

Kam Y J Zhang

List of Publications by Year in descending order

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143
papers

9,445
citations

101543

36
h-index

40979

93
g-index

151
all docs

151
docs citations

151
times ranked

12579
citing authors

#	ARTICLE	IF	CITATIONS
1	Clinical efficacy of a RAF inhibitor needs broad target blockade in BRAF-mutant melanoma. <i>Nature</i> , 2010, 467, 596-599.	27.8	1,610
2	Discovery of a selective inhibitor of oncogenic B-Raf kinase with potent antimelanoma activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3041-3046.	7.1	1,206
3	Germline KRAS mutations cause Noonan syndrome. <i>Nature Genetics</i> , 2006, 38, 331-336.	21.4	670
4	Keynote review: Phosphodiesterase-4 as a therapeutic target. <i>Drug Discovery Today</i> , 2005, 10, 1503-1519.	6.4	604
5	Antimycin A mimics a cell-death-inducing Bcl-2 homology domain 3. <i>Nature Cell Biology</i> , 2001, 3, 183-191.	10.3	436
6	Structural Basis for the Activity of Drugs that Inhibit Phosphodiesterases. <i>Structure</i> , 2004, 12, 2233-2247.	3.3	360
7	A Glutamine Switch Mechanism for Nucleotide Selectivity by Phosphodiesterases. <i>Molecular Cell</i> , 2004, 15, 279-286.	9.7	271
8	Density modification for macromolecular phase improvement. <i>Progress in Biophysics and Molecular Biology</i> , 1999, 72, 245-270.	2.9	242
9	A family of phosphodiesterase inhibitors discovered by cocrystallography and scaffold-based drug design. <i>Nature Biotechnology</i> , 2005, 23, 201-207.	17.5	220
10	Design of a peptide-based subunit vaccine against novel coronavirus SARS-CoV-2. <i>Microbial Pathogenesis</i> , 2020, 145, 104236.	2.9	154
11	Crystal structure of <i>E. coli</i> $\hat{\Gamma}^2$ -carbonic anhydrase, an enzyme with an unusual pH-dependent activity. <i>Protein Science</i> , 2001, 10, 911-922.	7.6	151
12	Scaffold-based discovery of indeglitazar, a PPAR pan-active anti-diabetic agent. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 262-267.	7.1	134
13	Mcl-1 is required for Akata6 B-lymphoma cell survival and is converted to a cell death molecule by efficient caspase-mediated cleavage. <i>Oncogene</i> , 2004, 23, 4818-4827.	5.9	133
14	Computational design of a self-assembling symmetrical $\hat{\Gamma}^2$ -propeller protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15102-15107.	7.1	122
15	Hierarchical virtual screening approaches in small molecule drug discovery. <i>Methods</i> , 2015, 71, 26-37.	3.8	121
16	[4] Combining constraints for electron-density modification. <i>Methods in Enzymology</i> , 1997, 277, 53-64.	1.0	109
17	The use of Sayre's equation with solvent flattening and histogram matching for phase extension and refinement of protein structures. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 1990, 46, 377-381.	0.3	105
18	Advances in the Development of Shape Similarity Methods and Their Application in Drug Discovery. <i>Frontiers in Chemistry</i> , 2018, 6, 315.	3.6	105

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19	Identification of a Novel Noncatalytic Bicarbonate Binding Site in Eubacterial $\hat{\Gamma}^2$ -Carbonic Anhydrase. <i>Biochemistry</i> , 2006, 45, 4351-4361.	2.5	97
20	Design and pharmacology of a highly specific dual FMS and KIT kinase inhibitor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5689-5694.	7.1	82
21	Biophysical Characterization of Recombinant Human Bcl-2 and Its Interactions with an Inhibitory Ligand, Antimycin A. <i>Biochemistry</i> , 2001, 40, 4911-4922.	2.5	81
22	Phosphodiesterase-4 as a potential drug target. <i>Expert Opinion on Therapeutic Targets</i> , 2005, 9, 1283-1305.	3.4	81
23	Spectomycin B1 as a Novel SUMOylation Inhibitor That Directly Binds to SUMO E2. <i>ACS Chemical Biology</i> , 2013, 8, 2635-2642.	3.4	80
24	Accurate computer-based design of a new backbone conformation in the second turn of protein L. <i>Journal of Molecular Biology</i> , 2002, 315, 471-477.	4.2	73
25	The Effect of F877L and T878A Mutations on Androgen Receptor Response to Enzalutamide. <i>Molecular Cancer Therapeutics</i> , 2016, 15, 1702-1712.	4.1	73
26	Conversion of monomeric protein L to an obligate dimer by computational protein design. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 10687-10691.	7.1	68
27	Bcl-XL Mutations Suppress Cellular Sensitivity to Antimycin A. <i>Journal of Biological Chemistry</i> , 2004, 279, 2159-2165.	3.4	68
28	Oncogene-dependent apoptosis in extracts from drug-resistant cells.. <i>Genes and Development</i> , 1997, 11, 1266-1276.	5.9	60
29	Structures of the B1 domain of protein L from <i>Peptostreptococcus magnus</i> with a tyrosine to tryptophan substitution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 480-487.	2.5	60
30	Advances in the development of SUMO specific protease (SEN1) inhibitors. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 204-211.	4.1	60
31	Single-Site Mutations Induce 3D Domain Swapping in the B1 Domain of Protein L from <i>Peptostreptococcus magnus</i> . <i>Structure</i> , 2001, 9, 1017-1027.	3.3	52
32	Pharmacophore modeling: advances, limitations, and current utility in drug discovery. <i>Journal of Receptor, Ligand and Channel Research</i> , 0, , 81.	0.7	48
33	Identification of 1,2,5-Oxadiazoles as a New Class of SEN2 Inhibitors Using Structure Based Virtual Screening. <i>Journal of Chemical Information and Modeling</i> , 2014, 54, 870-880.	5.4	47
34	Investigation on the Effect of Key Water Molecules on Docking Performance in CSARdock Exercise. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 1880-1892.	5.4	46
35	Synthesis, cholinesterase inhibition and molecular modelling studies of coumarin linked thiourea derivatives. <i>Bioorganic Chemistry</i> , 2015, 63, 58-63.	4.1	45
36	Post-translational modification of the N-terminal His tag interferes with the crystallization of the wild-type and mutant SH3 domains from chicken src tyrosine kinase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 759-762.	2.5	43

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37	EC359: A First-in-Class Small-Molecule Inhibitor for Targeting Oncogenic LIFR Signaling in Triple-Negative Breast Cancer. <i>Molecular Cancer Therapeutics</i> , 2019, 18, 1341-1354.	4.1	41
38	Identification of Sumoylation Activating Enzyme 1 Inhibitors by Structure-Based Virtual Screening. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 809-820.	5.4	40
39	A Probabilistic Fragment-Based Protein Structure Prediction Algorithm. <i>PLoS ONE</i> , 2012, 7, e38799.	2.5	40
40	Lean-Docking: Exploiting Ligands' Predicted Docking Scores to Accelerate Molecular Docking. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 2341-2352.	5.4	38
41	SQUASH – combining constraints for macromolecular phase refinement and extension. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1993, 49, 213-222.	2.5	36
42	Biominalization of a Cadmium Chloride Nanocrystal by a Designed Symmetrical Protein. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 9857-9860.	13.8	36
43	Targeting LIF/LIFR signaling in cancer. <i>Genes and Diseases</i> , 2022, 9, 973-980.	3.4	36
44	Protein Interface Pharmacophore Mapping Tools for Small Molecule Protein: Protein Interaction Inhibitor Discovery. <i>Current Topics in Medicinal Chemistry</i> , 2013, 13, 989-1001.	2.1	35
45	Computational design of a symmetrical β -trefoil lectin with cancer cell binding activity. <i>Scientific Reports</i> , 2017, 7, 5943.	3.3	35
46	Identification of new SUMO activating enzyme 1 inhibitors using virtual screening and scaffold hopping. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2016, 26, 1218-1223.	2.2	34
47	A variant in human AIOLOS impairs adaptive immunity by interfering with IKAROS. <i>Nature Immunology</i> , 2021, 22, 893-903.	14.5	33
48	Computational design of symmetrical eight-bladed β -propeller proteins. <i>IUCr</i> , 2019, 6, 46-55.	2.2	33
49	Discovery of Fungal Denitrification Inhibitors by Targeting Copper Nitrite Reductase from <i>Fusarium oxysporum</i> . <i>Journal of Chemical Information and Modeling</i> , 2017, 57, 203-213.	5.4	30
50	A Series of Compounds Bearing a Dipyrido-Pyrimidine Scaffold Acting as Novel Human and Insect Pest Chitinase Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 987-1001.	6.4	29
51	The Discovery of Novel Human Androgen Receptor Antagonist Chemotypes Using a Combined Pharmacophore Screening Procedure. <i>ChemMedChem</i> , 2013, 8, 644-651.	3.2	27
52	A Novel Scaffold for Developing Specific or Broad-Spectrum Chitinase Inhibitors. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 2413-2420.	5.4	27
53	Pharmacophore Modelling as a Virtual Screening Tool for the Discovery of Small Molecule Protein-protein Interaction Inhibitors. <i>Current Pharmaceutical Design</i> , 2012, 18, 4586-4598.	1.9	25
54	Combining in silico and in cerebra approaches for virtual screening and pose prediction in SAMPL4. <i>Journal of Computer-Aided Molecular Design</i> , 2014, 28, 363-373.	2.9	25

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55	Application of Shape Similarity in Pose Selection and Virtual Screening in CSARdock2014 Exercise. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 965-973.	5.4	24
56	A cross docking pipeline for improving pose prediction and virtual screening performance. <i>Journal of Computer-Aided Molecular Design</i> , 2018, 32, 163-173.	2.9	24
57	Human Chitinases: Structure, Function, and Inhibitor Discovery. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1142, 221-251.	1.6	23
58	Crystal structure of human acetylcholinesterase in complex with tacrine: Implications for drug discovery. <i>International Journal of Biological Macromolecules</i> , 2022, 210, 172-181.	7.5	23
59	Entropy-accelerated exact clustering of protein decoys. <i>Bioinformatics</i> , 2011, 27, 939-945.	4.1	22
60	Efficient Sampling in Fragment-Based Protein Structure Prediction Using an Estimation of Distribution Algorithm. <i>PLoS ONE</i> , 2013, 8, e68954.	2.5	22
61	Electrostatic Similarities between Protein and Small Molecule Ligands Facilitate the Design of Protein-Protein Interaction Inhibitors. <i>PLoS ONE</i> , 2013, 8, e75762.	2.5	21
62	A rotation-translation invariant molecular descriptor of partial charges and its use in ligand-based virtual screening. <i>Journal of Cheminformatics</i> , 2014, 6, 23.	6.1	21
63	Human glutamyl cyclase: Structure, function, inhibitors and involvement in Alzheimer's disease. <i>Pharmacological Research</i> , 2019, 147, 104342.	7.1	21
64	Durandal: Fast exact clustering of protein decoys. <i>Journal of Computational Chemistry</i> , 2012, 33, 471-474.	3.3	20
65	Identification of quinazolinyloxy biaryl urea as a new class of SUMO activating enzyme 1 inhibitors. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2013, 23, 5145-5149.	2.2	20
66	Balancing exploration and exploitation in population-based sampling improves fragment-based <i>de novo</i> protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 852-858.	2.6	20
67	A Novel Therapeutic Peptide Blocks SARS-CoV-2 Spike Protein Binding with Host Cell ACE2 Receptor. <i>Drugs in R and D</i> , 2021, 21, 273-283.	2.2	20
68	Evolutionary and codon usage preference insights into spike glycoprotein of SARS-CoV-2. <i>Briefings in Bioinformatics</i> , 2021, 22, 1006-1022.	6.5	20
69	Tumor Derived Extracellular Vesicles Drive T Cell Exhaustion in Tumor Microenvironment through Sphingosine Mediated Signaling and Impacting Immunotherapy Outcomes in Ovarian Cancer. <i>Advanced Science</i> , 2022, 9, e2104452.	11.2	20
70	Seven Amino Acid Types Suffice to Create the Core Fold of RNA Polymerase. <i>Journal of the American Chemical Society</i> , 2021, 143, 15998-16006.	13.7	18
71	Cloning, crystallization and preliminary characterization of a β -carbonic anhydrase from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1176-1179.	2.5	17
72	Cryo-EM structure of the human ELMO1-DOCK5-Rac1 complex. <i>Science Advances</i> , 2021, 7, .	10.3	17

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73	Neuroprotective derivatives of tacrine that target NMDA receptor and acetyl cholinesterase – Design, synthesis and biological evaluation. Computational and Structural Biotechnology Journal, 2021, 19, 4517-4537.	4.1	17
74	Comprehensive Intrinsic Disorder Analysis of 6108 Viral Proteomes: From the Extent of Intrinsic Disorder Penetrance to Functional Annotation of Disordered Viral Proteins. Journal of Proteome Research, 2021, 20, 2704-2713.	3.7	16
75	Computational fragment-based screening using RosettaLigand: the SAMPL3 challenge. Journal of Computer-Aided Molecular Design, 2012, 26, 603-616.	2.9	15
76	A fragmentation and reassembly method for ab initio phasing. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 304-312.	2.5	15
77	A pose prediction approach based on ligand 3D shape similarity. Journal of Computer-Aided Molecular Design, 2016, 30, 457-469.	2.9	15
78	Evolutionary Signatures Governing the Codon Usage Bias in Coronaviruses and Their Implications for Viruses Infecting Various Bat Species. Viruses, 2021, 13, 1847.	3.3	15
79	Mutation and Modeling Analysis of the <i>Saccharomyces cerevisiae</i> Swi6 Ankyrin Repeats. Biochemistry, 1998, 37, 4437-4450.	2.5	13
80	Accelerating ab initio phasing with de novo models. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 804-812.	2.5	13
81	Quality Assessment of Predicted Protein Models Using Energies Calculated by the Fragment Molecular Orbital Method. Molecular Informatics, 2015, 34, 97-104.	2.5	13
82	Identification of Novel Cathepsin B Inhibitors with Implications in Alzheimer's Disease: Computational Refining and Biochemical Evaluation. Cells, 2021, 10, 1946.	4.1	13
83	Piperidine-4-carboxamide as a new scaffold for designing secretory glutamyl cyclase inhibitors. International Journal of Biological Macromolecules, 2021, 170, 415-423.	7.5	13
84	Identification of Sumoylation Inhibitors Targeting a Predicted Pocket in Ubc9. Journal of Chemical Information and Modeling, 2014, 54, 2784-2793.	5.4	12
85	Prospective evaluation of shape similarity based pose prediction method in D3R Grand Challenge 2015. Journal of Computer-Aided Molecular Design, 2016, 30, 685-693.	2.9	12
86	Evolution-Inspired Computational Design of Symmetric Proteins. Methods in Molecular Biology, 2017, 1529, 309-322.	0.9	12
87	A protein sequence fitness function for identifying natural and nonnatural proteins: Structure, Function and Bioinformatics, 2020, 88, 1271-1284.	2.6	12
88	In-Silico Design of a Novel Tridecapeptide Targeting Spike Protein of SARS-CoV-2 Variants of Concern. International Journal of Peptide Research and Therapeutics, 2022, 28, 28.	1.9	12
89	An integrated fragment based screening approach for the discovery of small molecule modulators of the VWF-GPIIb/IIIa interaction. Chemical Communications, 2012, 48, 11349.	4.1	11
90	Glu-108 is essential for subunit assembly and dimer stability of d-phosphoglycerate dehydrogenase from <i>Entamoeba histolytica</i> . Molecular and Biochemical Parasitology, 2012, 181, 117-124.	1.1	11

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91	Identification and structure-activity relationship of purine derivatives as novel MTH1 inhibitors. <i>Chemical Biology and Drug Design</i> , 2017, 89, 862-869.	3.2	11
92	A loss-of-function variant in SUV39H2 identified in autism-spectrum disorder causes altered H3K9 trimethylation and dysregulation of protocadherin β -cluster genes in the developing brain. <i>Molecular Psychiatry</i> , 2021, 26, 7550-7559.	7.9	11
93	Improving fragment quality for de novo structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2240-2252.	2.6	10
94	Crystal Structure and Structure-Based Discovery of Inhibitors of the Nematode Chitinase <i>Ce</i> Cht1. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 3519-3526.	5.2	10
95	Role of conserved active site tryptophan-101 in functional activity and stability of phosphoserine aminotransferase from an enteric human parasite. <i>Amino Acids</i> , 2012, 43, 483-491.	2.7	9
96	Identification of small peptides inhibiting the integrase-LEDGF/p75 interaction through targeting the cellular cofactor. <i>Journal of Peptide Science</i> , 2013, 19, 651-658.	1.4	9
97	Discovery of small molecule inhibitors targeting the SUMO-SIM interaction using a protein interface consensus approach. <i>MedChemComm</i> , 2014, 5, 783-786.	3.4	9
98	Shape similarity guided pose prediction: lessons from D3R Grand Challenge 3. <i>Journal of Computer-Aided Molecular Design</i> , 2019, 33, 47-59.	2.9	9
99	Actin R256 Mono-methylation Is a Conserved Post-translational Modification Involved in Transcription. <i>Cell Reports</i> , 2020, 32, 108172.	6.4	9
100	EC330, a small-molecule compound, is a potential novel inhibitor of LIF signaling. <i>Journal of Molecular Cell Biology</i> , 2020, 12, 477-480.	3.3	9
101	Insights into the evolutionary forces that shape the codon usage in the viral genome segments encoding intrinsically disordered protein regions. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	9
102	The Two-Dimensional Histogram as a Constraint for Protein Phase Improvement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 1230-1244.	2.5	8
103	Scaffold-Based Drug Discovery. , 2007, , 129-153.		8
104	Understanding the Assembly of an Artificial Protein Nanotube. <i>Advanced Materials Interfaces</i> , 2016, 3, 1600846.	3.7	8
105	Mechanistic insights into the loss-of-function mechanisms of rare human D-amino acid oxidase variants implicated in amyotrophic lateral sclerosis. <i>Scientific Reports</i> , 2020, 10, 17146.	3.3	8
106	Structure-based virtual screening of highly potent inhibitors of the nematode chitinase <i>Ce</i> Cht1. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2021, 36, 1198-1204.	5.2	8
107	Chemical similarity assisted search for acetylcholinesterase inhibitors: Molecular modeling and evaluation of their neuroprotective properties. <i>International Journal of Biological Macromolecules</i> , 2021, 174, 466-476.	7.5	8
108	TIRAP-mediated activation of p38 MAPK in inflammatory signaling. <i>Scientific Reports</i> , 2022, 12, 5601.	3.3	8

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109	Cell-Free Mutant Analysis Combined with Structure Prediction of a Lasso Peptide Biosynthetic Protease B2. <i>ACS Synthetic Biology</i> , 2022, 11, 2022-2028.	3.8	8
110	A two-dimensional histogram-matching method for protein phase refinement and extension. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1893-1900.	2.5	7
111	PAR: a PARallel and distributed job crusher. <i>Bioinformatics</i> , 2010, 26, 2918-2919.	4.1	7
112	Assay methods for small ubiquitin-like modifier (SUMO)â€™SUMO-interacting motif (SIM) interactions in vivo and in vitro using a split-luciferase complementation system. <i>Analytical Biochemistry</i> , 2014, 448, 92-94.	2.4	7
113	ProFitFun: a protein tertiary structure fitness function for quantifying the accuracies of model structures. <i>Bioinformatics</i> , 2022, 38, 369-376.	4.1	7
114	Novel proteinâ€™protein interactions between <i>Entamoeba histolytica</i> d-phosphoglycerate dehydrogenase and phosphoserine aminotransferase. <i>Biochimie</i> , 2012, 94, 1676-1686.	2.6	6
115	Error-estimation-guided rebuilding of <i>de novo</i> models increases the success rate of <i>ab initio</i> phasing. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1522-1534.	2.5	6
116	Population-Based Sampling and Fragment-Based De Novo Protein Structure Prediction. , 2019, , 774-784.		6
117	A structural homology approach for computational protein design with flexible backbone. <i>Bioinformatics</i> , 2019, 35, 2418-2426.	4.1	6
118	A novel structure-based approach for identification of vertebrate susceptibility to SARS-CoV-2: Implications for future surveillance programmes. <i>Environmental Research</i> , 2022, 212, 113303.	7.5	6
119	Computational Investigation of SENP:SUMO Proteinâ€™Protein Interaction for Structure Based Drug Design. <i>Molecular Informatics</i> , 2013, 32, 267-280.	2.5	5
120	CDC25A-inhibitory RE derivatives bind to pocket adjacent to the catalytic site. <i>Molecular BioSystems</i> , 2013, 9, 1026.	2.9	5
121	Chemoinformatics and structural bioinformatics in OCaml. <i>Journal of Cheminformatics</i> , 2019, 11, 10.	6.1	5
122	NbX: Machine Learning-Guided Re-Ranking of Nanobodyâ€™Antigen Binding Poses. <i>Pharmaceuticals</i> , 2021, 14, 968.	3.8	5
123	Molecular dynamics simulations: Principles, methods, and applications in protein conformational dynamics. , 2022, , 439-454.		5
124	Solid-state phase transition in the crystal structure of ribulose 1,5-bisphosphate carboxylase/oxygenase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1994, 50, 258-262.	2.5	4
125	Crystallization and preliminary X-ray diffraction studies of mutants of B1 IgG-binding domain of protein L from <i>Peptostreptococcus magnus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 506-508.	2.5	4
126	EC313-a tissue selective SPRM reduces the growth and proliferation of uterine fibroids in a human uterine fibroid tissue xenograft model. <i>Scientific Reports</i> , 2019, 9, 17279.	3.3	4

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127	Understanding the molecular interactions of inhibitors against Bla1 beta-lactamase towards unraveling the mechanism of antimicrobial resistance. <i>International Journal of Biological Macromolecules</i> , 2021, 177, 337-350.	7.5	4
128	An integrated computational pipeline for designing high-affinity nanobodies with expanded genetic codes. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	4
129	A Glutamine Switch Mechanism for Nucleotide Selectivity by Phosphodiesterases. <i>Molecular Cell</i> , 2004, 15, 659.	9.7	3
130	Improving ligand 3D shape similarity-based pose prediction with a continuum solvent model. <i>Journal of Computer-Aided Molecular Design</i> , 2019, 33, 1045-1055.	2.9	3
131	ATP7A Clinical Genetics Resource – A comprehensive clinically annotated database and resource for genetic variants in ATP7A gene. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2347-2356.	4.1	3
132	Identification of a Selective RelA Inhibitor Based on DSE-FRET Screening Methods. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9150.	4.1	3
133	The symmetric designer protein Pizza as a scaffold for metal coordination. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 945-951.	2.6	3
134	Ambiguities in Ab Initio Phasing. <i>Science</i> , 1993, 259, 1771-1772.	12.6	2
135	Crystal Structure of Phosphodiesterase Families and the Potential for Rational Drug Design. , 2006, , .		2
136	Fragger: a protein fragment picker for structural queries. <i>F1000Research</i> , 2017, 6, 1722.	1.6	2
137	Fragger: a protein fragment picker for structural queries. <i>F1000Research</i> , 2017, 6, 1722.	1.6	2
138	Characterization of pH-induced transitions of <i>Entamoeba histolytica</i> d-phosphoglycerate dehydrogenase. <i>International Journal of Biological Macromolecules</i> , 2015, 79, 284-289.	7.5	1
139	The crystal and solution structure of YdiE from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 919-924.	0.8	1
140	A multidimensional computational exploration of congenital myasthenic syndrome causing mutations in human choline acetyltransferase. <i>Journal of Cellular Biochemistry</i> , 2021, 122, 787-800.	2.6	1
141	<sc>FPredX</sc>: Interpretable models for the prediction of spectral maxima, brightness, and oligomeric states of fluorescent proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 732-746.	2.6	1
142	Multidimensional Histograms for Density Modification. <i>Methods in Enzymology</i> , 2003, 374, 188-203.	1.0	0
143	Identification of 1,2,4-Triazolylthioethanone Scaffold for the Design of New Acetylcholinesterase Inhibitors. <i>Molecular Informatics</i> , 2021, 40, 2100020.	2.5	0