

# John Moul

## List of Publications by Year in descending order

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151  
papers

13,847  
citations

24978

57  
h-index

22764

112  
g-index

160  
all docs

160  
docs citations

160  
times ranked

11735  
citing authors

#	ARTICLE	IF	CITATIONS
1	CACHE (Critical Assessment of Computational Hit-finding Experiments): A public-private partnership benchmarking initiative to enable the development of computational methods for hit-finding. <i>Nature Reviews Chemistry</i> , 2022, 6, 287-295.	13.8	22
2	MecCog: a knowledge representation framework for genetic disease mechanism. <i>Bioinformatics</i> , 2021, 37, 4180-4186.	1.8	1
3	Modeling SARS-CoV-2 proteins in the CASP-commons experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1987-1996.	1.5	24
4	Computational models in the service of X-ray and cryo-electron microscopy structure determination. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1633-1646.	1.5	37
5	Target highlights in CASP14: Analysis of models by structure providers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1647-1672.	1.5	27
6	Critical assessment of methods of protein structure prediction (CASP) Round XIV. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1607-1617.	1.5	281
7	Matching whole genomes to rare genetic disorders: Identification of potential causative variants using phenotype-weighted knowledge in the CAGI SickKids5 clinical genomes challenge. <i>Human Mutation</i> , 2020, 41, 347-362.	1.1	4
8	CAGI SickKids challenges: Assessment of phenotype and variant predictions derived from clinical and genomic data of children with undiagnosed diseases. <i>Human Mutation</i> , 2019, 40, 1373-1391.	1.1	10
9	Assessing computational predictions of the phenotypic effect of cystathionine-beta-synthase variants. <i>Human Mutation</i> , 2019, 40, 1530-1545.	1.1	5
10	Assessment of predicted enzymatic activity of N-acetylglucosaminidase variants of unknown significance for CAGI 2016. <i>Human Mutation</i> , 2019, 40, 1519-1529.	1.1	10
11	Performance of computational methods for the evaluation of pericentriolar material 1 missense variants in CAGI5. <i>Human Mutation</i> , 2019, 40, 1474-1485.	1.1	8
12	Back Cover, Volume 40, Issue 9. <i>Human Mutation</i> , 2019, 40, ii.	1.1	0
13	Critical assessment of methods of protein structure prediction (CASP) Round XIII. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1011-1020.	1.5	380
14	Target highlights in CASP13: Experimental target structures through the eyes of their authors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1037-1057.	1.5	12
15	Assessment of methods for predicting the effects of PTEN and TPMT protein variants. <i>Human Mutation</i> , 2019, 40, 1495-1506.	1.1	16
16	Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. <i>Human Mutation</i> , 2019, 40, 1314-1320.	1.1	10
17	Assessment of patient clinical descriptions and pathogenic variants from gene panel sequences in the CAGI5 intellectual disability challenge. <i>Human Mutation</i> , 2019, 40, 1330-1345.	1.1	11
18	Cover Image, Volume 87, Issue 12. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, C4.	1.5	0

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19	latrogenic hypertension: a bioinformatic analysis. <i>Pharmacogenomics Journal</i> , 2019, 19, 337-346.	0.9	4
20	Target highlights from the first post-PSI CASP experiment (CASP12, May-August 2016). <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 27-50.	1.5	11
21	A tribute to Anna Tramontano (1957-2017). <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 5-6.	1.5	1
22	Critical assessment of methods of protein structure prediction (CASP) Round XII. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 7-15.	1.5	296
23	Evaluation of the template-based modeling in CASP12. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 321-334.	1.5	61
24	Harnessing formal concepts of biological mechanism to analyze human disease. <i>PLoS Computational Biology</i> , 2018, 14, e1006540.	1.5	14
25	The Product Guides the Process: Discovering Disease Mechanisms. <i>Studies in Applied Philosophy, Epistemology and Rational Ethics</i> , 2018, , 101-117.	0.2	4
26	Determination of disease phenotypes and pathogenic variants from exome sequence data in the CAGI 4 gene panel challenge. <i>Human Mutation</i> , 2017, 38, 1201-1216.	1.1	5
27	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. <i>Human Mutation</i> , 2017, 38, 1042-1050.	1.1	13
28	CAGI4 SickKids clinical genomes challenge: A pipeline for identifying pathogenic variants. <i>Human Mutation</i> , 2017, 38, 1169-1181.	1.1	11
29	CAGI4 Crohn's exome challenge: Marker SNP versus exome variant models for assigning risk of Crohn disease. <i>Human Mutation</i> , 2017, 38, 1225-1234.	1.1	15
30	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. <i>Human Mutation</i> , 2017, 38, 1182-1192.	1.1	39
31	Ensemble variant interpretation methods to predict enzyme activity and assign pathogenicity in the CAGI4 NAGLU (Human N-acetylglucosaminidase) and UBE2I (Human SUMO ligase) challenges. <i>Human Mutation</i> , 2017, 38, 1109-1122.	1.1	14
32	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. <i>Human Mutation</i> , 2017, 38, 1266-1276.	1.1	14
33	Reply to HU et al.: On the interpretation of gasdermin-B expression quantitative trait loci data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7863-E7864.	3.3	0
34	Reports from CAGI: The Critical Assessment of Genome Interpretation. <i>Human Mutation</i> , 2017, 38, 1039-1041.	1.1	38
35	Lessons from the CAGI Hopkins clinical panel challenge. <i>Human Mutation</i> , 2017, 38, 1155-1168.	1.1	6
36	Mapping genetic variations to three-dimensional protein structures to enhance variant interpretation: a proposed framework. <i>Genome Medicine</i> , 2017, 9, 113.	3.6	47

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37	Critical assessment of methods of protein structure prediction: Progress and new directions in round XI. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 4-14.	1.5	198
38	Some of the most interesting <scp>CASP</scp>11 targets through the eyes of their authors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 34-50.	1.5	16
39	Consensus Genome-Wide Expression Quantitative Trait Loci and Their Relationship with Human Complex Trait Disease. <i>OMICS A Journal of Integrative Biology</i> , 2016, 20, 400-414.	1.0	46
40	Cover Image, Volume 84, Issue S1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, C1-C1.	1.5	2
41	Cover Image, Volume 84, Issue S1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, C4.	1.5	13
42	A bacteriophage endolysin that eliminates intracellular streptococci. <i>ELife</i> , 2016, 5, .	2.8	64
43	Insights from GWAS: emerging landscape of mechanisms underlying complex trait disease. <i>BMC Genomics</i> , 2015, 16, S4.	1.2	16
44	Increasing the stability of the bacteriophage endolysin PlyC using rationale-based FoldX computational modeling. <i>Protein Engineering, Design and Selection</i> , 2015, 28, 85-92.	1.0	32
45	Genetic Basis of Common Human Disease: Insight into the Role of Missense SNPs from Genome-Wide Association Studies. <i>Journal of Molecular Biology</i> , 2015, 427, 2271-2289.	2.0	44
46	Critical assessment of methods of protein structure prediction (CASP) â€™ round x. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1-6.	1.5	366
47	Assessment of protein disorder region predictions in CASP10. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 127-137.	1.5	140
48	Challenging the state of the art in protein structure prediction: Highlights of experimental target structures for the 10th Critical Assessment of Techniques for Protein Structure Prediction Experiment CASP10. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 26-42.	1.5	53
49	CASP10 results compared to those of previous CASP experiments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 164-174.	1.5	91
50	GWAS and drug targets. <i>BMC Genomics</i> , 2014, 15, S5.	1.2	56
51	Neighbor Overlap Is Enriched in the Yeast Interaction Network: Analysis and Implications. <i>PLoS ONE</i> , 2012, 7, e39662.	1.1	2
52	Protein stability and <i>in vivo</i> concentration of missense mutations in phenylalanine hydroxylase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 61-70.	1.5	29
53	Genetic basis of common human disease: insight into the role of nonsynonymous SNPs from genome-wide association studies. <i>Genome Biology</i> , 2011, 12, .	13.9	0
54	Structural and Functional Impact of Cancer-Related Missense Somatic Mutations. <i>Journal of Molecular Biology</i> , 2011, 413, 495-512.	2.0	35

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55	Protein Characterization of a Candidate Mechanism SNP for Crohn's Disease: The Macrophage Stimulating Protein R689C Substitution. PLoS ONE, 2011, 6, e27269.	1.1	24
56	Evaluation of disorder predictions in CASP9. Proteins: Structure, Function and Bioinformatics, 2011, 79, 107-118.	1.5	102
57	CASP9 results compared to those of previous casp experiments. Proteins: Structure, Function and Bioinformatics, 2011, 79, 196-207.	1.5	91
58	Target highlights in CASP9: Experimental target structures for the critical assessment of techniques for protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2011, 79, 6-20.	1.5	19
59	Critical assessment of methods of protein structure prediction (CASP)â€”round IX. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1-5.	1.5	187
60	Composition bias and the origin of ORFan genes. Bioinformatics, 2010, 26, 996-999.	1.8	16
61	Structural Basis for the Mechanism and Substrate Specificity of Glycoamine Kinase, a Phosphagen Kinase Family Member<sup>, </sup>. Biochemistry, 2010, 49, 2031-2041.	1.2	22
62	Stochastic noise in splicing machinery. Nucleic Acids Research, 2009, 37, 4873-4886.	6.5	157
63	Structural implication of splicing stochastics. Nucleic Acids Research, 2009, 37, 4862-4872.	6.5	31
64	Evaluation of templateâ€”based models in CASP8 with standard measures. Proteins: Structure, Function and Bioinformatics, 2009, 77, 18-28.	1.5	114
65	CASP8 results in context of previous experiments. Proteins: Structure, Function and Bioinformatics, 2009, 77, 217-228.	1.5	38
66	Critical assessment of methods of protein structure predictionâ€”Round VIII. Proteins: Structure, Function and Bioinformatics, 2009, 77, 1-4.	1.5	229
67	Community-wide assessment of GPCR structure modelling and ligand docking: GPCR Dock 2008. Nature Reviews Drug Discovery, 2009, 8, 455-463.	21.5	260
68	A survey of proteins encoded by non-synonymous single nucleotide polymorphisms reveals a significant fraction with altered stability and activity. Biochemical Journal, 2009, 424, 15-26.	1.7	43
69	Comparative Modeling in Structural Genomics. Structure, 2008, 16, 14-16.	1.6	25
70	Flexibility of Aromatic Residues in the Active-Site Gorge of Acetylcholinesterase: X-ray versus Molecular Dynamics. Biophysical Journal, 2008, 95, 2500-2511.	0.2	104
71	Proteopedia - a scientific 'wiki' bridging the rift between 3D structure and function of biomacromolecules. Genome Biology, 2008, 9, R121.	13.9	98
72	Comparative Modeling in Structural Genomics. , 2008, , 121-134.		2

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73	Critical assessment of methods of protein structure predictionâ€”Round VII. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 3-9.	1.5	199
74	Progress from CASP6 to CASP7. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 194-207.	1.5	60
75	Rigorous performance evaluation in protein structure modelling and implications for computational biology. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 453-458.	1.8	34
76	Identification and Analysis of Deleterious Human SNPs. <i>Journal of Molecular Biology</i> , 2006, 356, 1263-1274.	2.0	237
77	Towards computing with proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 53-64.	1.5	87
78	Detection of operons. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 615-628.	1.5	14
79	Outcome of a Workshop on Archiving Structural Models of Biological Macromolecules. <i>Structure</i> , 2006, 14, 1211-1217.	1.6	60
80	SNPs3D: candidate gene and SNP selection for association studies. <i>BMC Bioinformatics</i> , 2006, 7, 166.	1.2	383
81	A decade of CASP: progress, bottlenecks and prognosis in protein structure prediction. <i>Current Opinion in Structural Biology</i> , 2005, 15, 285-289.	2.6	435
82	Critical assessment of methods of protein structure prediction (CASP)â€”Round 6. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 3-7.	1.5	162
83	Progress over the first decade of CASP experiments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 225-236.	1.5	172
84	The psychrophilic lifestyle as revealed by the genome sequence of <i>Colwellia psychrerythraea</i> 34H through genomic and proteomic analyses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10913-10918.	3.3	529
85	Loss of Protein Structure Stability as a Major Causative Factor in Monogenic Disease. <i>Journal of Molecular Biology</i> , 2005, 353, 459-473.	2.0	438
86	Protein Family Clustering for Structural Genomics. <i>Journal of Molecular Biology</i> , 2005, 353, 744-759.	2.0	27
87	Molecular modeling of protein function regions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 942-961.	1.5	43
88	CAPRI: A Critical Assessment of PRedicted Interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 2-9.	1.5	586
89	Three-dimensional structural location and molecular functional effects of missense SNPs in the T cell receptor V? domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 748-757.	1.5	25
90	Assessment of progress over the CASP experiments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 585-595.	1.5	110

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91	Evaluation of disorder predictions in CASP5. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 561-565.	1.5	90
92	Critical assessment of methods of protein structure prediction (CASP)-round V. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 334-339.	1.5	221
93	The Significance of Performance Ranking in CASPâ€™Response to Marti-Renom et al.. <i>Structure</i> , 2002, 10, 291-292.	1.6	5
94	A unfold, mesofold, and superfold model of protein fold use. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 46, 61-71.	1.5	85
95	Assisting Functional Assignment for Hypothetical <i>Heamophilus influenzae</i> Gene Products through Structural Genomics. <i>Current Drug Targets Infectious Disorders</i> , 2002, 2, 339-353.	2.1	7
96	Processing and evaluation of predictions in CASP4. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 13-21.	1.5	131
97	Comparison of performance in successive CASP experiments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 163-170.	1.5	62
98	Critical assessment of methods of protein structure prediction (CASP): Round IV. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 2-7.	1.5	146
99	SNPs, protein structure, and disease. <i>Human Mutation</i> , 2001, 17, 263-270.	1.1	649
100	Completeness in structural genomics. <i>Nature Structural Biology</i> , 2001, 8, 559-566.	9.7	336
101	We need both computer models and experiments. <i>Nature</i> , 2001, 409, 558-558.	13.7	13
102	From fold to function. <i>Current Opinion in Structural Biology</i> , 2000, 10, 384-389.	2.6	72
103	Local electrostatic optimization in proteins. <i>Protein Engineering, Design and Selection</i> , 1999, 12, 727-735.	1.0	4
104	Predicting protein three-dimensional structure. <i>Current Opinion in Biotechnology</i> , 1999, 10, 583-588.	3.3	79
105	Low Frequency Motion in Proteins. <i>Journal of Computational Physics</i> , 1999, 151, 169-189.	1.9	27
106	Critical assessment of methods of protein structure prediction (CASP): Round III. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 2-6.	1.5	137
107	Processing and analysis of CASP3 protein structure predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 22-29.	1.5	206
108	Some measures of comparative performance in the three CASPs. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 231-237.	1.5	39

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109	Processing and analysis of CASP3 protein structure predictions. Proteins: Structure, Function and Bioinformatics, 1999, 37, 22-29.	1.5	54
110	Critical assessment of methods of protein structure prediction (CASP): Round III. Proteins: Structure, Function and Bioinformatics, 1999, 37, 2-6.	1.5	27
111	Processing and analysis of CASP3 protein structure predictions. Proteins: Structure, Function and Bioinformatics, 1999, Suppl 3, 22-9.	1.5	142
112	Critical assessment of methods of protein structure prediction (CASP): Round III. , 1999, 37, 2.		103
113	Conformation of the sebacyl $\hat{I}^2$ 1Lys82 $\hat{A}^{\epsilon}$ $\hat{I}^2$ 2Lys82 crosslink in T-state human hemoglobin. , 1998, 30, 309-320.		5
114	pKaShifts in Small Molecules and HIV Protease: $\hat{A}$ Electrostatics and Conformation. Journal of the American Chemical Society, 1998, 120, 6138-6146.	6.6	55
115	An all-atom distance-dependent conditional probability discriminatory function for protein structure prediction 1 1 Edited by F. Cohen. Journal of Molecular Biology, 1998, 275, 895-916.	2.0	429
116	A graph-theoretic algorithm for comparative modeling of protein structure. Journal of Molecular Biology, 1998, 279, 287-302.	2.0	133
117	Dielectric Screening Treatment of Electrostatic Solvation. Journal of Physical Chemistry B, 1997, 101, 11226-11236.	1.2	37
118	Protein folding simulations with genetic algorithms and a detailed molecular description. Journal of Molecular Biology, 1997, 269, 240-259.	2.0	128
119	Ab initio protein folding simulations with genetic algorithms: Simulations on the complete sequence of small proteins. Proteins: Structure, Function and Bioinformatics, 1997, 29, 179-184.	1.5	20
120	Critical assessment of methods of protein structure prediction (CASP): Round II. , 1997, 29, 2-6.		114
121	Handling context-sensitivity in protein structures using graph theory: Bona fide prediction. Proteins: Structure, Function and Bioinformatics, 1997, 29, 43-49.	1.5	15
122	Criteria for evaluating protein structures derived from comparative modeling. Proteins: Structure, Function and Bioinformatics, 1997, 29, 7-13.	1.5	28
123	Chaos in protein dynamics. Proteins: Structure, Function and Bioinformatics, 1997, 29, 417-425.	1.5	63
124	Ab initio protein folding simulations with genetic algorithms: Simulations on the complete sequence of small proteins. Proteins: Structure, Function and Bioinformatics, 1997, 29, 179-184.	1.5	5
125	Critical assessment of methods of protein structure prediction (CASP): Round II. Proteins: Structure, Function and Bioinformatics, 1997, 29, 2-6.	1.5	22
126	Ab initio protein folding simulations with genetic algorithms: Simulations on the complete sequence of small proteins. Proteins: Structure, Function and Bioinformatics, 1997, 29, 179-184.	1.5	2



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127	Critical assessment of methods of protein structure prediction (CASP): Round II. , 1997, 29, 2.		82
128	Chaos in protein dynamics. , 1997, 29, 417.		1
129	Chaos in protein dynamics. Proteins: Structure, Function and Bioinformatics, 1997, 29, 417-425.	1.5	2
130	Local Interactions Dominate Folding in a Simple Protein Model. Journal of Molecular Biology, 1996, 259, 988-994.	2.0	95
131	The current state of the art in protein structure prediction. Current Opinion in Biotechnology, 1996, 7, 422-427.	3.3	61
132	Determination of the conformation of folding initiation sites in proteins by computer simulation. Proteins: Structure, Function and Bioinformatics, 1995, 23, 129-141.	1.5	43
133	A large-scale experiment to assess protein structure prediction methods. Proteins: Structure, Function and Bioinformatics, 1995, 23, ii-iv.	1.5	440
134	Confronting the problem of interconnected structural changes in the comparative modeling of proteins. Proteins: Structure, Function and Bioinformatics, 1995, 23, 327-336.	1.5	25
135	Ab initio structure prediction for small polypeptides and protein fragments using genetic algorithms. Proteins: Structure, Function and Bioinformatics, 1995, 23, 454-460.	1.5	60
136	Structure, Dynamics and Energetics of Initiation Sites in Protein Folding: I. Analysis of a 1 ns Molecular Dynamics Trajectory of an Early Folding Unit in Water: The Helix I/Loop I-Fragment of Barnase. Journal of Molecular Biology, 1995, 250, 239-257.	2.0	11
137	Comparison of systematic search and database methods for constructing segments of protein structure. Protein Engineering, Design and Selection, 1994, 7, 953-960.	1.0	113
138	An accurate simulation of the protein Streptomyces griseus protease A. Journal of Molecular Graphics, 1993, 11, 62-63.	1.7	0
139	Troponin-C mutants with increased calcium affinity. FEBS Journal, 1993, 213, 599-604.	0.2	34
140	Finding the lowest free energy conformation of a protein is an NP-hard problem: Proof and implications. Bulletin of Mathematical Biology, 1993, 55, 1183-1198.	0.9	109
141	Genetic Algorithms for Protein Folding Simulations. Journal of Molecular Biology, 1993, 231, 75-81.	2.0	484
142	Protein design on computers. Five new proteins: Shpilka, grendel, fingerclasp, leather, and aida. Proteins: Structure, Function and Bioinformatics, 1992, 12, 105-110.	1.5	26
143	Docking by least-squares fitting of molecular surface patterns. Journal of Molecular Biology, 1992, 225, 849-858.	2.0	93
144	The crystal packing interactions of two different crystal forms of bovine Ribonuclease A. Journal of Crystal Growth, 1991, 110, 119-130.	0.7	14

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145	Analysis of the steric strain in the polypeptide backbone of protein molecules. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991, 11, 223-229.	1.5	216
146	Comparative molecular model building of two serine proteinases from cytotoxic T lymphocytes. <i>Proteins: Structure, Function and Bioinformatics</i> , 1988, 4, 190-204.	1.5	78
147	[46] molecular structure of troponin C and its implications for the Ca <sup>2+</sup> triggering of muscle contraction. <i>Methods in Enzymology</i> , 1987, 139, 610-632.	0.4	18
148	Crystal structure of demetallized concanavalin A: the metal-binding region. <i>Journal of Molecular Biology</i> , 1979, 131, 137-155.	2.0	57
149	The effect of binding of metal ions on the three-dimensional structure of demetallized concanavalin A. <i>FEBS Letters</i> , 1978, 95, 54-56.	1.3	8
150	Binding of divalent copper ions to aspartic acid residue 52 in hen egg-white lysozyme. <i>Journal of Molecular Biology</i> , 1974, 87, 357-368.	2.0	38
151	The identification by X-ray crystallography of the site of attachment of an affinity label to hen egg-white lysozyme. <i>Journal of Molecular Biology</i> , 1973, 75, 1-4.	2.0	41