

Zhiping Weng

List of Publications by Year in descending order

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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	Factorbook: an updated catalog of transcription factor motifs and candidate regulatory motif sites. Nucleic Acids Research, 2022, 50, D141-D149.	14.5	16
2	Deletion and replacement of long genomic sequences using prime editing. Nature Biotechnology, 2022, 40, 227-234.	17.5	90
3	Spatial transcriptomic reconstruction of the mouse olfactory glomerular map suggests principles of odor processing. Nature Neuroscience, 2022, 25, 484-492.	14.8	27
4	Integration of high-resolution promoter profiling assays reveals novel, cell type-specific transcription start sites across 115 human cell and tissue types. Genome Research, 2022, 32, 389-402.	5.5	8
5	Ancestry-inclusive dog genomics challenges popular breed stereotypes. Science, 2022, 376, eabk0639.	12.6	77
6	MafB, WDR77, and β -catenin interact with each other and have similar genome association profiles. PLoS ONE, 2022, 17, e0264799.	2.5	0
7	YAP1 Withdrawal in Hepatoblastoma Drives Therapeutic Differentiation of Tumor Cells to Functional Hepatocyte-Like Cells. Hepatology, 2021, 73, 1011-1027.	7.3	10
8	High-throughput modeling and scoring of TCR-pMHC complexes to predict cross-reactive peptides. Bioinformatics, 2021, 36, 5377-5385.	4.1	13
9	Long first exons and epigenetic marks distinguish conserved pachytene piRNA clusters from other mammalian genes. Nature Communications, 2021, 12, 73.	12.8	17
10	A benchmark and an algorithm for detecting germline transposon insertions and measuring <i>de novo</i> transposon insertion frequencies. Nucleic Acids Research, 2021, 49, e44-e44.	14.5	26
11	Liquid chromatin Hi-C characterizes compartment-dependent chromatin interaction dynamics. Nature Genetics, 2021, 53, 367-378.	21.4	84
12	Annotation of chromatin states in 66 complete mouse epigenomes during development. Communications Biology, 2021, 4, 239.	4.4	34
13	Genetic and epigenetic features of promoters with ubiquitous chromatin accessibility support ubiquitous transcription of cell-essential genes. Nucleic Acids Research, 2021, 49, 5705-5725.	14.5	10
14	An expanded benchmark for antibody-antigen docking and affinity prediction reveals insights into antibody recognition determinants. Structure, 2021, 29, 606-621.e5.	3.3	65
15	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. Nature Communications, 2021, 12, 3968.	12.8	48
16	Genome-wide mapping of human DNA replication by optical replication mapping supports a stochastic model of eukaryotic replication. Molecular Cell, 2021, 81, 2975-2988.e6.	9.7	57
17	Investigating the Potential Roles of SINEs in the Human Genome. Annual Review of Genomics and Human Genetics, 2021, 22, 199-218.	6.2	16
18	YAP and TAZ are transcriptional co-activators of AP-1 proteins and STAT3 during breast cellular transformation. ELife, 2021, 10, .	6.0	56

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19	piRNA-independent transposon silencing by the Drosophila THO complex. <i>Developmental Cell</i> , 2021, 56, 2623-2635.e5.	7.0	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.	2.3	5
21	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
22	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
23	Evolutionarily conserved pachytene piRNA loci are highly divergent among modern humans. <i>Nature Ecology and Evolution</i> , 2020, 4, 156-168.	7.8	58
24	Performance of ZDOCK and IRAD in CAPRI rounds 39-45. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1050-1054.	2.6	8
25	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	27.8	123
26	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	27.8	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.	2.3	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.	21.4	146
29	LogoJS: a Javascript package for creating sequence logos and embedding them in web applications. <i>Bioinformatics</i> , 2020, 36, 3573-3575.	4.1	7
30	The evolutionarily conserved piRNA-producing locus pi6 is required for male mouse fertility. <i>Nature Genetics</i> , 2020, 52, 728-739.	21.4	96
31	Adaptive Evolution Targets a piRNA Precursor Transcription Network. <i>Cell Reports</i> , 2020, 30, 2672-2685.e5.	6.4	16
32	A chromosomal connectome for psychiatric and metabolic risk variants in adult dopaminergic neurons. <i>Genome Medicine</i> , 2020, 12, 19.	8.2	31
33	Integrated miRNA-/mRNA-Seq of the Habenulo-Interpeduncular Circuit During Acute Nicotine Withdrawal. <i>Scientific Reports</i> , 2020, 10, 813.	3.3	9
34	Comprehensive identification of alternative back-splicing in human tissue transcriptomes. <i>Nucleic Acids Research</i> , 2020, 48, 1779-1789.	14.5	33
35	Chemical modifications of adenine base editor mRNA and guide RNA expand its application scope. <i>Nature Communications</i> , 2020, 11, 1979.	12.8	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.	2.5	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.	10.3	29
38	A curated benchmark of enhancer-gene interactions for evaluating enhancer-target gene prediction methods. <i>Genome Biology</i> , 2020, 21, 17.	8.8	83
39	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
40	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
41	Chromatin profiling of cortical neurons identifies individual epigenetic signatures in schizophrenia. <i>Translational Psychiatry</i> , 2019, 9, 256.	4.8	18
42	The piRNA Response to Retroviral Invasion of the Koala Genome. <i>Cell</i> , 2019, 179, 632-643.e12.	28.9	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.	8.8	37
44	Spatial genome exploration in the context of cognitive and neurological disease. <i>Current Opinion in Neurobiology</i> , 2019, 59, 112-119.	4.2	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.	9.7	65
46	Epigeneticâ€“genetic chromatin footprinting identifies novel and subjectâ€“specific genes active in prefrontal cortex neurons. <i>FASEB Journal</i> , 2019, 33, 8161-8173.	0.5	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.	9.7	33
48	The Coding Regions of Germline mRNAs Confer Sensitivity to Argonaute Regulation in <i>C.Âlegans</i> . <i>Cell Reports</i> , 2018, 22, 2254-2264.	6.4	46
49	Integrating Cross-Linking Experiments with Ab Initio Proteinâ€“Protein Docking. <i>Journal of Molecular Biology</i> , 2018, 430, 1814-1828.	4.2	22
50	A Sex Chromosome piRNA Promotes Robust Dosage Compensation and Sex Determination in <i>C.Âlegans</i> . <i>Developmental Cell</i> , 2018, 44, 762-770.e3.	7.0	44
51	Identification of piRNA Binding Sites Reveals the Argonaute Regulatory Landscape of the <i>C.Âlegans</i> Germline. <i>Cell</i> , 2018, 172, 937-951.e18.	28.9	189
52	The piRNA targeting rules and the resistance to piRNA silencing in endogenous genes. <i>Science</i> , 2018, 359, 587-592.	12.6	198
53	Transcriptome-wide Interrogation of the Functional Intronome by Spliceosome Profiling. <i>Cell</i> , 2018, 173, 1031-1044.e13.	28.9	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.	2.7	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, .	6.0	13
56	Neuron-specific signatures in the chromosomal connectome associated with schizophrenia risk. <i>Science</i> , 2018, 362, .	12.6	162
57	Comprehensive functional genomic resource and integrative model for the human brain. <i>Science</i> , 2018, 362, .	12.6	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.	6.4	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.	2.6	4
60	The temporal landscape of recursive splicing during Pol II transcription elongation in human cells. <i>PLoS Genetics</i> , 2018, 14, e1007579.	3.5	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, .	6.0	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.	14.8	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.	6.3	13
64	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
65	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
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.	14.5	41
67	A benchmark testing ground for integrating homology modeling and protein docking. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 10-16.	2.6	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.	2.6	68
69	PCBD5 promotes site-specific oncogenic mutations in human tumors. <i>Nature Genetics</i> , 2017, 49, 1005-1014.	21.4	69
70	CRISPR/Cas9-mediated genome editing induces exon skipping by alternative splicing or exon deletion. <i>Genome Biology</i> , 2017, 18, 108.	8.8	141
71	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
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.	1.3	97

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73	Emerging Concepts in TCR Specificity: Rationalizing and (Maybe) Predicting Outcomes. Journal of Immunology, 2017, 199, 2203-2213.	0.8	77
74	The TREM2-APOE Pathway Drives the Transcriptional Phenotype of Dysfunctional Microglia in Neurodegenerative Diseases. Immunity, 2017, 47, 566-581.e9.	14.3	1,741
75	Adaptive Evolution Leads to Cross-Species Incompatibility in the piRNA Transposon Silencing Machinery. Developmental Cell, 2017, 43, 60-70.e5.	7.0	55
76	Structure-Based Design of Hepatitis C Virus Vaccines That Elicit Neutralizing Antibody Responses to a Conserved Epitope. Journal of Virology, 2017, 91, .	3.4	50
77	Performance of ZDOCK and IRAD in CAPRI rounds 28â€“34. Proteins: Structure, Function and Bioinformatics, 2017, 85, 408-416.	2.6	13
78	IRaPPA: information retrieval based integration of biophysical models for protein assembly selection. Bioinformatics, 2017, 33, 1806-1813.	4.1	36
79	Predicting human splicing branchpoints by combining sequence-derived features and multi-label learning methods. BMC Bioinformatics, 2017, 18, 464.	2.6	24
80	A systems level approach to temporal expression dynamics in Drosophila reveals clusters of long term memory genes. PLoS Genetics, 2017, 13, e1007054.	3.5	26
81	Evaluation of preprocessing, mapping and postprocessing algorithms for analyzing whole genome bisulfite sequencing data. Briefings in Bioinformatics, 2016, 17, bbv103.	6.5	20
82	Forward genetic screen of human transposase genomic rearrangements. BMC Genomics, 2016, 17, 548.	2.8	13
83	Prediction of homoprotein and heteroprotein complexes by protein docking and templateâ€“based modeling: A CASPâ€“CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2016, 84, 323-348.	2.6	148
84	Computational Reprogramming of T Cell Antigen Receptor Binding Properties. Methods in Molecular Biology, 2016, 1414, 305-318.	0.9	2
85	Computational Modeling of T Cell Receptor Complexes. Methods in Molecular Biology, 2016, 1414, 319-340.	0.9	11
86	A generalized framework for computational design and mutational scanning of T-cell receptor binding interfaces. Protein Engineering, Design and Selection, 2016, 29, 595-606.	2.1	16
87	Unexpected role of interferon-Î³ in regulating neuronal connectivity and social behaviour. Nature, 2016, 535, 425-429.	27.8	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 Î±Î² TCR repertoire. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1276-85.	7.1	55
90	Therapeutic genome editing by combined viral and non-viral delivery of CRISPR system components in vivo. Nature Biotechnology, 2016, 34, 328-333.	17.5	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.	28.9	121
92	DNApi: A De Novo Adapter Prediction Algorithm for Small RNA Sequencing Data. <i>PLoS ONE</i> , 2016, 11, e0164228.	2.5	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.	2.5	150
94	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
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.	4.5	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.	4.1	122
97	A versatile reporter system for CRISPR-mediated chromosomal rearrangements. <i>Genome Biology</i> , 2015, 16, 111.	9.6	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.	2.7	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.	14.5	38
100	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
101	piRNA-guided transposon cleavage initiates Zucchini-dependent, phased piRNA production. <i>Science</i> , 2015, 348, 817-821.	12.6	320
102	Pitfalls of Mapping High-Throughput Sequencing Data to Repetitive Sequences: Piwiâ€™s Genomic Targets Still Not Identified. <i>Developmental Cell</i> , 2015, 32, 765-771.	7.0	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.	8.1	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.	14.5	22
105	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
106	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
107	The PsychENCODE project. <i>Nature Neuroscience</i> , 2015, 18, 1707-1712.	14.8	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.	2.9	67

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109	The Role of H3K4me3 in Transcriptional Regulation Is Altered in Huntington's Disease. PLoS ONE, 2015, 10, e0144398.	2.5	47
110	Biophysical Characterization of TCR Variants with Reengineered Specificity and Affinity. FASEB Journal, 2015, 29, 571.30.	0.5	0
111	High-Throughput Sequencing Analysis of Post-Liver Transplantation HCV E2 Glycoprotein Evolution in the Presence and Absence of Neutralizing Monoclonal Antibody. PLoS ONE, 2014, 9, e100325.	2.5	23
112	Defining functional DNA elements in the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6131-6138.	7.1	635
113	Antisense piRNA amplification, but not piRNA production or nuage assembly, requires the Tudor-domain protein Qin. EMBO Journal, 2014, 33, 536-539.	7.8	21
114	Computational Design of the Affinity and Specificity of a Therapeutic T Cell Receptor. PLoS Computational Biology, 2014, 10, e1003478.	3.2	67
115	A System for Genome-Wide Histone Variant Dynamics In ES Cells Reveals Dynamic MacroH2A2 Replacement at Promoters. PLoS Genetics, 2014, 10, e1004515.	3.5	28
116	MicroRNAs Located in the Hox Gene Clusters Are Implicated in Huntington's Disease Pathogenesis. PLoS Genetics, 2014, 10, e1004188.	3.5	97
117	Crystal structure of <i>Streptococcus pyogenes</i> EndoS, an immunomodulatory endoglycosidase specific for human IgG antibodies. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6714-6719.	7.1	56
118	Evaluating template-based and template-free protein-protein complex structure prediction. Briefings in Bioinformatics, 2014, 15, 169-176.	6.5	35
119	The Initial Uridine of Primary piRNAs Does Not Create the Tenth Adenine that Is the Hallmark of Secondary piRNAs. Molecular Cell, 2014, 56, 708-716.	9.7	102
120	Endogenous U2-U5-U6 snRNA complexes in <i>S. pombe</i> are intron lariat spliceosomes. Rna, 2014, 20, 308-320.	3.5	40
121	TEMP: a computational method for analyzing transposable element polymorphism in populations. Nucleic Acids Research, 2014, 42, 6826-6838.	14.5	124
122	Modeling T cell receptor recognition of CD1-lipid and MR1-metabolite complexes. BMC Bioinformatics, 2014, 15, 319.	2.6	5
123	Binding interface prediction by combining protein-protein docking results. Proteins: Structure, Function and Bioinformatics, 2014, 82, 57-66.	2.6	38
124	Backbone Flexibility of CDR3 and Immune Recognition of Antigens. Journal of Molecular Biology, 2014, 426, 1583-1599.	4.2	16
125	Blind prediction of interfacial water positions in CAPRI. Proteins: Structure, Function and Bioinformatics, 2014, 82, 620-632.	2.6	50
126	Principles of regulatory information conservation between mouse and human. Nature, 2014, 515, 371-375.	27.8	259

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127	Regulation of histone H3K4 methylation in brain development and disease. Philosophical Transactions of the Royal Society B: Biological Sciences, 2014, 369, 20130514.	4.0	113
128	Reply to Brunet and Doolittle: Both selected effect and causal role elements can influence human biology and disease. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3366.	7.1	25
129	High-Resolution Mapping of Chromatin Packaging in Mouse Embryonic Stem Cells and Sperm. Developmental Cell, 2014, 30, 11-22.	7.0	207
130	ZDOCK server: interactive docking prediction of proteinâ€“protein complexes and symmetric multimers. Bioinformatics, 2014, 30, 1771-1773.	4.1	1,313
131	The HP1 Homolog Rhino Anchors a Nuclear Complex that Suppresses piRNA Precursor Splicing. Cell, 2014, 157, 1353-1363.	28.9	198
132	A flexible docking approach for prediction of T cell receptorâ€“peptideâ€“MHC complexes. Protein Science, 2013, 22, 35-46.	7.6	75
133	An Ancient Transcription Factor Initiates the Burst of piRNA Production during Early Meiosis in Mouse Testes. Molecular Cell, 2013, 50, 67-81.	9.7	322
134	Transposition-Driven Genomic Heterogeneity in the <i>Drosophila</i> Brain. Science, 2013, 340, 91-95.	12.6	212
135	The correlation between histone modifications and gene expression. Epigenomics, 2013, 5, 113-116.	2.1	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. PLoS Genetics, 2013, 9, e1003433.	3.5	68
138	Rapid Reassortment of Internal Genes in Avian Influenza A(H7N9) Virus. Clinical Infectious Diseases, 2013, 57, 1059-1061.	5.8	27
139	Factorbook.org: a Wiki-based database for transcription factor-binding data generated by the ENCODE consortium. Nucleic Acids Research, 2013, 41, D171-D176.	14.5	274
140	Substitution Rates of the Internal Genes in the Novel Avian H7N9 Influenza Virus. Clinical Infectious Diseases, 2013, 57, 1213-1215.	5.8	8
141	The Missing Heritability in T1D and Potential New Targets for Prevention. Journal of Diabetes Research, 2013, 2013, 1-10.	2.3	9
142	Performance of ZDOCK in CAPRI rounds 20â€“26. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2175-2182.	2.6	22
143	Networking development by Boolean logic. Nucleus, 2013, 4, 89-91.	2.2	6
144	Exploring Angular Distance in Protein-Protein Docking Algorithms. PLoS ONE, 2013, 8, e56645.	2.5	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.	2.6	87
146	Hdac6 regulates Tip60-p400 function in stem cells. <i>ELife</i> , 2013, 2, e01557.	6.0	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.	5.5	762
148	UAP56 Couples piRNA Clusters to the Perinuclear Transposon Silencing Machinery. <i>Cell</i> , 2012, 151, 871-884.	28.9	204
149	Long-term, efficient inhibition of microRNA function in mice using rAAV vectors. <i>Nature Methods</i> , 2012, 9, 403-409.	19.0	188
150	Dicer Partner Proteins Tune the Length of Mature miRNAs in Flies and Mammals. <i>Cell</i> , 2012, 151, 533-546.	28.9	158
151	Genome-wide identification and characterization of replication origins by deep sequencing. <i>Genome Biology</i> , 2012, 13, R27.	9.6	85
152	Functional analysis of transcription factor binding sites in human promoters. <i>Genome Biology</i> , 2012, 13, R50.	9.6	136
153	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
154	Cutting Edge: Evidence for a Dynamically Driven T Cell Signaling Mechanism. <i>Journal of Immunology</i> , 2012, 188, 5819-5823.	0.8	63
155	Epigenetic Signatures of Autism. <i>Archives of General Psychiatry</i> , 2012, 69, 314.	12.3	174
156	Exploring the DNA-recognition potential of homeodomains. <i>Genome Research</i> , 2012, 22, 1889-1898.	5.5	26
157	Unsupervised pattern discovery in human chromatin structure through genomic segmentation. <i>Nature Methods</i> , 2012, 9, 473-476.	19.0	562
158	Modeling gene expression using chromatin features in various cellular contexts. <i>Genome Biology</i> , 2012, 13, R53.	9.6	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.	8.1	122
160	Human-Specific Histone Methylation Signatures at Transcription Start Sites in Prefrontal Neurons. <i>PLoS Biology</i> , 2012, 10, e1001427.	5.6	113
161	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012, 22, 1658-1667.	5.5	166
162	Prediction of protein-protein binding free energies. <i>Protein Science</i> , 2012, 21, 396-404.	7.6	74

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163	Gene set enrichment analysis: performance evaluation and usage guidelines. <i>Briefings in Bioinformatics</i> , 2012, 13, 281-291.	6.5	217
164	Accelerating Protein Docking in ZDOCK Using an Advanced 3D Convolution Library. <i>PLoS ONE</i> , 2011, 6, e24657.	2.5	490
165	Adaptation to P Element Transposon Invasion in <i>Drosophila melanogaster</i> . <i>Cell</i> , 2011, 147, 1551-1563.	28.9	226
166	Mbd3/NURD Complex Regulates Expression of 5-Hydroxymethylcytosine Marked Genes in Embryonic Stem Cells. <i>Cell</i> , 2011, 147, 1498-1510.	28.9	424
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