

Zeng-Qiang Gao

List of Publications by Year in descending order

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73
papers

972
citations

394421
19
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526287
27
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75
all docs

75
docs citations

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times ranked

1539
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#	ARTICLE	IF	CITATIONS
1	Organic–inorganic hybrid metallic conductors based on bis(ethylenedithio)tetrathiafulvalene cations and antiferromagnetic oxalate-bridged copper(II) dinuclear anions. <i>Journal of Materials Chemistry C</i> , 2022, 10, 2845-2852.	5.5	2
2	Structure and Biochemical Characteristics of the Methyltransferase Domain of RNA Capping Enzyme from African Swine Fever Virus. <i>Journal of Virology</i> , 2021, 95, .	3.4	9
3	NUDIM: A non-uniform fast Fourier transform based dual-space constraint iterative reconstruction method in biological electron tomography. <i>Journal of Structural Biology</i> , 2021, 213, 107770.	2.8	2
4	Insights into the Neutralization and DNA Binding of Toxin–Antitoxin System ParESO-CopASO by Structure-Function Studies. <i>Microorganisms</i> , 2021, 9, 2506.	3.6	3
5	Structural and functional characterization of the deep-sea thermophilic bacteriophage GVE2 tailspike protein. <i>International Journal of Biological Macromolecules</i> , 2020, 164, 4415-4422.	7.5	3
6	Characterization of the <i>Pseudomonas aeruginosa</i> T6SS PldB immunity proteins PA5086, PA5087 and PA5088 explains a novel stockpiling mechanism. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 222-227.	0.8	3
7	Crystal structure of the nucleoid-associated protein Fis (PA4853) from <i>Pseudomonas aeruginosa</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 209-215.	0.8	0
8	A noise and artifact suppression using resampling (NASR) method to facilitate de novo protein structure determination. <i>Radiation Detection Technology and Methods</i> , 2019, 3, 1.	0.8	1
9	Conformational changes of antitoxin HigA from <i>Escherichia coli</i> str. K-12 upon binding of its cognate toxin HigB reveal a new regulation mechanism in toxin-antitoxin systems. <i>Biochemical and Biophysical Research Communications</i> , 2019, 514, 37-43.	2.1	7
10	Crystal structure of the type VI immunity protein Tdi1 (Atu4351) from <i>Agrobacterium tumefaciens</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 153-158.	0.8	1
11	Structural Insights Into the Transcriptional Regulation of HigBA Toxin–Antitoxin System by Antitoxin HigA in <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 3158.	3.5	16
12	Structure–function analyses reveal the molecular architecture and neutralization mechanism of a bacterial HEPN–MNT toxin–antitoxin system. <i>Journal of Biological Chemistry</i> , 2018, 293, 6812-6823.	3.4	24
13	Crystal structures of multicopper oxidase CueO G304K mutant: structural basis of the increased laccase activity. <i>Scientific Reports</i> , 2018, 8, 14252.	3.3	15
14	Structural and biochemical characterization of the yeast HD domain containing protein YGK1 reveals a metal-dependent nucleoside 5′-monophosphatase. <i>Biochemical and Biophysical Research Communications</i> , 2018, 501, 674-681.	2.1	4
15	An iterative refinement method combining detector geometry optimization and diffraction model refinement in serial femtosecond crystallography. <i>Radiation Detection Technology and Methods</i> , 2018, 2, 1.	0.8	1
16	The crystal structure of KSHV ORF57 reveals dimeric active sites important for protein stability and function. <i>PLoS Pathogens</i> , 2018, 14, e1007232.	4.7	15
17	(BEDT–TF) ₂ Cu ₂ (HCOO) ₅ : An Organic–Inorganic Hybrid Conducting Magnet. <i>ChemistryOpen</i> , 2017, 6, 320-324.	1.9	4
18	Exploring New Assembly Modes of Uranyl Terephthalate: Templated Syntheses and Structural Regulation of a Series of Rare 2D → 3D Polycatenated Frameworks. <i>Inorganic Chemistry</i> , 2017, 56, 7694-7706.	4.0	37

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19	Structural analysis of Wss1 protein from <i>saccharomyces cerevisiae</i> . Scientific Reports, 2017, 7, 8270.	3.3	10
20	Structural and SAXS analysis of Tle5-Tli5 complex reveals a novel inhibition mechanism of H2-T6SS in <i>Pseudomonas aeruginosa</i> . Protein Science, 2017, 26, 2083-2091.	7.6	6
21	Supramolecular Host-Guest Inclusion for Distinguishing Cucurbit[7]uril-Based Pseudorotaxanes from Small-Molecule Ligands in Coordination Assembly with a Uranyl Center. Chemistry - A European Journal, 2017, 23, 13995-14003.	3.3	33
22	HicAB toxin-antitoxin complex from <i>Escherichia coli</i> : expression and crystallization. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 505-510.	0.8	3
23	Crystal structure of the putative cytoplasmic protein STM0279 (Hcp2) from <i>Salmonella typhimurium</i> . Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 463-468.	0.8	5
24	Structural Insights into the Methylation of C1402 in 16S rRNA by Methyltransferase Rsml. PLoS ONE, 2016, 11, e0163816.	2.5	8
25	Structural insight into the <i>E. coli</i> HigBA complex. Biochemical and Biophysical Research Communications, 2016, 478, 1521-1527.	2.1	17
26	Novel Uranyl Coordination Polymers Based on Quinoline-Containing Dicarboxylate by Altering Auxiliary Ligands: From 1D Chain to 3D Framework. Crystal Growth and Design, 2016, 16, 4886-4896.	3.0	27
27	Structural analysis of <i>Pseudomonas aeruginosa</i> H3-T6SS immunity proteins. FEBS Letters, 2016, 590, 2787-2796.	2.8	9
28	Mechanism of the allosteric regulation of <i>Streptococcus mutans</i> 2-deoxycytidylate deaminase. Acta Crystallographica Section D: Structural Biology, 2016, 72, 883-891.	2.3	4
29	Structural insights into the inhibition mechanism of bacterial toxin LsoA by bacteriophage antitoxin Dmd. Molecular Microbiology, 2016, 101, 757-769.	2.5	16
30	Genome-Wide Mapping of the Binding Sites and Structural Analysis of Kaposi's Sarcoma-Associated Herpesvirus Viral Interferon Regulatory Factor 2 Reveal that It is a DNA-Binding Transcription Factor. Journal of Virology, 2016, 90, 1158-1168.	3.4	10
31	Structural characterizations of phage antitoxin Dmd and its interactions with bacterial toxin RnlA. Biochemical and Biophysical Research Communications, 2016, 472, 592-597.	2.1	16
32	Structural basis for the interaction of BamB with the POTRA3-4 domains of BamA. Acta Crystallographica Section D: Structural Biology, 2016, 72, 236-244.	2.3	14
33	Oxovanadium(IV) Schiff Base Complex Derived From Phenylalanine Analogue Containing 2,3-Diaminopropionic Acid (DAP): Synthesis, Computational Study, and Biological Evaluation. Synthesis and Reactivity in Inorganic, Metal Organic, and Nano Metal Chemistry, 2015, 45, 455-467.	0.6	2
34	New Insight of Coordination and Extraction of Uranium(VI) with N-Donating Ligands in Room Temperature Ionic Liquids: <i>N,N'</i> -diethyl- <i>N,N'</i> -ditolyldipicolinamide as a Case Study. Inorganic Chemistry, 2015, 54, 1992-1999.	4.0	20
35	Crystal structure of GnsA from <i>Escherichia coli</i> . Biochemical and Biophysical Research Communications, 2015, 462, 1-7.	2.1	5
36	Synthesis, structures and magnetic properties in 3d-electron-rich isostructural complexes based on chains with sole syn-anti carboxylate bridges. Dalton Transactions, 2015, 44, 7213-7222.	3.3	46

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37	Silver Ion-Mediated Heterometallic Three-Fold Interpenetrating Uranylâ€‘Organic Framework. <i>Inorganic Chemistry</i> , 2015, 54, 10934-10945.	4.0	44
38	Structural and functional analysis show that the <i>Escherichia coli</i> uncharacterized protein YjcS is likely an alkylsulfatase. <i>Protein Science</i> , 2014, 23, 1442-1450.	7.6	8
39	Crystal structures and kinetic properties of enoylâ€‘acyl carrier protein reductase I from <i>Candidatus Liberibacter asiaticus</i> . <i>Protein Science</i> , 2014, 23, 366-377.	7.6	5
40	Structure of the type VI secretion phospholipase effector Tle1 provides insight into its hydrolysis and membrane targeting. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2175-2185.	2.5	26
41	Application of a conic glass monocapillary in Beijing synchrotron radiation facility. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 2014, 754, 42-45.	1.6	1
42	Synthesis, Crystal Structure, and Characterization of the Charge-Transfer Salt (BEDT-TTF)[Fe(C ₂ O ₄)Cl ₂](CH ₂ Cl ₂), {BEDT-TTF = Bis(ethylenedithio)tetrathiafulvalene}. <i>European Journal of Inorganic Chemistry</i> , 2014, 2014, 4028-4032.	2.0	7
43	High-resolution crystal structure reveals a HEPN domain at the C-terminal region of <i>S. cerevisiae</i> RNA endonuclease Swt1. <i>Biochemical and Biophysical Research Communications</i> , 2014, 453, 826-832.	2.1	2
44	Structural and Functional Characterization of <i>Escherichia coli</i> Toxin-Antitoxin Complex DinJ-YafQ. <i>Journal of Biological Chemistry</i> , 2014, 289, 21191-21202.	3.4	29
45	Conserved residues that modulate protein trans-splicing of Npu DnaE split intein. <i>Biochemical Journal</i> , 2014, 461, 247-255.	3.7	11
46	Synthesis, crystal structures and characterization of two heterometallic compounds: Ba ₃ [Fe(C ₂ O ₄) ₄]·2H ₂ O·0.004H ₂ O. <i>Overlook 10</i> 399-404.	2.4	0
47	Cloning, purification, crystallization and preliminary X-ray studies of the putative type VI secretion immunity protein Tli5 (PA5088) from <i>Pseudomonas aeruginosa</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 903-905.	0.8	1
48	Structural basis for recognition of the type VI spike protein VgrG3 by a cognate immunity protein. <i>FEBS Letters</i> , 2014, 588, 1891-1898.	2.8	6
49	Structural Basis for Interaction between <i>Mycobacterium smegmatis</i> Ms6564, a TetR Family Master Regulator, and Its Target DNA. <i>Journal of Biological Chemistry</i> , 2013, 288, 23687-23695.	3.4	22
50	The crystal structure of human protein 11 reveals a chromophore-binding site and two putative proteinâ€‘protein interfaces. <i>Biochemical and Biophysical Research Communications</i> , 2013, 439, 346-350.	2.1	3
51	Structureâ€‘function studies of YjcS from <i>Escherichia coli</i> and RnlA reveal a novel toxin structure involved in bacteriophage resistance. <i>Molecular Microbiology</i> , 2013, 90, 956-965.	2.5	21
52	Structure analysis of the global metabolic regulator Crc from <i>Pseudomonas aeruginosa</i> . <i>IUBMB Life</i> , 2013, 65, 50-57.	3.4	5
53	NMR structure of the N-terminal-most HRDC1 domain of RecQ helicase from <i>Deinococcus radiodurans</i> . <i>FEBS Letters</i> , 2013, 587, 2635-2642.	2.8	5
54	Structural insights into the inhibition of type VI effector Tae3 by its immunity protein Tai3. <i>Biochemical Journal</i> , 2013, 454, 59-68.	3.7	26

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55	Purification, crystallization and preliminary crystallographic analysis of the 23S rRNA methyltransferase RlmM (Cm2498) from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 640-642.	0.7	1
56	Structure of the Type VI Effector-Immunity Complex (Tae4-Tai4) Provides Novel Insights into the Inhibition Mechanism of the Effector by Its Immunity Protein*. <i>Journal of Biological Chemistry</i> , 2013, 288, 5928-5939.	3.4	65
57	Insights into the Cross-Immunity Mechanism within Effector Families of Bacteria Type VI Secretion System from the Structure of StTae4-EcTai4 Complex. <i>PLoS ONE</i> , 2013, 8, e73782.	2.5	11
58	Structural insights into the function of 23S rRNA methyltransferase RlmG (m2G1835) from <i>Escherichia coli</i> . <i>Rna</i> , 2012, 18, 1500-1509.	3.5	1
59	Crystal structure of type VI effector Tse1 from <i>Pseudomonas aeruginosa</i> . <i>FEBS Letters</i> , 2012, 586, 3193-3199.	2.8	23
60	Crystal and solution structures of methyltransferase RsmH provide basis for methylation of C1402 in 16S rRNA. <i>Journal of Structural Biology</i> , 2012, 179, 29-40.	2.8	31
61	The structural basis of the response regulator DrRRA from <i>Deinococcus radiodurans</i> . <i>Biochemical and Biophysical Research Communications</i> , 2012, 417, 1206-1212.	2.1	2
62	Structural and SAXS analysis of the budding yeast SHU complex proteins. <i>FEBS Letters</i> , 2012, 586, 2306-2312.	2.8	18
63	Insights into the Catalytic Mechanism of 16S rRNA Methyltransferase RsmE (m3U1498) from Crystal and Solution Structures. <i>Journal of Molecular Biology</i> , 2012, 423, 576-589.	4.2	13
64	The crystal structure of the MPN domain from the COP9 signalosome subunit CSN6. <i>FEBS Letters</i> , 2012, 586, 1147-1153.	2.8	20
65	Cloning, purification, crystallization and preliminary X-ray studies of human β 1-microglobulin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 692-694.	0.7	1
66	Mononuclear copper(ii) complexes with 3,5-substituted-4-salicylidene-amino-3,5-dimethyl-1,2,4-triazole: synthesis, structure and potent inhibition of protein tyrosine phosphatases. <i>Dalton Transactions</i> , 2011, 40, 6532.	3.3	30
67	Crystal structure and site-directed mutagenesis of a nitroalkane oxidase from <i>Streptomyces ansochromogenes</i> . <i>Biochemical and Biophysical Research Communications</i> , 2011, 405, 344-348.	2.1	13
68	The 1.6Å... resolution structure of activated D138L mutant of catabolite gene activator protein with two cAMP bound in each monomer. <i>International Journal of Biological Macromolecules</i> , 2011, 48, 459-465.	7.5	2
69	Structure of the putative dihydroorotate dehydrogenase from <i>Streptococcus mutans</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 182-187.	0.7	8
70	High-resolution structure of a new crystal form of BamA POTRA4 from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 734-738.	0.7	30
71	Structure of orotate phosphoribosyltransferase from the caries pathogen <i>Streptococcus mutans</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 498-502.	0.7	7
72	Photonic Logic Gates Based on Control of FRET by a Solvatochromic Perylene Bisimide. <i>Journal of Organic Chemistry</i> , 2007, 72, 2878-2885.	3.2	76

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73	Protein Preparation, Crystallization and Preliminary X-Ray Crystallographic Studies of Smu.1392c from <i>Streptococcus mutans</i> . Protein and Peptide Letters, 2006, 13, 1051-1052.	0.9	0