## Yifan Cheng

List of Publications by Year in descending order

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YIEAN CHENC

#	Article	IF	CITATIONS
1	Selective G protein signaling driven by substance P–neurokinin receptor dynamics. Nature Chemical Biology, 2022, 18, 109-115.	8.0	40
2	Sensory TRP Channels in Three Dimensions. Annual Review of Biochemistry, 2022, 91, 629-649.	11.1	22
3	TRPV1 and Piezo: the 2021 Nobel Prize in Physiology or Medicine. IUCrJ, 2022, 9, 4-5.	2.2	4
4	Allostery Modulates Interactions between Proteasome Core Particles and Regulatory Particles. Biomolecules, 2022, 12, 764.	4.0	3
5	Molecular goniometers for single-particle cryo-electron microscopy of DNA-binding proteins. Nature Biotechnology, 2021, 39, 378-386.	17.5	26
6	Bi-paratopic and multivalent VH domains block ACE2 binding and neutralize SARS-CoV-2. Nature Chemical Biology, 2021, 17, 113-121.	8.0	78
7	A tumor-specific mechanism of T <sub>reg</sub> enrichment mediated by the integrin αvβ8. Science Immunology, 2021, 6, .	11.9	17
8	Identification of recombinant Fabs for structural and functional characterization of HIV-host factor complexes. PLoS ONE, 2021, 16, e0250318.	2.5	0
9	High-power near-concentric Fabry–Perot cavity for phase contrast electron microscopy. Review of Scientific Instruments, 2021, 92, 053005.	1.3	24
10	Structural snapshots of TRPV1 reveal mechanism of polymodal functionality. Cell, 2021, 184, 5138-5150.e12.	28.9	101
11	Classifying Liganded States in Heterogeneous Single-Particle Cryo-EM Datasets. Microscopy (Oxford,) Tj ETQq1 1	0,784314 1.5	∙ rgBT /Over
12	Dispatched uses Na+ flux to power release of lipid-modified Hedgehog. Nature, 2021, 599, 320-324.	27.8	16
13	Amino and PEG-amino graphene oxide grids enrich and protect samples for high-resolution single particle cryo-electron microscopy. Journal of Structural Biology, 2020, 209, 107437.	2.8	45
14	Structure of hepcidin-bound ferroportin reveals iron homeostatic mechanisms. Nature, 2020, 586, 807-811.	27.8	172
15	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. Science, 2020, 370, .	12.6	508
16	Protein nanoribbons template enamel mineralization. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 19201-19208.	7.1	46
17	Lipid Nanodiscs via Ordered Copolymers. CheM, 2020, 6, 2782-2795.	11.7	32
18	Allosteric coupling between α-rings of the 20S proteasome. Nature Communications, 2020, 11, 4580.	12.8	16

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19	Stoichiometry of Nucleotide Binding to Proteasome AAA+ ATPase Hexamer Established by Native Mass Spectrometry. Molecular and Cellular Proteomics, 2020, 19, 1997-2015.	3.8	2
20	General and robust covalently linked graphene oxide affinity grids for high-resolution cryo-EM. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 24269-24273.	7.1	71
21	Hedgehog pathway activation through nanobody-mediated conformational blockade of the Patched sterol conduit. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 28838-28846.	7.1	22
22	Ion transport and regulation in a synaptic vesicle glutamate transporter. Science, 2020, 368, 893-897.	12.6	53
23	Irritant-evoked activation and calcium modulation of the TRPA1 receptor. Nature, 2020, 585, 141-145.	27.8	93
24	Cryo-EM Reveals Integrin-Mediated TGF-β Activation without Release from Latent TGF-β. Cell, 2020, 180, 490-501.e16.	28.9	102
25	Highâ€resolution structures of <scp>transient receptor potential vanilloid</scp> channels: Unveiling a functionally diverse group of ion channels. Protein Science, 2020, 29, 1569-1580.	7.6	20
26	Enhancing the signal-to-noise ratio and generating contrast for cryo-EM images with convolutional neural networks. IUCrJ, 2020, 7, 1142-1150.	2.2	24
27	Membrane mimetic systems in CryoEM: keeping membrane proteins in their native environment. Current Opinion in Structural Biology, 2019, 58, 259-268.	5.7	60
28	Structural Studies αvβ8 Integrin by Single Particle Cryo-EM. Microscopy and Microanalysis, 2019, 25, 1312-1313.	0.4	0
29	Single-particle cryo-EM: beyond the resolution. National Science Review, 2019, 6, 864-866.	9.5	9
30	Antibody-Drug Conjugates Targeting the Urokinase Receptor (uPAR) as a Possible Treatment of Aggressive Breast Cancer. Antibodies, 2019, 8, 54.	2.5	16
31	Current outcomes when optimizing â€~standard' sample preparation for singleâ€particle cryoâ€EM. Journal of Microscopy, 2019, 276, 39-45.	1.8	41
32	Structural insights into TRPM8 inhibition and desensitization. Science, 2019, 365, 1434-1440.	12.6	118
33	Why recombinant antibodies — benefits and applications. Current Opinion in Biotechnology, 2019, 60, 153-158.	6.6	44
34	Structural insight into TRPV5 channel function and modulation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8869-8878.	7.1	78
35	Cryo-EM structures of remodeler-nucleosome intermediates suggest allosteric control through the nucleosome. ELife, 2019, 8, .	6.0	70
36	Structure of the human TRPM4 ion channel in a lipid nanodisc. Science, 2018, 359, 228-232.	12.6	219

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37	Integrin αvβ8–expressing tumor cells evade host immunity by regulating TGF-β activation in immune cells. JCI Insight, 2018, 3, .	5.0	82
38	Structural Basis for Cholesterol Transport-like Activity of the Hedgehog Receptor Patched. Cell, 2018, 175, 1352-1364.e14.	28.9	197
39	Membrane protein structural biology in the era of single particle cryo-EM. Current Opinion in Structural Biology, 2018, 52, 58-63.	5.7	122
40	Structural basis for activation of voltage sensor domains in an ion channel TPC1. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E9095-E9104.	7.1	40
41	Single-particle cryo-EM—How did it get here and where will it go. Science, 2018, 361, 876-880.	12.6	291
42	Cryo-EM structure of the αvβ8 integrin reveals a mechanism for stabilizing integrin extension. Nature Structural and Molecular Biology, 2018, 25, 698-704.	8.2	40
43	Cryo-EM structure of a fungal mitochondrial calcium uniporter. Nature, 2018, 559, 570-574.	27.8	125
44	A simple and robust procedure for preparing graphene-oxide cryo-EM grids. Journal of Structural Biology, 2018, 204, 80-84.	2.8	101
45	The first single particle analysis Map Challenge: A summary of the assessments. Journal of Structural Biology, 2018, 204, 291-300.	2.8	17
46	Fab-based inhibitors reveal ubiquitin independent functions for HIV Vif neutralization of APOBEC3 restriction factors. PLoS Pathogens, 2018, 14, e1006830.	4.7	17
47	MotionCor2: anisotropic correction of beam-induced motion for improved cryo-electron microscopy. Nature Methods, 2017, 14, 331-332.	19.0	6,166
48	Controlling Styrene Maleic Acid Lipid Particles through RAFT. Biomacromolecules, 2017, 18, 3706-3713.	5.4	44
49	Cryo-EM structures of the TMEM16A calcium-activated chloride channel. Nature, 2017, 552, 426-429.	27.8	274
50	Electron cryo-microscopy structure of the mechanotransduction channel NOMPC. Nature, 2017, 547, 118-122.	27.8	198
51	TRPV1 structures in nanodiscs reveal mechanisms of ligand and lipid action. Nature, 2016, 534, 347-351.	27.8	702
52	A saposin-lipoprotein nanoparticle system for membrane proteins. Nature Methods, 2016, 13, 345-351.	19.0	209
53	Automated structure refinement of macromolecular assemblies from cryo-EM maps using Rosetta. ELife, 2016, 5, .	6.0	407
54	Rqc2p and 60 <i>S</i> ribosomal subunits mediate mRNA-independent elongation of nascent chains. Science, 2015, 347, 75-78.	12.6	245

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55	Alignment of direct detection device micrographs using a robust Optical Flow approach. Journal of Structural Biology, 2015, 189, 163-176.	2.8	59
56	Mechanistic insights into the recycling machine of the SNARE complex. Nature, 2015, 518, 61-67.	27.8	216
57	A Primer to Single-Particle Cryo-Electron Microscopy. Cell, 2015, 161, 438-449.	28.9	478
58	Single-Particle Cryo-EM at Crystallographic Resolution. Cell, 2015, 161, 450-457.	28.9	481
59	Structure of the TRPA1 ion channel suggests regulatory mechanisms. Nature, 2015, 520, 511-517.	27.8	522
60	Asynchronous data acquisition and on-the-fly analysis of dose fractionated cryoEM images by UCSFImage. Journal of Structural Biology, 2015, 192, 174-178.	2.8	92
61	EMRinger: side chain–directed model and map validation for 3D cryo-electron microscopy. Nature Methods, 2015, 12, 943-946.	19.0	799
62	Glycine receptor mechanism elucidated by electron cryo-microscopy. Nature, 2015, 526, 224-229.	27.8	370
63	Subnanometre-resolution electron cryomicroscopy structure of a heterodimeric ABC exporter. Nature, 2015, 517, 396-400.	27.8	114
64	Selective Targeting of TGF-β Activation to Treat Fibroinflammatory Airway Disease. Science Translational Medicine, 2014, 6, 241ra79.	12.4	79
65	Structure of the TRPV1 ion channel determined by electron cryo-microscopy. Nature, 2013, 504, 107-112.	27.8	1,451
66	TRPV1 structures in distinct conformations reveal activation mechanisms. Nature, 2013, 504, 113-118.	27.8	895
67	Influence of electron dose rate on electron counting images recorded with the K2 camera. Journal of Structural Biology, 2013, 184, 251-260.	2.8	99
68	Acetylation-Mediated Proteasomal Degradation of Core Histones during DNA Repair and Spermatogenesis. Cell, 2013, 153, 1012-1024.	28.9	272
69	Electron counting and beam-induced motion correction enable near-atomic-resolution single-particle cryo-EM. Nature Methods, 2013, 10, 584-590.	19.0	1,707
70	Fabs Enable Single Particle cryoEM Studies of Small Proteins. Structure, 2012, 20, 582-592.	3.3	154
71	Visualizing Proteins and Macromolecular Complexes by Negative Stain EM: from Grid Preparation to Image Acquisition. Journal of Visualized Experiments, 2011, , .	0.3	109
72	Interactions of PAN's C-termini with archaeal 20S proteasome and implications for the eukaryotic proteasome–ATPase interactions. EMBO Journal, 2010, 29, 692-702.	7.8	100

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73	The chromatin remodeller ACF acts as a dimeric motor to space nucleosomes. Nature, 2009, 462, 1016-1021.	27.8	160
74	Mechanism of Gate Opening in the 20S Proteasome by the Proteasomal ATPases. Molecular Cell, 2008, 30, 360-368.	9.7	334
75	Docking of the Proteasomal ATPases' Carboxyl Termini in the 20S Proteasome's α Ring Opens the Gate for Substrate Entry. Molecular Cell, 2007, 27, 731-744.	9.7	460
76	Lipid–protein interactions in double-layered two-dimensional AQP0 crystals. Nature, 2005, 438, 633-638.	27.8	617
77	ATP Binding to PAN or the 26S ATPases Causes Association with the 20S Proteasome, Gate Opening, and Translocation of Unfolded Proteins. Molecular Cell, 2005, 20, 687-698.	9.7	230
78	Negative staining and image classification — powerful tools in modern electron microscopy. Biological Procedures Online, 2004, 6, 23-34.	2.9	598