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List of Publications by Year
in descending order

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185
papers

21,324
citations

36691

53
h-index

14386

132
g-index

204
all docs

204
docs citations

204
times ranked

31615
citing authors

#	Article	IF	Citations
1	PDBe-KB: collaboratively defining the biological context of structural data. Nucleic Acids Research, 2022, 50, D534-D542.	6.5	46
2	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. Nucleic Acids Research, 2022, 50, D480-D487.	6.5	117
3	ECO: the Evidence and Conclusion Ontology, an update for 2022. Nucleic Acids Research, 2022, 50, D1515-D1521.	6.5	21
4	FuzDB: a new phase in understanding fuzzy interactions. Nucleic Acids Research, 2022, 50, D509-D517.	6.5	25
5	ProSeqViewer: an interactive, responsive and efficient TypeScript library for visualization of sequences and alignments in web applications. Bioinformatics, 2022, 38, 1129-1130.	1.8	4
6	Databases for intrinsically disordered proteins. Acta Crystallographica Section D: Structural Biology, 2022, 78, 144-151.	1.1	3
7	SARSâ€CoVâ€2 variants preferentially emerge at intrinsically disordered protein sites helping immune evasion. FEBS Journal, 2022, 289, 4240-4250.	2.2	25
8	Characterization of the pVHL Interactome in Human Testis Using High-Throughput Library Screening. Cancers, 2022, 14, 1009.	1.7	1
9	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.	2.4	3
10	RING 3.0: fast generation of probabilistic residue interaction networks from structural ensembles. Nucleic Acids Research, 2022, 50, W651-W656.	6.5	75
11	FuzDrop on AlphaFold: visualizing the sequence-dependent propensity of liquidâ€“liquid phase separation and aggregation of proteins. Nucleic Acids Research, 2022, 50, W337-W344.	6.5	44
12	Exploring Manually Curated Annotations of Intrinsically Disordered Proteins with DisProt. Current Protocols, 2022, 2, .	1.3	2
13	The InterPro protein families and domains database: 20 years on. Nucleic Acids Research, 2021, 49, D344-D354.	6.5	1,385
14	MobiDB: intrinsically disordered proteins in 2021. Nucleic Acids Research, 2021, 49, D361-D367.	6.5	183
15	RepeatsDB in 2021: improved data and extended classification for protein tandem repeat structures. Nucleic Acids Research, 2021, 49, D452-D457.	6.5	37
16	Intrinsically Disordered Protein Ensembles Shape Evolutionary Rates Revealing Conformational Patterns. Journal of Molecular Biology, 2021, 433, 166751.	2.0	3
17	MobiDB-lite 3.0: fast consensus annotation of intrinsic disorder flavors in proteins. Bioinformatics, 2021, 36, 5533-5534.	1.8	47
18	Pfam: The protein families database in 2021. Nucleic Acids Research, 2021, 49, D412-D419.	6.5	3,068

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19	The MemMoRF database for recognizing disordered protein regions interacting with cellular membranes. Nucleic Acids Research, 2021, 49, D355-D360.	6.5	8
20	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.	0.7	5
21	â€œProteinâ€•no longer means what it used to. Current Research in Structural Biology, 2021, 3, 146-152.	1.1	3
22	FLIPPER: Predicting and Characterizing Linear Interacting Peptides in the Protein Data Bank. Journal of Molecular Biology, 2021, 433, 166900.	2.0	8
23	Critical assessment of protein intrinsic disorder prediction. Nature Methods, 2021, 18, 472-481.	9.0	187
24	The f subunit of human ATP synthase is essential for normal mitochondrial morphology and permeability transition. Cell Reports, 2021, 35, 109111.	2.9	22
25	HIF1Î±-dependent induction of the mitochondrial chaperone TRAP1 regulates bioenergetic adaptations to hypoxia. Cell Death and Disease, 2021, 12, 434.	2.7	17
26	Exploring Curated Conformational Ensembles of Intrinsically Disordered Proteins in the Protein Ensemble Database. Current Protocols, 2021, 1, e192.	1.3	4
27	DOME: recommendations for supervised machine learning validation in biology. Nature Methods, 2021, 18, 1122-1127.	9.0	105
28	APICURON: a database to credit and acknowledge the work of biocurators. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	10
29	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. Nucleic Acids Research, 2021, 49, D404-D411.	6.5	95
30	PhaSePro: the database of proteins driving liquidâ€“liquid phase separation. Nucleic Acids Research, 2020, 48, D360-D367.	6.5	100
31	DisProt: intrinsic protein disorder annotation in 2020. Nucleic Acids Research, 2020, 48, D269-D276.	6.5	141
32	Disentangling the complexity of low complexity proteins. Briefings in Bioinformatics, 2020, 21, 458-472.	3.2	70
33	The E3 ubiquitin-protein ligase MDM2 is a novel interactor of the von Hippelâ€“Lindau tumor suppressor. Scientific Reports, 2020, 10, 15850.	1.6	2
34	The pVHL neglected functions, a tale of hypoxia-dependent and -independent regulations in cancer. Open Biology, 2020, 10, 200109.	1.5	14
35	A novel approach to investigate the evolution of structured tandem repeat protein families by exon duplication. Journal of Structural Biology, 2020, 212, 107608.	1.3	8
36	Chasing coevolutionary signals in intrinsically disordered proteins complexes. Scientific Reports, 2020, 10, 17962.	1.6	7

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37	Exploring Manually Curated Annotations of Intrinsically Disordered Proteins with DisProt. Current Protocols in Bioinformatics, 2020, 72, e107.	25.8	2
38	PlaToLoCo: the first web meta-server for visualization and annotation of low complexity regions in proteins. Nucleic Acids Research, 2020, 48, W77-W84.	6.5	71
39	Assessing predictors for new post translational modification sites: AÂcase study on hydroxylation. PLoS Computational Biology, 2020, 16, e1007967.	1.5	10
40	Exploring Conformational Space with Thermal Fluctuations Obtained by Normal-Mode Analysis. Journal of Chemical Information and Modeling, 2020, 60, 3068-3080.	2.5	4
41	Experimentally Determined Long Intrinsically Disordered Protein Regions Are Now Abundant in the Protein Data Bank. International Journal of Molecular Sciences, 2020, 21, 4496.	1.8	25
42	In silico prediction of blood cholesterol levels from genotype data. PLoS ONE, 2020, 15, e0227191.	1.1	1
43	The Feature-Viewer: a visualization tool for positional annotations on a sequence. Bioinformatics, 2020, 36, 3244-3245.	1.8	18
44	Novel Missense Variant in <i>MYL2</i> Gene Associated With Hypertrophic Cardiomyopathy Showing High Incidence of Restrictive Physiology. Circulation Genomic and Precision Medicine, 2020, 13, e002824.	1.6	6
45	Exploring Protein Intrinsic Disorder with MobiDB. Methods in Molecular Biology, 2020, 2141, 127-143.	0.4	2
46	Assessing computational predictions of the phenotypic effect of cystathionineâ€betaâ€synthase variants. Human Mutation, 2019, 40, 1530-1545.	1.1	5
47	Network analysis of dynamically important residues in protein structures mediating ligand-binding conformational changes. European Biophysics Journal, 2019, 48, 559-568.	1.2	9
48	Performance of computational methods for the evaluation of pericentriolar material 1 missense variants in CAGIâ€5. Human Mutation, 2019, 40, 1474-1485.	1.1	8
49	Insights into the molecular features of the von Hippelâ€"Lindau-like protein. Amino Acids, 2019, 51, 1461-1474.	1.2	4
50	Ensembles from Ordered and Disordered Proteins Reveal Similar Structural Constraints during Evolution. Journal of Molecular Biology, 2019, 431, 1298-1307.	2.0	8
51	Characterization of intellectual disability and autism comorbidity through gene panel sequencing. Human Mutation, 2019, 40, 1346-1363.	1.1	54
52	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.	1.1	11
53	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.	1.6	32
54	INGA 2.0: improving protein function prediction for the dark proteome. Nucleic Acids Research, 2019, 47, W373-W378.	6.5	24

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55	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.	1.5	24
56	In silico Characterization of Human Prion-Like Proteins: Beyond Neurological Diseases. Frontiers in Physiology, 2019, 10, 314.	1.3	17
57	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	3.8	261
58	The Pfam protein families database in 2019. Nucleic Acids Research, 2019, 47, D427-D432.	6.5	3,937
59	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.	0.3	15
60	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. Nucleic Acids Research, 2019, 47, D351-D360.	6.5	1,291
61	An intrinsically disordered proteins community for ELIXIR. F1000Research, 2019, 8, 1753.	0.8	12
62	Editorial for special issue â€œProteins with tandem repeats: sequences, structures and functionsâ€•â˜†. Journal of Structural Biology, 2018, 201, 86-87.	1.3	2
63	A comprehensive assessment of long intrinsic protein disorder from the DisProt database. Bioinformatics, 2018, 34, 445-452.	1.8	53
64	Mobi 2.0: an improved method to define intrinsic disorder, mobility and linear binding regions in protein structures. Bioinformatics, 2018, 34, 122-123.	1.8	24
65	Classification of Î²-hairpin repeat proteins. Journal of Structural Biology, 2018, 201, 130-138.	1.3	25
66	PhytoTypeDB: a database of plant protein inter-cultivar variability and function. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	1
67	Where differences resemble: sequence-feature analysis in curated databases of intrinsically disordered proteins. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	9
68	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.	1.1	57
69	The clinical spectrum of CASQ1-related myopathy. Neurology, 2018, 91, e1629-e1641.	1.5	14
70	Calmodulin Enhances Cryptochrome Binding to INAD in Drosophila Photoreceptors. Frontiers in Molecular Neuroscience, 2018, 11, 280.	1.4	15
71	Whole-Exome Sequencing Identifies Pathogenic Variants in <i>TJP1</i> Gene Associated With Arrhythmogenic Cardiomyopathy. Circulation Genomic and Precision Medicine, 2018, 11, e002123.	1.6	38
72	RepeatsDB-lite: a web server for unit annotation of tandem repeat proteins. Nucleic Acids Research, 2018, 46, W402-W407.	6.5	18

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73	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. Nucleic Acids Research, 2018, 46, D471-D476.	6.5	190
74	CNTNAP2 mutations and autosomal dominant epilepsy with auditory features. Epilepsy Research, 2018, 139, 51-53.	0.8	3
75	Crohn disease risk predictionâ€"Best practices and pitfalls with exome data. Human Mutation, 2017, 38, 1193-1200.	1.1	12
76	Novel interactions of the von Hippel-Lindau (pVHL) tumor suppressor with the CDKN1 family of cell cycle inhibitors. Scientific Reports, 2017, 7, 46562.	1.6	6
77	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. Human Mutation, 2017, 38, 1042-1050.	1.1	13
78	FELLS: fast estimator of latent local structure. Bioinformatics, 2017, 33, 1889-1891.	1.8	72
79	DisProt 7.0: a major update of the database of disordered proteins. Nucleic Acids Research, 2017, 45, D219-D227.	6.5	242
80	Ca²⁺ binding to Fâ€ATP synthase Î² subunit triggers the mitochondrial permeability transition. EMBO Reports, 2017, 18, 1065-1076.	2.0	170
81	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2017, 38, 1182-1192.	1.1	39
82	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. Human Mutation, 2017, 38, 1266-1276.	1.1	14
83	InterPro in 2017â€"beyond protein family and domain annotations. Nucleic Acids Research, 2017, 45, D190-D199.	6.5	1,358
84	Simultaneous quantification of protein order and disorder. Nature Chemical Biology, 2017, 13, 339-342.	3.9	113
85	Dynamic scaffolds for neuronal signaling: in silico analysis of the TANC protein family. Scientific Reports, 2017, 7, 6829.	1.6	21
86	Lessons from the CAGIâ€4 Hopkins clinical panel challenge. Human Mutation, 2017, 38, 1155-1168.	1.1	6
87	MobiDB-lite: fast and highly specific consensus prediction of intrinsic disorder in proteins. Bioinformatics, 2017, 33, 1402-1404.	1.8	161
88	SODA: prediction of protein solubility from disorder and aggregation propensity. Nucleic Acids Research, 2017, 45, W236-W240.	6.5	47
89	Mapping pathogenic mutations suggests an innovative structural model for the pendrin (SLC26A4) transmembrane domain. Biochimie, 2017, 132, 109-120.	1.3	19
90	RepeatsDB 2.0: improved annotation, classification, search and visualization of repeat protein structures. Nucleic Acids Research, 2017, 45, D308-D312.	6.5	33

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91	The Origin of Personalized Medicine and the Systems Biology Revolution. , 2017, , 22-35.		0
92	Conformational diversity analysis reveals three functional mechanisms in proteins. PLoS Computational Biology, 2017, 13, e1005398.	1.5	46
93	Secretion-Positive LGI1 Mutations Linked to Lateral Temporal Epilepsy Impair Binding to ADAM22 and ADAM23 Receptors. PLoS Genetics, 2016, 12, e1006376.	1.5	23
94	VHLdb: A database of von Hippel-Lindau protein interactors and mutations. Scientific Reports, 2016, 6, 31128.	1.6	36
95	Computational analysis of prolyl hydroxylase domain-containing protein 2 (PHD2) mutations promoting polycythemia insurgence in humans. Scientific Reports, 2016, 6, 18716.	1.6	8
96	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	3.8	308
97	Largeâ€scale analysis of intrinsic disorder flavors and associated functions in the protein sequence universe. Protein Science, 2016, 25, 2164-2174.	3.1	52
98	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.	0.5	1
99	Disorder transitions and conformational diversity cooperatively modulate biological function in proteins. Protein Science, 2016, 25, 1138-1146.	3.1	23
100	The RING 2.0 web server for high quality residue interaction networks. Nucleic Acids Research, 2016, 44, W367-W374.	6.5	369
101	Tools and data services registry: a community effort to document bioinformatics resources. Nucleic Acids Research, 2016, 44, D38-D47.	6.5	113
102	Identification of repetitive units in protein structures with ReUPred. Amino Acids, 2016, 48, 1391-1400.	1.2	17
103	Correct machine learning on protein sequences: a peer-reviewing perspective. Briefings in Bioinformatics, 2016, 17, 831-840.	3.2	53
104	Comparison of protein repeat classifications based on structure and sequence families. Biochemical Society Transactions, 2015, 43, 832-837.	1.6	11
105	Isoform-specific interactions of the von Hippel-Lindau tumor suppressor protein. Scientific Reports, 2015, 5, 12605.	1.6	26
106	Exploration of alternative splicing events in ten different grapevine cultivars. BMC Genomics, 2015, 16, 706.	1.2	21
107	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.	1.3	11
108	MobiDB 2.0: an improved database of intrinsically disordered and mobile proteins. Nucleic Acids Research, 2015, 43, D315-D320.	6.5	177

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109	Heterozygous Reelin Mutations Cause Autosomal-Dominant Lateral Temporal Epilepsy. American Journal of Human Genetics, 2015, 96, 992-1000.	2.6	94
110	The Victor C++ library for protein representation and advanced manipulation. Bioinformatics, 2015, 31, 1138-1140.	1.8	6
111	Structural protein reorganization and fold emergence investigated through amino acid sequence permutations. Amino Acids, 2015, 47, 147-152.	1.2	3
112	Protein function prediction using guilty by association from interaction networks. Amino Acids, 2015, 47, 2583-2592.	1.2	40
113	INGA: protein function prediction combining interaction networks, domain assignments and sequence similarity. Nucleic Acids Research, 2015, 43, W134-W140.	6.5	73
114	BOOGIE: Predicting Blood Groups from High Throughput Sequencing Data. PLoS ONE, 2015, 10, e0124579.	1.1	31
115	Unfoldome variation upon plant-pathogen interactions: strawberry infection by Colletotrichum acutatum. Plant Molecular Biology, 2015, 89, 49-65.	2.0	3
116	Insights into the proline hydroxylase (PHD) family, molecular evolution and its impact on human health. Biochimie, 2015, 116, 114-124.	1.3	17
117	Comprehensive large-scale assessment of intrinsic protein disorder. Bioinformatics, 2015, 31, 201-208.	1.8	154
118	Design and Analysis of a Petri Net Model of the Von Hippel-Lindau (VHL) Tumor Suppressor Interaction Network. PLoS ONE, 2014, 9, e96986.	1.1	18
119	Evaluation of the steric impact of flavin adenine dinucleotide in Drosophila melanogaster cryptochrome function. Biochemical and Biophysical Research Communications, 2014, 450, 1606-1611.	1.0	13
120	RUBI: rapid proteomic-scale prediction of lysine ubiquitination and factors influencing predictor performance. Amino Acids, 2014, 46, 853-862.	1.2	24
121	<i>CDKN2A</i>Unclassified Variants in Familial Malignant Melanoma: Combining Functional and Computational Approaches for Their Assessment. Human Mutation, 2014, 35, 828-840.	1.1	17
122	RepeatsDB: a database of tandem repeat protein structures. Nucleic Acids Research, 2014, 42, D352-D357.	6.5	53
123	PASTA 2.0: an improved server for protein aggregation prediction. Nucleic Acids Research, 2014, 42, W301-W307.	6.5	349
124	NeEMO: a method using residue interaction networks to improve prediction of protein stability upon mutation. BMC Genomics, 2014, 15, S7.	1.2	83
125	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.	1.3	11
126	Analysis and consensus of currently available intrinsic protein disorder annotation sources in the MobiDB database. BMC Bioinformatics, 2013, 14, S3.	1.2	30

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127	The role of the Nâ€terminal tail for the oligomerization, folding and stability of human frataxin. FEBS Open Bio, 2013, 3, 310-320.	1.0	11
128	A novel <i><scp>SACS</scp></i> mutation results in nonâ€ataxic spastic paraplegia and peripheral neuropathy. European Journal of Neurology, 2013, 20, 1486-1491.	1.7	30
129	Fly cryptochrome and the visual system. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6163-6168.	3.3	103
130	2mit, an Intronic Gene of Drosophila melanogaster timeless2, Is Involved in Behavioral Plasticity. PLoS ONE, 2013, 8, e76351.	1.1	9
131	PANADA: Protein Association Network Annotation, Determination and Analysis. PLoS ONE, 2013, 8, e78383.	1.1	7
132	Studying Interactions by Molecular Dynamics Simulations at High Concentration. Journal of Biomedicine and Biotechnology, 2012, 2012, 1-9.	3.0	16
133	ESpritz: accurate and fast prediction of protein disorder. Bioinformatics, 2012, 28, 503-509.	1.8	445
134	Cardiomyopathy in patients with POMT1-related congenital and limb-girdle muscular dystrophy. European Journal of Human Genetics, 2012, 20, 1234-1239.	1.4	31
135	RAPHAEL: recognition, periodicity and insertion assignment of solenoid protein structures. Bioinformatics, 2012, 28, 3257-3264.	1.8	27
136	Bluues server: electrostatic properties of wild-type and mutated protein structures. Bioinformatics, 2012, 28, 2189-2190.	1.8	72
137	MobiDB: a comprehensive database of intrinsic protein disorder annotations. Bioinformatics, 2012, 28, 2080-2081.	1.8	142
138	Looking for putative phenoloxidases of compound ascidians: Haemocyanin-like proteins in Polyandrocarpa misakiensis and Botryllus schlosseri. Developmental and Comparative Immunology, 2012, 38, 232-242.	1.0	14
139	Immune roles of a rhamnose-binding lectin in the colonial ascidian Botryllus schlosseri. Immunobiology, 2011, 216, 725-736.	0.8	37
140	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.	0.3	19
141	Familial temporal lobe epilepsy with psychic auras associated with a novel <i>LGI1</i> mutation. Neurology, 2011, 76, 1173-1176.	1.5	49
142	RING: networking interacting residues, evolutionary information and energetics in protein structures. Bioinformatics, 2011, 27, 2003-2005.	1.8	116
143	CSpritz: accurate prediction of protein disorder segments with annotation for homology, secondary structure and linear motifs. Nucleic Acids Research, 2011, 39, W190-W196.	6.5	77
144	A Computational Model of the LGI1 Protein Suggests a Common Binding Site for ADAM Proteins. PLoS ONE, 2011, 6, e18142.	1.1	33

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145	FRASS: the web-server for RNA structural comparison. BMC Bioinformatics, 2010, 11, 327.	1.2	7
146	Deletions and Mutations in the Acidic Lipid-binding Region of the Plasma Membrane Ca2+ Pump. Journal of Biological Chemistry, 2010, 285, 30779-30791.	1.6	22
147	MOBI: a web server to define and visualize structural mobility in NMR protein ensembles. Bioinformatics, 2010, 26, 2916-2917.	1.8	35
148	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.	2.2	30
149	A<i>CRY</i>FROM THE KRILL. Chronobiology International, 2010, 27, 425-445.	0.9	41
150	REPETITA: detection and discrimination of the periodicity of protein solenoid repeats by discrete Fourier transform. Bioinformatics, 2009, 25, i289-i295.	1.8	57
151	Electric dipole reorientation in the interaction of botulinum neurotoxins with neuronal membranes. FEBS Letters, 2009, 583, 2321-2325.	1.3	17
152	Adding structural information to the von Hippelâ€“Lindau (VHL) tumor suppressor interaction network. FEBS Letters, 2009, 583, 3704-3710.	1.3	25
153	<i>LGI1</i>mutations in autosomal dominant and sporadic lateral temporal epilepsy. Human Mutation, 2009, 30, 530-536.	1.1	155
154	Global and local model quality estimation at CASP8 using the scoring functions QMEAN and QMEANclust. Proteins: Structure, Function and Bioinformatics, 2009, 77, 173-180.	1.5	56
155	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
156	Gammaâ€glutamyl transferase in the cell wall participates in extracellular glutathione salvage from the root apoplast. New Phytologist, 2009, 181, 115-126.	3.5	58
157	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.	1.0	80
158	QMEAN: A comprehensive scoring function for model quality assessment. Proteins: Structure, Function and Bioinformatics, 2008, 71, 261-277.	1.5	888
159	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.	3.8	16
160	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.	1.1	34
161	Evolutionary and Structural Insights Into the Multifaceted Glutathione Peroxidase (Gpx) Superfamily. Antioxidants and Redox Signaling, 2008, 10, 1501-1514.	2.5	205
162	The Catalytic Site of Glutathione Peroxidases. Antioxidants and Redox Signaling, 2008, 10, 1515-1526.	2.5	151

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163	TESE: generating specific protein structure test set ensembles. Bioinformatics, 2008, 24, 2632-2633.	1.8	9
164	Low density lipoprotein misfolding and amyloidogenesis. FASEB Journal, 2008, 22, 2350-2356.	0.2	48
165	The PASTA server for protein aggregation prediction. Protein Engineering, Design and Selection, 2007, 20, 521-523.	1.0	217
166	Linear motifs in the C-terminus of D. melanogaster cryptochrome. Biochemical and Biophysical Research Communications, 2007, 355, 531-537.	1.0	54
167	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.	2.0	113
168	TAP score: torsion angle propensity normalization applied to local protein structure evaluation. BMC Bioinformatics, 2007, 8, 155.	1.2	39
169	Functional insights from the structural modelling of a small Fe-hydrogenase. Biochemical and Biophysical Research Communications, 2006, 339, 277-283.	1.0	10
170	Improving the quality of protein structure models by selecting from alignment alternatives. BMC Bioinformatics, 2006, 7, 364.	1.2	17
171	Spritz: a server for the prediction of intrinsically disordered regions in protein sequences using kernel machines. Nucleic Acids Research, 2006, 34, W164-W168.	6.5	121
172	Large-Scale Prediction of Protein Structure and Function from Sequence. Current Pharmaceutical Design, 2006, 12, 2067-2086.	0.9	12
173	Fine-Grained Statistical Torsion Angle Potentials are Effective in Discriminating Native Protein Structures. Current Drug Discovery Technologies, 2006, 3, 75-81.	0.6	3
174	Align: a C++ Class Library and Web Server for Rapid Sequence Alignment Prototyping. Current Drug Discovery Technologies, 2006, 3, 167-173.	0.6	1
175	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.	3.1	41
176	A decoy set for the thermostable subdomain from chicken villin headpiece, comparison of different free energy estimators. BMC Bioinformatics, 2005, 6, 301.	1.2	14
177	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.	1.6	81
178	Decomposing protein networks into domain-domain interactions. Bioinformatics, 2005, 21, ii220-ii221.	1.8	19
179	The Victor/FRST Function for Model Quality Estimation. Journal of Computational Biology, 2005, 12, 1316-1327.	0.8	101
180	The SSEA server for protein secondary structure alignment. Bioinformatics, 2005, 21, 393-395.	1.8	35

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181	Structural insights into the function of human caveolin 1. Biochemical and Biophysical Research Communications, 2005, 338, 1383-1390.	1.0	55
182	Simple consensus procedures are effective and sufficient in secondary structure prediction. Protein Engineering, Design and Selection, 2003, 16, 459-462.	1.0	63
183	MANIFOLD: protein fold recognition based on secondary structure, sequence similarity and enzyme classification. Protein Engineering, Design and Selection, 2003, 16, 785-789.	1.0	29
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