

# Yuxing Chen

## List of Publications by Year in descending order

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81  
papers

1,809  
citations

293460

24  
h-index

388640

36  
g-index

84  
all docs

84  
docs citations

84  
times ranked

3111  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure and assembly pattern of a freshwater short-tailed cyanophage Pam1. <i>Structure</i> , 2022, 30, 240-251.e4.	1.6	9
2	Structure and transport mechanism of the human cholesterol transporter ABCG1. <i>Cell Reports</i> , 2022, 38, 110298.	2.9	18
3	Structures of human bile acid exporter ABCB11 reveal a transport mechanism facilitated by two tandem substrate-binding pockets. <i>Cell Research</i> , 2022, 32, 501-504.	5.7	17
4	Structural insights into the activation of autoinhibited human lipid flippase ATP8B1 upon substrate binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2118656119.	3.3	15
5	Inhibition of <i>Streptococcus pneumoniae</i> growth by masarimycin. <i>Microbiology (United Kingdom)</i> , 2022, 168, .	0.7	0
6	Structural basis of substrate recognition and translocation by human very long-chain fatty acid transporter ABCD1. <i>Nature Communications</i> , 2022, 13, .	5.8	13
7	Complex structure reveals <scp>CcmM</scp> and <scp>CcmN</scp> form a heterotrimeric adaptor in $\lambda$ 2â€carboxysome. <i>Protein Science</i> , 2021, 30, 1566-1576.	3.1	5
8	Structures of cyanobacterial bicarbonate transporter SbtA and its complex with PII-like SbtB. <i>Cell Discovery</i> , 2021, 7, 63.	3.1	16
9	Crystal structure of a novel fold protein Gp72 from the freshwater cyanophage Mic1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1226-1232.	1.5	1
10	The model cyanobacteria <i>Anabaena</i> sp. PCC 7120 possess an intact but partially degenerated gene cluster encoding gas vesicles. <i>BMC Microbiology</i> , 2020, 20, 110.	1.3	8
11	Cryo-electron Microscopy Structure and Transport Mechanism of a Wall Teichoic Acid ABC Transporter. <i>MBio</i> , 2020, 11, .	1.8	33
12	Cryo-EM structure of human bile salts exporter ABCB11. <i>Cell Research</i> , 2020, 30, 623-625.	5.7	30
13	Structural and functional insights into the Asp1/2/3 complex mediated secretion of pneumococcal serine-rich repeat protein PsrP. <i>Biochemical and Biophysical Research Communications</i> , 2020, 524, 784-790.	1.0	1
14	Genomic Analysis of Mic1 Reveals a Novel Freshwater Long-Tailed Cyanophage. <i>Frontiers in Microbiology</i> , 2020, 11, 484.	1.5	27
15	Molecular basis for the assembly of RuBisCO assisted by the chaperone Raf1. <i>Nature Plants</i> , 2020, 6, 708-717.	4.7	24
16	Capsid Structure of a Freshwater Cyanophage Siphoviridae Mic1. <i>Structure</i> , 2019, 27, 1508-1516.e3.	1.6	21
17	Structural insights into repression of the <i>Pneumococcal</i> fatty acid synthesis pathway by repressor FabT and coâ€repressor acylâ€ACP. <i>FEBS Letters</i> , 2019, 593, 2730-2741.	1.3	20
18	Cryo-EM structure of human lysosomal cobalamin exporter ABCD4. <i>Cell Research</i> , 2019, 29, 1039-1041.	5.7	42

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19	Crystal structure of pentameric shell protein CsoS4B of <i>Halothiobacillus neapolitanus</i> Î±-carboxysome. <i>Biochemical and Biophysical Research Communications</i> , 2019, 515, 510-515.	1.0	4
20	Crystal structure of the choline-binding protein CbpJ from <i>Streptococcus pneumoniae</i> . <i>Biochemical and Biophysical Research Communications</i> , 2019, 514, 1192-1197.	1.0	10
21	Structural insights into the catalysis and substrate specificity of cyanobacterial aspartate racemase McyF. <i>Biochemical and Biophysical Research Communications</i> , 2019, 514, 1108-1114.	1.0	6
22	Multi-functional regulator MapZ controls both positioning and timing of FtsZ polymerization. <i>Biochemical Journal</i> , 2019, 476, 1433-1444.	1.7	6
23	Structural and enzymatic analyses of <i>Anabaena</i> heterocyst-specific alkaline invertase InvB. <i>FEBS Letters</i> , 2018, 592, 1589-1601.	1.3	12
24	Structure of a MacAB-like efflux pump from <i>Streptococcus pneumoniae</i> . <i>Nature Communications</i> , 2018, 9, 196.	5.8	34
25	Coordinating carbon and nitrogen metabolic signaling through the cyanobacterial global repressor NdhR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 403-408.	3.3	65
26	The pore-forming protein Aep1 is an innate immune molecule that prevents zebrafish from bacterial infection. <i>Developmental and Comparative Immunology</i> , 2018, 82, 49-54.	1.0	16
27	The GDP-switched GAF domain of DcpA modulates the concerted synthesis/hydrolysis of c-di-GMP in <i>Mycobacterium smegmatis</i> . <i>Biochemical Journal</i> , 2018, 475, 1295-1308.	1.7	13
28	Structural and Biochemical Insights into the Multiple Functions of Yeast Grx3. <i>Journal of Molecular Biology</i> , 2018, 430, 1235-1248.	2.0	23
29	Defining the enzymatic pathway for polymorphic O-glycosylation of the pneumococcal serine-rich repeat protein PsrP. <i>Journal of Biological Chemistry</i> , 2017, 292, 6213-6224.	1.6	26
30	Crystal structure of yeast monothiol glutaredoxin Grx6 in complex with a glutathione-coordinated [2Fe-2S] cluster. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 732-737.	0.4	12
31	Structural Analysis of the Catalytic Mechanism and Substrate Specificity of <i>Anabaena</i> Alkaline Invertase InvA Reveals a Novel Glucosidase. <i>Journal of Biological Chemistry</i> , 2016, 291, 25667-25677.	1.6	24
32	Structure of a variable lymphocyte receptor-like protein from the amphioxus <i>Branchiostoma floridae</i> . <i>Scientific Reports</i> , 2016, 6, 19951.	1.6	12
33	Structural basis for receptor recognition and pore formation of a zebrafish aerolysin-like protein. <i>EMBO Reports</i> , 2016, 17, 235-248.	2.0	53
34	Structural Comparison and Simulation of Pneumococcal Peptidoglycan Hydrolase LytB. <i>Methods in Molecular Biology</i> , 2016, 1440, 271-283.	0.4	0
35	Structures of an all-Î± protein running along the DNA major groove. <i>Nucleic Acids Research</i> , 2016, 44, 3936-3945.	6.5	5
36	Structural and enzymatic analyses of a glucosyltransferase Alr3699/HepE involved in <i>Anabaena</i> heterocyst envelop polysaccharide biosynthesis. <i>Glycobiology</i> , 2016, 26, 520-531.	1.3	4

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37	Structural insights into HetR~PatS interaction involved in cyanobacterial pattern formation. <i>Scientific Reports</i> , 2015, 5, 16470.	1.6	29
38	Activity Augmentation of Amphioxus Peptidoglycan Recognition Protein BbtPGRP3 via Fusion with a Chitin Binding Domain. <i>PLoS ONE</i> , 2015, 10, e0140953.	1.1	3
39	Full-length structure of the major autolysin LytA. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1373-1381.	2.5	22
40	Structural and biochemical analyses of the <i>Streptococcus pneumoniae</i> L- and D-carboxypeptidase DacB. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 283-292.	2.5	2
41	Structure of the adenylation~peptidyl carrier protein didomain of the <i>Microcystis aeruginosa</i> microcystin synthetase McyG. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 873-881.	2.5	18
42	Structural and Enzymatic Characterization of the Choline Kinase LicA from <i>Streptococcus pneumoniae</i> . <i>PLoS ONE</i> , 2015, 10, e0120467.	1.1	11
43	Crystal structure of juvenile hormone epoxide hydrolase from the silkworm <i>Bombyx mori</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 3224-3229.	1.5	18
44	Structural Insights into SraP-Mediated <i>Staphylococcus aureus</i> Adhesion to Host Cells. <i>PLoS Pathogens</i> , 2014, 10, e1004169.	2.1	85
45	Structure of Pneumococcal Peptidoglycan Hydrolase LytB Reveals Insights into the Bacterial Cell Wall Remodeling and Pathogenesis. <i>Journal of Biological Chemistry</i> , 2014, 289, 23403-23416.	1.6	62
46	Crystal structures and catalytic mechanism of the C-methyltransferase Coq5 provide insights into a key step of the yeast coenzyme Q synthesis pathway. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2085-2092.	2.5	22
47	Structure of the gas vesicle protein GvpF from the cyanobacterium <i>Microcystis aeruginosa</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 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. <i>Journal of Biological Chemistry</i> , 2014, 289, 20898-20907.	1.6	49
49	Structural and biochemical analyses of <i>Microcystis aeruginosa</i> O-acetylserine sulfhydrylases reveal a negative feedback regulation of cysteine biosynthesis. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 308-315.	1.1	4
50	<i>Streptomyces coelicolor</i> SCO4226 Is a Nickel Binding Protein. <i>PLoS ONE</i> , 2014, 9, e109660.	1.1	9
51	Structures of Yeast Apa2 Reveal Catalytic Insights into a Canonical Ap4A Phosphorylase of the Histidine Triad Superfamily. <i>Journal of Molecular Biology</i> , 2013, 425, 2687-2698.	2.0	6
52	Structure and Catalytic Mechanism of Yeast 4-Amino-4-deoxychorismate Lyase. <i>Journal of Biological Chemistry</i> , 2013, 288, 22985-22992.	1.6	5
53	Structural Insights into the Substrate Specificity of a 6-Phospho- $\beta$ -glucosidase BglA-2 from <i>Streptococcus pneumoniae</i> TIGR4. <i>Journal of Biological Chemistry</i> , 2013, 288, 14949-14958.	1.6	18
54	The N-Terminal $\beta$ -Sheet of Peroxiredoxin 4 in the Large Yellow Croaker <i>Pseudosciaena crocea</i> Is Involved in Its Biological Functions. <i>PLoS ONE</i> , 2013, 8, e57061.	1.1	10

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55	Structures of <i>Streptococcus pneumoniae</i> PiaA and Its Complex with Ferrichrome Reveal Insights into the Substrate Binding and Release of High Affinity Iron Transporters. <i>PLoS ONE</i> , 2013, 8, e71451.	1.1	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. <i>Journal of Biological Chemistry</i> , 2012, 287, 17077-17087.	1.6	39
57	Structure of Yeast Sulfhydryl Oxidase Erv1 Reveals Electron Transfer of the Disulfide Relay System in the Mitochondrial Intermembrane Space. <i>Journal of Biological Chemistry</i> , 2012, 287, 34961-34969.	1.6	25
58	Structural Insights into the Substrate Specificity of <i>Streptococcus pneumoniae</i> $\beta$ (1,3)-Galactosidase BgaC. <i>Journal of Biological Chemistry</i> , 2012, 287, 22910-22918.	1.6	32
59	N-Terminal Domain of <i>Bombyx mori</i> Fibroin Mediates the Assembly of Silk in Response to pH Decrease. <i>Journal of Molecular Biology</i> , 2012, 418, 197-207.	2.0	107
60	Structural Basis for the Substrate Specificity of a Novel $\beta$ -N-Acetylhexosaminidase StrH Protein from <i>Streptococcus pneumoniae</i> R6. <i>Journal of Biological Chemistry</i> , 2011, 286, 43004-43012.	1.6	29
61	Crystal structure of the mucin-binding domain of Spr1345 from <i>Streptococcus pneumoniae</i> . <i>Journal of Structural Biology</i> , 2011, 174, 252-257.	1.3	31
62	Crystal structure of the 30 K protein from the silkworm <i>Bombyx mori</i> reveals a new member of the $\beta$ -trefoil superfamily. <i>Journal of Structural Biology</i> , 2011, 175, 97-103.	1.3	29
63	Structural insights into the cofactor-assisted substrate recognition of yeast quinone oxidoreductase Zta1. <i>Journal of Structural Biology</i> , 2011, 176, 112-118.	1.3	14
64	Structure-Guided Activity Restoration of the Silkworm Glutathione Transferase Omega GSTO3-3. <i>Journal of Molecular Biology</i> , 2011, 412, 204-211.	2.0	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. <i>Biochemical Journal</i> , 2011, 436, 283-289.	1.7	45
66	Structural and Enzymatic Characterization of the Streptococcal ATP/Diadenosine Polyphosphate and Phosphodiester Hydrolase Spr1479/SapH*. <i>Journal of Biological Chemistry</i> , 2011, 286, 35906-35914.	1.6	4
67	Structural Plasticity of the Thioredoxin Recognition Site of Yeast Methionine S-Sulfoxide Reductase Mxr1. <i>Journal of Biological Chemistry</i> , 2011, 286, 13430-13437.	1.6	26
68	Structural insights into the catalytic mechanism of the yeast pyridoxal 5-phosphate synthase Snz1. <i>Biochemical Journal</i> , 2010, 432, 445-454.	1.7	17
69	Crystal structures of holo and Cu-deficient Cu/Zn-SOD from the silkworm <i>Bombyx mori</i> and the implications in amyotrophic lateral sclerosis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1999-2004.	1.5	11
70	Crystal structures of the apo and GDP-bound forms of a cupin-like protein BbDUF985 from <i>Branchiostoma belcheri tsingtauense</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2714-2719.	1.5	3
71	Structural basis for the allosteric control of the global transcription factor NtcA by the nitrogen starvation signal 2-oxoglutarate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 12487-12492.	3.3	102
72	Structural and Biochemical Characterization of Yeast Monothiol Glutaredoxin Grx6. <i>Journal of Molecular Biology</i> , 2010, 398, 614-622.	2.0	45

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73	Crystal Structure of the Cyanobacterial Signal Transduction Protein PII in Complex with PipX. <i>Journal of Molecular Biology</i> , 2010, 402, 552-559.	2.0	36
74	Crystal structure of <i>Arabidopsis</i> translation initiation factor eIF5A2. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 736-740.	1.5	10
75	Structural insights into the substrate tunnel of <i>Saccharomyces cerevisiae</i> carbonic anhydrase Nce103. <i>BMC Structural Biology</i> , 2009, 9, 67.	2.3	27
76	Structures of yeast glutathione S-transferase Gtt2 reveal a new catalytic type of GST family. <i>EMBO Reports</i> , 2009, 10, 1320-1326.	2.0	27
77	Structural and kinetic analysis of <i>Saccharomyces cerevisiae</i> thioredoxin Trx1: Implications for the catalytic mechanism of GSSG reduced by the thioredoxin system. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 1218-1223.	1.1	22
78	Crystal structure of <i>Saccharomyces cerevisiae</i> cytoplasmic thioredoxin reductase Trr1 reveals the structural basis for species-specific recognition of thioredoxin. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 124-128.	1.1	24
79	Expression, purification, crystallization and preliminary X-ray diffraction analysis of thioredoxin Trx1 from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 323-325.	0.7	5
80	Crystal structure of glutathione-dependent phospholipid peroxidase Hyr1 from the yeast <i>Saccharomyces cerevisiae</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 1058-1062.	1.5	19
81	Crystal structure of the yeast cytoplasmic thioredoxin Trx2. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 66, 246-249.	1.5	20