Jianlin Cheng

List of Publications by Year
in descending order

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198	14,463	39113 52	27587 110
papers	citations	h-index	g-index

250	250	250	17126
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Improving protein tertiary structure prediction by deep learning and distance prediction in <scp>CASP14</scp>. Proteins: Structure, Function and Bioinformatics, 2022, 90, 58-72.	1.5	18
2	Artificial intelligence in the prediction of proteinâ€“ligand interactions: recent advances and future directions. Briefings in Bioinformatics, 2022, 23, .	3.2	78
3	Distanceâ€based reconstruction of protein quaternary structures from interâ€chain contacts. Proteins: Structure, Function and Bioinformatics, 2022, 90, 720-731.	1.5	8
4	A deep dilated convolutional residual network for predicting interchain contacts of protein homodimers. Bioinformatics, 2022, 38, 1904-1910.	1.8	29
5	Effect of aneuploidy of a nonâ€essential chromosome on gene expression in maize. Plant Journal, 2022, 110, 193-211.	2.8	8
6	DISTEMA: distance map-based estimation of single protein model accuracy with attentive 2D convolutional neural network. BMC Bioinformatics, 2022, 23, 141.	1.2	2
7	Allele-specific aberration of imprinted domain chromosome architecture associates with large offspring syndrome. IScience, 2022, 25, 104269.	1.9	6
8	Dosage-sensitive miRNAs trigger modulation of gene expression during genomic imbalance in maize. Nature Communications, 2022, 13, .	5.8	1
9	Multi-head attention-based U-Nets for predicting protein domain boundaries using 1D sequence features and 2D distance maps. BMC Bioinformatics, 2022, 23, .	1.2	2
10	<scp>DNSS2</scp>: Improved ab initio protein secondary structure prediction using advanced deep learning architectures. Proteins: Structure, Function and Bioinformatics, 2021, 89, 207-217.	1.5	24
11	DeepDist: real-value inter-residue distance prediction with deep residual convolutional network. BMC Bioinformatics, 2021, 22, 30.	1.2	37
12	Genomic imbalance determines positive and negative modulation of gene expression in diploid maize. Plant Cell, 2021, 33, 917-939.	3.1	22
13	DeepGRN: prediction of transcription factor binding site across cell-types using attention-based deep neural networks. BMC Bioinformatics, 2021, 22, 38.	1.2	35
14	Predominantly inverse modulation of gene expression in genomically unbalanced disomic haploid maize. Plant Cell, 2021, 33, 901-916.	3.1	22
15	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. Nature Methods, 2021, 18, 156-164.	9.0	73
16	Combination of deep neural network with attention mechanism enhances the explainability of protein contact prediction. Proteins: Structure, Function and Bioinformatics, 2021, 89, 697-707.	1.5	25
17	VEHiCLE: a Variationally Encoded Hi-C Loss Enhancement algorithm for improving and generating Hi-C data. Scientific Reports, 2021, 11, 8880.	1.6	17
18	Improving deep learning-based protein distance prediction in CASP14. Bioinformatics, 2021, 37, 3190-3196.	1.8	11

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19	Protein model accuracy estimation empowered by deep learning and inter-residue distance prediction in CASP14. Scientific Reports, 2021, 11, 10943.	1.6	10
20	Sequence of the supernumerary B chromosome of maize provides insight into its drive mechanism and evolution. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	25
21	MULTICOM2 open-source protein structure prediction system powered by deep learning and distance prediction. Scientific Reports, 2021, 11, 13155.	1.6	0
22	DNCON2_Inter: predicting interchain contacts for homodimeric and homomultimeric protein complexes using multiple sequence alignments of monomers and deep learning. Scientific Reports, 2021, 11, 12295.	1.6	19
23	DeepComplex: A Web Server of Predicting Protein Complex Structures by Deep Learning Inter-chain Contact Prediction and Distance-Based Modelling. Frontiers in Molecular Biosciences, 2021, 8, 716973.	1.6	15
24	De novo centromere formation on chromosome fragments with an inactive centromere in maize (Zea) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.6	4
25	Prediction of protein assemblies, the next frontier: The <scp>CASP14â€CAPRI</scp> experiment. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1800-1823.	1.5	73
26	Four-Dimensional Chromosome Structure Prediction. International Journal of Molecular Sciences, 2021, 22, 9785.	1.8	6
27	Deep Learning-Based Recommender Systems. Advances in Intelligent Systems and Computing, 2021, , 1-23.	0.5	7
28	High-Performance Deep Learning Toolbox for Genome-Scale Prediction of Protein Structure and Function. , 2021, 2021, 46-57.		8
29	Structural and functional analysis of â€œnon-smellyâ€•proteins. Cellular and Molecular Life Sciences, 2020, 77, 2423-2440.	2.4	16
30	Analysis of several key factors influencing deep learning-based inter-residue contact prediction. Bioinformatics, 2020, 36, 1091-1098.	1.8	29
31	GNET2: an R package for constructing gene regulatory networks from transcriptomic data. Bioinformatics, 2020, 37, 2068-2069.	1.8	1
32	DeepCryoPicker: fully automated deep neural network for single protein particle picking in cryo-EM. BMC Bioinformatics, 2020, 21, 509.	1.2	30
33	SMISS: a protein function prediction server by integrating multiple sources. International Journal of Computational Intelligence in Bioinformatics and Systems Biology, 2020, 2, 22.	0.1	1
34	Inverse design of two-dimensional graphene/h-BN hybrids by a regressional and conditional GAN. Carbon, 2020, 169, 9-16.	5.4	35
35	CATA++: A Collaborative Dual Attentive Autoencoder Method for Recommending Scientific Articles. IEEE Access, 2020, 8, 183633-183648.	2.6	9
36	GSDB: a database of 3D chromosome and genome structures reconstructed from Hi-C data. BMC Molecular and Cell Biology, 2020, 21, 60.	1.0	12

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37	Heme oxygenase promotes Bâ€Rafâ€dependent melanosphere formation. Pigment Cell and Melanoma Research, 2020, 33, 850-868.	1.5	8
38	Deep Learning to Predict Protein Backbone Structure from High-Resolution Cryo-EM Density Maps. Scientific Reports, 2020, 10, 4282.	1.6	56
39	Magnitude of modulation of gene expression in aneuploid maize depends on the extent of genomic imbalance. Journal of Genetics and Genomics, 2020, 47, 93-103.	1.7	15
40	SAXSDom: Modeling multidomain protein structures using smallâ€angle Xâ€ray scattering data. Proteins: Structure, Function and Bioinformatics, 2020, 88, 775-787.	1.5	9
41	Bioinformatics Methods for Mass Spectrometry-Based Proteomics Data Analysis. International Journal of Molecular Sciences, 2020, 21, 2873.	1.8	134
42	Quantitative Proteomics Reveals Docosahexaenoic Acid-Mediated Neuroprotective Effects in Lipopolysaccharide-Stimulated Microglial Cells. Journal of Proteome Research, 2020, 19, 2236-2246.	1.8	11
43	The Gene Balance Hypothesis: Epigenetics and Dosage Effects in Plants. Methods in Molecular Biology, 2020, 2093, 161-171.	0.4	14
44	The MULTICOM Protein Structure Prediction Server Empowered by Deep Learning and Contact Distance Prediction. Methods in Molecular Biology, 2020, 2165, 13-26.	0.4	23
45	Deep Ranking in Template-free Protein Structure Prediction. , 2020, , .		5
46	Auto3DCryoMap: an automated particle alignment approach for 3D cryo-EM density map reconstruction. BMC Bioinformatics, 2020, 21, 534.	1.2	5
47	SMISS: a protein function prediction server by integrating multiple sources. International Journal of Computational Intelligence in Bioinformatics and Systems Biology, 2020, 2, 22.	0.1	0
48	The renoprotective effects of soy protein in the aging kidney. Medical Research Archives, 2020, 8, .	0.1	4
49	Large-Scale Machine Learning and Optimization for Bioinformatics Data Analysis. , 2020, , .		2
50	PairedFB: a full hierarchical Bayesian model for paired RNA-seq data with heterogeneous treatment effects. Bioinformatics, 2019, 35, 787-797.	1.8	5
51	Estimation of model accuracy in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1361-1377.	1.5	78
52	Blind prediction of homoâ€and heteroâ€protein complexes: The CASP13â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	1.5	99
53	A Super-Clustering Approach for Fully Automated Single Particle Picking in Cryo-EM. Genes, 2019, 10, 666.	1.0	12
54	Introduction to 2019 ACM-BCB Highlights Session. , 2019, , .		0

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55	Identification and localization of Tospovirus genus-wide conserved residues in 3D models of the nucleocapsid and the silencing suppressor proteins. Virology Journal, 2019, 16, 7.	1.4	14
56	AutoCryoPicker: an unsupervised learning approach for fully automated single particle picking in Cryo-EM images. BMC Bioinformatics, 2019, 20, 326.	1.2	33
57	An Overview of Methods for Reconstructing 3-D Chromosome and Genome Structures from Hi-C Data. Biological Procedures Online, 2019, 21, 7.	1.4	96
58	Protein tertiary structure modeling driven by deep learning and contact distance prediction in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1165-1178.	1.5	149
59	Hierarchical Reconstruction of High-Resolution 3D Models of Large Chromosomes. Scientific Reports, 2019, 9, 4971.	1.6	19
60	Bandgap prediction by deep learning in configurationally hybridized graphene and boron nitride. Npj Computational Materials, 2019, 5, .	3.5	86
61	Collaborative Attentive Autoencoder for Scientific Article Recommendation. , 2019, , .		3
62	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	3.8	261
63	GenomeFlow: a comprehensive graphical tool for modeling and analyzing 3D genome structure. Bioinformatics, 2019, 35, 1416-1418.	1.8	19
64	From Analysis of Ischemic Mouse Brain Proteome to Identification of Human Serum Clusterin as a Potential Biomarker for Severity of Acute Ischemic Stroke. Translational Stroke Research, 2019, 10, 546-556.	2.3	20
65	Proteomic Analysis and Biochemical Correlates of Mitochondrial Dysfunction after Low-Intensity Primary Blast Exposure. Journal of Neurotrauma, 2019, 36, 1591-1605.	1.7	24
66	Protein Tertiary Structure Modeling Driven by Deep Learning and Contact Distance Prediction in CASP13. , 2019, , .		0
67	DeepSF: deep convolutional neural network for mapping protein sequences to folds. Bioinformatics, 2018, 34, 1295-1303.	1.8	127
68	DNCON2: improved protein contact prediction using two-level deep convolutional neural networks. Bioinformatics, 2018, 34, 1466-1472.	1.8	148
69	Protein contact prediction by integrating deep multiple sequence alignments, coevolution and machine learning. Proteins: Structure, Function and Bioinformatics, 2018, 86, 84-96.	1.5	15
70	DeepSF. , 2018, , .		8
71	Localized Deep-CNN Structure for Face Recognition. , 2018, , .		3
72	DeepHCF: A Deep Learning Based Hybrid Collaborative Filtering Approach for Recommendation Systems. , 2018, , .		10

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73	Global impacts of chromosomal imbalance on gene expression in Arabidopsis and other taxa. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11321-E11330.	3.3	51
74	Localized Deep Norm-CNN Structure for Face Verification. , 2018, , .		1
75	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. Scientific Reports, 2018, 8, 9939.	1.6	19
76	A maximum likelihood algorithm for reconstructing 3D structures of human chromosomes from chromosomal contact data. BMC Genomics, 2018, 19, 161.	1.2	44
77	CONFOLD2: improved contact-driven ab initio protein structure modeling. BMC Bioinformatics, 2018, 19, 22.	1.2	66
78	QAcon: single model quality assessment using protein structural and contact information with machine learning techniques. Bioinformatics, 2017, 33, 586-588.	1.8	91
79	Assessing Predicted Contacts for Building Protein Three-Dimensional Models. Methods in Molecular Biology, 2017, 1484, 115-126.	0.4	0
80	3D Genome Structure Modeling by Lorentzian Objective Function. , 2017, , .		0
81	A deep auto-encoder model for gene expression prediction. BMC Genomics, 2017, 18, 845.	1.2	79
82	Improved protein structure reconstruction using secondary structures, contacts at higher distance thresholds, and non-contacts. BMC Bioinformatics, 2017, 18, 380.	1.2	16
83	Deep learning methods for protein torsion angle prediction. BMC Bioinformatics, 2017, 18, 417.	1.2	46
84	ClusterTAD: an unsupervised machine learning approach to detecting topologically associated domains of chromosomes from Hi-C data. BMC Bioinformatics, 2017, 18, 480.	1.2	38
85	3D genome structure modeling by Lorentzian objective function. Nucleic Acids Research, 2017, 45, 1049-1058.	6.5	50
86	Genetic dissection of Arabidopsis MAP kinase phosphatase 1-dependent PAMP-induced transcriptional responses. Journal of Experimental Botany, 2017, 68, 5207-5220.	2.4	8
87	Chromosome3D: reconstructing three-dimensional chromosomal structures from Hi-C interaction frequency data using distance geometry simulated annealing. BMC Genomics, 2016, 17, 886.	1.2	44
88	A Template-Based Protein Structure Reconstruction Method Using Deep Autoencoder Learning. Journal of Proteomics and Bioinformatics, 2016, 9, 306-313.	0.4	8
89	UniCon3D: de novo protein structure prediction using united-residue conformational search via stepwise, probabilistic sampling. Bioinformatics, 2016, 32, 2791-2799.	1.8	40
90	Massive integration of diverse protein quality assessment methods to improve template based modeling in <scp>CASP11</scp>. Proteins: Structure, Function and Bioinformatics, 2016, 84, 247-259.	1.5	26

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91	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.	1.5	148
92	A predictive model of gene expression using a deep learning framework. , 2016, , .		5
93	A Stochastic Point Cloud Sampling Method for Multi-Template Protein Comparative Modeling. Scientific Reports, 2016, 6, 25687.	1.6	8
94	GMOL: An Interactive Tool for 3D Genome Structure Visualization. Scientific Reports, 2016, 6, 20802.	1.6	25
95	DeepQA: improving the estimation of single protein model quality with deep belief networks. BMC Bioinformatics, 2016, 17, 495.	1.2	156
96	A dominant TRPV4 variant underlies osteochondrodysplasia in Scottish fold cats. Osteoarthritis and Cartilage, 2016, 24, 1441-1450.	0.6	32
97	Protein Residue Contacts and Prediction Methods. Methods in Molecular Biology, 2016, 1415, 463-476.	0.4	23
98	Does Concurrent Use of Some Botanicals Interfere with Treatment of Tuberculosis?. NeuroMolecular Medicine, 2016, 18, 483-486.	1.8	4
99	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	3.8	308
100	Effects of aged garlic extract and FruArg on gene expression and signaling pathways in lipopolysaccharide-activated microglial cells. Scientific Reports, 2016, 6, 35323.	1.6	18
101	Protein single-model quality assessment by feature-based probability density functions. Scientific Reports, 2016, 6, 23990.	1.6	77
102	ConEVA: a toolbox for comprehensive assessment of protein contacts. BMC Bioinformatics, 2016, 17, 517.	1.2	23
103	3Drefine: an interactive web server for efficient protein structure refinement. Nucleic Acids Research, 2016, 44, W406-W409.	6.5	339
104	FRAGSION: ultra-fast protein fragment library generation by IOHMM sampling. Bioinformatics, 2016, 32, 2059-2061.	1.8	8
105	What if we ignore the random effects when analyzing RNA-seq data in a multifactor experiment. Statistical Applications in Genetics and Molecular Biology, 2016, 15, 87-105.	0.2	21
106	MOGEN: a tool for reconstructing 3D models of genomes from chromosomal conformation capturing data. Bioinformatics, 2016, 32, 1286-1292.	1.8	48
107	An overview of bioinformatics methods for modeling biological pathways in yeast. Briefings in Functional Genomics, 2016, 15, 95-108.	1.3	18
108	Integrated protein function prediction by mining function associations, sequences, and proteinâ€“protein and geneâ€“gene interaction networks. Methods, 2016, 93, 84-91.	1.9	76

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109	Improving Protein Fold Recognition by Deep Learning Networks. Scientific Reports, 2015, 5, 17573.	1.6	107
110	De novo protein conformational sampling using a probabilistic graphical model. Scientific Reports, 2015, 5, 16332.	1.6	18
111	A large-scale conformation sampling and evaluation server for protein tertiary structure prediction and its assessment in CASP11. BMC Bioinformatics, 2015, 16, 337.	1.2	19
112	Messenger RNA profile analysis deciphers new Esrrb responsive genes in prostate cancer cells. BMC Molecular Biology, 2015, 16, 21.	3.0	13
113	Iterative reconstruction of three-dimensional models of human chromosomes from chromosomal contact data. BMC Bioinformatics, 2015, 16, 338.	1.2	15
114	Deciphering the association between gene function and spatial gene-gene interactions in 3D human genome conformation. BMC Genomics, 2015, 16, 880.	1.2	17
115	Genes targeted by the Hedgehog-signaling pathway can be regulated by Estrogen related receptor Î². BMC Molecular Biology, 2015, 16, 19.	3.0	20
116	Exploring soybean metabolic pathways based on probabilistic graphical model and knowledge-based methods. Eurasip Journal on Bioinformatics and Systems Biology, 2015, 2015, 5.	1.4	3
117	CONFOLD: Residue-residue contact-guidedab initioprotein folding. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1436-1449.	1.5	152
118	An Overview of Practical Applications of Protein Disorder Prediction and Drive for Faster, More Accurate Predictions. International Journal of Molecular Sciences, 2015, 16, 15384-15404.	1.8	15
119	From Gigabyte to Kilobyte: A Bioinformatics Protocol for Mining Large RNA-Seq Transcriptomics Data. PLoS ONE, 2015, 10, e0125000.	1.1	7
120	Inhibition of Hedgehog-Signaling Driven Genes in Prostate Cancer Cells by Sutherlandia frutescens Extract. PLoS ONE, 2015, 10, e0145507.	1.1	7
121	A Deep Learning Network Approach to <italic>ab initio</italic> Protein Secondary Structure Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 103-112.	1.9	254
122	Large-scale model quality assessment for improving protein tertiary structure prediction. Bioinformatics, 2015, 31, i116-i123.	1.8	55
123	An Improved Integration of Template-Based and Template-Free Protein Structure Modeling Methods and its Assessment in CASP11. Protein and Peptide Letters, 2015, 22, 586-593.	0.4	11
124	Proteomic Analysis of the Effects of Aged Garlic Extract and Its FruArg Component on Lipopolysaccharide-Induced Neuroinflammatory Response in Microglial Cells. PLoS ONE, 2014, 9, e113531.	1.1	24
125	Reconstruction of metabolic pathways by combining probabilistic graphical model-based and knowledge-based methods. BMC Proceedings, 2014, 8, S5.	1.8	12
126	NitroDIGE analysis reveals inhibition of protein S-nitrosylation by epigallocatechin gallates in lipopolysaccharide-stimulated microglial cells. Journal of Neuroinflammation, 2014, 11, 17.	3.1	26

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127	WeFold: A coopetition for protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1850-1868.	1.5	48
128	Large-scale reconstruction of 3D structures of human chromosomes from chromosomal contact data. Nucleic Acids Research, 2014, 42, e52-e52.	6.5	63
129	Enhancing HMM-based protein profile-profile alignment with structural features and evolutionary coupling information. BMC Bioinformatics, 2014, 15, 252.	1.2	8
130	SMOQ: a tool for predicting the absolute residue-specific quality of a single protein model with support vector machines. BMC Bioinformatics, 2014, 15, 120.	1.2	99
131	Designing and evaluating the MULTICOM protein local and global model quality prediction methods in the CASP10 experiment. BMC Structural Biology, 2014, 14, 13.	2.3	44
132	Proteomic Quantification and Site-Mapping of S-Nitrosylated Proteins Using Isobaric iodoTMT Reagents. Journal of Proteome Research, 2014, 13, 3200-3211.	1.8	104
133	Transcriptomic Analysis Identifies Gene Networks Regulated by Estrogen Receptor Î± (ERÎ±) and ERÎ² that Control Distinct Effects of Different Botanical Estrogens. Nuclear Receptor Signaling, 2014, 12, nrs.12001.	1.0	59
134	Improving protein fold recognition by random forest. BMC Bioinformatics, 2014, 15, S14.	1.2	51
135	The MULTICOM Protein Tertiary Structure Prediction System. Methods in Molecular Biology, 2014, 1137, 29-41.	0.4	8
136	MSACompro: Improving Multiple Protein Sequence Alignment by Predicted Structural Features. Methods in Molecular Biology, 2014, 1079, 273-283.	0.4	2
137	Three-Level Prediction of Protein Function by Combining Profile-Sequence Search, Profile-Profile Search, and Domain Co-Occurrence Networks. BMC Bioinformatics, 2013, 14, S3.	1.2	23
138	DNdisorder: predicting protein disorder using boosting and deep networks. BMC Bioinformatics, 2013, 14, 88.	1.2	74
139	Designing and benchmarking the MULTICOM protein structure prediction system. BMC Structural Biology, 2013, 13, 2.	2.3	25
140	Predicting gene regulatory networks of soybean nodulation from RNA-Seq transcriptome data. BMC Bioinformatics, 2013, 14, 278.	1.2	22
141	A study and benchmark of DNcon: a method for protein residue-residue contact prediction using deep networks. BMC Bioinformatics, 2013, 14, S12.	1.2	28
142	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	9.0	789
143	Aberrant Epigenetic Gene Regulation in Lymphoid Malignancies. Seminars in Hematology, 2013, 50, 38-47.	1.8	17
144	Dosage compensation and inverse effects in triple X metafemales of Drosophila. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7383-7388.	3.3	51

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145	3Drefine: Consistent protein structure refinement by optimizing hydrogen bonding network and atomicâ€level energy minimization. Proteins: Structure, Function and Bioinformatics, 2013, 81, 119-131.	1.5	154
146	Protein Structure Refinement by Iterative Fragment Exchange. , 2013, , .		3
147	Automated protein structure refinement using i3Drefine software and its assessment in CASP10. , 2013, , .		0
148	Male-specific lethal complex in Drosophila counteracts histone acetylation and does not mediate dosage compensation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E808-17.	3.3	46
149	Differential effect of aneuploidy on the X chromosome and genes with sex-biased expression inDrosophila. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 16514-16519.	3.3	41
150	i3Drefine Software for Protein 3D Structure Refinement and Its Assessment in CASP10. PLoS ONE, 2013, 8, e69648.	1.1	47
151	The Properties of Genome Conformation and Spatial Gene Interaction and Regulation Networks of Normal and Malignant Human Cell Types. PLoS ONE, 2013, 8, e58793.	1.1	35
152	Predicting Protein Model Quality from Sequence Alignments by Support Vector Machines. Journal of Proteomics and Bioinformatics, 2013, s9, .	0.4	4
153	RECURSIVE PROTEIN MODELING: A DIVIDE AND CONQUER STRATEGY FOR PROTEIN STRUCTURE PREDICTION AND ITS CASE STUDY IN CASP9. Journal of Bioinformatics and Computational Biology, 2012, 10, 1242003.	0.3	9
154	Predicting protein residueâ€“residue contacts using deep networks and boosting. Bioinformatics, 2012, 28, 3066-3072.	1.8	149
155	A comprehensive overview of computational protein disorder prediction methods. Molecular BioSystems, 2012, 8, 114-121.	2.9	92
156	The MULTICOM toolbox for protein structure prediction. BMC Bioinformatics, 2012, 13, 65.	1.2	30
157	Reconstructing differentially co-expressed gene modules and regulatory networks of soybean cells. BMC Genomics, 2012, 13, 437.	1.2	21
158	Soybean Knowledge Base (SoyKB): a web resource for soybean translational genomics. BMC Genomics, 2012, 13, S15.	1.2	93
159	An iterative selfâ€refining and selfâ€evaluating approach for protein model quality estimation. Protein Science, 2012, 21, 142-151.	3.1	4
160	Evolutionary dynamics of protein domain architecture in plants. BMC Evolutionary Biology, 2012, 12, 6.	3.2	27
161	Recursive protein modeling: A divide and conquer strategy for protein structure prediction and its case study in CASP9. , 2011, , .		4
162	A Protein Domain Co-Occurrence Network Approach for Predicting Protein Function and Inferring Species Phylogeny. PLoS ONE, 2011, 6, e17906.	1.1	30

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163	MSACompro: protein multiple sequence alignment using predicted secondary structure, solvent accessibility, and residue-residue contacts. BMC Bioinformatics, 2011, 12, 472.	1.2	25
164	A conformation ensemble approach to protein residue-residue contact. BMC Structural Biology, 2011, 11, 38.	2.3	15
165	DoBo: Protein domain boundary prediction by integrating evolutionary signals and machine learning. BMC Bioinformatics, 2011, 12, 43.	1.2	52
166	APOLLO: a quality assessment service for single and multiple protein models. Bioinformatics, 2011, 27, 1715-1716.	1.8	89
167	Enzymatic Activity of the Soybean Ecto-Apyrase GS52 Is Essential for Stimulation of Nodulation Â Â. Plant Physiology, 2011, 155, 1988-1998.	2.3	38
168	INTRINSICALLY DISORDERED PROTEINS: ANALYSIS, PREDICTION, SIMULATION, AND BIOLOGY. , 2011, , .		0
169	SoyDB: a knowledge database of soybean transcription factors. BMC Plant Biology, 2010, 10, 14.	1.6	104
170	SeqRate: sequence-based protein folding type classification and rates prediction. BMC Bioinformatics, 2010, 11, S1.	1.2	26
171	Genome sequence of the palaeopolyploid soybean. Nature, 2010, 463, 178-183.	13.7	3,854
172	MULTICOM: a multi-level combination approach to protein structure prediction and its assessments in CASP8. Bioinformatics, 2010, 26, 882-888.	1.8	89
173	Root hair systems biology. Trends in Plant Science, 2010, 15, 641-650.	4.3	125
174	A Scalable and Integrative System for Pathway Bioinformatics and Systems Biology. Advances in Experimental Medicine and Biology, 2010, 680, 523-534.	0.8	0
175	Sequence-Based Prediction of Protein Folding Rates Using Contacts, Secondary Structures and Support Vector Machines. , 2009, , .		2
176	NNcon: improved protein contact map prediction using 2D-recursive neural networks. Nucleic Acids Research, 2009, 37, W515-W518.	6.5	124
177	PreDisorder: ab initio sequence-based prediction of protein disordered regions. BMC Bioinformatics, 2009, 10, 436.	1.2	92
178	Evaluating the absolute quality of a single protein model using structural features and support vector machines. Proteins: Structure, Function and Bioinformatics, 2009, 75, 638-647.	1.5	94
179	Prediction of global and local quality of CASP8 models by MULTICOM series. Proteins: Structure, Function and Bioinformatics, 2009, 77, 181-184.	1.5	66
180	The polycystic kidney disease-related proteins Bicc1 and SamCystin interact. Biochemical and Biophysical Research Communications, 2009, 383, 16-21.	1.0	41

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181	A multi-template combination algorithm for protein comparative modeling. BMC Structural Biology, 2008, 8, 18.	2.3	83
182	HMMEditor: a visual editing tool for profile hidden Markov model. BMC Genomics, 2008, 9, S8.	1.2	14
183	Protein disorder prediction at multiple levels of sensitivity and specificity. BMC Genomics, 2008, 9, S9.	1.2	47
184	Machine Learning Methods for Protein Structure Prediction. IEEE Reviews in Biomedical Engineering, 2008, 1, 41-49.	13.1	99
185	TMBpro: secondary structure, Î²-contact and tertiary structure prediction of transmembrane Î²-barrel proteins. Bioinformatics, 2008, 24, 513-520.	1.8	75
186	A neural network approach to ordinal regression. , 2008, , .		42
187	DOMAC: an accurate, hybrid protein domain prediction server. Nucleic Acids Research, 2007, 35, W354-W356.	6.5	40
188	Ty3 Capsid Mutations Reveal Early and Late Functions of the Amino-Terminal Domain. Journal of Virology, 2007, 81, 6957-6972.	1.5	29
189	Assessment of predictions submitted for the CASP7 domain prediction category. Proteins: Structure, Function and Bioinformatics, 2007, 69, 137-151.	1.5	51
190	Improved residue contact prediction using support vector machines and a large feature set. BMC Bioinformatics, 2007, 8, 113.	1.2	192
191	A machine learning information retrieval approach to protein fold recognition. Bioinformatics, 2006, 22, 1456-1463.	1.8	203
192	DOMpro: Protein Domain Prediction Using Profiles, Secondary Structure, Relative Solvent Accessibility, and Recursive Neural Networks. Data Mining and Knowledge Discovery, 2006, 13, 1-10.	2.4	93
193	Functional Census of Mutation Sequence Spaces: The Example of p53 Cancer Rescue Mutants. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006, 3, 114-125.	1.9	28
194	Accurate Prediction of Protein Disordered Regions by Mining Protein Structure Data. Data Mining and Knowledge Discovery, 2005, 11, 213-222.	2.4	187
195	Large-scale prediction of disulphide bridges using kernel methods, two-dimensional recursive neural networks, and weighted graph matching. Proteins: Structure, Function and Bioinformatics, 2005, 62, 617-629.	1.5	117
196	Prediction of protein stability changes for single-site mutations using support vector machines. Proteins: Structure, Function and Bioinformatics, 2005, 62, 1125-1132.	1.5	784
197	Sigmoid: A Software Infrastructure for Pathway Bioinformatics and Systems Biology. IEEE Intelligent Systems, 2005, 20, 68-75.	4.0	8
198	Three-stage prediction of protein Â-sheets by neural networks, alignments and graph algorithms. Bioinformatics, 2005, 21, i75-i84.	1.8	104