

Burkhard Rost

List of Publications by Citations

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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.

279
papers

27,214
citations

78
h-index

162
g-index

327
ext. papers

30,964
ext. citations

9.1
avg, IF

7.33
L-index

#	Paper	IF	Citations
279	Prediction of protein secondary structure at better than 70% accuracy. <i>Journal of Molecular Biology</i> , 1993 , 232, 584-99	6.5	2597
278	Combining evolutionary information and neural networks to predict protein secondary structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994 , 19, 55-72	4.2	1319
277	Twilight zone of protein sequence alignments. <i>Protein Engineering, Design and Selection</i> , 1999 , 12, 85-94	1.9	1129
276	The PredictProtein server. <i>Nucleic Acids Research</i> , 2004 , 32, W321-6	20.1	1082
275	PHD: predicting one-dimensional protein structure by profile-based neural networks. <i>Methods in Enzymology</i> , 1996 , 266, 525-39	1.7	1002
274	A mutation in VPS35, encoding a subunit of the retromer complex, causes late-onset Parkinson disease. <i>American Journal of Human Genetics</i> , 2011 , 89, 168-75	11	624
273	SNAP: predict effect of non-synonymous polymorphisms on function. <i>Nucleic Acids Research</i> , 2007 , 35, 3823-35	20.1	606
272	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013 , 10, 221-7	21.6	587
271	Finding nuclear localization signals. <i>EMBO Reports</i> , 2000 , 1, 411-5	6.5	566
270	Improving the prediction of protein secondary structure in three and eight classes using recurrent neural networks and profiles. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002 , 47, 228-35	4.2	561
269	Transmembrane helices predicted at 95% accuracy. <i>Protein Science</i> , 1995 , 4, 521-33	6.3	551
268	Topology prediction for helical transmembrane proteins at 86% accuracy. <i>Protein Science</i> , 1996 , 5, 1704-18	6.8	536
267	Conservation and prediction of solvent accessibility in protein families. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994 , 20, 216-26	4.2	523
266	PredictProtein--an open resource for online prediction of protein structural and functional features. <i>Nucleic Acids Research</i> , 2014 , 42, W337-43	20.1	433
265	Review: protein secondary structure prediction continues to rise. <i>Journal of Structural Biology</i> , 2001 , 134, 204-18	3.4	406
264	Three-dimensional structures of membrane proteins from genomic sequencing. <i>Cell</i> , 2012 , 149, 1607-21	56.2	395
263	A draft network of ligand-receptor-mediated multicellular signalling in human. <i>Nature Communications</i> , 2015 , 6, 7866	17.4	393

262	Analysing six types of protein-protein interfaces. <i>Journal of Molecular Biology</i> , 2003 , 325, 377-87	6.5	331
261	Enzyme function less conserved than anticipated. <i>Journal of Molecular Biology</i> , 2002 , 318, 595-608	6.5	319
260	Better prediction of functional effects for sequence variants. <i>BMC Genomics</i> , 2015 , 16 Suppl 8, S1	4.5	278
259	A modified definition of Sov, a segment-based measure for protein secondary structure prediction assessment. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , 34, 220-3	4.2	257
258	Redefining the goals of protein secondary structure prediction. <i>Journal of Molecular Biology</i> , 1994 , 235, 13-26	6.5	257
257	PHD--an automatic mail server for protein secondary structure prediction. <i>Bioinformatics</i> , 1994 , 10, 53-60	6.2	257
256	Mimicking cellular sorting improves prediction of subcellular localization. <i>Journal of Molecular Biology</i> , 2005 , 348, 85-100	6.5	253
255	Protein fold recognition by prediction-based threading. <i>Journal of Molecular Biology</i> , 1997 , 270, 471-80	6.5	238
254	Comparing function and structure between entire proteomes. <i>Protein Science</i> , 2001 , 10, 1970-9	6.3	223
253	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016 , 17, 184	18.3	218
252	ISIS: interaction sites identified from sequence. <i>Bioinformatics</i> , 2007 , 23, e13-6	7.2	199
251	Protein-protein interaction hotspots carved into sequences. <i>PLoS Computational Biology</i> , 2007 , 3, e119	5	192
250	Critical assessment of methods of protein structure prediction-Round VII. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69 Suppl 8, 3-9	4.2	189
249	LocTree3 prediction of localization. <i>Nucleic Acids Research</i> , 2014 , 42, W350-5	20.1	183
248	Predicted protein-protein interaction sites from local sequence information. <i>FEBS Letters</i> , 2003 , 544, 236-9	3.8	181
247	SNAP predicts effect of mutations on protein function. <i>Bioinformatics</i> , 2008 , 24, 2397-8	7.2	175
246	What's in a name? Why these proteins are intrinsically disordered: Why these proteins are intrinsically disordered. <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e24157		171
245	Loopy proteins appear conserved in evolution. <i>Journal of Molecular Biology</i> , 2002 , 322, 53-64	6.5	168

244	The PredictProtein server. <i>Nucleic Acids Research</i> , 2003 , 31, 3300-4	20.1	167
243	Improved disorder prediction by combination of orthogonal approaches. <i>PLoS ONE</i> , 2009 , 4, e4433	3.7	157
242	Critical assessment of methods of protein structure prediction - Round VIII. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 77 Suppl 9, 1-4	4.2	154
241	Transmembrane helix predictions revisited. <i>Protein Science</i> , 2002 , 11, 2774-91	6.3	149
240	Critical assessment of methods of protein structure prediction (CASP)--round 6. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61 Suppl 7, 3-7	4.2	148
239	Alignments grow, secondary structure prediction improves. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002 , 46, 197-205	4.2	146
238	Effective use of sequence correlation and conservation in fold recognition. <i>Journal of Molecular Biology</i> , 1999 , 293, 1221-39	6.5	142
237	Adaptation of protein surfaces to subcellular location. <i>Journal of Molecular Biology</i> , 1998 , 276, 517-25	6.5	136
236	EVA: Evaluation of protein structure prediction servers. <i>Nucleic Acids Research</i> , 2003 , 31, 3311-5	20.1	131
235	Protein flexibility and rigidity predicted from sequence. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61, 115-26	4.2	129
234	Protein structures sustain evolutionary drift. <i>Folding & Design</i> , 1997 , 2, S19-24		128
233	Sequence conserved for subcellular localization. <i>Protein Science</i> , 2002 , 11, 2836-47	6.3	126
232	PROFcon: novel prediction of long-range contacts. <i>Bioinformatics</i> , 2005 , 21, 2960-8	7.2	125
231	Protein structure. Structure and activity of tryptophan-rich TSPO proteins. <i>Science</i> , 2015 , 347, 551-5	33.3	124
230	Predicting transmembrane beta-barrels in proteomes. <i>Nucleic Acids Research</i> , 2004 , 32, 2566-77	20.1	123
229	Continuum secondary structure captures protein flexibility. <i>Structure</i> , 2002 , 10, 175-84	5.2	122
228	Prediction of DNA-binding residues from sequence. <i>Bioinformatics</i> , 2007 , 23, i347-53	7.2	120
227	Understanding the physical properties that control protein crystallization by analysis of large-scale experimental data. <i>Nature Biotechnology</i> , 2009 , 27, 51-7	44.5	118

226	NLSdb: database of nuclear localization signals. <i>Nucleic Acids Research</i> , 2003 , 31, 397-9	20.1	118
225	FreeContact: fast and free software for protein contact prediction from residue co-evolution. <i>BMC Bioinformatics</i> , 2014 , 15, 85	3.6	117
224	PROFbval: predict flexible and rigid residues in proteins. <i>Bioinformatics</i> , 2006 , 22, 891-3	7.2	117
223	Protein disorder--a breakthrough invention of evolution?. <i>Current Opinion in Structural Biology</i> , 2011 , 21, 412-8	8.1	111
222	Distinguishing protein-coding from non-coding RNAs through support vector machines. <i>PLoS Genetics</i> , 2006 , 2, e29	6	111
221	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019 , 20, 244	18.3	111
220	PSI-2: structural genomics to cover protein domain family space. <i>Structure</i> , 2009 , 17, 869-81	5.2	108
219	NORSp: Predictions of long regions without regular secondary structure. <i>Nucleic Acids Research</i> , 2003 , 31, 3833-5	20.1	107
218	Evaluation of template-based models in CASP8 with standard measures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 77 Suppl 9, 18-28	4.2	105
217	CAFASP-1: Critical assessment of fully automated structure prediction methods 1999 , 37, 209-217		105
216	Unexpected features of the dark proteome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 15898-903	11.5	103
215	Natively unstructured regions in proteins identified from contact predictions. <i>Bioinformatics</i> , 2007 , 23, 2376-84	7.2	102
214	Crystal structure of a potassium ion transporter, TrkH. <i>Nature</i> , 2011 , 471, 336-40	50.4	101
213	Membrane protein prediction methods. <i>Methods</i> , 2007 , 41, 460-74	4.6	97
212	Homologue structure of the SLAC1 anion channel for closing stomata in leaves. <i>Nature</i> , 2010 , 467, 1074-80	50.4	96
211	Modeling aspects of the language of life through transfer-learning protein sequences. <i>BMC Bioinformatics</i> , 2019 , 20, 723	3.6	96
210	CAFASP2: the second critical assessment of fully automated structure prediction methods. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , Suppl 5, 171-83	4.2	93
209	MSAViewer: interactive JavaScript visualization of multiple sequence alignments. <i>Bioinformatics</i> , 2016 , 32, 3501-3503	7.2	92

208	UniqueProt: Creating representative protein sequence sets. <i>Nucleic Acids Research</i> , 2003 , 31, 3789-91	20.1	88
207	Structure and selectivity in bestrophin ion channels. <i>Science</i> , 2014 , 346, 355-9	33.3	87
206	Reliability of assessment of protein structure prediction methods. <i>Structure</i> , 2002 , 10, 435-40	5.2	87
205	Protein-protein interactions more conserved within species than across species. <i>PLoS Computational Biology</i> , 2006 , 2, e79	5	85
204	Progress of 1D protein structure prediction at last. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995 , 23, 295-300	4.2	84
203	Tools and data services registry: a community effort to document bioinformatics resources. <i>Nucleic Acids Research</i> , 2016 , 44, D38-47	20.1	81
202	EVA: large-scale analysis of secondary structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , Suppl 5, 192-9	4.2	80
201	LocTree2 predicts localization for all domains of life. <i>Bioinformatics</i> , 2012 , 28, i458-i465	7.2	78
200	Protein folding rates estimated from contact predictions. <i>Journal of Molecular Biology</i> , 2005 , 348, 507-16	5	77
199	DSSPcont: Continuous secondary structure assignments for proteins. <i>Nucleic Acids Research</i> , 2003 , 31, 3293-5	20.1	77
198	Natively unstructured loops differ from other loops. <i>PLoS Computational Biology</i> , 2007 , 3, e140	5	76
197	Progress in protein structure prediction?. <i>Trends in Biochemical Sciences</i> , 1993 , 18, 120-3	10.3	76
196	Domains, motifs and clusters in the protein universe. <i>Current Opinion in Chemical Biology</i> , 2003 , 7, 5-11	9.7	75
195	Jury returns on structure prediction. <i>Nature</i> , 1992 , 360, 540	50.4	73
194	CASP6 assessment of contact prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61 Suppl 7, 214-24	4.2	72
193	Identifying cysteines and histidines in transition-metal-binding sites using support vector machines and neural networks. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 65, 305-16	4.2	71
192	Beyond annotation transfer by homology: novel protein-function prediction methods to assist drug discovery. <i>Drug Discovery Today</i> , 2005 , 10, 1475-82	8.8	71
191	Structures of aminoarabinose transferase ArnT suggest a molecular basis for lipid A glycosylation. <i>Science</i> , 2016 , 351, 608-12	33.3	70

190	Protein secondary structure appears to be robust under in silico evolution while protein disorder appears not to be. <i>Bioinformatics</i> , 2010 , 26, 625-31	7.2	70
189	Structural genomics is the largest contributor of novel structural leverage. <i>Journal of Structural and Functional Genomics</i> , 2009 , 10, 181-91		68
188	Crystal structure of a phosphorylation-coupled saccharide transporter. <i>Nature</i> , 2011 , 473, 50-4	50.4	67
187	Better prediction of sub-cellular localization by combining evolutionary and structural information. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 53, 917-30	4.2	67
186	Evolutionary profiles improve protein-protein interaction prediction from sequence. <i>Bioinformatics</i> , 2015 , 31, 1945-50	7.2	66
185	Comparisons of NMR spectral quality and success in crystallization demonstrate that NMR and X-ray crystallography are complementary methods for small protein structure determination. <i>Journal of the American Chemical Society</i> , 2005 , 127, 16505-11	16.4	66
184	Epitome: database of structure-inferred antigenic epitopes. <i>Nucleic Acids Research</i> , 2006 , 34, D777-80	20.1	66
183	Target space for structural genomics revisited. <i>Bioinformatics</i> , 2002 , 18, 922-33	7.2	66
182	Structural basis for a pH-sensitive calcium leak across membranes. <i>Science</i> , 2014 , 344, 1131-5	33.3	65
181	Marrying structure and genomics. <i>Structure</i> , 1998 , 6, 259-63	5.2	62
180	Sequence-based prediction of protein domains. <i>Nucleic Acids Research</i> , 2004 , 32, 3522-30	20.1	62
179	Large-scale analysis of thermostable, mammalian proteins provides insights into the intrinsically disordered proteome. <i>Journal of Proteome Research</i> , 2009 , 8, 211-26	5.6	61
178	Solution NMR structure of the NlpC/P60 domain of lipoprotein Spr from Escherichia coli: structural evidence for a novel cysteine peptidase catalytic triad. <i>Biochemistry</i> , 2008 , 47, 9715-7	3.2	61
177	Inferring sub-cellular localization through automated lexical analysis. <i>Bioinformatics</i> , 2002 , 18 Suppl 1, S78-86	7.2	61
176	Automatic target selection for structural genomics on eukaryotes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 188-200	4.2	58
175	Coordinating the impact of structural genomics on the human helical transmembrane proteome. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 135-8	17.6	57
174	Automated identification of complementarity determining regions (CDRs) reveals peculiar characteristics of CDRs and B cell epitopes. <i>Journal of Immunology</i> , 2008 , 181, 6230-5	5.3	56
173	News from the protein mutability landscape. <i>Journal of Molecular Biology</i> , 2013 , 425, 3937-48	6.5	55

172	Correlating protein function and stability through the analysis of single amino acid substitutions. <i>BMC Bioinformatics</i> , 2009 , 10 Suppl 8, S8	3.6	55
171	Novel leverage of structural genomics. <i>Nature Biotechnology</i> , 2007 , 25, 849-51	44.5	55
170	PROFtmb: a web server for predicting bacterial transmembrane beta barrel proteins. <i>Nucleic Acids Research</i> , 2006 , 34, W186-8	20.1	55
169	ProtTrans: Towards Cracking the Language of Lifs Code Through Self-Supervised Deep Learning and High Performance Computing. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 2021 , PP,	13.3	55
168	CHOP proteins into structural domain-like fragments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 55, 678-88	4.2	53
167	ProtTrans: Towards Cracking the Language of Life's Code Through Self-Supervised Learning		53
166	Radiomics in radiooncology - Challenging the medical physicist. <i>Physica Medica</i> , 2018 , 48, 27-36	2.7	49
165	Outcome of a workshop on archiving structural models of biological macromolecules. <i>Structure</i> , 2006 , 14, 1211-7	5.2	49
164	State-of-the-art in membrane protein prediction. <i>Applied Bioinformatics</i> , 2002 , 1, 21-35		49
163	Aquaria: simplifying discovery and insight from protein structures. <i>Nature Methods</i> , 2015 , 12, 98-9	21.6	48
162	The New York Consortium on Membrane Protein Structure (NYCOMPS): a high-throughput platform for structural genomics of integral membrane proteins. <i>Journal of Structural and Functional Genomics</i> , 2010 , 11, 191-9		48
161	NMPdb: Database of Nuclear Matrix Proteins. <i>Nucleic Acids Research</i> , 2005 , 33, D160-3	20.1	48
160	Improving fold recognition without folds. <i>Journal of Molecular Biology</i> , 2004 , 341, 255-69	6.5	47
159	Secondary structure prediction of all-helical proteins in two states. <i>Protein Engineering, Design and Selection</i> , 1993 , 6, 831-6	1.9	44
158	Comprehensive in silico mutagenesis highlights functionally important residues in proteins. <i>Bioinformatics</i> , 2008 , 24, i207-12	7.2	41
157	Did evolution leap to create the protein universe?. <i>Current Opinion in Structural Biology</i> , 2002 , 12, 409-163.1		41
156	MetalDetector: a web server for predicting metal-binding sites and disulfide bridges in proteins from sequence. <i>Bioinformatics</i> , 2008 , 24, 2094-5	7.2	40
155	SNPdbe: constructing an nsSNP functional impacts database. <i>Bioinformatics</i> , 2012 , 28, 601-2	7.2	39

154	Third generation prediction of secondary structures. <i>Methods in Molecular Biology</i> , 2000 , 143, 71-95	1.4	39
153	CAFASP-1: critical assessment of fully automated structure prediction methods. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , Suppl 3, 209-17	4.2	39
152	Structural genomics target selection for the New York consortium on membrane protein structure. <i>Journal of Structural and Functional Genomics</i> , 2009 , 10, 255-68		38
151	LocDB: experimental annotations of localization for Homo sapiens and Arabidopsis thaliana. <i>Nucleic Acids Research</i> , 2011 , 39, D230-4	20.1	38
150	LocText: relation extraction of protein localizations to assist database curation. <i>BMC Bioinformatics</i> , 2018 , 19, 15	3.6	37
149	In silico mutagenesis: a case study of the melanocortin 4 receptor. <i>FASEB Journal</i> , 2009 , 23, 3059-69	0.9	34
148	Physical protein-protein interactions predicted from microarrays. <i>Bioinformatics</i> , 2008 , 24, 2608-14	7.2	34
147	Structural genomics plucks high-hanging membrane proteins. <i>Current Opinion in Structural Biology</i> , 2012 , 22, 326-32	8.1	33
146	Predict impact of single amino acid change upon protein structure. <i>BMC Genomics</i> , 2012 , 13 Suppl 4, S4	4.5	33
145	Characterization of metalloproteins by high-throughput X-ray absorption spectroscopy. <i>Genome Research</i> , 2011 , 21, 898-907	9.7	33
144	Pitfalls of protein sequence analysis. <i>Current Opinion in Biotechnology</i> , 1996 , 7, 457-61	11.4	33
143	More challenges for machine-learning protein interactions. <i>Bioinformatics</i> , 2015 , 31, 1521-5	7.2	32
142	tagtog: interactive and text-mining-assisted annotation of gene mentions in PLOS full-text articles. <i>Database: the Journal of Biological Databases and Curation</i> , 2014 , 2014, bau033	5	32
141	MuD: an interactive web server for the prediction of non-neutral substitutions using protein structural data. <i>Nucleic Acids Research</i> , 2010 , 38, W523-8	20.1	32
140	NLProt: extracting protein names and sequences from papers. <i>Nucleic Acids Research</i> , 2004 , 32, W634-7	20.1	32
139	The protein target list of the Northeast Structural Genomics Consortium. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 181-7	4.2	32
138	Protein function in precision medicine: deep understanding with machine learning. <i>FEBS Letters</i> , 2016 , 590, 2327-41	3.8	31
137	LOC3D: annotate sub-cellular localization for protein structures. <i>Nucleic Acids Research</i> , 2003 , 31, 3337-40	20.1	31

136	PredictProtein - Predicting Protein Structure and Function for 29 Years. <i>Nucleic Acids Research</i> , 2021 , 49, W535-W540	20.1	31
135	Neutral and weakly nonneutral sequence variants may define individuality. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 14255-60	11.5	30
134	Static benchmarking of membrane helix predictions. <i>Nucleic Acids Research</i> , 2003 , 31, 3642-4	20.1	30
133	Protein names precisely peeled off free text. <i>Bioinformatics</i> , 2004 , 20 Suppl 1, i241-7	7.2	30
132	CT-based radiomic features predict tumor grading and have prognostic value in patients with soft tissue sarcomas treated with neoadjuvant radiation therapy. <i>Radiotherapy and Oncology</i> , 2019 , 135, 187-196	5.3	29
131	NLSdb-major update for database of nuclear localization signals and nuclear export signals. <i>Nucleic Acids Research</i> , 2018 , 46, D503-D508	20.1	29
130	LOCnet and LOcTarget: sub-cellular localization for structural genomics targets. <i>Nucleic Acids Research</i> , 2004 , 32, W517-21	20.1	29
129	CHOP: parsing proteins into structural domains. <i>Nucleic Acids Research</i> , 2004 , 32, W569-71	20.1	28
128	Structural elucidation of the Cys-His-Glu-Asn proteolytic relay in the secreted CHAP domain enzyme from the human pathogen <i>Staphylococcus saprophyticus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 74, 515-9	4.2	27
127	Computational prediction shines light on type III secretion origins. <i>Scientific Reports</i> , 2016 , 6, 34516	4.9	27
126	TMSEG: Novel prediction of transmembrane helices. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84, 1706-1716	4.2	26
125	Homology-based inference sets the bar high for protein function prediction. <i>BMC Bioinformatics</i> , 2013 , 14 Suppl 3, S7	3.6	26
124	Transmembrane domains in the functions of Fc receptors. <i>Biophysical Chemistry</i> , 2003 , 100, 555-75	3.5	26
123	PEP: Predictions for Entire Proteomes. <i>Nucleic Acids Research</i> , 2003 , 31, 410-3	20.1	26
122	Rising Accuracy of Protein Secondary Structure Prediction 2003 , 207-249		25
121	CAFASP3 in the spotlight of EVA. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 53 Suppl 6, 548-602	4.2	25
120	Translatomics combined with transcriptomics and proteomics reveals novel functional, recently evolved orphan genes in <i>Escherichia coli</i> O157:H7 (EHEC). <i>BMC Genomics</i> , 2016 , 17, 133	4.5	25
119	Embeddings from deep learning transfer GO annotations beyond homology. <i>Scientific Reports</i> , 2021 , 11, 1160	4.9	25

118	Alternative protein-protein interfaces are frequent exceptions. <i>PLoS Computational Biology</i> , 2012 , 8, e1002623	5	24
117	Validity of machine learning in biology and medicine increased through collaborations across fields of expertise. <i>Nature Machine Intelligence</i> , 2020 , 2, 18-24	22.5	23
116	Solution structure of <i>Archaeglobus fulgidis</i> peptidyl-tRNA hydrolase (Pth2) provides evidence for an extensive conserved family of Pth2 enzymes in archaea, bacteria, and eukaryotes. <i>Protein Science</i> , 2005 , 14, 2849-61	6.3	23
115	Better 1D predictions by experts with machines. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997 , 29, 192-197	4.2	22
114	Large-scale experimental studies show unexpected amino acid effects on protein expression and solubility in vivo in <i>E. coli</i> . <i>Microbial Informatics and Experimentation</i> , 2011 , 1, 6		21
113	Structural genomics reveals EVE as a new ASCH/PUA-related domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 75, 760-73	4.2	21
112	Long membrane helices and short loops predicted less accurately. <i>Protein Science</i> , 2002 , 11, 2766-73	6.3	21
111	Evaluation of transmembrane helix predictions in 2014. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015 , 83, 473-84	4.2	20
110	Using genetic algorithms to select most predictive protein features. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 75, 75-88	4.2	20
109	Prediction in 1D: secondary structure, membrane helices, and accessibility. <i>Methods of Biochemical Analysis</i> , 2003 , 44, 559-87		20
108	ProNA2020 predicts protein-DNA, protein-RNA, and protein-protein binding proteins and residues from sequence. <i>Journal of Molecular Biology</i> , 2020 , 432, 2428-2443	6.5	19
107	Structural basis of O6-alkylguanine recognition by a bacterial alkyltransferase-like DNA repair protein. <i>Journal of Biological Chemistry</i> , 2010 , 285, 13736-41	5.4	19
106	Solution NMR structure of the 30S ribosomal protein S28E from <i>Pyrococcus horikoshii</i> . <i>Protein Science</i> , 2003 , 12, 2823-30	6.3	19
105	Protein subcellular localization prediction using artificial intelligence technology. <i>Methods in Molecular Biology</i> , 2008 , 484, 435-63	1.4	19
104	EVAcon: a protein contact prediction evaluation service. <i>Nucleic Acids Research</i> , 2005 , 33, W347-51	20.1	18
103	Structure prediction of proteins--where are we now?. <i>Current Opinion in Biotechnology</i> , 1994 , 5, 372-80	11.4	18
102	Anatomy of BioJS, an open source community for the life sciences. <i>ELife</i> , 2015 , 4,	8.9	18
101	Modeling the language of life [Deep Learning Protein Sequences		18

100	Common sequence variants affect molecular function more than rare variants?. <i>Scientific Reports</i> , 2017 , 7, 1608	4.9	17
99	funtrp: identifying protein positions for variation driven functional tuning. <i>Nucleic Acids Research</i> , 2019 , 47, e142	20.1	17
98	Solution NMR structure of photosystem II reaction center protein Psb28 from <i>Synechocystis</i> sp. Strain PCC 6803. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79, 340-4	4.2	17
97	Discovery of numerous novel small genes in the intergenic regions of the <i>Escherichia coli</i> O157:H7 Sakai genome. <i>PLoS ONE</i> , 2017 , 12, e0184119	3.7	17
96	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 ubiquitination pathway. <i>Journal of Structural and Functional Genomics</i> , 2009 , 10, 127-36		16
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