Zhiheng Yu

List of Publications by Year in descending order

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586496 721071 1,177 22 16 23 h-index citations g-index papers 25 25 25 2138 docs citations times ranked citing authors all docs

#	Article	IF	Citations
1	Cryo-EM structures of the human GATOR1-Rag-Ragulator complex reveal a spatial-constraint regulated GAP mechanism. Molecular Cell, 2022, 82, 1836-1849.e5.	4.5	19
2	Cryo-EM structure of the EBV ribonucleotide reductase BORF2 and mechanism of APOBEC3B inhibition. Science Advances, 2022, 8, eabm2827.	4.7	15
3	Cryoâ€EM structures of the Human GATOR1â€Ragâ€Ragulator Complex Reveal a Spatialâ€Constraint Regulated GAP Mechanism. FASEB Journal, 2022, 36, .	0.2	0
4	Cryo-EM structures of excitatory amino acid transporter 3 visualize coupled substrate, sodium, and proton binding and transport. Science Advances, 2021, 7, .	4.7	28
5	CryoEM structure of the antibacterial target PBP1b at 3.3 Å resolution. Nature Communications, 2021, 12, 2775.	5.8	10
6	Structure and RNA template requirements of <i>Arabidopsis</i> RNA-DEPENDENT RNA POLYMERASE 2. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	25
7	Structural insight into the <i>Staphylococcus aureus</i> ATP-driven exporter of virulent peptide toxins. Science Advances, 2020, 6, .	4.7	9
8	The structural basis of Rubisco phase separation in the pyrenoid. Nature Plants, 2020, 6, 1480-1490.	4.7	68
9	Microdomains form on the luminal face of neuronal extracellular vesicle membranes. Scientific Reports, 2020, 10, 11953.	1.6	14
10	Structure of human GABAB receptor in an inactive state. Nature, 2020, 584, 304-309.	13.7	59
11	T3S injectisome needle complex structures in four distinct states reveal the basis of membrane coupling and assembly. Nature Microbiology, 2019, 4, 2010-2019.	5.9	58
12	Cryo-EM Structure of the Human FLCN-FNIP2-Rag-Ragulator Complex. Cell, 2019, 179, 1319-1329.e8.	13.5	98
13	Cryo-EM structure of the homohexameric T3SS ATPase-central stalk complex reveals rotary ATPase-like asymmetry. Nature Communications, 2019, 10, 626.	5.8	58
14	Structure of an endosomal signaling GPCR–G protein–β-arrestin megacomplex. Nature Structural and Molecular Biology, 2019, 26, 1123-1131.	3.6	139
15	Structure of Plasmodium falciparum Rh5–CyRPA–Ripr invasion complex. Nature, 2019, 565, 118-121.	13.7	74
16	Cryo-EM analysis of the T3S injectisome reveals the structure of the needle and open secretin. Nature Communications, 2018, 9, 3840.	5.8	106
17	Cryo-EM structure of an essential Plasmodium vivax invasion complex. Nature, 2018, 559, 135-139.	13.7	43
18	Near-atomic resolution cryoelectron microscopy structure of the 30-fold homooligomeric SpollIAG channel essential to spore formation in <i>Bacillus subtilis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E7073-E7081.	3.3	32

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#	Article	IF	CITATIONS
19	Structural basis of bacterial transcription activation. Science, 2017, 358, 947-951.	6.0	71
20	Near-atomic-resolution cryo-EM analysis of the Salmonella T3S injectisome basal body. Nature, 2016, 540, 597-601.	13.7	127
21	Unclosed HIV-1 Capsids Suggest a Curled Sheet Model of Assembly. Journal of Molecular Biology, 2013, 425, 112-123.	2.0	60
22	Lenalidomide plus high-dose dexamethasone provides improved overall survival compared to high-dose dexamethasone alone for relapsed or refractory multiple myeloma (MM): Results of a North American phase III study (MM-009). Journal of Clinical Oncology, 2006, 24, 7521-7521.	0.8	45