

Zhiping Weng

List of Publications by Year in descending order

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Version: 2024-02-01

263
papers

47,544
citations

2671

95
h-index

2125

203
g-index

299
all docs

299
docs citations

299
times ranked

56725
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | 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 28â€“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 templateâ€based modeling: A CASPâ€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 $\hat{\pm}^2$ TCR repertoire. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1276-85. | 3.3 | 55 |
| 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 |