

Steven Henikoff

List of Publications by Year in descending order

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363
papers

85,195
citations

587

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419
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419
times ranked

78146
citing authors

#	ARTICLE	IF	CITATIONS
1	Predicting the effects of coding non-synonymous variants on protein function using the SIFT algorithm. <i>Nature Protocols</i> , 2009, 4, 1073-1081.	5.5	6,149
2	Amino acid substitution matrices from protein blocks.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1992, 89, 10915-10919.	3.3	5,230
3	SIFT: predicting amino acid changes that affect protein function. <i>Nucleic Acids Research</i> , 2003, 31, 3812-3814.	6.5	5,120
4	Unidirectional digestion with exonuclease III creates targeted breakpoints for DNA sequencing. <i>Gene</i> , 1984, 28, 351-359.	1.0	4,616
5	Predicting Deleterious Amino Acid Substitutions. <i>Genome Research</i> , 2001, 11, 863-874.	2.4	2,186
6	SIFT web server: predicting effects of amino acid substitutions on proteins. <i>Nucleic Acids Research</i> , 2012, 40, W452-W457.	6.5	1,838
7	The epigenetic progenitor origin of human cancer. <i>Nature Reviews Genetics</i> , 2006, 7, 21-33.	7.7	1,642
8	Comparative Genomics of the Eukaryotes. <i>Science</i> , 2000, 287, 2204-2215.	6.0	1,573
9	Genome-wide analysis of <i>Arabidopsis thaliana</i> DNA methylation uncovers an interdependence between methylation and transcription. <i>Nature Genetics</i> , 2007, 39, 61-69.	9.4	1,257
10	The Centromere Paradox: Stable Inheritance with Rapidly Evolving DNA. <i>Science</i> , 2001, 293, 1098-1102.	6.0	1,138
11	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010, 330, 1787-1797.	6.0	1,124
12	An efficient targeted nuclease strategy for high-resolution mapping of DNA binding sites. <i>ELife</i> , 2017, 6, .	2.8	1,119
13	CUT&Tag for efficient epigenomic profiling of small samples and single cells. <i>Nature Communications</i> , 2019, 10, 1930.	5.8	1,101
14	The Histone Variant H3.3 Marks Active Chromatin by Replication-Independent Nucleosome Assembly. <i>Molecular Cell</i> , 2002, 9, 1191-1200.	4.5	1,023
15	[12] Unidirectional digestion with exonuclease III in DNA sequence analysis. <i>Methods in Enzymology</i> , 1987, 155, 156-165.	0.4	957
16	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787.	6.0	912
17	Requirement of CHROMOMETHYLASE3 for Maintenance of CpXpG Methylation. <i>Science</i> , 2001, 292, 2077-2080.	6.0	820
18	Targeting Induced Local Lesions IN Genomes (TILLING) for Plant Functional Genomics. <i>Plant Physiology</i> , 2000, 123, 439-442.	2.3	817

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19	Predicting the Effects of Amino Acid Substitutions on Protein Function. Annual Review of Genomics and Human Genetics, 2006, 7, 61-80.	2.5	811
20	Regulation of nucleosome dynamics by histone modifications. Nature Structural and Molecular Biology, 2013, 20, 259-266.	3.6	770
21	Unlocking the secrets of the genome. Nature, 2009, 459, 927-930.	13.7	744
22	Histone variants "ancient wrap artists of the epigenome. Nature Reviews Molecular Cell Biology, 2010, 11, 264-275.	16.1	699
23	Targeted screening for induced mutations. Nature Biotechnology, 2000, 18, 455-457.	9.4	689
24	Consensus-degenerate hybrid oligonucleotide primers for amplification of distantly related sequences. Nucleic Acids Research, 1998, 26, 1628-1635.	6.5	659
25	Accounting for Human Polymorphisms Predicted to Affect Protein Function. Genome Research, 2002, 12, 436-446.	2.4	630
26	Targeted in situ genome-wide profiling with high efficiency for low cell numbers. Nature Protocols, 2018, 13, 1006-1019.	5.5	572
27	Expansions of transgene repeats cause heterochromatin formation and gene silencing in Drosophila. Cell, 1994, 77, 993-1002.	13.5	557
28	Identification of in vivo DNA targets of chromatin proteins using tethered Dam methyltransferase. Nature Biotechnology, 2000, 18, 424-428.	9.4	544
29	Extensive Demethylation of Repetitive Elements During Seed Development Underlies Gene Imprinting. Science, 2009, 324, 1447-1451.	6.0	530
30	A large family of bacterial activator proteins.. Proceedings of the National Academy of Sciences of the United States of America, 1988, 85, 6602-6606.	3.3	524
31	Spectrum of Chemically Induced Mutations From a Large-Scale Reverse-Genetic Screen in Arabidopsis. Genetics, 2003, 164, 731-740.	1.2	512
32	Histone H2A.Z and DNA methylation are mutually antagonistic chromatin marks. Nature, 2008, 456, 125-129.	13.7	508
33	Large-Scale Discovery of Induced Point Mutations With High-Throughput TILLING. Genome Research, 2003, 13, 524-530.	2.4	505
34	Phylogenomics of the nucleosome. Nature Structural and Molecular Biology, 2003, 10, 882-891.	3.6	497
35	Sequencing of a rice centromere uncovers active genes. Nature Genetics, 2004, 36, 138-145.	9.4	489
36	High-Throughput Screening for Induced Point Mutations. Plant Physiology, 2001, 126, 480-484.	2.3	478

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37	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
38	From The Cover: Histone H3.3 is enriched in covalent modifications associated with active chromatin. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1525-1530.	3.3	468
39	Genome-scale profiling of histone H3.3 replacement patterns. Nature Genetics, 2005, 37, 1090-1097.	9.4	463
40	Automated assembly of protein blocks for database searching. Nucleic Acids Research, 1991, 19, 6565-6572.	6.5	449
41	Genome-Wide Kinetics of Nucleosome Turnover Determined by Metabolic Labeling of Histones. Science, 2010, 328, 1161-1164.	6.0	431
42	Efficient discovery of DNA polymorphisms in natural populations by Ecotilling. Plant Journal, 2004, 37, 778-786.	2.8	428
43	Histone modification: cause or cog?. Trends in Genetics, 2011, 27, 389-396.	2.9	415
44	Discovery of chemically induced mutations in rice by TILLING. BMC Plant Biology, 2007, 7, 19.	1.6	406
45	Nucleosome destabilization in the epigenetic regulation of gene expression. Nature Reviews Genetics, 2008, 9, 15-26.	7.7	404
46	Performance evaluation of amino acid substitution matrices. Proteins: Structure, Function and Bioinformatics, 1993, 17, 49-61.	1.5	395
47	Doxorubicin, DNA torsion, and chromatin dynamics. Biochimica Et Biophysica Acta: Reviews on Cancer, 2014, 1845, 84-89.	3.3	394
48	Position-based sequence weights. Journal of Molecular Biology, 1994, 243, 574-578.	2.0	392
49	Centromeric Localization and Adaptive Evolution of an Arabidopsis Histone H3 Variant. Plant Cell, 2002, 14, 1053-1066.	3.1	372
50	Protein Family Classification Based on Searching a Database of Blocks. Genomics, 1994, 19, 97-107.	1.3	370
51	Gene Families: The Taxonomy of Protein Paralogs and Chimeras. Science, 1997, 278, 609-614.	6.0	362
52	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
53	CODEHOP (COnsensus-DEgenerate Hybrid Oligonucleotide Primer) PCR primer design. Nucleic Acids Research, 2003, 31, 3763-3766.	6.5	359
54	The INTACT method for cell type-specific gene expression and chromatin profiling in Arabidopsis thaliana. Nature Protocols, 2011, 6, 56-68.	5.5	348

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55	Discovery of induced point mutations in maize genes by TILLING. <i>BMC Plant Biology</i> , 2004, 4, 12.	1.6	342
56	Position-effect variegation after 60 years. <i>Trends in Genetics</i> , 1990, 6, 422-426.	2.9	335
57	TILLING. Traditional Mutagenesis Meets Functional Genomics. <i>Plant Physiology</i> , 2004, 135, 630-636.	2.3	331
58	Epigenome characterization at single base-pair resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 18318-18323.	3.3	325
59	Genetic modification of heterochromatic association and nuclear organization in <i>Drosophila</i> . <i>Nature</i> , 1996, 381, 529-531.	13.7	324
60	Major Evolutionary Transitions in Centromere Complexity. <i>Cell</i> , 2009, 138, 1067-1082.	13.5	324
61	Localization of RNA from heat-induced polysomes at puff sites in <i>Drosophila melanogaster</i> .. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1975, 72, 1117-1121.	3.3	315
62	Nucleosomes Are Context-Specific, H2A.Z-Modulated Barriers to RNA Polymerase. <i>Molecular Cell</i> , 2014, 53, 819-830.	4.5	313
63	A Comprehensive Map of Insulator Elements for the <i>Drosophila</i> Genome. <i>PLoS Genetics</i> , 2010, 6, e1000814.	1.5	305
64	Poised for Contagion: Evolutionary Origins of the Infectious Abilities of Invertebrate Retroviruses. <i>Genome Research</i> , 2000, 10, 1307-1318.	2.4	303
65	Chromatin profiling using targeted DNA adenine methyltransferase. <i>Nature Genetics</i> , 2001, 27, 304-308.	9.4	303
66	Improved CUT&RUN chromatin profiling tools. <i>ELife</i> , 2019, 8, .	2.8	296
67	Automated construction and graphical presentation of protein blocks from unaligned sequences. <i>Gene</i> , 1995, 163, GC17-GC26.	1.0	289
68	Histone H3 variants specify modes of chromatin assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16477-16484.	3.3	288
69	Heterochromatic deposition of centromeric histone H3-like proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 716-721.	3.3	285
70	Increased coverage of protein families with the Blocks Database servers. <i>Nucleic Acids Research</i> , 2000, 28, 228-230.	6.5	281
71	Gene within a gene: Nested <i>Drosophila</i> genes encode unrelated proteins on opposite DNA strands. <i>Cell</i> , 1986, 44, 33-42.	13.5	275
72	Exploring and explaining epigenetic effects. <i>Trends in Genetics</i> , 1997, 13, 293-295.	2.9	275

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73	Histone Variants and Epigenetics. Cold Spring Harbor Perspectives in Biology, 2015, 7, a019364.	2.3	275
74	Adaptive Evolution of Cid, a Centromere-Specific Histone in Drosophila. Genetics, 2001, 157, 1293-1298.	1.2	274
75	Blocks+: a non-redundant database of protein alignment blocks derived from multiple compilations. Bioinformatics, 1999, 15, 471-479.	1.8	269
76	Histone variants on the move: substrates for chromatin dynamics. Nature Reviews Molecular Cell Biology, 2017, 18, 115-126.	16.1	268
77	Something from nothing: the evolution and utility of satellite repeats. Trends in Genetics, 1998, 14, 200-204.	2.9	267
78	Peak calling by Sparse Enrichment Analysis for CUT&RUN chromatin profiling. Epigenetics and Chromatin, 2019, 12, 42.	1.8	267
79	Histone variants, nucleosome assembly and epigenetic inheritance. Trends in Genetics, 2004, 20, 320-326.	2.9	265
80	A unified phylogeny-based nomenclature for histone variants. Epigenetics and Chromatin, 2012, 5, 7.	1.8	265
81	Spreading of silent chromatin: inaction at a distance. Nature Reviews Genetics, 2006, 7, 793-803.	7.7	264
82	TILLING to detect induced mutations in soybean. BMC Plant Biology, 2008, 8, 9.	1.6	259
83	Mediation of meiotic and early mitotic chromosome segregation in Drosophila by a protein related to kinesin. Nature, 1990, 345, 81-83.	13.7	256
84	Histone Replacement Marks the Boundaries of cis-Regulatory Domains. Science, 2007, 315, 1408-1411.	6.0	255
85	Chromatin Immunoprecipitation Reveals That the 180-bp Satellite Repeat Is the Key Functional DNA Element of <i>Arabidopsis thaliana</i> Centromeres. Genetics, 2003, 163, 1221-1225.	1.2	254
86	ASSEMBLY OF VARIANT HISTONES INTO CHROMATIN. Annual Review of Cell and Developmental Biology, 2005, 21, 133-153.	4.0	248
87	Histone variants: dynamic punctuation in transcription. Genes and Development, 2014, 28, 672-682.	2.7	247
88	Maize Centromeres: Organization and Functional Adaptation in the Genetic Background of Oat. Plant Cell, 2004, 16, 571-581.	3.1	241
89	SINGLE-NUCLEOTIDE MUTATIONS FOR PLANT FUNCTIONAL GENOMICS. Annual Review of Plant Biology, 2003, 54, 375-401.	8.6	238
90	A histone-H3-like protein in <i>C. elegans</i> . Nature, 1999, 401, 547-548.	13.7	233

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91	DNA demethylation by DNA repair. <i>Trends in Genetics</i> , 2009, 25, 82-90.	2.9	232
92	The HP1 chromo shadow domain binds a consensus peptide pentamer. <i>Current Biology</i> , 2000, 10, 27-30.	1.8	231
93	Mismatch cleavage by single-strand specific nucleases. <i>Nucleic Acids Research</i> , 2004, 32, 2632-2641.	6.5	225
94	TILLING: practical single-nucleotide mutation discovery. <i>Plant Journal</i> , 2006, 45, 684-694.	2.8	225
95	Genome-wide analysis of DNA methylation patterns. <i>Development (Cambridge)</i> , 2007, 134, 3959-3965.	1.2	224
96	A protocol for TILLING and Ecotilling in plants and animals. <i>Nature Protocols</i> , 2006, 1, 2465-2477.	5.5	219
97	Conspiracy of silence among repeated transgenes. <i>BioEssays</i> , 1998, 20, 532-535.	1.2	216
98	DNA Methylation Profiling Identifies CG Methylation Clusters in Arabidopsis Genes. <i>Current Biology</i> , 2005, 15, 154-159.	1.8	212
99	Tetrameric Structure of Centromeric Nucleosomes in Interphase Drosophila Cells. <i>PLoS Biology</i> , 2007, 5, e218.	2.6	210
100	Genome-wide profiling of salt fractions maps physical properties of chromatin. <i>Genome Research</i> , 2009, 19, 460-469.	2.4	204
101	Adaptive evolution of centromere proteins in plants and animals. <i>Journal of Biology</i> , 2004, 3, 18.	2.7	200
102	Transcription terminates in yeast distal to a control sequence. <i>Cell</i> , 1983, 33, 607-614.	13.5	198
103	Conserved Arrangement of Nested Genes at the Drosophila <i>Gart</i> Locus. <i>Genetics</i> , 1987, 117, 711-725.	1.2	195
104	Centromeric Nucleosomes Induce Positive DNA Supercoils. <i>Cell</i> , 2009, 138, 104-113.	13.5	193
105	A DNA Methyltransferase Homolog With a Chromodomain Exists in Multiple Polymorphic Forms in Arabidopsis. <i>Genetics</i> , 1998, 149, 307-318.	1.2	192
106	Transcription-generated torsional stress destabilizes nucleosomes. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 88-94.	3.6	183
107	Efficient low-cost chromatin profiling with CUT&Tag. <i>Nature Protocols</i> , 2020, 15, 3264-3283.	5.5	181
108	Conflict begets complexity: the evolution of centromeres. <i>Current Opinion in Genetics and Development</i> , 2002, 12, 711-718.	1.5	178

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109	Genomic Analysis of Parent-of-Origin Allelic Expression in Arabidopsis thaliana Seeds. PLoS ONE, 2011, 6, e23687.	1.1	178
110	Moving AHEAD with an international human epigenome project. Nature, 2008, 454, 711-715.	13.7	177
111	Recurrent loss of CenH3 is associated with independent transitions to holocentricity in insects. ELife, 2014, 3, .	2.8	174
112	High-resolution mapping of transcription factor binding sites on native chromatin. Nature Methods, 2014, 11, 203-209.	9.0	170
113	Genome-Wide Profiling of DNA Methylation Reveals Transposon Targets of CHROMOMETHYLASE3. Current Biology, 2002, 12, 65-68.	1.8	166
114	Transgene Repeat Arrays Interact With Distant Heterochromatin and Cause Silencing in <i>cis</i> and <i>trans</i> . Genetics, 1997, 147, 1181-1190.	1.2	158
115	Distinct HP1 and Su(var)3-9 complexes bind to sets of developmentally coexpressed genes depending on chromosomal location. Genes and Development, 2003, 17, 2825-2838.	2.7	153
116	ChEC-seq kinetics discriminates transcription factor binding sites by DNA sequence and shape in vivo. Nature Communications, 2015, 6, 8733.	5.8	153
117	DNA methylation dynamics in plant genomes. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2007, 1769, 276-286.	2.4	152
118	The Hinge and Chromo Shadow Domain Impart Distinct Targeting of HP1-Like Proteins. Molecular and Cellular Biology, 2001, 21, 2555-2569.	1.1	151
119	Centromeric chromatin: what makes it unique?. Current Opinion in Genetics and Development, 2005, 15, 177-184.	1.5	151
120	Methylation-Sensitive Expression of a DNA Demethylase Gene Serves As an Epigenetic Rheostat. PLoS Genetics, 2015, 11, e1005142.	1.5	150
121	Epigenetics, cellular memory and gene regulation. Current Biology, 2016, 26, R644-R648.	1.8	148
122	Trans-sensing effects from Drosophila to humans. Cell, 1991, 65, 201-203.	13.5	147
123	Modulation of a Transcription Factor Counteracts Heterochromatic Gene Silencing in Drosophila. Cell, 2001, 104, 839-847.	13.5	146
124	Centromeres Convert but Don't Cross. PLoS Biology, 2010, 8, e1000326.	2.6	143
125	Transcribing through the nucleosome. Trends in Biochemical Sciences, 2014, 39, 577-586.	3.7	141
126	Changes in Chromosomal Localization of Heterochromatin-binding Proteins during the Cell Cycle in Drosophila. Journal of Cell Biology, 1998, 140, 1297-1306.	2.3	140

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127	Transcriptional Regulators Compete with Nucleosomes Post-replication. <i>Cell</i> , 2016, 165, 580-592.	13.5	139
128	Centromeres Are Specialized Replication Domains in Heterochromatin. <i>Journal of Cell Biology</i> , 2001, 153, 101-110.	2.3	137
129	Histone variants and modifications in plant gene regulation. <i>Current Opinion in Plant Biology</i> , 2011, 14, 116-122.	3.5	132
130	Large-scale Chromosomal Movements During Interphase Progression in <i>Drosophila</i> . <i>Journal of Cell Biology</i> , 1998, 143, 13-22.	2.3	131
131	Maintenance of chromatin states: an open-and-shut case. <i>Current Opinion in Cell Biology</i> , 2003, 15, 266-274.	2.6	129
132	Chaperone-mediated assembly of centromeric chromatin in vitro. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6172-6177.	3.3	128
133	Precise genome-wide mapping of single nucleosomes and linkers in vivo. <i>Genome Biology</i> , 2018, 19, 19.	3.8	128
134	Histone variants in pluripotency and disease. <i>Development (Cambridge)</i> , 2013, 140, 2513-2524.	1.2	127
135	Amino acid substitution matrices. <i>Advances in Protein Chemistry</i> , 2000, 54, 73-97.	4.4	126
136	Positive Selection Drives the Evolution of rhino, a Member of the Heterochromatin Protein 1 Family in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2005, 1, e9.	1.5	125
137	Structure, dynamics, and evolution of centromeric nucleosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 15974-15981.	3.3	125
138	What makes a centromere?. <i>Experimental Cell Research</i> , 2020, 389, 111895.	1.2	123
139	Dosage-dependent modification of position-effect variegation in <i>Drosophila</i> . <i>BioEssays</i> , 1996, 18, 401-409.	1.2	121
140	Centromere Targeting Element within the Histone Fold Domain of Cid. <i>Molecular and Cellular Biology</i> , 2002, 22, 7553-7561.	1.1	121
141	Single-cell CUT&Tag analysis of chromatin modifications in differentiation and tumor progression. <i>Nature Biotechnology</i> , 2021, 39, 819-824.	9.4	121
142	Centromeres: Selfish drivers. <i>Nature</i> , 2002, 417, 227-227.	13.7	119
143	Environmental responses mediated by histone variants. <i>Trends in Cell Biology</i> , 2014, 24, 642-650.	3.6	114
144	Trans-inactivation of the <i>Drosophila brown</i> gene: evidence for transcriptional repression and somatic pairing dependence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1989, 86, 6704-6708.	3.3	112

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145	The Blocks database—a system for protein classification. <i>Nucleic Acids Research</i> , 1996, 24, 197-200.	6.5	112
146	Recurrent evolution of DNA-binding motifs in the <i>Drosophila</i> centromeric histone. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 1449-1454.	3.3	112
147	Germline histone dynamics and epigenetics. <i>Current Opinion in Cell Biology</i> , 2007, 19, 257-265.	2.6	112
148	Changes in H2A.Z occupancy and DNA methylation during B-cell lymphomagenesis. <i>Genome Research</i> , 2010, 20, 1383-1390.	2.4	112
149	Cell-type-specific nuclei purification from whole animals for genome-wide expression and chromatin profiling. <i>Genome Research</i> , 2012, 22, 766-777.	2.4	112
150	High-resolution digital profiling of the epigenome. <i>Nature Reviews Genetics</i> , 2014, 15, 814-827.	7.7	112
151	Epigenetic Consequences of Nucleosome Dynamics. <i>Cell</i> , 2002, 111, 281-284.	13.5	111
152	Non-B-Form DNA Is Enriched at Centromeres. <i>Molecular Biology and Evolution</i> , 2018, 35, 949-962.	3.5	110
153	H2A.Z nucleosomes enriched over active genes are homotypic. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1500-1507.	3.6	109
154	The nucleosomal barrier to promoter escape by RNA polymerase II is overcome by the chromatin remodeler Chd1. <i>ELife</i> , 2014, 3, e02042.	2.8	108
155	Transcription and Histone Modifications in the Recombination-Free Region Spanning a Rice Centromere[W]. <i>Plant Cell</i> , 2005, 17, 3227-3238.	3.1	107
156	Chromatin and siRNA pathways cooperate to maintain DNA methylation of small transposable elements in <i>Arabidopsis</i> . <i>Genome Biology</i> , 2005, 6, R90.	13.9	107
157	RSC-Associated Subnucleosomes Define MNase-Sensitive Promoters in Yeast. <i>Molecular Cell</i> , 2019, 73, 238-249.e3.	4.5	107
158	Isolation of a gene from <i>Drosophila</i> by complementation in yeast. <i>Nature</i> , 1981, 289, 33-37.	13.7	104
159	Histone H3.3 Variant Dynamics in the Germline of <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , 2006, 2, e97.	1.5	104
160	Transcription and Remodeling Produce Asymmetrically Unwrapped Nucleosomal Intermediates. <i>Molecular Cell</i> , 2017, 68, 1038-1053.e4.	4.5	104
161	Sequence, Chromatin and Evolution of Satellite DNA. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4309.	1.8	104
162	Holocentromeres are dispersed point centromeres localized at transcription factor hotspots. <i>ELife</i> , 2014, 3, e02025.	2.8	103

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163	[6] Blocks database and its applications. <i>Methods in Enzymology</i> , 1996, 266, 88-105.	0.4	101
164	Histone variants at a glance. <i>Journal of Cell Science</i> , 2021, 134, .	1.2	101
165	Nuclear organization and gene expression: homologous pairing and long-range interactions. <i>Current Opinion in Cell Biology</i> , 1997, 9, 388-395.	2.6	99
166	Pioneer Factor-Nucleosome Binding Events during Differentiation Are Motif Encoded. <i>Molecular Cell</i> , 2019, 75, 562-575.e5.	4.5	98
167	rbcR [correction of rcbR], a gene coding for a member of the LysR family of transcriptional regulators, is located upstream of the expressed set of ribulose 1,5-bisphosphate carboxylase/oxygenase genes in the photosynthetic bacterium <i>Chromatium vinosum</i> . <i>Journal of Bacteriology</i> , 1991, 173, 5224-5229.	1.0	97
168	A simple method for generating high-resolution maps of genome-wide protein binding. <i>ELife</i> , 2015, 4, e09225.	2.8	97
169	Position effect and related phenomena. <i>Current Opinion in Genetics and Development</i> , 1992, 2, 907-912.	1.5	96
170	Asymmetric nucleosomes flank promoters in the budding yeast genome. <i>Genome Research</i> , 2015, 25, 381-390.	2.4	96
171	Copy Number and Orientation Determine the Susceptibility of a Gene to Silencing by Nearby Heterochromatin in <i>Drosophila</i> . <i>Genetics</i> , 1996, 142, 447-458.	1.2	96
172	Using substitution probabilities to improve position-specific scoring matrices. <i>Bioinformatics</i> , 1996, 12, 135-143.	1.8	94
173	New features of the Blocks Database servers. <i>Nucleic Acids Research</i> , 1999, 27, 226-228.	6.5	94
174	High-Throughput TILLING for Functional Genomics. , 2003, 236, 205-220.		94
175	A pairing-sensitive element that mediates trans-inactivation is associated with the <i>Drosophila brown</i> gene.. <i>Genes and Development</i> , 1991, 5, 331-340.	2.7	92
176	Heterochromatin protein 1 binds transgene arrays. <i>Chromosoma</i> , 1998, 107, 286-292.	1.0	92
177	Centromeres put epigenetics in the driver's seat. <i>Trends in Biochemical Sciences</i> , 2006, 31, 662-669.	3.7	91
178	Tripartite organization of centromeric chromatin in budding yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 243-248.	3.3	91
179	Nucleotide sequence and initial functional characterization of the <i>clcR</i> gene encoding a LysR family activator of the <i>clcABD</i> chlorocatechol operon in <i>Pseudomonas putida</i> . <i>Journal of Bacteriology</i> , 1993, 175, 417-427.	1.0	90
180	Adaptive Evolution of the Histone Fold Domain in Centromeric Histones. <i>Molecular Biology and Evolution</i> , 2004, 21, 1712-1718.	3.5	89

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181	Heat shock reduces stalled RNA polymerase II and nucleosome turnover genome-wide. <i>Genes and Development</i> , 2011, 25, 2387-2397.	2.7	89
182	Doxorubicin Enhances Nucleosome Turnover around Promoters. <i>Current Biology</i> , 2013, 23, 782-787.	1.8	89
183	Trans-Sensing Effects: The Ups and Downs of Being Together. <i>Cell</i> , 1998, 93, 329-332.	13.5	88
184	Histone modifications: Combinatorial complexity or cumulative simplicity?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5308-5309.	3.3	88
185	Position-effect variegation and chromosome structure of a heat shock puff in <i>Drosophila</i> . <i>Chromosoma</i> , 1981, 83, 381-393.	1.0	86
186	A unique chromatin complex occupies young $\hat{\alpha}$ -satellite arrays of human centromeres. <i>Science Advances</i> , 2015, 1, .	4.7	86
187	Quantitative MNase-seq accurately maps nucleosome occupancy levels. <i>Genome Biology</i> , 2019, 20, 198.	3.8	86
188	Old cogs, new tricks: the evolution of gene expression in a chromatin context. <i>Nature Reviews Genetics</i> , 2019, 20, 283-297.	7.7	86
189	Evolutionary Turnover of Kinetochores: A Ship of Theseus?. <i>Trends in Cell Biology</i> , 2016, 26, 498-510.	3.6	84
190	Heterochromatin function in complex genomes. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2000, 1470, O1-O8.	3.3	82
191	Intergenic Locations of Rice Centromeric Chromatin. <i>PLoS Biology</i> , 2008, 6, e286.	2.6	81
192	Detecting dinosaur DNA. <i>Science</i> , 1995, 268, 1191-1192.	6.0	80
193	The <i>CentO</i> satellite confers translational and rotational phasing on cenH3 nucleosomes in rice centromeres. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4875-83.	3.3	80
194	Anthracyclines induce double-strand DNA breaks at active gene promoters. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2015, 773, 9-15.	0.4	80
195	ISWI and CHD Chromatin Remodelers Bind Promoters but Act in Gene Bodies. <i>PLoS Genetics</i> , 2013, 9, e1003317.	1.5	79
196	Efficient chromatin accessibility mapping in situ by nucleosome-tethered tagmentation. <i>ELife</i> , 2020, 9, .	2.8	78
197	The budding yeast Centromere DNA Element II wraps a stable Cse4 hemisome in either orientation in vivo. <i>ELife</i> , 2014, 3, e01861.	2.8	77
198	Transcription at two heat shock loci in <i>Drosophila</i> . <i>Cell</i> , 1977, 12, 441-451.	13.5	73

#	ARTICLE	IF	CITATIONS
199	A <i>Drosophila</i> metabolic gene transcript is alternatively processed. <i>Cell</i> , 1983, 34, 405-414.	13.5	73
200	Multiple purine pathway enzyme activities are encoded at a single genetic locus in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1986, 83, 720-724.	3.3	71
201	Transcribing Centromeres: Noncoding RNAs and Kinetochore Assembly. <i>Trends in Genetics</i> , 2018, 34, 587-599.	2.9	70
202	Epigenome Regulation by Dynamic Nucleosome Unwrapping. <i>Trends in Biochemical Sciences</i> , 2020, 45, 13-26.	3.7	69
203	A helix-turn-helix DNA-binding motif predicted for transposases of DNA transposons. <i>Molecular Genetics and Genomics</i> , 1997, 254, 689-695.	2.4	68
204	Diversity in the organization of centromeric chromatin. <i>Current Opinion in Genetics and Development</i> , 2015, 31, 28-35.	1.5	68
205	Replicating nucleosomes. <i>Science Advances</i> , 2015, 1, .	4.7	67
206	MYCN amplification and ATRX mutations are incompatible in neuroblastoma. <i>Nature Communications</i> , 2020, 11, 913.	5.8	66
207	Embedding strategies for effective use of information from multiple sequence alignments. <i>Protein Science</i> , 1997, 6, 698-705.	3.1	65
208	Automated band mapping in electrophoretic gel images using background information. <i>Nucleic Acids Research</i> , 2005, 33, 2806-2812.	6.5	65
209	A Reexamination of Spreading of Position-Effect Variegation in the white-roughest Region of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2000, 154, 259-272.	1.2	65
210	Blocks-based methods for detecting protein homology. <i>Electrophoresis</i> , 2000, 21, 1700-1706.	1.3	64
211	Mediator binding to <sc>UAS</sc> s is broadly uncoupled from transcription and cooperative with <sc>TFIID</sc> recruitment to promoters. <i>EMBO Journal</i> , 2016, 35, 2435-2446.	3.5	64
212	PHAGE DISPLAY: Affinity Selection from Biological Libraries. <i>Science</i> , 2002, 298, 621-622.	6.0	63
213	Positive Selection of Iris, a Retroviral Envelope-Derived Host Gene in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2005, 1, e44.	1.5	62
214	POSITION EFFECTS AND VARIATION ENHANCERS IN AN AUTOSOMAL REGION OF <i>DROSOPHILA MELANOGASTER</i> . <i>Genetics</i> , 1979, 93, 105-115.	1.2	61
215	Quantitative epigenetics. <i>Nature Genetics</i> , 2003, 33, 6-8.	9.4	60
216	The unconventional structure of centromeric nucleosomes. <i>Chromosoma</i> , 2012, 121, 341-352.	1.0	59

#	ARTICLE	IF	CITATIONS
217	A native chromatin purification system for epigenomic profiling in <i>Caenorhabditis elegans</i> . <i>Nucleic Acids Research</i> , 2010, 38, e26-e26.	6.5	58
218	Epigenomic profiling using microarrays. <i>BioTechniques</i> , 2003, 35, 346-357.	0.8	57
219	Superior performance in protein homology detection with the Blocks Database servers. <i>Nucleic Acids Research</i> , 1998, 26, 309-312.	6.5	56
220	The <i>Saccharomyces cerevisiae</i> ADE5,7 protein is homologous to overlapping <i>Drosophila melanogaster</i> Gart polypeptides. <i>Journal of Molecular Biology</i> , 1986, 190, 519-528.	2.0	55
221	Introduction of a DNA methyltransferase into <i>Drosophila</i> to probe chromatin structure in vivo. <i>Chromosoma</i> , 1996, 104, 332-340.	1.0	55
222	Applying whole-genome studies of epigenetic regulation to study human disease. <i>Cytogenetic and Genome Research</i> , 2006, 114, 1-15.	0.6	54
223	High-resolution mapping defines the cooperative architecture of Polycomb response elements. <i>Genome Research</i> , 2014, 24, 809-820.	2.4	53
224	Automated in situ chromatin profiling efficiently resolves cell types and gene regulatory programs. <i>Epigenetics and Chromatin</i> , 2018, 11, 74.	1.8	53
225	Dual recognitionâ€“incision enzymes might be involved in mismatch repair and meiosis. <i>Trends in Biochemical Sciences</i> , 2000, 25, 414-418.	3.7	52
226	Epigenetics, Histone H3 Variants, and the Inheritance of Chromatin States. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2004, 69, 235-244.	2.0	52
227	A Distal Heterochromatic Block Displays Centromeric Activity When Detached from a Natural Centromere. <i>Molecular Cell</i> , 1999, 4, 995-1004.	4.5	51
228	High-throughput discovery of rare human nucleotide polymorphisms by Ecotilling. <i>Nucleic Acids Research</i> , 2006, 34, e99-e99.	6.5	49
229	DNA torsion as a feedback mediator of transcription and chromatin dynamics. <i>Nucleus</i> , 2014, 5, 211-218.	0.6	49
230	Transcriptional activator components and poxvirus DNA-dependent ATPases comprise a single family. <i>Trends in Biochemical Sciences</i> , 1993, 18, 291-292.	3.7	48
231	Mot1 Redistributes TBP from TATA-Containing to TATA-Less Promoters. <i>Molecular and Cellular Biology</i> , 2013, 33, 4996-5004.	1.1	48
232	Silencing of transposons in plant genomes: kick them when they're down. <i>Genome Biology</i> , 2004, 5, 249.	13.9	46
233	Epigenetic Inheritance of Centromeres. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2010, 75, 51-60.	2.0	45
234	Capturing the dynamic epigenome. <i>Genome Biology</i> , 2010, 11, 218.	13.9	45

#	ARTICLE	IF	CITATIONS
235	Epigenetic inheritance in Arabidopsis: selective silence. <i>Current Opinion in Genetics and Development</i> , 2005, 15, 557-562.	1.5	44
236	“Point” Centromeres of <i>Saccharomyces</i> Harbor Single Centromere-Specific Nucleosomes. <i>Genetics</i> , 2012, 190, 1575-1577.	1.2	43
237	Simple and Complex Centromeric Satellites in <i>Drosophila</i> Sibling Species. <i>Genetics</i> , 2018, 208, 977-990.	1.2	43
238	Cloning exons for mapping of transcription: characterization of the <i>Drosophila melanogaster</i> alcohol dehydrogenase gene. <i>Nucleic Acids Research</i> , 1983, 11, 4735-4752.	6.5	42
239	Histone deposition pathways determine the chromatin landscapes of H3.1 and H3.3 K27M oncohistones. <i>ELife</i> , 2020, 9, .	2.8	42
240	Automated CUT&Tag profiling of chromatin heterogeneity in mixed-lineage leukemia. <i>Nature Genetics</i> , 2021, 53, 1586-1596.	9.4	42
241	Use of oligonucleotides to generate large deletions. <i>Nucleic Acids Research</i> , 1986, 14, 5115-5115.	6.5	41
242	Reconstitution of hemisomes on budding yeast centromeric DNA. <i>Nucleic Acids Research</i> , 2013, 41, 5769-5783.	6.5	41
243	CENPT bridges adjacent CENPA nucleosomes on young human α -satellite dimers. <i>Genome Research</i> , 2016, 26, 1178-1187.	2.4	41
244	<i>Max</i> deletion destabilizes MYC protein and abrogates E μ - <i>Myc</i> lymphomagenesis. <i>Genes and Development</i> , 2019, 33, 1252-1264.	2.7	41
245	The Yin and Yang of Histone Marks in Transcription. <i>Annual Review of Genomics and Human Genetics</i> , 2021, 22, 147-170.	2.5	41
246	The structure of a virus-encoded nucleosome. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 413-417.	3.6	40
247	Surveying the epigenomic landscape, one base at a time. <i>Genome Biology</i> , 2012, 13, 250.	13.9	40
248	Labile H3.3+H2A.Z nucleosomes mark 'nucleosome-free regions'. <i>Nature Genetics</i> , 2009, 41, 865-866.	9.4	38
249	Ordered deletions for DNA sequencing and in vitro mutagenesis by polymerase extension and exonuclease gapping of circular templates. <i>Nucleic Acids Research</i> , 1990, 18, 2961-2961.	6.5	37
250	Near the edge of a chromosome's “black hole”™. <i>Trends in Genetics</i> , 2002, 18, 165-167.	2.9	37
251	Architectural RNA in chromatin organization. <i>Biochemical Society Transactions</i> , 2020, 48, 1967-1978.	1.6	36
252	Pairing-Dependent Mislocalization of a <i>Drosophila</i> brown Gene Reporter to a Heterochromatic Environment. <i>Genetics</i> , 1999, 152, 595-604.	1.2	36

#	ARTICLE	IF	CITATIONS
253	Recent enhancements to the Blocks Database servers. <i>Nucleic Acids Research</i> , 1997, 25, 222-225.	6.5	34
254	DUX4-Induced Histone Variants H3.X and H3.Y Mark DUX4 Target Genes for Expression. <i>Cell Reports</i> , 2019, 29, 1812-1820.e5.	2.9	34
255	Retention of Induced Mutations in a <i>Drosophila</i> Reverse-Genetic Resource. <i>Genetics</i> , 2008, 180, 661-667.	1.2	33
256	Surveying the epigenomic landscape, one base at a time. <i>Genome Biology</i> , 2012, 13, 250.	3.8	33
257	Trans- and cis-acting effects of Firre on epigenetic features of the inactive X chromosome. <i>Nature Communications</i> , 2020, 11, 6053.	5.8	33
258	Multifunctional polypeptides for purinede novo synthesis. <i>BioEssays</i> , 1987, 6, 8-13.	1.2	32
259	Related transposons in <i>C.elegans</i> and <i>D.melanogaster</i> . <i>Nucleic Acids Research</i> , 1988, 16, 6234-6234.	6.5	32
260	Sequence analysis by electronic mail server. <i>Trends in Biochemical Sciences</i> , 1993, 18, 267-268.	3.7	32
261	Salt Fractionation of Nucleosomes for Genome-Wide Profiling. <i>Methods in Molecular Biology</i> , 2012, 833, 421-432.	0.4	32
262	Inner Kinetochoe Protein Interactions with Regional Centromeres of Fission Yeast. <i>Genetics</i> , 2015, 201, 543-561.	1.2	32
263	Tilling and Ecotilling for Crop Improvement. , 2007, , 333-349.		31
264	Heterochromatic <i>trans</i> -Inactivation of <i>Drosophila white</i> Transgenes. <i>Genetics</i> , 1997, 147, 671-677.	1.2	31
265	CUT&Tag2for1: a modified method for simultaneous profiling of the accessible and silenced regulome in single cells. <i>Genome Biology</i> , 2022, 23, 81.	3.8	30
266	Short H2A histone variants are expressed in cancer. <i>Nature Communications</i> , 2021, 12, 490.	5.8	29
267	Comparative Analysis of Position-Effect Variegation Mutations in <i>Drosophila melanogaster</i> Delineates the Targets of Modifiers. <i>Genetics</i> , 1998, 148, 733-741.	1.2	29
268	Sequence of a <i>Drosophila</i> DNA segment that functions in <i>Saccharomyces Cerevisiae</i> and its regulation by a yeast promoter. <i>Nucleic Acids Research</i> , 1983, 11, 789-800.	6.5	28
269	DNA Methylation and Demethylation in <i>Arabidopsis</i> . <i>The Arabidopsis Book</i> , 2008, 6, e0102.	0.5	27
270	Nucleosome dynamics during chromatin remodeling <i>in vivo</i> . <i>Nucleus</i> , 2016, 7, 20-26.	0.6	26

#	ARTICLE	IF	CITATIONS
271	Unexpected conformational variations of the human centromeric chromatin complex. <i>Genes and Development</i> , 2018, 32, 20-25.	2.7	25
272	Mechanisms of Nucleosome Dynamics In Vivo. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2016, 6, a026666.	2.9	24
273	High-Throughput TILLING for <i>Arabidopsis</i> . , 2006, 323, 127-136.		23
274	Single-epitope recognition imaging of native chromatin. <i>Epigenetics and Chromatin</i> , 2008, 1, 10.	1.8	23
275	Fly-TILL: Reverse genetics using a living point mutation resource. <i>Fly</i> , 2008, 2, 300-302.	0.9	23
276	A chromatin thermostat. <i>Nature</i> , 2010, 463, 887-888.	13.7	23
277	The genetics and epigenetics of satellite centromeres. <i>Genome Research</i> , 2022, 32, 608-615.	2.4	23
278	Chromatin-based transcriptional punctuation. <i>Genes and Development</i> , 2009, 23, 1037-1041.	2.7	21
279	Two <i>Drosophila melanogaster</i> mutations block successive steps of de novo purine synthesis.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1986, 83, 3919-3923.	3.3	20
280	Bugs on Drugs Go GAGAA. <i>Cell</i> , 2000, 103, 695-698.	13.5	20
281	CENP-A octamers do not confer a reduction in nucleosome height by AFM. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 4-5.	3.6	20
282	Mapping Regulatory Factors by Immunoprecipitation from Native Chromatin. <i>Current Protocols in Molecular Biology</i> , 2015, 110, 21.31.1-21.31.25.	2.9	20
283	Biotin-Tag Affinity Purification of a Centromeric Nucleosome Assembly Complex. <i>Cell Cycle</i> , 2006, 5, 1269-1274.	1.3	19
284	High-throughput single-cell epigenomic profiling by targeted insertion of promoters (TIP-seq). <i>Journal of Cell Biology</i> , 2021, 220, .	2.3	19
285	TILLING and Ecotilling for Rice. <i>Methods in Molecular Biology</i> , 2013, 956, 39-56.	0.4	18
286	Repetitive arrays containing a housekeeping gene have altered polytene chromosome morphology in <i>Drosophila</i> . <i>Chromosoma</i> , 1998, 107, 96-104.	1.0	17
287	The House & Garden guide to chromatin remodelling. <i>Nature Genetics</i> , 1999, 22, 6-7.	9.4	17
288	The heat shock response: A case study of chromatin dynamics in gene regulation. <i>Biochemistry and Cell Biology</i> , 2013, 91, 42-48.	0.9	17

#	ARTICLE	IF	CITATIONS
289	Epigenome editing made easy. <i>Nature Biotechnology</i> , 2015, 33, 606-607.	9.4	17
290	ENCODE and our very busy genome. <i>Nature Genetics</i> , 2007, 39, 817-818.	9.4	16
291	Phylogeny as the basis for naming histones. <i>Trends in Genetics</i> , 2013, 29, 499-500.	2.9	16
292	EvoChromo: towards a synthesis of chromatin biology and evolution. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	16
293	Managing the Steady State Chromatin Landscape by Nucleosome Dynamics. <i>Annual Review of Biochemistry</i> , 2022, 91, 183-195.	5.0	16
294	Rapid Changes in Plant Genomes. <i>Plant Cell</i> , 2005, 17, 2852-2855.	3.1	15
295	Capitalizing on disaster: Establishing chromatin specificity behind the replication fork. <i>BioEssays</i> , 2017, 39, 1600150.	1.2	15
296	Viral histones: pickpocketâ€™s prize or primordial progenitor?. <i>Epigenetics and Chromatin</i> , 2022, 15, .	1.8	15
297	Chemical- and Irradiation-Induced Mutants and TILLING. , 2007, , 148-180.		13
298	Biparental contributions of the H2A.B histone variant control embryonic development in mice. <i>PLoS Biology</i> , 2020, 18, e3001001.	2.6	13
299	The human mRNA that provides the N-terminus of chimeric G6PD encodes GMP reductase. <i>Cell</i> , 1989, 58, 1021-1022.	13.5	12
300	No strand left behind. <i>Science</i> , 2018, 361, 1311-1312.	6.0	12
301	Simplified Epigenome Profiling Using Antibody-tethered Tagmentation. <i>Bio-protocol</i> , 2021, 11, e4043.	0.2	12
302	Characterization of Sequences Responsible for trans-Inactivation of the <i>Drosophila</i> brown Gene. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 1993, 58, 577-584.	2.0	12
303	Nested genes take flight. <i>Current Biology</i> , 1993, 3, 372-374.	1.8	11
304	Connecting protein family resources using the proWeb network. <i>Trends in Biochemical Sciences</i> , 1996, 21, 444-445.	3.7	11
305	Measuring Genome-Wide Nucleosome Turnover Using CATCH-IT. <i>Methods in Enzymology</i> , 2012, 513, 169-184.	0.4	11
306	Chromatin: Packaging without Nucleosomes. <i>Current Biology</i> , 2012, 22, R1040-R1043.	1.8	11

#	ARTICLE	IF	CITATIONS
307	5-Aza-CdR Delivers a Gene Body Blow. <i>Cancer Cell</i> , 2014, 26, 449-451.	7.7	11
308	The H3.3K27M oncohistone antagonizes reprogramming in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2021, 17, e1009225.	1.5	11
309	Exploring protein homology with the Blocks server. <i>Trends in Genetics</i> , 1998, 14, 162-163.	2.9	10
310	Nucleosomes at Active Promoters: Unforgettable Loss. <i>Cancer Cell</i> , 2007, 12, 407-409.	7.7	10
311	Welcome to Epigenetics & Chromatin. <i>Epigenetics and Chromatin</i> , 2008, 1, 1.	1.8	10
312	Evolution of Centromeres and Kinetochores: A Two-Part Fugue. , 2009, , 1-37.		10
313	Response: Right-Handed Half-Nucleosomes at Centromeres. <i>Cell</i> , 2009, 139, 1217-1218.	13.5	10
314	Remarkable Evolutionary Plasticity of Centromeric Chromatin. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2017, 82, 71-82.	2.0	10
315	Unusual organizational features of the <i>Drosophila</i> Gart locus are not conserved within diptera. <i>Journal of Molecular Evolution</i> , 1992, 35, 51-59.	0.8	9
316	Epigenomics: A Roadmap to Chromatin. <i>Science</i> , 2008, 322, 853-853.	6.0	9
317	Distinct chromatin features characterize different classes of repeat sequences in <i>Drosophila melanogaster</i> . <i>BMC Genomics</i> , 2014, 15, 105.	1.2	9
318	Simultaneous Discovery of Cell-Free DNA and the Nucleosome Ladder. <i>Genetics</i> , 2018, 209, 27-29.	1.2	9
319	Chromatin Bottlenecks in Cancer. <i>Trends in Cancer</i> , 2019, 5, 183-194.	3.8	9
320	Speciation and Centromere Evolution. <i>Science</i> , 2001, 294, 2478-2480.	6.0	8
321	Predicting In Vivo Protein-Peptide Interactions with Random Phage Display. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2001, 4, 585-591.	0.6	7
322	So what's new?. <i>Nature</i> , 1991, 350, 9-9.	13.7	6
323	<i>Drosophila</i> Genomic Sequence Annotation Using the BLOCKS+ Database. <i>Genome Research</i> , 2000, 10, 543-546.	2.4	6
324	Catching a glimpse of nucleosome dynamics. <i>Cell Cycle</i> , 2010, 9, 3389-3390.	1.3	6

#	ARTICLE	IF	CITATIONS
325	MINCE-Seq: Mapping In Vivo Nascent Chromatin with EdU and Sequencing. <i>Methods in Molecular Biology</i> , 2018, 1832, 159-168.	0.4	6
326	Global and context-specific transcriptional consequences of oncogenic Fbw7 mutations. <i>ELife</i> , 2022, 11, .	2.8	6
327	Comparative methods for identifying functional domains in protein sequences. <i>Biotechnology Annual Review</i> , 1995, 1, 129-147.	2.1	5
328	Using the Blocks Database to Recognize Functional Domains. <i>Current Protocols in Bioinformatics</i> , 2003, 00, Unit 2.2.	25.8	5
329	Visualizing Gene Expression. <i>Cell</i> , 2004, 116, 633-634.	13.5	5
330	Baculovirus-encoded protein expression for epigenomic profiling in <i>Drosophila</i> cells. <i>Fly</i> , 2010, 4, 258-265.	0.9	5
331	GENOME MAPS 8: Building Gene Families. <i>Science</i> , 1997, 278, 615-615.	6.0	5
332	Orientation of repeating units in <i>Xenopus</i> chromosomal ribosomal DNA: A test of a stochastic model for maintaining intraspecies homogeneity. <i>Journal of Molecular Biology</i> , 1974, 85, 445-450.	2.0	4
333	Reaching for new heitz. <i>Genetica</i> , 2000, 109, 7-8.	0.5	4
334	Chromatin roadblocks to reprogramming 50 years on. <i>BMC Biology</i> , 2012, 10, 83.	1.7	4
335	Introduction of a DNA methyltransferase into <i>Drosophila</i> to probe chromatin structure in vivo. <i>Chromosoma</i> , 1996, 104, 332-340.	1.0	4
336	CUT&RUN Profiling of the Budding Yeast Epigenome. <i>Methods in Molecular Biology</i> , 2022, 2477, 129-147.	0.4	4
337	Fact and fiction in alignment. <i>Nature</i> , 1992, 358, 271-271.	13.7	3
338	You read it here first. <i>Nature</i> , 1997, 387, 843-843.	13.7	3
339	Summary: The Nucleus—A Close-Knit Community of Dynamic Structures. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2010, 75, 607-615.	2.0	3
340	Steven Henikoff. <i>Current Biology</i> , 2012, 22, R106-R107.	1.8	3
341	Epigenetics & Chromatin: interactions and processes. <i>Epigenetics and Chromatin</i> , 2013, 6, 2.	1.8	3
342	Pioneers Invade the Nucleosomal Landscape. <i>Molecular Cell</i> , 2018, 71, 193-194.	4.5	3

#	ARTICLE	IF	CITATIONS
343	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
344	Darwin meets Waddington. Current Biology, 2018, 28, R682-R684.	1.8	2
345	Bringing Oncohistones into the Fold. Cancer Discovery, 2019, 9, 1346-1348.	7.7	2
346	Evolution: Heterochromatin Diversity in Early-Branching Land Plants. Current Biology, 2020, 30, R161-R163.	1.8	2
347	Epigenetic Profiling of Histone Variants. , 2009, , 101-118.		2
348	Epigenomic Landscapes Reflect Neuronal Diversity. Neuron, 2015, 86, 1319-1321.	3.8	1
349	Structural Biology: Probing the Origins of Chromatin. Current Biology, 2017, 27, R1118-R1120.	1.8	1
350	Remodellerâ€™ variant tag team slams transposons. Nature Cell Biology, 2021, 23, 297-298.	4.6	1
351	Conspiracy of silence among repeated transgenes. , 1998, 20, 532.		1
352	Functional Organization of the Nucleus: A Laboratory Guide (Methods in Cell Biology Vol. 35). Trends in Genetics, 1992, 8, 259.	2.9	0
353	A Simple Method for Gene Expression and Chromatin Profiling of Individual Cell Types within a Tissue. Developmental Cell, 2011, 21, 1179.	3.1	0
354	Histones push the envelope. Nature Structural and Molecular Biology, 2014, 21, 651-652.	3.6	0
355	The Genetic Map Enters Its Second Century. Genetics, 2015, 200, 671-674.	1.2	0
356	Quantitative Measurement of Nucleosome Occupancy and DNA Accessibility. Biophysical Journal, 2019, 116, 73a.	0.2	0
357	DNA demethylation by the baseâ€™ excision DNA repair pathway in Arabidopsis. FASEB Journal, 2007, 21, .	0.2	0
358	Biparental contributions of the H2A.B histone variant control embryonic development in mice. , 2020, 18, e3001001.		0
359	Biparental contributions of the H2A.B histone variant control embryonic development in mice. , 2020, 18, e3001001.		0
360	Biparental contributions of the H2A.B histone variant control embryonic development in mice. , 2020, 18, e3001001.		0

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361	Biparental contributions of the H2A.B histone variant control embryonic development in mice. , 2020, 18, e3001001.		0
362	Biparental contributions of the H2A.B histone variant control embryonic development in mice. , 2020, 18, e3001001.		0
363	Biparental contributions of the H2A.B histone variant control embryonic development in mice. , 2020, 18, e3001001.		0