

# Yuequan Shen

## List of Publications by Year in descending order

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79  
papers

3,467  
citations

136950

32  
h-index

149698

56  
g-index

83  
all docs

83  
docs citations

83  
times ranked

5482  
citing authors

#	ARTICLE	IF	CITATIONS
1	Quantitative analysis of the effect of radiation on mitochondria structure using coherent diffraction imaging with a clustering algorithm. IUCr, 2022, 9, 223-230.	2.2	2
2	Cryo-EM structure of AMP-PNP-bound human mitochondrial ATP-binding cassette transporter ABCB7. Journal of Structural Biology, 2022, 214, 107832.	2.8	8
3	Expression, purification and microscopic characterization of transmembrane BAX Inhibitor-1 motif containing protein 5. Protein Expression and Purification, 2022, 193, 106045.	1.3	0
4	Cryo-EM structure of the heptameric calcium homeostasis modulator 1 channel. Journal of Biological Chemistry, 2022, 298, 101838.	3.4	6
5	Cryo-EM structure of the human TACAN in a closed state. Cell Reports, 2022, 38, 110445.	6.4	9
6	Mitochondrial heat-shock cognate protein 70 contributes to auxin-mediated embryo development. Plant Physiology, 2021, 186, 1101-1121.	4.8	4
7	The BAG2 and BAG6 Genes Are Involved in Multiple Abiotic Stress Tolerances in Arabidopsis Thaliana. International Journal of Molecular Sciences, 2021, 22, 5856.	4.1	17
8	Structural basis for activation and allosteric modulation of full-length calcium-sensing receptor. Science Advances, 2021, 7, .	10.3	32
9	Cryo-EM structure of human ABCB8 transporter in nucleotide binding state. Biochemical and Biophysical Research Communications, 2021, 557, 187-191.	2.1	13
10	Expression, purification and microscopic characterization of human ATP-binding cassette sub-family B member 7 protein. Protein Expression and Purification, 2021, 183, 105860.	1.3	2
11	Receptor-targeting nanomaterials alleviate binge drinking-induced neurodegeneration as artificial neurotrophins. Exploration, 2021, 1, 61-74.	11.0	28
12	Structural Insights into Ca <sup>2+</sup> Permeation through Orai Channels. Cells, 2021, 10, 3062.	4.1	2
13	Cryo-EM structure of the calcium homeostasis modulator 1 channel. Science Advances, 2020, 6, eaba8161.	10.3	17
14	Crystal Structures of the <i>C</i> -Glycosyltransferase UGT708C1 from Buckwheat Provide Insights into the Mechanism of <i>C</i> -Glycosylation. Plant Cell, 2020, 32, 2917-2931.	6.6	24
15	Expression, purification and oligomerization of the S-adenosylmethionine transporter. Protein Expression and Purification, 2020, 173, 105648.	1.3	0
16	Crystal structure and biochemical characterization of Striga hermonthica HYPO-SENSITIVE TO LIGHT 8 (ShHTL8) in strigolactone signaling pathway. Biochemical and Biophysical Research Communications, 2020, 523, 1040-1045.	2.1	10
17	Molecular architecture of the acetohydroxyacid synthase holoenzyme. Biochemical Journal, 2020, 477, 2439-2449.	3.7	8
18	Dimerization of MICU Proteins Controls Ca <sup>2+</sup> Influx through the Mitochondrial Ca <sup>2+</sup> Uniporter. Cell Reports, 2019, 26, 1203-1212.e4.	6.4	59

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19	Molecular understanding of calcium permeation through the open Orai channel. PLoS Biology, 2019, 17, e3000096.	5.6	52
20	Identification of a UDP-Glucosyltransferase favouring substrate- and regio-specific biosynthesis of flavonoid glucosides in Cyclocarya paliurus. Phytochemistry, 2019, 163, 75-88.	2.9	14
21	Crystal structures of rhamnosyltransferase <scp>UGT</scp>89C1 from <i>Arabidopsis thaliana</i> reveal the molecular basis of sugar donor specificity for <scp>UDP</scp>â€²â€œ<scp>l</scp>â€œrhamnose and rhamnosylation mechanism. Plant Journal, 2019, 99, 257-269.	5.7	44
22	Overexpression, purification, biochemical and structural characterization of rhamnosyltransferase UGT89C1 from Arabidopsis thaliana. Protein Expression and Purification, 2019, 156, 44-49.	1.3	7
23	Single channel recording of a mitochondrial calcium uniporter. Biochemical and Biophysical Research Communications, 2018, 496, 127-132.	2.1	11
24	The <scp>AAA</scp> protein spastin possesses two levels of basal <scp>ATP</scp>ase activity. FEBS Letters, 2018, 592, 1625-1633.	2.8	4
25	Identification of a single aspartate residue critical for both fast and slow calcium-dependent inactivation of the human TRPM1 channel. Journal of Biological Chemistry, 2018, 293, 11736-11745.	3.4	2
26	Synaptonemal complex protein 2 (SYCP2) mediates the association of the centromere with the synaptonemal complex. Protein and Cell, 2017, 8, 538-543.	11.0	26
27	Chronic mitochondrial calcium elevation suppresses leaf senescence. Biochemical and Biophysical Research Communications, 2017, 487, 672-677.	2.1	16
28	Calmodulin dissociates the STIM1-Orai1 complex and STIM1 oligomers. Nature Communications, 2017, 8, 1042.	12.8	43
29	CaM/BAG5/Hsc70 signaling complex dynamically regulates leaf senescence. Scientific Reports, 2016, 6, 31889.	3.3	44
30	Leucine zipper-EF-hand containing transmembrane protein 1 (LETM1) forms a Ca <sup>2+</sup> /H <sup>+</sup> antiporter. Scientific Reports, 2016, 6, 34174.	3.3	58
31	Auto-inhibitory Mechanism of the Human Mitochondrial RNase P Protein Complex. Scientific Reports, 2015, 5, 9878.	3.3	29
32	Angiotensin binding-induced activation of Merlin/NF2 in the Hippo pathway. Cell Research, 2015, 25, 801-817.	12.0	115
33	Molecular mechanism of mitochondrial calcium uptake. Cellular and Molecular Life Sciences, 2015, 72, 1489-1498.	5.4	28
34	The structure of WbnH in a near active state. Protein and Cell, 2015, 6, 615-618.	11.0	2
35	The Efp2 Subunit Is Essential for Elongator Complex Assembly and Functional Regulation. Structure, 2015, 23, 1078-1086.	3.3	27
36	Inside-out Ca <sup>2+</sup> signalling prompted by STIM1 conformational switch. Nature Communications, 2015, 6, 7826.	12.8	144

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37	Dimerization of elongator protein 1 is essential for Elongator complex assembly. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10697-10702.	7.1	41
38	Crystallographic analysis of the Arabidopsis thaliana BAG5-calmodulin protein complex. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 870-875.	0.8	3
39	A Regulatory Signaling Loop Comprising the PGAM5 Phosphatase and CK2 Controls Receptor-Mediated Mitophagy. Molecular Cell, 2014, 54, 362-377.	9.7	433
40	Gain-of-Function Mutation in STIM1 (P.R304W) Is Associated with Stormorken Syndrome. Human Mutation, 2014, 35, 1221-1232.	2.5	101
41	Crystal Structure of the Ubiquitin-like Domain-CUT Repeat-like Tandem of Special AT-rich Sequence Binding Protein 1 (SATB1) Reveals a Coordinating DNA-binding Mechanism. Journal of Biological Chemistry, 2014, 289, 27376-27385.	3.4	17
42	Structural Insight into the Central Element Assembly of the Synaptonemal Complex. Scientific Reports, 2014, 4, 7059.	3.3	30
43	Structure of the kinase domain of human RNA-dependent protein kinase with K296R mutation reveals a face-to-face dimer. Science Bulletin, 2013, 58, 998-1002.	1.7	8
44	Open-closed motion of Mint2 regulates APP metabolism. Journal of Molecular Cell Biology, 2013, 5, 48-56.	3.3	15
45	Structural insight into plant programmed cell death mediated by BAG proteins in Arabidopsis thaliana. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 934-945.	2.5	50
46	Structure of Neisseria meningitidis lipoprotein GNA1162. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 362-368.	0.7	6
47	Quantitative Structural Insight into Human Variegate Porphyria Disease. Journal of Biological Chemistry, 2013, 288, 11731-11740.	3.4	37
48	The Inhibitory Helix Controls the Intramolecular Conformational Switching of the C-Terminus of STIM1. PLoS ONE, 2013, 8, e74735.	2.5	40
49	The structural basis for the oligomerization of the N-terminal domain of SATB1. Nucleic Acids Research, 2012, 40, 4193-4202.	14.5	37
50	Structure of an L27 Domain Heterotrimer from Cell Polarity Complex Patj/Pals1/Mals2 Reveals Mutually Independent L27 Domain Assembly Mode. Journal of Biological Chemistry, 2012, 287, 11132-11140.	3.4	14
51	Crystal Structure of Elongator Subcomplex Elp4. Journal of Biological Chemistry, 2012, 287, 21501-21508.	3.4	38
52	Structural and mechanistic insights into the activation of Stromal interaction molecule 1 (STIM1). Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5657-5662.	7.1	185
53	Structure of Escherichia coli BamB and its interaction with POTRA domains of BamA. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1134-1139.	2.5	16
54	Structural Insights into TIR Domain Specificity of the Bridging Adaptor Mal in TLR4 Signaling. PLoS ONE, 2012, 7, e34202.	2.5	62

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55	Structural Insights into the Assembly of CARMA1 and BCL10. <i>PLoS ONE</i> , 2012, 7, e42775.	2.5	37
56	Structure of <i>Escherichia coli</i> BamD and its functional implications in outer membrane protein assembly. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 95-101.	2.5	40
57	Interactions of <i>Bordetella pertussis</i> adenylyl cyclase toxin CyaA with calmodulin mutants and calmodulin antagonists: Comparison with membranous adenylyl cyclase I. <i>Biochemical Pharmacology</i> , 2012, 83, 839-848.	4.4	9
58	Inhibition of the adenylyl cyclase toxin, edema factor, from <i>Bacillus anthracis</i> by a series of 18 mono- and bis-(M)ANT-substituted nucleoside 5'-triphosphates. <i>Naunyn-Schmiedeberg's Archives of Pharmacology</i> , 2012, 385, 57-68.	3.0	12
59	Structures of human pancreatic $\alpha$ -amylase in complex with acarviostatins: Implications for drug design against type II diabetes. <i>Journal of Structural Biology</i> , 2011, 174, 196-202.	2.8	49
60	Structural insight into substrate specificity of human intestinal maltase-glucoamylase. <i>Protein and Cell</i> , 2011, 2, 827-836.	11.0	185
61	Crystallization and preliminary X-ray data collection of the L27PAT(L27N,L27C)Pals1-L27MALStripartite complex. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1443-1447.	0.7	1
62	Bis-Halogen-Anthraniloyl-Substituted Nucleoside 5'-Triphosphates as Potent and Selective Inhibitors of <i>Bordetella pertussis</i> Adenylyl Cyclase Toxin. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2011, 336, 104-115.	2.5	23
63	Structural insight into human variegate porphyria disease. <i>FASEB Journal</i> , 2011, 25, 653-664.	0.5	54
64	Crystal Structure of Outer Membrane Protein NMB0315 from <i>Neisseria meningitidis</i> . <i>PLoS ONE</i> , 2011, 6, e26845.	2.5	28
65	Crystal structures of catalytic core domain of BIV integrase: implications for the interaction between integrase and target DNA. <i>Protein and Cell</i> , 2010, 1, 363-370.	11.0	3
66	Structural basis for tandem L27 domain-mediated polymerization. <i>FASEB Journal</i> , 2010, 24, 4806-4815.	0.5	9
67	Cytidylyl and Uridylyl Cyclase Activity of <i>Bacillus anthracis</i> Edema Factor and <i>Bordetella pertussis</i> CyaA. <i>Biochemistry</i> , 2010, 49, 5494-5503.	2.5	59
68	Structural insight into unique properties of protoporphyrinogen oxidase from <i>Bacillus subtilis</i> . <i>Journal of Structural Biology</i> , 2010, 170, 76-82.	2.8	55
69	Molecular Analysis of the Interaction of Anthrax Adenylyl Cyclase Toxin, Edema Factor, with 2'-O-(N-(methyl)anthraniloyl)-Substituted Purine and Pyrimidine Nucleotides. <i>Molecular Pharmacology</i> , 2009, 75, 693-703.	2.3	36
70	Crystal structures of catalytic and regulatory subunits of rat protein kinase CK2. <i>Science Bulletin</i> , 2009, 54, 220-226.	9.0	3
71	Crystal structure of lipoprotein GNA1946 from <i>Neisseria meningitidis</i> . <i>Journal of Structural Biology</i> , 2009, 168, 437-443.	2.8	13
72	A fluorimetric assay for real-time monitoring of adenylyl cyclase activity based on terbium norfloxacin. <i>Analytical Biochemistry</i> , 2008, 381, 86-93.	2.4	29

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73	Structural Basis of $\beta$ -Catenin Recognition by Tax-interacting Protein-1. <i>Journal of Molecular Biology</i> , 2008, 384, 255-263.	4.2	32
74	Molecular Analysis of the Interaction of <i>Bordetella pertussis</i> Adenylyl Cyclase with Fluorescent Nucleotides. <i>Molecular Pharmacology</i> , 2007, 72, 526-535.	2.3	37
75	Structures of human insulin-degrading enzyme reveal a new substrate recognition mechanism. <i>Nature</i> , 2006, 443, 870-874.	27.8	315
76	Calcium-independent calmodulin binding and two-metal <sup>+</sup> ion catalytic mechanism of anthrax edema factor. <i>EMBO Journal</i> , 2005, 24, 929-941.	7.8	127
77	Structural basis for the interaction of <i>Bordetella pertussis</i> adenylyl cyclase toxin with calmodulin. <i>EMBO Journal</i> , 2005, 24, 3190-3201.	7.8	127
78	Structural and Kinetic Analyses of the Interaction of Anthrax Adenylyl Cyclase Toxin with Reaction Products cAMP and Pyrophosphate. <i>Journal of Biological Chemistry</i> , 2004, 279, 29427-29435.	3.4	52
79	Physiological calcium concentrations regulate calmodulin binding and catalysis of adenylyl cyclase exotoxins. <i>EMBO Journal</i> , 2002, 21, 6721-6732.	7.8	91