Daisuke Kihara

List of Publications by Year
in descending order

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206	7,828	57758	74163
papers	citations	44 h-index	75 g-index

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

#	Article	IF	Citations
1	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	19.0	789
2	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
3	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261
4	Limitations and potentials of current motif discovery algorithms. Nucleic Acids Research, 2005, 33, 4899-4913.	14.5	203
5	Development and large scale benchmark testing of the PROSPECTOR_3 threading algorithm. Proteins: Structure, Function and Bioinformatics, 2004, 56, 502-518.	2.6	152
6	Protein-protein docking using region-based 3D Zernike descriptors. BMC Bioinformatics, 2009, 10, 407.	2.6	152
7	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.	2.6	148
8	TOUCHSTONE: An ab initio protein structure prediction method that uses threading-based tertiary restraints. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 10125-10130.	7.1	144
9	Structure and inhibition of EV-D68, a virus that causes respiratory illness in children. Science, 2015, 347, 71-74.	12.6	139
10	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	4.2	131
11	Local energy landscape flattening: Parallel hyperbolic Monte Carlo sampling of protein folding. Proteins: Structure, Function and Bioinformatics, 2002, 48, 192-201.	2.6	130
12	Enhanced automated function prediction using distantly related sequences and contextual association by PFP. Protein Science, 2006, 15, 1550-1556.	7.6	128
13	Defrosting the frozen approximation: PROSPECTOR? A new approach to threading. Proteins: Structure, Function and Bioinformatics, 2001, 42, 319-331.	2.6	124
14	De novo main-chain modeling for EM maps using MAINMAST. Nature Communications, 2018, 9, 1618.	12.8	117
15	The PDB is a Covering Set of Small Protein Structures. Journal of Molecular Biology, 2003, 334, 793-802.	4.2	110
16	Fast protein tertiary structure retrieval based on global surface shape similarity. Proteins: Structure, Function and Bioinformatics, 2008, 72, 1259-1273.	2.6	110
17	PFP: Automated prediction of gene ontology functional annotations with confidence scores using protein sequence data. Proteins: Structure, Function and Bioinformatics, 2009, 74, 566-582.	2.6	105
18	Blind prediction of homoâ€and heteroâ€protein complexes: The CASP13â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	2.6	99

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19	The effect of long-range interactions on the secondary structure formation of proteins. Protein Science, 2005, 14, 1955-1963.	7.6	92
20	FUNCTION PREDICTION OF UNCHARACTERIZED PROTEINS. Journal of Bioinformatics and Computational Biology, 2007, 05, 1-30.	0.8	87
21	ESG: extended similarity group method for automated protein function prediction. Bioinformatics, 2009, 25, 1739-1745.	4.1	87
22	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1980-1987.	2.6	87
23	Potential for Protein Surface Shape Analysis Using Spherical Harmonics and 3D Zernike Descriptors. Cell Biochemistry and Biophysics, 2009, 54, 23-32.	1.8	85
24	Protein docking model evaluation by 3D deep convolutional neural networks. Bioinformatics, 2020, 36, 2113-2118.	4.1	84
25	Characterization of local geometry of protein surfaces with the visibility criterion. Proteins: Structure, Function and Bioinformatics, 2008, 71, 670-683.	2.6	82
26	Molecular Surface Representation Using 3D Zernike Descriptors for Protein Shape Comparison and Docking. Current Protein and Peptide Science, 2011, 12, 520-530.	1.4	82
27	3D-SURFER: software for high-throughput protein surface comparison and analysis. Bioinformatics, 2009, 25, 2843-2844.	4.1	77
28	Protein secondary structure detection in intermediate-resolution cryo-EM maps using deep learning. Nature Methods, 2019, 16, 911-917.	19.0	76
29	Rapid comparison of properties on protein surface. Proteins: Structure, Function and Bioinformatics, 2008, 73, 1-10.	2.6	75
30	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. Nature Methods, 2021, 18, 156-164.	19.0	73
31	Prediction of protein assemblies, the next frontier: The <scp>CASP14â€CAPRI</scp> experiment. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1800-1823.	2.6	73
32	TOUCHSTONE: A unified approach to protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2003, 53, 469-479.	2.6	72
33	Multiâ€LZerD: Multiple protein docking for asymmetric complexes. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1818-1833.	2.6	71
34	In silico structure-based approaches to discover protein-protein interaction-targeting drugs. Methods, 2017, 131, 22-32.	3.8	69
35	The Structure of the Catalytic Domain of a Plant Cellulose Synthase and Its Assembly into Dimers. Plant Cell, 2014, 26, 2996-3009.	6.6	61
36	Protein docking prediction using predicted protein-protein interface. BMC Bioinformatics, 2012, 13, 7.	2.6	60

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37	Quality Assessment of Protein Structure Models. Current Protein and Peptide Science, 2009, 10, 216-228.	1.4	58
38	Detecting local ligandâ€binding site similarity in nonhomologous proteins by surface patch comparison. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1177-1195.	2.6	56
39	Computational identification of protein-protein interactions in model plant proteomes. Scientific Reports, 2019, 9, 8740.	3.3	56
40	Real-time ligand binding pocket database search using local surface descriptors. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2007-2028.	2.6	55
41	A Proteomic Strategy for Global Analysis of Plant Protein Complexes. Plant Cell, 2014, 26, 3867-3882.	6.6	55
42	NaviGO: interactive tool for visualization and functional similarity and coherence analysis with gene ontology. BMC Bioinformatics, 2017, 18, 177.	2.6	53
43	Energetics-Based Discovery of Proteinâ€“Ligand Interactions on a Proteomic Scale. Journal of Molecular Biology, 2011, 408, 147-162.	4.2	52
44	Tuning of Pectin Methylesterification. Journal of Biological Chemistry, 2015, 290, 23320-23335.	3.4	52
45	Modeling disordered protein interactions from biophysical principles. PLoS Computational Biology, 2017, 13, e1005485.	3.2	50
46	Three-Dimensional Compound Comparison Methods and Their Application in Drug Discovery. Molecules, 2015, 20, 12841-12862.	3.8	49
47	Large-scale binding ligand prediction by improved patch-based method Patch-Surfer2.0. Bioinformatics, 2015, 31, 707-713.	4.1	49
48	Application of 3D Zernike descriptors to shape-based ligand similarity searching. Journal of Cheminformatics, 2009, 1, 19.	6.1	48
49	Predicting permanent and transient proteinâ€“protein interfaces. Proteins: Structure, Function and Bioinformatics, 2013, 81, 805-818.	2.6	48
50	Computational Methods for Predicting Proteinâ€Protein Interactions Using Various Protein Features. Current Protocols in Protein Science, 2018, 93, e62.	2.8	47
51	Protein Docking Model Evaluation by Graph Neural Networks. Frontiers in Molecular Biosciences, 2021, 8, 647915.	3.5	47
52	Effective inter-residue contact definitions for accurate protein fold recognition. BMC Bioinformatics, 2012, 13, 292.	2.6	44
53	Ab initio protein structure prediction on a genomic scale: Application to the Mycoplasma genitalium genome. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 5993-5998.	7.1	41
54	EMD: an ensemble algorithm for discovering regulatory motifs in DNA sequences. BMC Bioinformatics, 2006, 7, 342.	2.6	41

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55	The Balancing Act of Intrinsically Disordered Proteins: Enabling Functional Diversity while Minimizing Promiscuity. Journal of Molecular Biology, 2019, 431, 1650-1670.	4.2	41
56	LZerD webserver for pairwise and multiple proteinâ€“protein docking. Nucleic Acids Research, 2021, 49, W359-W365.	14.5	41
57	Statistical potential-based amino acid similarity matrices for aligning distantly related protein sequences. Proteins: Structure, Function and Bioinformatics, 2006, 64, 587-600.	2.6	39
58	Fitting Multimeric Protein Complexes into Electron Microscopy Maps Using 3D Zernike Descriptors. Journal of Physical Chemistry B, 2012, 116, 6854-6861.	2.6	39
59	TOUCHSTONEX: Protein structure prediction with sparse NMR data. Proteins: Structure, Function and Bioinformatics, 2003, 53, 290-306.	2.6	38
60	Computational methods for constructing protein structure models from 3D electron microscopy maps. Journal of Structural Biology, 2013, 184, 93-102.	2.8	38
61	Genome-scale identification and characterization of moonlighting proteins. Biology Direct, 2014, 9, 30.	4.6	37
62	EnAET: A Self-Trained Framework for Semi-Supervised and Supervised Learning With Ensemble Transformations. IEEE Transactions on Image Processing, 2021, 30, 1639-1647.	9.8	36
63	Pairwise and Multimeric Proteinâ€“Protein Docking Using the LZerD Program Suite. Methods in Molecular Biology, 2014, 1137, 209-234.	0.9	36
64	N-Terminal Gly224â€“Gly411 Domain in Listeria Adhesion Protein Interacts with Host Receptor Hsp60. PLoS ONE, 2011, 6, e20694.	2.5	36
65	Ranking proteinâ€“protein docking results using steered molecular dynamics and potential of mean force calculations. Journal of Computational Chemistry, 2016, 37, 1861-1865.	3.3	35
66	Microbial genomes have over 72% structure assignment by the threading algorithm PROSPECTOR_Q. Proteins: Structure, Function and Bioinformatics, 2004, 55, 464-473.	2.6	34
67	Current Challenges and Opportunities in Designing Proteinâ€“Protein Interaction Targeted Drugs . Advances and Applications in Bioinformatics and Chemistry, 2020, Volume 13, 11-25.	2.6	34
68	Real-time structure search and structure classification for AlphaFold protein models. Communications Biology, 2022, 5, 316.	4.4	34
69	Binding Ligand Prediction for Proteins Using Partial Matching of Local Surface Patches. International Journal of Molecular Sciences, 2010, 11, 5009-5026.	4.1	33
70	SHREC 2020: Classification in cryo-electron tomograms. Computers and Graphics, 2020, 91, 279-289.	2.5	33
71	New paradigm in protein function prediction for large scale omics analysis. Molecular BioSystems, 2008, 4, 223.	2.9	31
72	Assessment of protein side-chain conformation prediction methods in different residue environments. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1971-1984.	2.6	30

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73	Modeling the assembly order of multimeric heteroprotein complexes. PLoS Computational Biology, 2018, 14, e1005937.	3.2	30
74	GenoBase: comprehensive resource database of Escherichia coli K-12. Nucleic Acids Research, 2015, 43, D606-D617.	14.5	29
75	Genome-scale prediction of moonlighting proteins using diverse protein association information. Bioinformatics, 2016, 32, 2281-2288.	4.1	29
76	Phylo-PFP: improved automated protein function prediction using phylogenetic distance of distantly related sequences. Bioinformatics, 2019, 35, 753-759.	4.1	29
77	Comparison of Image Patches Using Local Moment Invariants. IEEE Transactions on Image Processing, 2014, 23, 2369-2379.	9.8	28
78	An iterative compound screening contest method for identifying target protein inhibitors using the tyrosine-protein kinase Yes. Scientific Reports, 2017, 7, 12038.	3.3	28
79	Detecting protein and DNA/RNA structures in cryo-EM maps of intermediate resolution using deep learning. Nature Communications, 2021, 12, 2302.	12.8	28
80	A novel method for proteinâ€“protein interaction site prediction using phylogenetic substitution models. Proteins: Structure, Function and Bioinformatics, 2012, 80, 126-141.	2.6	27
81	Structure- and sequence-based function prediction for non-homologous proteins. Journal of Structural and Functional Genomics, 2012, 13, 111-123.	1.2	27
82	Estimating quality of templateâ€based protein models by alignment stability. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1255-1274.	2.6	26
83	Computational characterization of moonlighting proteins. Biochemical Society Transactions, 2014, 42, 1780-1785.	3.4	26
84	Structureâ€“Function Analysis of the DNA Translocating Portal of the Bacteriophage T4 Packaging Machine. Journal of Molecular Biology, 2014, 426, 1019-1038.	4.2	26
85	Advances in Structure Modeling Methods for Cryo-Electron Microscopy Maps. Molecules, 2020, 25, 82.	3.8	26
86	CryoFold: Determining protein structures and data-guided ensembles from cryo-EM density maps. Matter, 2021, 4, 3195-3216.	10.0	26
87	Survey of Machine Learning Techniques for Prediction of the Isoform Specificity of Cytochrome P450 Substrates. Current Drug Metabolism, 2019, 20, 229-235.	1.2	26
88	Effect of using suboptimal alignments in templateâ€based protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2011, 79, 315-334.	2.6	24
89	Protein domain recurrence and order can enhance prediction of protein functions. Bioinformatics, 2012, 28, i444-i450.	4.1	24
90	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.	5.4	24

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91	A global map of the protein shape universe. PLoS Computational Biology, 2019, 15, e1006969.	3.2	24
92	Improved protein surface comparison and application to low-resolution protein structure data. BMC Bioinformatics, 2010, 11, S2.	2.6	23
93	PFP/ESG: automated protein function prediction servers enhanced with Gene Ontology visualization tool. Bioinformatics, 2015, 31, 271-272.	4.1	23
94	PL-PatchSurfer: A Novel Molecular Local Surface-Based Method for Exploring Protein-Ligand Interactions. International Journal of Molecular Sciences, 2014, 15, 15122-15145.	4.1	22
95	Navigating 3D electron microscopy maps with EM-SURFER. BMC Bioinformatics, 2015, 16, 181.	2.6	22
96	Computational structure modeling for diverse categories of macromolecular interactions. Current Opinion in Structural Biology, 2020, 64, 1-8.	5.7	22
97	Evaluation of function predictions by PFP, ESG, and PSI-BLAST for moonlighting proteins. BMC Proceedings, 2012, 6, S5.	1.6	21
98	Current progress and future perspectives of polypharmacology : From the view of non-small cell lung cancer. Seminars in Cancer Biology, 2021, 68, 84-91.	9.6	21
99	Structural features that predict realâ€•value fluctuations of globular proteins. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1425-1435.	2.6	20
100	Protein structure prediction using residueâ€•and fragmentâ€•environment potentials in <scp>CASP</scp>11. Proteins: Structure, Function and Bioinformatics, 2016, 84, 105-117.	2.6	20
101	DextMP: deep dive into text for predicting moonlighting proteins. Bioinformatics, 2017, 33, i83-i91.	4.1	20
102	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.	2.6	20
103	LZerD Protein-Protein Docking Webserver Enhanced With de novo Structure Prediction. Frontiers in Molecular Biosciences, 2021, 8, 724947.	3.5	20
104	De novo main-chain modeling with MAINMAST in 2015/2016 EM Model Challenge. Journal of Structural Biology, 2018, 204, 351-359.	2.8	19
105	Analyzing effect of quadruple multiple sequence alignments on deep learning based protein inter-residue distance prediction. Scientific Reports, 2021, 11, 7574.	3.3	19
106	Mass spectrometryâ€‐based proteomic platforms for better understanding of SARSâ€‐CoVâ€‐2 induced pathogenesis and potential diagnostic approaches. Proteomics, 2021, 21, e2000279.	2.2	19
107	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.	7.6	18
108	On the Origin of Protein Superfamilies and Superfolds. Scientific Reports, 2015, 5, 8166.	3.3	18

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109	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.	2.6	18
110	A Gated Self-attention Memory Network for Answer Selection. , 2019, , .		18
111	Functional enrichment analyses and construction of functional similarity networks with high confidence function prediction by PFP. BMC Bioinformatics, 2010, 11, 265.	2.6	16
112	The PFP and ESG protein function prediction methods in 2014: effect of database updates and ensemble approaches. GigaScience, 2015, 4, 43.	6.4	16
113	Analysis of Protein Complexes in the Unicellular Cyanobacterium Cyanothece ATCC 51142. Journal of Proteome Research, 2018, 17, 3628-3643.	3.7	16
114	Sub-AQUA: real-value quality assessment of protein structure models. Protein Engineering, Design and Selection, 2010, 23, 617-632.	2.1	15
115	55 Years of the Rossmann Fold. Methods in Molecular Biology, 2019, 1958, 1-13.	0.9	15
116	A prospective compound screening contest identified broader inhibitors for Sirtuin 1. Scientific Reports, 2019, 9, 19585.	3.3	15
117	Identification of a novel effector domain of BIN1 for cancer suppression. Journal of Cellular Biochemistry, 2011, 112, 2992-3001.	2.6	14
118	SHREC 2020: Multi-domain protein shape retrieval challenge. Computers and Graphics, 2020, 91, 189-198.	2.5	14
119	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.	4.2	14
120	Three-dimensional Krawtchouk descriptors for protein local surface shape comparison. Pattern Recognition, 2019, 93, 534-545.	8.1	13
121	Performance and enhancement of the LZerD protein assembly pipeline in CAPRI 38â€46. Proteins: Structure, Function and Bioinformatics, 2020, 88, 948-961.	2.6	13
122	A Simple But Effective Bert Model for Dialog State Tracking on Resource-Limited Systems. , 2020, , .		13
123	Threading without optimizing weighting factors for scoring function. Proteins: Structure, Function and Bioinformatics, 2008, 73, 581-596.	2.6	12
124	Detecting local residue environment similarity for recognizing nearâ€native structure models. Proteins: Structure, Function and Bioinformatics, 2014, 82, 3255-3272.	2.6	12
125	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.	5.4	12
126	Variability of Protein Structure Models from Electron Microscopy. Structure, 2017, 25, 592-602.e2.	3.3	12

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127	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.	2.6	12
128	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
129	Quantification of protein group coherence and pathway assignment using functional association. BMC Bioinformatics, 2011, 12, 373.	2.6	11
130	Prediction of Local Quality of Protein Structure Models Considering Spatial Neighbors in Graphical Models. Scientific Reports, 2017, 7, 40629.	3.3	11
131	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.	3.7	11
132	IAS: Interaction Specific GO Term Associations for Predicting Protein-Protein Interaction Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1247-1258.	3.0	11
133	VESPER: global and local cryo-EM map alignment using local density vectors. Nature Communications, 2021, 12, 2090.	12.8	11
134	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.	5.4	11
135	NNTox: Gene Ontology-Based Protein Toxicity Prediction Using Neural Network. Scientific Reports, 2019, 9, 17923.	3.3	10
136	MAINMASTseg: Automated Map Segmentation Method for Cryo-EM Density Maps with Symmetry. Journal of Chemical Information and Modeling, 2020, 60, 2634-2643.	5.4	10
137	SHREC 2021: Retrieval and classification of protein surfaces equipped with physical and chemical properties. Computers and Graphics, 2021, 99, 1-21.	2.5	10
138	3D-SURFER 2.0: Web Platform for Real-Time Search and Characterization of Protein Surfaces. Methods in Molecular Biology, 2014, 1137, 105-117.	0.9	10
139	SHREC 2022: Proteinâ€“ligand binding site recognition. Computers and Graphics, 2022, 107, 20-31.	2.5	10
140	Evaluation of multiple protein docking structures using correctly predicted pairwise subunits. BMC Bioinformatics, 2012, 13, S6.	2.6	9
141	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
142	Protein contact map refinement for improving structure prediction using generative adversarial networks. Bioinformatics, 2021, 37, 3168-3174.	4.1	9
143	Bioinformatics Resources for Cancer Research with an Emphasis on Gene Function and Structure Prediction Tools. Cancer Informatics, 2006, 2, 117693510600200.	1.9	8
144	Constructing patch-based ligand-binding pocket database for predicting function of proteins. BMC Bioinformatics, 2012, 13, S7.	2.6	8

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145	PatchSurfers: Two methods for local molecular property-based binding ligand prediction. Methods, 2016, 93, 41-50.	3.8	8
146	Computational protein function predictions. Methods, 2016, 93, 1-2.	3.8	8
147	Genotype & phenotype in Lowe Syndrome: specificOCRL1patient mutations differentially impact cellular phenotypes. Human Molecular Genetics, 2021, 30, 198-212.	2.9	8
148	Super Resolution Cryo-EM Maps with 3D Deep Generative Networks. Biophysical Journal, 2021, 120, 283a.	0.5	8
149	Kinetic and structural parameters governing Fic-mediated adenylylation/AMPylation of the Hsp70 chaperone, BiP/GRP78. Cell Stress and Chaperones, 2021, 26, 639-656.	2.9	8
150	Computational Protein Function Prediction: Framework and Challenges. , 2011, , 1-17.		8
151	Protein Binding Ligand Prediction Using Moments-Based Methods. , 2011, , 145-163.		8
152	Bioinformatics resources for cancer research with an emphasis on gene function and structure prediction tools. Cancer Informatics, 2007, 2, 25-35.	1.9	8
153	Using PFP and ESG Protein Function Prediction Web Servers. Methods in Molecular Biology, 2017, 1611, 1-14.	0.9	7
154	Activation of gene expression by detergent-like protein domains. IScience, 2021, 24, 103017.	4.1	7
155	Ensemble-based evaluation for protein structure models. Bioinformatics, 2016, 32, i314-i321.	4.1	7
156	Combining gene sequence similarity and textual information for gene function annotation in the literature. Information Retrieval, 2008, 11, 389-404.	2.0	6
157	Energetic Coupling between Ligand Binding and Dimerization in Escherichia coli Phosphoglycerate Mutase. Biochemistry, 2016, 55, 1711-1723.	2.5	6
158	Virtual Ligand Screening Using PL-PatchSurfer2, a Molecular Surface-Based Proteinâ€“Ligand Docking Method. Methods in Molecular Biology, 2018, 1762, 105-121.	0.9	6
159	Identification of Moonlighting Proteins in Genomes Using Text Mining Techniques. Proteomics, 2018, 18, 1800083.	2.2	6
160	IDP-LZerD: Software for Modeling Disordered Protein Interactions. Methods in Molecular Biology, 2020, 2165, 231-244.	0.9	6
161	ContactPFP: Protein Function Prediction Using Predicted Contact Information. Frontiers in Bioinformatics, 2022, 2, .	2.1	6
162	Local surface shape-based protein function prediction using Zernike descriptors. Biophysical Journal, 2009, 96, 650a.	0.5	5

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163	Effect of conformation sampling strategies in genetic algorithm for multiple protein docking. BMC Proceedings, 2012, 6, S4.	1.6	5
164	In-depth performance evaluation of PFP and ESG sequence-based function prediction methods in CAFA 2011 experiment. BMC Bioinformatics, 2013, 14, S2.	2.6	5
165	Evolutionary Dynamics of Indels in SARS-CoV-2 Spike Glycoprotein. Evolutionary Bioinformatics, 2021, 17, 117693432110646.	1.2	5
166	OC_Finder: Osteoclast Segmentation, Counting, and Classification Using Watershed and Deep Learning. Frontiers in Bioinformatics, 2022, 2, .	2.1	5
167	Automated Prediction of Protein Function from Sequence. , 2008, , 63-85.		4
168	MPFit: Computational Tool for Predicting Moonlighting Proteins. Methods in Molecular Biology, 2017, 1611, 45-57.	0.9	4
169	BindML/BindML+: Detecting Protein-Protein Interaction Interface Propensity from Amino Acid Substitution Patterns. Methods in Molecular Biology, 2017, 1529, 279-289.	0.9	4
170	Predicting Real-Valued Protein Residue Fluctuation Using FlexPred. Methods in Molecular Biology, 2017, 1484, 175-186.	0.9	4
171	Lactose derivatives as potential inhibitors of pectin methylesterases. International Journal of Biological Macromolecules, 2019, 132, 1140-1146.	7.5	4
172	Prediction of protein group function by iterative classification on functional relevance network. Bioinformatics, 2019, 35, 1388-1394.	4.1	4
173	Tracing Lineage in Multi-version Scientific Databases. , 2007, , .		3
174	Missing gene identification using functional coherence scores. Scientific Reports, 2016, 6, 31725.	3.3	3
175	Implementation of pharmacophore-based 3D QSAR model and scaffold analysis in order to excavate pristine ALK inhibitors. Medicinal Chemistry Research, 2019, 28, 1726-1739.	2.4	3
176	Predicting binding poses and affinity ranking in D3R Grand Challenge using PL-PatchSurfer2.0. Journal of Computer-Aided Molecular Design, 2019, 33, 1083-1094.	2.9	3
177	Modeling protein-protein interactions with intrinsically disordered proteins. , 2019, , 189-206.		3
178	Benchmarking of structure refinement methods for protein complex models. Proteins: Structure, Function and Bioinformatics, 2022, 90, 83-95.	2.6	3
179	Multi-level analysis of intrinsically disordered protein docking methods. Methods, 2022, 204, 55-63.	3.8	3
180	Computing and Visualizing Gene Function Similarity and Coherence with NaviGO. Methods in Molecular Biology, 2018, 1807, 113-130.	0.9	2

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181	Study of the Variability of the Native Protein Structure. , 2019, , 606-619.		2
182	Protein Secondary Structure Detection in Intermediate-Resolution Cryo-EM Maps using Deep Learning. Biophysical Journal, 2020, 118, 43a.	0.5	2
183	Protein Structure Modeling from Cryo-EM Map Using MAINMAST and MAINMAST-GUI Plugin. Methods in Molecular Biology, 2020, 2165, 317-336.	0.9	2
184	Surface-based protein domains retrieval methods from a SHREC2021 challenge. Journal of Molecular Graphics and Modelling, 2022, 111, 108103.	2.4	2
185	Editorial: Computational Approaches to Study the Impact of Mutations on Disease and Drug Resistance. Frontiers in Molecular Biosciences, 2021, 8, 813552.	3.5	2
186	MAINMAST-MELD-MDFF: Denovo Structure-Determination with Data-Guided Molecular Dynamics. Biophysical Journal, 2019, 116, 287a-288a.	0.5	1
187	2DKD: a toolkit for content-based local image search. Source Code for Biology and Medicine, 2020, 15, 1.	1.7	1
188	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.	0.1	1
189	Enhanced Sequence-Based Function Prediction Methods and Application to Functional Similarity Networks. , 2011, , 19-34.		1
190	ESG: Extended Similarity Group method for automated protein function prediction. Nature Precedings, 2008, , .	0.1	0
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