

Steven Henikoff

List of Publications by Year in descending order

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363
papers

85,195
citations

588

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419
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419
docs citations

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. Nature Protocols, 2009, 4, 1073-1081.	12.0	6,149
2	Amino acid substitution matrices from protein blocks.. Proceedings of the National Academy of Sciences of the United States of America, 1992, 89, 10915-10919.	7.1	5,230
3	SIFT: predicting amino acid changes that affect protein function. Nucleic Acids Research, 2003, 31, 3812-3814.	14.5	5,120
4	Unidirectional digestion with exonuclease III creates targeted breakpoints for DNA sequencing. Gene, 1984, 28, 351-359.	2.2	4,616
5	Predicting Deleterious Amino Acid Substitutions. Genome Research, 2001, 11, 863-874.	5.5	2,186
6	SIFT web server: predicting effects of amino acid substitutions on proteins. Nucleic Acids Research, 2012, 40, W452-W457.	14.5	1,838
7	The epigenetic progenitor origin of human cancer. Nature Reviews Genetics, 2006, 7, 21-33.	16.3	1,642
8	Comparative Genomics of the Eukaryotes. Science, 2000, 287, 2204-2215.	12.6	1,573
9	Genome-wide analysis of Arabidopsis thaliana DNA methylation uncovers an interdependence between methylation and transcription. Nature Genetics, 2007, 39, 61-69.	21.4	1,257
10	The Centromere Paradox: Stable Inheritance with Rapidly Evolving DNA. Science, 2001, 293, 1098-1102.	12.6	1,138
11	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. Science, 2010, 330, 1787-1797.	12.6	1,124
12	An efficient targeted nuclease strategy for high-resolution mapping of DNA binding sites. ELife, 2017, 6, .	6.0	1,119
13	CUT&Tag for efficient epigenomic profiling of small samples and single cells. Nature Communications, 2019, 10, 1930.	12.8	1,101
14	The Histone Variant H3.3 Marks Active Chromatin by Replication-Independent Nucleosome Assembly. Molecular Cell, 2002, 9, 1191-1200.	9.7	1,023
15	[12] Unidirectional digestion with exonuclease III in DNA sequence analysis. Methods in Enzymology, 1987, 155, 156-165.	1.0	957
16	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. Science, 2010, 330, 1775-1787.	12.6	912
17	Requirement of CHROMOMETHYLASE3 for Maintenance of CpXpG Methylation. Science, 2001, 292, 2077-2080.	12.6	820
18	Targeting Induced Local Lesions IN Genomes (TILLING) for Plant Functional Genomics. Plant Physiology, 2000, 123, 439-442.	4.8	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.	6.2	811
20	Regulation of nucleosome dynamics by histone modifications. Nature Structural and Molecular Biology, 2013, 20, 259-266.	8.2	770
21	Unlocking the secrets of the genome. Nature, 2009, 459, 927-930.	27.8	744
22	Histone variants “ ancient wrap artists of the epigenome. Nature Reviews Molecular Cell Biology, 2010, 11, 264-275.	37.0	699
23	Targeted screening for induced mutations. Nature Biotechnology, 2000, 18, 455-457.	17.5	689
24	Consensus-degenerate hybrid oligonucleotide primers for amplification of distantly related sequences. Nucleic Acids Research, 1998, 26, 1628-1635.	14.5	659
25	Accounting for Human Polymorphisms Predicted to Affect Protein Function. Genome Research, 2002, 12, 436-446.	5.5	630
26	Targeted in situ genome-wide profiling with high efficiency for low cell numbers. Nature Protocols, 2018, 13, 1006-1019.	12.0	572
27	Expansions of transgene repeats cause heterochromatin formation and gene silencing in Drosophila. Cell, 1994, 77, 993-1002.	28.9	557
28	Identification of in vivo DNA targets of chromatin proteins using tethered Dam methyltransferase. Nature Biotechnology, 2000, 18, 424-428.	17.5	544
29	Extensive Demethylation of Repetitive Elements During Seed Development Underlies Gene Imprinting. Science, 2009, 324, 1447-1451.	12.6	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.	7.1	524
31	Spectrum of Chemically Induced Mutations From a Large-Scale Reverse-Genetic Screen in Arabidopsis. Genetics, 2003, 164, 731-740.	2.9	512
32	Histone H2A.Z and DNA methylation are mutually antagonistic chromatin marks. Nature, 2008, 456, 125-129.	27.8	508
33	Large-Scale Discovery of Induced Point Mutations With High-Throughput TILLING. Genome Research, 2003, 13, 524-530.	5.5	505
34	Phylogenomics of the nucleosome. Nature Structural and Molecular Biology, 2003, 10, 882-891.	8.2	497
35	Sequencing of a rice centromere uncovers active genes. Nature Genetics, 2004, 36, 138-145.	21.4	489
36	High-Throughput Screening for Induced Point Mutations. Plant Physiology, 2001, 126, 480-484.	4.8	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.	7.1	470
38	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.	7.1	468
39	Genome-scale profiling of histone H3.3 replacement patterns. Nature Genetics, 2005, 37, 1090-1097.	21.4	463
40	Automated assembly of protein blocks for database searching. Nucleic Acids Research, 1991, 19, 6565-6572.	14.5	449
41	Genome-Wide Kinetics of Nucleosome Turnover Determined by Metabolic Labeling of Histones. Science, 2010, 328, 1161-1164.	12.6	431
42	Efficient discovery of DNA polymorphisms in natural populations by Ecotilling. Plant Journal, 2004, 37, 778-786.	5.7	428
43	Histone modification: cause or cog?. Trends in Genetics, 2011, 27, 389-396.	6.7	415
44	Discovery of chemically induced mutations in rice by TILLING. BMC Plant Biology, 2007, 7, 19.	3.6	406
45	Nucleosome destabilization in the epigenetic regulation of gene expression. Nature Reviews Genetics, 2008, 9, 15-26.	16.3	404
46	Performance evaluation of amino acid substitution matrices. Proteins: Structure, Function and Bioinformatics, 1993, 17, 49-61.	2.6	395
47	Doxorubicin, DNA torsion, and chromatin dynamics. Biochimica Et Biophysica Acta: Reviews on Cancer, 2014, 1845, 84-89.	7.4	394
48	Position-based sequence weights. Journal of Molecular Biology, 1994, 243, 574-578.	4.2	392
49	Centromeric Localization and Adaptive Evolution of an Arabidopsis Histone H3 Variant. Plant Cell, 2002, 14, 1053-1066.	6.6	372
50	Protein Family Classification Based on Searching a Database of Blocks. Genomics, 1994, 19, 97-107.	2.9	370
51	Gene Families: The Taxonomy of Protein Paralogs and Chimeras. Science, 1997, 278, 609-614.	12.6	362
52	A Simple Method for Gene Expression and Chromatin Profiling of Individual Cell Types within a Tissue. Developmental Cell, 2010, 18, 1030-1040.	7.0	360
53	CODEHOP (COnsensus-DEgenerate Hybrid Oligonucleotide Primer) PCR primer design. Nucleic Acids Research, 2003, 31, 3763-3766.	14.5	359
54	The INTACT method for cell type-specific gene expression and chromatin profiling in Arabidopsis thaliana. Nature Protocols, 2011, 6, 56-68.	12.0	348

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55	Discovery of induced point mutations in maize genes by TILLING. BMC Plant Biology, 2004, 4, 12.	3.6	342
56	Position-effect variegation after 60 years. Trends in Genetics, 1990, 6, 422-426.	6.7	335
57	TILLING. Traditional Mutagenesis Meets Functional Genomics. Plant Physiology, 2004, 135, 630-636.	4.8	331
58	Epigenome characterization at single base-pair resolution. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18318-18323.	7.1	325
59	Genetic modification of heterochromatic association and nuclear organization in Drosophila. Nature, 1996, 381, 529-531.	27.8	324
60	Major Evolutionary Transitions in Centromere Complexity. Cell, 2009, 138, 1067-1082.	28.9	324
61	Localization of RNA from heat-induced polysomes at puff sites in Drosophila melanogaster.. Proceedings of the National Academy of Sciences of the United States of America, 1975, 72, 1117-1121.	7.1	315
62	Nucleosomes Are Context-Specific, H2A.Z-Modulated Barriers to RNA Polymerase. Molecular Cell, 2014, 53, 819-830.	9.7	313
63	A Comprehensive Map of Insulator Elements for the Drosophila Genome. PLoS Genetics, 2010, 6, e1000814.	3.5	305
64	Poised for Contagion: Evolutionary Origins of the Infectious Abilities of Invertebrate Retroviruses. Genome Research, 2000, 10, 1307-1318.	5.5	303
65	Chromatin profiling using targeted DNA adenine methyltransferase. Nature Genetics, 2001, 27, 304-308.	21.4	303
66	Improved CUT&RUN chromatin profiling tools. ELife, 2019, 8, .	6.0	296
67	Automated construction and graphical presentation of protein blocks from unaligned sequences. Gene, 1995, 163, GC17-GC26.	2.2	289
68	Histone H3 variants specify modes of chromatin assembly. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16477-16484.	7.1	288
69	Heterochromatic deposition of centromeric histone H3-like proteins. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 716-721.	7.1	285
70	Increased coverage of protein families with the Blocks Database servers. Nucleic Acids Research, 2000, 28, 228-230.	14.5	281
71	Gene within a gene: Nested Drosophila genes encode unrelated proteins on opposite DNA strands. Cell, 1986, 44, 33-42.	28.9	275
72	Exploring and explaining epigenetic effects. Trends in Genetics, 1997, 13, 293-295.	6.7	275

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73	Histone Variants and Epigenetics. Cold Spring Harbor Perspectives in Biology, 2015, 7, a019364.	5.5	275
74	Adaptive Evolution of Cid, a Centromere-Specific Histone in Drosophila. Genetics, 2001, 157, 1293-1298.	2.9	274
75	Blocks+: a non-redundant database of protein alignment blocks derived from multiple compilations. Bioinformatics, 1999, 15, 471-479.	4.1	269
76	Histone variants on the move: substrates for chromatin dynamics. Nature Reviews Molecular Cell Biology, 2017, 18, 115-126.	37.0	268
77	Something from nothing: the evolution and utility of satellite repeats. Trends in Genetics, 1998, 14, 200-204.	6.7	267
78	Peak calling by Sparse Enrichment Analysis for CUT&RUN chromatin profiling. Epigenetics and Chromatin, 2019, 12, 42.	3.9	267
79	Histone variants, nucleosome assembly and epigenetic inheritance. Trends in Genetics, 2004, 20, 320-326.	6.7	265
80	A unified phylogeny-based nomenclature for histone variants. Epigenetics and Chromatin, 2012, 5, 7.	3.9	265
81	Spreading of silent chromatin: inaction at a distance. Nature Reviews Genetics, 2006, 7, 793-803.	16.3	264
82	TILLING to detect induced mutations in soybean. BMC Plant Biology, 2008, 8, 9.	3.6	259
83	Mediation of meiotic and early mitotic chromosome segregation in Drosophila by a protein related to kinesin. Nature, 1990, 345, 81-83.	27.8	256
84	Histone Replacement Marks the Boundaries of cis-Regulatory Domains. Science, 2007, 315, 1408-1411.	12.6	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.	2.9	254
86	ASSEMBLY OF VARIANT HISTONES INTO CHROMATIN. Annual Review of Cell and Developmental Biology, 2005, 21, 133-153.	9.4	248
87	Histone variants: dynamic punctuation in transcription. Genes and Development, 2014, 28, 672-682.	5.9	247
88	Maize Centromeres: Organization and Functional Adaptation in the Genetic Background of Oat. Plant Cell, 2004, 16, 571-581.	6.6	241
89	SINGLE-NUCLEOTIDE MUTATIONS FOR PLANT FUNCTIONAL GENOMICS. Annual Review of Plant Biology, 2003, 54, 375-401.	18.7	238
90	A histone-H3-like protein in C. elegans. Nature, 1999, 401, 547-548.	27.8	233

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91	DNA demethylation by DNA repair. Trends in Genetics, 2009, 25, 82-90.	6.7	232
92	The HP1 chromo shadow domain binds a consensus peptide pentamer. Current Biology, 2000, 10, 27-30.	3.9	231
93	Mismatch cleavage by single-strand specific nucleases. Nucleic Acids Research, 2004, 32, 2632-2641.	14.5	225
94	TILLING: practical single-nucleotide mutation discovery. Plant Journal, 2006, 45, 684-694.	5.7	225
95	Genome-wide analysis of DNA methylation patterns. Development (Cambridge), 2007, 134, 3959-3965.	2.5	224
96	A protocol for TILLING and Ecotilling in plants and animals. Nature Protocols, 2006, 1, 2465-2477.	12.0	219
97	Conspiracy of silence among repeated transgenes. BioEssays, 1998, 20, 532-535.	2.5	216
98	DNA Methylation Profiling Identifies CG Methylation Clusters in Arabidopsis Genes. Current Biology, 2005, 15, 154-159.	3.9	212
99	Tetrameric Structure of Centromeric Nucleosomes in Interphase Drosophila Cells. PLoS Biology, 2007, 5, e218.	5.6	210
100	Genome-wide profiling of salt fractions maps physical properties of chromatin. Genome Research, 2009, 19, 460-469.	5.5	204
101	Adaptive evolution of centromere proteins in plants and animals. Journal of Biology, 2004, 3, 18.	2.7	200
102	Transcription terminates in yeast distal to a control sequence. Cell, 1983, 33, 607-614.	28.9	198
103	Conserved Arrangement of Nested Genes at the Drosophila <i>Cart</i> Locus. Genetics, 1987, 117, 711-725.	2.9	195
104	Centromeric Nucleosomes Induce Positive DNA Supercoils. Cell, 2009, 138, 104-113.	28.9	193
105	A DNA Methyltransferase Homolog With a Chromodomain Exists in Multiple Polymorphic Forms in Arabidopsis. Genetics, 1998, 149, 307-318.	2.9	192
106	Transcription-generated torsional stress destabilizes nucleosomes. Nature Structural and Molecular Biology, 2014, 21, 88-94.	8.2	183
107	Efficient low-cost chromatin profiling with CUT&Tag. Nature Protocols, 2020, 15, 3264-3283.	12.0	181
108	Conflict begets complexity: the evolution of centromeres. Current Opinion in Genetics and Development, 2002, 12, 711-718.	3.3	178

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109	Genomic Analysis of Parent-of-Origin Allelic Expression in Arabidopsis thaliana Seeds. PLoS ONE, 2011, 6, e23687.	2.5	178
110	Moving AHEAD with an international human epigenome project. Nature, 2008, 454, 711-715.	27.8	177
111	Recurrent loss of CenH3 is associated with independent transitions to holocentricity in insects. ELife, 2014, 3, .	6.0	174
112	High-resolution mapping of transcription factor binding sites on native chromatin. Nature Methods, 2014, 11, 203-209.	19.0	170
113	Genome-Wide Profiling of DNA Methylation Reveals Transposon Targets of CHROMOMETHYLASE3. Current Biology, 2002, 12, 65-68.	3.9	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.	2.9	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.	5.9	153
116	ChEC-seq kinetics discriminates transcription factor binding sites by DNA sequence and shape in vivo. Nature Communications, 2015, 6, 8733.	12.8	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.	2.3	151
119	Centromeric chromatin: what makes it unique?. Current Opinion in Genetics and Development, 2005, 15, 177-184.	3.3	151
120	Methylation-Sensitive Expression of a DNA Demethylase Gene Serves As an Epigenetic Rheostat. PLoS Genetics, 2015, 11, e1005142.	3.5	150
121	Epigenetics, cellular memory and gene regulation. Current Biology, 2016, 26, R644-R648.	3.9	148
122	Trans-sensing effects from Drosophila to humans. Cell, 1991, 65, 201-203.	28.9	147
123	Modulation of a Transcription Factor Counteracts Heterochromatic Gene Silencing in Drosophila. Cell, 2001, 104, 839-847.	28.9	146
124	Centromeres Convert but Don't Cross. PLoS Biology, 2010, 8, e1000326.	5.6	143
125	Transcribing through the nucleosome. Trends in Biochemical Sciences, 2014, 39, 577-586.	7.5	141
126	Changes in Chromosomal Localization of Heterochromatin-binding Proteins during the Cell Cycle in <i>Drosophila</i> . Journal of Cell Biology, 1998, 140, 1297-1306.	5.2	140

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127	Transcriptional Regulators Compete with Nucleosomes Post-replication. <i>Cell</i> , 2016, 165, 580-592.	28.9	139
128	Centromeres Are Specialized Replication Domains in Heterochromatin. <i>Journal of Cell Biology</i> , 2001, 153, 101-110.	5.2	137
129	Histone variants and modifications in plant gene regulation. <i>Current Opinion in Plant Biology</i> , 2011, 14, 116-122.	7.1	132
130	Large-scale Chromosomal Movements During Interphase Progression in <i>Drosophila</i> . <i>Journal of Cell Biology</i> , 1998, 143, 13-22.	5.2	131
131	Maintenance of chromatin states: an open-and-shut case. <i>Current Opinion in Cell Biology</i> , 2003, 15, 266-274.	5.4	129
132	Chaperone-mediated assembly of centromeric chromatin <i>in vitro</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6172-6177.	7.1	128
133	Precise genome-wide mapping of single nucleosomes and linkers <i>in vivo</i> . <i>Genome Biology</i> , 2018, 19, 19.	8.8	128
134	Histone variants in pluripotency and disease. <i>Development (Cambridge)</i> , 2013, 140, 2513-2524.	2.5	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.	3.5	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.	7.1	125
138	What makes a centromere?. <i>Experimental Cell Research</i> , 2020, 389, 111895.	2.6	123
139	Dosage-dependent modification of position-effect variegation in <i>Drosophila</i> . <i>BioEssays</i> , 1996, 18, 401-409.	2.5	121
140	Centromere Targeting Element within the Histone Fold Domain of Cid. <i>Molecular and Cellular Biology</i> , 2002, 22, 7553-7561.	2.3	121
141	Single-cell CUT&Tag analysis of chromatin modifications in differentiation and tumor progression. <i>Nature Biotechnology</i> , 2021, 39, 819-824.	17.5	121
142	Centromeres: Selfish drivers. <i>Nature</i> , 2002, 417, 227-227.	27.8	119
143	Environmental responses mediated by histone variants. <i>Trends in Cell Biology</i> , 2014, 24, 642-650.	7.9	114
144	Trans-inactivation of the <i>Drosophila</i> brown 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.	7.1	112

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145	The Blocks database—a system for protein classification. <i>Nucleic Acids Research</i> , 1996, 24, 197-200.	14.5	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.	7.1	112
147	Germline histone dynamics and epigenetics. <i>Current Opinion in Cell Biology</i> , 2007, 19, 257-265.	5.4	112
148	Changes in H2A.Z occupancy and DNA methylation during B-cell lymphomagenesis. <i>Genome Research</i> , 2010, 20, 1383-1390.	5.5	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.	5.5	112
150	High-resolution digital profiling of the epigenome. <i>Nature Reviews Genetics</i> , 2014, 15, 814-827.	16.3	112
151	Epigenetic Consequences of Nucleosome Dynamics. <i>Cell</i> , 2002, 111, 281-284.	28.9	111
152	Non-B-Form DNA Is Enriched at Centromeres. <i>Molecular Biology and Evolution</i> , 2018, 35, 949-962.	8.9	110
153	H2A.Z nucleosomes enriched over active genes are homotypic. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1500-1507.	8.2	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.	6.0	108
155	Transcription and Histone Modifications in the Recombination-Free Region Spanning a Rice Centromere[W]. <i>Plant Cell</i> , 2005, 17, 3227-3238.	6.6	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.	9.6	107
157	RSC-Associated Subnucleosomes Define MNase-Sensitive Promoters in Yeast. <i>Molecular Cell</i> , 2019, 73, 238-249.e3.	9.7	107
158	Isolation of a gene from <i>Drosophila</i> by complementation in yeast. <i>Nature</i> , 1981, 289, 33-37.	27.8	104
159	Histone H3.3 Variant Dynamics in the Germline of <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , 2006, 2, e97.	3.5	104
160	Transcription and Remodeling Produce Asymmetrically Unwrapped Nucleosomal Intermediates. <i>Molecular Cell</i> , 2017, 68, 1038-1053.e4.	9.7	104
161	Sequence, Chromatin and Evolution of Satellite DNA. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4309.	4.1	104
162	Holocentromeres are dispersed point centromeres localized at transcription factor hotspots. <i>ELife</i> , 2014, 3, e02025.	6.0	103

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163	[6] Blocks database and its applications. <i>Methods in Enzymology</i> , 1996, 266, 88-105.	1.0	101
164	Histone variants at a glance. <i>Journal of Cell Science</i> , 2021, 134, .	2.0	101
165	Nuclear organization and gene expression: homologous pairing and long-range interactions. <i>Current Opinion in Cell Biology</i> , 1997, 9, 388-395.	5.4	99
166	Pioneer Factor-Nucleosome Binding Events during Differentiation Are Motif Encoded. <i>Molecular Cell</i> , 2019, 75, 562-575.e5.	9.7	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.	2.2	97
168	A simple method for generating high-resolution maps of genome-wide protein binding. <i>ELife</i> , 2015, 4, e09225.	6.0	97
169	Position effect and related phenomena. <i>Current Opinion in Genetics and Development</i> , 1992, 2, 907-912.	3.3	96
170	Asymmetric nucleosomes flank promoters in the budding yeast genome. <i>Genome Research</i> , 2015, 25, 381-390.	5.5	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.	2.9	96
172	Using substitution probabilities to improve position-specific scoring matrices. <i>Bioinformatics</i> , 1996, 12, 135-143.	4.1	94
173	New features of the Blocks Database servers. <i>Nucleic Acids Research</i> , 1999, 27, 226-228.	14.5	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</i> brown gene.. <i>Genes and Development</i> , 1991, 5, 331-340.	5.9	92
176	Heterochromatin protein 1 binds transgene arrays. <i>Chromosoma</i> , 1998, 107, 286-292.	2.2	92
177	Centromeres put epigenetics in the driver's seat. <i>Trends in Biochemical Sciences</i> , 2006, 31, 662-669.	7.5	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.	7.1	91
179	Nucleotide sequence and initial functional characterization of the clcR gene encoding a LysR family activator of the clcABD chlorocatechol operon in <i>Pseudomonas putida</i> . <i>Journal of Bacteriology</i> , 1993, 175, 417-427.	2.2	90
180	Adaptive Evolution of the Histone Fold Domain in Centromeric Histones. <i>Molecular Biology and Evolution</i> , 2004, 21, 1712-1718.	8.9	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.	5.9	89
182	Doxorubicin Enhances Nucleosome Turnover around Promoters. <i>Current Biology</i> , 2013, 23, 782-787.	3.9	89
183	Trans-Sensing Effects: The Ups and Downs of Being Together. <i>Cell</i> , 1998, 93, 329-332.	28.9	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.	7.1	88
185	Position-effect variegation and chromosome structure of a heat shock puff in <i>Drosophila</i> . <i>Chromosoma</i> , 1981, 83, 381-393.	2.2	86
186	A unique chromatin complex occupies young α -satellite arrays of human centromeres. <i>Science Advances</i> , 2015, 1, .	10.3	86
187	Quantitative MNase-seq accurately maps nucleosome occupancy levels. <i>Genome Biology</i> , 2019, 20, 198.	8.8	86
188	Old cogs, new tricks: the evolution of gene expression in a chromatin context. <i>Nature Reviews Genetics</i> , 2019, 20, 283-297.	16.3	86
189	Evolutionary Turnover of Kinetochore Proteins: A Ship of Theseus?. <i>Trends in Cell Biology</i> , 2016, 26, 498-510.	7.9	84
190	Heterochromatin function in complex genomes. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2000, 1470, O1-O8.	7.4	82
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