Yuhui Dong

List of Publications by Year
in descending order

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81	1,971	471061 17	264894 42
papers	citations	h-index	g-index

83	83	83	3866
all docs	docs citations	times ranked	citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal structure of rhodopsin bound to arrestin by femtosecond X-ray laser. Nature, 2015, 523, 561-567.	13.7	683
2	Structure of the full-length glucagon class B G-protein-coupled receptor. Nature, 2017, 546, 259-264.	13.7	179
3	Quantification of Heterogeneous Degradation in Liâ€Ion Batteries. Advanced Energy Materials, 2019, 9, 1900674.	10.2	176
4	Structural insight into dGTP-dependent activation of tetrameric SAMHD1 deoxynucleoside triphosphate triphosphohydrolase. Nature Communications, 2013, 4, 2722.	5.8	102
5	Crystal Structure of Human Vacuolar Protein Sorting Protein 29 Reveals a Phosphodiesterase/Nuclease-like Fold and Two Protein-Protein Interaction Sites. Journal of Biological Chemistry, 2005, 280, 22962-22967.	1.6	56
6	Purification, partial characterization, crystallization and structural determination of AHP-LAAO, a novelL-amino-acid oxidase with cell apoptosis-inducing activity fromAgkistrodon halys pallasvenom. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 974-977.	2.5	52
7	Exploring Intertrimer CuÂ·Â·Â·Cu Interactions and Further Phosphorescent Properties of Aryl Trimer Copper(I) Pyrazolates via Substituent Changing and External Pressure. Inorganic Chemistry, 2010, 49, 1658-1666.	1.9	52
8	Structural insights into a dual-specificity histone demethylase ceKDM7A from Caenorhabditis elegans. Cell Research, 2010, 20, 886-898.	5.7	49
9	Synthesis, structures and magnetic properties in 3d-electron-rich isostructural complexes based on chains with sole synâ€“anti carboxylate bridges. Dalton Transactions, 2015, 44, 7213-7222.	1.6	46
10	Protein crystallography from the perspective of technology developments. Crystallography Reviews, 2015, 21, 122-153.	0.4	33
11	First-principles study of the pressure-induced phase transition in CaTiO3. Solid State Communications, 2005, 136, 416-420.	0.9	32
12	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. Dalton Transactions, 2011, 40, 6532.	1.6	30
13	Structural and Functional Characterization of Escherichia coli Toxin-Antitoxin Complex DinJ-YafQ. Journal of Biological Chemistry, 2014, 289, 21191-21202.	1.6	29
14	Crystal structure of DszC from <i>Rhodococcus</i> sp. XP at 1.79 Ã…. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1708-1720.	1.5	27
15	Structure of the type VI secretion phospholipase effector Tle1 provides insight into its hydrolysis and membrane targeting. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2175-2185.	2.5	26
16	Structural Basis for Interaction between Mycobacterium smegmatis Ms6564, a TetR Family Master Regulator, and Its Target DNA. Journal of Biological Chemistry, 2013, 288, 23687-23695.	1.6	22
17	Full-length structure of the major autolysin LytA. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1373-1381.	2.5	22
18	Structural insight into the E.Âcoli HigBA complex. Biochemical and Biophysical Research Communications, 2016, 478, 1521-1527.	1.0	17

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19	Structural characterizations of phage antitoxin Dmd and its interactions with bacterial toxin RnlA. Biochemical and Biophysical Research Communications, 2016, 472, 592-597.	1.0	16
20	Structural Insights Into the Transcriptional Regulation of HigBA Toxinâ€“Antitoxin System by Antitoxin HigA in Pseudomonas aeruginosa. Frontiers in Microbiology, 2019, 10, 3158.	1.5	16
21	A large-scale, high-efficiency and low-cost platform for structural genomics studies. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 843-851.	2.5	15
22	Crystal structures of multicopper oxidase CueO G304K mutant: structural basis of the increased laccase activity. Scientific Reports, 2018, 8, 14252.	1.6	15
23	A comparison of Remdesivir versus gold cluster in COVID-19 animal model: A better therapeutic outcome of gold cluster. Nano Today, 2022, 44, 101468.	6.2	15
24	Crystal structure and site-directed mutagenesis of a nitroalkane oxidase from Streptomyces ansochromogenes. Biochemical and Biophysical Research Communications, 2011, 405, 344-348.	1.0	13
25	How water molecules affect the catalytic activity of hydrolases - A XANES study of the local structures of peptide deformylase. Scientific Reports, 2014, 4, 7453.	1.6	13
26	Exascale image processing for next-generation beamlines in advanced light sources. Nature Reviews Physics, 2022, 4, 427-428.	11.9	12
27	Conserved residues that modulate protein <i>trans</i>-splicing of <i>Npu</i> DnaE split intein. Biochemical Journal, 2014, 461, 247-255.	1.7	11
28	Architectural roles of Cren7 in folding crenarchaeal chromatin filament. Molecular Microbiology, 2019, 111, 556-569.	1.2	11
29	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.	1.5	10
30	Structural analysis of Wss1 protein from saccharomyces cerevisiae. Scientific Reports, 2017, 7, 8270.	1.6	10
31	Local structure investigation of the active site of the imidazolonepropionase fromBacillus subtilisby XANES spectroscopy andab initiocalculations. Journal of Synchrotron Radiation, 2008, 15, 129-133.	1.0	9
32	Structural and functional analysis show that the <i>Escherichia coli</i> uncharacterized protein <scp>Y</scp>jc<scp>S</scp> is likely an alkylsulfatase. Protein Science, 2014, 23, 1442-1450.	3.1	8
33	Structural Insights into the Methylation of C1402 in 16S rRNA by Methyltransferase RsmI. PLoS ONE, 2016, 11, e0163816.	1.1	8
34	Beyond a Ribosomal RNA Methyltransferase, the Wider Role of MraW in DNA Methylation, Motility and Colonization in Escherichia coli O157:H7. Frontiers in Microbiology, 2019, 10, 2520.	1.5	8
35	Molecular to Macroscale Energy Absorption Mechanisms in Biological Body Armour Illuminated by Scanning X-ray Diffraction with In Situ Compression. ACS Nano, 2020, 14, 16535-16546.	7.3	8
36	The <i>PseudomonasÂaeruginosa PAAR2</i> cluster encodes a putative VRRâ€NUC domainâ€containing effector. FEBS Journal, 2021, 288, 5755-5767.	2.2	8

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37	Crystal and solution structures of human protein-disulfide isomerase-like protein of the testis (PDILT) provide insight into its chaperone activity. Journal of Biological Chemistry, 2018, 293, 1192-1202.	1.6	7
38	Structural insights into the mechanism of calmodulin binding to death receptors. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1604-1613.	2.5	6
39	Sequence-Dependent T:G Base Pair Opening in DNA Double Helix Bound by Cren7, a Chromatin Protein Conserved among Crenarchaea. PLoS ONE, 2016, 11, e0163361.	1.1	6
40	Studies of bromine modified single-walled carbon nanotubes using photoelectron spectroscopy and density-functional theory. Radiation Physics and Chemistry, 2006, 75, 1939-1942.	1.4	5
41	NMR structure of the Nâ€terminalâ€most HRDC1 domain of RecQ helicase from <i>Deinococcus radiodurans</i>. FEBS Letters, 2013, 587, 2635-2642.	1.3	5
42	Crystal structures and kinetic properties of enoylâ€acyl carrier protein reductase I from <i>Candidatus Liberibacter asiaticus</i>. Protein Science, 2014, 23, 366-377.	3.1	5
43	Crystal structure of GnsA from Escherichia coli. Biochemical and Biophysical Research Communications, 2015, 462, 1-7.	1.0	5
44	Roles of Leu28 side chain intercalation in the interaction between Cren7 and DNA. Biochemical Journal, 2017, 474, 1727-1739.	1.7	5
45	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.	0.4	5
46	Expression, purification, crystallization and preliminary X-ray characterization of the GRP carbohydrate-recognition domain fromHomo sapiens. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 474-476.	0.7	4
47	Solution Small Angle X-ray Scattering (SAXS) Studies of RecQ from Deinococcus radiodurans and Its Complexes with Junction DNA Substrates. Journal of Biological Chemistry, 2013, 288, 32414-32423.	1.6	4
48	Purification, crystallization and preliminary crystallographic analysis of the 16S rRNA methyltransferase RsmI from<i>Escherichia coli</i>. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1256-1259.	0.4	4
49	Influence of polychromaticity on particle structure determination in small-angle X-ray scattering. Journal of Applied Crystallography, 2015, 48, 1935-1942.	1.9	4
50	Mechanism of the allosteric regulation of<i>Streptococcus mutans</i>2â€²-deoxycytidylate deaminase. Acta Crystallographica Section D: Structural Biology, 2016, 72, 883-891.	1.1	4
51	Structural and biochemical characterization of the yeast HD domain containing protein YGK1 reveals a metal-dependent nucleoside 5Ê¹-monophosphatase. Biochemical and Biophysical Research Communications, 2018, 501, 674-681.	1.0	4
52	Structure and SAXS studies unveiled a novel inhibition mechanism of the Pseudomonas aeruginosa T6SS TseT-TsiT complex. International Journal of Biological Macromolecules, 2021, 188, 450-459.	3.6	4
53	A Freestanding Chitin-Derived Hierarchical Nanocomposite for Developing Electrodes in Future Supercapacitor Industry. Polymers, 2022, 14, 195.	2.0	4
54	Purification, characterization, crystallization and preliminary X-ray crystallographic analysis of two novel C-type lectin-like proteins: Aall-A and Aall-B fromDeinagkistrodon acutusvenom. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2035-2037.	2.5	3

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55	The crystal structure of human protein Î±1M reveals a chromophore-binding site and two putative proteinâ€“protein interfaces. Biochemical and Biophysical Research Communications, 2013, 439, 346-350.	1.0	3
56	Structural peculiarities of the (MHF1â€“MHF2)₄ octamer provide a long DNA binding patch to anchor the MHFâ€“FANCM complex to chromatin: A solution SAXS study. FEBS Letters, 2013, 587, 2912-2917.	1.3	3
57	HicAB toxinâ€“antitoxin complex fromEscherichia coli: expression and crystallization. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 505-510.	0.4	3
58	Structural and functional characterization of the deep-sea thermophilic bacteriophage GVE2 tailspike protein. International Journal of Biological Macromolecules, 2020, 164, 4415-4422.	3.6	3
59	Characterization of the<i>Pseudomonas aeruginosa</i>T6SS PldB immunity proteins PA5086, PA5087 and PA5088 explains a novel stockpiling mechanism. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 222-227.	0.4	3
60	A reference-based multi-lattice indexing method integrating prior information correction and iterative refinement in protein crystallography. Acta Crystallographica Section A: Foundations and Advances, 2021, 77, 277-288.	0.0	3
61	A micro-focusing and high-flux-throughput beamline design using a bending magnet for microscopic XAFS at the High Energy Photon Source. Journal of Synchrotron Radiation, 2019, 26, 1835-1842.	1.0	3
62	<i>In situ</i> determination of the extreme damage resistance behavior in stomatopod dactyl club. Journal of Synchrotron Radiation, 2022, 29, 775-786.	1.0	3
63	Texture and residual stress in FeMn/Ni80Fe20 multilayers. Materials Letters, 2005, 59, 2588-2592.	1.3	2
64	Crystallization and preliminary X-ray crystallographic analysis of agkicetin-C fromDeinagkistrodon acutusvenom. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 75-78.	0.7	2
65	The 1.6Ã… resolution structure of activated D138L mutant of catabolite gene activator protein with two cAMP bound in each monomer. International Journal of Biological Macromolecules, 2011, 48, 459-465.	3.6	2
66	Crystallization and preliminary X-ray study of TsiV3 from<i>Vibrio cholerae</i>. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 335-338.	0.4	2
67	High-resolution crystal structure reveals a HEPN domain at the C-terminal region of S. cerevisiae RNA endonuclease Swt1. Biochemical and Biophysical Research Communications, 2014, 453, 826-832.	1.0	2
68	Structure of tRNA-Modifying Enzyme TiaS and Motions of Its Substrate Binding Zinc Ribbon. Journal of Molecular Biology, 2018, 430, 4183-4194.	2.0	2
69	NUDIM: A non-uniform fast Fourier transform based dual-space constraint iterative reconstruction method in biological electron tomography. Journal of Structural Biology, 2021, 213, 107770.	1.3	2
70	Wave-optics simulation software for synchrotron radiation from 4th generation storage rings based on a coherent modes model. Optics Express, 2022, 30, 7625.	1.7	2
71	Cloning, purification, crystallization and preliminary X-ray studies of human Î±1-microglobulin. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 692-694.	0.7	1
72	Cloning, purification, crystallization and preliminary X-ray studies of the putative type VI secretion immunity protein Tli5 (PA5088) fromPseudomonas aeruginosa. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 903-905.	0.4	1

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73	A method to stabilize the incident X-ray energy for anomalous diffraction measurements. Journal of Synchrotron Radiation, 2017, 24, 781-786.	1.0	1
74	Electron density map evaluation functions for determining the quality of protein crystal structures. Radiation Detection Technology and Methods, 2018, 2, 1.	0.4	1
75	An iterative refinement method combining detector geometry optimization and diffraction model refinement in serial femtosecond crystallography. Radiation Detection Technology and Methods, 2018, 2, 1.	0.4	1
76	A noise and artifact suppression using resampling (NASR) method to facilitate de novo protein structure determination. Radiation Detection Technology and Methods, 2019, 3, 1.	0.4	1
77	Crystal structure of the type VI immunity protein Tdi1 (Atu4351) from <i>Agrobacterium tumefaciens</i>. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 153-158.	0.4	1
78	A wave optics model for the effect of partial coherence on coherent diffractive imaging. Journal of Synchrotron Radiation, 2021, 28, 499-504.	1.0	1
79	Effect of metal ion on the structure and function of LiPDF: The study of the fine structure around the metal site using XANES. Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment, 2010, 619, 115-118.	0.7	0
80	Crystal structure of the nucleoid-associated protein Fis (PA4853) from<i>Pseudomonas aeruginosa</i>. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 209-215.	0.4	0
81	Crystal structure of human APPL BAR-PH heterodimer reveals a flexible dimeric BAR curve: implication in mutual regulation of endosomal targeting. Biochemical Journal, 2020, 477, 4769-4783.	1.7	0