Yuxing Chen

List of Publications by Year in descending order

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Version: 2024-02-01

81 papers	1,809 citations	257450 24 h-index	345221 36 g-index
84 all docs	84 docs citations	84 times ranked	2854 citing authors

#	ARTICLE	IF	CITATIONS
1	Structure and assembly pattern of a freshwater short-tailed cyanophage Pam1. Structure, 2022, 30, 240-251.e4.	3.3	9
2	Structure and transport mechanism of the human cholesterol transporter ABCG1. Cell Reports, 2022, 38, 110298.	6.4	18
3	Structures of human bile acid exporter ABCB11 reveal a transport mechanism facilitated by two tandem substrate-binding pockets. Cell Research, 2022, 32, 501-504.	12.0	17
4	Structural insights into the activation of autoinhibited human lipid flippase ATP8B1 upon substrate binding. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2118656119.	7.1	15
5	Inhibition of Streptococcus pneumoniae growth by masarimycin. Microbiology (United Kingdom), 2022, 168, .	1.8	0
6	Structural basis of substrate recognition and translocation by human very long-chain fatty acid transporter ABCD1. Nature Communications, 2022, 13, .	12.8	13
7	Complex structure reveals <scp>CcmM</scp> and <scp>CcmN</scp> form a heterotrimeric adaptor in Î²â€•carboxysome. Protein Science, 2021, 30, 1566-1576.	7.6	5
8	Structures of cyanobacterial bicarbonate transporter SbtA and its complex with PII-like SbtB. Cell Discovery, 2021, 7, 63.	6.7	16
9	Crystal structure of a novel fold protein Gp72 from the freshwater cyanophage Mic1. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1226-1232.	2.6	1
10	The model cyanobacteria Anabaena sp. PCC 7120 possess an intact but partially degenerated gene cluster encoding gas vesicles. BMC Microbiology, 2020, 20, 110.	3.3	8
11	Cryo-electron Microscopy Structure and Transport Mechanism of a Wall Teichoic Acid ABC Transporter. MBio, 2020, 11, .	4.1	33
12	Cryo-EM structure of human bile salts exporter ABCB11. Cell Research, 2020, 30, 623-625.	12.0	30
13	Structural and functional insights into the Asp1/2/3 complex mediated secretion of pneumococcal serine-rich repeat protein PsrP. Biochemical and Biophysical Research Communications, 2020, 524, 784-790.	2.1	1
14	Genomic Analysis of Mic1 Reveals a Novel Freshwater Long-Tailed Cyanophage. Frontiers in Microbiology, 2020, 11, 484.	3.5	27
15	Molecular basis for the assembly of RuBisCO assisted by the chaperone Raf1. Nature Plants, 2020, 6, 708-717.	9.3	24
16	Capsid Structure of a Freshwater Cyanophage Siphoviridae Mic1. Structure, 2019, 27, 1508-1516.e3.	3.3	21
17	Structural insights into repression of the <i>Pneumococcal</i> fatty acid synthesis pathway by repressor FabT and coâ€•repressor acylâ€•ACP. FEBS Letters, 2019, 593, 2730-2741.	2.8	20
18	Cryo-EM structure of human lysosomal cobalamin exporter ABCD4. Cell Research, 2019, 29, 1039-1041.	12.0	42

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19	Crystal structure of pentameric shell protein CsoS4B of Halothiobacillus neapolitanus Î±-carboxysome. Biochemical and Biophysical Research Communications, 2019, 515, 510-515.	2.1	4
20	Crystal structure of the choline-binding protein CbpJ from Streptococcus pneumoniae. Biochemical and Biophysical Research Communications, 2019, 514, 1192-1197.	2.1	10
21	Structural insights into the catalysis and substrate specificity of cyanobacterial aspartate racemase McyF. Biochemical and Biophysical Research Communications, 2019, 514, 1108-1114.	2.1	6
22	Multi-functional regulator MapZ controls both positioning and timing of FtsZ polymerization. Biochemical Journal, 2019, 476, 1433-1444.	3.7	6
23	Structural and enzymatic analyses of <i>Anabaena</i> heterocystâ€specific alkaline invertase InvB. FEBS Letters, 2018, 592, 1589-1601.	2.8	12
24	Structure of a MacAB-like efflux pump from Streptococcus pneumoniae. Nature Communications, 2018, 9, 196.	12.8	34
25	Coordinating carbon and nitrogen metabolic signaling through the cyanobacterial global repressor NdhR. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 403-408.	7.1	65
26	The pore-forming protein Aep1 is an innate immune molecule that prevents zebrafish from bacterial infection. Developmental and Comparative Immunology, 2018, 82, 49-54.	2.3	16
27	The GDP-switched GAF domain of DcpA modulates the concerted synthesis/hydrolysis of c-di-GMP in Mycobacterium smegmatis. Biochemical Journal, 2018, 475, 1295-1308.	3.7	13
28	Structural and Biochemical Insights into the Multiple Functions of Yeast Grx3. Journal of Molecular Biology, 2018, 430, 1235-1248.	4.2	23
29	Defining the enzymatic pathway for polymorphic O-glycosylation of the pneumococcal serine-rich repeat protein PsrP. Journal of Biological Chemistry, 2017, 292, 6213-6224.	3.4	26
30	Crystal structure of yeast monothiol glutaredoxin Grx6 in complex with a glutathione-coordinated [2Feâ€“2S] cluster. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 732-737.	0.8	12
31	Structural Analysis of the Catalytic Mechanism and Substrate Specificity of Anabaena Alkaline Invertase InvA Reveals a Novel Glucosidase. Journal of Biological Chemistry, 2016, 291, 25667-25677.	3.4	24
32	Structure of a variable lymphocyte receptor-like protein from the amphioxus Branchiostoma floridae. Scientific Reports, 2016, 6, 19951.	3.3	12
33	Structural basis for receptor recognition and pore formation of a zebrafish aerolysinâ€like protein. EMBO Reports, 2016, 17, 235-248.	4.5	53
34	Structural Comparison and Simulation of Pneumococcal Peptidoglycan Hydrolase LytB. Methods in Molecular Biology, 2016, 1440, 271-283.	0.9	0
35	Structures of an all-Î± protein running along the DNA major groove. Nucleic Acids Research, 2016, 44, 3936-3945.	14.5	5
36	Structural and enzymatic analyses of a glucosyltransferase Alr3699/HepE involved in<i>Anabaena</i>heterocyst envelop polysaccharide biosynthesis. Glycobiology, 2016, 26, 520-531.	2.5	4

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37	Structural insights into HetRâˆ’PatS interaction involved in cyanobacterial pattern formation. Scientific Reports, 2015, 5, 16470.	3.3	29
38	Activity Augmentation of Amphioxus Peptidoglycan Recognition Protein BbtPGRP3 via Fusion with a Chitin Binding Domain. PLoS ONE, 2015, 10, e0140953.	2.5	3
39	Full-length structure of the major autolysin LytA. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1373-1381.	2.5	22
40	Structural and biochemical analyses of the<i>Streptococcus pneumoniae</i><scp>L</scp>,<scp>D</scp>-carboxypeptidase DacB. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 283-292.	2.5	2
41	Structure of the adenylationâ€“peptidyl carrier protein didomain of the<i>Microcystis aeruginosa</i>microcystin synthetase McyG. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 873-881.	2.5	18
42	Structural and Enzymatic Characterization of the Choline Kinase LicA from Streptococcus pneumoniae. PLoS ONE, 2015, 10, e0120467.	2.5	11
43	Crystal structure of juvenile hormone epoxide hydrolase from the silkworm<i>B</i><i>ombyx mori</i>. Proteins: Structure, Function and Bioinformatics, 2014, 82, 3224-3229.	2.6	18
44	Structural Insights into SraP-Mediated Staphylococcus aureus Adhesion to Host Cells. PLoS Pathogens, 2014, 10, e1004169.	4.7	85
45	Structure of Pneumococcal Peptidoglycan Hydrolase LytB Reveals Insights into the Bacterial Cell Wall Remodeling and Pathogenesis. Journal of Biological Chemistry, 2014, 289, 23403-23416.	3.4	62
46	Crystal structures and catalytic mechanism of the<i>C</i>-methyltransferase Coq5 provide insights into a key step of the yeast coenzyme Q synthesis pathway. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2085-2092.	2.5	22
47	Structure of the gas vesicle protein GvpF from the cyanobacterium<i>Microcystis aeruginosa</i>. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 3013-3022.	2.5	22
48	Structure of a Novel O-Linked N-Acetyl-d-glucosamine (O-GlcNAc) Transferase, GtfA, Reveals Insights into the Glycosylation of Pneumococcal Serine-rich Repeat Adhesins. Journal of Biological Chemistry, 2014, 289, 20898-20907.	3.4	49
49	Structural and biochemical analyses of Microcystis aeruginosa O-acetylserine sulfhydrylases reveal a negative feedback regulation of cysteine biosynthesis. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 308-315.	2.3	4
50	Streptomyces coelicolor SCO4226 Is a Nickel Binding Protein. PLoS ONE, 2014, 9, e109660.	2.5	9
51	Structures of Yeast Apa2 Reveal Catalytic Insights into a Canonical Ap4A Phosphorylase of the Histidine Triad Superfamily. Journal of Molecular Biology, 2013, 425, 2687-2698.	4.2	6
52	Structure and Catalytic Mechanism of Yeast 4-Amino-4-deoxychorismate Lyase. Journal of Biological Chemistry, 2013, 288, 22985-22992.	3.4	5
53	Structural Insights into the Substrate Specificity of a 6-Phospho-Î²-glucosidase BglA-2 from Streptococcus pneumoniae TIGR4. Journal of Biological Chemistry, 2013, 288, 14949-14958.	3.4	18
54	The N-Terminal Î²-Sheet of Peroxiredoxin 4 in the Large Yellow Croaker Pseudosciaena crocea Is Involved in Its Biological Functions. PLoS ONE, 2013, 8, e57061.	2.5	10

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55	Structures of Streptococcus pneumoniae PiaA and Its Complex with Ferrichrome Reveal Insights into the Substrate Binding and Release of High Affinity Iron Transporters. PLoS ONE, 2013, 8, e71451.	2.5	30
56	Structural Snapshots of Yeast Alkyl Hydroperoxide Reductase Ahp1 Peroxiredoxin Reveal a Novel Two-cysteine Mechanism of Electron Transfer to Eliminate Reactive Oxygen Species. Journal of Biological Chemistry, 2012, 287, 17077-17087.	3.4	39
57	Structure of Yeast Sulfhydryl Oxidase Erv1 Reveals Electron Transfer of the Disulfide Relay System in the Mitochondrial Intermembrane Space. Journal of Biological Chemistry, 2012, 287, 34961-34969.	3.4	25
58	Structural Insights into the Substrate Specificity of Streptococcus pneumoniae Î²(1,3)-Galactosidase BgaC. Journal of Biological Chemistry, 2012, 287, 22910-22918.	3.4	32
59	N-Terminal Domain of Bombyx mori Fibroin Mediates the Assembly of Silk in Response to pH Decrease. Journal of Molecular Biology, 2012, 418, 197-207.	4.2	107
60	Structural Basis for the Substrate Specificity of a Novel Î²-N-Acetylhexosaminidase StrH Protein from Streptococcus pneumoniae R6. Journal of Biological Chemistry, 2011, 286, 43004-43012.	3.4	29
61	Crystal structure of the mucin-binding domain of Spr1345 from Streptococcus pneumoniae. Journal of Structural Biology, 2011, 174, 252-257.	2.8	31
62	Crystal structure of the 30 K protein from the silkworm Bombyx mori reveals a new member of the Î²-trefoil superfamily. Journal of Structural Biology, 2011, 175, 97-103.	2.8	29
63	Structural insights into the cofactor-assisted substrate recognition of yeast quinone oxidoreductase Zta1. Journal of Structural Biology, 2011, 176, 112-118.	2.8	14
64	Structure-Guided Activity Restoration of the Silkworm Glutathione Transferase Omega GSTO3-3. Journal of Molecular Biology, 2011, 412, 204-211.	4.2	9
65	Structures of the substrate-binding protein provide insights into the multiple compatible solute binding specificities of the <i>Bacillus subtilis</i> ABC transporter OpuC. Biochemical Journal, 2011, 436, 283-289.	3.7	45
66	Structural and Enzymatic Characterization of the Streptococcal ATP/Diadenosine Polyphosphate and Phosphodiester Hydrolase Spr1479/SapH*. Journal of Biological Chemistry, 2011, 286, 35906-35914.	3.4	4
67	Structural Plasticity of the Thioredoxin Recognition Site of Yeast Methionine S-Sulfoxide Reductase Mxr1. Journal of Biological Chemistry, 2011, 286, 13430-13437.	3.4	26
68	Structural insights into the catalytic mechanism of the yeast pyridoxal 5-phosphate synthase Snz1. Biochemical Journal, 2010, 432, 445-454.	3.7	17
69	Crystal structures of holo and Cuâ€deficient Cu/Znâ€SOD from the silkworm <i>Bombyx mori</i> and the implications in amyotrophic lateral sclerosis. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1999-2004.	2.6	11
70	Crystal structures of the apo and GDPâ€bound forms of a cupinâ€like protein BbDUF985 from <i>Branchiostoma belcheri tsingtauense</i>. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2714-2719.	2.6	3
71	Structural basis for the allosteric control of the global transcription factor NtcA by the nitrogen starvation signal 2-oxoglutarate. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 12487-12492.	7.1	102
72	Structural and Biochemical Characterization of Yeast Monothiol Glutaredoxin Grx6. Journal of Molecular Biology, 2010, 398, 614-622.	4.2	45

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73	Crystal Structure of the Cyanobacterial Signal Transduction Protein PII in Complex with PipX. Journal of Molecular Biology, 2010, 402, 552-559.	4.2	36
74	Crystal structure of <i>Arabidopsis</i> translation initiation factor eIFâ€5A2. Proteins: Structure, Function and Bioinformatics, 2009, 77, 736-740.	2.6	10
75	Structural insights into the substrate tunnel of Saccharomyces cerevisiae carbonic anhydrase Nce103. BMC Structural Biology, 2009, 9, 67.	2.3	27
76	Structures of yeast glutathioneâ€<i>S</i>â€transferase Gtt2 reveal a new catalytic type of GST family. EMBO Reports, 2009, 10, 1320-1326.	4.5	27
77	Structural and kinetic analysis of Saccharomyces cerevisiae thioredoxin Trx1: Implications for the catalytic mechanism of GSSG reduced by the thioredoxin system. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2009, 1794, 1218-1223.	2.3	22
78	Crystal structure of Saccharomyces cerevisiae cytoplasmic thioredoxin reductase Trr1 reveals the structural basis for species-specific recognition of thioredoxin. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2009, 1794, 124-128.	2.3	24
79	Expression, purification, crystallization and preliminary X-ray diffraction analysis of thioredoxin Trx1 fromSaccharomyces cerevisiae. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 323-325.	0.7	5
80	Crystal structure of glutathioneâ€dependent phospholipid peroxidase Hyr1 from the yeast <i>Saccharomyces cerevisiae</i>. Proteins: Structure, Function and Bioinformatics, 2008, 73, 1058-1062.	2.6	19
81	Crystal structure of the yeast cytoplasmic thioredoxin Trx2. Proteins: Structure, Function and Bioinformatics, 2006, 66, 246-249.	2.6	20