

Yuhui Dong

List of Publications by Year in descending order

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Version: 2024-02-01

81
papers

1,971
citations

471061

17
h-index

264894

42
g-index

83
all docs

83
docs citations

83
times ranked

3866
citing authors

#	ARTICLE	IF	CITATIONS
1	A Freestanding Chitin-Derived Hierarchical Nanocomposite for Developing Electrodes in Future Supercapacitor Industry. <i>Polymers</i> , 2022, 14, 195.	2.0	4
2	Wave-optics simulation software for synchrotron radiation from 4th generation storage rings based on a coherent modes model. <i>Optics Express</i> , 2022, 30, 7625.	1.7	2
3	<i>In situ</i> determination of the extreme damage resistance behavior in stomatopod dactyl club. <i>Journal of Synchrotron Radiation</i> , 2022, 29, 775-786.	1.0	3
4	A comparison of Remdesivir versus gold cluster in COVID-19 animal model: A better therapeutic outcome of gold cluster. <i>Nano Today</i> , 2022, 44, 101468.	6.2	15
5	Exascale image processing for next-generation beamlines in advanced light sources. <i>Nature Reviews Physics</i> , 2022, 4, 427-428.	11.9	12
6	A wave optics model for the effect of partial coherence on coherent diffractive imaging. <i>Journal of Synchrotron Radiation</i> , 2021, 28, 499-504.	1.0	1
7	The <i>Pseudomonas aeruginosa</i> PAAR2 cluster encodes a putative VRR-NUC domain-containing effector. <i>FEBS Journal</i> , 2021, 288, 5755-5767.	2.2	8
8	A reference-based multi-lattice indexing method integrating prior information correction and iterative refinement in protein crystallography. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2021, 77, 277-288.	0.0	3
9	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.	1.3	2
10	Structure and SAXS studies unveiled a novel inhibition mechanism of the <i>Pseudomonas aeruginosa</i> T6SS TseT-TsiT complex. <i>International Journal of Biological Macromolecules</i> , 2021, 188, 450-459.	3.6	4
11	Molecular to Macroscale Energy Absorption Mechanisms in Biological Body Armour Illuminated by Scanning X-ray Diffraction with In Situ Compression. <i>ACS Nano</i> , 2020, 14, 16535-16546.	7.3	8
12	Structural and functional characterization of the deep-sea thermophilic bacteriophage GVE2 tailspike protein. <i>International Journal of Biological Macromolecules</i> , 2020, 164, 4415-4422.	3.6	3
13	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.	0.4	3
14	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.	0.4	0
15	Crystal structure of human APPL BAR-PH heterodimer reveals a flexible dimeric BAR curve: implication in mutual regulation of endosomal targeting. <i>Biochemical Journal</i> , 2020, 477, 4769-4783.	1.7	0
16	Beyond a Ribosomal RNA Methyltransferase, the Wider Role of MraW in DNA Methylation, Motility and Colonization in <i>Escherichia coli</i> O157:H7. <i>Frontiers in Microbiology</i> , 2019, 10, 2520.	1.5	8
17	Quantification of Heterogeneous Degradation in Li-Ion Batteries. <i>Advanced Energy Materials</i> , 2019, 9, 1900674.	10.2	176
18	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.	0.4	1

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19	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.	0.4	1
20	Architectural roles of Cren7 in folding crenarchaeal chromatin filament. <i>Molecular Microbiology</i> , 2019, 111, 556-569.	1.2	11
21	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.	1.5	16
22	A micro-focusing and high-flux-throughput beamline design using a bending magnet for microscopic XAFS at the High Energy Photon Source. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 1835-1842.	1.0	3
23	Crystal and solution structures of human protein-disulfide isomerase-like protein of the testis (PDILT) provide insight into its chaperone activity. <i>Journal of Biological Chemistry</i> , 2018, 293, 1192-1202.	1.6	7
24	Electron density map evaluation functions for determining the quality of protein crystal structures. <i>Radiation Detection Technology and Methods</i> , 2018, 2, 1.	0.4	1
25	Crystal structures of multicopper oxidase CueO G304K mutant: structural basis of the increased laccase activity. <i>Scientific Reports</i> , 2018, 8, 14252.	1.6	15
26	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.	1.0	4
27	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.	0.4	1
28	Structure of tRNA-Modifying Enzyme TiaS and Motions of Its Substrate Binding Zinc Ribbon. <i>Journal of Molecular Biology</i> , 2018, 430, 4183-4194.	2.0	2
29	Structure of the full-length glucagon class B G-protein-coupled receptor. <i>Nature</i> , 2017, 546, 259-264.	13.7	179
30	Roles of Leu28 side chain intercalation in the interaction between Cren7 and DNA. <i>Biochemical Journal</i> , 2017, 474, 1727-1739.	1.7	5
31	A method to stabilize the incident X-ray energy for anomalous diffraction measurements. <i>Journal of Synchrotron Radiation</i> , 2017, 24, 781-786.	1.0	1
32	Structural analysis of Wss1 protein from <i>Saccharomyces cerevisiae</i> . <i>Scientific Reports</i> , 2017, 7, 8270.	1.6	10
33	HicAB toxin-antitoxin complex from <i>Escherichia coli</i> : expression and crystallization. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 505-510.	0.4	3
34	Crystal structure of the putative cytoplasmic protein STM0279 (Hcp2) from <i>Salmonella typhimurium</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 463-468.	0.4	5
35	Sequence-Dependent T:C Base Pair Opening in DNA Double Helix Bound by Cren7, a Chromatin Protein Conserved among Crenarchaea. <i>PLoS ONE</i> , 2016, 11, e0163361.	1.1	6
36	Structural Insights into the Methylation of C1402 in 16S rRNA by Methyltransferase RsmI. <i>PLoS ONE</i> , 2016, 11, e0163816.	1.1	8

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37	Structural insight into the E. coli HlgBA complex. <i>Biochemical and Biophysical Research Communications</i> , 2016, 478, 1521-1527.	1.0	17
38	Mechanism of the allosteric regulation of <i>Streptococcus mutans</i> 2-deoxycytidylate deaminase. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 883-891.	1.1	4
39	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. <i>Journal of Virology</i> , 2016, 90, 1158-1168.	1.5	10
40	Structural characterizations of phage antitoxin Dmd and its interactions with bacterial toxin RnIA. <i>Biochemical and Biophysical Research Communications</i> , 2016, 472, 592-597.	1.0	16
41	Influence of polychromaticity on particle structure determination in small-angle X-ray scattering. <i>Journal of Applied Crystallography</i> , 2015, 48, 1935-1942.	1.9	4
42	Full-length structure of the major autolysin LytA. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1373-1381.	2.5	22
43	Crystal structure of GnsA from <i>Escherichia coli</i> . <i>Biochemical and Biophysical Research Communications</i> , 2015, 462, 1-7.	1.0	5
44	Crystal structure of rhodopsin bound to arrestin by femtosecond X-ray laser. <i>Nature</i> , 2015, 523, 561-567.	13.7	683
45	Synthesis, structures and magnetic properties in 3d-electron-rich isostructural complexes based on chains with sole syn-anti carboxylate bridges. <i>Dalton Transactions</i> , 2015, 44, 7213-7222.	1.6	46
46	Protein crystallography from the perspective of technology developments. <i>Crystallography Reviews</i> , 2015, 21, 122-153.	0.4	33
47	Crystal structure of DszC from <i>Rhodococcus</i> sp. XP at 1.79 Å... <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1708-1720.	1.5	27
48	Structural and functional analysis show that the <i>Escherichia coli</i> uncharacterized protein Y _{jc} S is likely an alkylsulfatase. <i>Protein Science</i> , 2014, 23, 1442-1450.	3.1	8
49	Crystal structures and kinetic properties of enoyl-acyl carrier protein reductase I from <i>Candidatus Liberibacter asiaticus</i> . <i>Protein Science</i> , 2014, 23, 366-377.	3.1	5
50	Crystallization and preliminary X-ray study of TsiV3 from <i>Vibrio cholerae</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 335-338.	0.4	2
51	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
52	Purification, crystallization and preliminary crystallographic analysis of the 16S rRNA methyltransferase RsmI from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1256-1259.	0.4	4
53	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.	1.0	2
54	Structural and Functional Characterization of <i>Escherichia coli</i> Toxin-Antitoxin Complex DinJ-YafQ. <i>Journal of Biological Chemistry</i> , 2014, 289, 21191-21202.	1.6	29

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55	Conserved residues that modulate protein <i>trans</i> -splicing of <i>Npu</i> DnaE split intein. <i>Biochemical Journal</i> , 2014, 461, 247-255.	1.7	11
56	Structural insights into the mechanism of calmodulin binding to death receptors. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1604-1613.	2.5	6
57	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.	0.4	1
58	How water molecules affect the catalytic activity of hydrolases - A XANES study of the local structures of peptide deformylase. <i>Scientific Reports</i> , 2014, 4, 7453.	1.6	13
59	Solution Small Angle X-ray Scattering (SAXS) Studies of RecQ from <i>Deinococcus radiodurans</i> and Its Complexes with Junction DNA Substrates. <i>Journal of Biological Chemistry</i> , 2013, 288, 32414-32423.	1.6	4
60	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.	1.6	22
61	The crystal structure of human protein $\hat{\pm}1M$ reveals a chromophore-binding site and two putative protein-protein interfaces. <i>Biochemical and Biophysical Research Communications</i> , 2013, 439, 346-350.	1.0	3
62	Structural peculiarities of the (MHF1 ₄ MHF2) ₄ octamer provide a long DNA binding patch to anchor the MHF-FANCM complex to chromatin: A solution SAXS study. <i>FEBS Letters</i> , 2013, 587, 2912-2917.	1.3	3
63	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.	1.3	5
64	Structural insight into dGTP-dependent activation of tetrameric SAMHD1 deoxynucleoside triphosphate triphosphohydrolase. <i>Nature Communications</i> , 2013, 4, 2722.	5.8	102
65	Cloning, purification, crystallization and preliminary X-ray studies of human $\hat{\pm}1$ -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.	1.6	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.	1.0	13
68	The 1.6 Å 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.	3.6	2
69	Effect of metal ion on the structure and function of LiPDF: The study of the fine structure around the metal site using XANES. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 2010, 619, 115-118.	0.7	0
70	Structural insights into a dual-specificity histone demethylase ceKDM7A from <i>Caenorhabditis elegans</i> . <i>Cell Research</i> , 2010, 20, 886-898.	5.7	49
71	Exploring Intertrimer Cu ⁺ -Cu Interactions and Further Phosphorescent Properties of Aryl Trimer Copper(I) Pyrazolates via Substituent Changing and External Pressure. <i>Inorganic Chemistry</i> , 2010, 49, 1658-1666.	1.9	52
72	Local structure investigation of the active site of the imidazolonepropionase from <i>Bacillus subtilis</i> by XANES spectroscopy and ab initio calculations. <i>Journal of Synchrotron Radiation</i> , 2008, 15, 129-133.	1.0	9

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73	A large-scale, high-efficiency and low-cost platform for structural genomics studies. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 843-851.	2.5	15
74	Expression, purification, crystallization and preliminary X-ray characterization of the GRP carbohydrate-recognition domain from <i>Homo sapiens</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 474-476.	0.7	4
75	Studies of bromine modified single-walled carbon nanotubes using photoelectron spectroscopy and density-functional theory. <i>Radiation Physics and Chemistry</i> , 2006, 75, 1939-1942.	1.4	5
76	First-principles study of the pressure-induced phase transition in CaTiO_3 . <i>Solid State Communications</i> , 2005, 136, 416-420.	0.9	32
77	Texture and residual stress in $\text{FeMn/Ni}_{80}\text{Fe}_{20}$ multilayers. <i>Materials Letters</i> , 2005, 59, 2588-2592.	1.3	2
78	Crystallization and preliminary X-ray crystallographic analysis of agkicetin-C from <i>Deinagkistrodon acutus</i> venom. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 75-78.	0.7	2
79	Crystal Structure of Human Vacuolar Protein Sorting Protein 29 Reveals a Phosphodiesterase/Nuclease-like Fold and Two Protein-Protein Interaction Sites. <i>Journal of Biological Chemistry</i> , 2005, 280, 22962-22967.	1.6	56
80	Purification, partial characterization, crystallization and structural determination of AHP-LAAO, a novel L-amino-acid oxidase with cell apoptosis-inducing activity from <i>Agkistrodon halys pallas</i> venom. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 974-977.	2.5	52
81	Purification, characterization, crystallization and preliminary X-ray crystallographic analysis of two novel C-type lectin-like proteins: Aall-A and Aall-B from <i>Deinagkistrodon acutus</i> venom. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2035-2037.	2.5	3