

Rong Xiao

List of Publications by Year in descending order

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106
papers

5,591
citations

101543

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times ranked

8527
citing authors

#	ARTICLE	IF	CITATIONS
1	Biofunctionalized "Kiwifruit" Assembly of Oxidoreductases in Mesoporous ZnO/Carbon Nanoparticles for Efficient Asymmetric Catalysis. <i>Advanced Materials</i> , 2018, 30, 1705443.	21.0	14
2	Backbone and Ile- α 1, Leu, Val methyl 1H, 15N, and 13C, chemical shift assignments for <i>Rhizopus chinensis</i> lipase. <i>Biomolecular NMR Assignments</i> , 2018, 12, 63-68.	0.8	3
3	X-ray crystal structure of the N-terminal region of <i>Moloney murine leukemia virus</i> integrase and its implications for viral DNA recognition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 647-656.	2.6	9
4	Principles for designing proteins with cavities formed by curved β^2 sheets. <i>Science</i> , 2017, 355, 201-206.	12.6	117
5	Sortase A-mediated crosslinked short-chain dehydrogenases/reductases as novel biocatalysts with improved thermostability and catalytic efficiency. <i>Scientific Reports</i> , 2017, 7, 3081.	3.3	10
6	In situ expression of (R)-carbonyl reductase rebalancing an asymmetric pathway improves stereoconversion efficiency of racemic mixture to (S)-phenyl-1,2-ethanediol in <i>Candida parapsilosis</i> CCTCC M203011. <i>Microbial Cell Factories</i> , 2016, 15, 143.	4.0	4
7	Introduction of a polar core into the de novo designed protein <i>Top7</i> . <i>Protein Science</i> , 2016, 25, 1299-1307.	7.6	7
8	Efficient production of 2H, 13C, 15N-enriched industrial enzyme <i>Rhizopus chinensis</i> lipase with native disulfide bonds. <i>Microbial Cell Factories</i> , 2016, 15, 123.	4.0	8
9	A community resource of experimental data for <i>NMR</i> / <i>X-ray</i> crystal structure pairs. <i>Protein Science</i> , 2016, 25, 30-45.	7.6	24
10	Lipases from the genus <i>Rhizopus</i> : Characteristics, expression, protein engineering and application. <i>Progress in Lipid Research</i> , 2016, 64, 57-68.	11.6	48
11	Disorder prediction-based construct optimization improves activity and catalytic efficiency of <i>Bacillus naganensis</i> pullulanase. <i>Scientific Reports</i> , 2016, 6, 24574.	3.3	20
12	Structural/Functional Properties of Human NFU1, an Intermediate [4Fe-4S] Carrier in Human Mitochondrial Iron-Sulfur Cluster Biogenesis. <i>Structure</i> , 2016, 24, 2080-2091.	3.3	45
13	Codon influence on protein expression in <i>E. coli</i> correlates with mRNA levels. <i>Nature</i> , 2016, 529, 358-363.	27.8	350
14	The detection and subsequent volume optimization of biological nanocrystals. <i>Structural Dynamics</i> , 2015, 2, 041710.	2.3	5
15	Precise assembly of complex beta sheet topologies from de novo designed building blocks. <i>ELife</i> , 2015, 4, .	6.0	15
16	A hybrid NMR/SAXS-based approach for discriminating oligomeric protein interfaces using <i>Rosetta</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 309-317.	2.6	33
17	The RAS-Binding Domain of Human BRAF Protein Serine/Threonine Kinase Exhibits Allosteric Conformational Changes upon Binding HRAS. <i>Structure</i> , 2015, 23, 1382-1393.	3.3	31
18	The second round of Critical Assessment of Automated Structure Determination of Proteins by NMR: CASD-NMR-2013. <i>Journal of Biomolecular NMR</i> , 2015, 62, 413-424.	2.8	27

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19	Redesigning alcohol dehydrogenases/reductases for more efficient biosynthesis of enantiopure isomers. <i>Biotechnology Advances</i> , 2015, 33, 1671-1684.	11.7	47
20	A General Computational Approach for Repeat Protein Design. <i>Journal of Molecular Biology</i> , 2015, 427, 563-575.	4.2	72
21	Polypeptide backbone, C α 2 and methyl group resonance assignments of the 24 kDa plectin repeat domain 6 from human protein plectin. <i>Biomolecular NMR Assignments</i> , 2015, 9, 135-138.	0.8	0
22	Structural and Functional Characterization of DUF1471 Domains of Salmonella Proteins SrfN, YdgH/SssB, and YahO. <i>PLoS ONE</i> , 2014, 9, e101787.	2.5	13
23	Mitochondrial COQ9 is a lipid-binding protein that associates with COQ7 to enable coenzyme Q biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4697-705.	7.1	113
24	Spatially Selective Heteronuclear Multiple-Quantum Coherence Spectroscopy for Biomolecular NMR Studies. <i>ChemPhysChem</i> , 2014, 15, 1872-1879.	2.1	6
25	Solution structure of the free Z α domain of human DLM-1 (ZBP1/DAI), a Z-DNA binding domain. <i>Journal of Biomolecular NMR</i> , 2014, 60, 189-195.	2.8	4
26	Allosteric regulation and substrate activation in cytosolic nucleotidase <i>YnfM</i> from <i>Legionella pneumophila</i> . <i>FEBS Journal</i> , 2014, 281, 1613-1628.	4.7	29
27	Conversion of a <i>Rhizopus chinensis</i> lipase into an esterase by lid swapping. <i>Journal of Lipid Research</i> , 2014, 55, 1044-1051.	4.2	32
28	Crystallization and preliminary X-ray diffraction analysis of (R)-carbonyl reductase from <i>Candida parapsilosis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 800-802.	0.8	2
29	Exploration of Alternate Catalytic Mechanisms and Optimization Strategies for Retroaldolase Design. <i>Journal of Molecular Biology</i> , 2014, 426, 256-271.	4.2	33
30	Structure of the DNA-Binding and RNA-Polymerase-Binding Region of Transcription Antitermination Factor λ Q. <i>Structure</i> , 2014, 22, 488-495.	3.3	14
31	Solution NMR structures of homeodomains from human proteins ALX4, ZHX1, and CASP8AP2 contribute to the structural coverage of the Human Cancer Protein Interaction Network. <i>Journal of Structural and Functional Genomics</i> , 2014, 15, 201-207.	1.2	1
32	Solution NMR structures of immunoglobulin-like domains 7 and 12 from obscurin-like protein 1 contribute to the structural coverage of the human cancer protein interaction network. <i>Journal of Structural and Functional Genomics</i> , 2014, 15, 209-214.	1.2	0
33	Solution NMR structure of the helicase associated domain BVU_0683(627-691) from <i>Bacteroides vulgatus</i> provides first structural coverage for protein domain family PF03457 and indicates domain binding to DNA. <i>Journal of Structural and Functional Genomics</i> , 2013, 14, 19-24.	1.2	0
34	A Bidirectional System for the Dynamic Small Molecule Control of Intracellular Fusion Proteins. <i>ACS Chemical Biology</i> , 2013, 8, 2293-2300.	3.4	38
35	Solution NMR structure of CD1104B from pathogenic <i>Clostridium difficile</i> reveals a distinct α -helical architecture and provides first structural representative of protein domain family PF14203. <i>Journal of Structural and Functional Genomics</i> , 2013, 14, 155-160.	1.2	2
36	Crystal Structures of Malonyl-Coenzyme A Decarboxylase Provide Insights into Its Catalytic Mechanism and Disease-Causing Mutations. <i>Structure</i> , 2013, 21, 1182-1192.	3.3	17

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37	Two Fe-S clusters catalyze sulfur insertion by radical-SAM methylthiotransferases. <i>Nature Chemical Biology</i> , 2013, 9, 333-338.	8.0	113
38	Solution NMR structures provide first structural coverage of the large protein domain family PF08369 and complementary structural coverage of dark operative protochlorophyllide oxidoreductase complexes. <i>Journal of Structural and Functional Genomics</i> , 2013, 14, 119-126.	1.2	0
39	High-Level Expression of <i>Bacillus naganoensis</i> Pullulanase from Recombinant <i>Escherichia coli</i> with Auto-Induction: Effect of lac Operator. <i>PLoS ONE</i> , 2013, 8, e78416.	2.5	38
40	Efficient (R)-Phenylethanol Production with Enantioselectivity-Altered (S)-Carbonyl Reductase II and NADPH Regeneration. <i>PLoS ONE</i> , 2013, 8, e83586.	2.5	14
41	Determination of solution structures of proteins up to 40 kDa using CS-Rosetta with sparse NMR data from deuterated samples. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 10873-10878.	7.1	188
42	Principles for designing ideal protein structures. <i>Nature</i> , 2012, 491, 222-227.	27.8	522
43	Computational Design of Catalytic Dyads and Oxyanion Holes for Ester Hydrolysis. <i>Journal of the American Chemical Society</i> , 2012, 134, 16197-16206.	13.7	138
44	Solution NMR structures reveal unique homodimer formation by a winged helix-turn-helix motif and provide first structures for protein domain family PF10771. <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 1-7.	1.2	2
45	Solution NMR structures reveal a distinct architecture and provide first structures for protein domain family PF04536. <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 9-14.	1.2	7
46	NMR Structure of Lipoprotein YxeF from <i>Bacillus subtilis</i> Reveals a Calycin Fold and Distant Homology with the Lipocalin Blc from <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2012, 7, e37404.	2.5	6
47	Coexpression of a carbonyl reductase and glucose 6-phosphate dehydrogenase in <i>Pichia pastoris</i> improves the production of (S)-1-phenyl-1,2-ethanediol. <i>Biocatalysis and Biotransformation</i> , 2011, 29, 172-178.	2.0	13
48	Solution Structure of 4-Phosphopantetheine - GmACP3 from <i>Geobacter metallireducens</i> : A Specialized Acyl Carrier Protein with Atypical Structural Features and a Putative Role in Lipopolysaccharide Biosynthesis. <i>Biochemistry</i> , 2011, 50, 1442-1453.	2.5	7
49	Preparation of Protein Samples for NMR Structure, Function, and Small-Molecule Screening Studies. <i>Methods in Enzymology</i> , 2011, 493, 21-60.	1.0	89
50	Novel anti-Prelog stereospecific carbonyl reductases from <i>Candida parapsilosis</i> for asymmetric reduction of prochiral ketones. <i>Organic and Biomolecular Chemistry</i> , 2011, 9, 4070.	2.8	74
51	UNC119 is required for G protein trafficking in sensory neurons. <i>Nature Neuroscience</i> , 2011, 14, 874-880.	14.8	154
52	Solution NMR and X-ray crystal structures of membrane-associated Lipoprotein-17 domain reveal a novel fold. <i>Journal of Structural and Functional Genomics</i> , 2011, 12, 27-32.	1.2	2
53	Solution NMR structure of MED25(391-543) comprising the activator-interacting domain (ACID) of human mediator subunit 25. <i>Journal of Structural and Functional Genomics</i> , 2011, 12, 159-166.	1.2	18
54	Large-scale experimental studies show unexpected amino acid effects on protein expression and solubility in vivo in <i>E. coli</i> . <i>Microbial Informatics and Experimentation</i> , 2011, 1, 6.	7.6	30

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55	A large conformational change in the putative ATP pyrophosphatase PF0828 induced by ATP binding. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1323-1327.	0.7	8
56	Solution NMR structure of the plasmid-encoded fimbriae regulatory protein PefI from <i>Salmonella enterica</i> serovar Typhimurium. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 335-339.	2.6	2
57	Structures of domains I and IV from YbbR are representative of a widely distributed protein family. <i>Protein Science</i> , 2011, 20, 396-405.	7.6	16
58	Novel C-terminal Motif within Sec7 Domain of Guanine Nucleotide Exchange Factors Regulates ADP-ribosylation Factor (ARF) Binding and Activation*. <i>Journal of Biological Chemistry</i> , 2011, 286, 36898-36906.	3.4	20
59	Dimer Interface of the Effector Domain of Non-structural Protein 1 from Influenza A Virus. <i>Journal of Biological Chemistry</i> , 2011, 286, 26050-26060.	3.4	58
60	A microscale protein NMR sample screening pipeline. <i>Journal of Biomolecular NMR</i> , 2010, 46, 11-22.	2.8	106
61	Structures of bacterial biosynthetic arginine decarboxylases. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1562-1566.	0.7	11
62	Solution NMR structures of proteins VPA0419 from <i>Vibrio parahaemolyticus</i> and yiiS from <i>Shigella flexneri</i> provide structural coverage for protein domain family PFAM 04175. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 779-784.	2.6	0
63	NMR structure of F-actin-binding domain of Arg/Abl2 from <i>Homo sapiens</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1326-1330.	2.6	7
64	Solution NMR structure of the ARID domain of human AT-rich interactive domain-containing protein 3A: A human cancer protein interaction network target. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2170-2175.	2.6	16
65	Solution NMR structure of Lin0431 protein from <i>Listeria innocua</i> reveals high structural similarity with domain II of bacterial transcription antitermination protein NusG. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2563-2568.	2.6	2
66	Solution structure and function of YndB, an AHSA1 protein from <i>Bacillus subtilis</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3328-3340.	2.6	13
67	Structural Basis of O6-Alkylguanine Recognition by a Bacterial Alkyltransferase-like DNA Repair Protein. <i>Journal of Biological Chemistry</i> , 2010, 285, 13736-13741.	3.4	25
68	The high-throughput protein sample production platform of the Northeast Structural Genomics Consortium. <i>Journal of Structural Biology</i> , 2010, 172, 21-33.	2.8	125
69	Enhancement of <i>Candida parapsilosis</i> catalyzing deracemization of (<i>R,S</i>)-1-phenyl-2-ethanediol: agitation speed control during cell cultivation. <i>Journal of Chemical Technology and Biotechnology</i> , 2009, 84, 468-472.	3.2	16
70	NMR and X-RAY structures of human E2-like ubiquitin-fold modifier conjugating enzyme 1 (UFC1) reveal structural and functional conservation in the metazoan UFM1-UBA5-UFC1 ubiquitination pathway. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 127-136.	1.2	26
71	¹ H, ¹³ C, and ¹⁵ N NMR assignments for the <i>Bacillus subtilis</i> yndB START domain. <i>Biomolecular NMR Assignments</i> , 2009, 3, 191-194.	0.8	4
72	Improving NMR protein structure quality by Rosetta refinement: A molecular replacement study. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 147-167.	2.6	57

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73	Structural elucidation of the Cys-His-Glu-Asn proteolytic relay in the secreted CHAP domain enzyme from the human pathogen <i>Staphylococcus saprophyticus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 515-519.	2.6	30
74	Crystal structure of human retinoblastoma binding protein 9. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 526-529.	2.6	12
75	Construct optimization for protein NMR structure analysis using amide hydrogen/deuterium exchange mass spectrometry. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 882-894.	2.6	33
76	NMR structure of protein YvyC from <i>Bacillus subtilis</i> reveals unexpected structural similarity between two PFAM families. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 1037-1041.	2.6	2
77	Understanding the physical properties that control protein crystallization by analysis of large-scale experimental data. <i>Nature Biotechnology</i> , 2009, 27, 51-57.	17.5	133
78	Structure of an acetyl-CoA binding protein from <i>Staphylococcus aureus</i> representing a novel subfamily of GCN5-related N-acetyltransferase-like proteins. <i>Journal of Structural and Functional Genomics</i> , 2008, 9, 7-20.	1.2	11
79	Protein chaperones Q8ZP25_SALTY from <i>Salmonella typhimurium</i> and HYAE_ECOLI from <i>Escherichia coli</i> exhibit thioredoxin-like structures despite lack of canonical thioredoxin active site sequence motif. <i>Journal of Structural and Functional Genomics</i> , 2008, 9, 41-49.	1.2	12
80	NMR structure of protein Cgl2762 from <i>Corynebacterium glutamicum</i> implicated in DNA transposition reveals a helix-turn-helix motif attached to a flexibly disordered leucine zipper. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 1650-1654.	2.6	1
81	NMR structure of the peptidyl-tRNA hydrolase domain from <i>Pseudomonas syringae</i> expands the structural coverage of the hydrolysis domains of class 1 peptide chain release factors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1027-1031.	2.6	8
82	Solution NMR structure of the SOS response protein YnzC from <i>Bacillus subtilis</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 526-530.	2.6	14
83	Protein production and purification. <i>Nature Methods</i> , 2008, 5, 135-146.	19.0	763
84	Solution NMR Structure of the NlpC/P60 Domain of Lipoprotein Spr from <i>Escherichia coli</i> : Structural Evidence for a Novel Cysteine Peptidase Catalytic Triad. <i>Biochemistry</i> , 2008, 47, 9715-9717.	2.5	71
85	Histidine 55 of Tryptophan 2,3-Dioxygenase Is Not an Active Site Base but Regulates Catalysis by Controlling Substrate Binding. <i>Biochemistry</i> , 2008, 47, 10677-10684.	2.5	40
86	Molecular Insights into the Biosynthesis of the F420 Coenzyme. <i>Journal of Biological Chemistry</i> , 2008, 283, 11832-11840.	3.4	46
87	Structural basis for suppression of a host antiviral response by influenza A virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 13093-13098.	7.1	193
88	Quantum chemical ^{13}C chemical shift calculations for protein NMR structure determination, refinement, and validation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 14389-14394.	7.1	56
89	Structural and Functional Studies of the Abundant Tegument Protein ORF52 from Murine Gammaherpesvirus 68. <i>Journal of Biological Chemistry</i> , 2007, 282, 31534-31541.	3.4	22
90	Molecular insights into substrate recognition and catalysis by tryptophan 2,3-dioxygenase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 473-478.	7.1	169

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91	NMR structure of protein yjbR from Escherichia coli reveals a "double-wing" DNA binding motif. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 501-504.	2.6	11
92	Solution NMR structure of Escherichia coli ytfP expands the structural coverage of the UPF0131 protein domain family. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 789-795.	2.6	4
93	Microgram-scale protein structure determination by NMR. <i>Nature Methods</i> , 2007, 4, 491-493.	19.0	41
94	Crystal structure of AGR_C_4470p from Agrobacterium tumefaciens. <i>Protein Science</i> , 2007, 16, 535-538.	7.6	3
95	Functional insights from structural genomics. <i>Journal of Structural and Functional Genomics</i> , 2007, 8, 37-44.	1.2	34
96	FAST-NMR: A Functional Annotation Screening Technology Using NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2006, 128, 15292-15299.	13.7	48
97	Structural and Functional Evidence for Bacillus subtilis PaiA as a Novel N1-Spermidine/Spermine Acetyltransferase. <i>Journal of Biological Chemistry</i> , 2005, 280, 40328-40336.	3.4	61
98	Robotic Cloning and Protein Production Platform of the Northeast Structural Genomics Consortium. <i>Methods in Enzymology</i> , 2005, 394, 210-243.	1.0	118
99	NMR data collection and analysis protocol for high-throughput protein structure determination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10487-10492.	7.1	108
100	Comparisons of NMR Spectral Quality and Success in Crystallization Demonstrate that NMR and X-ray Crystallography Are Complementary Methods for Small Protein Structure Determination. <i>Journal of the American Chemical Society</i> , 2005, 127, 16505-16511.	13.7	72
101	Biophysical Characterization of the Complex between Double-Stranded RNA and the N-Terminal Domain of the NS1 Protein from Influenza A Virus: Evidence for a Novel RNA-Binding Mode. <i>Biochemistry</i> , 2004, 43, 1950-1962.	2.5	107
102	Solution NMR Structure of the Iron-Sulfur Cluster Assembly Protein U (IsclU) with Zinc Bound at the Active Site. <i>Journal of Molecular Biology</i> , 2004, 344, 567-583.	4.2	135
103	The SufE Sulfur-acceptor Protein Contains a Conserved Core Structure that Mediates Interdomain Interactions in a Variety of Redox Protein Complexes. <i>Journal of Molecular Biology</i> , 2004, 344, 549-565.	4.2	53
104	SPINE 2: a system for collaborative structural proteomics within a federated database framework. <i>Nucleic Acids Research</i> , 2003, 31, 2833-2838.	14.5	55
105	X-ray crystal structure of MTH938 from Methanobacterium thermoautotrophicum at 2.2 Å resolution reveals a novel tertiary protein fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 486-488.	2.6	5
106	Resonance assignments for the N-terminal domain from human RNA-binding protein with multiple splicing (RBP-MS). <i>Journal of Biomolecular NMR</i> , 2001, 19, 285-286.	2.8	0