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List of Publications by Year
in descending order

185 papers	21,324 citations	31976 53 h-index	12597 132 g-index
204 all docs	204 docs citations	204 times ranked	28779 citing authors

#	Article	IF	Citations
1	The Pfam protein families database in 2019. Nucleic Acids Research, 2019, 47, D427-D432.	14.5	3,937
2	Pfam: The protein families database in 2021. Nucleic Acids Research, 2021, 49, D412-D419.	14.5	3,068
3	The InterPro protein families and domains database: 20 years on. Nucleic Acids Research, 2021, 49, D344-D354.	14.5	1,385
4	InterPro in 2017â€"beyond protein family and domain annotations. Nucleic Acids Research, 2017, 45, D190-D199.	14.5	1,358
5	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. Nucleic Acids Research, 2019, 47, D351-D360.	14.5	1,291
6	QMEAN: A comprehensive scoring function for model quality assessment. Proteins: Structure, Function and Bioinformatics, 2008, 71, 261-277.	2.6	888
7	ESpritz: accurate and fast prediction of protein disorder. Bioinformatics, 2012, 28, 503-509.	4.1	445
8	The RING 2.0 web server for high quality residue interaction networks. Nucleic Acids Research, 2016, 44, W367-W374.	14.5	369
9	PASTA 2.0: an improved server for protein aggregation prediction. Nucleic Acids Research, 2014, 42, W301-W307.	14.5	349
10	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
11	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261
12	DisProt 7.0: a major update of the database of disordered proteins. Nucleic Acids Research, 2017, 45, D219-D227.	14.5	242
13	The PASTA server for protein aggregation prediction. Protein Engineering, Design and Selection, 2007, 20, 521-523.	2.1	217
14	Evolutionary and Structural Insights Into the Multifaceted Glutathione Peroxidase (Gpx) Superfamily. Antioxidants and Redox Signaling, 2008, 10, 1501-1514.	5.4	205
15	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. Nucleic Acids Research, 2018, 46, D471-D476.	14.5	190
16	Critical assessment of protein intrinsic disorder prediction. Nature Methods, 2021, 18, 472-481.	19.0	187
17	MobiDB: intrinsically disordered proteins in 2021. Nucleic Acids Research, 2021, 49, D361-D367.	14.5	183
18	MobiDB 2.0: an improved database of intrinsically disordered and mobile proteins. Nucleic Acids Research, 2015, 43, D315-D320.	14.5	177

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19	Ca²⁺ binding to Fâ€ATP synthase Î² subunit triggers the mitochondrial permeability transition. EMBO Reports, 2017, 18, 1065-1076.	4.5	170
20	MobiDB-lite: fast and highly specific consensus prediction of intrinsic disorder in proteins. Bioinformatics, 2017, 33, 1402-1404.	4.1	161
21	LGI1mutations in autosomal dominant and sporadic lateral temporal epilepsy. Human Mutation, 2009, 30, 530-536.	2.5	155
22	Comprehensive large-scale assessment of intrinsic protein disorder. Bioinformatics, 2015, 31, 201-208.	4.1	154
23	The Catalytic Site of Glutathione Peroxidases. Antioxidants and Redox Signaling, 2008, 10, 1515-1526.	5.4	151
24	MobiDB: a comprehensive database of intrinsic protein disorder annotations. Bioinformatics, 2012, 28, 2080-2081.	4.1	142
25	DisProt: intrinsic protein disorder annotation in 2020. Nucleic Acids Research, 2020, 48, D269-D276.	14.5	141
26	QMEANclust: estimation of protein model quality by combining a composite scoring function with structural density information. BMC Structural Biology, 2009, 9, 35.	2.3	131
27	Spritz: a server for the prediction of intrinsically disordered regions in protein sequences using kernel machines. Nucleic Acids Research, 2006, 34, W164-W168.	14.5	121
28	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. Nucleic Acids Research, 2022, 50, D480-D487.	14.5	117
29	RING: networking interacting residues, evolutionary information and energetics in protein structures. Bioinformatics, 2011, 27, 2003-2005.	4.1	116
30	The Thioredoxin Specificity of Drosophila GPx: A Paradigm for a Peroxiredoxin-like Mechanism of many Glutathione Peroxidases. Journal of Molecular Biology, 2007, 365, 1033-1046.	4.2	113
31	Tools and data services registry: a community effort to document bioinformatics resources. Nucleic Acids Research, 2016, 44, D38-D47.	14.5	113
32	Simultaneous quantification of protein order and disorder. Nature Chemical Biology, 2017, 13, 339-342.	8.0	113
33	DOME: recommendations for supervised machine learning validation in biology. Nature Methods, 2021, 18, 1122-1127.	19.0	105
34	Fly cryptochrome and the visual system. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6163-6168.	7.1	103
35	The Victor/FRST Function for Model Quality Estimation. Journal of Computational Biology, 2005, 12, 1316-1327.	1.6	101
36	PhaSePro: the database of proteins driving liquidâ€“liquid phase separation. Nucleic Acids Research, 2020, 48, D360-D367.	14.5	100

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37	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. Nucleic Acids Research, 2021, 49, D404-D411.	14.5	95
38	Heterozygous Reelin Mutations Cause Autosomal-Dominant Lateral Temporal Epilepsy. American Journal of Human Genetics, 2015, 96, 992-1000.	6.2	94
39	NeEMO: a method using residue interaction networks to improve prediction of protein stability upon mutation. BMC Genomics, 2014, 15, S7.	2.8	83
40	Functional Interaction of Phospholipid Hydroperoxide Glutathione Peroxidase with Sperm Mitochondrion-associated Cysteine-rich Protein Discloses the Adjacent Cysteine Motif as a New Substrate of the Selenoperoxidase. Journal of Biological Chemistry, 2005, 280, 38395-38402.	3.4	81
41	The N-terminal half of the receptor domain of botulinum neurotoxin A binds to microdomains of the plasma membrane. Biochemical and Biophysical Research Communications, 2009, 380, 76-80.	2.1	80
42	CSpritz: accurate prediction of protein disorder segments with annotation for homology, secondary structure and linear motifs. Nucleic Acids Research, 2011, 39, W190-W196.	14.5	77
43	RING 3.0: fast generation of probabilistic residue interaction networks from structural ensembles. Nucleic Acids Research, 2022, 50, W651-W656.	14.5	75
44	INGA: protein function prediction combining interaction networks, domain assignments and sequence similarity. Nucleic Acids Research, 2015, 43, W134-W140.	14.5	73
45	Bluues server: electrostatic properties of wild-type and mutated protein structures. Bioinformatics, 2012, 28, 2189-2190.	4.1	72
46	FELLS: fast estimator of latent local structure. Bioinformatics, 2017, 33, 1889-1891.	4.1	72
47	PlaToLoCo: the first web meta-server for visualization and annotation of low complexity regions in proteins. Nucleic Acids Research, 2020, 48, W77-W84.	14.5	71
48	Disentangling the complexity of low complexity proteins. Briefings in Bioinformatics, 2020, 21, 458-472.	6.5	70
49	A divide and conquer approach to fast loop modeling. Protein Engineering, Design and Selection, 2002, 15, 279-286.	2.1	63
50	Simple consensus procedures are effective and sufficient in secondary structure prediction. Protein Engineering, Design and Selection, 2003, 16, 459-462.	2.1	63
51	Gammaâ€glutamyl transferase in the cell wall participates in extracellular glutathione salvage from the root apoplast. New Phytologist, 2009, 181, 115-126.	7.3	58
52	REPETITA: detection and discrimination of the periodicity of protein solenoid repeats by discrete Fourier transform. Bioinformatics, 2009, 25, i289-i295.	4.1	57
53	High-Conductance Channel Formation in Yeast Mitochondria is Mediated by F-ATP Synthase e and g Subunits. Cellular Physiology and Biochemistry, 2018, 50, 1840-1855.	1.6	57
54	Global and local model quality estimation at CASP8 using the scoring functions QMEAN and QMEANclust. Proteins: Structure, Function and Bioinformatics, 2009, 77, 173-180.	2.6	56

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55	Structural insights into the function of human caveolin 1. Biochemical and Biophysical Research Communications, 2005, 338, 1383-1390.	2.1	55
56	Linear motifs in the C-terminus of D. melanogaster cryptochrome. Biochemical and Biophysical Research Communications, 2007, 355, 531-537.	2.1	54
57	Characterization of intellectual disability and autism comorbidity through gene panel sequencing. Human Mutation, 2019, 40, 1346-1363.	2.5	54
58	RepeatsDB: a database of tandem repeat protein structures. Nucleic Acids Research, 2014, 42, D352-D357.	14.5	53
59	Correct machine learning on protein sequences: a peer-reviewing perspective. Briefings in Bioinformatics, 2016, 17, 831-840.	6.5	53
60	A comprehensive assessment of long intrinsic protein disorder from the DisProt database. Bioinformatics, 2018, 34, 445-452.	4.1	53
61	Largeâ€scale analysis of intrinsic disorder flavors and associated functions in the protein sequence universe. Protein Science, 2016, 25, 2164-2174.	7.6	52
62	Familial temporal lobe epilepsy with psychic auras associated with a novel LGI1 mutation. Neurology, 2011, 76, 1173-1176.	1.1	49
63	Low density lipoprotein misfolding and amyloidogenesis. FASEB Journal, 2008, 22, 2350-2356.	0.5	48
64	SODA: prediction of protein solubility from disorder and aggregation propensity. Nucleic Acids Research, 2017, 45, W236-W240.	14.5	47
65	MobiDB-lite 3.0: fast consensus annotation of intrinsic disorder flavors in proteins. Bioinformatics, 2021, 36, 5533-5534.	4.1	47
66	Conformational diversity analysis reveals three functional mechanisms in proteins. PLoS Computational Biology, 2017, 13, e1005398.	3.2	46
67	PDBe-KB: collaboratively defining the biological context of structural data. Nucleic Acids Research, 2022, 50, D534-D542.	14.5	46
68	FuzDrop on AlphaFold: visualizing the sequence-dependent propensity of liquidâ€“liquid phase separation and aggregation of proteins. Nucleic Acids Research, 2022, 50, W337-W344.	14.5	44
69	Application of MM/PBSA colony free energy to loop decoy discrimination: Toward correlation between energy and root mean square deviation. Protein Science, 2005, 14, 889-901.	7.6	41
70	ACRYFROM THE KRILL. Chronobiology International, 2010, 27, 425-445.	2.0	41
71	Protein function prediction using guilty by association from interaction networks. Amino Acids, 2015, 47, 2583-2592.	2.7	40
72	TAP score: torsion angle propensity normalization applied to local protein structure evaluation. BMC Bioinformatics, 2007, 8, 155.	2.6	39

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73	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2017, 38, 1182-1192.	2.5	39
74	Whole-Exome Sequencing Identifies Pathogenic Variants in TJP1 Gene Associated With Arrhythmogenic Cardiomyopathy. Circulation Genomic and Precision Medicine, 2018, 11, e002123.	3.6	38
75	Immune roles of a rhamnose-binding lectin in the colonial ascidian Botryllus schlosseri. Immunobiology, 2011, 216, 725-736.	1.9	37
76	RepeatsDB in 2021: improved data and extended classification for protein tandem repeat structures. Nucleic Acids Research, 2021, 49, D452-D457.	14.5	37
77	VHLdb: A database of von Hippel-Lindau protein interactors and mutations. Scientific Reports, 2016, 6, 31128.	3.3	36
78	The SSEA server for protein secondary structure alignment. Bioinformatics, 2005, 21, 393-395.	4.1	35
79	MOBI: a web server to define and visualize structural mobility in NMR protein ensembles. Bioinformatics, 2010, 26, 2916-2917.	4.1	35
80	Inhibitory interaction of the 14-3-3 proteins with ubiquitous (PMCA1) and tissue-specific (PMCA3) isoforms of the plasma membrane Ca2+ pump. Cell Calcium, 2008, 43, 550-561.	2.4	34
81	RepeatsDB 2.0: improved annotation, classification, search and visualization of repeat protein structures. Nucleic Acids Research, 2017, 45, D308-D312.	14.5	33
82	A Computational Model of the LGI1 Protein Suggests a Common Binding Site for ADAM Proteins. PLoS ONE, 2011, 6, e18142.	2.5	33
83	Arg-8 of yeast subunit e contributes to the stability of F-ATP synthase dimers and to the generation of the full-conductance mitochondrial megachannel. Journal of Biological Chemistry, 2019, 294, 10987-10997.	3.4	32
84	Cardiomyopathy in patients with POMT1-related congenital and limb-girdle muscular dystrophy. European Journal of Human Genetics, 2012, 20, 1234-1239.	2.8	31
85	BOOGIE: Predicting Blood Groups from High Throughput Sequencing Data. PLoS ONE, 2015, 10, e0124579.	2.5	31
86	A Novel WT1 Gene Mutation in a Three-Generation Family with Progressive Isolated Focal Segmental Glomerulosclerosis. Clinical Journal of the American Society of Nephrology: CJASN, 2010, 5, 698-702.	4.5	30
87	Analysis and consensus of currently available intrinsic protein disorder annotation sources in the MobiDB database. BMC Bioinformatics, 2013, 14, S3.	2.6	30
88	A novel <scp>SACS</scp> mutation results in nonâ€ataxic spastic paraplegia and peripheral neuropathy. European Journal of Neurology, 2013, 20, 1486-1491.	3.3	30
89	MANIFOLD: protein fold recognition based on secondary structure, sequence similarity and enzyme classification. Protein Engineering, Design and Selection, 2003, 16, 785-789.	2.1	29
90	RAPHAEL: recognition, periodicity and insertion assignment of solenoid protein structures. Bioinformatics, 2012, 28, 3257-3264.	4.1	27

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91	Isoform-specific interactions of the von Hippel-Lindau tumor suppressor protein. Scientific Reports, 2015, 5, 12605.	3.3	26
92	Adding structural information to the von Hippelâ€“Lindau (VHL) tumor suppressor interaction network. FEBS Letters, 2009, 583, 3704-3710.	2.8	25
93	Classification of Î²-hairpin repeat proteins. Journal of Structural Biology, 2018, 201, 130-138.	2.8	25
94	Experimentally Determined Long Intrinsically Disordered Protein Regions Are Now Abundant in the Protein Data Bank. International Journal of Molecular Sciences, 2020, 21, 4496.	4.1	25
95	FuzDB: a new phase in understanding fuzzy interactions. Nucleic Acids Research, 2022, 50, D509-D517.	14.5	25
96	SARSâ€CoVâ€2 variants preferentially emerge at intrinsically disordered protein sites helping immune evasion. FEBS Journal, 2022, 289, 4240-4250.	4.7	25
97	RUBI: rapid proteomic-scale prediction of lysine ubiquitination and factors influencing predictor performance. Amino Acids, 2014, 46, 853-862.	2.7	24
98	Mobi 2.0: an improved method to define intrinsic disorder, mobility and linear binding regions in protein structures. Bioinformatics, 2018, 34, 122-123.	4.1	24
99	INGA 2.0: improving protein function prediction for the dark proteome. Nucleic Acids Research, 2019, 47, W373-W378.	14.5	24
100	Genotype-phenotype relations of the von Hippel-Lindau tumor suppressor inferred from a large-scale analysis of disease mutations and interactors. PLoS Computational Biology, 2019, 15, e1006478.	3.2	24
101	Secretion-Positive LGI1 Mutations Linked to Lateral Temporal Epilepsy Impair Binding to ADAM22 and ADAM23 Receptors. PLoS Genetics, 2016, 12, e1006376.	3.5	23
102	Disorder transitions and conformational diversity cooperatively modulate biological function in proteins. Protein Science, 2016, 25, 1138-1146.	7.6	23
103	Deletions and Mutations in the Acidic Lipid-binding Region of the Plasma Membrane Ca2+ Pump. Journal of Biological Chemistry, 2010, 285, 30779-30791.	3.4	22
104	The f subunit of human ATP synthase is essential for normal mitochondrial morphology and permeability transition. Cell Reports, 2021, 35, 109111.	6.4	22
105	Exploration of alternative splicing events in ten different grapevine cultivars. BMC Genomics, 2015, 16, 706.	2.8	21
106	Dynamic scaffolds for neuronal signaling: in silico analysis of the TANC protein family. Scientific Reports, 2017, 7, 6829.	3.3	21
107	ECO: the Evidence and Conclusion Ontology, an update for 2022. Nucleic Acids Research, 2022, 50, D1515-D1521.	14.5	21
108	Decomposing protein networks into domain-domain interactions. Bioinformatics, 2005, 21, ii220-ii221.	4.1	19

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109	Identification and In Silico Analysis of Novel von Hippel-Lindau (VHL) Gene Variants from a Large Population. Annals of Human Genetics, 2011, 75, 483-496.	0.8	19
110	Mapping pathogenic mutations suggests an innovative structural model for the pendrin (SLC26A4) transmembrane domain. Biochimie, 2017, 132, 109-120.	2.6	19
111	Design and Analysis of a Petri Net Model of the Von Hippel-Lindau (VHL) Tumor Suppressor Interaction Network. PLoS ONE, 2014, 9, e96986.	2.5	18
112	RepeatsDB-lite: a web server for unit annotation of tandem repeat proteins. Nucleic Acids Research, 2018, 46, W402-W407.	14.5	18
113	The Feature-Viewer: a visualization tool for positional annotations on a sequence. Bioinformatics, 2020, 36, 3244-3245.	4.1	18
114	Improving the quality of protein structure models by selecting from alignment alternatives. BMC Bioinformatics, 2006, 7, 364.	2.6	17
115	Electric dipole reorientation in the interaction of botulinum neurotoxins with neuronal membranes. FEBS Letters, 2009, 583, 2321-2325.	2.8	17
116	CDKN2AUnclassified Variants in Familial Malignant Melanoma: Combining Functional and Computational Approaches for Their Assessment. Human Mutation, 2014, 35, 828-840.	2.5	17
117	Insights into the proline hydroxylase (PHD) family, molecular evolution and its impact on human health. Biochimie, 2015, 116, 114-124.	2.6	17
118	Identification of repetitive units in protein structures with ReUPred. Amino Acids, 2016, 48, 1391-1400.	2.7	17
119	In silico Characterization of Human Prion-Like Proteins: Beyond Neurological Diseases. Frontiers in Physiology, 2019, 10, 314.	2.8	17
120	HIF1Î±-dependent induction of the mitochondrial chaperone TRAP1 regulates bioenergetic adaptations to hypoxia. Cell Death and Disease, 2021, 12, 434.	6.3	17
121	Comparative analysis of [FeFe] hydrogenase from Thermotogales indicates the molecular basis of resistance to oxygen inactivation. International Journal of Hydrogen Energy, 2008, 33, 570-578.	7.1	16
122	Studying Interactions by Molecular Dynamics Simulations at High Concentration. Journal of Biomedicine and Biotechnology, 2012, 2012, 1-9.	3.0	16
123	Calmodulin Enhances Cryptochrome Binding to INAD in Drosophila Photoreceptors. Frontiers in Molecular Neuroscience, 2018, 11, 280.	2.9	15
124	A targeted next-generation gene panel reveals a novel heterozygous nonsense variant in the TP63 gene in patients with arrhythmogenic cardiomyopathy. Heart Rhythm, 2019, 16, 773-780.	0.7	15
125	A decoy set for the thermostable subdomain from chicken villin headpiece, comparison of different free energy estimators. BMC Bioinformatics, 2005, 6, 301.	2.6	14
126	Looking for putative phenoloxidases of compound ascidians: Haemocyanin-like proteins in Polyandrocarpa misakiensis and Botryllus schlosseri. Developmental and Comparative Immunology, 2012, 38, 232-242.	2.3	14

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127	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. Human Mutation, 2017, 38, 1266-1276.	2.5	14
128	The clinical spectrum of CASQ1-related myopathy. Neurology, 2018, 91, e1629-e1641.	1.1	14
129	The pVHL neglected functions, a tale of hypoxia-dependent and -independent regulations in cancer. Open Biology, 2020, 10, 200109.	3.6	14
130	Evaluation of the steric impact of flavin adenine dinucleotide in Drosophila melanogaster cryptochrome function. Biochemical and Biophysical Research Communications, 2014, 450, 1606-1611.	2.1	13
131	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. Human Mutation, 2017, 38, 1042-1050.	2.5	13
132	Large-Scale Prediction of Protein Structure and Function from Sequence. Current Pharmaceutical Design, 2006, 12, 2067-2086.	1.9	12
133	Crohn disease risk predictionâ€"Best practices and pitfalls with exome data. Human Mutation, 2017, 38, 1193-1200.	2.5	12
134	An intrinsically disordered proteins community for ELIXIR. F1000Research, 2019, 8, 1753.	1.6	12
135	In silico investigation of PHDâ€3 specific HIF1â€Î± proline 567 hydroxylation: A new player in the VHL/HIFâ€1Î± interaction pathway?. FEBS Letters, 2013, 587, 2996-3001.	2.8	11
136	The role of the Nâ€terminal tail for the oligomerization, folding and stability of human frataxin. FEBS Open Bio, 2013, 3, 310-320.	2.3	11
137	Comparison of protein repeat classifications based on structure and sequence families. Biochemical Society Transactions, 2015, 43, 832-837.	3.4	11
138	Structural in silico dissection of the collagen V interactome to identify genotypeâ€"phenotype correlations in classic Ehlersâ€"Danlos Syndrome (EDS). FEBS Letters, 2015, 589, 3871-3878.	2.8	11
139	Assessment of patient clinical descriptions and pathogenic variants from gene panel sequences in the CAGIâ€5 intellectual disability challenge. Human Mutation, 2019, 40, 1330-1345.	2.5	11
140	Functional insights from the structural modelling of a small Fe-hydrogenase. Biochemical and Biophysical Research Communications, 2006, 339, 277-283.	2.1	10
141	Assessing predictors for new post translational modification sites: AÂcase study on hydroxylation. PLoS Computational Biology, 2020, 16, e1007967.	3.2	10
142	APICURON: a database to credit and acknowledge the work of biocurators. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	3.0	10
143	TESE: generating specific protein structure test set ensembles. Bioinformatics, 2008, 24, 2632-2633.	4.1	9
144	Where differences resemble: sequence-feature analysis in curated databases of intrinsically disordered proteins. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	9

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145	Network analysis of dynamically important residues in protein structures mediating ligand-binding conformational changes. European Biophysics Journal, 2019, 48, 559-568.	2.2	9
146	2mit, an Intronic Gene of Drosophila melanogaster timeless2, Is Involved in Behavioral Plasticity. PLoS ONE, 2013, 8, e76351.	2.5	9
147	Computational analysis of prolyl hydroxylase domain-containing protein 2 (PHD2) mutations promoting polycythemia insurgence in humans. Scientific Reports, 2016, 6, 18716.	3.3	8
148	Performance of computational methods for the evaluation of pericentriolar material 1 missense variants in CAGIâ€5. Human Mutation, 2019, 40, 1474-1485.	2.5	8
149	Ensembles from Ordered and Disordered Proteins Reveal Similar Structural Constraints during Evolution. Journal of Molecular Biology, 2019, 431, 1298-1307.	4.2	8
150	A novel approach to investigate the evolution of structured tandem repeat protein families by exon duplication. Journal of Structural Biology, 2020, 212, 107608.	2.8	8
151	The MemMoRF database for recognizing disordered protein regions interacting with cellular membranes. Nucleic Acids Research, 2021, 49, D355-D360.	14.5	8
152	FLIPPER: Predicting and Characterizing Linear Interacting Peptides in the Protein Data Bank. Journal of Molecular Biology, 2021, 433, 166900.	4.2	8
153	FRASS: the web-server for RNA structural comparison. BMC Bioinformatics, 2010, 11, 327.	2.6	7
154	Chasing coevolutionary signals in intrinsically disordered proteins complexes. Scientific Reports, 2020, 10, 17962.	3.3	7
155	PANADA: Protein Association Network Annotation, Determination and Analysis. PLoS ONE, 2013, 8, e78383.	2.5	7
156	The Victor C++ library for protein representation and advanced manipulation. Bioinformatics, 2015, 31, 1138-1140.	4.1	6
157	Novel interactions of the von Hippel-Lindau (pVHL) tumor suppressor with the CDKN1 family of cell cycle inhibitors. Scientific Reports, 2017, 7, 46562.	3.3	6
158	Lessons from the CAGIâ€4 Hopkins clinical panel challenge. Human Mutation, 2017, 38, 1155-1168.	2.5	6
159	Novel Missense Variant in MYL2 Gene Associated With Hypertrophic Cardiomyopathy Showing High Incidence of Restrictive Physiology. Circulation Genomic and Precision Medicine, 2020, 13, e002824.	3.6	6
160	Assessing computational predictions of the phenotypic effect of cystathionineâ€betaâ€synthase variants. Human Mutation, 2019, 40, 1530-1545.	2.5	5
161	Neurocognitive assessment and DNA sequencing expand the phenotype and genotype spectrum of AlstrÃ¶m syndrome. American Journal of Medical Genetics, Part A, 2021, 185, 732-742.	1.2	5
162	Insights into the molecular features of the von Hippelâ€“Lindau-like protein. Amino Acids, 2019, 51, 1461-1474.	2.7	4

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163	Exploring Conformational Space with Thermal Fluctuations Obtained by Normal-Mode Analysis. Journal of Chemical Information and Modeling, 2020, 60, 3068-3080.	5.4	4
164	Exploring Curated Conformational Ensembles of Intrinsically Disordered Proteins in the Protein Ensemble Database. Current Protocols, 2021, 1, e192.	2.9	4
165	ProSeqViewer: an interactive, responsive and efficient TypeScript library for visualization of sequences and alignments in web applications. Bioinformatics, 2022, 38, 1129-1130.	4.1	4
166	Fine-Grained Statistical Torsion Angle Potentials are Effective in Discriminating Native Protein Structures. Current Drug Discovery Technologies, 2006, 3, 75-81.	1.2	3
167	Structural protein reorganization and fold emergence investigated through amino acid sequence permutations. Amino Acids, 2015, 47, 147-152.	2.7	3
168	Unfoldome variation upon plant-pathogen interactions: strawberry infection by Colletotrichum acutatum. Plant Molecular Biology, 2015, 89, 49-65.	3.9	3
169	Intrinsically Disordered Protein Ensembles Shape Evolutionary Rates Revealing Conformational Patterns. Journal of Molecular Biology, 2021, 433, 166751.	4.2	3
170	â€œProteinâ€•no longer means what it used to. Current Research in Structural Biology, 2021, 3, 146-152.	2.2	3
171	CNTNAP2 mutations and autosomal dominant epilepsy with auditory features. Epilepsy Research, 2018, 139, 51-53.	1.6	3
172	Databases for intrinsically disordered proteins. Acta Crystallographica Section D: Structural Biology, 2022, 78, 144-151.	2.3	3
173	Expanding the clinical-pathological and genetic spectrum of RYR1-related congenital myopathies with cores and minicores: an Italian population study. Acta Neuropathologica Communications, 2022, 10, 54.	5.2	3
174	Editorial for special issue â€œProteins with tandem repeats: sequences, structures and functionsâ€â˜†. Journal of Structural Biology, 2018, 201, 86-87.	2.8	2
175	The E3 ubiquitin-protein ligase MDM2 is a novel interactor of the von Hippelâ€“Lindau tumor suppressor. Scientific Reports, 2020, 10, 15850.	3.3	2
176	Exploring Manually Curated Annotations of Intrinsically Disordered Proteins with DisProt. Current Protocols in Bioinformatics, 2020, 72, e107.	25.8	2
177	Exploring Protein Intrinsic Disorder with MobiDB. Methods in Molecular Biology, 2020, 2141, 127-143.	0.9	2
178	Exploring Manually Curated Annotations of Intrinsically Disordered Proteins with DisProt. Current Protocols, 2022, 2, .	2.9	2
179	Align: a C++ Class Library and Web Server for Rapid Sequence Alignment Prototyping. Current Drug Discovery Technologies, 2006, 3, 167-173.	1.2	1
180	The Ca 2+ regulatory site of the permeability transition pore is within the catalytic core of F-ATP synthase. Biochimica Et Biophysica Acta - Bioenergetics, 2016, 1857, e65-e66.	1.0	1

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181	PhytoTypeDB: a database of plant protein inter-cultivar variability and function. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	1
182	In silico prediction of blood cholesterol levels from genotype data. PLoS ONE, 2020, 15, e0227191.	2.5	1
183	Characterization of the pVHL Interactome in Human Testis Using High-Throughput Library Screening. Cancers, 2022, 14, 1009.	3.7	1
184	The Origin of Personalized Medicine and the Systems Biology Revolution. , 2017, , 22-35.		0
185	Phenoloxidases and cytotoxicity in ascidians: an overview. Frontiers in Immunology, 0, 4, .	4.8	0