

Xiao-Dong Su

List of Publications by Year in descending order

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91
papers

3,949
citations

201674

27
h-index

128289

60
g-index

95
all docs

95
docs citations

95
times ranked

6587
citing authors

#	ARTICLE	IF	CITATIONS
1	Pathway-based classification of glioblastoma uncovers a mitochondrial subtype with therapeutic vulnerabilities. <i>Nature Cancer</i> , 2021, 2, 141-156.	13.2	163
2	Revealing atomic-scale molecular diffusion of a plant-transcription factor WRKY domain protein along DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	21
3	Protein crystallization benefits from the rough well surface of a 48-well polystyrene microplate. <i>Journal of Crystal Growth</i> , 2020, 532, 125425.	1.5	6
4	Crystal structures of N-terminal WRKY transcription factors and DNA complexes. <i>Protein and Cell</i> , 2020, 11, 208-213.	11.0	25
5	Mn ²⁺ Directly Activates cGAS and Structural Analysis Suggests Mn ²⁺ Induces a Noncanonical Catalytic Synthesis of 2'3'-cGAMP. <i>Cell Reports</i> , 2020, 32, 108053.	6.4	135
6	A map of tumor-host interactions in glioma at single-cell resolution. <i>GigaScience</i> , 2020, 9, .	6.4	32
7	Surveying brain tumor heterogeneity by single-cell RNA-sequencing of multi-sector biopsies. <i>National Science Review</i> , 2020, 7, 1306-1318.	9.5	84
8	Parkinson's disease associated mutation E46K of α -synuclein triggers the formation of a distinct fibril structure. <i>Nature Communications</i> , 2020, 11, 2643.	12.8	76
9	Cryo-EM structure of full-length α -synuclein amyloid fibril with Parkinson's disease familial A53T mutation. <i>Cell Research</i> , 2020, 30, 360-362.	12.0	94
10	Mutation Profile of Resected EGFR-Mutated Lung Adenocarcinoma by Next-Generation Sequencing. <i>Oncologist</i> , 2019, 24, 1368-1374.	3.7	15
11	HeLa-CCL2 cell heterogeneity studied by single-cell DNA and RNA sequencing. <i>PLoS ONE</i> , 2019, 14, e0225466.	2.5	17
12	Novel Mechanism for Cyclic Dinucleotide Degradation Revealed by Structural Studies of Vibrio Phosphodiesterase V-cGAP3. <i>Journal of Molecular Biology</i> , 2018, 430, 5080-5093.	4.2	13
13	Loss of MED12 Induces Tumor Dormancy in Human Epithelial Ovarian Cancer via Downregulation of EGFR. <i>Cancer Research</i> , 2018, 78, 3532-3543.	0.9	23
14	Single Mutations Reshape the Structural Correlation Network of the DMXAA-Human STING Complex. <i>Journal of Physical Chemistry B</i> , 2017, 121, 2073-2082.	2.6	14
15	Crystal Structure of Tetrameric Arabidopsis MYC2 Reveals the Mechanism of Enhanced Interaction with DNA. <i>Cell Reports</i> , 2017, 19, 1334-1342.	6.4	49
16	Effect of body mass index on survival of patients with stage I non-small cell lung cancer. <i>Chinese Journal of Cancer</i> , 2017, 36, 7.	4.9	15
17	Nonspecific DNA Binding of cGAS N Terminus Promotes cGAS Activation. <i>Journal of Immunology</i> , 2017, 198, 3627-3636.	0.8	67
18	Detection of Cyclic Dinucleotides by STING. <i>Methods in Molecular Biology</i> , 2017, 1657, 59-69.	0.9	7

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19	Polo-like kinase 1 (PLK1)-dependent phosphorylation of methylenetetrahydrofolate reductase (MTHFR) regulates replication via histone methylation. <i>Cell Cycle</i> , 2017, 16, 1933-1942.	2.6	14
20	T7 RNA polymerase translocation is facilitated by a helix opening on the fingers domain that may also prevent backtracking. <i>Nucleic Acids Research</i> , 2017, 45, 7909-7921.	14.5	25
21	The effects of cytosine methylation on general transcription factors. <i>Scientific Reports</i> , 2016, 6, 29119.	3.3	38
22	Rat and human STINGs profile similarly towards anticancer/antiviral compounds. <i>Scientific Reports</i> , 2015, 5, 18035.	3.3	26
23	Enhanced expression and phosphorylation of the MET oncoprotein by glioma-specific PTPRZ1-MET fusions. <i>FEBS Letters</i> , 2015, 589, 1437-1443.	2.8	20
24	Activation and Regulation of Caspase-6 and Its Role in Neurodegenerative Diseases. <i>Annual Review of Pharmacology and Toxicology</i> , 2015, 55, 553-572.	9.4	75
25	Prognostic impact of pattern-based grading system by the new IASLC/ATS/ERS classification in Asian patients with stage I lung adenocarcinoma. <i>Lung Cancer</i> , 2015, 90, 604-609.	2.0	30
26	Protein crystallography from the perspective of technology developments. <i>Crystallography Reviews</i> , 2015, 21, 122-153.	1.5	33
27	The regulatory mechanism of the caspase 6 pro-domain revealed by crystal structure and biochemical assays. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 58-67.	2.5	12
28	High-accuracy mapping of protein binding stability on nucleosomal DNA using a single-molecule method. <i>Journal of Molecular Cell Biology</i> , 2014, 6, 438-440.	3.3	3
29	Structural and functional characterization of a novel β -glucuronidase from cariogenic pathogen <i>Streptococcus mutans</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 695-700.	2.6	2
30	RNA-seq of 272 gliomas revealed a novel, recurrent PTPRZ1-MET fusion transcript in secondary glioblastomas. <i>Genome Research</i> , 2014, 24, 1765-1773.	5.5	316
31	Structural genomics studies of human caries pathogen <i>Streptococcus mutans</i> . <i>Journal of Structural and Functional Genomics</i> , 2014, 15, 91-99.	1.2	4
32	Reproducible copy number variation patterns among single circulating tumor cells of lung cancer patients. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 21083-21088.	7.1	396
33	Probing Allostery Through DNA. <i>Science</i> , 2013, 339, 816-819.	12.6	243
34	Intermolecular recognition revealed by the complex structure of human CLOCK-BMAL1 basic helix-loop-helix domains with E-box DNA. <i>Cell Research</i> , 2013, 23, 213-224.	12.0	84
35	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
36	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

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37	Structure of the bifunctional methyltransferase YcbY (RlmKL) that adds the m ⁷ G2069 and m ² G2445 modifications in <i>Escherichia coli</i> 23S rRNA. <i>Nucleic Acids Research</i> , 2012, 40, 5138-5148.	14.5	12
38	Inhibitory Mechanism of Caspase-6 Phosphorylation Revealed by Crystal Structures, Molecular Dynamics Simulations, and Biochemical Assays. <i>Journal of Biological Chemistry</i> , 2012, 287, 15371-15379.	3.4	28
39	Crystal structure of type VI effector Tse1 from <i>Pseudomonas aeruginosa</i> . <i>FEBS Letters</i> , 2012, 586, 3193-3199.	2.8	23
40	The structural basis for the sensing and binding of cyclic di-GMP by STING. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 728-730.	8.2	178
41	Ellman's reagent in promoting crystallization and structure determination of Anabaena CcbP. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1409-1414.	0.7	1
42	The crystal structure of the MPN domain from the COP9 signalosome subunit CSN6. <i>FEBS Letters</i> , 2012, 586, 1147-1153.	2.8	20
43	Structural basis for the autoinhibition of the C-terminal kinase domain of human RSK1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 680-685.	2.5	11
44	Crystal Structures of Cobalamin-Independent Methionine Synthase (MetE) from <i>Streptococcus mutans</i> : A Dynamic Zinc-Inversion Model. <i>Journal of Molecular Biology</i> , 2011, 412, 688-697.	4.2	14
45	Get Phases from Arsenic Anomalous Scattering: de novo SAD Phasing of Two Protein Structures Crystallized in Cacodylate Buffer. <i>PLoS ONE</i> , 2011, 6, e24227.	2.5	23
46	Davydov's "Pang model: An improved Davydov protein soliton theory. <i>Physics of Life Reviews</i> , 2011, 8, 300-301.	2.8	2
47	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
48	Structures of Anabaena Calcium-binding Protein CcbP. <i>Journal of Biological Chemistry</i> , 2011, 286, 12381-12388.	3.4	22
49	The structure of the hypothetical protein smu.1377c from <i>Streptococcus mutans</i> suggests a role in tRNA modification. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 771-775.	0.7	4
50	Purification, crystallization and preliminary X-ray crystallographic analysis of 23S RNA m ² G2445 methyltransferase RlmL from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1484-1486.	0.7	2
51	From signal perception to signal transduction: ligand-induced dimeric switch of DctB sensory domain in solution. <i>Molecular Microbiology</i> , 2010, 75, 1484-1494.	2.5	19
52	Crystal structures of human caspase 6 reveal a new mechanism for intramolecular cleavage self-activation. <i>EMBO Reports</i> , 2010, 11, 841-847.	4.5	86
53	Alternatively Spliced Caspase-6B Isoform Inhibits the Activation of Caspase-6A. <i>Journal of Biological Chemistry</i> , 2010, 285, 31974-31984.	3.4	18
54	Bioinformatics and Structural Characterization of a Hypothetical Protein from <i>Streptococcus mutans</i> : Implication of Antibiotic Resistance. <i>PLoS ONE</i> , 2009, 4, e7245.	2.5	16

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55	Structure of a fatty acid-binding protein from <i>Bacillus subtilis</i> determined by sulfur-SAD phasing using in-house chromium radiation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 440-448.	2.5	16
56	Crystallization and preliminary X-ray analysis of three dUTPases from Gram-positive bacteria. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 339-342.	0.7	2
57	Open/closed conformational change revealed by the crystal structures of 3-keto-l-gulonate 6-phosphate decarboxylase from <i>Streptococcus mutans</i> . <i>Biochemical and Biophysical Research Communications</i> , 2009, 381, 429-433.	2.1	1
58	Tailoring a low-molecular weight protein tyrosine phosphatase into an efficient reporting protein. <i>Biochemical and Biophysical Research Communications</i> , 2009, 382, 735-739.	2.1	2
59	Solid-liquid interface method (SLIM): A new crystallization method for proteins. <i>Biochemical and Biophysical Research Communications</i> , 2009, 386, 634-638.	2.1	3
60	Crystal Structures of Phosphotransferase System Enzymes PtxB (IIBAsc) and PtxA (IIAAsc) from <i>Streptococcus mutans</i> . <i>Journal of Molecular Biology</i> , 2009, 386, 465-475.	4.2	10
61	CLIC2-RyR1 Interaction and Structural Characterization by Cryo-electron Microscopy. <i>Journal of Molecular Biology</i> , 2009, 387, 320-334.	4.2	44
62	The crystal structure of human chloride intracellular channel protein 2: A disulfide bond with functional implications. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 509-513.	2.6	18
63	Crystal structure of <i>B. subtilis</i> YjcG characterizing the YjcG-like group of 2H phosphoesterase superfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 1071-1076.	2.6	4
64	Crystal structure of an alkaline serine protease from <i>Nesterenkonia</i> sp. defines a novel family of secreted bacterial proteases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 1072-1075.	2.6	3
65	Acceptor substrate binding revealed by crystal structure of human glucosamine-6-phosphate <i>N</i> -acetyltransferase 1. <i>FEBS Letters</i> , 2008, 582, 2973-2978.	2.8	30
66	Crystal Structures of <i>Streptococcus mutans</i> 2-Deoxycytidylate Deaminase and Its Complex with Substrate Analog and Allosteric Regulator dCTP-Mg ²⁺ . <i>Journal of Molecular Biology</i> , 2008, 377, 220-231.	4.2	34
67	Ring-Opening Mechanism Revealed by Crystal Structures of NagB and Its ES Intermediate Complex. <i>Journal of Molecular Biology</i> , 2008, 379, 73-81.	4.2	12
68	C4-Dicarboxylates Sensing Mechanism Revealed by the Crystal Structures of DctB Sensor Domain. <i>Journal of Molecular Biology</i> , 2008, 383, 49-61.	4.2	75
69	5,5-Dithio-bis(2-nitrobenzoic acid) modification of cysteine improves the crystal quality of human chloride intracellular channel protein 2. <i>Biochemical and Biophysical Research Communications</i> , 2008, 368, 919-922.	2.1	5
70	DNA binding mechanism revealed by high resolution crystal structure of <i>Arabidopsis thaliana</i> WRKY1 protein. <i>Nucleic Acids Research</i> , 2007, 35, 1145-1154.	14.5	131
71	An automated image-collection system for crystallization experiments using SBS standard microplates. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 119-125.	2.5	9
72	Protein preparation and preliminary X-ray crystallographic analysis of a putative glucosamine 6-phosphate deaminase from <i>Streptococcus mutans</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 809-811.	0.7	2

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73	Protein preparation, crystallization and preliminary X-ray analysis of the C-terminal domain of human RSK1 serine/threonine protein kinase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 1026-1028.	0.7	1
74	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
75	Preparation, crystallization and preliminary X-ray analysis of the methionine synthase (MetE) from <i>Streptococcus mutans</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 984-985.	0.7	1
76	Purification, crystallization and preliminary X-ray analysis of the glucosamine-6-phosphate N-acetyltransferase from human liver. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1097-1099.	0.7	3
77	Purification and preliminary X-ray crystallographic analysis of the ligand-binding domain of <i>Sinorhizobium meliloti</i> DctB. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 839-841.	2.3	8
78	Protein preparation, crystallization and preliminary X-ray analysis of imidazolonepropionase from <i>Bacillus subtilis</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 153-156.	2.3	4
79	A Catalytic Mechanism Revealed by the Crystal Structures of the Imidazolonepropionase from <i>Bacillus subtilis</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 36929-36936.	3.4	18
80	Crystallization and preliminary X-ray analysis of the C-terminal WRKY domain of <i>Arabidopsis thaliana</i> WRKY1 transcription factor. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2005, 1750, 14-16.	2.3	7
81	Preparation, crystallization and preliminary X-ray analysis of YjcG protein from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 496-498.	0.7	4
82	The crystal structure of human adenylate kinase 6: An adenylate kinase localized to the cell nucleus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 303-308.	7.1	88
83	Protein preparation, crystallization and preliminary X-ray analysis of human adrenal gland protein AD-004. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1292-1294.	2.5	9
84	Structural and Mutational Studies of the Carboxylate Cluster in Iron-Free Ribonucleotide Reductase R2. <i>Biochemistry</i> , 2004, 43, 7966-7972.	2.5	18
85	Crystallization and preliminary X-ray analysis of an alkaline serine protease from <i>Nesterenkonia</i> sp.. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 529-531.	2.5	10
86	Parallel cloning, expression, purification and crystallization of human proteins for structural genomics. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 2102-2108.	2.5	40
87	Insights into the Functional Architecture of the Catalytic Center of a Maize β -Glucosidase Zm-p60.1. <i>Plant Physiology</i> , 2001, 127, 973-985.	4.8	50
88	Purification, crystallization and preliminary X-ray analysis of a maize cytokinin glucoside specific β -glucosidase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 140-142.	2.5	6
89	Crystal structure of reduced protein R2 of ribonucleotide reductase: the structural basis for oxygen activation at a dinuclear iron site. <i>Structure</i> , 1996, 4, 1053-1064.	3.3	277
90	The crystal structure of a low-molecular-weight phosphotyrosine protein phosphatase. <i>Nature</i> , 1994, 370, 575-578.	27.8	224

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91	Crystallisation of a low molecular weight phosphotyrosine protein phosphatase from bovine liver. FEBS Letters, 1994, 343, 107-108.	2.8	3