Charlotte M Deane

List of Publications by Year
in descending order

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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	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
2	The Therapeutic Antibody Profiler for Computational Developability Assessment. Methods in Molecular Biology, 2022, 2313, 115-125.	0.4	7
3	DLAB: deep learning methods for structure-based virtual screening of antibodies. Bioinformatics, 2022, 38, 377-383.	1.8	48
4	SAbDab in the age of biotherapeutics: updates including SAbDab-nano, the nanobody structure tracker. Nucleic Acids Research, 2022, 50, D1368-D1372.	6.5	49
5	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
6	ABlooper: fast accurate antibody CDR loop structure prediction with accuracy estimation. Bioinformatics, 2022, 38, 1877-1880.	1.8	78
7	Current structure predictors are not learning the physics of protein folding. Bioinformatics, 2022, 38, 1881-1887.	1.8	50
8	Current advances in biopharmaceutical informatics: guidelines, impact and challenges in the computational developability assessment of antibody therapeutics. MAbs, 2022, 14, 2020082.	2.6	35
9	AI in 3D compound design. Current Opinion in Structural Biology, 2022, 73, 102326.	2.6	8
10	Challenges and Opportunities for Bayesian Statistics in Proteomics. Journal of Proteome Research, 2022, 21, 849-864.	1.8	5
11	Ranking of communities in multiplex spatiotemporal models of brain dynamics. Applied Network Science, 2022, 7, 15.	0.8	0
12	Membranome 3.0: Database of singleâ€pass membrane proteins with <scp>AlphaFold</scp> models. Protein Science, 2022, 31, e4318.	3.1	20
13	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
14	Advances in computational structure-based antibody design. Current Opinion in Structural Biology, 2022, 74, 102379.	2.6	32
15	Extracting Information from Gene Coexpression Networks of Rhizobium leguminosarum. Journal of Computational Biology, 2022, , .	0.8	1
16	Generating weighted and thresholded gene coexpression networks using signed distance correlation. Network Science, 2022, 10, 131-145.	0.8	1
17	AbLang: an antibody language model for completing antibody sequences. Bioinformatics Advances, 2022, 2, .	0.9	48
18	Empirical Bayes functional models for hydrogen deuterium exchange mass spectrometry. Communications Biology, 2022, 5, .	2.0	1

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19	CoV-AbDab: the coronavirus antibody database. Bioinformatics, 2021, 37, 734-735.	1.8	273
20	COGENT: evaluating the consistency of gene co-expression networks. Bioinformatics, 2021, 37, 1928-1929.	1.8	6
21	Ribosome occupancy profiles are conserved between structurally and evolutionarily related yeast domains. Bioinformatics, 2021, 37, 1853-1859.	1.8	4
22	Ab-Ligity: identifying sequence-dissimilar antibodies that bind to the same epitope. MAbs, 2021, 13, 1873478.	2.6	31
23	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
24	Robust gene coexpression networks using signed distance correlation. Bioinformatics, 2021, 37, 1982-1989.	1.8	10
25	The allosteric modulation of complement C5 by knob domain peptides. ELife, 2021, 10, .	2.8	21
26	Generating property-matched decoy molecules using deep learning. Bioinformatics, 2021, 37, 2134-2141.	1.8	30
27	Public Baseline and shared response structures support the theory of antibody repertoire functional commonality. PLoS Computational Biology, 2021, 17, e1008781.	1.5	26
28	Hypergraphs for predicting essential genes using multiprotein complex data. Journal of Complex Networks, 2021, 9, .	1.1	16
29	Humanization of antibodies using a machine learning approach on large-scale repertoire data. Bioinformatics, 2021, 37, 4041-4047.	1.8	49
30	Co-evolutionary distance predictions contain flexibility information. Bioinformatics, 2021, , .	1.8	9
31	The prospects of quantum computing in computational molecular biology. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2021, 11, e1481.	6.2	108
32	Deep generative design with 3D pharmacophoric constraints. Chemical Science, 2021, 12, 14577-14589.	3.7	36
33	Different B cell subpopulations show distinct patterns in their IgH repertoire metrics. ELife, 2021, 10, .	2.8	22
34	Current strategies for detecting functional convergence across B-cell receptor repertoires. MAbs, 2021, 13, 1996732.	2.6	18
35	Epitope profiling using computational structural modelling demonstrated on coronavirus-binding antibodies. PLoS Computational Biology, 2021, 17, e1009675.	1.5	33
36	Learning from the ligand: using ligand-based features to improve binding affinity prediction. Bioinformatics, 2020, 36, 758-764.	1.8	60

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37	The evolution of contact prediction: evidence that contact selection in statistical contact prediction is changing. Bioinformatics, 2020, 36, 1750-1756.	1.8	5
38	Thera-SAbDab: the Therapeutic Structural Antibody Database. Nucleic Acids Research, 2020, 48, D383-D388.	6.5	88
39	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
40	Maturation of the Human Immunoglobulin Heavy Chain Repertoire With Age. Frontiers in Immunology, 2020, 11, 1734.	2.2	46
41	Functional module detection through integration of single-cell RNA sequencing data with proteinâ€“protein interaction networks. BMC Genomics, 2020, 21, 756.	1.2	13
42	How repertoire data are changing antibody science. Journal of Biological Chemistry, 2020, 295, 9823-9837.	1.6	43
43	TCRBuilder: multi-state T-cell receptor structure prediction. Bioinformatics, 2020, 36, 3580-3581.	1.8	10
44	Deep Generative Models for 3D Linker Design. Journal of Chemical Information and Modeling, 2020, 60, 1983-1995.	2.5	126
45	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
46	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
47	Title is missing!. , 2020, 16, e1007636.		0
48	Title is missing!. , 2020, 16, e1007636.		0
49	Title is missing!. , 2020, 16, e1007636.		0
50	Title is missing!. , 2020, 16, e1007636.		0
51	Assessment of model fit via network comparison methods based on subgraph counts. Journal of Complex Networks, 2019, 7, 226-253.	1.1	3
52	Comparative Analysis of the CDR Loops of Antigen Receptors. Frontiers in Immunology, 2019, 10, 2454.	2.2	40
53	RFQAmodel: Random Forest Quality Assessment to identify a predicted protein structure in the correct fold. PLoS ONE, 2019, 14, e0218149.	1.1	3
54	Measuring rank robustness in scored protein interaction networks. BMC Bioinformatics, 2019, 20, 446.	1.2	30

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55	Looking for therapeutic antibodies in next-generation sequencing repositories. MAbs, 2019, 11, 1197-1205.	2.6	29
56	Modeling conformational flexibility of kinases in inactive states. Proteins: Structure, Function and Bioinformatics, 2019, 87, 943-951.	1.5	11
57	Ligity: A Non-Superpositional, Knowledge-Based Approach to Virtual Screening. Journal of Chemical Information and Modeling, 2019, 59, 2600-2616.	2.5	9
58	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
59	Antibodyâ€“antigen complex modelling in the era of immunoglobulin repertoire sequencing. Molecular Systems Design and Engineering, 2019, 4, 679-688.	1.7	20
60	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
61	MHC binding affects the dynamics of different T-cell receptors in different ways. PLoS Computational Biology, 2019, 15, e1007338.	1.5	13
62	Increasing the accuracy of protein loop structure prediction with evolutionary constraints. Bioinformatics, 2019, 35, 2585-2592.	1.8	8
63	SCALOP: sequence-based antibody canonical loop structure annotation. Bioinformatics, 2019, 35, 1774-1776.	1.8	29
64	High-Throughput Antibody Structure Modeling and Design Using ABodyBuilder. Methods in Molecular Biology, 2019, 1851, 367-380.	0.4	3
65	A Statistical Model for Helices with Applications. Biometrics, 2018, 74, 845-854.	0.8	2
66	Identifying networks with common organizational principles. Journal of Complex Networks, 2018, 6, 887-913.	1.1	20
67	Combining co-evolution and secondary structure prediction to improve fragment library generation. Bioinformatics, 2018, 34, 2219-2227.	1.8	7
68	pyHVis3D: visualising molecular simulation deduced H-bond networks in 3D: application to T-cell receptor interactions. Bioinformatics, 2018, 34, 1941-1943.	1.8	6
69	Predicting loop conformational ensembles. Bioinformatics, 2018, 34, 949-956.	1.8	20
70	Antibody side chain conformations are positionâ€dependent. Proteins: Structure, Function and Bioinformatics, 2018, 86, 383-392.	1.5	21
71	In silico structural modeling of multiple epigenetic marks on DNA. Bioinformatics, 2018, 34, 41-48.	1.8	4
72	STCRDab: the structural T-cell receptor database. Nucleic Acids Research, 2018, 46, D406-D412.	6.5	69

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73	Filtering Next-Generation Sequencing of the Ig Gene Repertoire Data Using Antibody Structural Information. Journal of Immunology, 2018, 201, 3694-3704.	0.4	11
74	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
75	Avoiding False Positive Conclusions in Molecular Simulation: The Importance of Replicas. Journal of Chemical Theory and Computation, 2018, 14, 6127-6138.	2.3	187
76	Observed Antibody Space: A Resource for Data Mining Next-Generation Sequencing of Antibody Repertoires. Journal of Immunology, 2018, 201, 2502-2509.	0.4	165
77	Sequential search leads to faster, more efficient fragment-basedde novoprotein structure prediction. Bioinformatics, 2018, 34, 1132-1140.	1.8	12
78	Structurally Mapping Antibody Repertoires. Frontiers in Immunology, 2018, 9, 1698.	2.2	36
79	Efficient Sampling for the Prediction of Long and Multidomain Protein Structures. Biophysical Journal, 2018, 114, 574a.	0.2	0
80	Comparing co-evolution methods and their application to template-free protein structure prediction. Bioinformatics, 2017, 33, 373-381.	1.8	28
81	Antibody H3 Structure Prediction. Computational and Structural Biotechnology Journal, 2017, 15, 222-231.	1.9	47
82	Association between a common immunoglobulin heavy chain allele and rheumatic heart disease risk in Oceania. Nature Communications, 2017, 8, 14946.	5.8	114
83	A multi-crystal method for extracting obscured crystallographic states from conventionally uninterpretable electron density. Nature Communications, 2017, 8, 15123.	5.8	186
84	Computational Tools for Aiding Rational Antibody Design. Methods in Molecular Biology, 2017, 1529, 399-416.	0.4	22
85	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
86	Investigating Cotranslational Folding in Membrane Proteins using Fragment-Based Structure Prediction. Biophysical Journal, 2017, 112, 61a.	0.2	1
87	The H3 loop of antibodies shows unique structural characteristics. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1311-1318.	1.5	89
88	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
89	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
90	Co-evolution techniques are reshaping the way we do structural bioinformatics. F1000Research, 2017, 6, 1224.	0.8	22

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91	How B-Cell Receptor Repertoire Sequencing Can Be Enriched with Structural Antibody Data. Frontiers in Immunology, 2017, 8, 1753.	2.2	48
92	Sphinx: merging knowledge-based and ab initio approaches to improve protein loop prediction. Bioinformatics, 2017, 33, 1346-1353.	1.8	49
93	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
94	Ten simple rules for surviving an interdisciplinary PhD. PLoS Computational Biology, 2017, 13, e1005512.	1.5	7
95	ANARCI: antigen receptor numbering and receptor classification. Bioinformatics, 2016, 32, 298-300.	1.8	237
96	Exploring peptide/MHC detachment processes using hierarchical natural move Monte Carlo. Bioinformatics, 2016, 32, 181-186.	1.8	21
97	Examining the Conservation of Kinks in Alpha Helices. PLoS ONE, 2016, 11, e0157553.	1.1	20
98	ABodyBuilder: Automated antibody structure prediction with dataâ€“driven accuracy estimation. MAbs, 2016, 8, 1259-1268.	2.6	208
99	Modeling Functional Motions of Biological Systems by Customized Natural Moves. Biophysical Journal, 2016, 111, 710-721.	0.2	7
100	Tertiary Element Interaction in HIV-1 TAR. Journal of Chemical Information and Modeling, 2016, 56, 1746-1754.	2.5	8
101	Comparison of large networks with sub-sampling strategies. Scientific Reports, 2016, 6, 28955.	1.6	9
102	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
103	SAbPred: a structure-based antibody prediction server. Nucleic Acids Research, 2016, 44, W474-W478.	6.5	155
104	Progress and challenges in predicting protein interfaces. Briefings in Bioinformatics, 2016, 17, 117-131.	3.2	115
105	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
106	Length-independent structural similarities enrich the antibody CDR canonical class model. MAbs, 2016, 8, 751-760.	2.6	49
107	Prediction of VHâ€“VL domain orientation for antibody variable domain modeling. Proteins: Structure, Function and Bioinformatics, 2015, 83, 681-695.	1.5	47
108	Building a Better Fragment Library for De Novo Protein Structure Prediction. PLoS ONE, 2015, 10, e0123998.	1.1	25

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109	Structural Bridges through Fold Space. PLoS Computational Biology, 2015, 11, e1004466.	1.5	16
110	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
111	Misato Controls Mitotic Microtubule Generation by Stabilizing the TCP-1 Tubulin Chaperone Complex. Current Biology, 2015, 25, 1777-1783.	1.8	25
112	Current status and future challenges in T-cell receptor/peptide/MHC molecular dynamics simulations. Briefings in Bioinformatics, 2015, 16, 1035-1044.	3.2	45
113	Ten Simple Rules for a Successful Cross-Disciplinary Collaboration. PLoS Computational Biology, 2015, 11, e1004214.	1.5	46
114	Type II Inhibitors Targeting CDK2. ACS Chemical Biology, 2015, 10, 2116-2125.	1.6	75
115	Identifying and quantifying radiation damage atÂtheÂatomic level. Journal of Synchrotron Radiation, 2015, 22, 201-212.	1.0	51
116	The Caenorhabditis elegans protein SAS-5 forms large oligomeric assemblies critical for centriole formation. ELife, 2015, 4, e07410.	2.8	37
117	Examining Variable Domain Orientations in Antigen Receptors Gives Insight into TCR-Like Antibody Design. PLoS Computational Biology, 2014, 10, e1003852.	1.5	29
118	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
119	Ten Simple Rules for Effective Computational Research. PLoS Computational Biology, 2014, 10, e1003506.	1.5	47
120	Improving B-cell epitope prediction and its application to global antibody-antigen docking. Bioinformatics, 2014, 30, 2288-2294.	1.8	137
121	Alignment-free protein interaction network comparison. Bioinformatics, 2014, 30, i430-i437.	1.8	48
122	Helix kinks are equally prevalent in soluble and membrane proteins. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1960-1970.	1.5	61
123	Protein Modeling and Structural Prediction. , 2014, , 171-182.		1
124	SAbDab: the structural antibody database. Nucleic Acids Research, 2014, 42, D1140-D1146.	6.5	374
125	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
126	Crowdsourcing Yields a New Standard for Kinks in Protein Helices. Journal of Chemical Information and Modeling, 2014, 54, 2585-2593.	2.5	7

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127	Gro2mat: A package to efficiently read gromacs output in MATLAB. Journal of Computational Chemistry, 2014, 35, 1528-1531.	1.5	18
128	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
129	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
130	MP-T: improving membrane protein alignment for structure prediction. Bioinformatics, 2013, 29, 54-61.	1.8	30
131	Interactions of Two Amphipathic Cell-Penetrating Peptides with Complex Model Membranes: Insights from Molecular Dynamics Simulations. Biophysical Journal, 2013, 104, 600a.	0.2	0
132	Exploring Fold Space Preferences of New-born and Ancient Protein Superfamilies. PLoS Computational Biology, 2013, 9, e1003325.	1.5	31
133	Memoir: template-based structure prediction for membrane proteins. Nucleic Acids Research, 2013, 41, W379-W383.	6.5	38
134	Local Network Patterns in Protein-Protein Interfaces. PLoS ONE, 2013, 8, e57031.	1.1	5
135	How long is a piece of loop?. PeerJ, 2013, 1, e1.	0.9	17
136	What Evidence Is There for the Homology of Protein-Protein Interactions?. PLoS Computational Biology, 2012, 8, e1002645.	1.5	41
137	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
138	Freely Available Conformer Generation Methods: How Good Are They?. Journal of Chemical Information and Modeling, 2012, 52, 1146-1158.	2.5	178
139	The Importance of Age and High Degree, in Protein-Protein Interaction Networks. Journal of Computational Biology, 2012, 19, 785-795.	0.8	11
140	Mutual information and variants for protein domain-domain contact prediction. BMC Research Notes, 2012, 5, 472.	0.6	5
141	Producing High-Accuracy Lattice Models from Protein Atomic Coordinates Including Side Chains. Advances in Bioinformatics, 2012, 2012, 1-6.	5.7	22
142	Predicting Inter-Species Cross-Talk in Two-Component Signalling Systems. PLoS ONE, 2012, 7, e37737.	1.1	2
143	Predicting antibody complementarity determining region structures without classification. Molecular BioSystems, 2011, 7, 3327.	2.9	39
144	The imprint of codons on protein structure. Biotechnology Journal, 2011, 6, 641-649.	1.8	17

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145	Signatures of coâ€translational folding. Biotechnology Journal, 2011, 6, 742-751.	1.8	15
146	Environment specific substitution tables improve membrane protein alignment. Bioinformatics, 2011, 27, i15-i23.	1.8	20
147	Directionality in protein fold prediction. BMC Bioinformatics, 2010, 11, 172.	1.2	17
148	The function of communities in protein interaction networks at multiple scales. BMC Systems Biology, 2010, 4, 100.	3.0	79
149	Deciphering chemotaxis pathways using cross species comparisons. BMC Systems Biology, 2010, 4, 3.	3.0	66
150	Protein structure prediction begins well but ends badly. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1282-1290.	1.5	15
151	FREAD revisited: Accurate loop structure prediction using a database search algorithm. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1431-1440.	1.5	154
152	iâ€Patch: Interprotein contact prediction using local network information. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2781-2797.	1.5	26
153	How threshold behaviour affects the use of subgraphs for network comparison. Bioinformatics, 2010, 26, i611-i617.	1.8	26
154	Exploring the potential of template-based modelling. Bioinformatics, 2010, 26, 1849-1856.	1.8	11
155	Revisiting Date and Party Hubs: Novel Approaches to Role Assignment in Protein Interaction Networks. PLoS Computational Biology, 2010, 6, e1000817.	1.5	128
156	MEDELLER: homology-based coordinate generation for membrane proteins. Bioinformatics, 2010, 26, 2833-2840.	1.8	103
157	Synonymous codon usage influences the local protein structure observed. Nucleic Acids Research, 2010, 38, 6719-6728.	6.5	148
158	Predicting proteinâ€“protein interactions in the context of protein evolution. Molecular BioSystems, 2010, 6, 55-64.	2.9	42
159	Evolutionary analysis reveals low coverage as the major challenge for protein interaction network alignment. Molecular BioSystems, 2010, 6, 2296.	2.9	11
160	iMembrane: homology-based membrane-insertion of proteins. Bioinformatics, 2009, 25, 1086-1088.	1.8	29
161	Reduced amounts and abnormal forms of phospholipase C zeta (PLCÂ) in spermatozoa from infertile men. Human Reproduction, 2009, 24, 2417-2428.	0.4	257
162	Proteomic Analysis of Microtubule-associated Proteins during Macrophage Activation. Molecular and Cellular Proteomics, 2009, 8, 2500-2514.	2.5	41

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163	Functionally guided alignment of protein interaction networks for module detection. Bioinformatics, 2009, 25, 3166-3173.	1.8	31
164	An assessment of the uses of homologous interactions. Bioinformatics, 2008, 24, 689-695.	1.8	22
165	The functional domain grouping of microtubule associated proteins. Communicative and Integrative Biology, 2008, 1, 47-50.	0.6	5
166	Predicting and Validating Protein Interactions Using Network Structure. PLoS Computational Biology, 2008, 4, e1000118.	1.5	30
167	A Microtubule Interactome: Complexes with Roles in Cell Cycle and Mitosis. PLoS Biology, 2008, 6, e98.	2.6	105
168	A statistical approach using network structure in the prediction of protein characteristics. Bioinformatics, 2007, 23, 2314-2321.	1.8	6
169	Using Phylogeny to Improve Genome-Wide Distant Homology Recognition. PLoS Computational Biology, 2007, 3, e3.	1.5	6
170	Cotranslational protein foldingâ€"fact or fiction?. Bioinformatics, 2007, 23, i142-i148.	1.8	28
171	Linking evolution of protein structures through fragments. BMC Systems Biology, 2007, 1, .	3.0	0
172	Protein protein interactions, evolutionary rate, abundance and age. BMC Bioinformatics, 2006, 7, 128.	1.2	64
173	Modelling sequential protein folding under kinetic control. Bioinformatics, 2006, 22, e203-e210.	1.8	23
174	Fold usage on genomes and protein fold evolution. Proteins: Structure, Function and Bioinformatics, 2005, 60, 690-700.	1.5	30
175	How old is your fold?. Bioinformatics, 2005, 21, i449-i458.	1.8	63
176	Using phylogeny to improve genome wide distant homology recognition. PLoS Computational Biology, 2005, preprint, e3.	1.5	0
177	Solution Structure and Dynamics of a Prototypical Chordin-like Cysteine-rich Repeat (von Willebrand) Tj ETQq1 1 0.784314 rgBT /Ove	1.6	83
178	PROTEIN COMPARATIVE MODELLING AND DRUG DISCOVERY. , 2003, , 445-458.		3
179	Protein Interactions. Molecular and Cellular Proteomics, 2002, 1, 349-356.	2.5	570
180	CODA: A combined algorithm for predicting the structurally variable regions of protein models. Protein Science, 2001, 10, 599-612.	3.1	147

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181	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
182	Improved protein loop prediction from sequence alone. Protein Engineering, Design and Selection, 2001, 14, 473-478.	1.0	32
183	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
184	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
185	An iterative structure-assisted approach to sequence alignment and comparative modeling. , 1999, 37, 55-60.		32
186	HOMSTRAD: A database of protein structure alignments for homologous families. Protein Science, 1998, 7, 2469-2471.	3.1	461
187	Protein Three-Dimensional Structural Databases: Domains, Structurally Aligned Homologues and Superfamilies. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 1168-1177.	2.5	6
188	A structural model of the human thrombopoietin receptor complex. Journal of Molecular Graphics and Modelling, 1997, 15, 170-188.	1.3	18
189	Investigating the potential for a limited quantum speedup on protein lattice problems. New Journal of Physics, 0, , .	1.2	6