

Bonnie Berger

List of Publications by Year in descending order

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Version: 2024-02-01

206
papers

20,981
citations

20817

60
h-index

13771

129
g-index

236
all docs

236
docs citations

236
times ranked

33429
citing authors

#	ARTICLE	IF	CITATIONS
1	Predicting the mutational drivers of future SARS-CoV-2 variants of concern. <i>Science Translational Medicine</i> , 2022, 14, eabk3445.	12.4	101
2	Deep learning guided optimization of human antibody against SARS-CoV-2 variants with broad neutralization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2122954119.	7.1	57
3	Topsy-Turvy: integrating a global view into sequence-based PPI prediction. <i>Bioinformatics</i> , 2022, 38, i264-i272.	4.1	28
4	Multimodal profiling of lung granulomas in macaques reveals cellular correlates of tuberculosis control. <i>Immunity</i> , 2022, 55, 827-846.e10.	14.3	92
5	Genome-wide mapping of somatic mutation rates uncovers drivers of cancer. <i>Nature Biotechnology</i> , 2022, 40, 1634-1643.	17.5	23
6	Levenshtein Distance, Sequence Comparison and Biological Database Search. <i>IEEE Transactions on Information Theory</i> , 2021, 67, 3287-3294.	2.4	51
7	Structures of radial spokes and associated complexes important for ciliary motility. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 29-37.	8.2	81
8	Learning the language of viral evolution and escape. <i>Science</i> , 2021, 371, 284-288.	12.6	184
9	Large mosaic copy number variations confer autism risk. <i>Nature Neuroscience</i> , 2021, 24, 197-203.	14.8	36
10	CryoDRGN: reconstruction of heterogeneous cryo-EM structures using neural networks. <i>Nature Methods</i> , 2021, 18, 176-185.	19.0	299
11	Human airway mast cells proliferate and acquire distinct inflammation-driven phenotypes during type 2 inflammation. <i>Science Immunology</i> , 2021, 6, .	11.9	79
12	Schema: metric learning enables interpretable synthesis of heterogeneous single-cell modalities. <i>Genome Biology</i> , 2021, 22, 131.	8.8	22
13	Learning the protein language: Evolution, structure, and function. <i>Cell Systems</i> , 2021, 12, 654-669.e3.	6.2	194
14	An engineered protein-phosphorylation toggle network with implications for endogenous network discovery. <i>Science</i> , 2021, 373, .	12.6	24
15	Bayesian information sharing enhances detection of regulatory associations in rare cell types. <i>Bioinformatics</i> , 2021, 37, i349-i357.	4.1	1
16	A Python-based programming language for high-performance computational genomics. <i>Nature Biotechnology</i> , 2021, 39, 1062-1064.	17.5	9
17	HIV infection drives interferon signaling within intestinal SARS-CoV-2 target cells. <i>JCI Insight</i> , 2021, 6, .	5.0	7
18	Minimizer-space de Bruijn graphs: Whole-genome assembly of long reads in minutes on a personal computer. <i>Cell Systems</i> , 2021, 12, 958-968.e6.	6.2	51

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19	Assessing single-cell transcriptomic variability through density-preserving data visualization. <i>Nature Biotechnology</i> , 2021, 39, 765-774.	17.5	74
20	D-SCRIPT translates genome to phenome with sequence-based, structure-aware, genome-scale predictions of protein-protein interactions. <i>Cell Systems</i> , 2021, 12, 969-982.e6.	6.2	78
21	Truly privacy-preserving federated analytics for precision medicine with multiparty homomorphic encryption. <i>Nature Communications</i> , 2021, 12, 5910.	12.8	64
22	CryoDRGN2: Ab initio neural reconstruction of 3D protein structures from real cryo-EM images. , 2021, , .		21
23	Meta-analysis of <i>Caenorhabditis elegans</i> single-cell developmental data reveals multi-frequency oscillation in gene activation. <i>Bioinformatics</i> , 2020, 36, 4047-4057.	4.1	6
24	Improved haplotype inference by exploiting long-range linking and allelic imbalance in RNA-seq datasets. <i>Nature Communications</i> , 2020, 11, 4662.	12.8	14
25	Leveraging Uncertainty in Machine Learning Accelerates Biological Discovery and Design. <i>Cell Systems</i> , 2020, 11, 461-477.e9.	6.2	92
26	Topaz-Denoise: general deep denoising models for cryoEM and cryoET. <i>Nature Communications</i> , 2020, 11, 5208.	12.8	313
27	Hopper: a mathematically optimal algorithm for sketching biological data. <i>Bioinformatics</i> , 2020, 36, i236-i241.	4.1	14
28	Privacy-Preserving Biomedical Database Queries with Optimal Privacy-Utility Trade-Offs. <i>Cell Systems</i> , 2020, 10, 408-416.e9.	6.2	14
29	Computational Methods for Single-Cell RNA Sequencing. <i>Annual Review of Biomedical Data Science</i> , 2020, 3, 339-364.	6.5	81
30	Integrated single-cell analysis of multicellular immune dynamics during hyperacute HIV-1 infection. <i>Nature Medicine</i> , 2020, 26, 511-518.	30.7	100
31	Carnelian uncovers hidden functional patterns across diverse study populations from whole metagenome sequencing reads. <i>Genome Biology</i> , 2020, 21, 47.	8.8	14
32	SARS-CoV-2 Receptor ACE2 Is an Interferon-Stimulated Gene in Human Airway Epithelial Cells and Is Detected in Specific Cell Subsets across Tissues. <i>Cell</i> , 2020, 181, 1016-1035.e19.	28.9	1,956
33	A Randomized Parallel Algorithm for Efficiently Finding Near-Optimal Universal Hitting Sets. <i>Lecture Notes in Computer Science</i> , 2020, , 37-53.	1.3	16
34	Metagenomic binning through low-density hashing. <i>Bioinformatics</i> , 2019, 35, 219-226.	4.1	21
35	Emerging technologies towards enhancing privacy in genomic data sharing. <i>Genome Biology</i> , 2019, 20, 128.	8.8	45
36	Seq: a high-performance language for bioinformatics. , 2019, 3, 1-29.		12

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37	TOPAZ: A Positive-Unlabeled Convolutional Neural Network CryoEM Particle Picker that can Pick Any Size and Shape Particle. <i>Microscopy and Microanalysis</i> , 2019, 25, 986-987.	0.4	14
38	Geometric Sketching Compactly Summarizes the Single-Cell Transcriptomic Landscape. <i>Cell Systems</i> , 2019, 8, 483-493.e7.	6.2	95
39	Efficient integration of heterogeneous single-cell transcriptomes using Scanorama. <i>Nature Biotechnology</i> , 2019, 37, 685-691.	17.5	557
40	Visualization of clustered protocadherin neuronal self-recognition complexes. <i>Nature</i> , 2019, 569, 280-283.	27.8	86
41	Positive-unlabeled convolutional neural networks for particle picking in cryo-electron micrographs. <i>Nature Methods</i> , 2019, 16, 1153-1160.	19.0	693
42	Protecting Genomic Data Privacy with Probabilistic Modeling. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2019, 24, 403-414.	0.7	1
43	Large-Margin Classification in Hyperbolic Space. <i>Proceedings of Machine Learning Research</i> , 2019, 89, 1832-1840.	0.3	1
44	Enhancing Evolutionary Couplings with Deep Convolutional Neural Networks. <i>Cell Systems</i> , 2018, 6, 65-74.e3.	6.2	97
45	Finding RNA structure in the unstructured RBPome. <i>BMC Genomics</i> , 2018, 19, 154.	2.8	7
46	Allelic decomposition and exact genotyping of highly polymorphic and structurally variant genes. <i>Nature Communications</i> , 2018, 9, 828.	12.8	67
47	Fast characterization of segmental duplications in genome assemblies. <i>Bioinformatics</i> , 2018, 34, i706-i714.	4.1	55
48	Realizing private and practical pharmacological collaboration. <i>Science</i> , 2018, 362, 347-350.	12.6	52
49	Joker de Bruijn: Covering k-Mers Using Joker Characters. <i>Journal of Computational Biology</i> , 2018, 25, 1171-1178.	1.6	0
50	Secure genome-wide association analysis using multiparty computation. <i>Nature Biotechnology</i> , 2018, 36, 547-551.	17.5	139
51	Statistical Binning for Barcoded Reads Improves Downstream Analyses. <i>Cell Systems</i> , 2018, 7, 219-226.e5.	6.2	18
52	Allergic inflammatory memory in human respiratory epithelial progenitor cells. <i>Nature</i> , 2018, 560, 649-654.	27.8	368
53	Generalizable and Scalable Visualization of Single-Cell Data Using Neural Networks. <i>Cell Systems</i> , 2018, 7, 185-191.e4.	6.2	49
54	Protecting Genomic Data Privacy with Probabilistic Modeling. , 2018, , .		5

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55	Positive-unlabeled convolutional neural networks for particle picking in cryo-electron micrographs. , 2018, 10812, 245-247.		12
56	Latent Variable Model for Aligning Barcoded Short-Reads Improves Downstream Analyses. , 2018, 10812, 280-282.		1
57	Genome-Scale Networks Link Neurodegenerative Disease Genes to α -Synuclein through Specific Molecular Pathways. Cell Systems, 2017, 4, 157-170.e14.	6.2	102
58	Research in Computational Molecular Biology. Lecture Notes in Computer Science, 2017, 10229, 389-390.	1.3	1
59	Identification of protein complexes by integrating multiple alignment of protein interaction networks. Bioinformatics, 2017, 33, 1681-1688.	4.1	72
60	Message from the ISCB: 2017 ISCB Overton Prize Awarded to Christoph Bock. Bioinformatics, 2017, 33, 2247-2248.	4.1	0
61	Optimized Sequence Library Design for Efficient In-Vitro Interaction Mapping. Cell Systems, 2017, 5, 230-236.e5.	6.2	0
62	Message from the ISCB: 2017 ISCB Innovator Award Given to Aviv Regev. Bioinformatics, 2017, 33, 2243-2244.	4.1	0
63	Message from the ISCB: 2017 ISCB Accomplishment by a Senior Scientist Award Given to Pavel Pevzner. Bioinformatics, 2017, 33, 2245-2246.	4.1	0
64	Message from the ISCB: 2017 Outstanding Contributions to ISCB Award Given to Fran Lewitter. Bioinformatics, 2017, 33, 2249-2250.	4.1	0
65	2017 ISCB Accomplishment by a Senior Scientist Award given to Pavel Pevzner. PLoS Computational Biology, 2017, 13, e1005561.	3.2	0
66	2017 Outstanding Contributions to ISCB Award: Fran Lewitter. F1000Research, 2017, 6, 1000.	1.6	4
67	2017 ISCB Innovator Award: Aviv Regev. F1000Research, 2017, 6, 998.	1.6	0
68	2017 ISCB Innovator Award: Aviv Regev. PLoS Computational Biology, 2017, 13, e1005558.	3.2	0
69	2017 ISCB Overton Prize: Christoph Bock. F1000Research, 2017, 6, 999.	1.6	0
70	2017 Outstanding Contributions to ISCB Award: Fran Lewitter. PLoS Computational Biology, 2017, 13, e1005560.	3.2	0
71	2017 ISCB Accomplishment by a Senior Scientist Award: Pavel Pevzner. F1000Research, 2017, 6, 1001.	1.6	0
72	2017 ISCB Overton Prize awarded to Christoph Bock. PLoS Computational Biology, 2017, 13, e1005559.	3.2	0

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73	Efficient Design of Compact Unstructured RNA Libraries Covering All k -mers. <i>Journal of Computational Biology</i> , 2016, 23, 67-79.	1.6	5
74	An Evaluation Framework for Lossy Compression of Genome Sequencing Quality Values. , 2016, 2016, 221-230.		13
75	Compressive mapping for next-generation sequencing. <i>Nature Biotechnology</i> , 2016, 34, 374-376.	17.5	33
76	Fast genotyping of known SNPs through approximate k -mer matching. <i>Bioinformatics</i> , 2016, 32, i538-i544.	4.1	51
77	Enabling Privacy-Preserving GWASs in Heterogeneous Human Populations. <i>Cell Systems</i> , 2016, 3, 54-61.	6.2	62
78	Computational biology in the 21st century. <i>Communications of the ACM</i> , 2016, 59, 72-80.	4.5	56
79	Compact Integration of Multi-Network Topology for Functional Analysis of Genes. <i>Cell Systems</i> , 2016, 3, 540-548.e5.	6.2	207
80	Structured States of Disordered Proteins from Genomic Sequences. <i>Cell</i> , 2016, 167, 158-170.e12.	28.9	127
81	Integrative analysis of genetic data sets reveals a shared innate immune component in autism spectrum disorder and its co-morbidities. <i>Genome Biology</i> , 2016, 17, 228.	8.8	46
82	RCK: accurate and efficient inference of sequence- and structure-based protein-RNA binding models from RNAcompete data. <i>Bioinformatics</i> , 2016, 32, i351-i359.	4.1	67
83	Realizing privacy preserving genome-wide association studies. <i>Bioinformatics</i> , 2016, 32, 1293-1300.	4.1	44
84	Reconstructing Causal Biological Networks through Active Learning. <i>PLoS ONE</i> , 2016, 11, e0150611.	2.5	13
85	Low-Density Locality-Sensitive Hashing Boosts Metagenomic Binning. , 2016, 9649, 255-257.		1
86	Entropy-Scaling Search of Massive Biological Data. <i>Cell Systems</i> , 2015, 1, 130-140.	6.2	64
87	Calibrating the Human Mutation Rate via Ancestral Recombination Density in Diploid Genomes. <i>PLoS Genetics</i> , 2015, 11, e1005550.	3.5	49
88	Conserved piRNA Expression from a Distinct Set of piRNA Cluster Loci in Eutherian Mammals. <i>PLoS Genetics</i> , 2015, 11, e1005652.	3.5	73
89	One Size Doesn't Fit All: Measuring Individual Privacy in Aggregate Genomic Data. , 2015, 2015, 41-49.		8
90	Message from the ISCB: ISCB Ebola award for important future research on the computational biology of Ebola virus. <i>Bioinformatics</i> , 2015, 31, 616-617.	4.1	3

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91	Efficient Bayesian mixed-model analysis increases association power in large cohorts. <i>Nature Genetics</i> , 2015, 47, 284-290.	21.4	1,285
92	Exploiting ontology graph for predicting sparsely annotated gene function. <i>Bioinformatics</i> , 2015, 31, i357-i364.	4.1	97
93	ISCB Ebola Award for Important Future Research on the Computational Biology of Ebola Virus. <i>PLoS Computational Biology</i> , 2015, 11, e1004087.	3.2	2
94	Discovering What Dimensionality Reduction Really Tells Us About RNA-Seq Data. <i>Journal of Computational Biology</i> , 2015, 22, 715-728.	1.6	9
95	ISCB Ebola Award for Important Future Research on the Computational Biology of Ebola Virus. <i>F1000Research</i> , 2015, 4, 12.	1.6	1
96	Widespread Macromolecular Interaction Perturbations in Human Genetic Disorders. <i>Cell</i> , 2015, 161, 647-660.	28.9	482
97	Quality score compression improves genotyping accuracy. <i>Nature Biotechnology</i> , 2015, 33, 240-243.	17.5	57
98	Two-Variance-Component Model Improves Genetic Prediction in Family Datasets. <i>American Journal of Human Genetics</i> , 2015, 97, 677-690.	6.2	26
99	HapTree-X: An Integrative Bayesian Framework for Haplotype Reconstruction from Transcriptome and Genome Sequencing Data. <i>Lecture Notes in Computer Science</i> , 2015, 9029, 28-29.	1.3	8
100	Diffusion Component Analysis: Unraveling Functional Topology in Biological Networks. <i>Lecture Notes in Computer Science</i> , 2015, 9029, 62-64.	1.3	63
101	Efficient Design of Compact Unstructured RNA Libraries Covering All k -mers. <i>Lecture Notes in Computer Science</i> , 2015, , 308-325.	1.3	0
102	Traversing the k -mer Landscape of NGS Read Datasets for Quality Score Sparsification. <i>Lecture Notes in Computer Science</i> , 2014, 8394, 385-399.	1.3	20
103	An exact arithmetic toolbox for a consistent and reproducible structural analysis of metabolic network models. <i>Nature Communications</i> , 2014, 5, 4893.	12.8	37
104	HapTree: A Novel Bayesian Framework for Single Individual Polyplototyping Using NGS Data. <i>PLoS Computational Biology</i> , 2014, 10, e1003502.	3.2	75
105	Reconstructing Austronesian population history in Island Southeast Asia. <i>Nature Communications</i> , 2014, 5, 4689.	12.8	158
106	Ancient west Eurasian ancestry in southern and eastern Africa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2632-2637.	7.1	246
107	Improving the Power of GWAS and Avoiding Confounding from Population Stratification with PC-Select. <i>Genetics</i> , 2014, 197, 1045-1049.	2.9	59
108	Simultaneous Alignment and Folding of Protein Sequences. <i>Journal of Computational Biology</i> , 2014, 21, 477-491.	1.6	0

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109	A Quantitative Chaperone Interaction Network Reveals the Architecture of Cellular Protein Homeostasis Pathways. <i>Cell</i> , 2014, 158, 434-448.	28.9	335
110	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , 2014, 513, 409-413.	27.8	1,179
111	HapTree: A Novel Bayesian Framework for Single Individual Polyplotyping Using NGS Data. <i>Lecture Notes in Computer Science</i> , 2014, , 18-19.	1.3	4
112	Genetic Evidence for Recent Population Mixture in India. <i>American Journal of Human Genetics</i> , 2013, 93, 422-438.	6.2	234
113	Reconstruction of phyletic trees by global alignment of multiple metabolic networks. <i>BMC Bioinformatics</i> , 2013, 14, S12.	2.6	9
114	Computational solutions for omics data. <i>Nature Reviews Genetics</i> , 2013, 14, 333-346.	16.3	288
115	Inferring Admixture Histories of Human Populations Using Linkage Disequilibrium. <i>Genetics</i> , 2013, 193, 1233-1254.	2.9	445
116	Efficient Moment-Based Inference of Admixture Parameters and Sources of Gene Flow. <i>Molecular Biology and Evolution</i> , 2013, 30, 1788-1802.	8.9	121
117	Compressive genomics for protein databases. <i>Bioinformatics</i> , 2013, 29, i283-i290.	4.1	53
118	Optimizing a global alignment of protein interaction networks. <i>Bioinformatics</i> , 2013, 29, 2765-2773.	4.1	53
119	A sampling framework for incorporating quantitative mass spectrometry data in protein interaction analysis. <i>BMC Bioinformatics</i> , 2013, 14, 299.	2.6	4
120	Reconstructing Roma History from Genome-Wide Data. <i>PLoS ONE</i> , 2013, 8, e58633.	2.5	61
121	Making sense out of massive data by going beyond differential expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5594-5599.	7.1	35
122	A global sampling approach to designing and reengineering RNA secondary structures. <i>Nucleic Acids Research</i> , 2012, 40, 10041-10052.	14.5	32
123	A gene expression profile of stem cell pluripotentiality and differentiation is conserved across diverse solid and hematopoietic cancers. <i>Genome Biology</i> , 2012, 13, R71.	9.6	69
124	Compressive genomics. <i>Nature Biotechnology</i> , 2012, 30, 627-630.	17.5	99
125	A computational framework for boosting confidence in high-throughput protein-protein interaction datasets. <i>Genome Biology</i> , 2012, 13, R76.	9.6	44
126	STITCHER: Dynamic assembly of likely amyloid and prion β -structures from secondary structure predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 410-420.	2.6	19

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127	Opposing Effects of Glutamine and Asparagine Govern Prion Formation by Intrinsically Disordered Proteins. <i>Molecular Cell</i> , 2011, 43, 72-84.	9.7	174
128	iWRAP: An Interface Threading Approach with Application to Prediction of Cancer-Related Protein-Protein Interactions. <i>Journal of Molecular Biology</i> , 2011, 405, 1295-1310.	4.2	56
129	Multicoil2: Predicting Coiled Coils and Their Oligomerization States from Sequence in the Twilight Zone. <i>PLoS ONE</i> , 2011, 6, e23519.	2.5	72
130	Phenotype Prediction Using Regularized Regression on Genetic Data in the DREAM5 Systems Genetics B Challenge. <i>PLoS ONE</i> , 2011, 6, e29095.	2.5	16
131	Sparse estimation for structural variability. <i>Algorithms for Molecular Biology</i> , 2011, 6, 12.	1.2	2
132	IsoBase: a database of functionally related proteins across PPI networks. <i>Nucleic Acids Research</i> , 2011, 39, D295-D300.	14.5	90
133	Proteomic and Functional Genomic Landscape of Receptor Tyrosine Kinase and Ras to Extracellular Signal-Regulated Kinase Signaling. <i>Science Signaling</i> , 2011, 4, rs10.	3.6	87
134	A method for probing the mutational landscape of amyloid structure. <i>Bioinformatics</i> , 2011, 27, i34-i42.	4.1	58
135	Structure-based prediction reveals capping motifs that inhibit α -helix aggregation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11099-11104.	7.1	37
136	Efficient Traversal of Beta-Sheet Protein Folding Pathways Using Ensemble Models. <i>Journal of Computational Biology</i> , 2011, 18, 1635-1647.	1.6	6
137	Unusually effective microRNA targeting within repeat-rich coding regions of mammalian mRNAs. <i>Genome Research</i> , 2011, 21, 1395-1403.	5.5	123
138	Efficient Traversal of Beta-Sheet Protein Folding Pathways Using Ensemble Models. <i>Lecture Notes in Computer Science</i> , 2011, , 408-423.	1.3	0
139	Metabolic Network Analysis Demystified. <i>Lecture Notes in Computer Science</i> , 2011, , 31-33.	1.3	0
140	Markov random fields reveal an N-terminal double beta-propeller motif as part of a bacterial hybrid two-component sensor system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4069-4074.	7.1	27
141	Struct2Net: a web service to predict protein-protein interactions using a structure-based approach. <i>Nucleic Acids Research</i> , 2010, 38, W508-W515.	14.5	121
142	Conserved microRNA targeting in <i>Drosophila</i> is as widespread in coding regions as in 3'UTRs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 15751-15756.	7.1	146
143	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010, 330, 1787-1797.	12.6	1,124
144	Novel Perspectives on Protein Structure Prediction. , 2010, , 179-207.		0

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145	Sparse Estimation for Structural Variability. Lecture Notes in Computer Science, 2010, , 13-27.	1.3	0
146	Large-scale identification of genetic design strategies using local search. Molecular Systems Biology, 2009, 5, 296.	7.2	143
147	IsoRankN: spectral methods for global alignment of multiple protein networks. Bioinformatics, 2009, 25, i253-i258.	4.1	322
148	BETASCAN: Probable β -amyloids Identified by Pairwise Probabilistic Analysis. PLoS Computational Biology, 2009, 5, e1000333.	3.2	91
149	RNAmutants: a web server to explore the mutational landscape of RNA secondary structures. Nucleic Acids Research, 2009, 37, W281-W286.	14.5	19
150	LOCAL OPTIMIZATION FOR GLOBAL ALIGNMENT OF PROTEIN INTERACTION NETWORKS. , 2009, , 123-132.		25
151	Simultaneous Alignment and Folding of Protein Sequences. Lecture Notes in Computer Science, 2009, , 339-355.	1.3	2
152	Modeling ensembles of transmembrane β -barrel proteins. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1097-1112.	2.6	26
153	LTHREADER: Prediction of extracellular ligand-receptor interactions in cytokines using localized threading. Protein Science, 2008, 17, 279-292.	7.6	8
154	Global alignment of multiple protein interaction networks with application to functional orthology detection. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 12763-12768.	7.1	500
155	Revealing the spatial distribution of a disease while preserving privacy. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17608-17613.	7.1	58
156	Matt: Local Flexibility Aids Protein Multiple Structure Alignment. PLoS Computational Biology, 2008, 4, e10.	3.2	185
157	Efficient Algorithms for Probing the RNA Mutation Landscape. PLoS Computational Biology, 2008, 4, e1000124.	3.2	38
158	Optimal contact map alignment of protein-protein interfaces. Bioinformatics, 2008, 24, 2324-2328.	4.1	24
159	Comprehensive Dissection of PDGF-PDGFR Signaling Pathways in PDGFR Genetically Defined Cells. PLoS ONE, 2008, 3, e3794.	2.5	99
160	GLOBAL ALIGNMENT OF MULTIPLE PROTEIN INTERACTION NETWORKS. , 2007, , .		23
161	Probabilistic modeling of systematic errors in two-hybrid experiments. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2007, , 445-57.	0.7	3
162	Fold recognition and accurate sequence-structure alignment of sequences directing β -sheet proteins. Proteins: Structure, Function and Bioinformatics, 2006, 63, 976-985.	2.6	24

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163	Predicting transmembrane β^2 -barrels and interstrand residue interactions from sequence. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 61-74.	2.6	36
164	Herpesviral Protein Networks and Their Interaction with the Human Proteome. <i>Science</i> , 2006, 311, 239-242.	12.6	399
165	transFold: a web server for predicting the structure and residue contacts of transmembrane beta-barrels. <i>Nucleic Acids Research</i> , 2006, 34, W189-W193.	14.5	34
166	Fast and accurate algorithms for protein side-chain packing. <i>Journal of the ACM</i> , 2006, 53, 533-557.	2.2	73
167	Pertactin beta-helix folding mechanism suggests common themes for the secretion and folding of autotransporter proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4918-4923.	7.1	187
168	PROBABILISTIC MODELING OF SYSTEMATIC ERRORS IN TWO-HYBRID EXPERIMENTS. , 2006, , .		3
169	LTHREADER: PREDICTION OF LIGAND-RECEPTOR INTERACTIONS USING LOCALIZED THREADING. , 2006, , .		0
170	Struct2net: integrating structure into protein-protein interaction prediction. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2006, , 403-14.	0.7	24
171	STRUCT2NET: INTEGRATING STRUCTURE INTO PROTEIN-PROTEIN INTERACTION PREDICTION. , 2005, , .		16
172	Wrap-and-Pack: A New Paradigm for Beta Structural Motif Recognition with Application to Recognizing Beta Trefoils. <i>Journal of Computational Biology</i> , 2005, 12, 777-795.	1.6	8
173	MSARI: Multiple sequence alignments for statistical detection of RNA secondary structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12102-12107.	7.1	77
174	Wrap-and-pack. , 2004, , .		2
175	Methods in Comparative Genomics: Genome Correspondence, Gene Identification and Regulatory Motif Discovery. <i>Journal of Computational Biology</i> , 2004, 11, 319-355.	1.6	88
176	CHAINTWEAK: SAMPLING FROM THE NEIGHBOURHOOD OF A PROTEIN CONFORMATION. , 2004, , .		5
177	Predicting the Beta-Helix Fold from Protein Sequence Data. <i>Journal of Computational Biology</i> , 2002, 9, 261-276.	1.6	37
178	ARACHNE: A Whole-Genome Shotgun Assembler. <i>Genome Research</i> , 2002, 12, 177-189.	5.5	508
179	Predicting the β^2 -helix fold from protein sequence data. , 2001, , .		7
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