Daisuke Kihara

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

194 papers	5,499 citations	39 h-index	67 g-index
223 ext. papers	6,771 ext. citations	5.3 avg, IF	6.01 L-index

#	Paper	IF	Citations
194	Real-time structure search and structure classification for AlphaFold protein models.. *Communications Biology*, **2022**, 5, 316	6.7	4
193	Multi-level analysis of intrinsically disordered protein docking methods. *Methods*, **2022**, 204, 55-63	4.6	0
192	Evolutionary Dynamics of Indels in SARS-CoV-2 Spike Glycoprotein.. *Evolutionary Bioinformatics*, **2021**, 17, 11769343211064616	1.9	0
191	Surface-based protein domains retrieval methods from a SHREC2021 challenge.. *Journal of Molecular Graphics and Modelling*, **2021**, 111, 108103	2.8	1
190	Protein Contact Map Refinement for Improving Structure Prediction Using Generative Adversarial Networks. *Bioinformatics*, **2021**,	7.2	2
189	VESPER: global and local cryo-EM map alignment using local density vectors. *Nature Communications*, **2021**, 12, 2090	17.4	1
188	Detecting protein and DNA/RNA structures in cryo-EM maps of intermediate resolution using deep learning. *Nature Communications*, **2021**, 12, 2302	17.4	7
187	Analyzing effect of quadruple multiple sequence alignments on deep learning based protein inter-residue distance prediction. *Scientific Reports*, **2021**, 11, 7574	4.9	6
186	Mass spectrometry-based proteomic platforms for better understanding of SARS-CoV-2 induced pathogenesis and potential diagnostic approaches. *Proteomics*, **2021**, 21, e2000279	4.8	7
185	Protein Docking Model Evaluation by Graph Neural Networks. *Frontiers in Molecular Biosciences*, **2021**, 8, 647915	5.6	7
184	Kinetic and structural parameters governing Fic-mediated adenylylation/AMPylation of the Hsp70 chaperone, BiP/GRP78. *Cell Stress and Chaperones*, **2021**, 26, 639-656	4	4
183	LZerD webserver for pairwise and multiple protein-protein docking. *Nucleic Acids Research*, **2021**, 49, W359-W365	20.1	14
182	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	6.1	0
181	Current progress and future perspectives of polypharmacology : From the view of non-small cell lung cancer. *Seminars in Cancer Biology*, **2021**, 68, 84-91	12.7	14
180	EnAET: A Self-Trained Framework for Semi-Supervised and Supervised Learning With Ensemble Transformations. *IEEE Transactions on Image Processing*, **2021**, 30, 1639-1647	8.7	8
179	Genotype & phenotype in Lowe Syndrome: specific OCRL1 patient mutations differentially impact cellular phenotypes. *Human Molecular Genetics*, **2021**, 30, 198-212	5.6	1
178	Turning Points in My Career Path. *Seibutsu Butsuri*, **2021**, 61, 044-045	0	

177	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. *Nature Methods*, **2021**, 18, 156-164	21.6	22
176	Benchmarking of structure refinement methods for protein complex models. *Proteins: Structure, Function and Bioinformatics*, **2021**, 90, 83	4.2	0
175	LZerD Protein-Protein Docking Webserver Enhanced With Structure Prediction. *Frontiers in Molecular Biosciences*, **2021**, 8, 724947	5.6	3
174	Prediction of protein assemblies, the next frontier: The CASP14-CAPRI experiment. *Proteins: Structure, Function and Bioinformatics*, **2021**, 89, 1800-1823	4.2	17
173	Activation of gene expression by detergent-like protein domains. *IScience*, **2021**, 24, 103017	6.1	0
172	CryoFold: Determining protein structures and data-guided ensembles from cryo-EM density maps. *Matter*, **2021**,	12.7	2
171	SHREC 2021: Retrieval and classification of protein surfaces equipped with physical and chemical properties. *Computers and Graphics*, **2021**, 99, 1-21	1.8	3
170	A Simple But Effective Bert Model for Dialog State Tracking on Resource-Limited Systems **2020**,		4
169	MAINMASTseg: Automated Map Segmentation Method for Cryo-EM Density Maps with Symmetry. *Journal of Chemical Information and Modeling*, **2020**, 60, 2634-2643	6.1	3
168	Computational structure modeling for diverse categories of macromolecular interactions. *Current Opinion in Structural Biology*, **2020**, 64, 1-8	8.1	9
167	2DKD: a toolkit for content-based local image search. *Source Code for Biology and Medicine*, **2020**, 15, 1	1.9	1
166	Protein Structure Modeling from Cryo-EM Map Using MAINMAST and MAINMAST-GUI Plugin. *Methods in Molecular Biology*, **2020**, 2165, 317-336	1.4	0
165	Path-LZerD: Predicting Assembly Order of Multimeric Protein Complexes. *Methods in Molecular Biology*, **2020**, 2074, 95-112	1.4	
164	Matching of EM Map Segments to Structurally-Relevant Bio-molecular Regions. *Communications in Computer and Information Science*, **2020**, 464-478	0.3	
163	IDP-LZerD: Software for Modeling Disordered Protein Interactions. *Methods in Molecular Biology*, **2020**, 2165, 231-244	1.4	1
162	Phage G Structure at 6.1 Å Resolution, Condensed DNA, and Host Identity Revision to a Lysinibacillus. *Journal of Molecular Biology*, **2020**, 432, 4139-4153	6.5	5
161	Performance and enhancement of the LZerD protein assembly pipeline in CAPRI 38-46. *Proteins: Structure, Function and Bioinformatics*, **2020**, 88, 948-961	4.2	6
160	Protein docking model evaluation by 3D deep convolutional neural networks. *Bioinformatics*, **2020**, 36, 2113-2118	7.2	27

159	SHREC 2020: Multi-domain protein shape retrieval challenge. *Computers and Graphics*, **2020**, 91, 189-198	1.8	5
158	Current Challenges and Opportunities in Designing Protein-Protein Interaction Targeted Drugs. *Advances and Applications in Bioinformatics and Chemistry*, **2020**, 13, 11-25	1.5	10
157	SHREC 2020: Classification in cryo-electron tomograms. *Computers and Graphics*, **2020**, 91, 279-289	1.8	6
156	Predicting binding poses and affinity ranking in D3R Grand Challenge using PL-PatchSurfer2.0. *Journal of Computer-Aided Molecular Design*, **2019**, 33, 1083-1094	4.2	0
155	Modeling protein-protein interactions with intrinsically disordered proteins **2019**, 189-206		2
154	Computational identification of protein-protein interactions in model plant proteomes. *Scientific Reports*, **2019**, 9, 8740	4.9	21
153	Three-Dimensional Krawtchouk Descriptors for Protein Local Surface Shape Comparison. *Pattern Recognition*, **2019**, 93, 534-545	7.7	8
152	Lactose derivatives as potential inhibitors of pectin methylesterases. *International Journal of Biological Macromolecules*, **2019**, 132, 1140-1146	7.9	4
151	The Balancing Act of Intrinsically Disordered Proteins: Enabling Functional Diversity while Minimizing Promiscuity. *Journal of Molecular Biology*, **2019**, 431, 1650-1670	6.5	24
150	A global map of the protein shape universe. *PLoS Computational Biology*, **2019**, 15, e1006969	5	12
149	55 Years of the Rossmann Fold. *Methods in Molecular Biology*, **2019**, 1958, 1-13	1.4	9
148	Study of the Variability of the Native Protein Structure **2019**, 606-619		2
147	Phylo-PFP: improved automated protein function prediction using phylogenetic distance of distantly related sequences. *Bioinformatics*, **2019**, 35, 753-759	7.2	12
146	Protein secondary structure detection in intermediate-resolution cryo-EM maps using deep learning. *Nature Methods*, **2019**, 16, 911-917	21.6	30
145	Implementation of pharmacophore-based 3D QSAR model and scaffold analysis in order to excavate pristine ALK inhibitors. *Medicinal Chemistry Research*, **2019**, 28, 1726-1739	2.2	3
144	Blind prediction of homo- and hetero-protein complexes: The CASP13-CAPRI experiment. *Proteins: Structure, Function and Bioinformatics*, **2019**, 87, 1200-1221	4.2	58
143	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	0.5	
142	A Gated Self-attention Memory Network for Answer Selection **2019**,		6

141	Survey of Machine Learning Techniques for Prediction of the Isoform Specificity of Cytochrome P450 Substrates. *Current Drug Metabolism*, **2019**, 20, 229-235	3.5	18
140	Advances in Structure Modeling Methods for Cryo-Electron Microscopy Maps. *Molecules*, **2019**, 25,	4.8	13
139	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. *Genome Biology*, **2019**, 20, 244	18.3	111
138	A prospective compound screening contest identified broader inhibitors for Sirtuin 1. *Scientific Reports*, **2019**, 9, 19585	4.9	5
137	NNTox: Gene Ontology-Based Protein Toxicity Prediction Using Neural Network. *Scientific Reports*, **2019**, 9, 17923	4.9	7
136	Prediction of protein group function by iterative classification on functional relevance network. *Bioinformatics*, **2019**, 35, 1388-1394	7.2	1
135	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	11
134	Virtual Ligand Screening Using PL-PatchSurfer2, a Molecular Surface-Based Protein-Ligand Docking Method. *Methods in Molecular Biology*, **2018**, 1762, 105-121	1.4	4
133	Improved performance in CAPRI round 37 using LZerD docking and template-based modeling with combined scoring functions. *Proteins: Structure, Function and Bioinformatics*, **2018**, 86 Suppl 1, 311-320	4.2	15
132	Protein structure model refinement in CASP12 using short and long molecular dynamics simulations in implicit solvent. *Proteins: Structure, Function and Bioinformatics*, **2018**, 86 Suppl 1, 189-201	4.2	10
131	Computational Methods for Predicting Protein-Protein Interactions Using Various Protein Features. *Current Protocols in Protein Science*, **2018**, 93, e62	3.1	30
130	Computing and Visualizing Gene Function Similarity and Coherence with NaviGO. *Methods in Molecular Biology*, **2018**, 1807, 113-130	1.4	1
129	De novo main-chain modeling for EM maps using MAINMAST. *Nature Communications*, **2018**, 9, 1618	17.4	39
128	Modeling the assembly order of multimeric heteroprotein complexes. *PLoS Computational Biology*, **2018**, 14, e1005937	5	14
127	Identification of Moonlighting Proteins in Genomes Using Text Mining Techniques. *Proteomics*, **2018**, 18, e1800083	4.8	4
126	De novo main-chain modeling with MAINMAST in 2015/2016 EM Model Challenge. *Journal of Structural Biology*, **2018**, 204, 351-359	3.4	12
125	Analysis of Protein Complexes in the Unicellular Cyanobacterium Cyanothece ATCC 51142. *Journal of Proteome Research*, **2018**, 17, 3628-3643	5.6	9
124	Prediction of Local Quality of Protein Structure Models Considering Spatial Neighbors in Graphical Models. *Scientific Reports*, **2017**, 7, 40629	4.9	7

123	Variability of Protein Structure Models from Electron Microscopy. *Structure*, **2017**, 25, 592-602.e2	5.2	10
122	MPFit: Computational Tool for Predicting Moonlighting Proteins. *Methods in Molecular Biology*, **2017**, 1611, 45-57	1.4	3
121	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	5.6	8
120	Using PFP and ESG Protein Function Prediction Web Servers. *Methods in Molecular Biology*, **2017**, 1611, 1-14	1.4	5
119	BindML/BindML+: Detecting Protein-Protein Interaction Interface Propensity from Amino Acid Substitution Patterns. *Methods in Molecular Biology*, **2017**, 1529, 279-289	1.4	4
118	DextMP: deep dive into text for predicting moonlighting proteins. *Bioinformatics*, **2017**, 33, i83-i91	7.2	14
117	An iterative compound screening contest method for identifying target protein inhibitors using the tyrosine-protein kinase Yes. *Scientific Reports*, **2017**, 7, 12038	4.9	18
116	In silico structure-based approaches to discover protein-protein interaction-targeting drugs. *Methods*, **2017**, 131, 22-32	4.6	44
115	NaviGO: interactive tool for visualization and functional similarity and coherence analysis with gene ontology. *BMC Bioinformatics*, **2017**, 18, 177	3.6	31
114	Human and server docking prediction for CAPRI round 30-35 using LZerD with combined scoring functions. *Proteins: Structure, Function and Bioinformatics*, **2017**, 85, 513-527	4.2	15
113	Predicting Real-Valued Protein Residue Fluctuation Using FlexPred. *Methods in Molecular Biology*, **2017**, 1484, 175-186	1.4	3
112	Protein 3D Structure and Electron Microscopy Map Retrieval Using 3D-SURFER2.0 and EM-SURFER. *Current Protocols in Bioinformatics*, **2017**, 60, 3.14.1-3.14.15	24.2	6
111	Modeling disordered protein interactions from biophysical principles. *PLoS Computational Biology*, **2017**, 13, e1005485	5	36
110	Missing gene identification using functional coherence scores. *Scientific Reports*, **2016**, 6, 31725	4.9	2
109	PatchSurfers: Two methods for local molecular property-based binding ligand prediction. *Methods*, **2016**, 93, 41-50	4.6	7
108	Genome-scale prediction of moonlighting proteins using diverse protein association information. *Bioinformatics*, **2016**, 32, 2281-8	7.2	24
107	Combined Approach of Patch-Surfer and PL-PatchSurfer for Protein-Ligand Binding Prediction in CSAR 2013 and 2014. *Journal of Chemical Information and Modeling*, **2016**, 56, 1088-99	6.1	9
106	Ensemble-based evaluation for protein structure models. *Bioinformatics*, **2016**, 32, i314-i321	7.2	5

105	Ranking protein-protein docking results using steered molecular dynamics and potential of mean force calculations. *Journal of Computational Chemistry*, **2016**, 37, 1861-5	3.5	13
104	Protein structure prediction using residue- and fragment-environment potentials in CASP11. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84 Suppl 1, 105-17	4.2	19
103	Prediction of homoprotein and heteroprotein complexes by protein docking and template-based modeling: A CASP-CAPRI experiment. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84 Suppl 1, 323-48	4.2	111
102	Energetic Coupling between Ligand Binding and Dimerization in Escherichia coli Phosphoglycerate Mutase. *Biochemistry*, **2016**, 55, 1711-23	3.2	6
101	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. *Genome Biology*, **2016**, 17, 184	18.3	218
100	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, 1676-91	6.1	17
99	On the origin of protein superfamilies and superfolds. *Scientific Reports*, **2015**, 5, 8166	4.9	10
98	Navigating 3D electron microscopy maps with EM-SURFER. *BMC Bioinformatics*, **2015**, 16, 181	3.6	17
97	PFP/ESG: automated protein function prediction servers enhanced with Gene Ontology visualization tool. *Bioinformatics*, **2015**, 31, 271-2	7.2	18
96	The PFP and ESG protein function prediction methods in 2014: effect of database updates and ensemble approaches. *GigaScience*, **2015**, 4, 43	7.6	13
95	Three-dimensional compound comparison methods and their application in drug discovery. *Molecules*, **2015**, 20, 12841-62	4.8	35
94	GenoBase: comprehensive resource database of Escherichia coli K-12. *Nucleic Acids Research*, **2015**, 43, D606-17	20.1	18
93	Tuning of Pectin Methylesterification: PECTIN METHYLESTERASE INHIBITOR 7 MODULATES THE PROCESSIVE ACTIVITY OF CO-EXPRESSED PECTIN METHYLESTERASE 3 IN A pH-DEPENDENT MANNER. *Journal of Biological Chemistry*, **2015**, 290, 23320-35	5.4	33
92	Large-scale binding ligand prediction by improved patch-based method Patch-Surfer2.0. *Bioinformatics*, **2015**, 31, 707-13	7.2	35
91	Structure and inhibition of EV-D68, a virus that causes respiratory illness in children. *Science*, **2015**, 347, 71-4	33.3	105
90	Comparison of image patches using local moment invariants. *IEEE Transactions on Image Processing*, **2014**, 23, 2369-79	8.7	21
89	Assessment of protein side-chain conformation prediction methods in different residue environments. *Proteins: Structure, Function and Bioinformatics*, **2014**, 82, 1971-84	4.2	25
88	Structure-function analysis of the DNA translocating portal of the bacteriophage T4 packaging machine. *Journal of Molecular Biology*, **2014**, 426, 1019-38	6.5	22

87	Detecting local residue environment similarity for recognizing near-native structure models. *Proteins: Structure, Function and Bioinformatics*, **2014**, 82, 3255-72	4.2	7
86	PL-PatchSurfer: a novel molecular local surface-based method for exploring protein-ligand interactions. *International Journal of Molecular Sciences*, **2014**, 15, 15122-45	6.3	16
85	A proteomic strategy for global analysis of plant protein complexes. *Plant Cell*, **2014**, 26, 3867-82	11.6	40
84	The structure of the catalytic domain of a plant cellulose synthase and its assembly into dimers. *Plant Cell*, **2014**, 26, 2996-3009	11.6	46
83	Computational characterization of moonlighting proteins. *Biochemical Society Transactions*, **2014**, 42, 1780-5	5.1	23
82	Genome-scale identification and characterization of moonlighting proteins. *Biology Direct*, **2014**, 9, 30	7.2	36
81	Pairwise and multimeric protein-protein docking using the LZerD program suite. *Methods in Molecular Biology*, **2014**, 1137, 209-34	1.4	29
80	3D-SURFER 2.0: web platform for real-time search and characterization of protein surfaces. *Methods in Molecular Biology*, **2014**, 1137, 105-17	1.4	7
79	In-depth performance evaluation of PFP and ESG sequence-based function prediction methods in CAFA 2011 experiment. *BMC Bioinformatics*, **2013**, 14 Suppl 3, S2	3.6	4
78	Computational methods for constructing protein structure models from 3D electron microscopy maps. *Journal of Structural Biology*, **2013**, 184, 93-102	3.4	31
77	Predicting permanent and transient protein-protein interfaces. *Proteins: Structure, Function and Bioinformatics*, **2013**, 81, 805-18	4.2	34
76	Graphical Models for Protein Function and Structure Prediction **2013**, 191-222		3
75	A large-scale evaluation of computational protein function prediction. *Nature Methods*, **2013**, 10, 221-7	21.6	587
74	Binding site identification in target proteins **2013**, 204-220		
73	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. *Proteins: Structure, Function and Bioinformatics*, **2013**, 81, 1980-7	4.2	78
72	Fitting multimeric protein complexes into electron microscopy maps using 3D Zernike descriptors. *Journal of Physical Chemistry B*, **2012**, 116, 6854-61	3.4	32
71	Evaluation of multiple protein docking structures using correctly predicted pairwise subunits. *BMC Bioinformatics*, **2012**, 13 Suppl 2, S6	3.6	9
70	Effective inter-residue contact definitions for accurate protein fold recognition. *BMC Bioinformatics* , **2012**, 13, 292	3.6	29

69	Protein docking prediction using predicted protein-protein interface. *BMC Bioinformatics*, **2012**, 13, 7	3.6	48
68	Constructing patch-based ligand-binding pocket database for predicting function of proteins. *BMC Bioinformatics*, **2012**, 13 Suppl 2, S7	3.6	7
67	Evaluation of function predictions by PFP, ESG,and PSI-BLAST for moonlighting proteins. *BMC Proceedings*, **2012**, 6 Suppl 7, S5	2.3	18
66	Effect of conformation sampling strategies in genetic algorithm for multiple protein docking. *BMC Proceedings*, **2012**, 6 Suppl 7, S4	2.3	4
65	A novel method for protein-protein interaction site prediction using phylogenetic substitution models. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 126-41	4.2	22
64	Detecting local ligand-binding site similarity in nonhomologous proteins by surface patch comparison. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 1177-95	4.2	44
63	Formyl-coenzyme A (CoA):oxalate CoA-transferase from the acidophile Acetobacter aceti has a distinctive electrostatic surface and inherent acid stability. *Protein Science*, **2012**, 21, 686-96	6.3	14
62	Structural features that predict real-value fluctuations of globular proteins. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 1425-35	4.2	18
61	Multi-LZerD: multiple protein docking for asymmetric complexes. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 1818-33	4.2	53
60	Structure- and sequence-based function prediction for non-homologous proteins. *Journal of Structural and Functional Genomics*, **2012**, 13, 111-23		21
59	Protein domain recurrence and order can enhance prediction of protein functions. *Bioinformatics*, **2012**, 28, i444-i450	7.2	18
58	Error Estimation of Template-Based Protein Structure Models **2011**, 295-314		
57	Energetics-based discovery of protein-ligand interactions on a proteomic scale. *Journal of Molecular Biology*, **2011**, 408, 147-62	6.5	46
56	Community-wide assessment of protein-interface modeling suggests improvements to design methodology. *Journal of Molecular Biology*, **2011**, 414, 289-302	6.5	114
55	Molecular surface representation using 3D Zernike descriptors for protein shape comparison and docking. *Current Protein and Peptide Science*, **2011**, 12, 520-30	2.8	67
54	Quantification of protein group coherence and pathway assignment using functional association. *BMC Bioinformatics*, **2011**, 12, 373	3.6	10
53	Effect of using suboptimal alignments in template-based protein structure prediction. *Proteins: Structure, Function and Bioinformatics*, **2011**, 79, 315-34	4.2	20
52	Identification of a novel effector domain of BIN1 for cancer suppression. *Journal of Cellular Biochemistry*, **2011**, 112, 2992-3001	4.7	9

51	N-terminal Gly(224)-Gly(411) domain in Listeria adhesion protein interacts with host receptor Hsp60. *PLoS ONE*, **2011**, 6, e20694	3.7	27
50	Computational Protein Function Prediction: Framework and Challenges **2011**, 1-17		5
49	Protein Binding Ligand Prediction Using Moments-Based Methods **2011**, 145-163		4
48	Enhanced Sequence-Based Function Prediction Methods and Application to Functional Similarity Networks **2011**, 19-34		1
47	Sub-AQUA: real-value quality assessment of protein structure models. *Protein Engineering, Design and Selection*, **2010**, 23, 617-32	1.9	12
46	Binding ligand prediction for proteins using partial matching of local surface patches. *International Journal of Molecular Sciences*, **2010**, 11, 5009-26	6.3	31
45	Functional enrichment analyses and construction of functional similarity networks with high confidence function prediction by PFP. *BMC Bioinformatics*, **2010**, 11, 265	3.6	16
44	Improved protein surface comparison and application to low-resolution protein structure data. *BMC Bioinformatics*, **2010**, 11 Suppl 11, S2	3.6	19
43	Real-time ligand binding pocket database search using local surface descriptors. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 2007-28	4.2	49
42	Characterization and Classification of Local Protein Surfaces Using Self-Organizing Map. *International Journal of Knowledge Discovery in Bioinformatics*, **2010**, 1, 32-47		8
41	Quality assessment of protein structure models. *Current Protein and Peptide Science*, **2009**, 10, 216-28	2.8	53
40	3D-SURFER: software for high-throughput protein surface comparison and analysis. *Bioinformatics*, **2009**, 25, 2843-4	7.2	62
39	ESG: extended similarity group method for automated protein function prediction. *Bioinformatics*, **2009**, 25, 1739-45	7.2	71
38	Protein-protein docking using region-based 3D Zernike descriptors. *BMC Bioinformatics*, **2009**, 10, 407	3.6	116
37	Potential for protein surface shape analysis using spherical harmonics and 3D Zernike descriptors. *Cell Biochemistry and Biophysics*, **2009**, 54, 23-32	3.2	68
36	PFP: Automated prediction of gene ontology functional annotations with confidence scores using protein sequence data. *Proteins: Structure, Function and Bioinformatics*, **2009**, 74, 566-82	4.2	89
35	Application of 3D Zernike descriptors to shape-based ligand similarity searching. *Journal of Cheminformatics*, **2009**, 1, 19	8.6	39
34	Local surface shape-based protein function prediction using Zernike descriptors. *Biophysical Journal*, **2009**, 96, 650a	2.9	5

33	Automated Prediction of Protein Function from Sequence **2008**, 63-85		3
32	Estimating quality of template-based protein models by alignment stability. *Proteins: Structure, Function and Bioinformatics*, **2008**, 71, 1255-74	4.2	20
31	Combining gene sequence similarity and textual information for gene function annotation in the literature. *Information Retrieval*, **2008**, 11, 389-404	1.8	4
30	Characterization of local geometry of protein surfaces with the visibility criterion. *Proteins: Structure, Function and Bioinformatics*, **2008**, 71, 670-83	4.2	72
29	Fast protein tertiary structure retrieval based on global surface shape similarity. *Proteins: Structure, Function and Bioinformatics*, **2008**, 72, 1259-73	4.2	92
28	Threading without optimizing weighting factors for scoring function. *Proteins: Structure, Function and Bioinformatics*, **2008**, 73, 581-96	4.2	10
27	Rapid comparison of properties on protein surface. *Proteins: Structure, Function and Bioinformatics*, **2008**, 73, 1-10	4.2	63
26	New paradigm in protein function prediction for large scale omics analysis. *Molecular BioSystems*, **2008**, 4, 223-31		27
25	Function prediction of uncharacterized proteins. *Journal of Bioinformatics and Computational Biology*, **2007**, 5, 1-30	1	70
24	Tracing Lineage in Multi-version Scientific Databases **2007**,		2
23	Bioinformatics resources for cancer research with an emphasis on gene function and structure prediction tools. *Cancer Informatics*, **2007**, 2, 25-35	2.4	5
22	Protein Function Prediction in Proteomics Era **2007**, 143-148		
21	EMD: an ensemble algorithm for discovering regulatory motifs in DNA sequences. *BMC Bioinformatics*, **2006**, 7, 342	3.6	32
20	Bioinformatics Resources for Cancer Research with an Emphasis on Gene Function and Structure Prediction Tools. *Cancer Informatics*, **2006**, 2, 117693510600200	2.4	4
19	Statistical potential-based amino acid similarity matrices for aligning distantly related protein sequences. *Proteins: Structure, Function and Bioinformatics*, **2006**, 64, 587-600	4.2	34
18	Enhanced automated function prediction using distantly related sequences and contextual association by PFP. *Protein Science*, **2006**, 15, 1550-6	6.3	109
17	Limitations and potentials of current motif discovery algorithms. *Nucleic Acids Research*, **2005**, 33, 4899-913	2.31	166
16	The effect of long-range interactions on the secondary structure formation of proteins. *Protein Science*, **2005**, 14, 1955-63	6.3	81

15	Microbial genomes have over 72% structure assignment by the threading algorithm PROSPECTOR_Q. *Proteins: Structure, Function and Bioinformatics*, **2004**, 55, 464-73	4.2	30
14	Development and large scale benchmark testing of the PROSPECTOR_3 threading algorithm. *Proteins: Structure, Function and Bioinformatics*, **2004**, 56, 502-18	4.2	137
13	TOUCHSTONEX: protein structure prediction with sparse NMR data. *Proteins: Structure, Function and Bioinformatics*, **2003**, 53, 290-306	4.2	35
12	TOUCHSTONE: a unified approach to protein structure prediction. *Proteins: Structure, Function and Bioinformatics*, **2003**, 53 Suppl 6, 469-79	4.2	69
11	The PDB is a covering set of small protein structures. *Journal of Molecular Biology*, **2003**, 334, 793-802	6.5	101
10	Local energy landscape flattening: parallel hyperbolic Monte Carlo sampling of protein folding. *Proteins: Structure, Function and Bioinformatics*, **2002**, 48, 192-201	4.2	118
9	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, 5993-8	11.5	39
8	Defrosting the frozen approximation: PROSPECTOR□A new approach to threading. *Proteins: Structure, Function and Bioinformatics*, **2001**, 42, 319-331	4.2	117
7	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, 10125-30	11.5	131
6	Characterization and Classification of Local Protein Surfaces Using Self-Organizing Map49-65		
5	Real-Time Structure Search and Structure Classification for AlphaFold Protein Models		2
4	Protein Contact Map Denoising Using Generative Adversarial Networks		1
3	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens		7
2	CryoFold: determining protein structures and ensembles from cryo-EM data		2
1	Super-Resolution Cryo-EM Maps With 3D Deep Generative Networks		2