

Bi-Cheng Wang

List of Publications by Year in descending order

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101
papers

5,693
citations

117625

34
h-index

76900

74
g-index

104
all docs

104
docs citations

104
times ranked

4814
citing authors

#	ARTICLE	IF	CITATIONS
1	The SER-CAT Virtual Beamline: Providing Light when You Need it in Your Home Lab. Nihon Kessho Gakkaishi, 2021, 63, 44-52.	0.0	0
2	SAD phasing: History, current impact and future opportunities. Archives of Biochemistry and Biophysics, 2016, 602, 80-94.	3.0	21
3	Structural Insights into Substrate Specificity of Feruloyl-CoA 6- β -Hydroxylase from Arabidopsis thaliana. Scientific Reports, 2015, 5, 10355.	3.3	21
4	Crystal structure of Cry51Aa1: A potential novel insecticidal aerolysin-type β -pore-forming toxin from Bacillus thuringiensis. Biochemical and Biophysical Research Communications, 2015, 462, 184-189.	2.1	32
5	Fast native-SAD phasing for routine macromolecular structure determination. Nature Methods, 2015, 12, 131-133.	19.0	120
6	Native SAD is maturing. IUCr, 2015, 2, 431-440.	2.2	50
7	Structural Insights into Bacillus thuringiensis Cry, Cyt and Parasporin Toxins. Toxins, 2014, 6, 2732-2770.	3.4	144
8	Spatial structure of the novel light-sensitive photoprotein berovin from the ctenophore Beroë abyssicola in the Ca ²⁺ -loaded apoprotein conformation state. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 2139-2146.	2.3	25
9	The structure of augments of liver regeneration crystallized in the presence of 50 μ M CdCl ₂ reveals a novel Cd ₂ Cl ₄ O ₆ cluster that aids in crystal packing. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1128-1133.	2.5	4
10	Structure of the Archaeoglobus fulgidus orphan ORF AF1382 determined by sulfur SAD from a moderately diffracting crystal. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1242-1252.	2.5	5
11	Structural View of a Non Pfam Singleton and Crystal Packing Analysis. PLoS ONE, 2012, 7, e31673.	2.5	2
12	A multi-dataset data-collection strategy produces better diffraction data. Acta Crystallographica Section A: Foundations and Advances, 2011, 67, 544-549.	0.3	25
13	Crystal structure of a novel non-Pfam protein PF2046 solved using low resolution B-factor sharpening and multi-crystal averaging methods. Protein and Cell, 2010, 1, 453-458.	11.0	13
14	Single amino acid changes in the predicted RNase H domain of Escherichia coli RNase G lead to complementation of RNase E deletion mutants. Rna, 2010, 16, 1371-1385.	3.5	31
15	NMR-derived Topology of a GFP-photoprotein Energy Transfer Complex*. Journal of Biological Chemistry, 2010, 285, 40891-40900.	3.4	47
16	Structure based mechanism of the Ca ²⁺ -induced release of coelenterazine from the Renilla binding protein. Proteins: Structure, Function and Bioinformatics, 2009, 74, 583-593.	2.6	19
17	Purification, crystallization and preliminary crystallographic analysis of the non-Pfam protein AF1514 from Archaeoglobus fulgidus DSM 4304. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 91-93.	0.7	0
18	Crystal structure solution of a ParB-like nuclease at atomic resolution. Proteins: Structure, Function and Bioinformatics, 2008, 70, 263-267.	2.6	7

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19	Crystal structure of a novel non-β-barrel protein AF1514 from <i>Archeoglobus fulgidus</i> DSM 4304 solved by SAD using a Cr Kα source. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 2109-2113.	2.6	8
20	Crystal structure of coelenterazine-binding protein from <i>Renilla muelleri</i> at 1.7 Å: Why it is not a calcium-regulated photoprotein. <i>Photochemical and Photobiological Sciences</i> , 2008, 7, 442.	2.9	31
21	Expression, purification and characterization of the secreted luciferase of the copepod <i>Metridia longa</i> from Sf9 insect cells. <i>Protein Expression and Purification</i> , 2008, 61, 142-148.	1.3	30
22	Intragenic suppressors of temperature-sensitive <i>rne</i> mutations lead to the dissociation of RNase E activity on mRNA and tRNA substrates in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2008, 36, 5306-5318.	14.5	19
23	The First Agmatine/Cadaverine Aminopropyl Transferase: Biochemical and Structural Characterization of an Enzyme Involved in Polyamine Biosynthesis in the Hyperthermophilic Archaeon <i>Pyrococcus furiosus</i> . <i>Journal of Bacteriology</i> , 2007, 189, 6057-6067.	2.2	31
24	Crystal structure of an aerobic FMN-dependent azoreductase (AzoA) from <i>Enterococcus faecalis</i> . <i>Archives of Biochemistry and Biophysics</i> , 2007, 463, 68-77.	3.0	66
25	Structure of the hypothetical protein PF0899 from <i>Pyrococcus furiosus</i> at 1.85 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 549-552.	0.7	6
26	(NZ)CH...O Contacts assist crystallization of a ParB-like nuclease. <i>BMC Structural Biology</i> , 2007, 7, 46.	2.3	17
27	Characterization of a corrinoid protein involved in the C1 metabolism of strict anaerobic bacterium <i>Moorella thermoacetica</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 167-176.	2.6	28
28	Structural basis of CoA recognition by the <i>Pyrococcus</i> single-domain CoA-binding proteins. <i>Journal of Structural and Functional Genomics</i> , 2007, 7, 119-129.	1.2	3
29	Structural and transcriptional analyses of a purine nucleotide-binding protein from <i>Pyrococcus furiosus</i> : a component of a novel, membrane-bound multiprotein complex unique to this hyperthermophilic archaeon. <i>Journal of Structural and Functional Genomics</i> , 2007, 8, 1-10.	1.2	0
30	Crystal Structures of Tyrosyl-tRNA Synthetases from Archaea. <i>Journal of Molecular Biology</i> , 2006, 355, 395-408.	4.2	27
31	Crystal structure of obelin after Ca ²⁺ -triggered bioluminescence suggests neutral coelenteramide as the primary excited state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2570-2575.	7.1	84
32	All three Ca ²⁺ -binding loops of photoproteins bind calcium ions: The crystal structures of calcium-loaded apo-aequorin and apo-obelin. <i>Protein Science</i> , 2005, 14, 663-675.	7.6	85
33	Life in the fast lane for protein crystallization and X-ray crystallography. <i>Progress in Biophysics and Molecular Biology</i> , 2005, 88, 359-386.	2.9	77
34	Protein Production and Crystallization at SECSG – An Overview. <i>Journal of Structural and Functional Genomics</i> , 2005, 6, 233-243.	1.2	14
35	A test of enhancing model accuracy in high-throughput crystallography. <i>Journal of Structural and Functional Genomics</i> , 2005, 6, 1-11.	1.2	45
36	Salvaging <i>Pyrococcus furiosus</i> Protein Targets at SECSG. <i>Journal of Structural and Functional Genomics</i> , 2005, 6, 121-127.	1.2	2

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37	On increasing protein-crystallization throughput for X-ray diffraction studies. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 123-129.	2.5	17
38	Parameter-space screening: a powerful tool for high-throughput crystal structure determination. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 520-527.	2.5	25
39	SGXPro: a parallel workflow engine enabling optimization of program performance and automation of structure determination. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 951-959.	2.5	23
40	Away from the edge II: in-house Se-SAS phasing with chromium radiation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 960-966.	2.5	10
41	The high-throughput protein-to-structure pipeline at SECSG. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 679-684.	2.5	22
42	Isolation, crystallization and preliminary X-ray analysis of a methanol-induced corrinoid protein from <i>Moorella thermoacetica</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 537-540.	0.7	8
43	Three-dimensional structure of GlcNAc β 1-4Gal releasing Endo- β 2-Galactosidase from <i>Clostridium perfringens</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 141-144.	2.6	12
44	Mechanism of Class 1 (Glycosylhydrolase Family 47) β -Mannosidases Involved in N-Glycan Processing and Endoplasmic Reticulum Quality Control. <i>Journal of Biological Chemistry</i> , 2005, 280, 16197-16207.	3.4	106
45	Crystal Structure of a Ca ²⁺ -discharged Photoprotein. <i>Journal of Biological Chemistry</i> , 2004, 279, 33647-33652.	3.4	51
46	Structure of Mouse Golgi β -Mannosidase IA Reveals the Molecular Basis for Substrate Specificity among Class 1 (Family 47 Glycosylhydrolase) β 1,2-Mannosidases. <i>Journal of Biological Chemistry</i> , 2004, 279, 29774-29786.	3.4	48
47	Structural genomics of <i>Pyrococcus furiosus</i> : X-ray crystallography reveals 3D domain swapping in rubrerythrin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 878-882.	2.6	18
48	Preparation and X-ray crystallographic analysis of the Ca ²⁺ -discharged photoprotein obelin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 512-514.	2.5	7
49	Crystallization and preliminary X-ray analysis of GlcNAc β 1,4Gal-releasing endo- β 2-galactosidase from <i>Clostridium perfringens</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 537-538.	2.5	2
50	Monitoring the anomalous scattering signal and noise levels in X-ray diffraction of crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 499-506.	2.5	5
51	Displacement of iron by zinc at the diiron site of <i>Desulfovibrio vulgaris</i> rubrerythrin: X-ray crystal structure and anomalous scattering analysis. <i>Journal of Inorganic Biochemistry</i> , 2004, 98, 786-796.	3.5	19
52	X-ray Crystal Structure of <i>Desulfovibrio vulgaris</i> Rubrerythrin with Zinc Substituted into the [Fe(SCys) ₄] Site and Alternative Diiron Site Structures. <i>Biochemistry</i> , 2004, 43, 3204-3213.	2.5	14
53	Structure determination of fibrillar protein from the hyperthermophilic archaeon <i>Pyrococcus furiosus</i> . <i>Biochemical and Biophysical Research Communications</i> , 2004, 315, 726-732.	2.1	19
54	The Hyperthermophile Protein Sso10a is a Dimer of Winged Helix DNA-binding Domains Linked by an Antiparallel Coiled Coil Rod. <i>Journal of Molecular Biology</i> , 2004, 341, 73-91.	4.2	35

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55	The Southeast Collaboratory for Structural Genomics: A High-Throughput Gene to Structural Factory. <i>ChemInform</i> , 2003, 34, no.	0.0	0
56	The crystal structure of augmeter of liver regeneration: A mammalian FAD-dependent sulfhydryl oxidase. <i>Protein Science</i> , 2003, 12, 1109-1118.	7.6	99
57	The Southeast Collaboratory for Structural Genomics: A High-Throughput Gene to Structure Factory. <i>Accounts of Chemical Research</i> , 2003, 36, 191-198.	15.6	76
58	Atomic resolution structure of obelin: soaking with calcium enhances electron density of the second oxygen atom substituted at the C2-position of coelenterazine. <i>Biochemical and Biophysical Research Communications</i> , 2003, 311, 433-439.	2.1	56
59	Violet Bioluminescence and Fast Kinetics from W92F Obelin: A Structure-Based Proposals for the Bioluminescence Triggering and the Identification of the Emitting Species. <i>Biochemistry</i> , 2003, 42, 6013-6024.	2.5	57
60	Crystal Structure of the Cytoskeleton-associated Protein Glycine-rich (CAP-Gly) Domain. <i>Journal of Biological Chemistry</i> , 2002, 277, 48596-48601.	3.4	88
61	X-ray Crystal Structures of Reduced Rubrerythrin and Its Azide Adduct: A Structure-Based Mechanism for a Non-Heme Diiron Peroxidase. <i>Journal of the American Chemical Society</i> , 2002, 124, 9845-9855.	13.7	76
62	Structural basis for the emission of violet bioluminescence from a W92F obelin mutant. <i>FEBS Letters</i> , 2001, 506, 281-285.	2.8	44
63	Aldehyde dehydrogenase. <i>FEBS Journal</i> , 2001, 268, 722-726.	0.2	34
64	Structures of an unliganded neurophysin and its vasopressin complex: Implications for binding and allosteric mechanisms. <i>Protein Science</i> , 2001, 10, 1869-1880.	7.6	42
65	Crystal structure of the transcription factor sc-mtTFB offers insights into mitochondrial transcription. <i>Protein Science</i> , 2001, 10, 1980-1988.	7.6	93
66	The 2.0 Å structure of human ferrochelatase, the terminal enzyme of heme biosynthesis. <i>Nature Structural Biology</i> , 2001, 8, 156-160.	9.7	200
67	Beyond the catalytic core of ALDH: a web of important residues begins to emerge. <i>Chemico-Biological Interactions</i> , 2001, 130-132, 39-46.	4.0	8
68	Protein Crystallography. , 2001, , .		2
69	Crystallization and preliminary X-ray diffraction analysis of the mitochondrial transcription factor sc-mtTFB from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 902-903.	2.5	2
70	Structure of the Ca ²⁺ -regulated photoprotein obelin at 1.7 Å... resolution determined directly from its sulfur substructure. <i>Protein Science</i> , 2000, 9, 2085-2093.	7.6	170
71	Low-salt crystallization of T7 RNA polymerase: a first step towards the transcription bubble complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1188-1192.	2.5	2
72	Human ferrochelatase: crystallization, characterization of the [2Fe-2S] cluster and determination that the enzyme is a homodimer. <i>BBA - Proteins and Proteomics</i> , 1999, 1435, 191-197.	2.1	60

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73	Relationships within the aldehyde dehydrogenase extended family. <i>Protein Science</i> , 1999, 8, 137-146.	7.6	247
74	Structural basis of neurophysin hormone specificity: Geometry, polarity, and polarizability in aromatic ring interactions. <i>Protein Science</i> , 1999, 8, 820-831.	7.6	9
75	Aldehyde Dehydrogenase Catalytic Mechanism. <i>Advances in Experimental Medicine and Biology</i> , 1999, 463, 53-59.	1.6	47
76	The structure of glutamine-binding protein complexed with glutamine at 1.94 Å... resolution: comparisons with other amino acid binding proteins. <i>Journal of Molecular Biology</i> , 1998, 278, 219-229.	4.2	180
77	The first structure of an aldehyde dehydrogenase reveals novel interactions between NAD and the Rossmann fold. <i>Nature Structural Biology</i> , 1997, 4, 317-326.	9.7	289
78	The Crystal Structure of Glutamine-binding Protein from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1996, 262, 225-242.	4.2	165
79	Crystal structure of the neurophysin-oxytocin complex. <i>Nature Structural Biology</i> , 1996, 3, 163-169.	9.7	94
80	Crystal Structure of a Class 3 Aldehyde Dehydrogenase at 2.6 Å... Resolution. <i>Advances in Experimental Medicine and Biology</i> , 1996, 414, 1-7.	1.6	12
81	Conserved Residues in the Aldehyde Dehydrogenase Family. <i>Advances in Experimental Medicine and Biology</i> , 1996, 414, 9-13.	1.6	12
82	Progress Toward the Tertiary Structure of (Class 3) Aldehyde Dehydrogenase. <i>Advances in Experimental Medicine and Biology</i> , 1995, 372, 71-77.	1.6	0
83	The Octameric Histone Core of the Nucleosome. <i>Journal of Molecular Biology</i> , 1994, 236, 179-188.	4.2	31
84	Crystals of Glutamine-binding Protein in Various Conformational States. <i>Journal of Molecular Biology</i> , 1994, 240, 87-91.	4.2	13
85	Crystal structure of bacteriophage T7 RNA polymerase at 3.3 Å... resolution. <i>Nature</i> , 1993, 364, 593-599.	27.8	381
86	Crystallographic analysis of the neurophysin-oxytocin complex. <i>Journal of Molecular Biology</i> , 1991, 221, 43-45.	4.2	8
87	Crystals of a bovine neurophysin II tripeptide complex. <i>Journal of Molecular Biology</i> , 1991, 222, 23-25.	4.2	5
88	Preliminary crystallographic analysis of class 3 rat liver aldehyde dehydrogenase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990, 8, 305-308.	2.6	20
89	Single crystals of bacteriophage T7 RNA polymerase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1989, 5, 266-270.	2.6	25
90	Crystals of modified bovine neurophysin II. <i>FEBS Journal</i> , 1988, 174, 145-147.	0.2	6

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91	Structure and recognition mechanism of EcoRI endonuclease. Trends in Biochemical Sciences, 1987, 12, 395-398.	7.5	12
92	Structure of the DNA-EcoRI Endonuclease Recognition Complex. , 1987, , 251-256.		1
93	Structure of the DNA-EcoRI Endonuclease Recognition Complex. Springer Series in Biophysics, 1987, , 255-259.	0.4	0
94	Resolution of phase ambiguity in macromolecular crystallography. Methods in Enzymology, 1985, 115, 90-112.	1.0	989
95	Kinked DNA in crystalline complex with EcoRI endonuclease. Nature, 1984, 309, 327-331.	27.8	328
96	Crystals of a bovine neurophysin II-dipeptide amide complex. Journal of Molecular Biology, 1979, 127, 241-242.	4.2	13
97	Automated interpretation of electron density maps as applied to Bence-Jones protein rhe. Journal of Molecular Biology, 1979, 135, 305-308.	4.2	1
98	Crystal structure of bence jones protein Rhe (3 Å...) and its unique domain-domain association. Journal of Molecular Biology, 1979, 129, 657-674.	4.2	29
99	Structure of a dimeric fragment related to the lambda-type Bence-Jones protein: A preliminary study. Journal of Molecular Biology, 1974, 87, 505-508.	4.2	15
100	Crystal structure of pentacyanocobalt(III)-mu.-cyano-pentaamminecobalt(III) monohydrate. Inorganic Chemistry, 1971, 10, 1492-1497.	4.0	51
101	Crystal structure of dipyrindinium(II) oxytetrachloroselenate(IV),C10H8N2H22+SeOCl42-. Highly coordinated selenium compound. Inorganic Chemistry, 1970, 9, 1643-1650.	4.0	21