

Zhiping Weng

List of Publications by Year in descending order

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Version: 2024-02-01

263
papers

47,544
citations

3116

95
h-index

2453

203
g-index

299
all docs

299
docs citations

299
times ranked

63610
citing authors

#	ARTICLE	IF	CITATIONS
1	Factorbook: an updated catalog of transcription factor motifs and candidate regulatory motif sites. <i>Nucleic Acids Research</i> , 2022, 50, D141-D149.	6.5	16
2	Deletion and replacement of long genomic sequences using prime editing. <i>Nature Biotechnology</i> , 2022, 40, 227-234.	9.4	90
3	Spatial transcriptomic reconstruction of the mouse olfactory glomerular map suggests principles of odor processing. <i>Nature Neuroscience</i> , 2022, 25, 484-492.	7.1	27
4	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.	2.4	8
5	Ancestry-inclusive dog genomics challenges popular breed stereotypes. <i>Science</i> , 2022, 376, eabk0639.	6.0	77
6	MafB, WDR77, and β -catenin interact with each other and have similar genome association profiles. <i>PLoS ONE</i> , 2022, 17, e0264799.	1.1	0
7	YAP1 Withdrawal in Hepatoblastoma Drives Therapeutic Differentiation of Tumor Cells to Functional Hepatocyte-Like Cells. <i>Hepatology</i> , 2021, 73, 1011-1027.	3.6	10
8	High-throughput modeling and scoring of TCR-pMHC complexes to predict cross-reactive peptides. <i>Bioinformatics</i> , 2021, 36, 5377-5385.	1.8	13
9	Long first exons and epigenetic marks distinguish conserved pachytene piRNA clusters from other mammalian genes. <i>Nature Communications</i> , 2021, 12, 73.	5.8	17
10	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.	6.5	26
11	Liquid chromatin Hi-C characterizes compartment-dependent chromatin interaction dynamics. <i>Nature Genetics</i> , 2021, 53, 367-378.	9.4	84
12	Annotation of chromatin states in 66 complete mouse epigenomes during development. <i>Communications Biology</i> , 2021, 4, 239.	2.0	34
13	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.	6.5	10
14	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
15	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. <i>Nature Communications</i> , 2021, 12, 3968.	5.8	48
16	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
17	Investigating the Potential Roles of SINEs in the Human Genome. <i>Annual Review of Genomics and Human Genetics</i> , 2021, 22, 199-218.	2.5	16
18	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

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19	piRNA-independent transposon silencing by the Drosophila THO complex. <i>Developmental Cell</i> , 2021, 56, 2623-2635.e5.	3.1	10
20	Somatic piRNAs and Transposons are Differentially Expressed Coincident with Skeletal Muscle Atrophy and Programmed Cell Death. <i>Frontiers in Genetics</i> , 2021, 12, 775369.	1.1	5
21	Depletion of TRRAP Induces p53-independent Senescence in Liver Cancer by Down-regulating Mitotic Genes. <i>Hepatology</i> , 2020, 71, 275-290.	3.6	43
22	Integrating <i>ab initio</i> and template-based algorithms for protein-protein complex structure prediction. <i>Bioinformatics</i> , 2020, 36, 751-757.	1.8	14
23	Evolutionarily conserved pachytene piRNA loci are highly divergent among modern humans. <i>Nature Ecology and Evolution</i> , 2020, 4, 156-168.	3.4	58
24	Performance of ZDOCK and IRAD in CAPRI rounds 39-45. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1050-1054.	1.5	8
25	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	13.7	123
26	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	13.7	1,252
27	High-resolution analysis of differential gene expression during skeletal muscle atrophy and programmed cell death. <i>Physiological Genomics</i> , 2020, 52, 492-511.	1.0	8
28	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
29	LogoJS: a Javascript package for creating sequence logos and embedding them in web applications. <i>Bioinformatics</i> , 2020, 36, 3573-3575.	1.8	7
30	The evolutionarily conserved piRNA-producing locus pi6 is required for male mouse fertility. <i>Nature Genetics</i> , 2020, 52, 728-739.	9.4	96
31	Adaptive Evolution Targets a piRNA Precursor Transcription Network. <i>Cell Reports</i> , 2020, 30, 2672-2685.e5.	2.9	16
32	A chromosomal connectome for psychiatric and metabolic risk variants in adult dopaminergic neurons. <i>Genome Medicine</i> , 2020, 12, 19.	3.6	31
33	Integrated miRNA-/mRNA-Seq of the Habenulo-Interpeduncular Circuit During Acute Nicotine Withdrawal. <i>Scientific Reports</i> , 2020, 10, 813.	1.6	9
34	Comprehensive identification of alternative back-splicing in human tissue transcriptomes. <i>Nucleic Acids Research</i> , 2020, 48, 1779-1789.	6.5	33
35	Chemical modifications of adenine base editor mRNA and guide RNA expand its application scope. <i>Nature Communications</i> , 2020, 11, 1979.	5.8	66
36	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.	1.1	17

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37	Ribosomes guide pachytene piRNA formation on long intergenic piRNA precursors. <i>Nature Cell Biology</i> , 2020, 22, 200-212.	4.6	29
38	A curated benchmark of enhancer-gene interactions for evaluating enhancer-target gene prediction methods. <i>Genome Biology</i> , 2020, 21, 17.	3.8	83
39	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
40	Blind prediction of homo- and hetero-protein complexes: The CASP13-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1200-1221.	1.5	99
41	Chromatin profiling of cortical neurons identifies individual epigenetic signatures in schizophrenia. <i>Translational Psychiatry</i> , 2019, 9, 256.	2.4	18
42	The piRNA Response to Retroviral Invasion of the Koala Genome. <i>Cell</i> , 2019, 179, 632-643.e12.	13.5	73
43	A unified encyclopedia of human functional DNA elements through fully automated annotation of 164 human cell types. <i>Genome Biology</i> , 2019, 20, 180.	3.8	37
44	Spatial genome exploration in the context of cognitive and neurological disease. <i>Current Opinion in Neurobiology</i> , 2019, 59, 112-119.	2.0	12
45	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
46	Epigenetic-genetic chromatin footprinting identifies novel and subject-specific genes active in prefrontal cortex neurons. <i>FASEB Journal</i> , 2019, 33, 8161-8173.	0.2	12
47	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.	4.5	33
48	The Coding Regions of Germline mRNAs Confer Sensitivity to Argonaute Regulation in <i>C.Âelegans</i> . <i>Cell Reports</i> , 2018, 22, 2254-2264.	2.9	46
49	Integrating Cross-Linking Experiments with Ab Initio Protein-Protein Docking. <i>Journal of Molecular Biology</i> , 2018, 430, 1814-1828.	2.0	22
50	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.	3.1	44
51	Identification of piRNA Binding Sites Reveals the Argonaute Regulatory Landscape of the <i>C.Âelegans</i> Germline. <i>Cell</i> , 2018, 172, 937-951.e18.	13.5	189
52	The piRNA targeting rules and the resistance to piRNA silencing in endogenous genes. <i>Science</i> , 2018, 359, 587-592.	6.0	198
53	Transcriptome-wide Interrogation of the Functional Intronome by Spliceosome Profiling. <i>Cell</i> , 2018, 173, 1031-1044.e13.	13.5	26
54	<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

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55	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, .	2.8	13
56	Neuron-specific signatures in the chromosomal connectome associated with schizophrenia risk. <i>Science</i> , 2018, 362, .	6.0	162
57	Comprehensive functional genomic resource and integrative model for the human brain. <i>Science</i> , 2018, 362, .	6.0	618
58	Co-dependent Assembly of <i>Drosophila</i> piRNA Precursor Complexes and piRNA Cluster Heterochromatin. <i>Cell Reports</i> , 2018, 24, 3413-3422.e4.	2.9	29
59	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.	1.3	4
60	The temporal landscape of recursive splicing during Pol II transcription elongation in human cells. <i>PLoS Genetics</i> , 2018, 14, e1007579.	1.5	17
61	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
62	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
63	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.	2.7	13
64	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
65	Differential analysis of chromatin accessibility and histone modifications for predicting mouse developmental enhancers. <i>Nucleic Acids Research</i> , 2018, 46, 11184-11201.	6.5	36
66	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.	6.5	41
67	A benchmark testing ground for integrating homology modeling and protein docking. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 10-16.	1.5	29
68	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
69	PGBD5 promotes site-specific oncogenic mutations in human tumors. <i>Nature Genetics</i> , 2017, 49, 1005-1014.	9.4	69
70	CRISPR/Cas9-mediated genome editing induces exon skipping by alternative splicing or exon deletion. <i>Genome Biology</i> , 2017, 18, 108.	3.8	141
71	Genetic disruption of oncogenic <i>Kras</i> 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.	3.3	32
72	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

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73	Emerging Concepts in TCR Specificity: Rationalizing and (Maybe) Predicting Outcomes. <i>Journal of Immunology</i> , 2017, 199, 2203-2213.	0.4	77
74	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
75	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
76	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
77	Performance of ZDOCK and IRAD in CAPRI rounds 28-34. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 408-416.	1.5	13
78	IRaPPA: information retrieval based integration of biophysical models for protein assembly selection. <i>Bioinformatics</i> , 2017, 33, 1806-1813.	1.8	36
79	Predicting human splicing branchpoints by combining sequence-derived features and multi-label learning methods. <i>BMC Bioinformatics</i> , 2017, 18, 464.	1.2	24
80	A systems level approach to temporal expression dynamics in <i>Drosophila</i> reveals clusters of long term memory genes. <i>PLoS Genetics</i> , 2017, 13, e1007054.	1.5	26
81	Evaluation of preprocessing, mapping and postprocessing algorithms for analyzing whole genome bisulfite sequencing data. <i>Briefings in Bioinformatics</i> , 2016, 17, bbv103.	3.2	20
82	Forward genetic screen of human transposase genomic rearrangements. <i>BMC Genomics</i> , 2016, 17, 548.	1.2	13
83	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
84	Computational Reprogramming of T Cell Antigen Receptor Binding Properties. <i>Methods in Molecular Biology</i> , 2016, 1414, 305-318.	0.4	2
85	Computational Modeling of T Cell Receptor Complexes. <i>Methods in Molecular Biology</i> , 2016, 1414, 319-340.	0.4	11
86	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.	1.0	16
87	Unexpected role of interferon- β in regulating neuronal connectivity and social behaviour. <i>Nature</i> , 2016, 535, 425-429.	13.7	507
88	The prediction of human splicing branchpoints by multi-label learning. , 2016, , .		3
89	How structural adaptability exists alongside HLA-A2 bias in the human TCR repertoire. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1276-85.	3.3	55
90	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

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91	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
92	DNApi: A De Novo Adapter Prediction Algorithm for Small RNA Sequencing Data. <i>PLoS ONE</i> , 2016, 11, e0164228.	1.1	36
93	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
94	Tailor: a computational framework for detecting non-templated tailing of small silencing RNAs. <i>Nucleic Acids Research</i> , 2015, 43, e109-e109.	6.5	31
95	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.	2.0	14
96	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
97	A versatile reporter system for CRISPR-mediated chromosomal rearrangements. <i>Genome Biology</i> , 2015, 16, 111.	13.9	52
98	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
99	Comparative functional characterization of the CSR-1 22G-RNA pathway in <i>Caenorhabditis</i> nematodes. <i>Nucleic Acids Research</i> , 2015, 43, 208-224.	6.5	38
100	miR-10b-5p expression in Huntington'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
101	piRNA-guided transposon cleavage initiates Zucchini-dependent, phased piRNA production. <i>Science</i> , 2015, 348, 817-821.	6.0	320
102	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.	3.1	26
103	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
104	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.	6.5	22
105	Updates to the Integrated Protein-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
106	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
107	The PsychENCODE project. <i>Nature Neuroscience</i> , 2015, 18, 1707-1712.	7.1	371
108	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

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109	The Role of H3K4me3 in Transcriptional Regulation Is Altered in Huntington's Disease. <i>PLoS ONE</i> , 2015, 10, e0144398.	1.1	47
110	Biophysical Characterization of TCR Variants with Reengineered Specificity and Affinity. <i>FASEB Journal</i> , 2015, 29, 571.30.	0.2	0
111	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.	1.1	23
112	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
113	Antisense piRNA amplification, but not piRNA production or nuage assembly, requires the Tudor-domain protein Qin. <i>EMBO Journal</i> , 2014, 33, 536-539.	3.5	21
114	Computational Design of the Affinity and Specificity of a Therapeutic T Cell Receptor. <i>PLoS Computational Biology</i> , 2014, 10, e1003478.	1.5	67
115	A System for Genome-Wide Histone Variant Dynamics In ES Cells Reveals Dynamic MacroH2A2 Replacement at Promoters. <i>PLoS Genetics</i> , 2014, 10, e1004515.	1.5	28
116	MicroRNAs Located in the Hox Gene Clusters Are Implicated in Huntington's Disease Pathogenesis. <i>PLoS Genetics</i> , 2014, 10, e1004188.	1.5	97
117	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
118	Evaluating template-based and template-free protein-protein complex structure prediction. <i>Briefings in Bioinformatics</i> , 2014, 15, 169-176.	3.2	35
119	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
120	Endogenous U2-U5-U6 snRNA complexes in <i>S. pombe</i> are intron lariat spliceosomes. <i>Rna</i> , 2014, 20, 308-320.	1.6	40
121	TEMP: a computational method for analyzing transposable element polymorphism in populations. <i>Nucleic Acids Research</i> , 2014, 42, 6826-6838.	6.5	124
122	Modeling T cell receptor recognition of CD1-lipid and MR1-metabolite complexes. <i>BMC Bioinformatics</i> , 2014, 15, 319.	1.2	5
123	Binding interface prediction by combining protein-protein docking results. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 57-66.	1.5	38
124	Backbone Flexibility of CDR3 and Immune Recognition of Antigens. <i>Journal of Molecular Biology</i> , 2014, 426, 1583-1599.	2.0	16
125	Blind prediction of interfacial water positions in CAPRI. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 620-632.	1.5	50
126	Principles of regulatory information conservation between mouse and human. <i>Nature</i> , 2014, 515, 371-375.	13.7	259

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127	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
128	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.	3.3	25
129	High-Resolution Mapping of Chromatin Packaging in Mouse Embryonic Stem Cells and Sperm. <i>Developmental Cell</i> , 2014, 30, 11-22.	3.1	207
130	ZDOCK server: interactive docking prediction of proteinâ€“protein complexes and symmetric multimers. <i>Bioinformatics</i> , 2014, 30, 1771-1773.	1.8	1,313
131	The HP1 Homolog Rhino Anchors a Nuclear Complex that Suppresses piRNA Precursor Splicing. <i>Cell</i> , 2014, 157, 1353-1363.	13.5	198
132	A flexible docking approach for prediction of T cell receptorâ€“peptideâ€“MHC complexes. <i>Protein Science</i> , 2013, 22, 35-46.	3.1	75
133	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
134	Transposition-Driven Genomic Heterogeneity in the <i>Drosophila</i> Brain. <i>Science</i> , 2013, 340, 91-95.	6.0	212
135	The correlation between histone modifications and gene expression. <i>Epigenomics</i> , 2013, 5, 113-116.	1.0	154
136	Unsupervised pattern discovery in human chromatin structure through genomic segmentation. , 2013, , .		216
137	Coordinated Cell Typeâ€“Specific Epigenetic Remodeling in Prefrontal Cortex Begins before Birth and Continues into Early Adulthood. <i>PLoS Genetics</i> , 2013, 9, e1003433.	1.5	68
138	Rapid Reassortment of Internal Genes in Avian Influenza A(H7N9) Virus. <i>Clinical Infectious Diseases</i> , 2013, 57, 1059-1061.	2.9	27
139	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
140	Substitution Rates of the Internal Genes in the Novel Avian H7N9 Influenza Virus. <i>Clinical Infectious Diseases</i> , 2013, 57, 1213-1215.	2.9	8
141	The Missing Heritability in T1D and Potential New Targets for Prevention. <i>Journal of Diabetes Research</i> , 2013, 2013, 1-10.	1.0	9
142	Performance of ZDOCK in CAPRI rounds 20â€“26. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 2175-2182.	1.5	22
143	Networking development by Boolean logic. <i>Nucleus</i> , 2013, 4, 89-91.	0.6	6
144	Exploring Angular Distance in Protein-Protein Docking Algorithms. <i>PLoS ONE</i> , 2013, 8, e56645.	1.1	11

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145	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
146	Hdac6 regulates Tip60-p400 function in stem cells. <i>ELife</i> , 2013, 2, e01557.	2.8	53
147	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
148	UAP56 Couples piRNA Clusters to the Perinuclear Transposon Silencing Machinery. <i>Cell</i> , 2012, 151, 871-884.	13.5	204
149	Long-term, efficient inhibition of microRNA function in mice using rAAV vectors. <i>Nature Methods</i> , 2012, 9, 403-409.	9.0	188
150	Dicer Partner Proteins Tune the Length of Mature miRNAs in Flies and Mammals. <i>Cell</i> , 2012, 151, 533-546.	13.5	158
151	Genome-wide identification and characterization of replication origins by deep sequencing. <i>Genome Biology</i> , 2012, 13, R27.	13.9	85
152	Functional analysis of transcription factor binding sites in human promoters. <i>Genome Biology</i> , 2012, 13, R50.	13.9	136
153	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
154	Cutting Edge: Evidence for a Dynamically Driven T Cell Signaling Mechanism. <i>Journal of Immunology</i> , 2012, 188, 5819-5823.	0.4	63
155	Epigenetic Signatures of Autism. <i>Archives of General Psychiatry</i> , 2012, 69, 314.	13.8	174
156	Exploring the DNA-recognition potential of homeodomains. <i>Genome Research</i> , 2012, 22, 1889-1898.	2.4	26
157	Unsupervised pattern discovery in human chromatin structure through genomic segmentation. <i>Nature Methods</i> , 2012, 9, 473-476.	9.0	562
158	Modeling gene expression using chromatin features in various cellular contexts. <i>Genome Biology</i> , 2012, 13, R53.	13.9	231
159	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
160	Human-Specific Histone Methylation Signatures at Transcription Start Sites in Prefrontal Neurons. <i>PLoS Biology</i> , 2012, 10, e1001427.	2.6	113
161	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012, 22, 1658-1667.	2.4	166
162	Prediction of protein-protein binding free energies. <i>Protein Science</i> , 2012, 21, 396-404.	3.1	74

#	ARTICLE	IF	CITATIONS
163	Gene set enrichment analysis: performance evaluation and usage guidelines. <i>Briefings in Bioinformatics</i> , 2012, 13, 281-291.	3.2	217
164	Accelerating Protein Docking in ZDOCK Using an Advanced 3D Convolution Library. <i>PLoS ONE</i> , 2011, 6, e24657.	1.1	490
165	Adaptation to P Element Transposon Invasion in <i>Drosophila melanogaster</i> . <i>Cell</i> , 2011, 147, 1551-1563.	13.5	226
166	Mbd3/NURD Complex Regulates Expression of 5-Hydroxymethylcytosine Marked Genes in Embryonic Stem Cells. <i>Cell</i> , 2011, 147, 1498-1510.	13.5	424
167	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
168	Molecular Basis of a Million-Fold Affinity Maturation Process in a Protein-Protein Interaction. <i>Journal of Molecular Biology</i> , 2011, 411, 321-328.	2.0	7
169	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
170	The 3' to-5' Exoribonuclease Nibbler Shapes the 3' Ends of MicroRNAs Bound to <i>Drosophila</i> Argonaute1. <i>Current Biology</i> , 2011, 21, 1878-1887.	1.8	143
171	A machine learning approach for the prediction of protein surface loop flexibility. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2467-2474.	1.5	8
172	A structure-based benchmark for protein-protein binding affinity. <i>Protein Science</i> , 2011, 20, 482-491.	3.1	252
173	Integrating atom-based and residue-based scoring functions for protein-protein docking. <i>Protein Science</i> , 2011, 20, 1576-1586.	3.1	80
174	MicroRNA-regulated, Systemically Delivered rAAV9: A Step Closer to CNS-restricted Transgene Expression. <i>Molecular Therapy</i> , 2011, 19, 526-535.	3.7	143
175	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
176	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
177	Performance of ZDOCK and ZRANK in CAPRI rounds 13-19. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3104-3110.	1.5	72
178	Protein-protein docking benchmark version 4.0. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3111-3114.	1.5	390
179	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
180	Sequence features that drive human promoter function and tissue specificity. <i>Genome Research</i> , 2010, 20, 890-898.	2.4	87

#	ARTICLE	IF	CITATIONS
181	Distinct Functions for the <i>Drosophila</i> piRNA Pathway in Genome Maintenance and Telomere Protection. <i>PLoS Genetics</i> , 2010, 6, e1001246.	1.5	86
182	A simple method for improving the specificity of anti-methyl histone antibodies. <i>Epigenetics</i> , 2010, 5, 392-395.	1.3	7
183	Target RNA-directed Trimming and Tailing of Small Silencing RNAs. <i>Science</i> , 2010, 328, 1534-1539.	6.0	514
184	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
185	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.	1.2	10
186	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
187	Paternally Induced Transgenerational Environmental Reprogramming of Metabolic Gene Expression in Mammals. <i>Cell</i> , 2010, 143, 1084-1096.	13.5	990
188	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
189	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
190	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
191	Collapse of Germline piRNAs in the Absence of Argonaute3 Reveals Somatic piRNAs in Flies. <i>Cell</i> , 2009, 137, 509-521.	13.5	503
192	The <i>Drosophila</i> 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
193	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
194	Protein-protein docking benchmark version 3.0. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 705-709.	1.5	224
195	Epitope tagging of endogenous proteins for genome-wide ChIP-chip studies. <i>Nature Methods</i> , 2008, 5, 163-165.	9.0	92
196	High-Resolution Mapping and Characterization of Open Chromatin across the Genome. <i>Cell</i> , 2008, 132, 311-322.	13.5	1,246
197	Endogenous siRNAs Derived from Transposons and mRNAs in <i>Drosophila</i> Somatic Cells. <i>Science</i> , 2008, 320, 1077-1081.	6.0	594
198	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

#	ARTICLE	IF	CITATIONS
199	Systematic evaluation of variability in ChIP-chip experiments using predefined DNA targets. <i>Genome Research</i> , 2008, 18, 393-403.	2.4	117
200	Quantitative Analysis of Single Nucleotide Polymorphisms within Copy Number Variation. <i>PLoS ONE</i> , 2008, 3, e3906.	1.1	34
201	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
202	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
203	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
204	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
205	Transcription factor binding and modified histones in human bidirectional promoters. <i>Genome Research</i> , 2007, 17, 818-827.	2.4	131
206	Nucleosome positioning signals in genomic DNA. <i>Genome Research</i> , 2007, 17, 1170-1177.	2.4	287
207	Integrated analysis of experimental data sets reveals many novel promoters in 1% of the human genome. <i>Genome Research</i> , 2007, 17, 720-731.	2.4	31
208	ZRANK: Reranking protein docking predictions with an optimized energy function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 1078-1086.	1.5	401
209	Integrating statistical pair potentials into protein complex prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 511-520.	1.5	273
210	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
211	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
212	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
213	A Global Map of p53 Transcription-Factor Binding Sites in the Human Genome. <i>Cell</i> , 2006, 124, 207-219.	13.5	1,060
214	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
215	Systematic detection of statistically overrepresented DNA motif association rules. <i>Genome Informatics</i> , 2006, 17, 124-33.	0.4	1
216	Assessing computational tools for the discovery of transcription factor binding sites. <i>Nature Biotechnology</i> , 2005, 23, 137-144.	9.4	1,121

#	ARTICLE	IF	CITATIONS
217	Main-chain conformational tendencies of amino acids. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 679-689.	1.5	139
218	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
219	Protein-protein docking benchmark 2.0: An update. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 214-216.	1.5	254
220	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.	1.0	17
221	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
222	M-ZDOCK: a grid-based approach for Cn symmetric multimer docking. <i>Bioinformatics</i> , 2005, 21, 1472-1478.	1.8	160
223	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.	3.1	10
224	Identification and characterization of cell type-specific and ubiquitous chromatin regulatory structures in the human genome. <i>PLoS Genetics</i> , 2005, preprint, e136.	1.5	0
225	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
226	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
227	Finding functional sequence elements by multiple local alignment. <i>Nucleic Acids Research</i> , 2004, 32, 189-200.	6.5	195
228	Detection of functional DNA motifs via statistical over-representation. <i>Nucleic Acids Research</i> , 2004, 32, 1372-1381.	6.5	383
229	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
230	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
231	FAST: A novel protein structure alignment algorithm. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 618-627.	1.5	153
232	Optimizing protein representations with information theory. <i>Genome Informatics</i> , 2004, 15, 160-9.	0.4	13
233	SeqVISTA: a graphical tool for sequence feature visualization and comparison. <i>BMC Bioinformatics</i> , 2003, 4, 1.	1.2	179
234	A novel shape complementarity scoring function for protein-protein docking. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 51, 397-408.	1.5	277

#	ARTICLE	IF	CITATIONS
235	ZDOCK predictions for the CAPRI challenge. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 68-73.	1.5	83
236	ZDOCK: An initial-stage protein-docking algorithm. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 80-87.	1.5	1,220
237	A protein-protein docking benchmark. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 88-91.	1.5	242
238	Atomic contact vectors in protein-protein recognition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 629-639.	1.5	116
239	RDOCK: Refinement of rigid-body protein docking predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 693-707.	1.5	289
240	PromoSer: a large-scale mammalian promoter and transcription start site identification service. <i>Nucleic Acids Research</i> , 2003, 31, 3554-3559.	6.5	75
241	Managing Biological Sequence and Protein Structure Data. <i>OMICS A Journal of Integrative Biology</i> , 2003, 7, 25-26.	1.0	0
242	Cluster-Buster: finding dense clusters of motifs in DNA sequences. <i>Nucleic Acids Research</i> , 2003, 31, 3666-3668.	6.5	268
243	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
244	A computational framework for optimal masking in the synthesis of oligonucleotide microarrays. <i>Nucleic Acids Research</i> , 2002, 30, 106e-106.	6.5	23
245	HugeIndex: a database with visualization tools for high-density oligonucleotide array data from normal human tissues. <i>Nucleic Acids Research</i> , 2002, 30, 214-217.	6.5	44
246	Protein therapeutics: promises and challenges for the 21st century. <i>Trends in Biotechnology</i> , 2002, 20, 29-35.	4.9	68
247	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.	0.9	26
248	Docking unbound proteins using shape complementarity, desolvation, and electrostatics. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 281-294.	1.5	339
249	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.	5.7	33
250	A compendium of gene expression in normal human tissues. <i>Physiological Genomics</i> , 2001, 7, 97-104.	1.0	376
251	Protein structure alignment using a genetic algorithm. , 2000, 38, 428-440.		92
252	VRDD: applying virtual reality visualization to protein docking and design. <i>Journal of Molecular Graphics and Modelling</i> , 1999, 17, 180-186.	1.3	39

#	ARTICLE	IF	CITATIONS
253	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.	1.6	17
254	Free Energy Landscapes of Encounter Complexes in Protein-Protein Association. <i>Biophysical Journal</i> , 1999, 76, 1166-1178.	0.2	181
255	The waters of life. <i>Journal of the Franklin Institute</i> , 1998, 335, 213-240.	1.9	4
256	Toward a predictive understanding of molecular recognition. <i>Immunological Reviews</i> , 1998, 163, 251-266.	2.8	14
257	Computational determination of the structure of rat fc bound to the neonatal fc receptor 1 Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 1998, 282, 217-225.	2.0	22
258	Hedgehogs, foxes, and a new science. <i>Nature Biotechnology</i> , 1997, 15, 819-819.	9.4	1
259	Empirical free energy calculation: Comparison to calorimetric data. <i>Protein Science</i> , 1997, 6, 1976-1984.	3.1	29
260	Prediction of protein complexes using empirical free energy functions. <i>Protein Science</i> , 1996, 5, 614-626.	3.1	91
261	Extracting hydrophobicity parameters from solute partition and protein mutation/unfolding experiments. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 1081-1092.	1.0	26
262	Co-Dependent Assembly of <i>Drosophila</i> piRNA Precursor Complexes and piRNA Cluster Heterochromatin. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
263	Mutational analysis verifies that "kneed" sequence of fibronectin participates in cell-substrate interactions. , 0, , .		0