

Liam James Mcguffin

List of Publications by Year in descending order

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66
papers

6,684
citations

101543
36
h-index

110387
64
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68
all docs

68
docs citations

68
times ranked

8978
citing authors

#	ARTICLE	IF	CITATIONS
1	Prediction and Functional Analysis of Native Disorder in Proteins from the Three Kingdoms of Life. Journal of Molecular Biology, 2004, 337, 635-645.	4.2	1,828
2	The DISOPRED server for the prediction of protein disorder. Bioinformatics, 2004, 20, 2138-2139.	4.1	659
3	Protein structure prediction servers at University College London. Nucleic Acids Research, 2005, 33, W36-W38.	14.5	646
4	Improvement of the GenTHREADER method for genomic fold recognition. Bioinformatics, 2003, 19, 874-881.	4.1	337
5	Structure and evolution of barley powdery mildew effector candidates. BMC Genomics, 2012, 13, 694.	2.8	238
6	Secondary structure prediction with support vector machines. Bioinformatics, 2003, 19, 1650-1655.	4.1	213
7	Predicting Metal-binding Site Residues in Low-resolution Structural Models. Journal of Molecular Biology, 2004, 342, 307-320.	4.2	126
8	The ModFOLD server for the quality assessment of protein structural models. Bioinformatics, 2008, 24, 586-587.	4.1	123
9	Rapid protein domain assignment from amino acid sequence using predicted secondary structure. Protein Science, 2009, 11, 2814-2824.	7.6	122
10	Dominant β^2 -catenin mutations cause intellectual disability with recognizable syndromic features. Journal of Clinical Investigation, 2014, 124, 1468-1482.	8.2	110
11	The ModFOLD4 server for the quality assessment of 3D protein models. Nucleic Acids Research, 2013, 41, W368-W372.	14.5	108
12	Intrinsic disorder prediction from the analysis of multiple protein fold recognition models. Bioinformatics, 2008, 24, 1798-1804.	4.1	106
13	Rapid model quality assessment for protein structure predictions using the comparison of multiple models without structural alignments. Bioinformatics, 2010, 26, 182-188.	4.1	105
14	ModFOLD6: an accurate web server for the global and local quality estimation of 3D protein models. Nucleic Acids Research, 2017, 45, W416-W421.	14.5	104
15	The IntFOLD server: an integrated web resource for protein fold recognition, 3D model quality assessment, intrinsic disorder prediction, domain prediction and ligand binding site prediction. Nucleic Acids Research, 2011, 39, W171-W176.	14.5	101
16	IntFOLD: an integrated web resource for high performance protein structure and function prediction. Nucleic Acids Research, 2019, 47, W408-W413.	14.5	100
17	IntFOLD: an integrated server for modelling protein structures and functions from amino acid sequences: Figure 1.. Nucleic Acids Research, 2015, 43, W169-W173.	14.5	98
18	Prediction of novel and analogous folds using fragment assembly and fold recognition. Proteins: Structure, Function and Bioinformatics, 2005, 61, 143-151.	2.6	78

#	ARTICLE	IF	CITATIONS
19	Estimation of model accuracy in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1361-1377.	2.6	78
20	Assembling novel protein folds from super-secondary structural fragments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 480-485.	2.6	73
21	Benchmarking consensus model quality assessment for protein fold recognition. <i>BMC Bioinformatics</i> , 2007, 8, 345.	2.6	73
22	Proteins and Their Interacting Partners: An Introduction to Proteinâ€“Ligand Binding Site Prediction Methods. <i>International Journal of Molecular Sciences</i> , 2015, 16, 29829-29842.	4.1	66
23	Improving sequence-based fold recognition by using 3D model quality assessment. <i>Bioinformatics</i> , 2005, 21, 3509-3515.	4.1	65
24	FunFOLD: an improved automated method for the prediction of ligand binding residues using 3D models of proteins. <i>BMC Bioinformatics</i> , 2011, 12, 160.	2.6	64
25	Disorder Prediction Methods, Their Applicability to Different Protein Targets and Their Usefulness for Guiding Experimental Studies. <i>International Journal of Molecular Sciences</i> , 2015, 16, 19040-19054.	4.1	61
26	Evolutionary resurrection of flagellar motility via rewiring of the nitrogen regulation system. <i>Science</i> , 2015, 347, 1014-1017.	12.6	61
27	Proteogenomics and in silico structural and functional annotation of the barley powdery mildew <i>Blumeria graminis</i> f. sp. <i>hordei</i> . <i>Methods</i> , 2011, 54, 432-441.	3.8	57
28	ModFOLD8: accurate global and local quality estimates for 3D protein models. <i>Nucleic Acids Research</i> , 2021, 49, W425-W430.	14.5	56
29	Accurate templateâ€“based modeling in CASP12 using the IntFOLD4â€“TS, ModFOLD6, and ReFOLD methods. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 335-344.	2.6	48
30	The FunFOLD2 server for the prediction of proteinâ€“ligand interactions. <i>Nucleic Acids Research</i> , 2013, 41, W303-W307.	14.5	47
31	Prediction of global and local model quality in CASP8 using the ModFOLD server. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 185-190.	2.6	45
32	Improvement of 3D protein models using multiple templates guided by single-template model quality assessment. <i>Bioinformatics</i> , 2012, 28, 1851-1857.	4.1	44
33	The mysterious presence of a 5-methylcytosine oxidase in the <i>Drosophila</i> genome. <i>Cell Cycle</i> , 2013, 12, 3357-3365.	2.6	44
34	Methods for the Refinement of Protein Structure 3D Models. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2301.	4.1	44
35	SOcK, MiSTs, MASK and STickS: the GCKIII (germinal centre kinase III) kinases and their heterologous proteinâ€“protein interactions. <i>Biochemical Journal</i> , 2013, 454, 13-30.	3.7	41
36	The Genomic Threading Database: a comprehensive resource for structural annotations of the genomes from key organisms. <i>Nucleic Acids Research</i> , 2004, 32, 196D-199.	14.5	40

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37	Benchmarking secondary structure prediction for fold recognition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 166-175.	2.6	36
38	Targeting novel folds for structural genomics. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 48, 44-52.	2.6	34
39	A novel non-canonical mechanism of regulation of MST3 (mammalian Sterile20-related kinase 3). <i>Biochemical Journal</i> , 2012, 442, 595-610.	3.7	33
40	Automated tertiary structure prediction with accurate local model quality assessment using the <i>intfold</i> method. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 137-146.	2.6	32
41	ReFOLD: a server for the refinement of 3D protein models guided by accurate quality estimates. <i>Nucleic Acids Research</i> , 2017, 45, W422-W428.	14.5	32
42	Methods for estimation of model accuracy in CASP12. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 361-373.	2.6	27
43	The Genomic Threading Database. <i>Bioinformatics</i> , 2004, 20, 131-132.	4.1	25
44	Assessing the Quality of Modelled 3D Protein Structures Using the ModFOLD Server. <i>Methods in Molecular Biology</i> , 2014, 1137, 83-103.	0.9	24
45	The binding site distance test score: a robust method for the assessment of predicted protein binding sites. <i>Bioinformatics</i> , 2010, 26, 2920-2921.	4.1	23
46	PINOT: an intuitive resource for integrating protein-protein interactions. <i>Cell Communication and Signaling</i> , 2020, 18, 92.	6.5	21
47	FunFOLDQA: A Quality Assessment Tool for Protein-Ligand Binding Site Residue Predictions. <i>PLoS ONE</i> , 2012, 7, e38219.	2.5	20
48	GRID and docking analyses reveal a molecular basis for flavonoid inhibition of Src family kinase activity. <i>Journal of Nutritional Biochemistry</i> , 2015, 26, 1156-1165.	4.2	20
49	High throughput profile-profile based fold recognition for the entire human proteome. <i>BMC Bioinformatics</i> , 2006, 7, 288.	2.6	19
50	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. <i>Scientific Reports</i> , 2018, 8, 9939.	3.3	19
51	Predictive and Experimental Approaches for Elucidating Protein-Protein Interactions and Quaternary Structures. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2623.	4.1	18
52	Estimating the Quality of 3D Protein Models Using the ModFOLD7 Server. <i>Methods in Molecular Biology</i> , 2020, 2165, 69-81.	0.9	16
53	<i>In silico</i> identification and three-dimensional modelling of the missense mutation in <i>ADAMTS2</i> in a sheep flock with dermatosparaxis. <i>Veterinary Dermatology</i> , 2015, 26, 49.	1.2	9
54	Structural, functional, and mechanistic insights uncover the fundamental role of orphan connexin-62 in platelets. <i>Blood</i> , 2021, 137, 830-843.	1.4	9

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55	ReFOLD3: refinement of 3D protein models with gradual restraints based on predicted local quality and residue contacts. <i>Nucleic Acids Research</i> , 2021, 49, W589-W596.	14.5	8
56	In silico Identification and Characterization of Protein-Ligand Binding Sites. <i>Methods in Molecular Biology</i> , 2016, 1414, 1-21.	0.9	7
57	MAP4K4 expression in cardiomyocytes: multiple isoforms, multiple phosphorylations and interactions with striatins. <i>Biochemical Journal</i> , 2021, 478, 2121-2143.	3.7	7
58	Genetic diversity at the Dhn3 locus in Turkish <i>Hordeum spontaneum</i> populations with comparative structural analyses. <i>Scientific Reports</i> , 2016, 6, 20966.	3.3	7
59	Characterisation of HvVIP1 and expression profile analysis of stress response regulators in barley under <i>Agrobacterium</i> and <i>Fusarium</i> infections. <i>PLoS ONE</i> , 2019, 14, e0218120.	2.5	6
60	Toolbox for Protein Structure Prediction. <i>Methods in Molecular Biology</i> , 2016, 1369, 363-377.	0.9	6
61	Evolutionary rewiring of bacterial regulatory networks. <i>Microbial Cell</i> , 2015, 2, 256-258.	3.2	4
62	RAPIDSnpS: A new computational pipeline for rapidly identifying key genetic variants reveals previously unidentified SNPs that are significantly associated with individual platelet responses. <i>PLoS ONE</i> , 2017, 12, e0175957.	2.5	3
63	Aligning Sequences to Structures. , 2008, 413, 61-90.		2
64	Proteins and Their Interacting Partners: An Introduction to Proteinâ€“Ligand Binding Site Prediction Methods with a Focus on FunFOLD3. <i>Methods in Molecular Biology</i> , 2021, 2365, 43-58.	0.9	1
65	Computational Methods for the Elucidation of Protein Structure and Interactions. <i>Methods in Molecular Biology</i> , 2021, 2305, 23-52.	0.9	1
66	Protein Structure Prediction and Structural Annotation of Proteomes. , 2018, , 1-9.		0