Yuedong Yang

List of Publications by Year
in descending order

140	7,213	81434	81351
papers	citations	41 h-index	76 g-index

169	169	169	8171
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Mendelian randomization study reveals a population-specific putative causal effect of type 2 diabetes in risk of cataract. International Journal of Epidemiology, 2022, 50, 2024-2037.	0.9	11
2	Cancer survival prognosis with Deep Bayesian Perturbation Cox Network. Computers in Biology and Medicine, 2022, 141, 105012.	3.9	9
3	A coarseâ€refine segmentation network for COVIDâ€19 CT images. IET Image Processing, 2022, 16, 333-343.	1.4	8
4	A robust and scalable graph neural network for accurate single-cell classification. Briefings in Bioinformatics, 2022, 23, .	3.2	15
5	AlphaFold2-aware proteinâ€“DNA binding site prediction using graph transformer. Briefings in Bioinformatics, 2022, 23, .	3.2	48
6	Structure-Aware Multimodal Deep Learning for Drugâ€“Protein Interaction Prediction. Journal of Chemical Information and Modeling, 2022, 62, 1308-1317.	2.5	28
7	Cardiac ISL1-Interacting Protein, a Cardioprotective Factor, Inhibits the Transition From Cardiac Hypertrophy to Heart Failure. Frontiers in Cardiovascular Medicine, 2022, 9, 857049.	1.1	0
8	Optimization Extraction and Antioxidant Activity of Crude Polysaccharide from Chestnut Mushroom (Agrocybe aegerita) by Accelerated Solvent Extraction Combined with Response Surface Methodology (ASE-RSM). Molecules, 2022, 27, 2380.	1.7	14
9	A parameter-free deep embedded clustering method for single-cell RNA-seq data. Briefings in Bioinformatics, 2022, 23, .	3.2	6
10	Subgraph-aware Few-Shot Inductive Link Prediction via Meta-Learning. IEEE Transactions on Knowledge and Data Engineering, 2022, , 1-1.	4.0	3
11	Deep learning driven biosynthetic pathways navigation for natural products with BioNavi-NP. Nature Communications, 2022, 13, .	5.8	35
12	A Multi-constraint Deep Semi-supervised Learning Method for Ovarian Cancer Prognosis Prediction. Lecture Notes in Computer Science, 2022, , 219-229.	1.0	1
13	Identification of Putative Causal Relationships Between Type 2 Diabetes and Blood-Based Biomarkers in East Asians by Mendelian Randomization. American Journal of Epidemiology, 2022, 191, 1867-1876.	1.6	5
14	Communicative Subgraph Representation Learning for Multi-Relational Inductive Drug-Gene Interaction Prediction. , 2022, , .		2
15	PharmKG: a dedicated knowledge graph benchmark for bomedical data mining. Briefings in Bioinformatics, 2021, 22, .	3.2	70
16	EVLncRNAs 2.0: an updated database of manually curated functional long non-coding RNAs validated by low-throughput experiments. Nucleic Acids Research, 2021, 49, D86-D91.	6.5	42
17	Systematic analysis to identify transcriptome-wide dysregulation of Alzheimerâ€™s disease in genes and isoforms. Human Genetics, 2021, 140, 609-623.	1.8	13
18	scAdapt: virtual adversarial domain adaptation network for single cell RNA-seq data classification across platforms and species. Briefings in Bioinformatics, 2021, 22, .	3.2	13

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19	Deep Learning Enables Accurate Diagnosis of Novel Coronavirus (COVID-19) With CT Images. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2775-2780.	1.9	531
20	Structure-aware protein solubility prediction from sequence through graph convolutional network and predicted contact map. Journal of Cheminformatics, 2021, 13, 7.	2.8	57
21	Accurately Discriminating COVID-19 from Viral and Bacterial Pneumonia According to CT Images Via Deep Learning. Interdisciplinary Sciences, Computational Life Sciences, 2021, 13, 273-285.	2.2	19
22	Prioritization of schizophrenia risk genes from GWAS results by integrating multi-omics data. Translational Psychiatry, 2021, 11, 175.	2.4	10
23	Meta Learning for Low-Resource Molecular Optimization. Journal of Chemical Information and Modeling, 2021, 61, 1627-1636.	2.5	17
24	Rapid isolation and immune profiling of SARS-CoV-2 specific memory B cell in convalescent COVID-19 patients via LIBRA-seq. Signal Transduction and Targeted Therapy, 2021, 6, 195.	7.1	45
25	Imputing single-cell RNA-seq data by combining graph convolution and autoencoder neural networks. IScience, 2021, 24, 102393.	1.9	50
26	Integrating multi-omics data through deep learning for accurate cancer prognosis prediction. Computers in Biology and Medicine, 2021, 134, 104481.	3.9	68
27	Learning Attributed Graph Representation with Communicative Message Passing Transformer. , 2021, , .		19
28	Predicting bladder cancer prognosis by integrating multi-omics data through a transfer learning-based Cox proportional hazards network. CCF Transactions on High Performance Computing, 2021, 3, 311-319.	1.1	6
29	Structure-aware proteinâ€“protein interaction site prediction using deep graph convolutional network. Bioinformatics, 2021, 38, 125-132.	1.8	64
30	Identification of Novel Single-Nucleotide Variants With Potential of Mediating Malfunction of MicroRNA in Congenital Heart Disease. Frontiers in Cardiovascular Medicine, 2021, 8, 739598.	1.1	0
31	An Adaptive Transfer-Learning-Based Deep Cox Neural Network for Hepatocellular Carcinoma Prognosis Prediction. Frontiers in Oncology, 2021, 11, 692774.	1.3	7
32	Reply to: â€œA global survey of alternative splicing of HBV transcriptome using long-read sequencingâ€• Journal of Hepatology, 2021, , .	1.8	0
33	Exploring complex and heterogeneous correlations on hypergraph for the prediction of drug-target interactions. Patterns, 2021, 2, 100390.	3.1	9
34	Deep scaffold hopping with multimodal transformer neural networks. Journal of Cheminformatics, 2021, 13, 87.	2.8	24
35	Multi-omics Cancer Prognosis Analysis Based on Graph Convolution Network. , 2021, , .		5
36	DGAT-onco: A differential analysis method to detect oncogenes by integrating functional information of mutations. , 2021, , .		0

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37	SEGEM: a Fast and Accurate Automated Protein Backbone Structure Modeling Method for Cryo-EM. , 2021, , .		2
38	DeepANIS: Predicting antibody paratope from concatenated CDR sequences by integrating bidirectional long-short-term memory and transformer neural networks. , 2021, , .		1
39	Getting to Know Your Neighbor: Protein Structure Prediction Comes of Age with Contextual Machine Learning. Journal of Computational Biology, 2020, 27, 796-814.	0.8	15
40	All-Atom Knowledge-Based Potential for RNA Structure Discrimination Based on the Distance-Scaled Finite Ideal-Gas Reference State. Journal of Computational Biology, 2020, 27, 856-867.	0.8	15
41	Predicting Retrosynthetic Reactions Using Self-Corrected Transformer Neural Networks. Journal of Chemical Information and Modeling, 2020, 60, 47-55.	2.5	112
42	SPOTâ€Fold: Fragmentâ€Free Protein Structure Prediction Guided by Predicted Backbone Structure and Contact Map. Journal of Computational Chemistry, 2020, 41, 745-750.	1.5	9
43	To Improve Protein Sequence Profile Prediction through Image Captioning on Pairwise Residue Distance Map. Journal of Chemical Information and Modeling, 2020, 60, 391-399.	2.5	33
44	Imputing missing RNA-sequencing data from DNA methylation by using a transfer learningâ€“based neural network. GigaScience, 2020, 9, .	3.3	33
45	Accurate prediction of genome-wide RNA secondary structure profile based on extreme gradient boosting. Bioinformatics, 2020, 36, 4576-4582.	1.8	7
46	Moraxella catarrhalis phase-variable loci show differences in expression during conditions relevant to disease. PLoS ONE, 2020, 15, e0234306.	1.1	5
47	Accurately Predicting Mutation-Caused Stability Changes from Protein Sequences Using Extreme Gradient Boosting. Journal of Chemical Information and Modeling, 2020, 60, 2388-2395.	2.5	22
48	Predicting drugâ€“protein interaction using quasi-visual question answering system. Nature Machine Intelligence, 2020, 2, 134-140.	8.3	154
49	Accurately Clustering Single-cell RNA-seq data by Capturing Structural Relations between Cells through Graph Convolutional Network. , 2020, , .		26
50	Communicative Representation Learning on Attributed Molecular Graphs. , 2020, , .		50
51	An End-to-end Oxford Nanopore Basecaller Using Convolution-augmented Transformer. , 2020, , .		11
52	DLIGAND2: an improved knowledge-based energy function for proteinâ€“ligand interactions using the distance-scaled, finite, ideal-gas reference state. Journal of Cheminformatics, 2019, 11, 52.	2.8	35
53	Assessing predictions of the impact of variants on splicing in CAGI5. Human Mutation, 2019, 40, 1215-1224.	1.1	18
54	Predicting functional long non-coding RNAs validated by low throughput experiments. RNA Biology, 2019, 16, 1555-1564.	1.5	6

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55	LSA: a local-weighted structural alignment tool for pharmaceutical virtual screening. RSC Advances, 2019, 9, 3912-3917.	1.7	2
56	SPOT-Peptide: Template-Based Prediction of Peptide-Binding Proteins and Peptide-Binding Sites. Journal of Chemical Information and Modeling, 2019, 59, 924-930.	2.5	19
57	Identifying Structureâ€“Property Relationships through SMILES Syntax Analysis with Self-Attention Mechanism. Journal of Chemical Information and Modeling, 2019, 59, 914-923.	2.5	78
58	Predicting the change of exon splicing caused by genetic variant using support vector regression. Human Mutation, 2019, 40, 1235-1242.	1.1	6
59	Experimentally Validated Plant lncRNAs in EVLncRNAs Database. Methods in Molecular Biology, 2019, 1933, 431-437.	0.4	5
60	QBMG: quasi-biogenic molecule generator with deep recurrent neural network. Journal of Cheminformatics, 2019, 11, 5.	2.8	52
61	Identifying Common Genes, Cell Types and Brain Regions Between Diseases of the Nervous System. Frontiers in Genetics, 2019, 10, 1202.	1.1	4
62	Improving prediction of protein secondary structure, backbone angles, solvent accessibility and contact numbers by using predicted contact maps and an ensemble of recurrent and residual convolutional neural networks. Bioinformatics, 2019, 35, 2403-2410.	1.8	145
63	Selfâ€derived structureâ€disrupting peptides targeting methionine aminopeptidase in pathogenic bacteria: a new strategy to generate antimicrobial peptides. FASEB Journal, 2019, 33, 2095-2104.	0.2	7
64	Sixty-five years of the long march in protein secondary structure prediction: the final stretch?. Briefings in Bioinformatics, 2018, 19, bbw129.	3.2	168
65	SPIN2: Predicting sequence profiles from protein structures using deep neural networks. Proteins: Structure, Function and Bioinformatics, 2018, 86, 629-633.	1.5	62
66	EVLncRNAs: a manually curated database for long non-coding RNAs validated by low-throughput experiments. Nucleic Acids Research, 2018, 46, D100-D105.	6.5	75
67	Transcriptome profiling of lentil (Lens culinaris) through the first 24 hours of Ascochyta lentis infection reveals key defence response genes. BMC Genomics, 2018, 19, 108.	1.2	53
68	A survey of Type III restriction-modification systems reveals numerous, novel epigenetic regulators controlling phase-variable regulons; phasevarions. Nucleic Acids Research, 2018, 46, 3532-3542.	6.5	43
69	Quantitative mapping of genetic similarity in human heritable diseases by shared mutations. Human Mutation, 2018, 39, 292-301.	1.1	8
70	Structure-based prediction of proteinâ€“ peptide binding regions using Random Forest. Bioinformatics, 2018, 34, 477-484.	1.8	62
71	Bâ€factor profile prediction for RNA flexibility using support vector machines. Journal of Computational Chemistry, 2018, 39, 407-411.	1.5	13
72	Singleâ€sequenceâ€based prediction of protein secondary structures and solvent accessibility by deep wholeâ€sequence learning. Journal of Computational Chemistry, 2018, 39, 2210-2216.	1.5	84

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73	YesU from Bacillus subtilis preferentially binds fucosylated glycans. Scientific Reports, 2018, 8, 13139.	1.6	7
74	Predicting lysineâ€malonylation sites of proteins using sequence and predicted structural features. Journal of Computational Chemistry, 2018, 39, 1757-1763.	1.5	30
75	Bias-Exchange Metadynamics Simulation of Membrane Permeation of 20 Amino Acids. International Journal of Molecular Sciences, 2018, 19, 885.	1.8	14
76	Grid-based prediction of torsion angle probabilities of protein backbone and its application to discrimination of protein intrinsic disorder regions and selection of model structures. BMC Bioinformatics, 2018, 19, 29.	1.2	17
77	Detecting Proline and Non-Proline Cis Isomers in Protein Structures from Sequences Using Deep Residual Ensemble Learning. Journal of Chemical Information and Modeling, 2018, 58, 2033-2042.	2.5	13
78	Computational Prediction of Carbohydrateâ€Binding Proteins and Binding Sites. Current Protocols in Protein Science, 2018, 94, e75.	2.8	5
79	Accurate prediction of protein contact maps by coupling residual two-dimensional bidirectional long short-term memory with convolutional neural networks. Bioinformatics, 2018, 34, 4039-4045.	1.8	155
80	Improving protein disorder prediction by deep bidirectional long short-term memory recurrent neural networks. Bioinformatics, 2017, 33, 685-692.	1.8	235
81	LRFragLib: an effective algorithm to identify fragments for de novo protein structure prediction. Bioinformatics, 2017, 33, 677-684.	1.8	10
82	A heuristic for the time constrained asymmetric linear sum assignment problem. Journal of Combinatorial Optimization, 2017, 33, 551-566.	0.8	4
83	regSNPs-splicing: a tool for prioritizing synonymous single-nucleotide substitution. Human Genetics, 2017, 136, 1279-1289.	1.8	27
84	Capturing non-local interactions by long short-term memory bidirectional recurrent neural networks for improving prediction of protein secondary structure, backbone angles, contact numbers and solvent accessibility. Bioinformatics, 2017, 33, 2842-2849.	1.8	300
85	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. Human Mutation, 2017, 38, 1042-1050.	1.1	13
86	SPOT-ligand 2: improving structure-based virtual screening by binding-homology search on an expanded structural template library. Bioinformatics, 2017, 33, 1238-1240.	1.8	18
87	Systems-level understanding of ethanol-induced stresses and adaptation in E. coli. Scientific Reports, 2017, 7, 44150.	1.6	43
88	Investigating DNA-, RNA-, and protein-based features as a means to discriminate pathogenic synonymous variants. Human Mutation, 2017, 38, 1336-1347.	1.1	37
89	Improving the detection of pathways in genome-wide association studies by combined effects of SNPs from Linkage Disequilibrium blocks. Scientific Reports, 2017, 7, 3512.	1.6	9
90	Genome-scale characterization of RNA tertiary structures and their functional impact by RNA solvent accessibility prediction. Rna, 2017, 23, 14-22.	1.6	28

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91	SPIDER2: A Package to Predict Secondary Structure, Accessible Surface Area, and Main-Chain Torsional Angles by Deep Neural Networks. Methods in Molecular Biology, 2017, 1484, 55-63.	0.4	137
92	ExonImpact: Prioritizing Pathogenic Alternative Splicing Events. Human Mutation, 2017, 38, 16-24.	1.1	12
93	JAK2-binding long noncoding RNA promotes breast cancer brain metastasis. Journal of Clinical Investigation, 2017, 127, 4498-4515.	3.9	177
94	Structural signatures of thermal adaptation of bacterial ribosomal RNA, transfer RNA, and messenger RNA. PLoS ONE, 2017, 12, e0184722.	1.1	15
95	Investigation the Possibility of Using Peptides with a Helical Repeating Pattern of Hydro-Phobic and Hydrophilic Residues to Inhibit IL-10. PLoS ONE, 2016, 11, e0153939.	1.1	14
96	s<scp>DFIRE</scp>: Sequenceâ€specific statistical energy function for protein structure prediction by decoy selections. Journal of Computational Chemistry, 2016, 37, 1119-1124.	1.5	16
97	SPOTâ€Ligand: Fast and effective structureâ€based virtual screening by binding homology search according to ligand and receptor similarity. Journal of Computational Chemistry, 2016, 37, 1734-1739.	1.5	15
98	Enrichment of SNPs in Functional Categories Reveals Genes Affecting Complex Traits. Human Mutation, 2016, 37, 820-826.	1.1	3
99	Sequenceâ€based prediction of proteinâ€“peptide binding sites using support vector machine. Journal of Computational Chemistry, 2016, 37, 1223-1229.	1.5	81
100	Infectivity of Plasmodium falciparum in Malaria-Naive Individuals Is Related to Knob Expression and Cytoadherence of the Parasite. Infection and Immunity, 2016, 84, 2689-2696.	1.0	14
101	Effective protein conformational sampling based on predicted torsion angles. Journal of Computational Chemistry, 2016, 37, 976-980.	1.5	2
102	Optimal secretion of alkali-tolerant xylanase in Bacillus subtilis by signal peptide screening. Applied Microbiology and Biotechnology, 2016, 100, 8745-8756.	1.7	35
103	Predicting the errors of predicted local backbone angles and non-local solvent- accessibilities of proteins by deep neural networks. Bioinformatics, 2016, 32, 3768-3773.	1.8	25
104	Sequence-Based Prediction of Proteinâ€“Carbohydrate Binding Sites Using Support Vector Machines. Journal of Chemical Information and Modeling, 2016, 56, 2115-2122.	2.5	59
105	Natural protein sequences are more intrinsically disordered than random sequences. Cellular and Molecular Life Sciences, 2016, 73, 2949-2957.	2.4	37
106	Highly accurate sequence-based prediction of half-sphere exposures of amino acid residues in proteins. Bioinformatics, 2016, 32, 843-849.	1.8	79
107	Fast and accurate non-sequential protein structure alignment using a new asymmetric linear sum assignment heuristic. Bioinformatics, 2016, 32, 370-377.	1.8	19
108	Sequence and Structure Analysis of Biological Molecules Based on Computational Methods. BioMed Research International, 2015, 2015, 1-3.	0.9	0

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109	DDIG-in: detecting disease-causing genetic variations due to frameshifting indels and nonsense mutations employing sequence and structural properties at nucleotide and protein levels. Bioinformatics, 2015, 31, 1599-1606.	1.8	52
110	Improving prediction of secondary structure, local backbone angles and solvent accessible surface area of proteins by iterative deep learning. Scientific Reports, 2015, 5, 11476.	1.6	290
111	Advancing the Accuracy of Protein Fold Recognition by Utilizing Profiles From Hidden Markov Models. IEEE Transactions on Nanobioscience, 2015, 14, 761-772.	2.2	34
112	Predicting DNA-Binding Proteins and Binding Residues by Complex Structure Prediction and Application to Human Proteome. PLoS ONE, 2014, 9, e96694.	1.1	32
113	Direct prediction of profiles of sequences compatible with a protein structure by neural networks with fragment-based local and energy-based nonlocal profiles. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2565-2573.	1.5	46
114	Predicting backbone CÎ± angles and dihedrals from protein sequences by stacked sparse autoâ€•encoder deep neural network. Journal of Computational Chemistry, 2014, 35, 2040-2046.	1.5	133
115	Carbohydrate-binding protein identification by coupling structural similarity searching with binding affinity prediction. Journal of Computational Chemistry, 2014, 35, 2177-2183.	1.5	20
116	Prediction and validation of the unexplored RNAâ€•binding protein atlas of the human proteome. Proteins: Structure, Function and Bioinformatics, 2014, 82, 640-647.	1.5	22
117	SPOT-Seq-RNA: Predicting Proteinâ€“RNA Complex Structure and RNA-Binding Function by Fold Recognition and Binding Affinity Prediction. Methods in Molecular Biology, 2014, 1137, 119-130.	0.4	39
118	DDIG-in: discriminating between disease-associated and neutral non-frameshifting micro-indels. Genome Biology, 2013, 14, R23.	13.9	63
119	Structural insights into the histone H1-nucleosome complex. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19390-19395.	3.3	178
120	The Role of Semidisorder in Temperature Adaptation of Bacterial FlgM Proteins. Biophysical Journal, 2013, 105, 2598-2605.	0.2	5
121	Energy Functions in De Novo Protein Design: Current Challenges and Future Prospects. Annual Review of Biophysics, 2013, 42, 315-335.	4.5	75
122	Prediction of RNA binding proteins comes of age from low resolution to high resolution. Molecular BioSystems, 2013, 9, 2417.	2.9	37
123	Templateâ€•based structure prediction and classification of transcription factors in Arabidopsis thaliana. Protein Science, 2012, 21, 828-838.	3.1	11
124	A new sizeâ€•independent score for pairwise protein structure alignment and its application to structure classification and nucleicâ€•acid binding prediction. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2080-2088.	1.5	69
125	SPINE X: Improving protein secondary structure prediction by multistep learning coupled with prediction of solvent accessible surface area and backbone torsion angles. Journal of Computational Chemistry, 2012, 33, 259-267.	1.5	209
126	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	2.0	131

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127	Trends in template/fragment-free protein structure prediction. Theoretical Chemistry Accounts, 2011, 128, 3-16.	0.5	48
128	Highly accurate and high-resolution function prediction of RNA binding proteins by fold recognition and binding affinity prediction. RNA Biology, 2011, 8, 988-996.	1.5	53
129	Improving protein fold recognition and template-based modeling by employing probabilistic-based matching between predicted one-dimensional structural properties of query and corresponding native properties of templates. Bioinformatics, 2011, 27, 2076-2082.	1.8	288
130	Structure-based prediction of RNA-binding domains and RNA-binding sites and application to structural genomics targets. Nucleic Acids Research, 2011, 39, 3017-3025.	6.5	100
131	Improving computational protein design by using structureâ€derived sequence profile. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2338-2348.	1.5	23
132	Structure-based prediction of DNA-binding proteins by structural alignment and a volume-fraction corrected DFIRE-based energy function. Bioinformatics, 2010, 26, 1857-1863.	1.8	81
133	Predicting Continuous Local Structure and the Effect of Its Substitution for Secondary Structure in Fragment-Free Protein Structure Prediction. Structure, 2009, 17, 1515-1527.	1.6	108
134	An allâ€atom knowledgeâ€based energy function for proteinâ€DNA threading, docking decoy discrimination, and prediction of transcriptionâ€factor binding profiles. Proteins: Structure, Function and Bioinformatics, 2009, 76, 718-730.	1.5	46
135	Specific interactions for ab initio folding of protein terminal regions with secondary structures. Proteins: Structure, Function and Bioinformatics, 2008, 72, 793-803.	1.5	219
136	Ab initio folding of terminal segments with secondary structures reveals the fine difference between two closely related allâ€atom statistical energy functions. Protein Science, 2008, 17, 1212-1219.	3.1	131
137	Genetic algorithms for protein conformation sampling and optimization in a discrete backbone dihedral angle space. Journal of Computational Chemistry, 2006, 27, 1593-1602.	1.5	14
138	Structural basis for SUMO-E2 interaction revealed by a complex model using docking approach in combination with NMR data. Proteins: Structure, Function and Bioinformatics, 2005, 61, 1050-1058.	1.5	9
139	Solution Structure of AF-6 PDZ Domain and Its Interaction with the C-terminal Peptides from Neurexin and Bcr. Journal of Biological Chemistry, 2005, 280, 13841-13847.	1.6	25
140	Transition State Ensemble for the Folding of B Domain of Protein A:â€‰ A Comparison of Distributed Molecular Dynamics Simulations with Experiments. Journal of Physical Chemistry B, 2005, 109, 23645-23654.	1.2	15