

Zhiping Weng

List of Publications by Year in descending order

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Version: 2024-02-01

263
papers

47,544
citations

2671

95
h-index

2125

203
g-index

299
all docs

299
docs citations

299
times ranked

56725
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	13.7	4,709
2	Distinct and predictive chromatin signatures of transcriptional promoters and enhancers in the human genome. <i>Nature Genetics</i> , 2007, 39, 311-318.	9.4	2,898
3	The TREM2-APOE Pathway Drives the Transcriptional Phenotype of Dysfunctional Microglia in Neurodegenerative Diseases. <i>Immunity</i> , 2017, 47, 566-581.e9.	6.6	1,741
4	ZDOCK server: interactive docking prediction of protein-protein complexes and symmetric multimers. <i>Bioinformatics</i> , 2014, 30, 1771-1773.	1.8	1,313
5	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	13.7	1,252
6	High-Resolution Mapping and Characterization of Open Chromatin across the Genome. <i>Cell</i> , 2008, 132, 311-322.	13.5	1,246
7	ZDOCK: An initial-stage protein-docking algorithm. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 80-87.	1.5	1,220
8	Assessing computational tools for the discovery of transcription factor binding sites. <i>Nature Biotechnology</i> , 2005, 23, 137-144.	9.4	1,121
9	A Global Map of p53 Transcription-Factor Binding Sites in the Human Genome. <i>Cell</i> , 2006, 124, 207-219.	13.5	1,060
10	Paternally Induced Transgenerational Environmental Reprogramming of Metabolic Gene Expression in Mammals. <i>Cell</i> , 2010, 143, 1084-1096.	13.5	990
11	Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. <i>Genome Research</i> , 2012, 22, 1798-1812.	2.4	762
12	Therapeutic genome editing by combined viral and non-viral delivery of CRISPR system components in vivo. <i>Nature Biotechnology</i> , 2016, 34, 328-333.	9.4	732
13	Defining functional DNA elements in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6131-6138.	3.3	635
14	Comprehensive functional genomic resource and integrative model for the human brain. <i>Science</i> , 2018, 362, .	6.0	618
15	Endogenous siRNAs Derived from Transposons and mRNAs in <i>Drosophila</i> Somatic Cells. <i>Science</i> , 2008, 320, 1077-1081.	6.0	594
16	Unsupervised pattern discovery in human chromatin structure through genomic segmentation. <i>Nature Methods</i> , 2012, 9, 473-476.	9.0	562
17	Target RNA-Directed Trimming and Tailing of Small Silencing RNAs. <i>Science</i> , 2010, 328, 1534-1539.	6.0	514
18	Unexpected role of interferon- β in regulating neuronal connectivity and social behaviour. <i>Nature</i> , 2016, 535, 425-429.	13.7	507

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19	Collapse of Germline piRNAs in the Absence of Argonaute3 Reveals Somatic piRNAs in Flies. <i>Cell</i> , 2009, 137, 509-521.	13.5	503
20	Accelerating Protein Docking in ZDOCK Using an Advanced 3D Convolution Library. <i>PLoS ONE</i> , 2011, 6, e24657.	1.1	490
21	Global mapping of c-Myc binding sites and target gene networks in human B cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17834-17839.	3.3	462
22	Mbd3/NURD Complex Regulates Expression of 5-Hydroxymethylcytosine Marked Genes in Embryonic Stem Cells. <i>Cell</i> , 2011, 147, 1498-1510.	13.5	424
23	ZRANK: Reranking protein docking predictions with an optimized energy function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 1078-1086.	1.5	401
24	Proteinâ€“protein docking benchmark version 4.0. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3111-3114.	1.5	390
25	Detection of functional DNA motifs via statistical over-representation. <i>Nucleic Acids Research</i> , 2004, 32, 1372-1381.	6.5	383
26	The Drosophila HP1 Homolog Rhino Is Required for Transposon Silencing and piRNA Production by Dual-Strand Clusters. <i>Cell</i> , 2009, 138, 1137-1149.	13.5	382
27	A compendium of gene expression in normal human tissues. <i>Physiological Genomics</i> , 2001, 7, 97-104.	1.0	376
28	The PsychENCODE project. <i>Nature Neuroscience</i> , 2015, 18, 1707-1712.	7.1	371
29	The landscape of histone modifications across 1% of the human genome in five human cell lines. <i>Genome Research</i> , 2007, 17, 691-707.	2.4	353
30	Updates to the Integrated Proteinâ€“Protein Interaction Benchmarks: Docking Benchmark Version 5 and Affinity Benchmark Version 2. <i>Journal of Molecular Biology</i> , 2015, 427, 3031-3041.	2.0	348
31	Docking unbound proteins using shape complementarity, desolvation, and electrostatics. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 281-294.	1.5	339
32	Structure, function, and evolution of transient and obligate protein-protein interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10930-10935.	3.3	335
33	An Ancient Transcription Factor Initiates the Burst of piRNA Production during Early Meiosis in Mouse Testes. <i>Molecular Cell</i> , 2013, 50, 67-81.	4.5	322
34	The Insulator Binding Protein CTCF Positions 20 Nucleosomes around Its Binding Sites across the Human Genome. <i>PLoS Genetics</i> , 2008, 4, e1000138.	1.5	321
35	piRNA-guided transposon cleavage initiates Zucchini-dependent, phased piRNA production. <i>Science</i> , 2015, 348, 817-821.	6.0	320
36	Sorting of <i>Drosophila</i> small silencing RNAs partitions microRNA* strands into the RNA interference pathway. <i>Rna</i> , 2010, 16, 43-56.	1.6	304

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37	Adenovirus-Mediated Somatic Genome Editing of <i>Pten</i> by CRISPR/Cas9 in Mouse Liver in Spite of Cas9-Specific Immune Responses. <i>Human Gene Therapy</i> , 2015, 26, 432-442.	1.4	291
38	RDOCK: Refinement of rigid-body protein docking predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 693-707.	1.5	289
39	Nucleosome positioning signals in genomic DNA. <i>Genome Research</i> , 2007, 17, 1170-1177.	2.4	287
40	The Cellular EJC Interactome Reveals Higher-Order mRNP Structure and an EJC-SR Protein Nexus. <i>Cell</i> , 2012, 151, 750-764.	13.5	287
41	A novel shape complementarity scoring function for protein-protein docking. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 51, 397-408.	1.5	277
42	Factorbook.org: a Wiki-based database for transcription factor-binding data generated by the ENCODE consortium. <i>Nucleic Acids Research</i> , 2013, 41, D171-D176.	6.5	274
43	Integrating statistical pair potentials into protein complex prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 511-520.	1.5	273
44	Cluster-Buster: finding dense clusters of motifs in DNA sequences. <i>Nucleic Acids Research</i> , 2003, 31, 3666-3668.	6.5	268
45	Principles of regulatory information conservation between mouse and human. <i>Nature</i> , 2014, 515, 371-375.	13.7	259
46	Optical Recognition of Converted DNA Nucleotides for Single-Molecule DNA Sequencing Using Nanopore Arrays. <i>Nano Letters</i> , 2010, 10, 2237-2244.	4.5	257
47	Protein-protein docking benchmark 2.0: An update. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 214-216.	1.5	254
48	A structure-based benchmark for protein-protein binding affinity. <i>Protein Science</i> , 2011, 20, 482-491.	3.1	252
49	A protein-protein docking benchmark. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 88-91.	1.5	242
50	Modeling gene expression using chromatin features in various cellular contexts. <i>Genome Biology</i> , 2012, 13, R53.	13.9	231
51	Adaptation to P Element Transposon Invasion in <i>Drosophila melanogaster</i> . <i>Cell</i> , 2011, 147, 1551-1563.	13.5	226
52	Protein-protein docking benchmark version 3.0. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 705-709.	1.5	224
53	Developmental regulation and individual differences of neuronal H3K4me3 epigenomes in the prefrontal cortex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 8824-8829.	3.3	218
54	Gene set enrichment analysis: performance evaluation and usage guidelines. <i>Briefings in Bioinformatics</i> , 2012, 13, 281-291.	3.2	217

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55	Unsupervised pattern discovery in human chromatin structure through genomic segmentation. , 2013, , ,		216
56	Transposition-Driven Genomic Heterogeneity in the <i>Drosophila</i> Brain. <i>Science</i> , 2013, 340, 91-95.	6.0	212
57	Deep annotation of <i>Drosophila melanogaster</i> microRNAs yields insights into their processing, modification, and emergence. <i>Genome Research</i> , 2011, 21, 203-215.	2.4	207
58	High-Resolution Mapping of Chromatin Packaging in Mouse Embryonic Stem Cells and Sperm. <i>Developmental Cell</i> , 2014, 30, 11-22.	3.1	207
59	UAP56 Couples piRNA Clusters to the Perinuclear Transposon Silencing Machinery. <i>Cell</i> , 2012, 151, 871-884.	13.5	204
60	The HP1 Homolog Rhino Anchors a Nuclear Complex that Suppresses piRNA Precursor Splicing. <i>Cell</i> , 2014, 157, 1353-1363.	13.5	198
61	The piRNA targeting rules and the resistance to piRNA silencing in endogenous genes. <i>Science</i> , 2018, 359, 587-592.	6.0	198
62	Genomic binding profiles of functionally distinct RNA polymerase III transcription complexes in human cells. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 635-640.	3.6	197
63	Identification and Characterization of Cell Type-Specific and Ubiquitous Chromatin Regulatory Structures in the Human Genome. <i>PLoS Genetics</i> , 2007, 3, e136.	1.5	196
64	Finding functional sequence elements by multiple local alignment. <i>Nucleic Acids Research</i> , 2004, 32, 189-200.	6.5	195
65	Identification of piRNA Binding Sites Reveals the Argonaute Regulatory Landscape of the <i>C.Âlegans</i> Germline. <i>Cell</i> , 2018, 172, 937-951.e18.	13.5	189
66	Long-term, efficient inhibition of microRNA function in mice using rAAV vectors. <i>Nature Methods</i> , 2012, 9, 403-409.	9.0	188
67	Free Energy Landscapes of Encounter Complexes in Protein-Protein Association. <i>Biophysical Journal</i> , 1999, 76, 1166-1178.	0.2	181
68	SeqVISTA: a graphical tool for sequence feature visualization and comparison. <i>BMC Bioinformatics</i> , 2003, 4, 1.	1.2	179
69	Differential Toxicity of Nuclear RNA Foci versus Dipeptide Repeat Proteins in a <i>Drosophila</i> Model of C9ORF72 FTD/ALS. <i>Neuron</i> , 2015, 87, 1207-1214.	3.8	176
70	Epigenetic Signatures of Autism. <i>Archives of General Psychiatry</i> , 2012, 69, 314.	13.8	174
71	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012, 22, 1658-1667.	2.4	166
72	Neuron-specific signatures in the chromosomal connectome associated with schizophrenia risk. <i>Science</i> , 2018, 362, .	6.0	162

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73	M-ZDOCK: a grid-based approach for Cn symmetric multimer docking. <i>Bioinformatics</i> , 2005, 21, 1472-1478.	1.8	160
74	Dicer Partner Proteins Tune the Length of Mature miRNAs in Flies and Mammals. <i>Cell</i> , 2012, 151, 533-546.	13.5	158
75	Heterotypic piRNA Ping-Pong Requires Qin, a Protein with Both E3 Ligase and Tudor Domains. <i>Molecular Cell</i> , 2011, 44, 572-584.	4.5	156
76	The correlation between histone modifications and gene expression. <i>Epigenomics</i> , 2013, 5, 113-116.	1.0	154
77	FAST: A novel protein structure alignment algorithm. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 618-627.	1.5	153
78	RNA Sequence Analysis of Human Huntington Disease Brain Reveals an Extensive Increase in Inflammatory and Developmental Gene Expression. <i>PLoS ONE</i> , 2015, 10, e0143563.	1.1	150
79	Prediction of homoprotein and heteroprotein complexes by protein docking and template-based modeling: A CASP-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 323-348.	1.5	148
80	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. <i>Nature Genetics</i> , 2020, 52, 969-983.	9.4	146
81	The 3' to 5' Exoribonuclease Nibbler Shapes the 3' Ends of MicroRNAs Bound to Drosophila Argonaute1. <i>Current Biology</i> , 2011, 21, 1878-1887.	1.8	143
82	MicroRNA-regulated, Systemically Delivered rAAV9: A Step Closer to CNS-restricted Transgene Expression. <i>Molecular Therapy</i> , 2011, 19, 526-535.	3.7	143
83	CRISPR/Cas9-mediated genome editing induces exon skipping by alternative splicing or exon deletion. <i>Genome Biology</i> , 2017, 18, 108.	3.8	141
84	Main-chain conformational tendencies of amino acids. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 679-689.	1.5	139
85	Functional analysis of transcription factor binding sites in human promoters. <i>Genome Biology</i> , 2012, 13, R50.	13.9	136
86	Transcription factor binding and modified histones in human bidirectional promoters. <i>Genome Research</i> , 2007, 17, 818-827.	2.4	131
87	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. <i>Journal of Molecular Biology</i> , 2011, 414, 289-302.	2.0	131
88	A combination of rescoring and refinement significantly improves protein docking performance. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 270-279.	1.5	126
89	TEMP: a computational method for analyzing transposable element polymorphism in populations. <i>Nucleic Acids Research</i> , 2014, 42, 6826-6838.	6.5	124
90	Elimination of PCR duplicates in RNA-seq and small RNA-seq using unique molecular identifiers. <i>BMC Genomics</i> , 2018, 19, 531.	1.2	123

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91	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	13.7	123
92	Strand-specific libraries for high throughput RNA sequencing (RNA-Seq) prepared without poly(A) selection. <i>Silence: A Journal of RNA Regulation</i> , 2012, 3, 9.	8.0	122
93	piPipes: a set of pipelines for piRNA and transposon analysis via small RNA-seq, RNA-seq, degradome- and CAGE-seq, ChIP-seq and genomic DNA sequencing. <i>Bioinformatics</i> , 2015, 31, 593-595.	1.8	122
94	The RNase PARN-1 Trims piRNA 3' Ends to Promote Transcriptome Surveillance in <i>C.Âelegans</i> . <i>Cell</i> , 2016, 164, 974-984.	13.5	121
95	Systematic evaluation of variability in ChIP-chip experiments using predefined DNA targets. <i>Genome Research</i> , 2008, 18, 393-403.	2.4	117
96	Atomic contact vectors in protein-protein recognition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 629-639.	1.5	116
97	miR-10b-5p expression in Huntingtonâ€™s disease brain relates to age of onset and the extent of striatal involvement. <i>BMC Medical Genomics</i> , 2015, 8, 10.	0.7	114
98	Human-Specific Histone Methylation Signatures at Transcription Start Sites in Prefrontal Neurons. <i>PLoS Biology</i> , 2012, 10, e1001427.	2.6	113
99	Regulation of histone H3K4 methylation in brain development and disease. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2014, 369, 20130514.	1.8	113
100	Slicing and Binding by Ago3 or Aub Trigger Piwi-Bound piRNA Production by Distinct Mechanisms. <i>Molecular Cell</i> , 2015, 59, 819-830.	4.5	112
101	Cell-specific histone modification maps in the human frontal lobe link schizophrenia risk to the neuronal epigenome. <i>Nature Neuroscience</i> , 2018, 21, 1126-1136.	7.1	112
102	Statistical significance of clusters of motifs represented by position specific scoring matrices in nucleotide sequences. <i>Nucleic Acids Research</i> , 2002, 30, 3214-3224.	6.5	106
103	ZDOCK and RDOCK performance in CAPRI rounds 3, 4, and 5. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 207-213.	1.5	102
104	The Initial Uridine of Primary piRNAs Does Not Create the Tenth Adenine that Is the Hallmark of Secondary piRNAs. <i>Molecular Cell</i> , 2014, 56, 708-716.	4.5	102
105	Analysis of overrepresented motifs in human core promoters reveals dual regulatory roles of YY1. <i>Genome Research</i> , 2007, 17, 798-806.	2.4	101
106	Computational inference of transcriptional regulatory networks from expression profiling and transcription factor binding site identification. <i>Nucleic Acids Research</i> , 2004, 32, 179-188.	6.5	99
107	Blind prediction of homoâ€™and heteroâ€™protein complexes: The CASP13â€™CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1200-1221.	1.5	99
108	MicroRNAs Located in the Hox Gene Clusters Are Implicated in Huntington's Disease Pathogenesis. <i>PLoS Genetics</i> , 2014, 10, e1004188.	1.5	97

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109	Genome-Wide CRISPR Screen Identifies Regulators of Mitogen-Activated Protein Kinase as Suppressors of Liver Tumors in Mice. <i>Gastroenterology</i> , 2017, 152, 1161-1173.e1.	0.6	97
110	The evolutionarily conserved piRNA-producing locus pi6 is required for male mouse fertility. <i>Nature Genetics</i> , 2020, 52, 728-739.	9.4	96
111	Protein structure alignment using a genetic algorithm. , 2000, 38, 428-440.		92
112	Epitope tagging of endogenous proteins for genome-wide CHIP-chip studies. <i>Nature Methods</i> , 2008, 5, 163-165.	9.0	92
113	Prediction of protein complexes using empirical free energy functions. <i>Protein Science</i> , 1996, 5, 614-626.	3.1	91
114	Deletion and replacement of long genomic sequences using prime editing. <i>Nature Biotechnology</i> , 2022, 40, 227-234.	9.4	90
115	Sequence features that drive human promoter function and tissue specificity. <i>Genome Research</i> , 2010, 20, 890-898.	2.4	87
116	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1980-1987.	1.5	87
117	Distinct Functions for the Drosophila piRNA Pathway in Genome Maintenance and Telomere Protection. <i>PLoS Genetics</i> , 2010, 6, e1001246.	1.5	86
118	Genome-wide identification and characterization of replication origins by deep sequencing. <i>Genome Biology</i> , 2012, 13, R27.	13.9	85
119	Liquid chromatin Hi-C characterizes compartment-dependent chromatin interaction dynamics. <i>Nature Genetics</i> , 2021, 53, 367-378.	9.4	84
120	ZDOCK predictions for the CAPRI challenge. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 68-73.	1.5	83
121	A curated benchmark of enhancer-gene interactions for evaluating enhancer-target gene prediction methods. <i>Genome Biology</i> , 2020, 21, 17.	3.8	83
122	Integrating atomâ€based and residueâ€based scoring functions for proteinâ€protein docking. <i>Protein Science</i> , 2011, 20, 1576-1586.	3.1	80
123	Emerging Concepts in TCR Specificity: Rationalizing and (Maybe) Predicting Outcomes. <i>Journal of Immunology</i> , 2017, 199, 2203-2213.	0.4	77
124	Ancestry-inclusive dog genomics challenges popular breed stereotypes. <i>Science</i> , 2022, 376, eabk0639.	6.0	77
125	PromoSer: a large-scale mammalian promoter and transcription start site identification service. <i>Nucleic Acids Research</i> , 2003, 31, 3554-3559.	6.5	75
126	A flexible docking approach for prediction of T cell receptorâ€peptideâ€MHC complexes. <i>Protein Science</i> , 2013, 22, 35-46.	3.1	75

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127	Prediction of protein-protein binding free energies. <i>Protein Science</i> , 2012, 21, 396-404.	3.1	74
128	The piRNA Response to Retroviral Invasion of the Koala Genome. <i>Cell</i> , 2019, 179, 632-643.e12.	13.5	73
129	Performance of ZDOCK and ZRANK in CAPRI rounds 13-19. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3104-3110.	1.5	72
130	PGBD5 promotes site-specific oncogenic mutations in human tumors. <i>Nature Genetics</i> , 2017, 49, 1005-1014.	9.4	69
131	Genome-wide analysis of polymerase III-transcribed Alu elements suggests cell-type-specific enhancer function. <i>Genome Research</i> , 2019, 29, 1402-1414.	2.4	69
132	Protein therapeutics: promises and challenges for the 21st century. <i>Trends in Biotechnology</i> , 2002, 20, 29-35.	4.9	68
133	Coordinated Cell Type-Specific Epigenetic Remodeling in Prefrontal Cortex Begins before Birth and Continues into Early Adulthood. <i>PLoS Genetics</i> , 2013, 9, e1003433.	1.5	68
134	ATLAS: A database linking binding affinities with structures for wild-type and mutant TCR-pMHC complexes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 908-916.	1.5	68
135	The genome of the Hi5 germ cell line from <i>Trichoplusia ni</i> , an agricultural pest and novel model for small RNA biology. <i>ELife</i> , 2018, 7, .	2.8	68
136	Computational Design of the Affinity and Specificity of a Therapeutic T Cell Receptor. <i>PLoS Computational Biology</i> , 2014, 10, e1003478.	1.5	67
137	Epigenetic dysregulation of hairy and enhancer of split 4 (HES4) is associated with striatal degeneration in postmortem Huntington brains. <i>Human Molecular Genetics</i> , 2015, 24, 1441-1456.	1.4	67
138	Structure-based design of a T cell receptor leads to nearly 100-fold improvement in binding affinity for pepMHC. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 948-960.	1.5	66
139	Chemical modifications of adenine base editor mRNA and guide RNA expand its application scope. <i>Nature Communications</i> , 2020, 11, 1979.	5.8	66
140	The RNA-Binding ATPase, Armitage, Couples piRNA Amplification in Nuage to Phased piRNA Production on Mitochondria. <i>Molecular Cell</i> , 2019, 74, 982-995.e6.	4.5	65
141	An expanded benchmark for antibody-antigen docking and affinity prediction reveals insights into antibody recognition determinants. <i>Structure</i> , 2021, 29, 606-621.e5.	1.6	65
142	Cutting Edge: Evidence for a Dynamically Driven T Cell Signaling Mechanism. <i>Journal of Immunology</i> , 2012, 188, 5819-5823.	0.4	63
143	The performance of ZDOCK and ZRANK in rounds 6-11 of CAPRI. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 719-725.	1.5	61
144	Uncovering multiple molecular targets for caffeine using a drug target validation strategy combining A _{2A} receptor knockout mice with microarray profiling. <i>Physiological Genomics</i> , 2009, 37, 199-210.	1.0	59

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145	Evolutionarily conserved pachytene piRNA loci are highly divergent among modern humans. <i>Nature Ecology and Evolution</i> , 2020, 4, 156-168.	3.4	58
146	Genome-wide mapping of human DNA replication by optical replication mapping supports a stochastic model of eukaryotic replication. <i>Molecular Cell</i> , 2021, 81, 2975-2988.e6.	4.5	57
147	Characterization of genomic organization of the adenosine A2A receptor gene by molecular and bioinformatics analyses. <i>Brain Research</i> , 2004, 1000, 156-173.	1.1	56
148	Statistical analysis of the genomic distribution and correlation of regulatory elements in the ENCODE regions. <i>Genome Research</i> , 2007, 17, 787-797.	2.4	56
149	Crystal structure of <i>Streptococcus pyogenes</i> EndoS, an immunomodulatory endoglycosidase specific for human IgG antibodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6714-6719.	3.3	56
150	YAP and TAZ are transcriptional co-activators of AP-1 proteins and STAT3 during breast cellular transformation. <i>ELife</i> , 2021, 10, .	2.8	56
151	How structural adaptability exists alongside HLA-A2 bias in the human $\hat{\mu}^2$ TCR repertoire. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1276-85.	3.3	55
152	Adaptive Evolution Leads to Cross-Species Incompatibility in the piRNA Transposon Silencing Machinery. <i>Developmental Cell</i> , 2017, 43, 60-70.e5.	3.1	55
153	<i>In Vivo</i> Genome Editing Partially Restores Alpha1-Antitrypsin in a Murine Model of AAT Deficiency. <i>Human Gene Therapy</i> , 2018, 29, 853-860.	1.4	54
154	Hdac6 regulates Tip60-p400 function in stem cells. <i>ELife</i> , 2013, 2, e01557.	2.8	53
155	A versatile reporter system for CRISPR-mediated chromosomal rearrangements. <i>Genome Biology</i> , 2015, 16, 111.	13.9	52
156	Target RNA-directed tailing and trimming purifies the sorting of endo-siRNAs between the two <i>Drosophila</i> Argonaute proteins. <i>Rna</i> , 2011, 17, 54-63.	1.6	51
157	Blind prediction of interfacial water positions in CAPRI. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 620-632.	1.5	50
158	Structure-Based Design of Hepatitis C Virus Vaccines That Elicit Neutralizing Antibody Responses to a Conserved Epitope. <i>Journal of Virology</i> , 2017, 91, .	1.5	50
159	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. <i>Nature Communications</i> , 2021, 12, 3968.	5.8	48
160	The Role of H3K4me3 in Transcriptional Regulation Is Altered in Huntington's Disease. <i>PLoS ONE</i> , 2015, 10, e0144398.	1.1	47
161	The Coding Regions of Germline mRNAs Confer Sensitivity to Argonaute Regulation in <i>C.Âlegans</i> . <i>Cell Reports</i> , 2018, 22, 2254-2264.	2.9	46
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