Charlotte M Deane

List of Publications by Year
in descending order

189 papers	9,609 citations	57631 44 h-index	58464 82 g-index
290 all docs	290 docs citations	290 times ranked	10289 citing authors

#	Article	IF	Citations
1	Protein Interactions. Molecular and Cellular Proteomics, 2002, 1, 349-356.	2.5	570
2	HOMSTRAD: A database of protein structure alignments for homologous families. Protein Science, 1998, 7, 2469-2471.	3.1	461
3	SAbDab: the structural antibody database. Nucleic Acids Research, 2014, 42, D1140-D1146.	6.5	374
4	CoV-AbDab: the coronavirus antibody database. Bioinformatics, 2021, 37, 734-735.	1.8	273
5	Reduced amounts and abnormal forms of phospholipase C zeta (PLCÂ) in spermatozoa from infertile men. Human Reproduction, 2009, 24, 2417-2428.	0.4	257
6	ANARCI: antigen receptor numbering and receptor classification. Bioinformatics, 2016, 32, 298-300.	1.8	237
7	Five computational developability guidelines for therapeutic antibody profiling. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 4025-4030.	3.3	221
8	ABodyBuilder: Automated antibody structure prediction with dataâ€“driven accuracy estimation. MAbs, 2016, 8, 1259-1268.	2.6	208
9	Avoiding False Positive Conclusions in Molecular Simulation: The Importance of Replicas. Journal of Chemical Theory and Computation, 2018, 14, 6127-6138.	2.3	187
10	A multi-crystal method for extracting obscured crystallographic states from conventionally uninterpretable electron density. Nature Communications, 2017, 8, 15123.	5.8	186
11	Freely Available Conformer Generation Methods: How Good Are They?. Journal of Chemical Information and Modeling, 2012, 52, 1146-1158.	2.5	178
12	Observed Antibody Space: A Resource for Data Mining Next-Generation Sequencing of Antibody Repertoires. Journal of Immunology, 2018, 201, 2502-2509.	0.4	165
13	SAbPred: a structure-based antibody prediction server. Nucleic Acids Research, 2016, 44, W474-W478.	6.5	155
14	FREAD revisited: Accurate loop structure prediction using a database search algorithm. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1431-1440.	1.5	154
15	Synonymous codon usage influences the local protein structure observed. Nucleic Acids Research, 2010, 38, 6719-6728.	6.5	148
16	CODA: A combined algorithm for predicting the structurally variable regions of protein models. Protein Science, 2001, 10, 599-612.	3.1	147
17	Improving B-cell epitope prediction and its application to global antibody-antigen docking. Bioinformatics, 2014, 30, 2288-2294.	1.8	137
18	Revisiting Date and Party Hubs: Novel Approaches to Role Assignment in Protein Interaction Networks. PLoS Computational Biology, 2010, 6, e1000817.	1.5	128

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19	Deep Generative Models for 3D Linker Design. Journal of Chemical Information and Modeling, 2020, 60, 1983-1995.	2.5	126
20	Rapid, Precise, and Reproducible Prediction of Peptideâ€“MHC Binding Affinities from Molecular Dynamics That Correlate Well with Experiment. Journal of Chemical Theory and Computation, 2015, 11, 3346-3356.	2.3	122
21	A maternally inherited autosomal point mutation in human phospholipase C zeta (PLCÂ) leads to male infertility. Human Reproduction, 2012, 27, 222-231.	0.4	117
22	Progress and challenges in predicting protein interfaces. Briefings in Bioinformatics, 2016, 17, 117-131.	3.2	115
23	Association between a common immunoglobulin heavy chain allele and rheumatic heart disease risk in Oceania. Nature Communications, 2017, 8, 14946.	5.8	114
24	The prospects of quantum computing in computational molecular biology. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2021, 11, e1481.	6.2	108
25	Protein Family-Specific Models Using Deep Neural Networks and Transfer Learning Improve Virtual Screening and Highlight the Need for More Data. Journal of Chemical Information and Modeling, 2018, 58, 2319-2330.	2.5	106
26	A Microtubule Interactome: Complexes with Roles in Cell Cycle and Mitosis. PLoS Biology, 2008, 6, e98.	2.6	105
27	MEDELLER: homology-based coordinate generation for membrane proteins. Bioinformatics, 2010, 26, 2833-2840.	1.8	103
28	Deep Sequencing of B Cell Receptor Repertoires From COVID-19 Patients Reveals Strong Convergent Immune Signatures. Frontiers in Immunology, 2020, 11, 605170.	2.2	101
29	Observed Antibody Space: A diverse database of cleaned, annotated, and translated unpaired and paired antibody sequences. Protein Science, 2022, 31, 141-146.	3.1	98
30	Carbonylâ€“carbonyl interactions stabilize the partially allowed Ramachandran conformations of asparagine and aspartic acid. Protein Engineering, Design and Selection, 1999, 12, 1025-1028.	1.0	90
31	The H3 loop of antibodies shows unique structural characteristics. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1311-1318.	1.5	89
32	Thera-SAbDab: the Therapeutic Structural Antibody Database. Nucleic Acids Research, 2020, 48, D383-D388.	6.5	88
33	Solution Structure and Dynamics of a Prototypical Chordin-like Cysteine-rich Repeat (von Willebrand) Tj ETQq1 1 0.784314 rgBT /Ove	1.6	83
34	Antibody i-Patch prediction of the antibody binding site improves rigid local antibody-antigen docking. Protein Engineering, Design and Selection, 2013, 26, 621-629.	1.0	80
35	The function of communities in protein interaction networks at multiple scales. BMC Systems Biology, 2010, 4, 100.	3.0	79
36	ABlooper: fast accurate antibody CDR loop structure prediction with accuracy estimation. Bioinformatics, 2022, 38, 1877-1880.	1.8	78

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37	Type II Inhibitors Targeting CDK2. ACS Chemical Biology, 2015, 10, 2116-2125.	1.6	75
38	STCRDab: the structural T-cell receptor database. Nucleic Acids Research, 2018, 46, D406-D412.	6.5	69
39	Deciphering chemotaxis pathways using cross species comparisons. BMC Systems Biology, 2010, 4, 3.	3.0	66
40	Protein protein interactions, evolutionary rate, abundance and age. BMC Bioinformatics, 2006, 7, 128.	1.2	64
41	How old is your fold?. Bioinformatics, 2005, 21, i449-i458.	1.8	63
42	Helix kinks are equally prevalent in soluble and membrane proteins. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1960-1970.	1.5	61
43	A novel exhaustive search algorithm for predicting the conformation of polypeptide segments in proteins. Proteins: Structure, Function and Bioinformatics, 2000, 40, 135-144.	1.5	60
44	Learning from the ligand: using ligand-based features to improve binding affinity prediction. Bioinformatics, 2020, 36, 758-764.	1.8	60
45	Identifying and quantifying radiation damage atÂtheÂatomic level. Journal of Synchrotron Radiation, 2015, 22, 201-212.	1.0	51
46	Current structure predictors are not learning the physics of protein folding. Bioinformatics, 2022, 38, 1881-1887.	1.8	50
47	Length-independent structural similarities enrich the antibody CDR canonical class model. MAbs, 2016, 8, 751-760.	2.6	49
48	Sphinx: merging knowledge-based and ab initio approaches to improve protein loop prediction. Bioinformatics, 2017, 33, 1346-1353.	1.8	49
49	Humanization of antibodies using a machine learning approach on large-scale repertoire data. Bioinformatics, 2021, 37, 4041-4047.	1.8	49
50	SAbDab in the age of biotherapeutics: updates including SAbDab-nano, the nanobody structure tracker. Nucleic Acids Research, 2022, 50, D1368-D1372.	6.5	49
51	Alignment-free protein interaction network comparison. Bioinformatics, 2014, 30, i430-i437.	1.8	48
52	How B-Cell Receptor Repertoire Sequencing Can Be Enriched with Structural Antibody Data. Frontiers in Immunology, 2017, 8, 1753.	2.2	48
53	DLAB: deep learning methods for structure-based virtual screening of antibodies. Bioinformatics, 2022, 38, 377-383.	1.8	48
54	AbLang: an antibody language model for completing antibody sequences. Bioinformatics Advances, 2022, 2, .	0.9	48

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55	Ten Simple Rules for Effective Computational Research. PLoS Computational Biology, 2014, 10, e1003506.	1.5	47
56	Prediction of VHâ€“VL domain orientation for antibody variable domain modeling. Proteins: Structure, Function and Bioinformatics, 2015, 83, 681-695.	1.5	47
57	Antibody H3 Structure Prediction. Computational and Structural Biotechnology Journal, 2017, 15, 222-231.	1.9	47
58	Ten Simple Rules for a Successful Cross-Disciplinary Collaboration. PLoS Computational Biology, 2015, 11, e1004214.	1.5	46
59	Maturation of the Human Immunoglobulin Heavy Chain Repertoire With Age. Frontiers in Immunology, 2020, 11, 1734.	2.2	46
60	Current status and future challenges in T-cell receptor/peptide/MHC molecular dynamics simulations. Briefings in Bioinformatics, 2015, 16, 1035-1044.	3.2	45
61	How repertoire data are changing antibody science. Journal of Biological Chemistry, 2020, 295, 9823-9837.	1.6	43
62	Predicting proteinâ€“protein interactions in the context of protein evolution. Molecular BioSystems, 2010, 6, 55-64.	2.9	42
63	Proteomic Analysis of Microtubule-associated Proteins during Macrophage Activation. Molecular and Cellular Proteomics, 2009, 8, 2500-2514.	2.5	41
64	What Evidence Is There for the Homology of Protein-Protein Interactions?. PLoS Computational Biology, 2012, 8, e1002645.	1.5	41
65	Comparative Analysis of the CDR Loops of Antigen Receptors. Frontiers in Immunology, 2019, 10, 2454.	2.2	40
66	Predicting antibody complementarity determining region structures without classification. Molecular BioSystems, 2011, 7, 3327.	2.9	39
67	Memoir: template-based structure prediction for membrane proteins. Nucleic Acids Research, 2013, 41, W379-W383.	6.5	38
68	The Caenorhabditis elegans protein SAS-5 forms large oligomeric assemblies critical for centriole formation. ELife, 2015, 4, e07410.	2.8	37
69	Structurally Mapping Antibody Repertoires. Frontiers in Immunology, 2018, 9, 1698.	2.2	36
70	Data Set Augmentation Allows Deep Learning-Based Virtual Screening to Better Generalize to Unseen Target Classes and Highlight Important Binding Interactions. Journal of Chemical Information and Modeling, 2020, 60, 3722-3730.	2.5	36
71	Deep generative design with 3D pharmacophoric constraints. Chemical Science, 2021, 12, 14577-14589.	3.7	36
72	The Role and Predicted Propensity of Conserved Proline Residues in the 5-HT3 Receptor. Journal of Biological Chemistry, 2001, 276, 37962-37966.	1.6	35

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73	Current advances in biopharmaceutical informatics: guidelines, impact and challenges in the computational developability assessment of antibody therapeutics. MAbs, 2022, 14, 2020082.	2.6	35
74	Epitope profiling using computational structural modelling demonstrated on coronavirus-binding antibodies. PLoS Computational Biology, 2021, 17, e1009675.	1.5	33
75	An iterative structure-assisted approach to sequence alignment and comparative modeling. , 1999, 37, 55-60.		32
76	Improved protein loop prediction from sequence alone. Protein Engineering, Design and Selection, 2001, 14, 473-478.	1.0	32
77	Large Scale Characterization of the LC13 TCR and HLA-B8 Structural Landscape in Reaction to 172 Altered Peptide Ligands: A Molecular Dynamics Simulation Study. PLoS Computational Biology, 2014, 10, e1003748.	1.5	32
78	Advances in computational structure-based antibody design. Current Opinion in Structural Biology, 2022, 74, 102379.	2.6	32
79	Functionally guided alignment of protein interaction networks for module detection. Bioinformatics, 2009, 25, 3166-3173.	1.8	31
80	Exploring Fold Space Preferences of New-born and Ancient Protein Superfamilies. PLoS Computational Biology, 2013, 9, e1003325.	1.5	31
81	Ab-Ligity: identifying sequence-dissimilar antibodies that bind to the same epitope. MAbs, 2021, 13, 1873478.	2.6	31
82	A computational method for immune repertoire mining that identifies novel binders from different clonotypes, demonstrated by identifying anti-pertussis toxoid antibodies. MAbs, 2021, 13, 1869406.	2.6	31
83	Fold usage on genomes and protein fold evolution. Proteins: Structure, Function and Bioinformatics, 2005, 60, 690-700.	1.5	30
84	Predicting and Validating Protein Interactions Using Network Structure. PLoS Computational Biology, 2008, 4, e1000118.	1.5	30
85	MP-T: improving membrane protein alignment for structure prediction. Bioinformatics, 2013, 29, 54-61.	1.8	30
86	Measuring rank robustness in scored protein interaction networks. BMC Bioinformatics, 2019, 20, 446.	1.2	30
87	Generating property-matched decoy molecules using deep learning. Bioinformatics, 2021, 37, 2134-2141.	1.8	30
88	iMembrane: homology-based membrane-insertion of proteins. Bioinformatics, 2009, 25, 1086-1088.	1.8	29
89	Examining Variable Domain Orientations in Antigen Receptors Gives Insight into TCR-Like Antibody Design. PLoS Computational Biology, 2014, 10, e1003852.	1.5	29
90	Looking for therapeutic antibodies in next-generation sequencing repositories. MAbs, 2019, 11, 1197-1205.	2.6	29

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91	SCALOP: sequence-based antibody canonical loop structure annotation. Bioinformatics, 2019, 35, 1774-1776.	1.8	29
92	Cotranslational protein foldingâ€"fact or fiction?. Bioinformatics, 2007, 23, i142-i148.	1.8	28
93	Comparing co-evolution methods and their application to template-free protein structure prediction. Bioinformatics, 2017, 33, 373-381.	1.8	28
94	Structural diversity of B-cell receptor repertoires along the B-cell differentiation axis in humans and mice. PLoS Computational Biology, 2020, 16, e1007636.	1.5	27
95	iâ€Patch: Interprotein contact prediction using local network information. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2781-2797.	1.5	26
96	How threshold behaviour affects the use of subgraphs for network comparison. Bioinformatics, 2010, 26, i611-i617.	1.8	26
97	Public Baseline and shared response structures support the theory of antibody repertoire functional commonality. PLoS Computational Biology, 2021, 17, e1008781.	1.5	26
98	Building a Better Fragment Library for De Novo Protein Structure Prediction. PLoS ONE, 2015, 10, e0123998.	1.1	25
99	Misato Controls Mitotic Microtubule Generation by Stabilizing the TCP-1 Tubulin Chaperone Complex. Current Biology, 2015, 25, 1777-1783.	1.8	25
100	Partial-occupancy binders identified by the Pan-Dataset Density Analysis method offer new chemical opportunities and reveal cryptic binding sites. Structural Dynamics, 2017, 4, 032104.	0.9	25
101	Cross-linking mass spectrometry identifies new interfaces of Augmin required to localise the Î³-Tubulin Ring Complex to the mitotic spindle. Biology Open, 2017, 6, 654-663.	0.6	25
102	Modelling sequential protein folding under kinetic control. Bioinformatics, 2006, 22, e203-e210.	1.8	23
103	An assessment of the uses of homologous interactions. Bioinformatics, 2008, 24, 689-695.	1.8	22
104	Producing High-Accuracy Lattice Models from Protein Atomic Coordinates Including Side Chains. Advances in Bioinformatics, 2012, 2012, 1-6.	5.7	22
105	Computational Tools for Aiding Rational Antibody Design. Methods in Molecular Biology, 2017, 1529, 399-416.	0.4	22
106	Co-evolution techniques are reshaping the way we do structural bioinformatics. F1000Research, 2017, 6, 1224.	0.8	22
107	Different B cell subpopulations show distinct patterns in their IgH repertoire metrics. ELife, 2021, 10, .	2.8	22
108	Exploring peptide/MHC detachment processes using hierarchical natural move Monte Carlo. Bioinformatics, 2016, 32, 181-186.	1.8	21

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109	T-Cell Receptor Binding Affects the Dynamics of the Peptide/MHC-I Complex. Journal of Chemical Information and Modeling, 2016, 56, 46-53.	2.5	21
110	Variable Regions of Antibodies and T-Cell Receptors May Not Be Sufficient in Molecular Simulations Investigating Binding. Journal of Chemical Theory and Computation, 2017, 13, 3097-3105.	2.3	21
111	Antibody side chain conformations are positionâ€dependent. Proteins: Structure, Function and Bioinformatics, 2018, 86, 383-392.	1.5	21
112	The allosteric modulation of complement C5 by knob domain peptides. ELife, 2021, 10, .	2.8	21
113	Environment specific substitution tables improve membrane protein alignment. Bioinformatics, 2011, 27, i15-i23.	1.8	20
114	Examining the Conservation of Kinks in Alpha Helices. PLoS ONE, 2016, 11, e0157553.	1.1	20
115	Identifying networks with common organizational principles. Journal of Complex Networks, 2018, 6, 887-913.	1.1	20
116	Predicting loop conformational ensembles. Bioinformatics, 2018, 34, 949-956.	1.8	20
117	Antibodyâ€“antigen complex modelling in the era of immunoglobulin repertoire sequencing. Molecular Systems Design and Engineering, 2019, 4, 679-688.	1.7	20
118	Membranome 3.0: Database of singleâ€pass membrane proteins with <scp>AlphaFold</scp> models. Protein Science, 2022, 31, e4318.	3.1	20
119	A structural model of the human thrombopoietin receptor complex. Journal of Molecular Graphics and Modelling, 1997, 15, 170-188.	1.3	18
120	Gro2mat: A package to efficiently read gromacs output in MATLAB. Journal of Computational Chemistry, 2014, 35, 1528-1531.	1.5	18
121	The contribution of major histocompatibility complex contacts to the affinity and kinetics of T cell receptor binding. Scientific Reports, 2016, 6, 35326.	1.6	18
122	Current strategies for detecting functional convergence across B-cell receptor repertoires. MAbs, 2021, 13, 1996732.	2.6	18
123	Directionality in protein fold prediction. BMC Bioinformatics, 2010, 11, 172.	1.2	17
124	The imprint of codons on protein structure. Biotechnology Journal, 2011, 6, 641-649.	1.8	17
125	How long is a piece of loop?. PeerJ, 2013, 1, e1.	0.9	17
126	Structural Bridges through Fold Space. PLoS Computational Biology, 2015, 11, e1004466.	1.5	16

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127	Hypergraphs for predicting essential genes using multiprotein complex data. Journal of Complex Networks, 2021, 9, .	1.1	16
128	Protein structure prediction begins well but ends badly. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1282-1290.	1.5	15
129	Signatures of coâ€translational folding. Biotechnology Journal, 2011, 6, 742-751.	1.8	15
130	Fragment-based modeling of membrane protein loops: Successes, failures, and prospects for the future. Proteins: Structure, Function and Bioinformatics, 2014, 82, 175-186.	1.5	15
131	MHC binding affects the dynamics of different T-cell receptors in different ways. PLoS Computational Biology, 2019, 15, e1007338.	1.5	13
132	Functional module detection through integration of single-cell RNA sequencing data with proteinâ€“protein interaction networks. BMC Genomics, 2020, 21, 756.	1.2	13
133	Sequential search leads to faster, more efficient fragment-basedde novoprotein structure prediction. Bioinformatics, 2018, 34, 1132-1140.	1.8	12
134	Exploring the potential of template-based modelling. Bioinformatics, 2010, 26, 1849-1856.	1.8	11
135	Evolutionary analysis reveals low coverage as the major challenge for protein interaction network alignment. Molecular BioSystems, 2010, 6, 2296.	2.9	11
136	The Importance of Age and High Degree, in Protein-Protein Interaction Networks. Journal of Computational Biology, 2012, 19, 785-795.	0.8	11
137	Filtering Next-Generation Sequencing of the Ig Gene Repertoire Data Using Antibody Structural Information. Journal of Immunology, 2018, 201, 3694-3704.	0.4	11
138	Modeling conformational flexibility of kinases in inactive states. Proteins: Structure, Function and Bioinformatics, 2019, 87, 943-951.	1.5	11
139	TCRBuilder: multi-state T-cell receptor structure prediction. Bioinformatics, 2020, 36, 3580-3581.	1.8	10
140	Robust gene coexpression networks using signed distance correlation. Bioinformatics, 2021, 37, 1982-1989.	1.8	10
141	Learning from Docked Ligands: Ligand-Based Features Rescue Structure-Based Scoring Functions When Trained on Docked Poses. Journal of Chemical Information and Modeling, 2022, 62, 5329-5341.	2.5	10
142	Incorporating Target-Specific Pharmacophoric Information into Deep Generative Models for Fragment Elaboration. Journal of Chemical Information and Modeling, 2022, 62, 2280-2292.	2.5	10
143	OOMMPPAA: A Tool To Aid Directed Synthesis by the Combined Analysis of Activity and Structural Data. Journal of Chemical Information and Modeling, 2014, 54, 2636-2646.	2.5	9
144	Comparison of large networks with sub-sampling strategies. Scientific Reports, 2016, 6, 28955.	1.6	9

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145	Ligity: A Non-Superpositional, Knowledge-Based Approach to Virtual Screening. Journal of Chemical Information and Modeling, 2019, 59, 2600-2616.	2.5	9
146	Co-evolutionary distance predictions contain flexibility information. Bioinformatics, 2021, , .	1.8	9
147	Tertiary Element Interaction in HIV-1 TAR. Journal of Chemical Information and Modeling, 2016, 56, 1746-1754.	2.5	8
148	Increasing the accuracy of protein loop structure prediction with evolutionary constraints. Bioinformatics, 2019, 35, 2585-2592.	1.8	8
149	AI in 3D compound design. Current Opinion in Structural Biology, 2022, 73, 102326.	2.6	8
150	Crowdsourcing Yields a New Standard for Kinks in Protein Helices. Journal of Chemical Information and Modeling, 2014, 54, 2585-2593.	2.5	7
151	Modeling Functional Motions of Biological Systems by Customized Natural Moves. Biophysical Journal, 2016, 111, 710-721.	0.2	7
152	Combining co-evolution and secondary structure prediction to improve fragment library generation. Bioinformatics, 2018, 34, 2219-2227.	1.8	7
153	The Therapeutic Antibody Profiler for Computational Developability Assessment. Methods in Molecular Biology, 2022, 2313, 115-125.	0.4	7
154	Ten simple rules for surviving an interdisciplinary PhD. PLoS Computational Biology, 2017, 13, e1005512.	1.5	7
155	Protein Three-Dimensional Structural Databases: Domains, Structurally Aligned Homologues and Superfamilies. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 1168-1177.	2.5	6
156	A statistical approach using network structure in the prediction of protein characteristics. Bioinformatics, 2007, 23, 2314-2321.	1.8	6
157	Using Phylogeny to Improve Genome-Wide Distant Homology Recognition. PLoS Computational Biology, 2007, 3, e3.	1.5	6
158	pyHVis3D: visualising molecular simulation deduced H-bond networks in 3D: application to T-cell receptor interactions. Bioinformatics, 2018, 34, 1941-1943.	1.8	6
159	COGENT: evaluating the consistency of gene co-expression networks. Bioinformatics, 2021, 37, 1928-1929.	1.8	6
160	Investigating the potential for a limited quantum speedup on protein lattice problems. New Journal of Physics, 0, , .	1.2	6
161	The functional domain grouping of microtubule associated proteins. Communicative and Integrative Biology, 2008, 1, 47-50.	0.6	5
162	Mutual information and variants for protein domain-domain contact prediction. BMC Research Notes, 2012, 5, 472.	0.6	5

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163	Local Network Patterns in Protein-Protein Interfaces. PLoS ONE, 2013, 8, e57031.	1.1	5
164	The evolution of contact prediction: evidence that contact selection in statistical contact prediction is changing. Bioinformatics, 2020, 36, 1750-1756.	1.8	5
165	WONKAandOOMMPPAA: analysis of proteinâ€“ligand interaction data to direct structure-based drug design. Acta Crystallographica Section D: Structural Biology, 2017, 73, 279-285.	1.1	5
166	Challenges and Opportunities for Bayesian Statistics in Proteomics. Journal of Proteome Research, 2022, 21, 849-864.	1.8	5
167	In silico structural modeling of multiple epigenetic marks on DNA. Bioinformatics, 2018, 34, 41-48.	1.8	4
168	Ribosome occupancy profiles are conserved between structurally and evolutionarily related yeast domains. Bioinformatics, 2021, 37, 1853-1859.	1.8	4
169	Assessment of model fit via network comparison methods based on subgraph counts. Journal of Complex Networks, 2019, 7, 226-253.	1.1	3
170	RFQAmodel: Random Forest Quality Assessment to identify a predicted protein structure in the correct fold. PLoS ONE, 2019, 14, e0218149.	1.1	3
171	High-Throughput Antibody Structure Modeling and Design Using ABodyBuilder. Methods in Molecular Biology, 2019, 1851, 367-380.	0.4	3
172	PROTEIN COMPARATIVE MODELLING AND DRUG DISCOVERY. , 2003, , 445-458.		3
173	A Statistical Model for Helices with Applications. Biometrics, 2018, 74, 845-854.	0.8	2
174	Predicting Inter-Species Cross-Talk in Two-Component Signalling Systems. PLoS ONE, 2012, 7, e37737.	1.1	2
175	Protein Modeling and Structural Prediction. , 2014, , 171-182.		1
176	Investigating Cotranslational Folding in Membrane Proteins using Fragment-Based Structure Prediction. Biophysical Journal, 2017, 112, 61a.	0.2	1
177	HLA-DM Stabilizes the Empty MHCII Binding Groove: A Model Using Customized Natural Move Monte Carlo. Journal of Chemical Information and Modeling, 2019, 59, 2894-2899.	2.5	1
178	Extracting Information from Gene Coexpression Networks of Rhizobium leguminosarum. Journal of Computational Biology, 2022, , .	0.8	1
179	Generating weighted and thresholded gene coexpression networks using signed distance correlation. Network Science, 2022, 10, 131-145.	0.8	1
180	Empirical Bayes functional models for hydrogen deuterium exchange mass spectrometry. Communications Biology, 2022, 5, .	2.0	1

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181	Linking evolution of protein structures through fragments. BMC Systems Biology, 2007, 1, .	3.0	0
182	Interactions of Two Amphipathic Cell-Penetrating Peptides with Complex Model Membranes: Insights from Molecular Dynamics Simulations. Biophysical Journal, 2013, 104, 600a.	0.2	0
183	Efficient Sampling for the Prediction of Long and Multidomain Protein Structures. Biophysical Journal, 2018, 114, 574a.	0.2	0
184	Using phylogeny to improve genome wide distant homology recognition. PLoS Computational Biology, 2005, preprint, e3.	1.5	0
185	Ranking of communities in multiplex spatiotemporal models of brain dynamics. Applied Network Science, 2022, 7, 15.	0.8	0
186	Title is missing!. , 2020, 16, e1007636.		0
187	Title is missing!. , 2020, 16, e1007636.		0
188	Title is missing!. , 2020, 16, e1007636.		0
189	Title is missing!. , 2020, 16, e1007636.		0