Burkhard Rost

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/7266712/burkhard-rost-publications-by-year.pdf
Version: 2024-04-27

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	ProteomicsDB: toward a FAIR open-source resource for life-science research. *Nucleic Acids Research* , **2021**,	20.1	7
278	Protein matchmaking through representation learning. *Cell Systems*, **2021**, 12, 948-950	10.6	
277	PredictProtein - Predicting Protein Structure and Function for 29 Years. *Nucleic Acids Research*, **2021**, 49, W535-W540	20.1	31
276	Clustering FunFams using sequence embeddings improves EC purity. *Bioinformatics*, **2021**,	7.2	5
275	Learned Embeddings from Deep Learning to Visualize and Predict Protein Sets. *Current Protocols*, **2021**, 1, e113		15
274	Spectrum of Protein Location in Proteomes Captures Evolutionary Relationship Between Species. *Journal of Molecular Evolution*, **2021**, 89, 544-553	3.1	1
273	Mutations in transmembrane proteins: diseases, evolutionary insights, prediction and comparison with globular proteins. *Briefings in Bioinformatics*, **2021**, 22,	13.4	6
272	ProtTrans: Towards Cracking the Language of Lifes Code Through Self-Supervised Deep Learning and High Performance Computing. *IEEE Transactions on Pattern Analysis and Machine Intelligence*, **2021**, PP,	13.3	55
271	SARS-CoV-2 structural coverage map reveals viral protein assembly, mimicry, and hijacking mechanisms. *Molecular Systems Biology*, **2021**, 17, e10079	12.2	5
270	Embeddings from deep learning transfer GO annotations beyond homology. *Scientific Reports*, **2021**, 11, 1160	4.9	25
269	Protein embeddings and deep learning predict binding residues for various ligand classes.. *Scientific Reports*, **2021**, 11, 23916	4.9	4
268	Embeddings from protein language models predict conservation and variant effects.. *Human Genetics*, **2021**, 1	6.3	2
267	Evolutionary model of protein secondary structure capable of revealing new biological relationships. *Proteins: Structure, Function and Bioinformatics*, **2020**, 88, 1251-1259	4.2	
266	Family-specific analysis of variant pathogenicity prediction tools. *NAR Genomics and Bioinformatics*, **2020**, 2, lqaa014	3.7	2
265	Visualizing Human Protein-Protein Interactions and Subcellular Localizations on Cell Images Through CellMap. *Current Protocols in Bioinformatics*, **2020**, 69, e97	24.2	2
264	Variant effect predictions capture some aspects of deep mutational scanning experiments. *BMC Bioinformatics*, **2020**, 21, 107	3.6	12
263	ProNA2020 predicts protein-DNA, protein-RNA, and protein-protein binding proteins and residues from sequence. *Journal of Molecular Biology*, **2020**, 432, 2428-2443	6.5	19

262	Validity of machine learning in biology and medicine increased through collaborations across fields of expertise. *Nature Machine Intelligence*, **2020**, 2, 18-24	22.5	23
261	Protein-protein and protein-nucleic acid binding residues important for common and rare sequence variants in human. *BMC Bioinformatics*, **2020**, 21, 452	3.6	3
260	funtrp: identifying protein positions for variation driven functional tuning. *Nucleic Acids Research*, **2019**, 47, e142	20.1	17
259	Detailed prediction of protein sub-nuclear localization. *BMC Bioinformatics*, **2019**, 20, 205	3.6	0
258	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	5.3	29
257	Secondary Structure Prediction **2019**, 488-496		5
256	FunFam protein families improve residue level molecular function prediction. *BMC Bioinformatics*, **2019**, 20, 400	3.6	10
255	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
254	Modeling aspects of the language of life through transfer-learning protein sequences. *BMC Bioinformatics*, **2019**, 20, 723	3.6	96
253	NLSdb-major update for database of nuclear localization signals and nuclear export signals. *Nucleic Acids Research*, **2018**, 46, D503-D508	20.1	29
252	Radiomics in radiooncology - Challenging the medical physicist. *Physica Medica*, **2018**, 48, 27-36	2.7	49
251	Treatment-related features improve machine learning prediction of prognosis in soft tissue sarcoma patients. *Strahlentherapie Und Onkologie*, **2018**, 194, 824-834	4.3	7
250	HFSP: high speed homology-driven function annotation of proteins. *Bioinformatics*, **2018**, 34, i304-i312	7.2	10
249	ProfPPIdb: Pairs of physical protein-protein interactions predicted for entire proteomes. *PLoS ONE*, **2018**, 13, e0199988	3.7	3
248	Evolutionary couplings and sequence variation effect predict protein binding sites. *Proteins: Structure, Function and Bioinformatics*, **2018**, 86, 1064-1074	4.2	14
247	LocText: relation extraction of protein localizations to assist database curation. *BMC Bioinformatics*, **2018**, 19, 15	3.6	37
246	Structure-based analysis of CysZ-mediated cellular uptake of sulfate. *ELife*, **2018**, 7,	8.9	6
245	Dark Proteins Important for Cellular Function. *Proteomics*, **2018**, 18, e1800227	4.8	5

244	Correcting mistakes in predicting distributions. *Bioinformatics*, **2018**, 34, 3385-3386	7.2	5
243	Bioinformatics advances biology and medicine by turning big data troves into knowledge. *Informatik-Spektrum*, **2017**, 40, 153-160	0.3	1
242	Common sequence variants affect molecular function more than rare variants?. *Scientific Reports*, **2017**, 7, 1608	4.9	17
241	nala: text mining natural language mutation mentions. *Bioinformatics*, **2017**, 33, 1852-1858	7.2	9
240	CellMap visualizes protein-protein interactions and subcellular localization. *F1000Research*, **2017**, 6, 1824	3.6	2
239	CellMap visualizes protein-protein interactions and subcellular localization. *F1000Research*, **2017**, 6, 1824	3.6	3
238	Discovery of numerous novel small genes in the intergenic regions of the Escherichia coli O157:H7 Sakai genome. *PLoS ONE*, **2017**, 12, e0184119	3.7	17
237	Bioinformatics Advances Biology and Medicine by Turning Big Data Troves into Knowledge **2017**, 33-45		
236	TMSEG: Novel prediction of transmembrane helices. *Proteins: Structure, Function and Bioinformatics* , **2016**, 84, 1706-1716	4.2	26
235	Protein function in precision medicine: deep understanding with machine learning. *FEBS Letters*, **2016**, 590, 2327-41	3.8	31
234	MSAViewer: interactive JavaScript visualization of multiple sequence alignments. *Bioinformatics*, **2016**, 32, 3501-3503	7.2	92
233	Tools and data services registry: a community effort to document bioinformatics resources. *Nucleic Acids Research*, **2016**, 44, D38-47	20.1	81
232	Structures of aminoarabinose transferase ArnT suggest a molecular basis for lipid A glycosylation. *Science*, **2016**, 351, 608-12	33.3	70
231	Predicted Molecular Effects of Sequence Variants Link to System Level of Disease. *PLoS Computational Biology*, **2016**, 12, e1005047	5	13
230	Computational prediction shines light on type III secretion origins. *Scientific Reports*, **2016**, 6, 34516	4.9	27
229	Translatomics combined with transcriptomics and proteomics reveals novel functional, recently evolved orphan genes in Escherichia coli O157:H7 (EHEC). *BMC Genomics*, **2016**, 17, 133	4.5	25
228	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. *Genome Biology*, **2016**, 17, 184	18.3	218
227	A draft network of ligand-receptor-mediated multicellular signalling in human. *Nature Communications*, **2015**, 6, 7866	17.4	393

226	ISCB Ebola Award for Important Future Research on the Computational Biology of Ebola Virus. *PLoS Computational Biology*, **2015**, 11, e1004087	5	2
225	ISCB Ebola Award for Important Future Research on the Computational Biology of Ebola Virus. *F1000Research*, **2015**, 4, 12	3.6	1
224	Linked annotations: a middle ground for manual curation of biomedical databases and text corpora. *BMC Proceedings*, **2015**, 9, A4	2.3	4
223	Better prediction of functional effects for sequence variants. *BMC Genomics*, **2015**, 16 Suppl 8, S1	4.5	278
222	Unexpected features of the dark proteome. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 15898-903	11.5	103
221	Evaluation of transmembrane helix predictions in 2014. *Proteins: Structure, Function and Bioinformatics*, **2015**, 83, 473-84	4.2	20
220	More challenges for machine-learning protein interactions. *Bioinformatics*, **2015**, 31, 1521-5	7.2	32
219	Message from the ISCB: ISCB Ebola award for important future research on the computational biology of Ebola virus. *Bioinformatics*, **2015**, 31, 616-7	7.2	2
218	Aquaria: simplifying discovery and insight from protein structures. *Nature Methods*, **2015**, 12, 98-9	21.6	48
217	Protein structure. Structure and activity of tryptophan-rich TSPO proteins. *Science*, **2015**, 347, 551-5	33.3	124
216	Evolutionary profiles improve protein-protein interaction prediction from sequence. *Bioinformatics*, **2015**, 31, 1945-50	7.2	66
215	Environmental Pressure May Change the Composition Protein Disorder in Prokaryotes. *PLoS ONE*, **2015**, 10, e0133990	3.7	7
214	Anatomy of BioJS, an open source community for the life sciences. *ELife*, **2015**, 4,	8.9	18
213	Protein disorder reduced in Saccharomyces cerevisiae to survive heat shock. *F1000Research*, **2015**, 4, 1222	3.6	0
212	Structure and selectivity in bestrophin ion channels. *Science*, **2014**, 346, 355-9	33.3	87
211	Co-expression and co-localization of hub proteins and their partners are encoded in protein sequence. *Molecular BioSystems*, **2014**, 10, 787-94		1
210	Taking structure searches to the next dimension. *Structure*, **2014**, 22, 938-9	5.2	
209	FreeContact: fast and free software for protein contact prediction from residue co-evolution. *BMC Bioinformatics*, **2014**, 15, 85	3.6	117

208	Structural basis for a pH-sensitive calcium leak across membranes. *Science*, **2014**, 344, 1131-5	33.3	65
207	ISCB: past-present perspective for the International Society for Computational Biology. *Bioinformatics*, **2014**, 30, 143-5	7.2	2
206	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	5	32
205	LocTree3 prediction of localization. *Nucleic Acids Research*, **2014**, 42, W350-5	20.1	183
204	PredictProtein--an open resource for online prediction of protein structural and functional features. *Nucleic Acids Research*, **2014**, 42, W337-43	20.1	433
203	HeatMapViewer: interactive display of 2D data in biology. *F1000Research*, **2014**, 3, 48	3.6	14
202	Coordinating the impact of structural genomics on the human αhelical transmembrane proteome. *Nature Structural and Molecular Biology*, **2013**, 20, 135-8	17.6	57
201	Homology-based inference sets the bar high for protein function prediction. *BMC Bioinformatics*, **2013**, 14 Suppl 3, S7	3.6	26
200	News from the protein mutability landscape. *Journal of Molecular Biology*, **2013**, 425, 3937-48	6.5	55
199	A large-scale evaluation of computational protein function prediction. *Nature Methods*, **2013**, 10, 221-7	21.6	587
198	ISCB: past-present perspective for the International Society for Computational Biology. *Bioinformatics*, **2013**, 29, 3243-5	7.2	
197	What's in a name? Why these proteins are intrinsically disordered: Why these proteins are intrinsically disordered. *Intrinsically Disordered Proteins*, **2013**, 1, e24157		171
196	ISCB computational biology Wikipedia competition. *PLoS Computational Biology*, **2013**, 9, e1003242	5	3
195	Cloud prediction of protein structure and function with PredictProtein for Debian. *BioMed Research International*, **2013**, 2013, 398968	3	14
194	An estimated 5% of new protein structures solved today represent a new Pfam family. *Acta Crystallographica Section D: Biological Crystallography*, **2013**, 69, 2186-93		11
193	Neutral and weakly nonneutral sequence variants may define individuality. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 14255-60	11.5	30
192	Accelerating the Original Profile Kernel. *PLoS ONE*, **2013**, 8, e68459	3.7	10
191	Structural genomics plucks high-hanging membrane proteins. *Current Opinion in Structural Biology*, **2012**, 22, 326-32	8.1	33

190	Disease-related mutations predicted to impact protein function. *BMC Genomics*, **2012**, 13 Suppl 4, S11	4.5	15
189	Predict impact of single amino acid change upon protein structure. *BMC Genomics*, **2012**, 13 Suppl 4, S4	4.5	33
188	Three-dimensional structures of membrane proteins from genomic sequencing. *Cell*, **2012**, 149, 1607-21	56.2	395
187	Solution NMR structure of the ribosomal protein RP-L35Ae from Pyrococcus furiosus. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 1901-6	4.2	3
186	SNPdbe: constructing an nsSNP functional impacts database. *Bioinformatics*, **2012**, 28, 601-2	7.2	39
185	LocTree2 predicts localization for all domains of life. *Bioinformatics*, **2012**, 28, i458-i465	7.2	78
184	Alternative protein-protein interfaces are frequent exceptions. *PLoS Computational Biology*, **2012**, 8, e1002623	5	24
183	NMR structure of lipoprotein YxeF from Bacillus subtilis reveals a calycin fold and distant homology with the lipocalin Blc from Escherichia coli. *PLoS ONE*, **2012**, 7, e37404	3.7	4
182	Crystal structure of a potassium ion transporter, TrkH. *Nature*, **2011**, 471, 336-40	50.4	101
181	Crystal structure of a phosphorylation-coupled saccharide transporter. *Nature*, **2011**, 473, 50-4	50.4	67
180	Protein disorder--a breakthrough invention of evolution?. *Current Opinion in Structural Biology*, **2011**, 21, 412-8	8.1	111
179	A mutation in VPS35, encoding a subunit of the retromer complex, causes late-onset Parkinson disease. *American Journal of Human Genetics*, **2011**, 89, 168-75	11	624
178	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		21
177	Towards big data science in the decade ahead from ten years of InCoB and the 1st ISCB-Asia Joint Conference. *BMC Bioinformatics*, **2011**, 12 Suppl 13, S1	3.6	15
176	Solution NMR structure of photosystem II reaction center protein Psb28 from Synechocystis sp. Strain PCC 6803. *Proteins: Structure, Function and Bioinformatics*, **2011**, 79, 340-4	4.2	17
175	Comparison of a molecular dynamics model with the X-ray structure of the N370S acid-beta-glucosidase mutant that causes Gaucher disease. *Protein Engineering, Design and Selection*, **2011**, 24, 773-5	1.9	12
174	ISCB public policy statement on open access to scientific and technical research literature. *Bioinformatics*, **2011**, 27, 291-4	7.2	6
173	LocDB: experimental annotations of localization for Homo sapiens and Arabidopsis thaliana. *Nucleic Acids Research*, **2011**, 39, D230-4	20.1	38

172	Characterization of metalloproteins by high-throughput X-ray absorption spectroscopy. *Genome Research*, **2011**, 21, 898-907	9.7	33
171	ISCB Public Policy Statement on Open Access to Scientific and Technical Research Literature. *PLoS Computational Biology*, **2011**, 7, e1002014	5	6
170	Homologue structure of the SLAC1 anion channel for closing stomata in leaves. *Nature*, **2010**, 467, 1074-80	36.4	96
169	MuD: an interactive web server for the prediction of non-neutral substitutions using protein structural data. *Nucleic Acids Research*, **2010**, 38, W523-8	20.1	32
168	Protein secondary structure appears to be robust under in silico evolution while protein disorder appears not to be. *Bioinformatics*, **2010**, 26, 625-31	7.2	70
167	The Protein Structure Initiative **2010**, 33-44		
166	Structural basis of O6-alkylguanine recognition by a bacterial alkyltransferase-like DNA repair protein. *Journal of Biological Chemistry*, **2010**, 285, 13736-41	5.4	19
165	Bioinformatics predictions of localization and targeting. *Methods in Molecular Biology*, **2010**, 619, 285-305	1.4	6
164	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, 191-9		48
163	Solution NMR structures of proteins VPA0419 from Vibrio parahaemolyticus and yiiS from Shigella flexneri provide structural coverage for protein domain family PFAM 04175. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 779-84	4.2	
162	Solution NMR structure of Lin0431 protein from Listeria innocua reveals high structural similarity with domain II of bacterial transcription antitermination protein NusG. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 2563-8	4.2	2
161	Annotation of Entirely Sequenced Genomes **2010**, 733-745		
160	In silico mutagenesis: a case study of the melanocortin 4 receptor. *FASEB Journal*, **2009**, 23, 3059-69	0.9	34
159	PSI-2: structural genomics to cover protein domain family space. *Structure*, **2009**, 17, 869-81	5.2	108
158	Correlating protein function and stability through the analysis of single amino acid substitutions. *BMC Bioinformatics*, **2009**, 10 Suppl 8, S8	3.6	55
157	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, 127-36		16
156	Structural genomics is the largest contributor of novel structural leverage. *Journal of Structural and Functional Genomics*, **2009**, 10, 181-91		68
155	Structural genomics target selection for the New York consortium on membrane protein structure. *Journal of Structural and Functional Genomics*, **2009**, 10, 255-68		38

154	Cell cycle kinases predicted from conserved biophysical properties. *Proteins: Structure, Function and Bioinformatics*, **2009**, 74, 655-68	4.2	2
153	Using genetic algorithms to select most predictive protein features. *Proteins: Structure, Function and Bioinformatics*, **2009**, 75, 75-88	4.2	20
152	Structural elucidation of the Cys-His-Glu-Asn proteolytic relay in the secreted CHAP domain enzyme from the human pathogen Staphylococcus saprophyticus. *Proteins: Structure, Function and Bioinformatics*, **2009**, 74, 515-9	4.2	27
151	Structural genomics reveals EVE as a new ASCH/PUA-related domain. *Proteins: Structure, Function and Bioinformatics*, **2009**, 75, 760-73	4.2	21
150	NMR structure of protein YvyC from Bacillus subtilis reveals unexpected structural similarity between two PFAM families. *Proteins: Structure, Function and Bioinformatics*, **2009**, 76, 1037-41	4.2	2
149	Evaluation of template-based models in CASP8 with standard measures. *Proteins: Structure, Function and Bioinformatics*, **2009**, 77 Suppl 9, 18-28	4.2	105
148	Critical assessment of methods of protein structure prediction - Round VIII. *Proteins: Structure, Function and Bioinformatics*, **2009**, 77 Suppl 9, 1-4	4.2	154
147	Understanding the physical properties that control protein crystallization by analysis of large-scale experimental data. *Nature Biotechnology*, **2009**, 27, 51-7	44.5	118
146	Large-scale analysis of thermostable, mammalian proteins provides insights into the intrinsically disordered proteome. *Journal of Proteome Research*, **2009**, 8, 211-26	5.6	61
145	Online tools for predicting integral membrane proteins. *Methods in Molecular Biology*, **2009**, 528, 3-23	1.4	8
144	Improved disorder prediction by combination of orthogonal approaches. *PLoS ONE*, **2009**, 4, e4433	3.7	157
143	New in protein structure and function annotation: hotspots, single nucleotide polymorphisms and the 'Deep Web'. *Current Opinion in Drug Discovery & Development*, **2009**, 12, 408-19		5
142	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, 9715-7	3.2	61
141	Comprehensive in silico mutagenesis highlights functionally important residues in proteins. *Bioinformatics*, **2008**, 24, i207-12	7.2	41
140	Powerful fusion: PSI-BLAST and consensus sequences. *Bioinformatics*, **2008**, 24, 1987-93	7.2	9
139	Physical protein-protein interactions predicted from microarrays. *Bioinformatics*, **2008**, 24, 2608-14	7.2	34
138	ISMB 2008 Toronto. *PLoS Computational Biology*, **2008**, 4, e1000094	5	
137	MetalDetector: a web server for predicting metal-binding sites and disulfide bridges in proteins from sequence. *Bioinformatics*, **2008**, 24, 2094-5	7.2	40

136	Automated identification of complementarity determining regions (CDRs) reveals peculiar characteristics of CDRs and B cell epitopes. *Journal of Immunology*, **2008**, 181, 6230-5	5.3	56
135	SNAP predicts effect of mutations on protein function. *Bioinformatics*, **2008**, 24, 2397-8	7.2	175
134	NMR structure of the peptidyl-tRNA hydrolase domain from Pseudomonas syringae expands the structural coverage of the hydrolysis domains of class 1 peptide chain release factors. *Proteins: Structure, Function and Bioinformatics*, **2008**, 71, 1027-31	4.2	7
133	Solution NMR structure of the SOS response protein YnzC from Bacillus subtilis. *Proteins: Structure, Function and Bioinformatics*, **2008**, 72, 526-30	4.2	13
132	Protein conformational flexibility prediction using machine learning. *Journal of Magnetic Resonance* , **2008**, 192, 37-47	3	10
131	Protein subcellular localization prediction using artificial intelligence technology. *Methods in Molecular Biology*, **2008**, 484, 435-63	1.4	19
130	Neural networks predict protein structure and function. *Methods in Molecular Biology*, **2008**, 458, 203-30	1.4	6
129	Solution NMR structure of Escherichia coli ytfP expands the structural coverage of the UPF0131 protein domain family. *Proteins: Structure, Function and Bioinformatics*, **2007**, 68, 789-95	4.2	4
128	Critical assessment of methods of protein structure prediction-Round VII. *Proteins: Structure, Function and Bioinformatics*, **2007**, 69 Suppl 8, 3-9	4.2	189
127	Novel leverage of structural genomics. *Nature Biotechnology*, **2007**, 25, 849-51	44.5	55
126	SNAP: predict effect of non-synonymous polymorphisms on function. *Nucleic Acids Research*, **2007**, 35, 3823-35	20.1	606
125	Consensus sequences improve PSI-BLAST through mimicking profile-profile alignments. *Nucleic Acids Research*, **2007**, 35, 2238-46	20.1	8
124	Natively unstructured loops differ from other loops. *PLoS Computational Biology*, **2007**, 3, e140	5	76
123	Protein-protein interaction hotspots carved into sequences. *PLoS Computational Biology*, **2007**, 3, e119	5	192
122	Prediction of DNA-binding residues from sequence. *Bioinformatics*, **2007**, 23, i347-53	7.2	120
121	ISIS: interaction sites identified from sequence. *Bioinformatics*, **2007**, 23, e13-6	7.2	199
120	Natively unstructured regions in proteins identified from contact predictions. *Bioinformatics*, **2007**, 23, 2376-84	7.2	102
119	Membrane protein prediction methods. *Methods*, **2007**, 41, 460-74	4.6	97

118	Outcome of a workshop on archiving structural models of biological macromolecules. *Structure*, **2006**, 14, 1211-7	5.2	49
117	PROFbval: predict flexible and rigid residues in proteins. *Bioinformatics*, **2006**, 22, 891-3	7.2	117
116	Create and assess protein networks through molecular characteristics of individual proteins. *Bioinformatics*, **2006**, 22, e402-7	7.2	6
115	PROFtmb: a web server for predicting bacterial transmembrane beta barrel proteins. *Nucleic Acids Research*, **2006**, 34, W186-8	20.1	55
114	Distinguishing protein-coding from non-coding RNAs through support vector machines. *PLoS Genetics*, **2006**, 2, e29	6	111
113	Protein-protein interactions more conserved within species than across species. *PLoS Computational Biology*, **2006**, 2, e79	5	85
112	Epitome: database of structure-inferred antigenic epitopes. *Nucleic Acids Research*, **2006**, 34, D777-80	20.1	66
111	Identifying cysteines and histidines in transition-metal-binding sites using support vector machines and neural networks. *Proteins: Structure, Function and Bioinformatics*, **2006**, 65, 305-16	4.2	71
110	EVAcon: a protein contact prediction evaluation service. *Nucleic Acids Research*, **2005**, 33, W347-51	20.1	18
109	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, 16505-11	16.4	66
108	Mimicking cellular sorting improves prediction of subcellular localization. *Journal of Molecular Biology*, **2005**, 348, 85-100	6.5	253
107	Protein folding rates estimated from contact predictions. *Journal of Molecular Biology*, **2005**, 348, 507-12	6.5	77
106	NMPdb: Database of Nuclear Matrix Proteins. *Nucleic Acids Research*, **2005**, 33, D160-3	20.1	48
105	Secondary Structure Assignment. *Methods of Biochemical Analysis*, **2005**, 339-363		3
104	Prediction in 1D: Secondary Structure, Membrane Helices, and Accessibility. *Methods of Biochemical Analysis*, **2005**, 559-587		7
103	Solution structure of Archaeglobus fulgidis peptidyl-tRNA hydrolase (Pth2) provides evidence for an extensive conserved family of Pth2 enzymes in archea, bacteria, and eukaryotes. *Protein Science*, **2005**, 14, 2849-61	6.3	23
102	Beyond annotation transfer by homology: novel protein-function prediction methods to assist drug discovery. *Drug Discovery Today*, **2005**, 10, 1475-82	8.8	71
101	The 2.35 A structure of the TenA homolog from Pyrococcus furiosus supports an enzymatic function in thiamine metabolism. *Acta Crystallographica Section D: Biological Crystallography*, **2005**, 61, 589-98		10

100	Protein flexibility and rigidity predicted from sequence. *Proteins: Structure, Function and Bioinformatics*, **2005**, 61, 115-26	4.2	129
99	Critical assessment of methods of protein structure prediction (CASP)--round 6. *Proteins: Structure, Function and Bioinformatics*, **2005**, 61 Suppl 7, 3-7	4.2	148
98	CASP6 assessment of contact prediction. *Proteins: Structure, Function and Bioinformatics*, **2005**, 61 Suppl 7, 214-24	4.2	72
97	PROFcon: novel prediction of long-range contacts. *Bioinformatics*, **2005**, 21, 2960-8	7.2	125
96	How to Use Protein 1- D Structure Predicted by PROFphd **2005**, 875-901		14
95	CHOP: parsing proteins into structural domains. *Nucleic Acids Research*, **2004**, 32, W569-71	20.1	28
94	Sequence-based prediction of protein domains. *Nucleic Acids Research*, **2004**, 32, 3522-30	20.1	62
93	Protein names precisely peeled off free text. *Bioinformatics*, **2004**, 20 Suppl 1, i241-7	7.2	30
92	Predicting transmembrane beta-barrels in proteomes. *Nucleic Acids Research*, **2004**, 32, 2566-77	20.1	123
91	NLProt: extracting protein names and sequences from papers. *Nucleic Acids Research*, **2004**, 32, W634-7	20.1	32
90	LOCnet and LOCtarget: sub-cellular localization for structural genomics targets. *Nucleic Acids Research*, **2004**, 32, W517-21	20.1	29
89	The PredictProtein server. *Nucleic Acids Research*, **2004**, 32, W321-6	20.1	1082
88	(1)H, (13)C and (15)N assignments for the Archaeglobus fulgidis protein AF2095. *Journal of Biomolecular NMR*, **2004**, 30, 107-8	3	1
87	Automatic target selection for structural genomics on eukaryotes. *Proteins: Structure, Function and Bioinformatics*, **2004**, 56, 188-200	4.2	58
86	The protein target list of the Northeast Structural Genomics Consortium. *Proteins: Structure, Function and Bioinformatics*, **2004**, 56, 181-7	4.2	32
85	CHOP proteins into structural domain-like fragments. *Proteins: Structure, Function and Bioinformatics*, **2004**, 55, 678-88	4.2	53
84	Cataloging proteins in cell cycle control. *Methods in Molecular Biology*, **2004**, 241, 219-33	1.4	4
83	Improving fold recognition without folds. *Journal of Molecular Biology*, **2004**, 341, 255-69	6.5	47

82	Static benchmarking of membrane helix predictions. *Nucleic Acids Research*, **2003**, 31, 3642-4	20.1	30
81	Rising Accuracy of Protein Secondary Structure Prediction **2003**, 207-249		25
80	Transmembrane domains in the functions of Fc receptors. *Biophysical Chemistry*, **2003**, 100, 555-75	3.5	26
79	Domains, motifs and clusters in the protein universe. *Current Opinion in Chemical Biology*, **2003**, 7, 5-11	9.7	75
78	Better prediction of sub-cellular localization by combining evolutionary and structural information. *Proteins: Structure, Function and Bioinformatics*, **2003**, 53, 917-30	4.2	67
77	CAFASP3 in the spotlight of EVA. *Proteins: Structure, Function and Bioinformatics*, **2003**, 53 Suppl 6, 548-60	4.2	25
76	Solution NMR structure of the 30S ribosomal protein S28E from Pyrococcus horikoshii. *Protein Science*, **2003**, 12, 2823-30	6.3	19
75	Analysing six types of protein-protein interfaces. *Journal of Molecular Biology*, **2003**, 325, 377-87	6.5	331
74	Predicted protein-protein interaction sites from local sequence information. *FEBS Letters*, **2003**, 544, 236-9	3.8	181
73	LOC3D: annotate sub-cellular localization for protein structures. *Nucleic Acids Research*, **2003**, 31, 3337-40	20.1	31
72	NORSp: Predictions of long regions without regular secondary structure. *Nucleic Acids Research*, **2003**, 31, 3833-5	20.1	107
71	META-PP: single interface to crucial prediction servers. *Nucleic Acids Research*, **2003**, 31, 3308-10	20.1	10
70	DSSPcont: Continuous secondary structure assignments for proteins. *Nucleic Acids Research*, **2003**, 31, 3293-5	20.1	77
69	The PredictProtein server. *Nucleic Acids Research*, **2003**, 31, 3300-4	20.1	167
68	EVA: Evaluation of protein structure prediction servers. *Nucleic Acids Research*, **2003**, 31, 3311-5	20.1	131
67	UniqueProt: Creating representative protein sequence sets. *Nucleic Acids Research*, **2003**, 31, 3789-91	20.1	88
66	PEP: Predictions for Entire Proteomes. *Nucleic Acids Research*, **2003**, 31, 410-3	20.1	26
65	NLSdb: database of nuclear localization signals. *Nucleic Acids Research*, **2003**, 31, 397-9	20.1	118

64	Prediction in 1D: secondary structure, membrane helices, and accessibility. *Methods of Biochemical Analysis*, **2003**, 44, 559-87		20
63	Long membrane helices and short loops predicted less accurately. *Protein Science*, **2002**, 11, 2766-73	6.3	21
62	Sequence conserved for subcellular localization. *Protein Science*, **2002**, 11, 2836-47	6.3	126
61	Transmembrane helix predictions revisited. *Protein Science*, **2002**, 11, 2774-91	6.3	149
60	Continuum secondary structure captures protein flexibility. *Structure*, **2002**, 10, 175-84	5.2	122
59	Reliability of assessment of protein structure prediction methods. *Structure*, **2002**, 10, 435-40	5.2	87
58	Did evolution leap to create the protein universe?. *Current Opinion in Structural Biology*, **2002**, 12, 409-16	8.1	41
57	Alignments grow, secondary structure prediction improves. *Proteins: Structure, Function and Bioinformatics*, **2002**, 46, 197-205	4.2	146
56	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, 228-35	4.2	561
55	Inferring sub-cellular localization through automated lexical analysis. *Bioinformatics*, **2002**, 18 Suppl 1, S78-86	7.2	61
54	Target space for structural genomics revisited. *Bioinformatics*, **2002**, 18, 922-33	7.2	66
53	Enzyme function less conserved than anticipated. *Journal of Molecular Biology*, **2002**, 318, 595-608	6.5	319
52	Loopy proteins appear conserved in evolution. *Journal of Molecular Biology*, **2002**, 322, 53-64	6.5	168
51	State-of-the-art in membrane protein prediction. *Applied Bioinformatics*, **2002**, 1, 21-35		49
50	CAFASP2: the second critical assessment of fully automated structure prediction methods. *Proteins: Structure, Function and Bioinformatics*, **2001**, Suppl 5, 171-83	4.2	93
49	EVA: large-scale analysis of secondary structure prediction. *Proteins: Structure, Function and Bioinformatics*, **2001**, Suppl 5, 192-9	4.2	80
48	Comparing function and structure between entire proteomes. *Protein Science*, **2001**, 10, 1970-9	6.3	223
47	Review: protein secondary structure prediction continues to rise. *Journal of Structural Biology*, **2001** , 134, 204-18	3.4	406

46	Finding nuclear localization signals. *EMBO Reports*, **2000**, 1, 411-5	6.5	566
45	Third generation prediction of secondary structures. *Methods in Molecular Biology*, **2000**, 143, 71-95	1.4	39
44	Evolution teaches neural networks to predict protein structure **1999**, 207-223		1
43	Twilight zone of protein sequence alignments. *Protein Engineering, Design and Selection*, **1999**, 12, 85-94	1.9	1129
42	CAFASP-1: Critical assessment of fully automated structure prediction methods **1999**, 37, 209-217		105
41	A modified definition of Sov, a segment-based measure for protein secondary structure prediction assessment. *Proteins: Structure, Function and Bioinformatics*, **1999**, 34, 220-3	4.2	257
40	Effective use of sequence correlation and conservation in fold recognition. *Journal of Molecular Biology*, **1999**, 293, 1221-39	6.5	142
39	CAFASP-1: critical assessment of fully automated structure prediction methods. *Proteins: Structure, Function and Bioinformatics*, **1999**, Suppl 3, 209-17	4.2	39
38	Marrying structure and genomics. *Structure*, **1998**, 6, 259-63	5.2	62
37	Role of transmembrane domains in the functions of B- and T-cell receptors. *Immunology Letters*, **1998**, 64, 97-107	4.1	13
36	Adaptation of protein surfaces to subcellular location. *Journal of Molecular Biology*, **1998**, 276, 517-25	6.5	136
35	Sisyphus and prediction of protein structure. *Bioinformatics*, **1997**, 13, 345-56	7.2	10
34	Protein fold recognition by prediction-based threading. *Journal of Molecular Biology*, **1997**, 270, 471-80	6.5	238
33	Protein structures sustain evolutionary drift. *Folding & Design*, **1997**, 2, S19-24		128
32	Better 1D predictions by experts with machines. *Proteins: Structure, Function and Bioinformatics*, **1997**, 29, 192-197	4.2	22
31	PHD: predicting one-dimensional protein structure by profile-based neural networks. *Methods in Enzymology*, **1996**, 266, 525-39	1.7	1002
30	Pitfalls of protein sequence analysis. *Current Opinion in Biotechnology*, **1996**, 7, 457-61	11.4	33
29	Topology prediction for helical transmembrane proteins at 86% accuracy. *Protein Science*, **1996**, 5, 1704-18	6.5	536

28	Transmembrane helices predicted at 95% accuracy. *Protein Science*, **1995**, 4, 521-33	6.3	551
27	Progress of 1D protein structure prediction at last. *Proteins: Structure, Function and Bioinformatics*, **1995**, 23, 295-300	4.2	84
26	Combining evolutionary information and neural networks to predict protein secondary structure. *Proteins: Structure, Function and Bioinformatics*, **1994**, 19, 55-72	4.2	1319
25	Conservation and prediction of solvent accessibility in protein families. *Proteins: Structure, Function and Bioinformatics*, **1994**, 20, 216-26	4.2	523
24	Structure prediction of proteins--where are we now?. *Current Opinion in Biotechnology*, **1994**, 5, 372-80	11.4	18
23	Redefining the goals of protein secondary structure prediction. *Journal of Molecular Biology*, **1994**, 235, 13-26	6.5	257
22	PHD--an automatic mail server for protein secondary structure prediction. *Bioinformatics*, **1994**, 10, 53-60	7.2	257
21	Prediction of protein secondary structure at better than 70% accuracy. *Journal of Molecular Biology* , **1993**, 232, 584-99	6.5	2597
20	Progress in protein structure prediction?. *Trends in Biochemical Sciences*, **1993**, 18, 120-3	10.3	76
19	Secondary structure prediction of all-helical proteins in two states. *Protein Engineering, Design and Selection*, **1993**, 6, 831-6	1.9	44
18	EXERCISING MULTI-LAYERED NETWORKS ON PROTEIN SECONDARY STRUCTURE. *International Journal of Neural Systems*, **1992**, 03, 209-220	6.2	2
17	Jury returns on structure prediction. *Nature*, **1992**, 360, 540	50.4	73
16	Predicting Simplified Features of Protein Structure261-295		
15	Variant effect predictions capture some aspects of deep mutational scanning experiments		2
14	An exhaustive analysis of single amino acid variants in helical transmembrane proteins		1
13	ProtTrans: Towards Cracking the Language of Life▯ Code Through Self-Supervised Learning		53
12	SARS-CoV-2 structural coverage map reveals state changes that disrupt host immunity		5
11	Embeddings from deep learning transfer GO annotations beyond homology		1

List of Publications

10	Evolutionary model of protein secondary structure capable of revealing new biological relationships	1
9	fuNTRp: Identifying protein positions for variation driven functional tuning	3
8	Modeling the language of life – Deep Learning Protein Sequences	18
7	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens	7
6	End-to-end multitask learning, from protein language to protein features without alignments	2
5	Light Attention Predicts Protein Location from the Language of Life	4
4	PredictProtein – Predicting Protein Structure and Function for 29 Years	2
3	Protein language model embeddings for fast, accurate, alignment-free protein structure prediction	5
2	Protein embeddings and deep learning predict binding residues for various ligand classes	1
1	Prediction of Protein Structure Through Evolution1789-1811	5