Liam James Mcguffin

List of Publications by Year
in descending order

66 papers	6,684 citations	101384 36 h-index	110170 64 g-index
68 all docs	68 docs citations	68 times ranked	8978 citing authors

#	Article	IF	Citations
1	Structural, functional, and mechanistic insights uncover the fundamental role of orphan connexin-62 in platelets. Blood, 2021, 137, 830-843.	0.6	9
2	Proteins and Their Interacting Partners: An Introduction to Protein–Ligand Binding Site Prediction Methods with a Focus on FunFOLD3. Methods in Molecular Biology, 2021, 2365, 43-58.	0.4	1
3	Computational Methods for the Elucidation of Protein Structure and Interactions. Methods in Molecular Biology, 2021, 2305, 23-52.	0.4	1
4	ReFOLD3: refinement of 3D protein models with gradual restraints based on predicted local quality and residue contacts. Nucleic Acids Research, 2021, 49, W589-W596.	6.5	8
5	ModFOLD8: accurate global and local quality estimates for 3D protein models. Nucleic Acids Research, 2021, 49, W425-W430.	6.5	56
6	MAP4K4 expression in cardiomyocytes: multiple isoforms, multiple phosphorylations and interactions with striatins. Biochemical Journal, 2021, 478, 2121-2143.	1.7	7
7	PINOT: an intuitive resource for integrating protein-protein interactions. Cell Communication and Signaling, 2020, 18, 92.	2.7	21
8	Estimating the Quality of 3D Protein Models Using the ModFOLD7 Server. Methods in Molecular Biology, 2020, 2165, 69-81.	0.4	16
9	Estimation of model accuracy in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1361-1377.	1.5	78
10	Characterisation of HvVIP1 and expression profile analysis of stress response regulators in barley under Agrobacterium and Fusarium infections. PLoS ONE, 2019, 14, e0218120.	1.1	6
11	IntFOLD: an integrated web resource for high performance protein structure and function prediction. Nucleic Acids Research, 2019, 47, W408-W413.	6.5	100
12	Methods for the Refinement of Protein Structure 3D Models. International Journal of Molecular Sciences, 2019, 20, 2301.	1.8	44
13	Methods for estimation of model accuracy in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 361-373.	1.5	27
14	Accurate template–based modeling in CASP12 using the IntFOLD4–TS, ModFOLD6, and ReFOLD methods. Proteins: Structure, Function and Bioinformatics, 2018, 86, 335-344.	1.5	48
15	Protein Structure Prediction and Structural Annotation of Proteomes. , 2018, , 1-9.		0
16	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. Scientific Reports, 2018, 8, 9939.	1.6	19
17	Predictive and Experimental Approaches for Elucidating Protein–Protein Interactions and Quaternary Structures. International Journal of Molecular Sciences, 2017, 18, 2623.	1.8	18
18	ReFOLD: a server for the refinement of 3D protein models guided by accurate quality estimates. Nucleic Acids Research, 2017, 45, W422-W428.	6.5	32

#	Article	IF	Citations
19	ModFOLD6: an accurate web server for the global and local quality estimation of 3D protein models. Nucleic Acids Research, 2017, 45, W416-W421.	6.5	104
20	RAPIDSNPs: A new computational pipeline for rapidly identifying key genetic variants reveals previously unidentified SNPs that are significantly associated with individual platelet responses. PLoS ONE, 2017, 12, e0175957.	1.1	3
21	In silico Identification and Characterization of Protein-Ligand Binding Sites. Methods in Molecular Biology, 2016, 1414, 1-21.	0.4	7
22	Toolbox for Protein Structure Prediction. Methods in Molecular Biology, 2016, 1369, 363-377.	0.4	6
23	Genetic diversity at the Dhn3 locus in Turkish Hordeum spontaneum populations with comparative structural analyses. Scientific Reports, 2016, 6, 20966.	1.6	7
24	*In silico* identification and three‐dimensional modelling of the missense mutation in ADAMTS2 in a sheep flock with dermatosparaxis. Veterinary Dermatology, 2015, 26, 49.	0.4	9
25	Disorder Prediction Methods, Their Applicability to Different Protein Targets and Their Usefulness for Guiding Experimental Studies. International Journal of Molecular Sciences, 2015, 16, 19040-19054.	1.8	61
26	Proteins and Their Interacting Partners: An Introduction to Protein‐Ligand Binding Site Prediction Methods. International Journal of Molecular Sciences, 2015, 16, 29829-29842.	1.8	66
27	IntFOLD: an integrated server for modelling protein structures and functions from amino acid sequences: Figure 1.. Nucleic Acids Research, 2015, 43, W169-W173.	6.5	98
28	Evolutionary resurrection of flagellar motility via rewiring of the nitrogen regulation system. Science, 2015, 347, 1014-1017.	6.0	61
29	GRID and docking analyses reveal a molecular basis for flavonoid inhibition of Src family kinase activity. Journal of Nutritional Biochemistry, 2015, 26, 1156-1165.	1.9	20
30	Evolutionary rewiring of bacterial regulatory networks. Microbial Cell, 2015, 2, 256-258.	1.4	4
31	Dominant β-catenin mutations cause intellectual disability with recognizable syndromic features. Journal of Clinical Investigation, 2014, 124, 1468-1482.	3.9	110
32	Assessing the Quality of Modelled 3D Protein Structures Using the ModFOLD Server. Methods in Molecular Biology, 2014, 1137, 83-103.	0.4	24
33	SOcK, MiSTs, MASK and STicKs: the GCKIII (germinal centre kinase III) kinases and their heterologous protein‐protein interactions. Biochemical Journal, 2013, 454, 13-30.	1.7	41
34	The mysterious presence of a 5-methylcytosine oxidase in the *Drosophila* genome. Cell Cycle, 2013, 12, 3357-3365.	1.3	44
35	The FunFOLD2 server for the prediction of protein‐ligand interactions. Nucleic Acids Research, 2013, 41, W303-W307.	6.5	47
36	The ModFOLD4 server for the quality assessment of 3D protein models. Nucleic Acids Research, 2013, 41, W368-W372.	6.5	108

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37	Improvement of 3D protein models using multiple templates guided by single-template model quality assessment. Bioinformatics, 2012, 28, 1851-1857.	1.8	44
38	A novel non-canonical mechanism of regulation of MST3 (mammalian Sterile20-related kinase 3). Biochemical Journal, 2012, 442, 595-610.	1.7	33
39	Structure and evolution of barley powdery mildew effector candidates. BMC Genomics, 2012, 13, 694.	1.2	238
40	FunFOLDQA: A Quality Assessment Tool for Protein-Ligand Binding Site Residue Predictions. PLoS ONE, 2012, 7, e38219.	1.1	20
41	Proteogenomics and in silico structural and functional annotation of the barley powdery mildew Blumeria graminis f. sp. hordei. Methods, 2011, 54, 432-441.	1.9	57
42	FunFOLD: an improved automated method for the prediction of ligand binding residues using 3D models of proteins. BMC Bioinformatics, 2011, 12, 160.	1.2	64
43	Automated tertiary structure prediction with accurate local model quality assessment using the intfoldâ€ts method. Proteins: Structure, Function and Bioinformatics, 2011, 79, 137-146.	1.5	32
44	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.	6.5	101
45	Rapid model quality assessment for protein structure predictions using the comparison of multiple models without structural alignments. Bioinformatics, 2010, 26, 182-188.	1.8	105
46	The binding site distance test score: a robust method for the assessment of predicted protein binding sites. Bioinformatics, 2010, 26, 2920-2921.	1.8	23
47	Prediction of global and local model quality in CASP8 using the ModFOLD server. Proteins: Structure, Function and Bioinformatics, 2009, 77, 185-190.	1.5	45
48	Rapid protein domain assignment from amino acid sequence using predicted secondary structure. Protein Science, 2009, 11, 2814-2824.	3.1	122
49	Aligning Sequences to Structures. , 2008, 413, 61-90.		2
50	The ModFOLD server for the quality assessment of protein structural models. Bioinformatics, 2008, 24, 586-587.	1.8	123
51	Intrinsic disorder prediction from the analysis of multiple protein fold recognition models. Bioinformatics, 2008, 24, 1798-1804.	1.8	106
52	Benchmarking consensus model quality assessment for protein fold recognition. BMC Bioinformatics, 2007, 8, 345.	1.2	73
53	High throughput profile-profile based fold recognition for the entire human proteome. BMC Bioinformatics, 2006, 7, 288.	1.2	19
54	Prediction of novel and analogous folds using fragment assembly and fold recognition. Proteins: Structure, Function and Bioinformatics, 2005, 61, 143-151.	1.5	78

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55	Improving sequence-based fold recognition by using 3D model quality assessment. Bioinformatics, 2005, 21, 3509-3515.	1.8	65
56	Protein structure prediction servers at University College London. Nucleic Acids Research, 2005, 33, W36-W38.	6.5	646
57	The Genomic Threading Database: a comprehensive resource for structural annotations of the genomes from key organisms. Nucleic Acids Research, 2004, 32, 196D-199.	6.5	40
58	The Genomic Threading Database. Bioinformatics, 2004, 20, 131-132.	1.8	25
59	The DISOPRED server for the prediction of protein disorder. Bioinformatics, 2004, 20, 2138-2139.	1.8	659
60	Prediction and Functional Analysis of Native Disorder in Proteins from the Three Kingdoms of Life. Journal of Molecular Biology, 2004, 337, 635-645.	2.0	1,828
61	Predicting Metal-binding Site Residues in Low-resolution Structural Models. Journal of Molecular Biology, 2004, 342, 307-320.	2.0	126
62	Benchmarking secondary structure prediction for fold recognition. Proteins: Structure, Function and Bioinformatics, 2003, 52, 166-175.	1.5	36
63	Assembling novel protein folds from super-secondary structural fragments. Proteins: Structure, Function and Bioinformatics, 2003, 53, 480-485.	1.5	73
64	Secondary structure prediction with support vector machines. Bioinformatics, 2003, 19, 1650-1655.	1.8	213
65	Improvement of the GenTHREADER method for genomic fold recognition. Bioinformatics, 2003, 19, 874-881.	1.8	337
66	Targeting novel folds for structural genomics. Proteins: Structure, Function and Bioinformatics, 2002, 48, 44-52.	1.5	34