Daisuke Kihara

List of Publications by Year
in descending order

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206	7,828	57631	74018
papers	citations	44 h-index	75 g-index

223	223	223	6993
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Benchmarking of structure refinement methods for protein complex models. Proteins: Structure, Function and Bioinformatics, 2022, 90, 83-95.	1.5	3
2	Surface-based protein domains retrieval methods from a SHREC2021 challenge. Journal of Molecular Graphics and Modelling, 2022, 111, 108103.	1.3	2
3	Deep learning-based local quality estimation for protein structure models from cryo-EM maps. Biophysical Journal, 2022, 121, 129a.	0.2	0
4	OC_Finder: Osteoclast Segmentation, Counting, and Classification Using Watershed and Deep Learning. Frontiers in Bioinformatics, 2022, 2, .	1.0	5
5	Real-time structure search and structure classification for AlphaFold protein models. Communications Biology, 2022, 5, 316.	2.0	34
6	Using steered molecular dynamic tension for assessing quality of computational protein structure models. Journal of Computational Chemistry, 2022, , .	1.5	0
7	ContactPFP: Protein Function Prediction Using Predicted Contact Information. Frontiers in Bioinformatics, 2022, 2, .	1.0	6
8	Multi-level analysis of intrinsically disordered protein docking methods. Methods, 2022, 204, 55-63.	1.9	3
9	SHREC 2022: Proteinâ€“ligand binding site recognition. Computers and Graphics, 2022, 107, 20-31.	1.4	10
10	Current progress and future perspectives of polypharmacology : From the view of non-small cell lung cancer. Seminars in Cancer Biology, 2021, 68, 84-91.	4.3	21
11	EnAET: A Self-Trained Framework for Semi-Supervised and Supervised Learning With Ensemble Transformations. IEEE Transactions on Image Processing, 2021, 30, 1639-1647.	6.0	36
12	Genotype & phenotype in Lowe Syndrome: specificOCRL1patient mutations differentially impact cellular phenotypes. Human Molecular Genetics, 2021, 30, 198-212.	1.4	8
13	Turning Points in My Career Path. Seibutsu Butsuri, 2021, 61, 044-045.	0.0	0
14	Super Resolution Cryo-EM Maps with 3D Deep Generative Networks. Biophysical Journal, 2021, 120, 283a.	0.2	8
15	Vesper: Global and Local Cryo-Em Map Alignment and Database Search using Local Density Vectors. Biophysical Journal, 2021, 120, 84a.	0.2	0
16	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. Nature Methods, 2021, 18, 156-164.	9.0	73
17	Detecting Protein and DNA/RNA Structures in Cryo-Em Maps of Intermediate Resolution using Deep Learning. Biophysical Journal, 2021, 120, 81a.	0.2	0
18	Protein contact map refinement for improving structure prediction using generative adversarial networks. Bioinformatics, 2021, 37, 3168-3174.	1.8	9

#	Article	IF	Citations
19	VESPER: global and local cryo-EM map alignment using local density vectors. Nature Communications, 2021, 12, 2090.	5.8	11
20	Detecting protein and DNA/RNA structures in cryo-EM maps of intermediate resolution using deep learning. Nature Communications, 2021, 12, 2302.	5.8	28
21	Analyzing effect of quadruple multiple sequence alignments on deep learning based protein inter-residue distance prediction. Scientific Reports, 2021, 11, 7574.	1.6	19
22	Mass spectrometryâ€based proteomic platforms for better understanding of SARSâ€CoVâ€2 induced pathogenesis and potential diagnostic approaches. Proteomics, 2021, 21, e2000279.	1.3	19
23	Protein Docking Model Evaluation by Graph Neural Networks. Frontiers in Molecular Biosciences, 2021, 8, 647915.	1.6	47
24	Kinetic and structural parameters governing Fic-mediated adenylylation/AMPylation of the Hsp70 chaperone, BiP/GRP78. Cell Stress and Chaperones, 2021, 26, 639-656.	1.2	8
25	LZerD webserver for pairwise and multiple proteinâ€“protein docking. Nucleic Acids Research, 2021, 49, W359-W365.	6.5	41
26	Efficient Flexible Fitting Refinement with Automatic Error Fixing for De Novo Structure Modeling from Cryo-EM Density Maps. Journal of Chemical Information and Modeling, 2021, 61, 3516-3528.	2.5	11
27	LZerD Protein-Protein Docking Webserver Enhanced With de novo Structure Prediction. Frontiers in Molecular Biosciences, 2021, 8, 724947.	1.6	20
28	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
29	Activation of gene expression by detergent-like protein domains. IScience, 2021, 24, 103017.	1.9	7
30	CryoFold: Determining protein structures and data-guided ensembles from cryo-EM density maps. Matter, 2021, 4, 3195-3216.	5.0	26
31	SHREC 2021: Retrieval and classification of protein surfaces equipped with physical and chemical properties. Computers and Graphics, 2021, 99, 1-21.	1.4	10
32	Emap2sec+: detecting protein and DNA/RNA structures in cryo-EM maps of intermediate resolution using deep learning. Acta Crystallographica Section A: Foundations and Advances, 2021, 77, a84-a84.	0.0	1
33	MAINMAST: de novo protein structure modeling for cryo-EM maps assisted by structure feature detection by deep learning. Acta Crystallographica Section A: Foundations and Advances, 2021, 77, a97-a97.	0.0	0
34	Evolutionary Dynamics of Indels in SARS-CoV-2 Spike Glycoprotein. Evolutionary Bioinformatics, 2021, 17, 117693432110646.	0.6	5
35	Editorial: Computational Approaches to Study the Impact of Mutations on Disease and Drug Resistance. Frontiers in Molecular Biosciences, 2021, 8, 813552.	1.6	2
36	Performance and enhancement of the LZerD protein assembly pipeline in CAPRI 38â€46. Proteins: Structure, Function and Bioinformatics, 2020, 88, 948-961.	1.5	13

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37	Protein docking model evaluation by 3D deep convolutional neural networks. Bioinformatics, 2020, 36, 2113-2118.	1.8	84
38	Advances in Structure Modeling Methods for Cryo-Electron Microscopy Maps. Molecules, 2020, 25, 82.	1.7	26
39	SHREC 2020: Multi-domain protein shape retrieval challenge. Computers and Graphics, 2020, 91, 189-198.	1.4	14
40	De Novo Protein Structure Modeling Tool MAINMAST Enhanced for Multiple Chain Complexes and Bound Ligands. Biophysical Journal, 2020, 118, 481a.	0.2	0
41	Current Challenges and Opportunities in Designing Proteinâ€“Protein Interaction Targeted Drugs . Advances and Applications in Bioinformatics and Chemistry, 2020, Volume 13, 11-25.	1.6	34
42	De Novo Computational Protein Tertiary Structure Modeling Pipeline for Cryo-EM Maps of Intermediate Resolution. Biophysical Journal, 2020, 118, 292a.	0.2	0
43	SHREC 2020: Classification in cryo-electron tomograms. Computers and Graphics, 2020, 91, 279-289.	1.4	33
44	A Simple But Effective Bert Model for Dialog State Tracking on Resource-Limited Systems. , 2020, , .		13
45	MAINMASTseg: Automated Map Segmentation Method for Cryo-EM Density Maps with Symmetry. Journal of Chemical Information and Modeling, 2020, 60, 2634-2643.	2.5	10
46	Computational structure modeling for diverse categories of macromolecular interactions. Current Opinion in Structural Biology, 2020, 64, 1-8.	2.6	22
47	2DKD: a toolkit for content-based local image search. Source Code for Biology and Medicine, 2020, 15, 1.	1.7	1
48	Protein Secondary Structure Detection in Intermediate-Resolution Cryo-EM Maps using Deep Learning. Biophysical Journal, 2020, 118, 43a.	0.2	2
49	Phage G Structure at 6.1â€Ã… Resolution, Condensed DNA, and Host Identity Revision to a Lysinibacillus. Journal of Molecular Biology, 2020, 432, 4139-4153.	2.0	14
50	Path-LZerD: Predicting Assembly Order of Multimeric Protein Complexes. Methods in Molecular Biology, 2020, 2074, 95-112.	0.4	0
51	Matching of EM Map Segments to Structurally-Relevant Bio-molecular Regions. Communications in Computer and Information Science, 2020, , 464-478.	0.4	0
52	IDP-LZerD: Software for Modeling Disordered Protein Interactions. Methods in Molecular Biology, 2020, 2165, 231-244.	0.4	6
53	Protein Structure Modeling from Cryo-EM Map Using MAINMAST and MAINMAST-GUI Plugin. Methods in Molecular Biology, 2020, 2165, 317-336.	0.4	2
54	Study of the Variability of the Native Protein Structure. , 2019, , 606-619.		2

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55	Phylo-PFP: improved automated protein function prediction using phylogenetic distance of distantly related sequences. Bioinformatics, 2019, 35, 753-759.	1.8	29
56	Protein secondary structure detection in intermediate-resolution cryo-EM maps using deep learning. Nature Methods, 2019, 16, 911-917.	9.0	76
57	Implementation of pharmacophore-based 3D QSAR model and scaffold analysis in order to excavate pristine ALK inhibitors. Medicinal Chemistry Research, 2019, 28, 1726-1739.	1.1	3
58	Blind prediction of homoâ€•and heteroâ€protein complexes: The CASP13â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	1.5	99
59	Enhancement for MAINMAST, De Novo Main-Chain Tracing Method: Symmetric Multi-Chain Modeling, Local Refinement, and Graphical User Interface. Microscopy and Microanalysis, 2019, 25, 146-147.	0.2	0
60	Predicting binding poses and affinity ranking in D3R Grand Challenge using PL-PatchSurfer2.0. Journal of Computer-Aided Molecular Design, 2019, 33, 1083-1094.	1.3	3
61	Modeling the Assembly Order of Multimeric Heteroprotein Complexes. Biophysical Journal, 2019, 116, 194a-195a.	0.2	0
62	Modeling protein-protein interactions with intrinsically disordered proteins. , 2019, , 189-206.		3
63	Computational identification of protein-protein interactions in model plant proteomes. Scientific Reports, 2019, 9, 8740.	1.6	56
64	MAINMAST-MELD-MDFF: Denovo Structure-Determination with Data-Guided Molecular Dynamics. Biophysical Journal, 2019, 116, 287a-288a.	0.2	1
65	Three-dimensional Krawtchouk descriptors for protein local surface shape comparison. Pattern Recognition, 2019, 93, 534-545.	5.1	13
66	Lactose derivatives as potential inhibitors of pectin methylesterases. International Journal of Biological Macromolecules, 2019, 132, 1140-1146.	3.6	4
67	The Balancing Act of Intrinsically Disordered Proteins: Enabling Functional Diversity while Minimizing Promiscuity. Journal of Molecular Biology, 2019, 431, 1650-1670.	2.0	41
68	A global map of the protein shape universe. PLoS Computational Biology, 2019, 15, e1006969.	1.5	24
69	55 Years of the Rossmann Fold. Methods in Molecular Biology, 2019, 1958, 1-13.	0.4	15
70	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
71	A prospective compound screening contest identified broader inhibitors for Sirtuin 1. Scientific Reports, 2019, 9, 19585.	1.6	15
72	NNTox: Gene Ontology-Based Protein Toxicity Prediction Using Neural Network. Scientific Reports, 2019, 9, 17923.	1.6	10

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73	Prediction of protein group function by iterative classification on functional relevance network. Bioinformatics, 2019, 35, 1388-1394.	1.8	4
74	A Gated Self-attention Memory Network for Answer Selection. , 2019, , .		18
75	Survey of Machine Learning Techniques for Prediction of the Isoform Specificity of Cytochrome P450 Substrates. Current Drug Metabolism, 2019, 20, 229-235.	0.7	26
76	IAS: Interaction Specific GO Term Associations for Predicting Protein-Protein Interaction Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1247-1258.	1.9	11
77	Virtual Ligand Screening Using PL-PatchSurfer2, a Molecular Surface-Based Proteinâ€“Ligand Docking Method. Methods in Molecular Biology, 2018, 1762, 105-121.	0.4	6
78	Improved performance in CAPRI round 37 using LZerD docking and templateâ€based modeling with combined scoring functions. Proteins: Structure, Function and Bioinformatics, 2018, 86, 311-320.	1.5	20
79	Protein structure model refinement in CASP12 using short and long molecular dynamics simulations in implicit solvent. Proteins: Structure, Function and Bioinformatics, 2018, 86, 189-201.	1.5	12
80	Identification of Moonlighting Proteins in Genomes Using Text Mining Techniques. Proteomics, 2018, 18, 1800083.	1.3	6
81	De novo main-chain modeling with MAINMAST in 2015/2016 EM Model Challenge. Journal of Structural Biology, 2018, 204, 351-359.	1.3	19
82	Analysis of Protein Complexes in the Unicellular Cyanobacterium Cyanothece ATCC 51142. Journal of Proteome Research, 2018, 17, 3628-3643.	1.8	16
83	Computational Methods for Predicting Proteinâ€Protein Interactions Using Various Protein Features. Current Protocols in Protein Science, 2018, 93, e62.	2.8	47
84	Computing and Visualizing Gene Function Similarity and Coherence with NaviGO. Methods in Molecular Biology, 2018, 1807, 113-130.	0.4	2
85	De novo main-chain modeling for EM maps using MAINMAST. Nature Communications, 2018, 9, 1618.	5.8	117
86	Modeling the assembly order of multimeric heteroprotein complexes. PLoS Computational Biology, 2018, 14, e1005937.	1.5	30
87	Prediction of Local Quality of Protein Structure Models Considering Spatial Neighbors in Graphical Models. Scientific Reports, 2017, 7, 40629.	1.6	11
88	Variability of Protein Structure Models from Electron Microscopy. Structure, 2017, 25, 592-602.e2.	1.6	12
89	MPFit: Computational Tool for Predicting Moonlighting Proteins. Methods in Molecular Biology, 2017, 1611, 45-57.	0.4	4
90	Discovery of Nicotinamide Adenine Dinucleotide Binding Proteins in the Escherichia coli Proteome Using a Combined Energetic- and Structural-Bioinformatics-Based Approach. Journal of Proteome Research, 2017, 16, 470-480.	1.8	11

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91	Using PFP and ESG Protein Function Prediction Web Servers. Methods in Molecular Biology, 2017, 1611, 1-14.	0.4	7
92	BindML/BindML+: Detecting Protein-Protein Interaction Interface Propensity from Amino Acid Substitution Patterns. Methods in Molecular Biology, 2017, 1529, 279-289.	0.4	4
93	An iterative compound screening contest method for identifying target protein inhibitors using the tyrosine-protein kinase Yes. Scientific Reports, 2017, 7, 12038.	1.6	28
94	In silico structure-based approaches to discover protein-protein interaction-targeting drugs. Methods, 2017, 131, 22-32.	1.9	69
95	NaviGO: interactive tool for visualization and functional similarity and coherence analysis with gene ontology. BMC Bioinformatics, 2017, 18, 177.	1.2	53
96	Human and server docking prediction for CAPRI round 30â€35 using LZerD with combined scoring functions. Proteins: Structure, Function and Bioinformatics, 2017, 85, 513-527.	1.5	18
97	Predicting Real-Valued Protein Residue Fluctuation Using FlexPred. Methods in Molecular Biology, 2017, 1484, 175-186.	0.4	4
98	Protein 3D Structure and Electron Microscopy Map Retrieval Using 3Dâ€SURFER2.0 and EMâ€SURFER. Current Protocols in Bioinformatics, 2017, 60, 3.14.1-3.14.15.	25.8	9
99	DextMP: deep dive into text for predicting moonlighting proteins. Bioinformatics, 2017, 33, i83-i91.	1.8	20
100	Modeling disordered protein interactions from biophysical principles. PLoS Computational Biology, 2017, 13, e1005485.	1.5	50
101	Ranking proteinâ€“protein docking results using steered molecular dynamics and potential of mean force calculations. Journal of Computational Chemistry, 2016, 37, 1861-1865.	1.5	35
102	Protein structure prediction using residueâ€•and fragmentâ€environment potentials in <scp>CASP</scp>11. Proteins: Structure, Function and Bioinformatics, 2016, 84, 105-117.	1.5	20
103	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
104	Pl-Patchsurfer: A Fast, Surface-Patch-Based Virtual Screening Program using Three-Dimensional Zernike Descriptors. Biophysical Journal, 2016, 110, 187a.	0.2	0
105	Energetic Coupling between Ligand Binding and Dimerization in Escherichia coli Phosphoglycerate Mutase. Biochemistry, 2016, 55, 1711-1723.	1.2	6
106	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	3.8	308
107	PL-PatchSurfer2: Improved Local Surface Matching-Based Virtual Screening Method That Is Tolerant to Target and Ligand Structure Variation. Journal of Chemical Information and Modeling, 2016, 56, 1676-1691.	2.5	24
108	Missing gene identification using functional coherence scores. Scientific Reports, 2016, 6, 31725.	1.6	3

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109	PatchSurfers: Two methods for local molecular property-based binding ligand prediction. Methods, 2016, 93, 41-50.	1.9	8
110	Genome-scale prediction of moonlighting proteins using diverse protein association information. Bioinformatics, 2016, 32, 2281-2288.	1.8	29
111	Combined Approach of Patch-Surfer and PL-PatchSurfer for Proteinâ€“Ligand Binding Prediction in CSAR 2013 and 2014. Journal of Chemical Information and Modeling, 2016, 56, 1088-1099.	2.5	12
112	Computational protein function predictions. Methods, 2016, 93, 1-2.	1.9	8
113	Ensemble-based evaluation for protein structure models. Bioinformatics, 2016, 32, i314-i321.	1.8	7
114	The PFP and ESG protein function prediction methods in 2014: effect of database updates and ensemble approaches. GigaScience, 2015, 4, 43.	3.3	16
115	Three-Dimensional Compound Comparison Methods and Their Application in Drug Discovery. Molecules, 2015, 20, 12841-12862.	1.7	49
116	GenoBase: comprehensive resource database of Escherichia coli K-12. Nucleic Acids Research, 2015, 43, D606-D617.	6.5	29
117	Tuning of Pectin Methylesterification. Journal of Biological Chemistry, 2015, 290, 23320-23335.	1.6	52
118	Large-scale binding ligand prediction by improved patch-based method Patch-Surfer2.0. Bioinformatics, 2015, 31, 707-713.	1.8	49
119	Structure and inhibition of EV-D68, a virus that causes respiratory illness in children. Science, 2015, 347, 71-74.	6.0	139
120	On the Origin of Protein Superfamilies and Superfolds. Scientific Reports, 2015, 5, 8166.	1.6	18
121	Navigating 3D electron microscopy maps with EM-SURFER. BMC Bioinformatics, 2015, 16, 181.	1.2	22
122	PFP/ESG: automated protein function prediction servers enhanced with Gene Ontology visualization tool. Bioinformatics, 2015, 31, 271-272.	1.8	23
123	PL-PatchSurfer: A Novel Molecular Local Surface-Based Method for Exploring Protein-Ligand Interactions. International Journal of Molecular Sciences, 2014, 15, 15122-15145.	1.8	22
124	A Proteomic Strategy for Global Analysis of Plant Protein Complexes. Plant Cell, 2014, 26, 3867-3882.	3.1	55
125	The Structure of the Catalytic Domain of a Plant Cellulose Synthase and Its Assembly into Dimers. Plant Cell, 2014, 26, 2996-3009.	3.1	61
126	Computational characterization of moonlighting proteins. Biochemical Society Transactions, 2014, 42, 1780-1785.	1.6	26

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127	Genome-scale identification and characterization of moonlighting proteins. Biology Direct, 2014, 9, 30.	1.9	37
128	Comparison of Image Patches Using Local Moment Invariants. IEEE Transactions on Image Processing, 2014, 23, 2369-2379.	6.0	28
129	Assessment of protein side-chain conformation prediction methods in different residue environments. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1971-1984.	1.5	30
130	Structureâ€“Function Analysis of the DNA Translocating Portal of the Bacteriophage T4 Packaging Machine. Journal of Molecular Biology, 2014, 426, 1019-1038.	2.0	26
131	Detecting local residue environment similarity for recognizing nearâ€native structure models. Proteins: Structure, Function and Bioinformatics, 2014, 82, 3255-3272.	1.5	12
132	Pairwise and Multimeric Proteinâ€“Protein Docking Using the LZerD Program Suite. Methods in Molecular Biology, 2014, 1137, 209-234.	0.4	36
133	3D-SURFER 2.0: Web Platform for Real-Time Search and Characterization of Protein Surfaces. Methods in Molecular Biology, 2014, 1137, 105-117.	0.4	10
134	In-depth performance evaluation of PFP and ESG sequence-based function prediction methods in CAFA 2011 experiment. BMC Bioinformatics, 2013, 14, S2.	1.2	5
135	Computational methods for constructing protein structure models from 3D electron microscopy maps. Journal of Structural Biology, 2013, 184, 93-102.	1.3	38
136	Predicting permanent and transient proteinâ€“protein interfaces. Proteins: Structure, Function and Bioinformatics, 2013, 81, 805-818.	1.5	48
137	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	9.0	789
138	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1980-1987.	1.5	87
139	Protein domain recurrence and order can enhance prediction of protein functions. Bioinformatics, 2012, 28, i444-i450.	1.8	24
140	Fitting Multimeric Protein Complexes into Electron Microscopy Maps Using 3D Zernike Descriptors. Journal of Physical Chemistry B, 2012, 116, 6854-6861.	1.2	39
141	Evaluation of multiple protein docking structures using correctly predicted pairwise subunits. BMC Bioinformatics, 2012, 13, S6.	1.2	9
142	Effective inter-residue contact definitions for accurate protein fold recognition. BMC Bioinformatics, 2012, 13, 292.	1.2	44
143	Protein docking prediction using predicted protein-protein interface. BMC Bioinformatics, 2012, 13, 7.	1.2	60
144	Constructing patch-based ligand-binding pocket database for predicting function of proteins. BMC Bioinformatics, 2012, 13, S7.	1.2	8

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145	Evaluation of function predictions by PFP, ESG, and PSI-BLAST for moonlighting proteins. BMC Proceedings, 2012, 6, S5.	1.8	21
146	Effect of conformation sampling strategies in genetic algorithm for multiple protein docking. BMC Proceedings, 2012, 6, S4.	1.8	5
147	A novel method for proteinâ€"protein interaction site prediction using phylogenetic substitution models. Proteins: Structure, Function and Bioinformatics, 2012, 80, 126-141.	1.5	27
148	Detecting local ligandâ€binding site similarity in nonhomologous proteins by surface patch comparison. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1177-1195.	1.5	56
149	Formylâ€coenzyme A (CoA):oxalate CoAâ€transferase from the acidophile Acetobacter aceti has a distinctive electrostatic surface and inherent acid stability. Protein Science, 2012, 21, 686-696.	3.1	18
150	Structural features that predict realâ€value fluctuations of globular proteins. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1425-1435.	1.5	20
151	Multiâ€LZerD: Multiple protein docking for asymmetric complexes. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1818-1833.	1.5	71
152	Structure- and sequence-based function prediction for non-homologous proteins. Journal of Structural and Functional Genomics, 2012, 13, 111-123.	1.2	27
153	Error Estimation of Template-Based Protein Structure Models. , 2011, , 295-314.		0
154	Energetics-Based Discovery of Proteinâ€"Ligand Interactions on a Proteomic Scale. Journal of Molecular Biology, 2011, 408, 147-162.	2.0	52
155	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	2.0	131
156	Molecular Surface Representation Using 3D Zernike Descriptors for Protein Shape Comparison and Docking. Current Protein and Peptide Science, 2011, 12, 520-530.	0.7	82
157	Quantification of protein group coherence and pathway assignment using functional association. BMC Bioinformatics, 2011, 12, 373.	1.2	11
158	Effect of using suboptimal alignments in templateâ€based protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2011, 79, 315-334.	1.5	24
159	Identification of a novel effector domain of BIN1 for cancer suppression. Journal of Cellular Biochemistry, 2011, 112, 2992-3001.	1.2	14
160	Computational Protein Function Prediction: Framework and Challenges. , 2011, , 1-17.		8
161	Protein Binding Ligand Prediction Using Moments-Based Methods. , 2011, , 145-163.		8
162	N-Terminal Gly224â€"Gly411 Domain in Listeria Adhesion Protein Interacts with Host Receptor Hsp60. PLoS ONE, 2011, 6, e20694.	1.1	36

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163	Enhanced Sequence-Based Function Prediction Methods and Application to Functional Similarity Networks. , 2011, , 19-34.		1
164	Functional enrichment analyses and construction of functional similarity networks with high confidence function prediction by PFP. BMC Bioinformatics, 2010, 11, 265.	1.2	16
165	Improved protein surface comparison and application to low-resolution protein structure data. BMC Bioinformatics, 2010, 11, S2.	1.2	23
166	Real-time ligand binding pocket database search using local surface descriptors. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2007-2028.	1.5	55
167	Sub-AQUA: real-value quality assessment of protein structure models. Protein Engineering, Design and Selection, 2010, 23, 617-632.	1.0	15
168	Binding Ligand Prediction for Proteins Using Partial Matching of Local Surface Patches. International Journal of Molecular Sciences, 2010, 11, 5009-5026.	1.8	33
169	Characterization and Classification of Local Protein Surfaces Using Self-Organizing Map. International Journal of Knowledge Discovery in Bioinformatics, 2010, 1, 32-47.	0.8	12
170	Quality Assessment of Protein Structure Models. Current Protein and Peptide Science, 2009, 10, 216-228.	0.7	58
171	3D-SURFER: software for high-throughput protein surface comparison and analysis. Bioinformatics, 2009, 25, 2843-2844.	1.8	77
172	ESG: extended similarity group method for automated protein function prediction. Bioinformatics, 2009, 25, 1739-1745.	1.8	87
173	Protein-protein docking using region-based 3D Zernike descriptors. BMC Bioinformatics, 2009, 10, 407.	1.2	152
174	Potential for Protein Surface Shape Analysis Using Spherical Harmonics and 3D Zernike Descriptors. Cell Biochemistry and Biophysics, 2009, 54, 23-32.	0.9	85
175	PFP: Automated prediction of gene ontology functional annotations with confidence scores using protein sequence data. Proteins: Structure, Function and Bioinformatics, 2009, 74, 566-582.	1.5	105
176	Application of 3D Zernike descriptors to shape-based ligand similarity searching. Journal of Cheminformatics, 2009, 1, 19.	2.8	48
177	Local surface shape-based protein function prediction using Zernike descriptors. Biophysical Journal, 2009, 96, 650a.	0.2	5
178	Estimating quality of templateâ€based protein models by alignment stability. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1255-1274.	1.5	26
179	Combining gene sequence similarity and textual information for gene function annotation in the literature. Information Retrieval, 2008, 11, 389-404.	1.6	6
180	Characterization of local geometry of protein surfaces with the visibility criterion. Proteins: Structure, Function and Bioinformatics, 2008, 71, 670-683.	1.5	82

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181	Fast protein tertiary structure retrieval based on global surface shape similarity. Proteins: Structure, Function and Bioinformatics, 2008, 72, 1259-1273.	1.5	110
182	Threading without optimizing weighting factors for scoring function. Proteins: Structure, Function and Bioinformatics, 2008, 73, 581-596.	1.5	12
183	Rapid comparison of properties on protein surface. Proteins: Structure, Function and Bioinformatics, 2008, 73, 1-10.	1.5	75
184	New paradigm in protein function prediction for large scale omics analysis. Molecular BioSystems, 2008, 4, 223.	2.9	31
185	Automated Prediction of Protein Function from Sequence. , 2008, , 63-85.		4
186	ESG: Extended Similarity Group method for automated protein function prediction. Nature Precedings, 2008, , .	0.1	0
187	FUNCTION PREDICTION OF UNCHARACTERIZED PROTEINS. Journal of Bioinformatics and Computational Biology, 2007, 05, 1-30.	0.3	87
188	Tracing Lineage in Multi-version Scientific Databases. , 2007, , .		3
189	Protein Function Prediction in Proteomics Era. , 2007, , 143-148.		0
190	Bioinformatics resources for cancer research with an emphasis on gene function and structure prediction tools. Cancer Informatics, 2007, 2, 25-35.	0.9	8
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