Burkhard Rost

List of Publications by Year
in descending order

268 papers	34,700 citations	5261 83 h-index	4338 173 g-index
327 all docs	327 docs citations	327 times ranked	33204 citing authors

#	ARTICLE	IF	CITATIONS
1	Prediction of Protein Secondary Structure at Better than 70% Accuracy. Journal of Molecular Biology, 1993, 232, 584-599.	2.0	2,860
2	Combining evolutionary information and neural networks to predict protein secondary structure. Proteins: Structure, Function and Bioinformatics, 1994, 19, 55-72.	1.5	1,465
3	Twilight zone of protein sequence alignments. Protein Engineering, Design and Selection, 1999, 12, 85-94.	1.0	1,446
4	The PredictProtein server. Nucleic Acids Research, 2004, 32, W321-W326.	6.5	1,246
5	[31] PHD: Predicting one-dimensional protein structure by profile-based neural networks. Methods in Enzymology, 1996, 266, 525-539.	0.4	1,147
6	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	9.0	789
7	A Mutation in VPS35, Encoding a Subunit of the Retromer Complex, Causes Late-Onset Parkinson Disease. American Journal of Human Genetics, 2011, 89, 168-175.	2.6	757
8	SNAP: predict effect of non-synonymous polymorphisms on function. Nucleic Acids Research, 2007, 35, 3823-3835.	6.5	728
9	A draft network of ligand–receptor-mediated multicellular signalling in human. Nature Communications, 2015, 6, 7866.	5.8	676
10	Improving the prediction of protein secondary structure in three and eight classes using recurrent neural networks and profiles. Proteins: Structure, Function and Bioinformatics, 2002, 47, 228-235.	1.5	652
11	Transmembrane helices predicted at 95% accuracy. Protein Science, 1995, 4, 521-533.	3.1	628
12	Finding nuclear localization signals. EMBO Reports, 2000, 1, 411-415.	2.0	626
13	Conservation and prediction of solvent accessibility in protein families. Proteins: Structure, Function and Bioinformatics, 1994, 20, 216-226.	1.5	623
14	PredictProtein—an open resource for online prediction of protein structural and functional features. Nucleic Acids Research, 2014, 42, W337-W343.	6.5	589
15	Topology prediction for helical transmembrane proteins at 86% accuracy–Topology prediction at 86% accuracy. Protein Science, 1996, 5, 1704-1718.	3.1	574
16	ProtTrans: Toward Understanding the Language of Life Through Self-Supervised Learning. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2022, 44, 7112-7127.	9.7	496
17	Review: Protein Secondary Structure Prediction Continues to Rise. Journal of Structural Biology, 2001, 134, 204-218.	1.3	487
18	Three-Dimensional Structures of Membrane Proteins from Genomic Sequencing. Cell, 2012, 149, 1607-1621.	13.5	478

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19	Better prediction of functional effects for sequence variants. BMC Genomics, 2015, 16, S1.	1.2	478
20	Analysing Six Types of Protein–Protein Interfaces. Journal of Molecular Biology, 2003, 325, 377-387.	2.0	378
21	Enzyme Function Less Conserved than Anticipated. Journal of Molecular Biology, 2002, 318, 595-608.	2.0	355
22	PHD-an automatic mail server for protein secondary structure prediction. Bioinformatics, 1994, 10, 53-60.	1.8	344
23	A modified definition of Sov, a segment-based measure for protein secondary structure prediction assessment. , 1999, 34, 220-223.		323
24	Redefining the goals of protein secondary structure prediction. Journal of Molecular Biology, 1994, 235, 13-26.	2.0	320
25	Modeling aspects of the language of life through transfer-learning protein sequences. BMC Bioinformatics, 2019, 20, 723.	1.2	319
26	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	3.8	308
27	Mimicking Cellular Sorting Improves Prediction of Subcellular Localization. Journal of Molecular Biology, 2005, 348, 85-100.	2.0	273
28	LocTree3 prediction of localization. Nucleic Acids Research, 2014, 42, W350-W355.	6.5	272
29	Protein fold recognition by prediction-based threading. Journal of Molecular Biology, 1997, 270, 471-480.	2.0	263
30	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
31	Comparing function and structure between entire proteomes. Protein Science, 2001, 10, 1970-1979.	3.1	248
32	ISIS: interaction sites identified from sequence. Bioinformatics, 2007, 23, e13-e16.	1.8	243
33	Protein–Protein Interaction Hotspots Carved into Sequences. PLoS Computational Biology, 2007, 3, e119.	1.5	229
34	Critical assessment of methods of protein structure prediction—Round VIII. Proteins: Structure, Function and Bioinformatics, 2009, 77, 1-4.	1.5	229
35	What's in a name? Why these proteins are intrinsically disordered. Intrinsically Disordered Proteins, 2013, 1, e24157.	1.9	226
36	SNAP predicts effect of mutations on protein function. Bioinformatics, 2008, 24, 2397-2398.	1.8	225

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37	Predicted protein-protein interaction sites from local sequence information. FEBS Letters, 2003, 544, 236-239.	1.3	222
38	Critical assessment of methods of protein structure prediction—Round VII. Proteins: Structure, Function and Bioinformatics, 2007, 69, 3-9.	1.5	199
39	Loopy Proteins Appear Conserved in Evolution. Journal of Molecular Biology, 2002, 322, 53-64.	2.0	187
40	Transmembrane helix predictions revisited. Protein Science, 2009, 11, 2774-2791.	3.1	181
41	Alignments grow, secondary structure prediction improves. Proteins: Structure, Function and Bioinformatics, 2002, 46, 197-205.	1.5	179
42	The PredictProtein server. Nucleic Acids Research, 2003, 31, 3300-3304.	6.5	176
43	Unexpected features of the dark proteome. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15898-15903.	3.3	170
44	Improved Disorder Prediction by Combination of Orthogonal Approaches. PLoS ONE, 2009, 4, e4433.	1.1	170
45	Protein structures sustain evolutionary drift. Folding & Design, 1997, 2, S19-S24.	4.5	168
46	Critical assessment of methods of protein structure prediction (CASP)—Round 6. Proteins: Structure, Function and Bioinformatics, 2005, 61, 3-7.	1.5	162
47	Protein flexibility and rigidity predicted from sequence. Proteins: Structure, Function and Bioinformatics, 2005, 61, 115-126.	1.5	161
48	Adaptation of protein surfaces to subcellular location 1 1Edited by F. E. Cohen. Journal of Molecular Biology, 1998, 276, 517-525.	2.0	158
49	Effective use of sequence correlation and conservation in fold recognition 1 1Edited by J. M. Thornton. Journal of Molecular Biology, 1999, 293, 1221-1239.	2.0	157
50	Prediction of DNA-binding residues from sequence. Bioinformatics, 2007, 23, i347-i353.	1.8	157
51	MSAViewer: interactive JavaScript visualization of multiple sequence alignments. Bioinformatics, 2016, 32, 3501-3503.	1.8	156
52	EVA: evaluation of protein structure prediction servers. Nucleic Acids Research, 2003, 31, 3311-3315.	6.5	154
53	Structure and activity of tryptophan-rich TSPO proteins. Science, 2015, 347, 551-555.	6.0	149
54	Sequence conserved for subcellular localization. Protein Science, 2009, 11, 2836-2847.	3.1	147

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55	FreeContact: fast and free software for protein contact prediction from residue co-evolution. BMC Bioinformatics, 2014, 15, 85.	1.2	146
56	NLSdb: database of nuclear localization signals. Nucleic Acids Research, 2003, 31, 397-399.	6.5	140
57	PROFcon: novel prediction of long-range contacts. Bioinformatics, 2005, 21, 2960-2968.	1.8	138
58	Predicting transmembrane beta-barrels in proteomes. Nucleic Acids Research, 2004, 32, 2566-2577.	6.5	137
59	Continuum Secondary Structure Captures Protein Flexibility. Structure, 2002, 10, 175-184.	1.6	135
60	PROFbval: predict flexible and rigid residues in proteins. Bioinformatics, 2006, 22, 891-893.	1.8	135
61	PredictProtein - Predicting Protein Structure and Function for 29 Years. Nucleic Acids Research, 2021, 49, W535-W540.	6.5	135
62	Protein disorder—a breakthrough invention of evolution?. Current Opinion in Structural Biology, 2011, 21, 412-418.	2.6	134
63	Distinguishing Protein-Coding from Non-Coding RNAs through Support Vector Machines. PLoS Genetics, 2006, 2, e29.	1.5	133
64	Understanding the physical properties that control protein crystallization by analysis of large-scale experimental data. Nature Biotechnology, 2009, 27, 51-57.	9.4	133
65	Structure and selectivity in bestrophin ion channels. Science, 2014, 346, 355-359.	6.0	133
66	CAFASP2: The second critical assessment of fully automated structure prediction methods. Proteins: Structure, Function and Bioinformatics, 2001, 45, 171-183.	1.5	130
67	NORSp: predictions of long regions without regular secondary structure. Nucleic Acids Research, 2003, 31, 3833-3835.	6.5	124
68	PSI-2: Structural Genomics to Cover Protein Domain Family Space. Structure, 2009, 17, 869-881.	1.6	120
69	Crystal structure of a potassium ion transporter, TrkH. Nature, 2011, 471, 336-340.	13.7	120
70	LocText: relation extraction of protein localizations to assist database curation. BMC Bioinformatics, 2018, 19, 15.	1.2	120
71	Natively unstructured regions in proteins identified from contact predictions. Bioinformatics, 2007, 23, 2376-2384.	1.8	118
72	Homologue structure of the SLAC1 anion channel for closing stomata in leaves. Nature, 2010, 467, 1074-1080.	13.7	118

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73	Evaluation of template‐based models in CASP8 with standard measures. Proteins: Structure, Function and Bioinformatics, 2009, 77, 18-28.	1.5	114
74	Tools and data services registry: a community effort to document bioinformatics resources. Nucleic Acids Research, 2016, 44, D38-D47.	6.5	113
75	CAFASP-1: Critical assessment of fully automated structure prediction methods. , 1999, 37, 209-217.		110
76	Evolutionary profiles improve protein–protein interaction prediction from sequence. Bioinformatics, 2015, 31, 1945-1950.	1.8	109
77	EVA: Large-scale analysis of secondary structure prediction. Proteins: Structure, Function and Bioinformatics, 2001, 45, 192-199.	1.5	108
78	UniqueProt: creating representative protein sequence sets. Nucleic Acids Research, 2003, 31, 3789-3791.	6.5	108
79	Protein–Protein Interactions More Conserved within Species than across Species. PLoS Computational Biology, 2006, 2, e79.	1.5	106
80	Membrane protein prediction methods. Methods, 2007, 41, 460-474.	1.9	104
81	Progress of 1D protein structure prediction at last. Proteins: Structure, Function and Bioinformatics, 1995, 23, 295-300.	1.5	97
82	Reliability of Assessment of Protein Structure Prediction Methods. Structure, 2002, 10, 435-440.	1.6	95
83	Embeddings from deep learning transfer GO annotations beyond homology. Scientific Reports, 2021, 11, 1160.	1.6	95
84	Structures of aminoarabinose transferase ArnT suggest a molecular basis for lipid A glycosylation. Science, 2016, 351, 608-612.	6.0	94
85	Progress in protein structure prediction?. Trends in Biochemical Sciences, 1993, 18, 120-123.	3.7	91
86	LocTree2 predicts localization for all domains of life. Bioinformatics, 2012, 28, i458-i465.	1.8	91
87	Jury returns on structure prediction. Nature, 1992, 360, 540-540.	13.7	89
88	Domains, motifs and clusters in the protein universe. Current Opinion in Chemical Biology, 2003, 7, 5-11.	2.8	87
89	DSSPcont: continuous secondary structure assignments for proteins. Nucleic Acids Research, 2003, 31, 3293-3295.	6.5	87
90	CASP6 assessment of contact prediction. Proteins: Structure, Function and Bioinformatics, 2005, 61, 214-224.	1.5	86

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91	Identifying cysteines and histidines in transition-metal-binding sites using support vector machines and neural networks. Proteins: Structure, Function and Bioinformatics, 2006, 65, 305-316.	1.5	86
92	Structural basis for a pH-sensitive calcium leak across membranes. Science, 2014, 344, 1131-1135.	6.0	86
93	Beyond annotation transfer by homology: novel protein-function prediction methods to assist drug discovery. Drug Discovery Today, 2005, 10, 1475-1482.	3.2	84
94	Protein Folding Rates Estimated from Contact Predictions. Journal of Molecular Biology, 2005, 348, 507-512.	2.0	84
95	Natively Unstructured Loops Differ from Other Loops. PLoS Computational Biology, 2007, 3, e140.	1.5	84
96	Protein secondary structure appears to be robust under *in silico* evolution while protein disorder appears not to be. Bioinformatics, 2010, 26, 625-631.	1.8	81
97	Better prediction of sub-cellular localization by combining evolutionary and structural information. Proteins: Structure, Function and Bioinformatics, 2003, 53, 917-930.	1.5	80
98	Inferring sub-cellular localization through automated lexical analysis. Bioinformatics, 2002, 18, S78-S86.	1.8	78
99	Epitome: database of structure-inferred antigenic epitopes. Nucleic Acids Research, 2006, 34, D777-D780.	6.5	78
100	Crystal structure of a phosphorylation-coupled saccharide transporter. Nature, 2011, 473, 50-54.	13.7	77
101	Correlating protein function and stability through the analysis of single amino acid substitutions. BMC Bioinformatics, 2009, 10, S8.	1.2	76
102	Large-Scale Analysis of Thermostable, Mammalian Proteins Provides Insights into the Intrinsically Disordered Proteome. Journal of Proteome Research, 2009, 8, 211-226.	1.8	76
103	Sequence-based prediction of protein domains. Nucleic Acids Research, 2004, 32, 3522-3530.	6.5	73
104	Automated Identification of Complementarity Determining Regions (CDRs) Reveals Peculiar Characteristics of CDRs and B Cell Epitopes. Journal of Immunology, 2008, 181, 6230-6235.	0.4	73
105	Comparisons of NMR Spectral Quality and Success in Crystallization Demonstrate that NMR and X-ray Crystallography Are Complementary Methods for Small Protein Structure Determination. Journal of the American Chemical Society, 2005, 127, 16505-16511.	6.6	72
106	News from the Protein Mutability Landscape. Journal of Molecular Biology, 2013, 425, 3937-3948.	2.0	72
107	Target space for structural genomics revisited. Bioinformatics, 2002, 18, 922-933.	1.8	71
108	Solution NMR Structure of the NlpC/P60 Domain of Lipoprotein Spr from *Escherichia coli*: Structural Evidence for a Novel Cysteine Peptidase Catalytic Triad. Biochemistry, 2008, 47, 9715-9717.	1.2	71

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109	Radiomics in radiooncology â€" Challenging the medical physicist. Physica Medica, 2018, 48, 27-36.	0.4	71
110	Marrying structure and genomics. Structure, 1998, 6, 259-263.	1.6	70
111	Structural genomics is the largest contributor of novel structural leverage. Journal of Structural and Functional Genomics, 2009, 10, 181-191.	1.2	69
112	CHOP proteins into structural domain-like fragments. Proteins: Structure, Function and Bioinformatics, 2004, 55, 678-688.	1.5	68
113	ProNA2020 predicts proteinâ€"DNA, proteinâ€"RNA, and proteinâ€"protein binding proteins and residues from sequence. Journal of Molecular Biology, 2020, 432, 2428-2443.	2.0	67
114	Coordinating the impact of structural genomics on the human Î±-helical transmembrane proteome. Nature Structural and Molecular Biology, 2013, 20, 135-138.	3.6	64
115	PROFtmb: a web server for predicting bacterial transmembrane beta barrel proteins. Nucleic Acids Research, 2006, 34, W186-W188.	6.5	63
116	Protein embeddings and deep learning predict binding residues for various ligand classes. Scientific Reports, 2021, 11, 23916.	1.6	63
117	Automatic target selection for structural genomics on eukaryotes. Proteins: Structure, Function and Bioinformatics, 2004, 56, 188-200.	1.5	62
118	More challenges for machine-learning protein interactions. Bioinformatics, 2015, 31, 1521-1525.	1.8	62
119	NLSdbâ€"major update for database of nuclear localization signals and nuclear export signals. Nucleic Acids Research, 2018, 46, D503-D508.	6.5	61
120	Learned Embeddings from Deep Learning to Visualize and Predict Protein Sets. Current Protocols, 2021, 1, e113.	1.3	61
121	Third Generation Prediction of Secondary Structures. , 2000, 143, 71-95.		60
122	Outcome of a Workshop on Archiving Structural Models of Biological Macromolecules. Structure, 2006, 14, 1211-1217.	1.6	60
123	CAFASPâ€1: Critical assessment of fully automated structure prediction methods. Proteins: Structure, Function and Bioinformatics, 1999, 37, 209-217.	1.5	60
124	Embeddings from protein language models predict conservation and variant effects. Human Genetics, 2022, 141, 1629-1647.	1.8	60
125	Novel leverage of structural genomics. Nature Biotechnology, 2007, 25, 849-851.	9.4	59
126	Aquaria: simplifying discovery and insight from protein structures. Nature Methods, 2015, 12, 98-99.	9.0	58

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127	The New York Consortium on Membrane Protein Structure (NYCOMPS): a high-throughput platform for structural genomics of integral membrane proteins. Journal of Structural and Functional Genomics, 2010, 11, 191-199.	1.2	57
128	CT-based radiomic features predict tumor grading and have prognostic value in patients with soft tissue sarcomas treated with neoadjuvant radiation therapy. Radiotherapy and Oncology, 2019, 135, 187-196.	0.3	57
129	Light attention predicts protein location from the language of life. Bioinformatics Advances, 2021, 1, .	0.9	57
130	Improving Fold Recognition Without Folds. Journal of Molecular Biology, 2004, 341, 255-269.	2.0	54
131	Secondary structure prediction of all-helical proteins in two states. Protein Engineering, Design and Selection, 1993, 6, 831-836.	1.0	52
132	NMPdb: Database of Nuclear Matrix Proteins. Nucleic Acids Research, 2004, 33, D160-D163.	6.5	52
133	Protein language-model embeddings for fast, accurate, and alignment-free protein structure prediction. Structure, 2022, 30, 1169-1177.e4.	1.6	52
134	State-of-the-art in membrane protein prediction. Applied Bioinformatics, 2002, 1, 21-35.	1.7	51
135	TMSEG: Novel prediction of transmembrane helices. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1706-1716.	1.5	49
136	Predict impact of single amino acid change upon protein structure. BMC Genomics, 2012, 13, S4.	1.2	48
137	Comprehensive *in silico* mutagenesis highlights functionally important residues in proteins. Bioinformatics, 2008, 24, i207-i212.	1.8	47
138	MetalDetector: a web server for predicting metal-binding sites and disulfide bridges in proteins from sequence. Bioinformatics, 2008, 24, 2094-2095.	1.8	47
139	LocDB: experimental annotations of localization for Homo sapiens and Arabidopsis thaliana. Nucleic Acids Research, 2011, 39, D230-D234.	6.5	47
140	tagtog: interactive and text-mining-assisted annotation of gene mentions in PLOS full-text articles. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau033-bau033.	1.4	47
141	Did evolution leap to create the protein universe?. Current Opinion in Structural Biology, 2002, 12, 409-416.	2.6	46
142	Structural genomics target selection for the New York consortium on membrane protein structure. Journal of Structural and Functional Genomics, 2009, 10, 255-268.	1.2	46
143	SNPdbe: constructing an nsSNP functional impacts database. Bioinformatics, 2012, 28, 601-602.	1.8	44
144	Rising Accuracy of Protein Secondary Structure Prediction. , 2003, , 207-249.		43

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145	Protein names precisely peeled off free text. Bioinformatics, 2004, 20, i241-i247.	1.8	43
146	Protein function in precision medicine: deep understanding with machine learning. FEBS Letters, 2016, 590, 2327-2341.	1.3	43
147	Validity of machine learning in biology and medicine increased through collaborations across fields of expertise. Nature Machine Intelligence, 2020, 2, 18-24.	8.3	43
148	Translatomics combined with transcriptomics and proteomics reveals novel functional, recently evolved orphan genes in Escherichia coli O157:H7 (EHEC). BMC Genomics, 2016, 17, 133.	1.2	42
149	Pitfalls of protein sequence analysis. Current Opinion in Biotechnology, 1996, 7, 457-461.	3.3	41
150	Characterization of metalloproteins by high-throughput X-ray absorption spectroscopy. Genome Research, 2011, 21, 898-907.	2.4	41
151	Physical protein–protein interactions predicted from microarrays. Bioinformatics, 2008, 24, 2608-2614.	1.8	40
152	Structural genomics plucks high-hanging membrane proteins. Current Opinion in Structural Biology, 2012, 22, 326-332.	2.6	38
153	Homology-based inference sets the bar high for protein function prediction. BMC Bioinformatics, 2013, 14, S7.	1.2	38
154	Discovery of numerous novel small genes in the intergenic regions of the Escherichia coli O157:H7 Sakai genome. PLoS ONE, 2017, 12, e0184119.	1.1	38
155	Contrastive learning on protein embeddings enlightens midnight zone. NAR Genomics and Bioinformatics, 2022, 4, .	1.5	38
156	*In silico* mutagenesis: a case study of the melanocortin 4 receptor. FASEB Journal, 2009, 23, 3059-3069.	0.2	37
157	Computational prediction shines light on type III secretion origins. Scientific Reports, 2016, 6, 34516.	1.6	37
158	Neutral and weakly nonneutral sequence variants may define individuality. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14255-14260.	3.3	36
159	LOC3D: annotate sub-cellular localization for protein structures. Nucleic Acids Research, 2003, 31, 3337-3340.	6.5	35
160	Static benchmarking of membrane helix predictions. Nucleic Acids Research, 2003, 31, 3642-3644.	6.5	35
161	NLProt: extracting protein names and sequences from papers. Nucleic Acids Research, 2004, 32, W634-W637.	6.5	35
162	ProteomicsDB: toward a FAIR open-source resource for life-science research. Nucleic Acids Research, 2022, 50, D1541-D1552.	6.5	35

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163	The protein target list of the Northeast Structural Genomics Consortium. Proteins: Structure, Function and Bioinformatics, 2004, 56, 181-187.	1.5	34
164	MuD: an interactive web server for the prediction of non-neutral substitutions using protein structural data. Nucleic Acids Research, 2010, 38, W523-W528.	6.5	34
165	CAFASP3 in the spotlight of EVA. Proteins: Structure, Function and Bioinformatics, 2003, 53, 548-560.	1.5	32
166	LOCnet and LOCtarget: sub-cellular localization for structural genomics targets. Nucleic Acids Research, 2004, 32, W517-W521.	6.5	32
167	CHOP: parsing proteins into structural domains. Nucleic Acids Research, 2004, 32, W569-W571.	6.5	30
168	Structural elucidation of the Cysâ€His€Gluâ€Asn proteolytic relay in the secreted CHAP domain enzyme from the human pathogen <i>Staphylococcus saprophyticus</i>. Proteins: Structure, Function and Bioinformatics, 2009, 74, 515-519.	1.5	30
169	Large-scale experimental studies show unexpected amino acid effects on protein expression and solubility in vivo in E. coli. Microbial Informatics and Experimentation, 2011, 1, 6.	7.6	30
170	PEP: Predictions for Entire Proteomes. Nucleic Acids Research, 2003, 31, 410-413.	6.5	29
171	Structural genomics reveals EVE as a new ASCH/PUAâ€related domain. Proteins: Structure, Function and Bioinformatics, 2009, 75, 760-773.	1.5	29
172	funtrp: identifying protein positions for variation driven functional tuning. Nucleic Acids Research, 2019, 47, e142-e142.	6.5	29
173	Anatomy of BioJS, an open source community for the life sciences. ELife, 2015, 4, .	2.8	29
174	Evaluation of transmembrane helix predictions in 2014. Proteins: Structure, Function and Bioinformatics, 2015, 83, 473-484.	1.5	27
175	Transmembrane domains in the functions of Fc receptors. Biophysical Chemistry, 2002, 100, 555-575.	1.5	26
176	NMR and X-RAY structures of human E2-like ubiquitin-fold modifier conjugating enzyme 1 (UFC1) reveal structural and functional conservation in the metazoan UFM1-UBA5-UFC1 ubiquination pathway. Journal of Structural and Functional Genomics, 2009, 10, 127-136.	1.2	26
177	Variant effect predictions capture some aspects of deep mutational scanning experiments. BMC Bioinformatics, 2020, 21, 107.	1.2	26
178	Alternative Protein-Protein Interfaces Are Frequent Exceptions. PLoS Computational Biology, 2012, 8, e1002623.	1.5	26
179	Prediction in 1D: Secondary Structure, Membrane Helices, and Accessibility. Methods of Biochemical Analysis, 2005, , 559-587.	0.2	25
180	Solution structure ofArchaeglobus fulgidispeptidyl-tRNA hydrolase (Pth2) provides evidence for an extensive conserved family of Pth2 enzymes in archea, bacteria, and eukaryotes. Protein Science, 2005, 14, 2849-2861.	3.1	25

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181	Long membrane helices and short loops predicted less accurately. Protein Science, 2009, 11, 2766-2773.	3.1	25
182	Structural Basis of O6-Alkylguanine Recognition by a Bacterial Alkyltransferase-like DNA Repair Protein. Journal of Biological Chemistry, 2010, 285, 13736-13741.	1.6	25
183	Clustering FunFams using sequence embeddings improves EC purity. Bioinformatics, 2021, 37, 3449-3455.	1.8	25
184	Protein Subcellular Localization Prediction Using Artificial Intelligence Technology. Methods in Molecular Biology, 2008, 484, 435-463.	0.4	25
185	Structure prediction of proteinsâ€"where are we now?. Current Opinion in Biotechnology, 1994, 5, 372-380.	3.3	24
186	Sisyphus and prediction of protein structure. Bioinformatics, 1997, 13, 345-356.	1.8	24
187	Better 1D predictions by experts with machines. Proteins: Structure, Function and Bioinformatics, 1997, 29, 192-197.	1.5	22
188	Using genetic algorithms to select most predictive protein features. Proteins: Structure, Function and Bioinformatics, 2009, 75, 75-88.	1.5	22
189	HFSP: high speed homology-driven function annotation of proteins. Bioinformatics, 2018, 34, i304-i312.	1.8	22
190	SARSâ€"CoVâ€"2 structural coverage map reveals viral protein assembly, mimicry, and hijacking mechanisms. Molecular Systems Biology, 2021, 17, e10079.	3.2	22
191	Prediction in 1D: secondary structure, membrane helices, and accessibility. Methods of Biochemical Analysis, 2003, 44, 559-87.	0.2	21
192	Solution NMR structure of the 30S ribosomal protein S28E fromPyrococcus horikoshii. Protein Science, 2003, 12, 2823-2830.	3.1	20
193	Towards big data science in the decade ahead from ten years of InCoB and the 1st ISCB-Asia Joint Conference. BMC Bioinformatics, 2011, 12, S1.	1.2	20
194	Solution NMR structure of photosystem II reaction center protein Psb28 from <i>Synechocystis sp</i>. Strain PCC 6803. Proteins: Structure, Function and Bioinformatics, 2011, 79, 340-344.	1.5	20
195	Common sequence variants affect molecular function more than rare variants?. Scientific Reports, 2017, 7, 1608.	1.6	20
196	FunFam protein families improve residue level molecular function prediction. BMC Bioinformatics, 2019, 20, 400.	1.2	20
197	EVAcon: a protein contact prediction evaluation service. Nucleic Acids Research, 2005, 33, W347-W351.	6.5	19
198	Disease-related mutations predicted to impact protein function. BMC Genomics, 2012, 13, S11.	1.2	19

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199	Evolutionary couplings and sequence variation effect predict protein binding sites. Proteins: Structure, Function and Bioinformatics, 2018, 86, 1064-1074.	1.5	18
200	Secondary Structure Prediction. , 2019, , 488-496.		18
201	<i>nala</i>: text mining natural language mutation mentions. Bioinformatics, 2017, 33, 1852-1858.	1.8	17
202	Mutations in transmembrane proteins: diseases, evolutionary insights, prediction and comparison with globular proteins. Briefings in Bioinformatics, 2021, 22, .	3.2	17
203	HeatMapViewer: interactive display of 2D data in biology. F1000Research, 2014, 3, 48.	0.8	17
204	META-PP: single interface to crucial prediction servers. Nucleic Acids Research, 2003, 31, 3308-3310.	6.5	16
205	Cloud Prediction of Protein Structure and Function with PredictProtein for Debian. BioMed Research International, 2013, 2013, 1-6.	0.9	16
206	Role of transmembrane domains in the functions of B- and T-cell receptors. Immunology Letters, 1998, 64, 97-107.	1.1	14
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