

Zhiping Weng

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3847907/publications.pdf>

Version: 2024-02-01

263
papers

47,544
citations

2675

95
h-index

2127

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.	27.8	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.	21.4	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.	14.3	1,741
4	ZDOCK server: interactive docking prediction of protein-protein complexes and symmetric multimers. <i>Bioinformatics</i> , 2014, 30, 1771-1773.	4.1	1,313
5	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	27.8	1,252
6	High-Resolution Mapping and Characterization of Open Chromatin across the Genome. <i>Cell</i> , 2008, 132, 311-322.	28.9	1,246
7	ZDOCK: An initial-stage protein-docking algorithm. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 80-87.	2.6	1,220
8	Assessing computational tools for the discovery of transcription factor binding sites. <i>Nature Biotechnology</i> , 2005, 23, 137-144.	17.5	1,121
9	A Global Map of p53 Transcription-Factor Binding Sites in the Human Genome. <i>Cell</i> , 2006, 124, 207-219.	28.9	1,060
10	Paternally Induced Transgenerational Environmental Reprogramming of Metabolic Gene Expression in Mammals. <i>Cell</i> , 2010, 143, 1084-1096.	28.9	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.	5.5	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.	17.5	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.	7.1	635
14	Comprehensive functional genomic resource and integrative model for the human brain. <i>Science</i> , 2018, 362, .	12.6	618
15	Endogenous siRNAs Derived from Transposons and mRNAs in <i>Drosophila</i> Somatic Cells. <i>Science</i> , 2008, 320, 1077-1081.	12.6	594
16	Unsupervised pattern discovery in human chromatin structure through genomic segmentation. <i>Nature Methods</i> , 2012, 9, 473-476.	19.0	562
17	Target RNA-Directed Trimming and Tailing of Small Silencing RNAs. <i>Science</i> , 2010, 328, 1534-1539.	12.6	514
18	Unexpected role of interferon- β in regulating neuronal connectivity and social behaviour. <i>Nature</i> , 2016, 535, 425-429.	27.8	507

#	ARTICLE	IF	CITATIONS
19	Collapse of Germline piRNAs in the Absence of Argonaute3 Reveals Somatic piRNAs in Flies. <i>Cell</i> , 2009, 137, 509-521.	28.9	503
20	Accelerating Protein Docking in ZDOCK Using an Advanced 3D Convolution Library. <i>PLoS ONE</i> , 2011, 6, e24657.	2.5	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.	7.1	462
22	Mbd3/NURD Complex Regulates Expression of 5-Hydroxymethylcytosine Marked Genes in Embryonic Stem Cells. <i>Cell</i> , 2011, 147, 1498-1510.	28.9	424
23	ZRANK: Reranking protein docking predictions with an optimized energy function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 1078-1086.	2.6	401
24	Proteinâ€“protein docking benchmark version 4.0. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3111-3114.	2.6	390
25	Detection of functional DNA motifs via statistical over-representation. <i>Nucleic Acids Research</i> , 2004, 32, 1372-1381.	14.5	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.	28.9	382
27	A compendium of gene expression in normal human tissues. <i>Physiological Genomics</i> , 2001, 7, 97-104.	2.3	376
28	The PsychENCODE project. <i>Nature Neuroscience</i> , 2015, 18, 1707-1712.	14.8	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.	5.5	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.	4.2	348
31	Docking unbound proteins using shape complementarity, desolvation, and electrostatics. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 281-294.	2.6	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.	7.1	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.	9.7	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.	3.5	321
35	piRNA-guided transposon cleavage initiates Zucchini-dependent, phased piRNA production. <i>Science</i> , 2015, 348, 817-821.	12.6	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.	3.5	304

#	ARTICLE	IF	CITATIONS
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.	2.7	291
38	RDOCK: Refinement of rigid-body protein docking predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 693-707.	2.6	289
39	Nucleosome positioning signals in genomic DNA. <i>Genome Research</i> , 2007, 17, 1170-1177.	5.5	287
40	The Cellular EJC Interactome Reveals Higher-Order mRNP Structure and an EJC-SR Protein Nexus. <i>Cell</i> , 2012, 151, 750-764.	28.9	287
41	A novel shape complementarity scoring function for protein-protein docking. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 51, 397-408.	2.6	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.	14.5	274
43	Integrating statistical pair potentials into protein complex prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 511-520.	2.6	273
44	Cluster-Buster: finding dense clusters of motifs in DNA sequences. <i>Nucleic Acids Research</i> , 2003, 31, 3666-3668.	14.5	268
45	Principles of regulatory information conservation between mouse and human. <i>Nature</i> , 2014, 515, 371-375.	27.8	259
46	Optical Recognition of Converted DNA Nucleotides for Single-Molecule DNA Sequencing Using Nanopore Arrays. <i>Nano Letters</i> , 2010, 10, 2237-2244.	9.1	257
47	Protein-protein docking benchmark 2.0: An update. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 214-216.	2.6	254
48	A structure-based benchmark for protein-protein binding affinity. <i>Protein Science</i> , 2011, 20, 482-491.	7.6	252
49	A protein-protein docking benchmark. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 88-91.	2.6	242
50	Modeling gene expression using chromatin features in various cellular contexts. <i>Genome Biology</i> , 2012, 13, R53.	9.6	231
51	Adaptation to P Element Transposon Invasion in <i>Drosophila melanogaster</i> . <i>Cell</i> , 2011, 147, 1551-1563.	28.9	226
52	Protein-protein docking benchmark version 3.0. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 705-709.	2.6	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.	7.1	218
54	Gene set enrichment analysis: performance evaluation and usage guidelines. <i>Briefings in Bioinformatics</i> , 2012, 13, 281-291.	6.5	217

#	ARTICLE	IF	CITATIONS
55	Unsupervised pattern discovery in human chromatin structure through genomic segmentation. , 2013, , ,		216
56	Transposition-Driven Genomic Heterogeneity in the <i>Drosophila</i> Brain. Science, 2013, 340, 91-95.	12.6	212
57	Deep annotation of <i>Drosophila melanogaster</i> microRNAs yields insights into their processing, modification, and emergence. Genome Research, 2011, 21, 203-215.	5.5	207
58	High-Resolution Mapping of Chromatin Packaging in Mouse Embryonic Stem Cells and Sperm. Developmental Cell, 2014, 30, 11-22.	7.0	207
59	UAP56 Couples piRNA Clusters to the Perinuclear Transposon Silencing Machinery. Cell, 2012, 151, 871-884.	28.9	204
60	The HP1 Homolog Rhino Anchors a Nuclear Complex that Suppresses piRNA Precursor Splicing. Cell, 2014, 157, 1353-1363.	28.9	198
61	The piRNA targeting rules and the resistance to piRNA silencing in endogenous genes. Science, 2018, 359, 587-592.	12.6	198
62	Genomic binding profiles of functionally distinct RNA polymerase III transcription complexes in human cells. Nature Structural and Molecular Biology, 2010, 17, 635-640.	8.2	197
63	Identification and Characterization of Cell Type-Specific and Ubiquitous Chromatin Regulatory Structures in the Human Genome. PLoS Genetics, 2007, 3, e136.	3.5	196
64	Finding functional sequence elements by multiple local alignment. Nucleic Acids Research, 2004, 32, 189-200.	14.5	195
65	Identification of piRNA Binding Sites Reveals the Argonaute Regulatory Landscape of the <i>C.Âlegans</i> Germline. Cell, 2018, 172, 937-951.e18.	28.9	189
66	Long-term, efficient inhibition of microRNA function in mice using rAAV vectors. Nature Methods, 2012, 9, 403-409.	19.0	188
67	Free Energy Landscapes of Encounter Complexes in Protein-Protein Association. Biophysical Journal, 1999, 76, 1166-1178.	0.5	181
68	SeqVISTA: a graphical tool for sequence feature visualization and comparison. BMC Bioinformatics, 2003, 4, 1.	2.6	179
69	Differential Toxicity of Nuclear RNA Foci versus Dipeptide Repeat Proteins in a <i>Drosophila</i> Model of C9ORF72 FTD/ALS. Neuron, 2015, 87, 1207-1214.	8.1	176
70	Epigenetic Signatures of Autism. Archives of General Psychiatry, 2012, 69, 314.	12.3	174
71	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. Genome Research, 2012, 22, 1658-1667.	5.5	166
72	Neuron-specific signatures in the chromosomal connectome associated with schizophrenia risk. Science, 2018, 362, .	12.6	162

#	ARTICLE	IF	CITATIONS
73	M-ZDOCK: a grid-based approach for Cn symmetric multimer docking. <i>Bioinformatics</i> , 2005, 21, 1472-1478.	4.1	160
74	Dicer Partner Proteins Tune the Length of Mature miRNAs in Flies and Mammals. <i>Cell</i> , 2012, 151, 533-546.	28.9	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.	9.7	156
76	The correlation between histone modifications and gene expression. <i>Epigenomics</i> , 2013, 5, 113-116.	2.1	154
77	FAST: A novel protein structure alignment algorithm. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 618-627.	2.6	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.	2.5	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.	2.6	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.	21.4	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.	3.9	143
82	MicroRNA-regulated, Systemically Delivered rAAV9: A Step Closer to CNS-restricted Transgene Expression. <i>Molecular Therapy</i> , 2011, 19, 526-535.	8.2	143
83	CRISPR/Cas9-mediated genome editing induces exon skipping by alternative splicing or exon deletion. <i>Genome Biology</i> , 2017, 18, 108.	8.8	141
84	Main-chain conformational tendencies of amino acids. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 679-689.	2.6	139
85	Functional analysis of transcription factor binding sites in human promoters. <i>Genome Biology</i> , 2012, 13, R50.	9.6	136
86	Transcription factor binding and modified histones in human bidirectional promoters. <i>Genome Research</i> , 2007, 17, 818-827.	5.5	131
87	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. <i>Journal of Molecular Biology</i> , 2011, 414, 289-302.	4.2	131
88	A combination of rescoring and refinement significantly improves protein docking performance. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 270-279.	2.6	126
89	TEMP: a computational method for analyzing transposable element polymorphism in populations. <i>Nucleic Acids Research</i> , 2014, 42, 6826-6838.	14.5	124
90	Elimination of PCR duplicates in RNA-seq and small RNA-seq using unique molecular identifiers. <i>BMC Genomics</i> , 2018, 19, 531.	2.8	123

#	ARTICLE	IF	CITATIONS
91	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	27.8	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.	8.1	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.	4.1	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.	28.9	121
95	Systematic evaluation of variability in ChIP-chip experiments using predefined DNA targets. <i>Genome Research</i> , 2008, 18, 393-403.	5.5	117
96	Atomic contact vectors in protein-protein recognition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 629-639.	2.6	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.	1.5	114
98	Human-Specific Histone Methylation Signatures at Transcription Start Sites in Prefrontal Neurons. <i>PLoS Biology</i> , 2012, 10, e1001427.	5.6	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.	4.0	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.	9.7	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.	14.8	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.	14.5	106
103	ZDOCK and RDOCK performance in CAPRI rounds 3, 4, and 5. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 207-213.	2.6	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.	9.7	102
105	Analysis of overrepresented motifs in human core promoters reveals dual regulatory roles of YY1. <i>Genome Research</i> , 2007, 17, 798-806.	5.5	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.	14.5	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.	2.6	99
108	MicroRNAs Located in the Hox Gene Clusters Are Implicated in Huntington's Disease Pathogenesis. <i>PLoS Genetics</i> , 2014, 10, e1004188.	3.5	97

#	ARTICLE	IF	CITATIONS
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.	1.3	97
110	The evolutionarily conserved piRNA-producing locus pi6 is required for male mouse fertility. <i>Nature Genetics</i> , 2020, 52, 728-739.	21.4	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.	19.0	92
113	Prediction of protein complexes using empirical free energy functions. <i>Protein Science</i> , 1996, 5, 614-626.	7.6	91
114	Deletion and replacement of long genomic sequences using prime editing. <i>Nature Biotechnology</i> , 2022, 40, 227-234.	17.5	90
115	Sequence features that drive human promoter function and tissue specificity. <i>Genome Research</i> , 2010, 20, 890-898.	5.5	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.	2.6	87
117	Distinct Functions for the Drosophila piRNA Pathway in Genome Maintenance and Telomere Protection. <i>PLoS Genetics</i> , 2010, 6, e1001246.	3.5	86
118	Genome-wide identification and characterization of replication origins by deep sequencing. <i>Genome Biology</i> , 2012, 13, R27.	9.6	85
119	Liquid chromatin Hi-C characterizes compartment-dependent chromatin interaction dynamics. <i>Nature Genetics</i> , 2021, 53, 367-378.	21.4	84
120	ZDOCK predictions for the CAPRI challenge. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 68-73.	2.6	83
121	A curated benchmark of enhancer-gene interactions for evaluating enhancer-target gene prediction methods. <i>Genome Biology</i> , 2020, 21, 17.	8.8	83
122	Integrating atom-based and residue-based scoring functions for protein-protein docking. <i>Protein Science</i> , 2011, 20, 1576-1586.	7.6	80
123	Emerging Concepts in TCR Specificity: Rationalizing and (Maybe) Predicting Outcomes. <i>Journal of Immunology</i> , 2017, 199, 2203-2213.	0.8	77
124	Ancestry-inclusive dog genomics challenges popular breed stereotypes. <i>Science</i> , 2022, 376, eabk0639.	12.6	77
125	PromoSer: a large-scale mammalian promoter and transcription start site identification service. <i>Nucleic Acids Research</i> , 2003, 31, 3554-3559.	14.5	75
126	A flexible docking approach for prediction of T cell receptor-peptide-MHC complexes. <i>Protein Science</i> , 2013, 22, 35-46.	7.6	75

#	ARTICLE	IF	CITATIONS
127	Prediction of proteinâ€“protein binding free energies. <i>Protein Science</i> , 2012, 21, 396-404.	7.6	74
128	The piRNA Response to Retroviral Invasion of the Koala Genome. <i>Cell</i> , 2019, 179, 632-643.e12.	28.9	73
129	Performance of ZDOCK and ZRANK in CAPRI rounds 13â€“19. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3104-3110.	2.6	72
130	PGBD5 promotes site-specific oncogenic mutations in human tumors. <i>Nature Genetics</i> , 2017, 49, 1005-1014.	21.4	69
131	Genome-wide analysis of polymerase IIIâ€“transcribed <i>Alu</i> elements suggests cell-typeâ€“specific enhancer function. <i>Genome Research</i> , 2019, 29, 1402-1414.	5.5	69
132	Protein therapeutics: promises and challenges for the 21st century. <i>Trends in Biotechnology</i> , 2002, 20, 29-35.	9.3	68
133	Coordinated Cell Typeâ€“Specific Epigenetic Remodeling in Prefrontal Cortex Begins before Birth and Continues into Early Adulthood. <i>PLoS Genetics</i> , 2013, 9, e1003433.	3.5	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.	2.6	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, .	6.0	68
136	Computational Design of the Affinity and Specificity of a Therapeutic T Cell Receptor. <i>PLoS Computational Biology</i> , 2014, 10, e1003478.	3.2	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.	2.9	67
138	Structureâ€“based design of a Tâ€“cell receptor leads to nearly 100â€“fold improvement in binding affinity for pepMHC. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 948-960.	2.6	66
139	Chemical modifications of adenine base editor mRNA and guide RNA expand its application scope. <i>Nature Communications</i> , 2020, 11, 1979.	12.8	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.	9.7	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.	3.3	65
142	Cutting Edge: Evidence for a Dynamically Driven T Cell Signaling Mechanism. <i>Journal of Immunology</i> , 2012, 188, 5819-5823.	0.8	63
143	The performance of ZDOCK and ZRANK in rounds 6â€“11 of CAPRI. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 719-725.	2.6	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.	2.3	59

#	ARTICLE	IF	CITATIONS
145	Evolutionarily conserved pachytene piRNA loci are highly divergent among modern humans. <i>Nature Ecology and Evolution</i> , 2020, 4, 156-168.	7.8	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.	9.7	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.	2.2	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.	5.5	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.	7.1	56
150	YAP and TAZ are transcriptional co-activators of AP-1 proteins and STAT3 during breast cellular transformation. <i>ELife</i> , 2021, 10, .	6.0	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.	7.1	55
152	Adaptive Evolution Leads to Cross-Species Incompatibility in the piRNA Transposon Silencing Machinery. <i>Developmental Cell</i> , 2017, 43, 60-70.e5.	7.0	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.	2.7	54
154	Hdac6 regulates Tip60-p400 function in stem cells. <i>ELife</i> , 2013, 2, e01557.	6.0	53
155	A versatile reporter system for CRISPR-mediated chromosomal rearrangements. <i>Genome Biology</i> , 2015, 16, 111.	9.6	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.	3.5	51
157	Blind prediction of interfacial water positions in CAPRI. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 620-632.	2.6	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, .	3.4	50
159	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. <i>Nature Communications</i> , 2021, 12, 3968.	12.8	48
160	The Role of H3K4me3 in Transcriptional Regulation Is Altered in Huntington's Disease. <i>PLoS ONE</i> , 2015, 10, e0144398.	2.5	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.	6.4	46
162	HugelIndex: a database with visualization tools for high-density oligonucleotide array data from normal human tissues. <i>Nucleic Acids Research</i> , 2002, 30, 214-217.	14.5	44

#	ARTICLE	IF	CITATIONS
163	A Sex Chromosome piRNA Promotes Robust Dosage Compensation and Sex Determination in <i>C.Âelegans</i> . <i>Developmental Cell</i> , 2018, 44, 762-770.e3.	7.0	44
164	Depletion of TRRAP Induces p53-Independent Senescence in Liver Cancer by Down-Regulating Mitotic Genes. <i>Hepatology</i> , 2020, 71, 275-290.	7.3	43
165	pirScan: a webserver to predict piRNA targeting sites and to avoid transgene silencing in <i>C. elegans</i> . <i>Nucleic Acids Research</i> , 2018, 46, W43-W48.	14.5	41
166	Endogenous U2-U5-U6 snRNA complexes in <i>S. pombe</i> are intron lariat spliceosomes. <i>Rna</i> , 2014, 20, 308-320.	3.5	40
167	VRDD: applying virtual reality visualization to protein docking and design. <i>Journal of Molecular Graphics and Modelling</i> , 1999, 17, 180-186.	2.4	39
168	Binding interface prediction by combining protein-protein docking results. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 57-66.	2.6	38
169	Comparative functional characterization of the CSR-1 22G-RNA pathway in <i>Caenorhabditis nematodes</i> . <i>Nucleic Acids Research</i> , 2015, 43, 208-224.	14.5	38
170	A unified encyclopedia of human functional DNA elements through fully automated annotation of 164 human cell types. <i>Genome Biology</i> , 2019, 20, 180.	8.8	37
171	IRaPPA: information retrieval based integration of biophysical models for protein assembly selection. <i>Bioinformatics</i> , 2017, 33, 1806-1813.	4.1	36
172	Differential analysis of chromatin accessibility and histone modifications for predicting mouse developmental enhancers. <i>Nucleic Acids Research</i> , 2018, 46, 11184-11201.	14.5	36
173	DNApi: A De Novo Adapter Prediction Algorithm for Small RNA Sequencing Data. <i>PLoS ONE</i> , 2016, 11, e0164228.	2.5	36
174	Evaluating template-based and template-free protein-protein complex structure prediction. <i>Briefings in Bioinformatics</i> , 2014, 15, 169-176.	6.5	35
175	Quantitative Analysis of Single Nucleotide Polymorphisms within Copy Number Variation. <i>PLoS ONE</i> , 2008, 3, e3906.	2.5	34
176	Annotation of chromatin states in 66 complete mouse epigenomes during development. <i>Communications Biology</i> , 2021, 4, 239.	4.4	34
177	Identification and validation of a novel cell-recognition site (KNEED) on the 8th type III domain of fibronectin. <i>Biomaterials</i> , 2002, 23, 3865-3870.	11.4	33
178	Maelstrom Represses Canonical Polymerase II Transcription within Bi-directional piRNA Clusters in <i>Drosophila melanogaster</i> . <i>Molecular Cell</i> , 2019, 73, 291-303.e6.	9.7	33
179	Comprehensive identification of alternative back-splicing in human tissue transcriptomes. <i>Nucleic Acids Research</i> , 2020, 48, 1779-1789.	14.5	33
180	Genetic disruption of oncogenic Kras sensitizes lung cancer cells to Fas receptor-mediated apoptosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 3648-3653.	7.1	32

#	ARTICLE	IF	CITATIONS
181	Integrated analysis of experimental data sets reveals many novel promoters in 1% of the human genome. <i>Genome Research</i> , 2007, 17, 720-731.	5.5	31
182	Tailor: a computational framework for detecting non-templated tailing of small silencing RNAs. <i>Nucleic Acids Research</i> , 2015, 43, e109-e109.	14.5	31
183	A chromosomal connectome for psychiatric and metabolic risk variants in adult dopaminergic neurons. <i>Genome Medicine</i> , 2020, 12, 19.	8.2	31
184	Empirical free energy calculation: Comparison to calorimetric data. <i>Protein Science</i> , 1997, 6, 1976-1984.	7.6	29
185	A benchmark testing ground for integrating homology modeling and protein docking. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 10-16.	2.6	29
186	Co-dependent Assembly of Drosophila piRNA Precursor Complexes and piRNA Cluster Heterochromatin. <i>Cell Reports</i> , 2018, 24, 3413-3422.e4.	6.4	29
187	Ribosomes guide pachytene piRNA formation on long intergenic piRNA precursors. <i>Nature Cell Biology</i> , 2020, 22, 200-212.	10.3	29
188	A System for Genome-Wide Histone Variant Dynamics In ES Cells Reveals Dynamic MacroH2A2 Replacement at Promoters. <i>PLoS Genetics</i> , 2014, 10, e1004515.	3.5	28
189	Rapid Reassortment of Internal Genes in Avian Influenza A(H7N9) Virus. <i>Clinical Infectious Diseases</i> , 2013, 57, 1059-1061.	5.8	27
190	Spatial transcriptomic reconstruction of the mouse olfactory glomerular map suggests principles of odor processing. <i>Nature Neuroscience</i> , 2022, 25, 484-492.	14.8	27
191	Extracting hydrophobicity parameters from solute partition and protein mutation/unfolding experiments. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 1081-1092.	2.1	26
192	Gene Discovery in the Auditory System: Characterization of Additional Cochlear-Expressed Sequences. <i>JARO - Journal of the Association for Research in Otolaryngology</i> , 2002, 3, 45-53.	1.8	26
193	Exploring the DNA-recognition potential of homeodomains. <i>Genome Research</i> , 2012, 22, 1889-1898.	5.5	26
194	Pitfalls of Mapping High-Throughput Sequencing Data to Repetitive Sequences: Piwi's Genomic Targets Still Not Identified. <i>Developmental Cell</i> , 2015, 32, 765-771.	7.0	26
195	Transcriptome-wide Interrogation of the Functional Intronome by Spliceosome Profiling. <i>Cell</i> , 2018, 173, 1031-1044.e13.	28.9	26
196	A benchmark and an algorithm for detecting germline transposon insertions and measuring <i>de novo</i> transposon insertion frequencies. <i>Nucleic Acids Research</i> , 2021, 49, e44-e44.	14.5	26
197	A systems level approach to temporal expression dynamics in Drosophila reveals clusters of long term memory genes. <i>PLoS Genetics</i> , 2017, 13, e1007054.	3.5	26
198	Reply to Brunet and Doolittle: Both selected effect and causal role elements can influence human biology and disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3366.	7.1	25

#	ARTICLE	IF	CITATIONS
199	Predicting human splicing branchpoints by combining sequence-derived features and multi-label learning methods. <i>BMC Bioinformatics</i> , 2017, 18, 464.	2.6	24
200	A computational framework for optimal masking in the synthesis of oligonucleotide microarrays. <i>Nucleic Acids Research</i> , 2002, 30, 106e-106.	14.5	23
201	High-Throughput Sequencing Analysis of Post-Liver Transplantation HCV E2 Glycoprotein Evolution in the Presence and Absence of Neutralizing Monoclonal Antibody. <i>PLoS ONE</i> , 2014, 9, e100325.	2.5	23
202	Computational determination of the structure of rat fc bound to the neonatal fc receptor 1 1Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 1998, 282, 217-225.	4.2	22
203	Performance of ZDOCK in CAPRI rounds 20â€“26. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 2175-2182.	2.6	22
204	Local sequence assembly reveals a high-resolution profile of somatic structural variations in 97 cancer genomes. <i>Nucleic Acids Research</i> , 2015, 43, 8146-8156.	14.5	22
205	Integrating Cross-Linking Experiments with Ab Initio Proteinâ€“Protein Docking. <i>Journal of Molecular Biology</i> , 2018, 430, 1814-1828.	4.2	22
206	Antisense piRNA amplification, but not piRNA production or nuage assembly, requires the Tudor-domain protein Qin. <i>EMBO Journal</i> , 2014, 33, 536-539.	7.8	21
207	Evaluation of preprocessing, mapping and postprocessing algorithms for analyzing whole genome bisulfite sequencing data. <i>Briefings in Bioinformatics</i> , 2016, 17, bbv103.	6.5	20
208	Chromatin profiling of cortical neurons identifies individual epigenetic signatures in schizophrenia. <i>Translational Psychiatry</i> , 2019, 9, 256.	4.8	18
209	Cytotoxic T cell recognition of allelic variants of HLA B35 bound to an Epstein-Barr virus epitope: influence of peptide conformation and TCR-peptide interaction. <i>European Journal of Immunology</i> , 1999, 29, 1587-1597.	2.9	17
210	Genetic and pharmacological inactivation of adenosine A2A receptor reveals an Egr-2-mediated transcriptional regulatory network in the mouse striatum. <i>Physiological Genomics</i> , 2005, 23, 89-102.	2.3	17
211	The temporal landscape of recursive splicing during Pol II transcription elongation in human cells. <i>PLoS Genetics</i> , 2018, 14, e1007579.	3.5	17
212	Transcriptomic Profiling Reveals Extraordinary Diversity of Venom Peptides in Unexplored Predatory Gastropods of the Genus <i>Clavus</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 684-700.	2.5	17
213	Long first exons and epigenetic marks distinguish conserved pachytene piRNA clusters from other mammalian genes. <i>Nature Communications</i> , 2021, 12, 73.	12.8	17
214	Backbone Flexibility of CDR3 and Immune Recognition of Antigens. <i>Journal of Molecular Biology</i> , 2014, 426, 1583-1599.	4.2	16
215	A generalized framework for computational design and mutational scanning of T-cell receptor binding interfaces. <i>Protein Engineering, Design and Selection</i> , 2016, 29, 595-606.	2.1	16
216	Adaptive Evolution Targets a piRNA Precursor Transcription Network. <i>Cell Reports</i> , 2020, 30, 2672-2685.e5.	6.4	16

#	ARTICLE	IF	CITATIONS
217	Investigating the Potential Roles of SINEs in the Human Genome. <i>Annual Review of Genomics and Human Genetics</i> , 2021, 22, 199-218.	6.2	16
218	Factorbook: an updated catalog of transcription factor motifs and candidate regulatory motif sites. <i>Nucleic Acids Research</i> , 2022, 50, D141-D149.	14.5	16
219	Toward a predictive understanding of molecular recognition. <i>Immunological Reviews</i> , 1998, 163, 251-266.	6.0	14
220	Glycolytic enzymes localize to ribonucleoprotein granules in <i>Drosophila</i> germ cells, bind Tudor and protect from transposable elements. <i>EMBO Reports</i> , 2015, 16, 379-386.	4.5	14
221	Integrating <i>ab initio</i> and template-based algorithms for protein-protein complex structure prediction. <i>Bioinformatics</i> , 2020, 36, 751-757.	4.1	14
222	Forward genetic screen of human transposase genomic rearrangements. <i>BMC Genomics</i> , 2016, 17, 548.	2.8	13
223	Performance of ZDOCK and IRAD in CAPRI rounds 28-34. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 408-416.	2.6	13
224	The TRIM-NHL protein NHL-2 is a co-factor in the nuclear and somatic RNAi pathways in <i>C. elegans</i> . <i>ELife</i> , 2018, 7, .	6.0	13
225	Dynamic placement of the linker histone H1 associated with nucleosome arrangement and gene transcription in early <i>Drosophila</i> embryonic development. <i>Cell Death and Disease</i> , 2018, 9, 765.	6.3	13
226	High-throughput modeling and scoring of TCR-pMHC complexes to predict cross-reactive peptides. <i>Bioinformatics</i> , 2021, 36, 5377-5385.	4.1	13
227	Optimizing protein representations with information theory. <i>Genome Informatics</i> , 2004, 15, 160-9.	0.4	13
228	Spatial genome exploration in the context of cognitive and neurological disease. <i>Current Opinion in Neurobiology</i> , 2019, 59, 112-119.	4.2	12
229	Epigenetic-genetic chromatin footprinting identifies novel and subject-specific genes active in prefrontal cortex neurons. <i>FASEB Journal</i> , 2019, 33, 8161-8173.	0.5	12
230	Exploring Angular Distance in Protein-Protein Docking Algorithms. <i>PLoS ONE</i> , 2013, 8, e56645.	2.5	11
231	Computational Modeling of T Cell Receptor Complexes. <i>Methods in Molecular Biology</i> , 2016, 1414, 319-340.	0.9	11
232	An avidin-like domain that does not bind biotin is adopted for oligomerization by the extracellular mosaic protein fibropellin. <i>Protein Science</i> , 2005, 14, 417-423.	7.6	10
233	Combinations of Affinity-Enhancing Mutations in a T Cell Receptor Reveal Highly Nonadditive Effects within and between Complementarity Determining Regions and Chains. <i>Biochemistry</i> , 2010, 49, 7050-7059.	2.5	10
234	YAP1 Withdrawal in Hepatoblastoma Drives Therapeutic Differentiation of Tumor Cells to Functional Hepatocyte-Like Cells. <i>Hepatology</i> , 2021, 73, 1011-1027.	7.3	10

#	ARTICLE	IF	CITATIONS
235	Genetic and epigenetic features of promoters with ubiquitous chromatin accessibility support ubiquitous transcription of cell-essential genes. <i>Nucleic Acids Research</i> , 2021, 49, 5705-5725.	14.5	10
236	piRNA-independent transposon silencing by the Drosophila THO complex. <i>Developmental Cell</i> , 2021, 56, 2623-2635.e5.	7.0	10
237	The Missing Heritability in T1D and Potential New Targets for Prevention. <i>Journal of Diabetes Research</i> , 2013, 2013, 1-10.	2.3	9
238	Integrated miRNA-/mRNA-Seq of the Habenulo-Interpeduncular Circuit During Acute Nicotine Withdrawal. <i>Scientific Reports</i> , 2020, 10, 813.	3.3	9
239	A machine learning approach for the prediction of protein surface loop flexibility. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2467-2474.	2.6	8
240	Substitution Rates of the Internal Genes in the Novel Avian H7N9 Influenza Virus. <i>Clinical Infectious Diseases</i> , 2013, 57, 1213-1215.	5.8	8
241	Performance of ZDOCK and IRAD in CAPRI rounds 39–45. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1050-1054.	2.6	8
242	High-resolution analysis of differential gene expression during skeletal muscle atrophy and programmed cell death. <i>Physiological Genomics</i> , 2020, 52, 492-511.	2.3	8
243	Integration of high-resolution promoter profiling assays reveals novel, cell type“specific transcription start sites across 115 human cell and tissue types. <i>Genome Research</i> , 2022, 32, 389-402.	5.5	8
244	A simple method for improving the specificity of anti-methyl histone antibodies. <i>Epigenetics</i> , 2010, 5, 392-395.	2.7	7
245	Molecular Basis of a Million-Fold Affinity Maturation Process in a Protein“Protein Interaction. <i>Journal of Molecular Biology</i> , 2011, 411, 321-328.	4.2	7
246	LogoJS: a Javascript package for creating sequence logos and embedding them in web applications. <i>Bioinformatics</i> , 2020, 36, 3573-3575.	4.1	7
247	Networking development by Boolean logic. <i>Nucleus</i> , 2013, 4, 89-91.	2.2	6
248	Identification of conserved structural features at sequentially degenerate locations in transcription factor binding sites. <i>Genome Informatics</i> , 2005, 16, 49-58.	0.4	6
249	Improvement of TRANSFAC matrices using multiple local alignment of transcription factor binding site sequences. <i>Genome Informatics</i> , 2005, 16, 68-72.	0.4	6
250	Modeling T cell receptor recognition of CD1-lipid and MR1-metabolite complexes. <i>BMC Bioinformatics</i> , 2014, 15, 319.	2.6	5
251	Somatic piRNAs and Transposons are Differentially Expressed Coincident with Skeletal Muscle Atrophy and Programmed Cell Death. <i>Frontiers in Genetics</i> , 2021, 12, 775369.	2.3	5
252	The waters of life. <i>Journal of the Franklin Institute</i> , 1998, 335, 213-240.	3.4	4

#	ARTICLE	IF	CITATIONS
253	Decoding the non-coding genome: Opportunities and challenges of genomic and epigenomic consortium data. <i>Current Opinion in Systems Biology</i> , 2018, 11, 82-90.	2.6	4
254	The prediction of human splicing branchpoints by multi-label learning. , 2016, , .		3
255	Computational Reprogramming of T Cell Antigen Receptor Binding Properties. <i>Methods in Molecular Biology</i> , 2016, 1414, 305-318.	0.9	2
256	Hedgehogs, foxes, and a new science. <i>Nature Biotechnology</i> , 1997, 15, 819-819.	17.5	1
257	Systematic detection of statistically overrepresented DNA motif association rules. <i>Genome Informatics</i> , 2006, 17, 124-33.	0.4	1
258	Managing Biological Sequence and Protein Structure Data. <i>OMICS A Journal of Integrative Biology</i> , 2003, 7, 25-26.	2.0	0
259	Identification and characterization of cell type-specific and ubiquitous chromatin regulatory structures in the human genome. <i>PLoS Genetics</i> , 2005, preprint, e136.	3.5	0
260	Biophysical Characterization of TCR Variants with Reengineered Specificity and Affinity. <i>FASEB Journal</i> , 2015, 29, 571.30.	0.5	0
261	Co-Dependent Assembly of <i>Drosophila</i> piRNA Precursor Complexes and piRNA Cluster Heterochromatin. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
262	Mutational analysis verifies that "kneed" sequence of fibronectin participates in cell-substrate interactions. , 0, , .		0
263	MafB, WDR77, and β -catenin interact with each other and have similar genome association profiles. <i>PLoS ONE</i> , 2022, 17, e0264799.	2.5	0