.	2.7	121
159	Cuticular Hydrocarbon Pheromones for Social Behavior and Their Coding in the Ant Antenna. <i>Cell Reports</i> , 2015, 12, 1261-1271.	2.9	121
160	The Human Immunodeficiency Virus Transactivator Tat Interacts with the RNA Polymerase II Holoenzyme. <i>Molecular and Cellular Biology</i> , 1997, 17, 1817-1823.	1.1	120
161	The 62- and 80-kDa subunits of transcription factor IIIH mediate the interaction with Epstein-Barr virus nuclear protein 2.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 3259-3263.	3.3	118
162	Chromatin domains rich in inheritance. <i>Science</i> , 2018, 361, 33-34.	6.0	118

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