Steven Henikoff

List of Publications by Year
in descending order

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363 papers	85,195 citations	587 125 h-index	407 277 g-index
419 all docs	419 docs citations	419 times ranked	78146 citing authors

#	Article	IF	Citations
1	Global and context-specific transcriptional consequences of oncogenic Fbw7 mutations. ELife, 2022, 11, .	2.8	6
2	Managing the Steady State Chromatin Landscape by Nucleosome Dynamics. Annual Review of Biochemistry, 2022, 91, 183-195.	5.0	16
3	CUT&Tag2for1: a modified method for simultaneous profiling of the accessible and silenced regulome in singleÂcells. Genome Biology, 2022, 23, 81.	3.8	30
4	The genetics and epigenetics of satellite centromeres. Genome Research, 2022, 32, 608-615.	2.4	23
5	CUT&RUN Profiling of the Budding Yeast Epigenome. Methods in Molecular Biology, 2022, 2477, 129-147.	0.4	4
6	Viral histones: pickpocketâ€™s prize or primordial progenitor?. Epigenetics and Chromatin, 2022, 15, .	1.8	15
7	Histone variants at a glance. Journal of Cell Science, 2021, 134, .	1.2	101
8	Sequence, Chromatin and Evolution of Satellite DNA. International Journal of Molecular Sciences, 2021, 22, 4309.	1.8	104
9	The structure of a virus-encoded nucleosome. Nature Structural and Molecular Biology, 2021, 28, 413-417.	3.6	40
10	Single-cell CUT&Tag analysis of chromatin modifications in differentiation and tumor progression. Nature Biotechnology, 2021, 39, 819-824.	9.4	121
11	Remodellerâ€"variant tag team slams transposons. Nature Cell Biology, 2021, 23, 297-298.	4.6	1
12	The H3.3K27M oncohistone antagonizes reprogramming in Drosophila. PLoS Genetics, 2021, 17, e1009225.	1.5	11
13	The Yin and Yang of Histone Marks in Transcription. Annual Review of Genomics and Human Genetics, 2021, 22, 147-170.	2.5	41
14	Simplified Epigenome Profiling Using Antibody-tethered Tagmentation. Bio-protocol, 2021, 11, e4043.	0.2	12
15	Short H2A histone variants are expressed in cancer. Nature Communications, 2021, 12, 490.	5.8	29
16	Automated CUT&Tag profiling of chromatin heterogeneity in mixed-lineage leukemia. Nature Genetics, 2021, 53, 1586-1596.	9.4	42
17	High-throughput single-cell epigenomic profiling by targeted insertion of promoters (TIP-seq). Journal of Cell Biology, 2021, 220, .	2.3	19
18	Epigenome Regulation by Dynamic Nucleosome Unwrapping. Trends in Biochemical Sciences, 2020, 45, 13-26.	3.7	69

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19	Efficient low-cost chromatin profiling with CUT&Tag. Nature Protocols, 2020, 15, 3264-3283.	5.5	181
20	Trans- and cis-acting effects of Firre on epigenetic features of the inactive X chromosome. Nature Communications, 2020, 11, 6053.	5.8	33
21	Evolution: Heterochromatin Diversity in Early-Branching Land Plants. Current Biology, 2020, 30, R161-R163.	1.8	2
22	MYCN amplification and ATRX mutations are incompatible in neuroblastoma. Nature Communications, 2020, 11, 913.	5.8	66
23	What makes a centromere?. Experimental Cell Research, 2020, 389, 111895.	1.2	123
24	Architectural RNA in chromatin organization. Biochemical Society Transactions, 2020, 48, 1967-1978.	1.6	36
25	Biparental contributions of the H2A.B histone variant control embryonic development in mice. PLoS Biology, 2020, 18, e3001001.	2.6	13
26	Histone deposition pathways determine the chromatin landscapes of H3.1 and H3.3 K27M oncohistones. ELife, 2020, 9, .	2.8	42
27	Efficient chromatin accessibility mapping in situ by nucleosome-tethered tagmentation. ELife, 2020, 9, .	2.8	78
28	Biparental contributions of the H2A.B histone variant control embryonic development in mice. , 2020, 18, e3001001.		0
29	Biparental contributions of the H2A.B histone variant control embryonic development in mice. , 2020, 18, e3001001.		0
30	Biparental contributions of the H2A.B histone variant control embryonic development in mice. , 2020, 18, e3001001.		0
31	Biparental contributions of the H2A.B histone variant control embryonic development in mice. , 2020, 18, e3001001.		0
32	Biparental contributions of the H2A.B histone variant control embryonic development in mice. , 2020, 18, e3001001.		0
33	Biparental contributions of the H2A.B histone variant control embryonic development in mice. , 2020, 18, e3001001.		0
34	<i>Max</i> deletion destabilizes MYC protein and abrogates EÂµ-<i>Myc</i> lymphomagenesis. Genes and Development, 2019, 33, 1252-1264.	2.7	41
35	Peak calling by Sparse Enrichment Analysis for CUT&RUN chromatin profiling. Epigenetics and Chromatin, 2019, 12, 42.	1.8	267
36	Pioneer Factor-Nucleosome Binding Events during Differentiation Are Motif Encoded. Molecular Cell, 2019, 75, 562-575.e5.	4.5	98

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37	Bringing Oncohistones into the Fold. Cancer Discovery, 2019, 9, 1346-1348.	7.7	2
38	DUX4-Induced Histone Variants H3.X and H3.Y Mark DUX4 Target Genes for Expression. Cell Reports, 2019, 29, 1812-1820.e5.	2.9	34
39	Nucleosomes remember where they were. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 20254-20256.	3.3	3
40	Quantitative MNase-seq accurately maps nucleosome occupancy levels. Genome Biology, 2019, 20, 198.	3.8	86
41	EvoChromo: towards a synthesis of chromatin biology and evolution. Development (Cambridge), 2019, 146, .	1.2	16
42	CUT&Tag for efficient epigenomic profiling of small samples and single cells. Nature Communications, 2019, 10, 1930.	5.8	1,101
43	Chromatin Bottlenecks in Cancer. Trends in Cancer, 2019, 5, 183-194.	3.8	9
44	Old cogs, new tricks: the evolution of gene expression in a chromatin context. Nature Reviews Genetics, 2019, 20, 283-297.	7.7	86
45	Quantitative Measurement of Nucleosome Occupancy and DNA Accessibility. Biophysical Journal, 2019, 116, 73a.	0.2	0
46	RSC-Associated Subnucleosomes Define MNase-Sensitive Promoters in Yeast. Molecular Cell, 2019, 73, 238-249.e3.	4.5	107
47	Improved CUT&RUN chromatin profiling tools. ELife, 2019, 8, .	2.8	296
48	Targeted in situ genome-wide profiling with high efficiency for low cell numbers. Nature Protocols, 2018, 13, 1006-1019.	5.5	572
49	Unexpected conformational variations of the human centromeric chromatin complex. Genes and Development, 2018, 32, 20-25.	2.7	25
50	Non-B-Form DNA Is Enriched at Centromeres. Molecular Biology and Evolution, 2018, 35, 949-962.	3.5	110
51	Simple and Complex Centromeric Satellites in <i>Drosophila</i> Sibling Species. Genetics, 2018, 208, 977-990.	1.2	43
52	Simultaneous Discovery of Cell-Free DNA and the Nucleosome Ladder. Genetics, 2018, 209, 27-29.	1.2	9
53	Automated in situ chromatin profiling efficiently resolves cell types and gene regulatory programs. Epigenetics and Chromatin, 2018, 11, 74.	1.8	53
54	No strand left behind. Science, 2018, 361, 1311-1312.	6.0	12

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55	MINCE-Seq: Mapping In Vivo Nascent Chromatin with EdU and Sequencing. Methods in Molecular Biology, 2018, 1832, 159-168.	0.4	6
56	Pioneers Invade the Nucleosomal Landscape. Molecular Cell, 2018, 71, 193-194.	4.5	3
57	Precise genome-wide mapping of single nucleosomes and linkers in vivo. Genome Biology, 2018, 19, 19.	3.8	128
58	Transcribing Centromeres: Noncoding RNAs and Kinetochore Assembly. Trends in Genetics, 2018, 34, 587-599.	2.9	70
59	Darwin meets Waddington. Current Biology, 2018, 28, R682-R684.	1.8	2
60	Capitalizing on disaster: Establishing chromatin specificity behind the replication fork. BioEssays, 2017, 39, 1600150.	1.2	15
61	Histone variants on the move: substrates for chromatin dynamics. Nature Reviews Molecular Cell Biology, 2017, 18, 115-126.	16.1	268
62	Structural Biology: Probing the Origins of Chromatin. Current Biology, 2017, 27, R1118-R1120.	1.8	1
63	Transcription and Remodeling Produce Asymmetrically Unwrapped Nucleosomal Intermediates. Molecular Cell, 2017, 68, 1038-1053.e4.	4.5	104
64	Remarkable Evolutionary Plasticity of Centromeric Chromatin. Cold Spring Harbor Symposia on Quantitative Biology, 2017, 82, 71-82.	2.0	10
65	An efficient targeted nuclease strategy for high-resolution mapping of DNA binding sites. ELife, 2017, 6, .	2.8	1,119
66	CENPT bridges adjacent CENPA nucleosomes on young human Î±-satellite dimers. Genome Research, 2016, 26, 1178-1187.	2.4	41
67	Transcriptional Regulators Compete with Nucleosomes Post-replication. Cell, 2016, 165, 580-592.	13.5	139
68	Nucleosome dynamics during chromatin remodelingin vivo. Nucleus, 2016, 7, 20-26.	0.6	26
69	Mechanisms of Nucleosome Dynamics In Vivo. Cold Spring Harbor Perspectives in Medicine, 2016, 6, a026666.	2.9	24
70	Epigenetics, cellular memory and gene regulation. Current Biology, 2016, 26, R644-R648.	1.8	148
71	Mediator binding to <scp>UAS</scp> s is broadly uncoupled from transcription and cooperative with <scp>TFIID</scp> recruitment to promoters. EMBO Journal, 2016, 35, 2435-2446.	3.5	64
72	Evolutionary Turnover of Kinetochore Proteins: A Ship of Theseus?. Trends in Cell Biology, 2016, 26, 498-510.	3.6	84

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73	Epigenome editing made easy. Nature Biotechnology, 2015, 33, 606-607.	9.4	17
74	A unique chromatin complex occupies young Î±-satellite arrays of human centromeres. Science Advances, 2015, 1, .	4.7	86
75	Histone Variants and Epigenetics. Cold Spring Harbor Perspectives in Biology, 2015, 7, a019364.	2.3	275
76	Anthracyclines induce double-strand DNA breaks at active gene promoters. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2015, 773, 9-15.	0.4	80
77	Methylation-Sensitive Expression of a DNA Demethylase Gene Serves As an Epigenetic Rheostat. PLoS Genetics, 2015, 11, e1005142.	1.5	150
78	Epigenomic Landscapes Reflect Neuronal Diversity. Neuron, 2015, 86, 1319-1321.	3.8	1
79	Mapping Regulatory Factors by Immunoprecipitation from Native Chromatin. Current Protocols in Molecular Biology, 2015, 110, 21.31.1-21.31.25.	2.9	20
80	Diversity in the organization of centromeric chromatin. Current Opinion in Genetics and Development, 2015, 31, 28-35.	1.5	68
81	Inner Kinetochore Protein Interactions with Regional Centromeres of Fission Yeast. Genetics, 2015, 201, 543-561.	1.2	32
82	ChEC-seq kinetics discriminates transcription factor binding sites by DNA sequence and shape in vivo. Nature Communications, 2015, 6, 8733.	5.8	153
83	The Genetic Map Enters Its Second Century. Genetics, 2015, 200, 671-674.	1.2	0
84	Replicating nucleosomes. Science Advances, 2015, 1, .	4.7	67
85	Asymmetric nucleosomes flank promoters in the budding yeast genome. Genome Research, 2015, 25, 381-390.	2.4	96
86	A simple method for generating high-resolution maps of genome-wide protein binding. ELife, 2015, 4, e09225.	2.8	97
87	Holocentromeres are dispersed point centromeres localized at transcription factor hotspots. ELife, 2014, 3, e02025.	2.8	103
88	CENP-A octamers do not confer a reduction in nucleosome height by AFM. Nature Structural and Molecular Biology, 2014, 21, 4-5.	3.6	20
89	Histones push the envelope. Nature Structural and Molecular Biology, 2014, 21, 651-652.	3.6	0
90	Transcribing through the nucleosome. Trends in Biochemical Sciences, 2014, 39, 577-586.	3.7	141

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91	DNA torsion as a feedback mediator of transcription and chromatin dynamics. Nucleus, 2014, 5, 211-218.	0.6	49
92	Distinct chromatin features characterize different classes of repeat sequences in Drosophila melanogaster. BMC Genomics, 2014, 15, 105.	1.2	9
93	Nucleosomes Are Context-Specific, H2A.Z-Modulated Barriers to RNA Polymerase. Molecular Cell, 2014, 53, 819-830.	4.5	313
94	High-resolution mapping defines the cooperative architecture of Polycomb response elements. Genome Research, 2014, 24, 809-820.	2.4	53
95	Histone variants: dynamic punctuation in transcription. Genes and Development, 2014, 28, 672-682.	2.7	247
96	High-resolution mapping of transcription factor binding sites on native chromatin. Nature Methods, 2014, 11, 203-209.	9.0	170
97	Transcription-generated torsional stress destabilizes nucleosomes. Nature Structural and Molecular Biology, 2014, 21, 88-94.	3.6	183
98	5-Aza-CdR Delivers a Gene Body Blow. Cancer Cell, 2014, 26, 449-451.	7.7	11
99	Environmental responses mediated by histone variants. Trends in Cell Biology, 2014, 24, 642-650.	3.6	114
100	High-resolution digital profiling of the epigenome. Nature Reviews Genetics, 2014, 15, 814-827.	7.7	112
101	Doxorubicin, DNA torsion, and chromatin dynamics. Biochimica Et Biophysica Acta: Reviews on Cancer, 2014, 1845, 84-89.	3.3	394
102	The budding yeast Centromere DNA Element II wraps a stable Cse4 hemisome in either orientation in vivo. ELife, 2014, 3, e01861.	2.8	77
103	The nucleosomal barrier to promoter escape by RNA polymerase II is overcome by the chromatin remodeler Chd1. ELife, 2014, 3, e02042.	2.8	108
104	Recurrent loss of CenH3 is associated with independent transitions to holocentricity in insects. ELife, 2014, 3, .	2.8	174
105	Epigenetics & Chromatin: interactions and processes. Epigenetics and Chromatin, 2013, 6, 2.	1.8	3
106	Phylogeny as the basis for naming histones. Trends in Genetics, 2013, 29, 499-500.	2.9	16
107	Histone variants in pluripotency and disease. Development (Cambridge), 2013, 140, 2513-2524.	1.2	127
108	TILLING and Ecotilling for Rice. Methods in Molecular Biology, 2013, 956, 39-56.	0.4	18

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109	Doxorubicin Enhances Nucleosome Turnover around Promoters. Current Biology, 2013, 23, 782-787.	1.8	89
110	The heat shock response: A case study of chromatin dynamics in gene regulation. Biochemistry and Cell Biology, 2013, 91, 42-48.	0.9	17
111	Regulation of nucleosome dynamics by histone modifications. Nature Structural and Molecular Biology, 2013, 20, 259-266.	3.6	770
112	Mot1 Redistributes TBP from TATA-Containing to TATA-Less Promoters. Molecular and Cellular Biology, 2013, 33, 4996-5004.	1.1	48
113	ISWI and CHD Chromatin Remodelers Bind Promoters but Act in Gene Bodies. PLoS Genetics, 2013, 9, e1003317.	1.5	79
114	Reconstitution of hemisomes on budding yeast centromeric DNA. Nucleic Acids Research, 2013, 41, 5769-5783.	6.5	41
115	The <i>CentO</i> satellite confers translational and rotational phasing on cenH3 nucleosomes in rice centromeres. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E4875-83.	3.3	80
116	Cell-type-specific nuclei purification from whole animals for genome-wide expression and chromatin profiling. Genome Research, 2012, 22, 766-777.	2.4	112
117	Measuring Genome-Wide Nucleosome Turnover Using CATCH-IT. Methods in Enzymology, 2012, 513, 169-184.	0.4	11
118	Tripartite organization of centromeric chromatin in budding yeast. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 243-248.	3.3	91
119	â€œPointâ€•Centromeres of <i>Saccharomyces</i> Harbor Single Centromere-Specific Nucleosomes. Genetics, 2012, 190, 1575-1577.	1.2	43
120	Surveying the epigenomic landscape, one base at a time. Genome Biology, 2012, 13, 250.	3.8	33
121	SIFT web server: predicting effects of amino acid substitutions on proteins. Nucleic Acids Research, 2012, 40, W452-W457.	6.5	1,838
122	Salt Fractionation of Nucleosomes for Genome-Wide Profiling. Methods in Molecular Biology, 2012, 833, 421-432.	0.4	32
123	Chromatin roadblocks to reprogramming 50 years on. BMC Biology, 2012, 10, 83.	1.7	4
124	A unified phylogeny-based nomenclature for histone variants. Epigenetics and Chromatin, 2012, 5, 7.	1.8	265
125	Chromatin: Packaging without Nucleosomes. Current Biology, 2012, 22, R1040-R1043.	1.8	11
126	The unconventional structure of centromeric nucleosomes. Chromosoma, 2012, 121, 341-352.	1.0	59

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127	Steven Henikoff. Current Biology, 2012, 22, R106-R107.	1.8	3
128	Surveying the epigenomic landscape, one base at a time. Genome Biology, 2012, 13, 250.	13.9	40
129	A Simple Method for Gene Expression and Chromatin Profiling of Individual Cell Types within a Tissue. Developmental Cell, 2011, 21, 1179.	3.1	0
130	Epigenome characterization at single base-pair resolution. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18318-18323.	3.3	325
131	Genomic Analysis of Parent-of-Origin Allelic Expression in Arabidopsis thaliana Seeds. PLoS ONE, 2011, 6, e23687.	1.1	178
132	The INTACT method for cell typeâ€“specific gene expression and chromatin profiling in Arabidopsis thaliana. Nature Protocols, 2011, 6, 56-68.	5.5	348
133	Histone modification: cause or cog?. Trends in Genetics, 2011, 27, 389-396.	2.9	415
134	Histone variants and modifications in plant gene regulation. Current Opinion in Plant Biology, 2011, 14, 116-122.	3.5	132
135	Heat shock reduces stalled RNA polymerase II and nucleosome turnover genome-wide. Genes and Development, 2011, 25, 2387-2397.	2.7	89
136	Epigenetic Inheritance of Centromeres. Cold Spring Harbor Symposia on Quantitative Biology, 2010, 75, 51-60.	2.0	45
137	Summary: The Nucleus--A Close-Knit Community of Dynamic Structures. Cold Spring Harbor Symposia on Quantitative Biology, 2010, 75, 607-615.	2.0	3
138	H2A.Z nucleosomes enriched over active genes are homotypic. Nature Structural and Molecular Biology, 2010, 17, 1500-1507.	3.6	109
139	A chromatin thermostat. Nature, 2010, 463, 887-888.	13.7	23
140	Histone variants â€” ancient wrap artists of the epigenome. Nature Reviews Molecular Cell Biology, 2010, 11, 264-275.	16.1	699
141	Genome-Wide Kinetics of Nucleosome Turnover Determined by Metabolic Labeling of Histones. Science, 2010, 328, 1161-1164.	6.0	431
142	Changes in H2A.Z occupancy and DNA methylation during B-cell lymphomagenesis. Genome Research, 2010, 20, 1383-1390.	2.4	112
143	Centromeres Convert but Don't Cross. PLoS Biology, 2010, 8, e1000326.	2.6	143
144	A Comprehensive Map of Insulator Elements for the Drosophila Genome. PLoS Genetics, 2010, 6, e1000814.	1.5	305

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145	A native chromatin purification system for epigenomic profiling in Caenorhabditis elegans. Nucleic Acids Research, 2010, 38, e26-e26.	6.5	58
146	Catching a glimpse of nucleosome dynamics. Cell Cycle, 2010, 9, 3389-3390.	1.3	6
147	Baculovirus-encoded protein expression for epigenomic profiling in Drosophila cells. Fly, 2010, 4, 258-265.	0.9	5
148	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. Science, 2010, 330, 1775-1787.	6.0	912
149	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. Science, 2010, 330, 1787-1797.	6.0	1,124
150	A Simple Method for Gene Expression and Chromatin Profiling of Individual Cell Types within a Tissue. Developmental Cell, 2010, 18, 1030-1040.	3.1	360
151	Capturing the dynamic epigenome. Genome Biology, 2010, 11, 218.	13.9	45
152	Genome-wide profiling of salt fractions maps physical properties of chromatin. Genome Research, 2009, 19, 460-469.	2.4	204
153	Chromatin-based transcriptional punctuation. Genes and Development, 2009, 23, 1037-1041.	2.7	21
154	DNA demethylation by DNA repair. Trends in Genetics, 2009, 25, 82-90.	2.9	232
155	Unlocking the secrets of the genome. Nature, 2009, 459, 927-930.	13.7	744
156	Labile H3.3+H2A.Z nucleosomes mark 'nucleosome-free regions'. Nature Genetics, 2009, 41, 865-866.	9.4	38
157	Predicting the effects of coding non-synonymous variants on protein function using the SIFT algorithm. Nature Protocols, 2009, 4, 1073-1081.	5.5	6,149
158	Evolution of Centromeres and Kinetochores: A Two-Part Fugue. , 2009, , 1-37.		10
159	Centromeric Nucleosomes Induce Positive DNA Supercoils. Cell, 2009, 138, 104-113.	13.5	193
160	Major Evolutionary Transitions in Centromere Complexity. Cell, 2009, 138, 1067-1082.	13.5	324
161	Response: Right-Handed Half-Nucleosomes at Centromeres. Cell, 2009, 139, 1217-1218.	13.5	10
162	Extensive Demethylation of Repetitive Elements During Seed Development Underlies Gene Imprinting. Science, 2009, 324, 1447-1451.	6.0	530

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163	Epigenetic Profiling of Histone Variants. , 2009, , 101-118.		2
164	Welcome to Epigenetics & Chromatin. Epigenetics and Chromatin, 2008, 1, 1.	1.8	10
165	Single-epitope recognition imaging of native chromatin. Epigenetics and Chromatin, 2008, 1, 10.	1.8	23
166	Histone H2A.Z and DNA methylation are mutually antagonistic chromatin marks. Nature, 2008, 456, 125-129.	13.7	508
167	Moving AHEAD with an international human epigenome project. Nature, 2008, 454, 711-715.	13.7	177
168	Nucleosome destabilization in the epigenetic regulation of gene expression. Nature Reviews Genetics, 2008, 9, 15-26.	7.7	404
169	TILLING to detect induced mutations in soybean. BMC Plant Biology, 2008, 8, 9.	1.6	259
170	Fly-TILL: Reverse genetics using a living point mutation resource. Fly, 2008, 2, 300-302.	0.9	23
171	Retention of Induced Mutations in a Drosophila Reverse-Genetic Resource. Genetics, 2008, 180, 661-667.	1.2	33
172	DNA Methylation and Demethylation in Arabidopsis. The Arabidopsis Book, 2008, 6, e0102.	0.5	27
173	Epigenomics: A Roadmap to Chromatin. Science, 2008, 322, 853-853.	6.0	9
174	Intergenic Locations of Rice Centromeric Chromatin. PLoS Biology, 2008, 6, e286.	2.6	81
175	DNA demethylation in the Arabidopsis genome. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6752-6757.	3.3	470
176	Tetrameric Structure of Centromeric Nucleosomes in Interphase Drosophila Cells. PLoS Biology, 2007, 5, e218.	2.6	210
177	Histone Replacement Marks the Boundaries of cis-Regulatory Domains. Science, 2007, 315, 1408-1411.	6.0	255
178	Germline histone dynamics and epigenetics. Current Opinion in Cell Biology, 2007, 19, 257-265.	2.6	112
179	Tilling and Ecotilling for Crop Improvement. , 2007, , 333-349.		31
180	Chemical- and Irradiation-Induced Mutants and TILLING. , 2007, , 148-180.		13

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181	Genome-wide analysis of DNA methylation patterns. Development (Cambridge), 2007, 134, 3959-3965.	1.2	224
182	Structure, dynamics, and evolution of centromeric nucleosomes. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 15974-15981.	3.3	125
183	ENCODE and our very busy genome. Nature Genetics, 2007, 39, 817-818.	9.4	16
184	Genome-wide analysis of Arabidopsis thaliana DNA methylation uncovers an interdependence between methylation and transcription. Nature Genetics, 2007, 39, 61-69.	9.4	1,257
185	Discovery of chemically induced mutations in rice by TILLING. BMC Plant Biology, 2007, 7, 19.	1.6	406
186	DNA methylation dynamics in plant genomes. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2007, 1769, 276-286.	2.4	152
187	Nucleosomes at Active Promoters: Unforgettable Loss. Cancer Cell, 2007, 12, 407-409.	7.7	10
188	DNA demethylation by the baseâ€excision DNA repair pathway in Arabidopsis. FASEB Journal, 2007, 21, .	0.2	0
189	Applying whole-genome studies of epigenetic regulation to study human disease. Cytogenetic and Genome Research, 2006, 114, 1-15.	0.6	54
190	Predicting the Effects of Amino Acid Substitutions on Protein Function. Annual Review of Genomics and Human Genetics, 2006, 7, 61-80.	2.5	811
191	High-throughput discovery of rare human nucleotide polymorphisms by Ecotilling. Nucleic Acids Research, 2006, 34, e99-e99.	6.5	49
192	TILLING: practical single-nucleotide mutation discovery. Plant Journal, 2006, 45, 684-694.	2.8	225
193	The epigenetic progenitor origin of human cancer. Nature Reviews Genetics, 2006, 7, 21-33.	7.7	1,642
194	Spreading of silent chromatin: inaction at a distance. Nature Reviews Genetics, 2006, 7, 793-803.	7.7	264
195	A protocol for TILLING and Ecotilling in plants and animals. Nature Protocols, 2006, 1, 2465-2477.	5.5	219
196	Centromeres put epigenetics in the driver's seat. Trends in Biochemical Sciences, 2006, 31, 662-669.	3.7	91
197	Biotin-Tag Affinity Purification of a Centromeric Nucleosome Assembly Complex. Cell Cycle, 2006, 5, 1269-1274.	1.3	19
198	High-Throughput TILLING for <i>Arabidopsis</i>. , 2006, 323, 127-136.		23

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199	Histone H3.3 Variant Dynamics in the Germline of Caenorhabditis elegans. PLoS Genetics, 2006, 2, e97.	1.5	104
200	Chaperone-mediated assembly of centromeric chromatin in vitro. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6172-6177.	3.3	128
201	Genome-scale profiling of histone H3.3 replacement patterns. Nature Genetics, 2005, 37, 1090-1097.	9.4	463
202	DNA Methylation Profiling Identifies CG Methylation Clusters in Arabidopsis Genes. Current Biology, 2005, 15, 154-159.	1.8	212
203	Positive Selection Drives the Evolution of rhino, a Member of the Heterochromatin Protein 1 Family in Drosophila. PLoS Genetics, 2005, 1, e9.	1.5	125
204	Positive Selection of Iris, a Retroviral Envelopeâ€"Derived Host Gene in Drosophila melanogaster. PLoS Genetics, 2005, 1, e44.	1.5	62
205	Transcription and Histone Modifications in the Recombination-Free Region Spanning a Rice Centromere[W]. Plant Cell, 2005, 17, 3227-3238.	3.1	107
206	Rapid Changes in Plant Genomes. Plant Cell, 2005, 17, 2852-2855.	3.1	15
207	Histone modifications: Combinatorial complexity or cumulative simplicity?. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 5308-5309.	3.3	88
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