Kam Y J Zhang

List of Publications by Year
in descending order

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	Targeting LIF/LIFR signaling in cancer. Genes and Diseases, 2022, 9, 973-980.	3.4	36
2	ProFitFun: a protein tertiary structure fitness function for quantifying the accuracies of model structures. Bioinformatics, 2022, 38, 369-376.	4.1	7
3	<scp>FPredX</scp>: Interpretable models for the prediction of spectral maxima, brightness, and oligomeric states of fluorescent proteins. Proteins: Structure, Function and Bioinformatics, 2022, 90, 732-746.	2.6	1
4	Molecular dynamics simulations: Principles, methods, and applications in protein conformational dynamics. , 2022, , 439-454.		5
5	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
6	Tumor Derived Extracellular Vesicles Drive T Cell Exhaustion in Tumor Microenvironment through Sphingosine Mediated Signaling and Impacting Immunotherapy Outcomes in Ovarian Cancer. Advanced Science, 2022, 9, e2104452.	11.2	20
7	TIRAP-mediated activation of p38 MAPK in inflammatory signaling. Scientific Reports, 2022, 12, 5601.	3.3	8
8	A novel structure-based approach for identification of vertebrate susceptibility to SARS-CoV-2: Implications for future surveillance programmes. Environmental Research, 2022, 212, 113303.	7.5	6
9	Crystal structure of human acetylcholinesterase in complex with tacrine: Implications for drug discovery. International Journal of Biological Macromolecules, 2022, 210, 172-181.	7.5	23
10	Cell-Free Mutant Analysis Combined with Structure Prediction of a Lasso Peptide Biosynthetic Protease B2. ACS Synthetic Biology, 2022, 11, 2022-2028.	3.8	8
11	Structure-based virtual screening of highly potent inhibitors of the nematode chitinase CeCht1. Journal of Enzyme Inhibition and Medicinal Chemistry, 2021, 36, 1198-1204.	5.2	8
12	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
13	Chemical similarity assisted search for acetylcholinesterase inhibitors: Molecular modeling and evaluation of their neuroprotective properties. International Journal of Biological Macromolecules, 2021, 174, 466-476.	7.5	8
14	Crystal Structure and Structure-Based Discovery of Inhibitors of the Nematode Chitinase CeCht1. Journal of Agricultural and Food Chemistry, 2021, 69, 3519-3526.	5.2	10
15	The symmetric designer protein Pizza as a scaffold for metal coordination. Proteins: Structure, Function and Bioinformatics, 2021, 89, 945-951.	2.6	3
16	A multidimensional computational exploration of congenital myasthenic syndrome causing mutations in human choline acetyltransferase. Journal of Cellular Biochemistry, 2021, 122, 787-800.	2.6	1
17	Lean-Docking: Exploiting Ligandsâ€™ Predicted Docking Scores to Accelerate Molecular Docking. Journal of Chemical Information and Modeling, 2021, 61, 2341-2352.	5.4	38
18	Understanding the molecular interactions of inhibitors against Bla1 beta-lactamase towards unraveling the mechanism of antimicrobial resistance. International Journal of Biological Macromolecules, 2021, 177, 337-350.	7.5	4

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19	Insights into the evolutionary forces that shape the codon usage in the viral genome segments encoding intrinsically disordered protein regions. Briefings in Bioinformatics, 2021, 22, .	6.5	9
20	Identification of 1,2,4â€Triazolylthioethanone Scaffold for the Design of New Acetylcholinesterase Inhibitors. Molecular Informatics, 2021, 40, 2100020.	2.5	0
21	A variant in human AIOLOS impairs adaptive immunity by interfering with IKAROS. Nature Immunology, 2021, 22, 893-903.	14.5	33
22	A loss-of-function variant in SUV39H2 identified in autism-spectrum disorder causes altered H3K9 trimethylation and dysregulation of protocadherin Î²-cluster genes in the developing brain. Molecular Psychiatry, 2021, 26, 7550-7559.	7.9	11
23	Cryo-EM structure of the human ELMO1-DOCK5-Rac1 complex. Science Advances, 2021, 7, .	10.3	17
24	Identification of Novel Cathepsin B Inhibitors with Implications in Alzheimerâ€™s Disease: Computational Refining and Biochemical Evaluation. Cells, 2021, 10, 1946.	4.1	13
25	A Novel Therapeutic Peptide Blocks SARS-CoV-2 Spike Protein Binding with Host Cell ACE2 Receptor. Drugs in R and D, 2021, 21, 273-283.	2.2	20
26	An integrated computational pipeline for designing high-affinity nanobodies with expanded genetic codes. Briefings in Bioinformatics, 2021, 22, .	6.5	4
27	NbX: Machine Learning-Guided Re-Ranking of Nanobodyâ€“Antigen Binding Poses. Pharmaceuticals, 2021, 14, 968.	3.8	5
28	Seven Amino Acid Types Suffice to Create the Core Fold of RNA Polymerase. Journal of the American Chemical Society, 2021, 143, 15998-16006.	13.7	18
29	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
30	Neuroprotective derivatives of tacrine that target NMDA receptor and acetyl cholinesterase â€“ Design, synthesis and biological evaluation. Computational and Structural Biotechnology Journal, 2021, 19, 4517-4537.	4.1	17
31	Piperidine-4-carboxamide as a new scaffold for designing secretory glutaminyl cyclase inhibitors. International Journal of Biological Macromolecules, 2021, 170, 415-423.	7.5	13
32	Evolutionary and codon usage preference insights into spike glycoprotein of SARS-CoV-2. Briefings in Bioinformatics, 2021, 22, 1006-1022.	6.5	20
33	A Series of Compounds Bearing a Dipyrido-Pyrimidine Scaffold Acting as Novel Human and Insect Pest Chitinase Inhibitors. Journal of Medicinal Chemistry, 2020, 63, 987-1001.	6.4	29
34	ATP7A Clinical Genetics Resource â€“ A comprehensive clinically annotated database and resource for genetic variants in ATP7A gene. Computational and Structural Biotechnology Journal, 2020, 18, 2347-2356.	4.1	3
35	Mechanistic insights into the loss-of-function mechanisms of rare human D-amino acid oxidase variants implicated in amyotrophic lateral sclerosis. Scientific Reports, 2020, 10, 17146.	3.3	8
36	Identification of a Selective RelA Inhibitor Based on DSE-FRET Screening Methods. International Journal of Molecular Sciences, 2020, 21, 9150.	4.1	3

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37	Actin R256 Mono-methylation Is a Conserved Post-translational Modification Involved in Transcription. Cell Reports, 2020, 32, 108172.	6.4	9
38	Design of a peptide-based subunit vaccine against novel coronavirus SARS-CoV-2. Microbial Pathogenesis, 2020, 145, 104236.	2.9	154
39	A protein sequence fitness function for identifying natural and <scp>nonnatural</scp> proteins. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1271-1284.	2.6	12
40	EC330, a small-molecule compound, is a potential novel inhibitor of LIF signaling. Journal of Molecular Cell Biology, 2020, 12, 477-480.	3.3	9
41	Shape similarity guided pose prediction: lessons from D3R Grand Challenge 3. Journal of Computer-Aided Molecular Design, 2019, 33, 47-59.	2.9	9
42	Population-Based Sampling and Fragment-Based De Novo Protein Structure Prediction. , 2019, , 774-784.		6
43	Human glutaminyl cyclase: Structure, function, inhibitors and involvement in Alzheimerâ€™s disease. Pharmacological Research, 2019, 147, 104342.	7.1	21
44	Improving ligand 3D shape similarity-based pose prediction with a continuum solvent model. Journal of Computer-Aided Molecular Design, 2019, 33, 1045-1055.	2.9	3
45	EC359: A First-in-Class Small-Molecule Inhibitor for Targeting Oncogenic LIFR Signaling in Triple-Negative Breast Cancer. Molecular Cancer Therapeutics, 2019, 18, 1341-1354.	4.1	41
46	Human Chitinases: Structure, Function, and Inhibitor Discovery. Advances in Experimental Medicine and Biology, 2019, 1142, 221-251.	1.6	23
47	Chemoinformatics and structural bioinformatics in OCaml. Journal of Cheminformatics, 2019, 11, 10.	6.1	5
48	EC313-a tissue selective SPRM reduces the growth and proliferation of uterine fibroids in a human uterine fibroid tissue xenograft model. Scientific Reports, 2019, 9, 17279.	3.3	4
49	A structural homology approach for computational protein design with flexible backbone. Bioinformatics, 2019, 35, 2418-2426.	4.1	6
50	Computational design of symmetrical eight-bladed Î²-propeller proteins. IUCrJ, 2019, 6, 46-55.	2.2	33
51	A cross docking pipeline for improving pose prediction and virtual screening performance. Journal of Computer-Aided Molecular Design, 2018, 32, 163-173.	2.9	24
52	Advances in the Development of Shape Similarity Methods and Their Application in Drug Discovery. Frontiers in Chemistry, 2018, 6, 315.	3.6	105
53	Discovery of Fungal Denitrification Inhibitors by Targeting Copper Nitrite Reductase from Fusarium oxysporum. Journal of Chemical Information and Modeling, 2017, 57, 203-213.	5.4	30
54	Balancing exploration and exploitation in population-based sampling improves fragment-basedde novoprotein structure prediction. Proteins: Structure, Function and Bioinformatics, 2017, 85, 852-858.	2.6	20

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55	Evolution-Inspired Computational Design of Symmetric Proteins. Methods in Molecular Biology, 2017, 1529, 309-322.	0.9	12
56	Computational design of a symmetrical Î²-trefoil lectin with cancer cell binding activity. Scientific Reports, 2017, 7, 5943.	3.3	35
57	Identification and structureâ€“activity relationship of purine derivatives as novel <scp>MTH</scp>1 inhibitors. Chemical Biology and Drug Design, 2017, 89, 862-869.	3.2	11
58	Fragger: a protein fragment picker for structural queries. F1000Research, 2017, 6, 1722.	1.6	2
59	Fragger: a protein fragment picker for structural queries. F1000Research, 2017, 6, 1722.	1.6	2
60	A pose prediction approach based on ligand 3D shape similarity. Journal of Computer-Aided Molecular Design, 2016, 30, 457-469.	2.9	15
61	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
62	Understanding the Assembly of an Artificial Protein Nanotube. Advanced Materials Interfaces, 2016, 3, 1600846.	3.7	8
63	A Novel Scaffold for Developing Specific or Broad-Spectrum Chitinase Inhibitors. Journal of Chemical Information and Modeling, 2016, 56, 2413-2420.	5.4	27
64	The Effect of F877L and T878A Mutations on Androgen Receptor Response to Enzalutamide. Molecular Cancer Therapeutics, 2016, 15, 1702-1712.	4.1	73
65	Identification of new SUMO activating enzyme 1 inhibitors using virtual screening and scaffold hopping. Bioorganic and Medicinal Chemistry Letters, 2016, 26, 1218-1223.	2.2	34
66	Application of Shape Similarity in Pose Selection and Virtual Screening in CSARdock2014 Exercise. Journal of Chemical Information and Modeling, 2016, 56, 965-973.	5.4	24
67	Characterization of pH-induced transitions of Entamoeba histolytica d-phosphoglycerate dehydrogenase. International Journal of Biological Macromolecules, 2015, 79, 284-289.	7.5	1
68	The crystal and solution structure of YdiE fromEscherichia coli. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 919-924.	0.8	1
69	A fragmentation and reassembly method forab initiophasing. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 304-312.	2.5	15
70	Quality Assessment of Predicted Protein Models Using Energies Calculated by the Fragment Molecular Orbital Method. Molecular Informatics, 2015, 34, 97-104.	2.5	13
71	Advances in the development of SUMO specific protease (SENP) inhibitors. Computational and Structural Biotechnology Journal, 2015, 13, 204-211.	4.1	60
72	Synthesis, cholinesterase inhibition and molecular modelling studies of coumarin linked thiourea derivatives. Bioorganic Chemistry, 2015, 63, 58-63.	4.1	45

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73	Biomineralization of a Cadmium Chloride Nanocrystal by a Designed Symmetrical Protein. Angewandte Chemie - International Edition, 2015, 54, 9857-9860.	13.8	36
74	Hierarchical virtual screening approaches in small molecule drug discovery. Methods, 2015, 71, 26-37.	3.8	121
75	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. Analytical Biochemistry, 2014, 448, 92-94.	2.4	7
76	Combining in silico and in cerebro approaches for virtual screening and pose prediction in SAMPL4. Journal of Computer-Aided Molecular Design, 2014, 28, 363-373.	2.9	25
77	Improving fragment quality for de novo structure prediction. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2240-2252.	2.6	10
78	Discovery of small molecule inhibitors targeting the SUMOâ€“SIM interaction using a protein interface consensus approach. MedChemComm, 2014, 5, 783-786.	3.4	9
79	Identification of Sumoylation Inhibitors Targeting a Predicted Pocket in Ubc9. Journal of Chemical Information and Modeling, 2014, 54, 2784-2793.	5.4	12
80	Identification of 1,2,5-Oxadiazoles as a New Class of SENP2 Inhibitors Using Structure Based Virtual Screening. Journal of Chemical Information and Modeling, 2014, 54, 870-880.	5.4	47
81	Computational design of a self-assembling symmetrical Î²-propeller protein. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15102-15107.	7.1	122
82	A rotation-translation invariant molecular descriptor of partial charges and its use in ligand-based virtual screening. Journal of Cheminformatics, 2014, 6, 23.	6.1	21
83	Computational Investigation of SENP:SUMO Proteinâ€Protein Interaction for Structure Based Drug Design. Molecular Informatics, 2013, 32, 267-280.	2.5	5
84	Identification of small peptides inhibiting the integraseâ€LEDGF/p75 interaction through targeting the cellular coâ€factor. Journal of Peptide Science, 2013, 19, 651-658.	1.4	9
85	CDC25A-inhibitory RE derivatives bind to pocket adjacent to the catalytic site. Molecular BioSystems, 2013, 9, 1026.	2.9	5
86	Identification of quinazolinyloxy biaryl urea as a new class of SUMO activating enzyme 1 inhibitors. Bioorganic and Medicinal Chemistry Letters, 2013, 23, 5145-5149.	2.2	20
87	The Discovery of Novel Human Androgen Receptor Antagonist Chemotypes Using a Combined Pharmacophore Screening Procedure. ChemMedChem, 2013, 8, 644-651.	3.2	27
88	Identification of Sumoylation Activating Enzyme 1 Inhibitors by Structure-Based Virtual Screening. Journal of Chemical Information and Modeling, 2013, 53, 809-820.	5.4	40
89	Investigation on the Effect of Key Water Molecules on Docking Performance in CSARdock Exercise. Journal of Chemical Information and Modeling, 2013, 53, 1880-1892.	5.4	46
90	Spectomycin B1 as a Novel SUMOylation Inhibitor That Directly Binds to SUMO E2. ACS Chemical Biology, 2013, 8, 2635-2642.	3.4	80

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91	Protein Interface Pharmacophore Mapping Tools for Small Molecule Protein: Protein Interaction Inhibitor Discovery. Current Topics in Medicinal Chemistry, 2013, 13, 989-1001.	2.1	35
92	Design and pharmacology of a highly specific dual FMS and KIT kinase inhibitor. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5689-5694.	7.1	82
93	Efficient Sampling in Fragment-Based Protein Structure Prediction Using an Estimation of Distribution Algorithm. PLoS ONE, 2013, 8, e68954.	2.5	22
94	Electrostatic Similarities between Protein and Small Molecule Ligands Facilitate the Design of Protein-Protein Interaction Inhibitors. PLoS ONE, 2013, 8, e75762.	2.5	21
95	Pharmacophore Modelling as a Virtual Screening Tool for the Discovery of Small Molecule Protein-protein Interaction Inhibitors. Current Pharmaceutical Design, 2012, 18, 4586-4598.	1.9	25
96	An integrated fragment based screening approach for the discovery of small molecule modulators of the VWFâ€“GPIbÎ± interaction. Chemical Communications, 2012, 48, 11349.	4.1	11
97	Novel proteinâ€“protein interactions between Entamoeba histolytica d-phosphoglycerate dehydrogenase and phosphoserine aminotransferase. Biochimie, 2012, 94, 1676-1686.	2.6	6
98	Error-estimation-guided rebuilding ofde novomodels increases the success rate ofab initiophasing. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1522-1534.	2.5	6
99	Computational fragment-based screening using RosettaLigand: the SAMPL3 challenge. Journal of Computer-Aided Molecular Design, 2012, 26, 603-616.	2.9	15
100	Role of conserved active site tryptophan-101 in functional activity and stability of phosphoserine aminotransferase from an enteric human parasite. Amino Acids, 2012, 43, 483-491.	2.7	9
101	Glu-108 is essential for subunit assembly and dimer stability of d-phosphoglycerate dehydrogenase from Entamoeba histolytica. Molecular and Biochemical Parasitology, 2012, 181, 117-124.	1.1	11
102	Durandal: Fast exact clustering of protein decoys. Journal of Computational Chemistry, 2012, 33, 471-474.	3.3	20
103	A Probabilistic Fragment-Based Protein Structure Prediction Algorithm. PLoS ONE, 2012, 7, e38799.	2.5	40
104	Acceleratingab initiophasing withde novomodels. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 804-812.	2.5	13
105	Entropy-accelerated exact clustering of protein decoys. Bioinformatics, 2011, 27, 939-945.	4.1	22
106	Clinical efficacy of a RAF inhibitor needs broad target blockade in BRAF-mutant melanoma. Nature, 2010, 467, 596-599.	27.8	1,610
107	PAR: a PARallel and distributed job crusher. Bioinformatics, 2010, 26, 2918-2919.	4.1	7
108	Scaffold-based discovery of indeglitazar, a PPAR pan-active anti-diabetic agent. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 262-267.	7.1	134

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109	Discovery of a selective inhibitor of oncogenic B-Raf kinase with potent antimelanoma activity. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3041-3046.	7.1	1,206
110	Scaffold-Based Drug Discovery. , 2007, , 129-153.		8
111	Identification of a Novel Noncatalytic Bicarbonate Binding Site in Eubacterial Î²-Carbonic Anhydrase. Biochemistry, 2006, 45, 4351-4361.	2.5	97
112	Germline KRAS mutations cause Noonan syndrome. Nature Genetics, 2006, 38, 331-336.	21.4	670
113	Crystal Structure of Phosphodiesterase Families and the Potential for Rational Drug Design. , 2006, , .		2
114	A family of phosphodiesterase inhibitors discovered by cocrystallography and scaffold-based drug design. Nature Biotechnology, 2005, 23, 201-207.	17.5	220
115	Keynote review: Phosphodiesterase-4 as a therapeutic target. Drug Discovery Today, 2005, 10, 1503-1519.	6.4	604
116	Phosphodiesterase-4 as a potential drug target. Expert Opinion on Therapeutic Targets, 2005, 9, 1283-1305.	3.4	81
117	Bcl-XL Mutations Suppress Cellular Sensitivity to Antimycin A. Journal of Biological Chemistry, 2004, 279, 2159-2165.	3.4	68
118	Mcl-1 is required for Akata6 B-lymphoma cell survival and is converted to a cell death molecule by efficient caspase-mediated cleavage. Oncogene, 2004, 23, 4818-4827.	5.9	133
119	Structural Basis for the Activity of Drugs that Inhibit Phosphodiesterases. Structure, 2004, 12, 2233-2247.	3.3	360
120	A Glutamine Switch Mechanism for Nucleotide Selectivity by Phosphodiesterases. Molecular Cell, 2004, 15, 279-286.	9.7	271
121	A Glutamine Switch Mechanism for Nucleotide Selectivity by Phosphodiesterases. Molecular Cell, 2004, 15, 659.	9.7	3
122	Multidimensional Histograms for Density Modification. Methods in Enzymology, 2003, 374, 188-203.	1.0	0
123	Accurate computer-based design of a new backbone conformation in the second turn of protein L. Journal of Molecular Biology, 2002, 315, 471-477.	4.2	73
124	Biophysical Characterization of Recombinant Human Bcl-2 and Its Interactions with an Inhibitory Ligand, Antimycin A. Biochemistry, 2001, 40, 4911-4922.	2.5	81
125	Structures of the B1 domain of protein L fromPeptostreptococcus magnuswith a tyrosine to tryptophan substitution. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 480-487.	2.5	60
126	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. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 759-762.	2.5	43

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127	Crystal structure of E. coli Î²-carbonic anhydrase, an enzyme with an unusual pH-dependent activity. Protein Science, 2001, 10, 911-922.	7.6	151
128	Antimycin A mimics a cell-death-inducing Bcl-2 homology domain 3. Nature Cell Biology, 2001, 3, 183-191.	10.3	436
129	Single-Site Mutations Induce 3D Domain Swapping in the B1 Domain of Protein L from Peptostreptococcus magnus. Structure, 2001, 9, 1017-1027.	3.3	52
130	Conversion of monomeric protein L to an obligate dimer by computational protein design. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 10687-10691.	7.1	68
131	Crystallization and preliminary X-ray diffraction studies of mutants of B1 IgG-binding domain of protein L fromPeptostreptococcus magnus. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 506-508.	2.5	4
132	Cloning, crystallization and preliminary characterization of a Î²-carbonic anhydrase fromEscherichia coli. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1176-1179.	2.5	17
133	A two-dimensional histogram-matching method for protein phase refinement and extension. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1893-1900.	2.5	7
134	Density modification for macromolecular phase improvement. Progress in Biophysics and Molecular Biology, 1999, 72, 245-270.	2.9	242
135	The Two-Dimensional Histogram as a Constraint for Protein Phase Improvement. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 1230-1244.	2.5	8
136	Mutation and Modeling Analysis of theSaccharomyces cerevisiaeSwi6 Ankyrin Repeatsâ€. Biochemistry, 1998, 37, 4437-4450.	2.5	13
137	Oncogene-dependent apoptosis in extracts from drug-resistant cells.. Genes and Development, 1997, 11, 1266-1276.	5.9	60
138	[4] Combining constraints for electron-density modification. Methods in Enzymology, 1997, 277, 53-64.	1.0	109
139	Solid-state phase transition in the crystal structure of ribulose 1,5-bisphosphate carboxylase/oxygenase. Acta Crystallographica Section D: Biological Crystallography, 1994, 50, 258-262.	2.5	4
140	SQUASH â€“ combining constraints for macromolecular phase refinement and extension. Acta Crystallographica Section D: Biological Crystallography, 1993, 49, 213-222.	2.5	36
141	Ambiguities in Ab Initio Phasing. Science, 1993, 259, 1771-1772.	12.6	2
142	The use of Sayre's equation with solvent flattening and histogram matching for phase extension and refinement of protein structures. Acta Crystallographica Section A: Foundations and Advances, 1990, 46, 377-381.	0.3	105
143	Pharmacophore modeling: advances, limitations, and current utility in drug discovery. Journal of Receptor, Ligand and Channel Research, 0, , 81.	0.7	48