Mu Gao

List of Publications by Year
in descending order

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50 papers	3,747 citations	186265 28 h-index	206112 48 g-index
53 all docs	53 docs citations	53 times ranked	4231 citing authors

#	Article	IF	Citations
1	AF2Complex predicts direct physical interactions in multimeric proteins with deep learning. Nature Communications, 2022, 13, 1744.	12.8	128
2	The role of local versus nonlocal physicochemical restraints in determining protein native structure. Current Opinion in Structural Biology, 2021, 68, 1-8.	5.7	14
3	A novel sequence alignment algorithm based on deep learning of the protein folding code. Bioinformatics, 2021, 37, 490-496.	4.1	19
4	On the emergence of homochirality and life itself. Biochemist, 2021, 43, 4-12.	0.5	2
5	A General Framework to Learn Tertiary Structure for Protein Sequence Characterization. Frontiers in Bioinformatics, 2021, 1, .	2.1	3
6	AlphaFold 2: Why It Works and Its Implications for Understanding the Relationships of Protein Sequence, Structure, and Function. Journal of Chemical Information and Modeling, 2021, 61, 4827-4831.	5.4	109
7	High-Performance Deep Learning Toolbox for Genome-Scale Prediction of Protein Structure and Function. , 2021, 2021, 46-57.		8
8	Differential kinase activity of ACVR1 G328V and R206H mutations with implications to possible TÎ²RI cross-talk in diffuse intrinsic pontine glioma. Scientific Reports, 2020, 10, 6140.	3.3	5
9	DESTINI: A deep-learning approach to contact-driven protein structure prediction. Scientific Reports, 2019, 9, 3514.	3.3	44
10	On the possible origin of protein homochirality, structure, and biochemical function. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 26571-26579.	7.1	30
11	Repurposed FDA-approved drugs targeting genes influencing aging can extend lifespan and healthspan in rotifers. Biogerontology, 2018, 19, 145-157.	3.9	16
12	Brain activity patterns in high-throughput electrophysiology screen predict bothÂdrug efficacies and side effects. Nature Communications, 2018, 9, 219.	12.8	55
13	The crystal structure of a tetrahydrofolate-bound dihydrofolate reductase reveals the origin of slow product release. Communications Biology, 2018, 1, 226.	4.4	23
14	ENTPRISE-X: Predicting disease-associated frameshift and nonsense mutations. PLoS ONE, 2018, 13, e0196849.	2.5	20
15	Repurposing FDA-approved drugs for anti-aging therapies. Biogerontology, 2016, 17, 907-920.	3.9	31
16	How special is the biochemical function of native proteins?. F1000Research, 2016, 5, 207.	1.6	9
17	ENTPRISE: An Algorithm for Predicting Human Disease-Associated Amino Acid Substitutions from Sequence Entropy and Predicted Protein Structures. PLoS ONE, 2016, 11, e0150965.	2.5	23
18	Insights into Disease-Associated Mutations in the Human Proteome through Protein Structural Analysis. Structure, 2015, 23, 1362-1369.	3.3	103

#	Article	IF	Citations
19	Comprehensive prediction of drug-protein interactions and side effects for the human proteome. Scientific Reports, 2015, 5, 11090.	3.3	90
20	Implications of the small number of distinct ligand binding pockets in proteins for drug discovery, evolution and biochemical function. Bioorganic and Medicinal Chemistry Letters, 2015, 25, 1163-1170.	2.2	27
21	Hurt, tired and queasy: Specific variants in the ATPase domain of the TRAP1 mitochondrial chaperone are associated with common, chronic â€œfunctionalâ€•symptomatology including pain, fatigue and gastrointestinal dysmotility. Mitochondrion, 2015, 23, 64-70.	3.4	15
22	On the Role of Physics and Evolution in Dictating Protein Structure and Function. Israel Journal of Chemistry, 2014, 54, 1176-1188.	2.3	10
23	Are predicted protein structures of any value for binding site prediction and virtual ligand screening?. Current Opinion in Structural Biology, 2013, 23, 191-197.	5.7	29
24	APoc: large-scale identification of similar protein pockets. Bioinformatics, 2013, 29, 597-604.	4.1	109
25	A Comprehensive Survey of Small-Molecule Binding Pockets in Proteins. PLoS Computational Biology, 2013, 9, e1003302.	3.2	103
26	Interplay of physics and evolution in the likely origin of protein biochemical function. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 9344-9349.	7.1	59
27	The distribution of ligand-binding pockets around protein-protein interfaces suggests a general mechanism for pocket formation. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3784-3789.	7.1	82
28	Why not consider a spherical protein? Implications of backbone hydrogen bonding for protein structure and function. Physical Chemistry Chemical Physics, 2011, 13, 17044.	2.8	16
29	New benchmark metrics for proteinâ€protein docking methods. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1623-1634.	2.6	31
30	iAlign: a method for the structural comparison of proteinâ€“protein interfaces. Bioinformatics, 2010, 26, 2259-2265.	4.1	81
31	PSiFR: an integrated resource for prediction of protein structure and function. Bioinformatics, 2010, 26, 687-688.	4.1	13
32	Structural space of proteinâ€“protein interfaces is degenerate, close to complete, and highly connected. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 22517-22522.	7.1	133
33	A Threading-Based Method for the Prediction of DNA-Binding Proteins with Application to the Human Genome. PLoS Computational Biology, 2009, 5, e1000567.	3.2	74
34	From Nonspecific DNAâ€“Protein Encounter Complexes to the Prediction of DNAâ€“Protein Interactions. PLoS Computational Biology, 2009, 5, e1000341.	3.2	32
35	DBD-Hunter: a knowledge-based method for the prediction of DNAâ€“protein interactions. Nucleic Acids Research, 2008, 36, 3978-3992.	14.5	142
36	Molecular mechanisms of cellular mechanics. Physical Chemistry Chemical Physics, 2006, 8, 3692.	2.8	76

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37	Onset of Anthrax Toxin Pore Formation. Biophysical Journal, 2006, 90, 3267-3279.	0.5	17
38	Mechanical Strength of the Titin Z1Z2-Telethonin Complex. Structure, 2006, 14, 497-509.	3.3	70
39	How the headpiece hinge angle is opened: new insights into the dynamics of integrin activation. Journal of Cell Biology, 2006, 175, 349-360.	5.2	181
40	Tuning the Mechanical Stability of Fibronectin Type III Modules through Sequence Variations. Structure, 2004, 12, 21-30.	3.3	98
41	Structural Insights into How the MIDAS Ion Stabilizes Integrin Binding to an RGD Peptide under Force. Structure, 2004, 12, 2049-2058.	3.3	75
42	Integrin Activation In Vivo and In Silico. Structure, 2004, 12, 2096-2098.	3.3	7
43	Structure and functional significance of mechanically unfolded fibronectin type III1 intermediates. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 14784-14789.	7.1	187
44	Large Scale Simulation of Protein Mechanics and Function. Advances in Protein Chemistry, 2003, 66, 195-247.	4.4	31
45	Unfolding of titin domains studied by molecular dynamics simulations. , 2003, , 513-521.		1
46	Identifying Unfolding Intermediates of FN-III10 by Steered Molecular Dynamics. Journal of Molecular Biology, 2002, 323, 939-950.	4.2	159
47	Steered Molecular Dynamics Studies of Titin I1 Domain Unfolding. Biophysical Journal, 2002, 83, 3435-3445.	0.5	111
48	Unfolding of titin domains studied by molecular dynamics simulations. Journal of Muscle Research and Cell Motility, 2002, 23, 513-521.	2.0	61
49	Simulated Refolding of Stretched Titin Immunoglobulin Domains. Biophysical Journal, 2001, 81, 2268-2277.	0.5	48
50	Steered molecular dynamics and mechanical functions of proteins. Current Opinion in Structural Biology, 2001, 11, 224-230.	5.7	934