

# Danny Reinberg

## 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.

279  
papers

55,403  
citations

131  
h-index

234  
g-index

301  
ext. papers

61,032  
ext. citations

19.3  
avg, IF

7.74  
L-index

#	Paper	IF	Citations
279	CRISPR and biochemical screens identify MAZ as a cofactor in CTCF-mediated insulation at Hox clusters.. <i>Nature Genetics</i> , <b>2022</b> , 54, 202-212	36.3	2
278	Inheritance of repressed chromatin domains during S phase requires the histone chaperone NPM1.. <i>Science Advances</i> , <b>2022</b> , 8, eabm3945	14.3	0
277	NRF1 association with AUTS2-Polycomb mediates specific gene activation in the brain. <i>Molecular Cell</i> , <b>2021</b> , 81, 4663-4676.e8	17.6	4
276	Reversible plasticity in brain size, behaviour and physiology characterizes caste transitions in a socially flexible ant (). <i>Proceedings of the Royal Society B: Biological Sciences</i> , <b>2021</b> , 288, 20210141	4.4	14
275	The H3K36me2 writer-reader dependency in H3K27M-DIPG. <i>Science Advances</i> , <b>2021</b> , 7,	14.3	6
274	Parental nucleosome segregation and the inheritance of cellular identity. <i>Nature Reviews Genetics</i> , <b>2021</b> , 22, 379-392	30.1	14
273	Structures of monomeric and dimeric PRC2:EZH1 reveal flexible modules involved in chromatin compaction. <i>Nature Communications</i> , <b>2021</b> , 12, 714	17.4	8
272	Early behavioral and molecular events leading to caste switching in the ant. <i>Genes and Development</i> , <b>2021</b> , 35, 410-424	12.6	9
271	A molecular toolkit for superorganisms. <i>Trends in Genetics</i> , <b>2021</b> , 37, 846-859	8.5	2
270	The missing link: emerging trends for H1 variant-specific functions. <i>Genes and Development</i> , <b>2021</b> , 35, 40-58	12.6	11
269	Evolution, developmental expression and function of odorant receptors in insects. <i>Journal of Experimental Biology</i> , <b>2020</b> , 223,	3	37
268	Automethylation of PRC2 promotes H3K27 methylation and is impaired in H3K27M pediatric glioma. <i>Genes and Development</i> , <b>2019</b> , 33, 1428-1440	12.6	46
267	Distinct Classes of Chromatin Loops Revealed by Deletion of an RNA-Binding Region in CTCF. <i>Molecular Cell</i> , <b>2019</b> , 76, 395-411.e13	17.6	97
266	RNA Interactions Are Essential for CTCF-Mediated Genome Organization. <i>Molecular Cell</i> , <b>2019</b> , 76, 412-422.e5	17.6	92
265	LEDGF and HDGF2 relieve the nucleosome-induced barrier to transcription in differentiated cells. <i>Science Advances</i> , <b>2019</b> , 5, eaay3068	14.3	32
264	PRC2 is high maintenance. <i>Genes and Development</i> , <b>2019</b> , 33, 903-935	12.6	93
263	Active and Repressed Chromatin Domains Exhibit Distinct Nucleosome Segregation during DNA Replication. <i>Cell</i> , <b>2019</b> , 179, 953-963.e11	56.2	63

262	Distinct Stimulatory Mechanisms Regulate the Catalytic Activity of Polycomb Repressive Complex 2. <i>Molecular Cell</i> , <b>2018</b> , 70, 435-448.e5	17.6	48
261	Allosteric Activation Dictates PRC2 Activity Independent of Its Recruitment to Chromatin. <i>Molecular Cell</i> , <b>2018</b> , 70, 422-434.e6	17.6	67
260	Functions of FACT in Breaking the Nucleosome and Maintaining Its Integrity at the Single-Nucleosome Level. <i>Molecular Cell</i> , <b>2018</b> , 71, 284-293.e4	17.6	50
259	Capturing the Onset of PRC2-Mediated Repressive Domain Formation. <i>Molecular Cell</i> , <b>2018</b> , 70, 1149-1162.e5	17.6	117
258	Multiple modes of PRC2 inhibition elicit global chromatin alterations in H3K27M pediatric glioma. <i>Science Advances</i> , <b>2018</b> , 4, eaau5935	14.3	76
257	Antennal Olfactory Physiology and Behavior of Males of the Ponerine Ant <i>Harpegnathos saltator</i> . <i>Journal of Chemical Ecology</i> , <b>2018</b> , 44, 999-1007	2.7	6
256	Recent Advances in Behavioral (Epi)Genetics in Eusocial Insects. <i>Annual Review of Genetics</i> , <b>2018</b> , 52, 489-510	14.5	27
255	Chromatin domains rich in inheritance. <i>Science</i> , <b>2018</b> , 361, 33-34	33.3	72
254	RNA Binding to CBP Stimulates Histone Acetylation and Transcription. <i>Cell</i> , <b>2017</b> , 168, 135-149.e22	56.2	198
253	Chemosensory sensitivity reflects reproductive status in the ant <i>Harpegnathos saltator</i> . <i>Scientific Reports</i> , <b>2017</b> , 7, 3732	4.9	21
252	Low-Grade Astrocytoma Mutations in IDH1, P53, and ATRX Cooperate to Block Differentiation of Human Neural Stem Cells via Repression of SOX2. <i>Cell Reports</i> , <b>2017</b> , 21, 1267-1280	10.6	64
251	Specialized odorant receptors in social insects that detect cuticular hydrocarbon cues and candidate pheromones. <i>Nature Communications</i> , <b>2017</b> , 8, 297	17.4	59
250	PR-Set7 deficiency limits uterine epithelial population growth hampering postnatal gland formation in mice. <i>Cell Death and Differentiation</i> , <b>2017</b> , 24, 2013-2021	12.7	5
249	Phospho-H1 Decorates the Inter-chromatid Axis and Is Evicted along with Shugoshin by SET during Mitosis. <i>Molecular Cell</i> , <b>2017</b> , 67, 579-593.e6	17.6	16
248	An Engineered orco Mutation Produces Aberrant Social Behavior and Defective Neural Development in Ants. <i>Cell</i> , <b>2017</b> , 170, 736-747.e9	56.2	126
247	The Neuropeptide Corazonin Controls Social Behavior and Caste Identity in Ants. <i>Cell</i> , <b>2017</b> , 170, 748-759.e12	56.2	94
246	Functional characterization of odorant receptors in the ponerine ant, <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, 8586-8591	11.5	50
245	The chromatin remodeling factor CHD7 controls cerebellar development by regulating reelin expression. <i>Journal of Clinical Investigation</i> , <b>2017</b> , 127, 874-887	15.9	40

244	MED12 Regulates HSC-Specific Enhancers Independently of Mediator Kinase Activity to Control Hematopoiesis. <i>Cell Stem Cell</i> , <b>2016</b> , 19, 784-799	18	60
243	Structural basis of oncogenic histone H3K27M inhibition of human polycomb repressive complex 2. <i>Nature Communications</i> , <b>2016</b> , 7, 11316	17.4	245
242	Chromatin Starts to Come Clean. <i>Molecular Cell</i> , <b>2016</b> , 64, 439-441	17.6	2
241	Co-repressor CBFA2T2 regulates pluripotency and germline development. <i>Nature</i> , <b>2016</b> , 534, 387-90	50.4	46
240	Epigenetic (re)programming of caste-specific behavior in the ant <i>Camponotus floridanus</i> . <i>Science</i> , <b>2016</b> , 351, aac6633	33.3	131
239	CTCF-mediated topological boundaries during development foster appropriate gene regulation. <i>Genes and Development</i> , <b>2016</b> , 30, 2657-2662	12.6	107
238	ISL1 and JMJD3 synergistically control cardiac differentiation of embryonic stem cells. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 6741-55	20.1	28
237	USP7 cooperates with SCML2 to regulate the activity of PRC1. <i>Molecular and Cellular Biology</i> , <b>2015</b> , 35, 1157-68	4.8	39
236	CTCF establishes discrete functional chromatin domains at the Hox clusters during differentiation. <i>Science</i> , <b>2015</b> , 347, 1017-21	33.3	375
235	Spontaneous development of hepatocellular carcinoma with cancer stem cell properties in PR-SET7-deficient livers. <i>EMBO Journal</i> , <b>2015</b> , 34, 430-47	13	30
234	Analysis of the Histone H3.1 Interactome: A Suitable Chaperone for the Right Event. <i>Molecular Cell</i> , <b>2015</b> , 60, 697-709	17.6	45
233	Cuticular Hydrocarbon Pheromones for Social Behavior and Their Coding in the Ant Antenna. <i>Cell Reports</i> , <b>2015</b> , 12, 1261-71	10.6	80
232	DNA methylation in social insects: how epigenetics can control behavior and longevity. <i>Annual Review of Entomology</i> , <b>2015</b> , 60, 435-52	21.8	121
231	CTCF regulates the human p53 gene through direct interaction with its natural antisense transcript, Wrap53. <i>Genes and Development</i> , <b>2014</b> , 28, 723-34	12.6	131
230	Selective methylation of histone H3 variant H3.1 regulates heterochromatin replication. <i>Science</i> , <b>2014</b> , 343, 1249-53	33.3	119
229	Interactions between JARID2 and noncoding RNAs regulate PRC2 recruitment to chromatin. <i>Molecular Cell</i> , <b>2014</b> , 53, 290-300	17.6	273
228	Jarid2 Is Implicated in the Initial Xist-Induced Targeting of PRC2 to the Inactive X Chromosome. <i>Molecular Cell</i> , <b>2014</b> , 53, 301-16	17.6	191
227	BRD4 assists elongation of both coding and enhancer RNAs by interacting with acetylated histones. <i>Nature Structural and Molecular Biology</i> , <b>2014</b> , 21, 1047-57	17.6	185

226	Nascent RNA interaction keeps PRC2 activity poised and in check. <i>Genes and Development</i> , <b>2014</b> , 28, 1983-86	13.2	133
225	Eusocial insects as emerging models for behavioural epigenetics. <i>Nature Reviews Genetics</i> , <b>2014</b> , 15, 677-81	3.8	133
224	Epigenetic inheritance: histone bookmarks across generations. <i>Trends in Cell Biology</i> , <b>2014</b> , 24, 664-74	18.3	107
223	Chromatin features and the epigenetic regulation of pluripotency states in ESCs. <i>Development (Cambridge)</i> , <b>2014</b> , 141, 2376-90	6.6	67
222	An AUTS2-Polycomb complex activates gene expression in the CNS. <i>Nature</i> , <b>2014</b> , 516, 349-54	50.4	181
221	Erk1/2 activity promotes chromatin features and RNAPII phosphorylation at developmental promoters in mouse ESCs. <i>Cell</i> , <b>2014</b> , 156, 678-90	56.2	106
220	Interactions with RNA direct the Polycomb group protein SCML2 to chromatin where it represses target genes. <i>ELife</i> , <b>2014</b> , 3, e02637	8.9	37
219	PRC2 binds active promoters and contacts nascent RNAs in embryonic stem cells. <i>Nature Structural and Molecular Biology</i> , <b>2013</b> , 20, 1258-64	17.6	221
218	Nucleosome-binding activities within JARID2 and EZH1 regulate the function of PRC2 on chromatin. <i>Genes and Development</i> , <b>2013</b> , 27, 2663-77	12.6	121
217	Social insect genomes exhibit dramatic evolution in gene composition and regulation while preserving regulatory features linked to sociality. <i>Genome Research</i> , <b>2013</b> , 23, 1235-47	9.7	166
216	Putting a halt on PRC2 in pediatric glioblastoma. <i>Nature Genetics</i> , <b>2013</b> , 45, 587-9	36.3	6
215	SFMBT1 functions with LSD1 to regulate expression of canonical histone genes and chromatin-related factors. <i>Genes and Development</i> , <b>2013</b> , 27, 749-66	12.6	53
214	A chromatin link to caste identity in the carpenter ant <i>Camponotus floridanus</i> . <i>Genome Research</i> , <b>2013</b> , 23, 486-96	9.7	104
213	Polycomb protein SCML2 regulates the cell cycle by binding and modulating CDK/CYCLIN/p21 complexes. <i>PLoS Biology</i> , <b>2013</b> , 11, e1001737	9.7	22
212	A double take on bivalent promoters. <i>Genes and Development</i> , <b>2013</b> , 27, 1318-38	12.6	543
211	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> , <b>2013</b> , 110, 7654-9	11.5	138
210	Deregulated FGF and homeotic gene expression underlies cerebellar vermis hypoplasia in CHARGE syndrome. <i>ELife</i> , <b>2013</b> , 2, e01305	8.9	49
209	The role of PR-Set7 in replication licensing depends on Suv4-20h. <i>Genes and Development</i> , <b>2012</b> , 26, 2580-96	2.6	85

208	Trans-tail regulation of MLL4-catalyzed H3K4 methylation by H4R3 symmetric dimethylation is mediated by a tandem PHD of MLL4. <i>Genes and Development</i> , <b>2012</b> , 26, 2749-62	12.6	124
207	PR-Set7 and H4K20me1: at the crossroads of genome integrity, cell cycle, chromosome condensation, and transcription. <i>Genes and Development</i> , <b>2012</b> , 26, 325-37	12.6	212
206	SIRT3 functions in the nucleus in the control of stress-related gene expression. <i>Molecular and Cellular Biology</i> , <b>2012</b> , 32, 5022-34	4.8	131
205	Prdm3 and Prdm16 are H3K9me1 methyltransferases required for mammalian heterochromatin integrity. <i>Cell</i> , <b>2012</b> , 150, 948-60	56.2	207
204	Asymmetrically modified nucleosomes. <i>Cell</i> , <b>2012</b> , 151, 181-93	56.2	306
203	PCGF homologs, CBX proteins, and RYBP define functionally distinct PRC1 family complexes. <i>Molecular Cell</i> , <b>2012</b> , 45, 344-56	17.6	583
202	Genome-wide and caste-specific DNA methylomes of the ants <i>Camponotus floridanus</i> and <i>Harpegnathos saltator</i> . <i>Current Biology</i> , <b>2012</b> , 22, 1755-64	6.3	266
201	Crystal structure of TDRD3 and methyl-arginine binding characterization of TDRD3, SMN and SPF30. <i>PLoS ONE</i> , <b>2012</b> , 7, e30375	3.7	62
200	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> , <b>2012</b> , 8, e1002930	6	150
199	EZH2 couples pancreatic regeneration to neoplastic progression. <i>Genes and Development</i> , <b>2012</b> , 26, 439-46	11.6	84
198	Fcp1 dephosphorylation of the RNA polymerase II C-terminal domain is required for efficient transcription of heat shock genes. <i>Molecular and Cellular Biology</i> , <b>2012</b> , 32, 3428-37	4.8	24
197	Chromatin higher-order structures and gene regulation. <i>Current Opinion in Genetics and Development</i> , <b>2011</b> , 21, 175-86	4.9	313
196	L3MBTL2 protein acts in concert with PcG protein-mediated monoubiquitination of H2A to establish a repressive chromatin structure. <i>Molecular Cell</i> , <b>2011</b> , 42, 438-50	17.6	109
195	The C-terminal domain of RNA polymerase II is modified by site-specific methylation. <i>Science</i> , <b>2011</b> , 332, 99-103	33.3	161
194	The Polycomb complex PRC2 and its mark in life. <i>Nature</i> , <b>2011</b> , 469, 343-9	50.4	2172
193	Histone tails: ideal motifs for probing epigenetics through chemical biology approaches. <i>ChemBioChem</i> , <b>2011</b> , 12, 236-52	3.8	29
192	BRD4 jump-starts transcription after mitotic silencing. <i>Genome Biology</i> , <b>2011</b> , 12, 133	18.3	8
191	Epigenetic inheritance: uncontested?. <i>Cell Research</i> , <b>2011</b> , 21, 435-41	24.7	80

190	A dual flip-out mechanism for 5mC recognition by the Arabidopsis SUVH5 SRA domain and its impact on DNA methylation and H3K9 dimethylation in vivo. <i>Genes and Development</i> , <b>2011</b> , 25, 137-52	12.6	83
189	The structure of NSD1 reveals an autoregulatory mechanism underlying histone H3K36 methylation. <i>Journal of Biological Chemistry</i> , <b>2011</b> , 286, 8361-8368	5.4	123
188	The program for processing newly synthesized histones H3.1 and H4. <i>Nature Structural and Molecular Biology</i> , <b>2010</b> , 17, 1343-51	17.6	169
187	Chromatin structure and the inheritance of epigenetic information. <i>Nature Reviews Genetics</i> , <b>2010</b> , 11, 285-96	30.1	535
186	New chaps in the histone chaperone arena. <i>Genes and Development</i> , <b>2010</b> , 24, 1334-8	12.6	32
185	Jarid2 and PRC2, partners in regulating gene expression. <i>Genes and Development</i> , <b>2010</b> , 24, 368-80	12.6	384
184	Phosphorylation of the PRC2 component Ezh2 is cell cycle-regulated and up-regulates its binding to ncRNA. <i>Genes and Development</i> , <b>2010</b> , 24, 2615-20	12.6	296
183	Genomic comparison of the ants <i>Camponotus floridanus</i> and <i>Harpegnathos saltator</i> . <i>Science</i> , <b>2010</b> , 329, 1068-71	33.3	353
182	G9a and Glp methylate lysine 373 in the tumor suppressor p53. <i>Journal of Biological Chemistry</i> , <b>2010</b> , 285, 9636-9641	5.4	284
181	Molecular signals of epigenetic states. <i>Science</i> , <b>2010</b> , 330, 612-6	33.3	670
180	Highly compacted chromatin formed in vitro reflects the dynamics of transcription activation in vivo. <i>Molecular Cell</i> , <b>2010</b> , 38, 41-53	17.6	73
179	Regulation of the histone H4 monomethylase PR-Set7 by CRL4(Cdt2)-mediated PCNA-dependent degradation during DNA damage. <i>Molecular Cell</i> , <b>2010</b> , 40, 364-76	17.6	187
178	MBT domain proteins in development and disease. <i>Seminars in Cell and Developmental Biology</i> , <b>2010</b> , 21, 221-30	7.5	110
177	Monomethylation of histone H4-lysine 20 is involved in chromosome structure and stability and is essential for mouse development. <i>Molecular and Cellular Biology</i> , <b>2009</b> , 29, 2278-95	4.8	234
176	Heterogeneous nuclear ribonucleoprotein L is a subunit of human KMT3a/Set2 complex required for H3 Lys-36 trimethylation activity in vivo. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 15701-7	5.4	76
175	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> , <b>2009</b> , 284, 8395-405	5.4	146
174	Calorie restriction and the exercise of chromatin. <i>Genes and Development</i> , <b>2009</b> , 23, 1849-69	12.6	118
173	The target of the NSD family of histone lysine methyltransferases depends on the nature of the substrate. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 34283-95	5.4	209

172	Role of the polycomb protein EED in the propagation of repressive histone marks. <i>Nature</i> , <b>2009</b> , 461, 762-7	50.4	849
171	Histones: annotating chromatin. <i>Annual Review of Genetics</i> , <b>2009</b> , 43, 559-99	14.5	647
170	Is there a code embedded in proteins that is based on post-translational modifications?. <i>Nature Reviews Molecular Cell Biology</i> , <b>2008</b> , 9, 815-20	48.7	247
169	Ezh1 and Ezh2 maintain repressive chromatin through different mechanisms. <i>Molecular Cell</i> , <b>2008</b> , 32, 503-18	17.6	602
168	Ezh2 requires PHF1 to efficiently catalyze H3 lysine 27 trimethylation in vivo. <i>Molecular and Cellular Biology</i> , <b>2008</b> , 28, 2718-31	4.8	231
167	Nonradioactive, ultrasensitive site-specific protein-protein photocrosslinking: interactions of alpha-helix 2 of TATA-binding protein with general transcription factor TFIIA and transcriptional repressor NC2. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, 6143-54	20.1	4
166	Beyond histone methyl-lysine binding: how malignant brain tumor (MBT) protein L3MBTL1 impacts chromatin structure. <i>Cell Cycle</i> , <b>2008</b> , 7, 578-85	4.7	27
165	NAD <sup>+</sup> -dependent deacetylation of H4 lysine 16 by class III HDACs. <i>Oncogene</i> , <b>2007</b> , 26, 5505-20	9.2	230
164	SIRT1 regulates the histone methyl-transferase SUV39H1 during heterochromatin formation. <i>Nature</i> , <b>2007</b> , 450, 440-4	50.4	336
163	Methylation-acetylation interplay activates p53 in response to DNA damage. <i>Molecular and Cellular Biology</i> , <b>2007</b> , 27, 6756-69	4.8	138
162	SirT3 is a nuclear NAD <sup>+</sup> -dependent histone deacetylase that translocates to the mitochondria upon cellular stress. <i>Genes and Development</i> , <b>2007</b> , 21, 920-8	12.6	332
161	L3MBTL1, a histone-methylation-dependent chromatin lock. <i>Cell</i> , <b>2007</b> , 129, 915-28	56.2	279
160	New nomenclature for chromatin-modifying enzymes. <i>Cell</i> , <b>2007</b> , 131, 633-6	56.2	745
159	Facultative heterochromatin: is there a distinctive molecular signature?. <i>Molecular Cell</i> , <b>2007</b> , 28, 1-13	17.6	356
158	Recognition of trimethylated histone H3 lysine 4 facilitates the recruitment of transcription postinitiation factors and pre-mRNA splicing. <i>Molecular Cell</i> , <b>2007</b> , 28, 665-76	17.6	426
157	Demethylation of H3K27 regulates polycomb recruitment and H2A ubiquitination. <i>Science</i> , <b>2007</b> , 318, 447-50	33.3	591
156	Histone H3 Lys 4 methylation: caught in a bind?. <i>Genes and Development</i> , <b>2006</b> , 20, 2779-86	12.6	189
155	de FACTo nucleosome dynamics. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 23297-301	5.4	182



154	Drosophila Paf1 modulates chromatin structure at actively transcribed genes. <i>Molecular and Cellular Biology</i> , <b>2006</b> , 26, 250-60	4.8	98
153	Suz12 binds to silenced regions of the genome in a cell-type-specific manner. <i>Genome Research</i> , <b>2006</b> , 16, 890-900	9.7	251
152	SirT2 is a histone deacetylase with preference for histone H4 Lys 16 during mitosis. <i>Genes and Development</i> , <b>2006</b> , 20, 1256-61	12.6	466
151	Histone lysine demethylases and their impact on epigenetics. <i>Cell</i> , <b>2006</b> , 125, 213-7	56.2	175
150	Histone H2B monoubiquitination functions cooperatively with FACT to regulate elongation by RNA polymerase II. <i>Cell</i> , <b>2006</b> , 125, 703-17	56.2	545
149	Methods to identify and functionally analyze factors that specifically recognize histone lysine methylation. <i>Methods</i> , <b>2006</b> , 40, 331-8	4.6	8
148	Biochemistry of Multiprotein HDAC Complexes <b>2006</b> , 23-60		6
147	PARP-1 determines specificity in a retinoid signaling pathway via direct modulation of mediator. <i>Molecular Cell</i> , <b>2005</b> , 18, 83-96	17.6	193
146	Functional characterization of core promoter elements: DPE-specific transcription requires the protein kinase CK2 and the PC4 coactivator. <i>Molecular Cell</i> , <b>2005</b> , 18, 471-81	17.6	54
145	Monoubiquitination of human histone H2B: the factors involved and their roles in HOX gene regulation. <i>Molecular Cell</i> , <b>2005</b> , 20, 601-11	17.6	367
144	The key to development: interpreting the histone code?. <i>Current Opinion in Genetics and Development</i> , <b>2005</b> , 15, 163-76	4.9	605
143	Polycomb group protein ezh2 controls actin polymerization and cell signaling. <i>Cell</i> , <b>2005</b> , 121, 425-36	56.2	293
142	The human PAF complex coordinates transcription with events downstream of RNA synthesis. <i>Genes and Development</i> , <b>2005</b> , 19, 1668-73	12.6	165
141	Histone variants meet their match. <i>Nature Reviews Molecular Cell Biology</i> , <b>2005</b> , 6, 139-49	48.7	238
140	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> , <b>2005</b> , 19, 431-5	12.6	137
139	Specificity and mechanism of the histone methyltransferase Pr-Set7. <i>Genes and Development</i> , <b>2005</b> , 19, 1444-54	12.6	144
138	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> , <b>2005</b> , 280, 41789-92	5.4	284
137	Functional characterization of core promoter elements: the downstream core element is recognized by TAF1. <i>Molecular and Cellular Biology</i> , <b>2005</b> , 25, 9674-86	4.8	84

136	Composition and histone substrates of polycomb repressive group complexes change during cellular differentiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 1859-64	11.5	344
135	Silencing of human polycomb target genes is associated with methylation of histone H3 Lys 27. <i>Genes and Development</i> , <b>2004</b> , 18, 1592-605	12.6	396
134	Differential histone H3 Lys-9 and Lys-27 methylation profiles on the X chromosome. <i>Molecular and Cellular Biology</i> , <b>2004</b> , 24, 5475-84	4.8	176
133	Human Spt6 stimulates transcription elongation by RNA polymerase II in vitro. <i>Molecular and Cellular Biology</i> , <b>2004</b> , 24, 3324-36	4.8	89
132	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> , <b>2004</b> , 101, 7572-7	11.5	130
131	Elongation by RNA polymerase II: the short and long of it. <i>Genes and Development</i> , <b>2004</b> , 18, 2437-68	12.6	547
130	Regulation of p53 activity through lysine methylation. <i>Nature</i> , <b>2004</b> , 432, 353-60	50.4	620
129	Transcription through chromatin: understanding a complex FACT. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , <b>2004</b> , 1677, 87-99		60
128	Recent highlights of RNA-polymerase-II-mediated transcription. <i>Current Opinion in Cell Biology</i> , <b>2004</b> , 16, 263-71	9	148
127	Steps toward understanding the inheritance of repressive methyl-lysine marks in histones. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , <b>2004</b> , 69, 171-82	3.9	13
126	Tips in analyzing antibodies directed against specific histone tail modifications. <i>Methods in Enzymology</i> , <b>2004</b> , 376, 255-69	1.7	20
125	Techniques used to study transcription on chromatin templates. <i>Methods in Enzymology</i> , <b>2004</b> , 377, 474-99		10
124	Facts about FACT and transcript elongation through chromatin. <i>Current Opinion in Genetics and Development</i> , <b>2004</b> , 14, 139-46	4.9	100
123	A unified nomenclature for protein subunits of mediator complexes linking transcriptional regulators to RNA polymerase II. <i>Molecular Cell</i> , <b>2004</b> , 14, 553-7	17.6	209
122	Human SirT1 interacts with histone H1 and promotes formation of facultative heterochromatin. <i>Molecular Cell</i> , <b>2004</b> , 16, 93-105	17.6	696
121	Different EZH2-containing complexes target methylation of histone H1 or nucleosomal histone H3. <i>Molecular Cell</i> , <b>2004</b> , 14, 183-93	17.6	374
120	Epigenetic dynamics of imprinted X inactivation during early mouse development. <i>Science</i> , <b>2004</b> , 303, 644-9	33.3	638
119	A silencing pathway to induce H3-K9 and H4-K20 trimethylation at constitutive heterochromatin. <i>Genes and Development</i> , <b>2004</b> , 18, 1251-62	12.6	812

118	Functional analysis of the subunits of the chromatin assembly factor RSF. <i>Molecular and Cellular Biology</i> , <b>2003</b> , 23, 6759-68	4.8	89
117	The C-terminal domain phosphatase and transcription elongation activities of FCP1 are regulated by phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 2328-33	11.5	26
116	Histone lysine methylation: a signature for chromatin function. <i>Trends in Genetics</i> , <b>2003</b> , 19, 629-39	8.5	538
115	FACT facilitates transcription-dependent nucleosome alteration. <i>Science</i> , <b>2003</b> , 301, 1090-3	33.3	660
114	Tracking FACT and the RNA polymerase II elongation complex through chromatin in vivo. <i>Science</i> , <b>2003</b> , 301, 1094-6	33.3	233
113	Tails of intrigue: phosphorylation of RNA polymerase II mediates histone methylation. <i>Cell</i> , <b>2003</b> , 113, 429-32	56.2	257
112	Methods and tips for the purification of human histone methyltransferases. <i>Methods</i> , <b>2003</b> , 31, 49-58	4.6	51
111	Histone deposition and chromatin assembly by RSF. <i>Methods</i> , <b>2003</b> , 31, 96-103	4.6	17
110	ASAP, a novel protein complex involved in RNA processing and apoptosis. <i>Molecular and Cellular Biology</i> , <b>2003</b> , 23, 2981-90	4.8	99
109	Facile synthesis of site-specifically acetylated and methylated histone proteins: reagents for evaluation of the histone code hypothesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 12033-8	11.5	104
108	The mediator coactivator complex: functional and physical roles in transcriptional regulation. <i>Journal of Cell Science</i> , <b>2003</b> , 116, 3667-75	5.3	112
107	The constantly changing face of chromatin. <i>Science of Aging Knowledge Environment: SAGE KE</i> , <b>2003</b> , 2003, RE4		126
106	Human Elongator facilitates RNA polymerase II transcription through chromatin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2002</b> , 99, 1241-6	11.5	130
105	FCP1, a phosphatase specific for the heptapeptide repeat of the largest subunit of RNA polymerase II, stimulates transcription elongation. <i>Molecular and Cellular Biology</i> , <b>2002</b> , 22, 7543-52	4.8	56
104	Role of the Sin3-histone deacetylase complex in growth regulation by the candidate tumor suppressor p33(ING1). <i>Molecular and Cellular Biology</i> , <b>2002</b> , 22, 835-48	4.8	193
103	Histone methyltransferase activity associated with a human multiprotein complex containing the Enhancer of Zeste protein. <i>Genes and Development</i> , <b>2002</b> , 16, 2893-905	12.6	1223
102	Set9, a novel histone H3 methyltransferase that facilitates transcription by precluding histone tail modifications required for heterochromatin formation. <i>Genes and Development</i> , <b>2002</b> , 16, 479-89	12.6	426
101	Mitotic-specific methylation of histone H4 Lys 20 follows increased PR-Set7 expression and its localization to mitotic chromosomes. <i>Genes and Development</i> , <b>2002</b> , 16, 2225-30	12.6	186

100	Inhibition of excess nodal signaling during mouse gastrulation by the transcriptional corepressor DRAP1. <i>Science</i> , <b>2002</b> , 298, 1996-9	33.3	69
99	A unified theory of gene expression. <i>Cell</i> , <b>2002</b> , 108, 439-51	56.2	705
98	PR-Set7 is a nucleosome-specific methyltransferase that modifies lysine 20 of histone H4 and is associated with silent chromatin. <i>Molecular Cell</i> , <b>2002</b> , 9, 1201-13	17.6	462
97	Interaction of FACT, SSRP1, and the high mobility group (HMG) domain of SSRP1 with DNA damaged by the anticancer drug cisplatin. <i>Journal of Biological Chemistry</i> , <b>2001</b> , 276, 25736-41	5.4	74
96	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> , <b>2001</b> , 21, 2918-32	4.8	162
95	Transcription. Switching partners in a regulatory tango. <i>Science</i> , <b>2001</b> , 294, 2497-8	33.3	8
94	Defective interplay of activators and repressors with TFIH in xeroderma pigmentosum. <i>Cell</i> , <b>2001</b> , 104, 353-63	56.2	106
93	Transcription regulation by histone methylation: interplay between different covalent modifications of the core histone tails. <i>Genes and Development</i> , <b>2001</b> , 15, 2343-60	12.6	1153
92	Reconstitution of recombinant chromatin establishes a requirement for histone-tail modifications during chromatin assembly and transcription. <i>Genes and Development</i> , <b>2001</b> , 15, 2837-51	12.6	94
91	TFIIH is negatively regulated by cdk8-containing mediator complexes. <i>Nature</i> , <b>2000</b> , 407, 102-6	50.4	312
90	RNA polymerase II elongation through chromatin. <i>Nature</i> , <b>2000</b> , 407, 471-5	50.4	218
89	Purification and characterization of a human factor that assembles and remodels chromatin. <i>Journal of Biological Chemistry</i> , <b>2000</b> , 275, 14787-90	5.4	134
88	Genetic analysis of the YDR1-BUR6 repressor complex reveals an intricate balance among transcriptional regulatory proteins in yeast. <i>Molecular and Cellular Biology</i> , <b>2000</b> , 20, 2455-65	4.8	19
87	FACT relieves DSIF/NELF-mediated inhibition of transcriptional elongation and reveals functional differences between P-TEFb and TFIIH. <i>Molecular Cell</i> , <b>2000</b> , 5, 1067-72	17.6	88
86	Mechanism of ATP-dependent promoter melting by transcription factor IIH. <i>Science</i> , <b>2000</b> , 288, 1418-22	33.3	214
85	MBD2 is a transcriptional repressor belonging to the MeCP1 histone deacetylase complex. <i>Nature Genetics</i> , <b>1999</b> , 23, 58-61	36.3	692
84	The chromatin-specific transcription elongation factor FACT comprises human SPT16 and SSRP1 proteins. <i>Nature</i> , <b>1999</b> , 400, 284-8	50.4	436
83	RNA polymerase II as a control panel for multiple coactivator complexes. <i>Current Opinion in Genetics and Development</i> , <b>1999</b> , 9, 132-9	4.9	139

82	Repression: targeting the heart of the matter. <i>Cell</i> , <b>1999</b> , 99, 455-8	56.2	98
81	The general transcription factors IIA, IIB, IIF, and IIE are required for RNA polymerase II transcription from the human U1 small nuclear RNA promoter. <i>Molecular and Cellular Biology</i> , <b>1999</b> , 19, 2130-41	4.8	52
80	Analysis of the NuRD subunits reveals a histone deacetylase core complex and a connection with DNA methylation. <i>Genes and Development</i> , <b>1999</b> , 13, 1924-35	12.6	846
79	A protein phosphatase functions to recycle RNA polymerase II. <i>Genes and Development</i> , <b>1999</b> , 13, 1540-52	2.6	162
78	SAP30, a novel protein conserved between human and yeast, is a component of a histone deacetylase complex. <i>Molecular Cell</i> , <b>1998</b> , 1, 1021-31	17.6	245
77	NAT, a human complex containing Srb polypeptides that functions as a negative regulator of activated transcription. <i>Molecular Cell</i> , <b>1998</b> , 2, 213-22	17.6	201
76	FACT, a factor that facilitates transcript elongation through nucleosomes. <i>Cell</i> , <b>1998</b> , 92, 105-16	56.2	494
75	The dermatomyositis-specific autoantigen Mi2 is a component of a complex containing histone deacetylase and nucleosome remodeling activities. <i>Cell</i> , <b>1998</b> , 95, 279-89	56.2	688
74	Human general transcription factor TFIIB: conformational variability and interaction with VP16 activation domain. <i>Biochemistry</i> , <b>1998</b> , 37, 7941-51	3.2	41
73	The mammalian transcriptional repressor RBP (CBF1) targets TFIID and TFIIA to prevent activated transcription. <i>Genes and Development</i> , <b>1998</b> , 12, 1621-37	12.6	71
72	The molecular mechanism of mitotic inhibition of TFIH is mediated by phosphorylation of CDK7. <i>Genes and Development</i> , <b>1998</b> , 12, 3541-50	12.6	73
71	New core promoter element in RNA polymerase II-dependent transcription: sequence-specific DNA binding by transcription factor IIB. <i>Genes and Development</i> , <b>1998</b> , 12, 34-44	12.6	294
70	Immunoaffinity purification of the human multisubunit transcription factor IIH. <i>Journal of Biological Chemistry</i> , <b>1998</b> , 273, 7134-40	5.4	24
69	A human RNA polymerase II complex containing factors that modify chromatin structure. <i>Molecular and Cellular Biology</i> , <b>1998</b> , 18, 5355-63	4.8	255
68	Promoter-proximal stalling results from the inability to recruit transcription factor IIH to the transcription complex and is a regulated event. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1998</b> , 95, 9767-72	11.5	69
67	RNA polymerase II stalled at a thymine dimer: footprint and effect on excision repair. <i>Nucleic Acids Research</i> , <b>1997</b> , 25, 787-93	20.1	159
66	Functional dissection of a human Dr1-DRAP1 repressor complex. <i>Molecular and Cellular Biology</i> , <b>1997</b> , 17, 36-45	4.8	34
65	The human immunodeficiency virus transactivator Tat interacts with the RNA polymerase II holoenzyme. <i>Molecular and Cellular Biology</i> , <b>1997</b> , 17, 1817-23	4.8	110

64	Accurate positioning of RNA polymerase II on a natural TATA-less promoter is independent of TATA-binding-protein-associated factors and initiator-binding proteins. <i>Molecular and Cellular Biology</i> , <b>1997</b> , 17, 2973-84	4.8	89
63	Histone deacetylases and SAP18, a novel polypeptide, are components of a human Sin3 complex. <i>Cell</i> , <b>1997</b> , 89, 357-64	56.2	500
62	Trajectory of DNA in the RNA polymerase II transcription preinitiation complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1997</b> , 94, 12268-73	11.5	91
61	Affinity purification of a human RNA polymerase II complex using monoclonal antibodies against transcription factor IIF. <i>Journal of Biological Chemistry</i> , <b>1997</b> , 272, 11495-502	5.4	23
60	The Dr1/DRAP1 heterodimer is a global repressor of transcription in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1997</b> , 94, 820-5	11.5	81
59	Transcription: why are TAFs essential?. <i>Current Biology</i> , <b>1997</b> , 7, R44-6	6.3	15
58	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> , <b>1997</b> , 94, 12898-903	11.5	195
57	Requirement of a corepressor for Dr1-mediated repression of transcription. <i>Genes and Development</i> , <b>1996</b> , 10, 1033-48	12.6	108
56	Purification of human RNA polymerase II and general transcription factors. <i>Methods in Enzymology</i> , <b>1996</b> , 274, 72-100	1.7	75
55	The general transcription factors of RNA polymerase II. <i>Genes and Development</i> , <b>1996</b> , 10, 2657-83	12.6	800
54	High-resolution mapping of nucleoprotein complexes by site-specific protein-DNA photocrosslinking: organization of the human TBP-TFIIA-TFIIB-DNA quaternary complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1996</b> , 93, 10620-5	11.5	95
53	Separation of the transcriptional coactivator and antirepression functions of transcription factor IIA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1996</b> , 93, 6583-8	11.5	39
52	Protein-protein interactions in eukaryotic transcription initiation: structure of the preinitiation complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1996</b> , 93, 11119-24	11.5	96
51	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> , <b>1996</b> , 93, 6488-93	11.5	147
50	A human RNA polymerase II complex associated with SRB and DNA-repair proteins. <i>Nature</i> , <b>1996</b> , 381, 86-9	50.4	312
49	Cdk-activating kinase complex is a component of human transcription factor TFIIH. <i>Nature</i> , <b>1995</b> , 374, 283-7	50.4	381
48	Requirement for TFIIH kinase activity in transcription by RNA polymerase II. <i>Nature</i> , <b>1995</b> , 377, 557-60	50.4	166
47	Recycling of the general transcription factors during RNA polymerase II transcription. <i>Genes and Development</i> , <b>1995</b> , 9, 1479-90	12.6	266

46	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> , <b>1995</b> , 92, 3259-63	11.5	103
45	Common themes in assembly and function of eukaryotic transcription complexes. <i>Annual Review of Biochemistry</i> , <b>1995</b> , 64, 533-61	29.1	408
44	News on initiation and elongation of transcription by RNA polymerase II. <i>Current Opinion in Cell Biology</i> , <b>1995</b> , 7, 352-61	9	80
43	Solution structure of the C-terminal core domain of human TFIIB: similarity to cyclin A and interaction with TATA-binding protein. <i>Cell</i> , <b>1995</b> , 82, 857-67	56.2	122
42	Visualization of TBP oligomers binding and bending the HIV-1 and adeno promoters. <i>Journal of Molecular Biology</i> , <b>1995</b> , 246, 576-84	6.5	18
41	Differential regulation of RNA polymerases I, II, and III by the TBP-binding repressor Dr1. <i>Science</i> , <b>1994</b> , 266, 448-50	33.3	65
40	Structure-function analysis of the TBP-binding protein Dr1 reveals a mechanism for repression of class II gene transcription. <i>Genes and Development</i> , <b>1994</b> , 8, 2097-109	12.6	85
39	Reconstitution of human TFIIA activity from recombinant polypeptides: a role in TFIID-mediated transcription. <i>Genes and Development</i> , <b>1994</b> , 8, 2336-48	12.6	101
38	The multifunctional TFIIH complex and transcriptional control. <i>Trends in Biochemical Sciences</i> , <b>1994</b> , 19, 504-8	10.3	80
37	Dual role of TFIIH in DNA excision repair and in transcription by RNA polymerase II. <i>Nature</i> , <b>1994</b> , 368, 769-72	50.4	635
36	Where transcription meets repair. <i>Cell</i> , <b>1994</b> , 77, 9-12	56.2	146
35	Interaction of the Dr1 inhibitory factor with the TATA binding protein is disrupted by adenovirus E1A. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1994</b> , 91, 6279-82	11.5	66
34	Regulation of RNA polymerase II transcription. <i>Current Opinion in Cell Biology</i> , <b>1993</b> , 5, 469-76	9	89
33	Initiation of transcription by RNA polymerase II: a multi-step process. <i>Progress in Molecular Biology and Translational Science</i> , <b>1993</b> , 44, 67-108		305
32	Isolation of a cDNA encoding the largest subunit of TFIIA reveals functions important for activated transcription. <i>Genes and Development</i> , <b>1993</b> , 7, 2246-57	12.6	77
31	Multiple functional domains of human transcription factor IIB: distinct interactions with two general transcription factors and RNA polymerase II. <i>Genes and Development</i> , <b>1993</b> , 7, 1021-32	12.6	198
30	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> , <b>1993</b> , 90, 8832-6	11.5	287
29	Interaction between an acidic activator and transcription factor TFIIB is required for transcriptional activation. <i>Nature</i> , <b>1993</b> , 363, 741-4	50.4	222

28	DNA topoisomerase I is involved in both repression and activation of transcription. <i>Nature</i> , <b>1993</b> , 365, 227-32	50.4	332
27	The cycling of RNA polymerase II during transcription. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , <b>1993</b> , 58, 187-98	3.9	25
26	Advances in RNA polymerase II transcription. <i>Current Opinion in Cell Biology</i> , <b>1992</b> , 4, 488-95	9	210
25	Dr1, a TATA-binding protein-associated phosphoprotein and inhibitor of class II gene transcription. <i>Cell</i> , <b>1992</b> , 70, 477-89	56.2	359
24	Specific interaction between the nonphosphorylated form of RNA polymerase II and the TATA-binding protein. <i>Cell</i> , <b>1992</b> , 69, 871-81	56.2	211
23	Transcription by RNA polymerase II: initiator-directed formation of transcription-competent complexes. <i>FASEB Journal</i> , <b>1992</b> , 6, 3300-9	0.9	397
22	Human general transcription factor IIH phosphorylates the C-terminal domain of RNA polymerase II. <i>Nature</i> , <b>1992</b> , 358, 641-5	50.4	583
21	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> , <b>1991</b> , 88, 9999-10003 <sup>158</sup>	11.5	160
20	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> , <b>1991</b> , 88, 8052-6	11.5	160
19	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> , <b>1991</b> , 88, 10004-8 <sup>5</sup>	11.5	283
18	Cloning of a human gene encoding the general transcription initiation factor IIB. <i>Nature</i> , <b>1991</b> , 352, 689-95.4	50.4	283
17	Binding of general transcription factor TFIIB to an acidic activating region. <i>Nature</i> , <b>1991</b> , 353, 569-71	50.4	375
16	Structure and functional properties of human general transcription factor IIE. <i>Nature</i> , <b>1991</b> , 354, 369-73	50.4	198
15	Direct interaction between adenovirus E1A protein and the TATA box binding transcription factor IID. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1991</b> , 88, 5124-8	11.5	240
14	A TATA-like sequence located downstream of the transcription initiation site is required for expression of an RNA polymerase II transcribed gene. <i>Genes and Development</i> , <b>1990</b> , 4, 1611-22	12.6	76
13	Initiation of transcription by RNA polymerase II. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , <b>1989</b> , 1009, 1-10		56
12	EivF, a factor required for transcription of the adenovirus EIV promoter, binds to an element involved in Ela-dependent activation and cAMP induction. <i>Genes and Development</i> , <b>1988</b> , 2, 975-90	12.6	59
11	Analysis of the phiX174 gene A protein using in vitro DNA replication systems. <i>Methods in Enzymology</i> , <b>1983</b> , 100, 217-39	1.7	



10	6 Priming Enzymes. <i>The Enzymes</i> , <b>1982</b> , 155-182	2.3	1
9	A CRISPR Screen Identifies Myc-associated Zinc Finger Protein (MAZ) as an Insulator Functioning at CTCF boundaries in Hox Clusters		1
8	ChIPSeqSpike: A R/Bioconductor package for ChIP-Seq data scaling according to spike-in control		1
7	Capturing the onset of PRC2-mediated repressive domain formation		2
6	Automethylation of PRC2 fine-tunes its catalytic activity on chromatin		5
5	Active and repressed chromatin domains exhibit distinct nucleosome segregation during DNA replication		4
4	Multiple modes of PRC2 inhibition elicit global chromatin alterations in H3K27M pediatric glioma		2
3	RNA interactions with CTCF are essential for its proper function		7
2	Allosteric activation dictates PRC2 activity independent of its recruitment to chromatin		3
1	Distinct stimulatory mechanisms regulate the catalytic activity of Polycomb Repressive Complex 2 (PRC2)		1