Yifan Cheng

List of Publications by Year
in descending order

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78	21,959	44069	74163
papers	citations	48 h-index	75 g-index

99	99	99	23826
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	MotionCor2: anisotropic correction of beam-induced motion for improved cryo-electron microscopy. Nature Methods, 2017, 14, 331-332.	19.0	6,166
2	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
3	Structure of the TRPV1 ion channel determined by electron cryo-microscopy. Nature, 2013, 504, 107-112.	27.8	1,451
4	TRPV1 structures in distinct conformations reveal activation mechanisms. Nature, 2013, 504, 113-118.	27.8	895
5	EMRinger: side chainâ€“directed model and map validation for 3D cryo-electron microscopy. Nature Methods, 2015, 12, 943-946.	19.0	799
6	TRPV1 structures in nanodiscs reveal mechanisms of ligand and lipid action. Nature, 2016, 534, 347-351.	27.8	702
7	Lipidâ€“protein interactions in double-layered two-dimensional AQP0 crystals. Nature, 2005, 438, 633-638.	27.8	617
8	Negative staining and image classification â€” powerful tools in modern electron microscopy. Biological Procedures Online, 2004, 6, 23-34.	2.9	598
9	Structure of the TRPA1 ion channel suggests regulatory mechanisms. Nature, 2015, 520, 511-517.	27.8	522
10	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. Science, 2020, 370, .	12.6	508
11	Single-Particle Cryo-EM at Crystallographic Resolution. Cell, 2015, 161, 450-457.	28.9	481
12	A Primer to Single-Particle Cryo-Electron Microscopy. Cell, 2015, 161, 438-449.	28.9	478
13	Docking of the Proteasomal ATPases' Carboxyl Termini in the 20S Proteasome's Î± Ring Opens the Gate for Substrate Entry. Molecular Cell, 2007, 27, 731-744.	9.7	460
14	Automated structure refinement of macromolecular assemblies from cryo-EM maps using Rosetta. ELife, 2016, 5, .	6.0	407
15	Glycine receptor mechanism elucidated by electron cryo-microscopy. Nature, 2015, 526, 224-229.	27.8	370
16	Mechanism of Gate Opening in the 20S Proteasome by the Proteasomal ATPases. Molecular Cell, 2008, 30, 360-368.	9.7	334
17	Single-particle cryo-EMâ€”How did it get here and where will it go. Science, 2018, 361, 876-880.	12.6	291
18	Cryo-EM structures of the TMEM16A calcium-activated chloride channel. Nature, 2017, 552, 426-429.	27.8	274

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19	Acetylation-Mediated Proteasomal Degradation of Core Histones during DNA Repair and Spermatogenesis. Cell, 2013, 153, 1012-1024.	28.9	272
20	Rqc2p and 60 S ribosomal subunits mediate mRNA-independent elongation of nascent chains. Science, 2015, 347, 75-78.	12.6	245
21	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
22	Structure of the human TRPM4 ion channel in a lipid nanodisc. Science, 2018, 359, 228-232.	12.6	219
23	Mechanistic insights into the recycling machine of the SNARE complex. Nature, 2015, 518, 61-67.	27.8	216
24	A saposin-lipoprotein nanoparticle system for membrane proteins. Nature Methods, 2016, 13, 345-351.	19.0	209
25	Electron cryo-microscopy structure of the mechanotransduction channel NOMPC. Nature, 2017, 547, 118-122.	27.8	198
26	Structural Basis for Cholesterol Transport-like Activity of the Hedgehog Receptor Patched. Cell, 2018, 175, 1352-1364.e14.	28.9	197
27	Structure of hepcidin-bound ferroportin reveals iron homeostatic mechanisms. Nature, 2020, 586, 807-811.	27.8	172
28	The chromatin remodeller ACF acts as a dimeric motor to space nucleosomes. Nature, 2009, 462, 1016-1021.	27.8	160
29	Fabs Enable Single Particle cryoEM Studies of Small Proteins. Structure, 2012, 20, 582-592.	3.3	154
30	Cryo-EM structure of a fungal mitochondrial calcium uniporter. Nature, 2018, 559, 570-574.	27.8	125
31	Membrane protein structural biology in the era of single particle cryo-EM. Current Opinion in Structural Biology, 2018, 52, 58-63.	5.7	122
32	Structural insights into TRPM8 inhibition and desensitization. Science, 2019, 365, 1434-1440.	12.6	118
33	Subnanometre-resolution electron cryomicroscopy structure of a heterodimeric ABC exporter. Nature, 2015, 517, 396-400.	27.8	114
34	Visualizing Proteins and Macromolecular Complexes by Negative Stain EM: from Grid Preparation to Image Acquisition. Journal of Visualized Experiments, 2011, , .	0.3	109
35	Cryo-EM Reveals Integrin-Mediated TGF-Î² Activation without Release from Latent TGF-Î². Cell, 2020, 180, 490-501.e16.	28.9	102
36	A simple and robust procedure for preparing graphene-oxide cryo-EM grids. Journal of Structural Biology, 2018, 204, 80-84.	2.8	101

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37	Structural snapshots of TRPV1 reveal mechanism of polymodal functionality. Cell, 2021, 184, 5138-5150.e12.	28.9	101
38	Interactions of PAN's C-termini with archaeal 20S proteasome and implications for the eukaryotic proteasomeâ€“ATPase interactions. EMBO Journal, 2010, 29, 692-702.	7.8	100
39	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
40	Irritant-evoked activation and calcium modulation of the TRPA1 receptor. Nature, 2020, 585, 141-145.	27.8	93
41	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
42	Integrin Î±vÎ²8â€“expressing tumor cells evade host immunity by regulating TGF-Î² activation in immune cells. JCI Insight, 2018, 3, .	5.0	82
43	Selective Targeting of TGF-Î² Activation to Treat Fibroinflammatory Airway Disease. Science Translational Medicine, 2014, 6, 241ra79.	12.4	79
44	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
45	Bi-paratopic and multivalent VH domains block ACE2 binding and neutralize SARS-CoV-2. Nature Chemical Biology, 2021, 17, 113-121.	8.0	78
46	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
47	Cryo-EM structures of remodeler-nucleosome intermediates suggest allosteric control through the nucleosome. ELife, 2019, 8, .	6.0	70
48	Membrane mimetic systems in CryoEM: keeping membrane proteins in their native environment. Current Opinion in Structural Biology, 2019, 58, 259-268.	5.7	60
49	Alignment of direct detection device micrographs using a robust Optical Flow approach. Journal of Structural Biology, 2015, 189, 163-176.	2.8	59
50	Ion transport and regulation in a synaptic vesicle glutamate transporter. Science, 2020, 368, 893-897.	12.6	53
51	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
52	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
53	Controlling Styrene Maleic Acid Lipid Particles through RAFT. Biomacromolecules, 2017, 18, 3706-3713.	5.4	44
54	Why recombinant antibodies â€" benefits and applications. Current Opinion in Biotechnology, 2019, 60, 153-158.	6.6	44

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55	Current outcomes when optimizing â€˜standardâ€™ sample preparation for singleâ€particle cryoâ€EM. Journal of Microscopy, 2019, 276, 39-45.	1.8	41
56	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
57	Cryo-EM structure of the Î±vÎ²8 integrin reveals a mechanism for stabilizing integrin extension. Nature Structural and Molecular Biology, 2018, 25, 698-704.	8.2	40
58	Selective G protein signaling driven by substance Pâ€“neurokinin receptor dynamics. Nature Chemical Biology, 2022, 18, 109-115.	8.0	40
59	Lipid Nanodiscs via Ordered Copolymers. CheM, 2020, 6, 2782-2795.	11.7	32
60	Molecular goniometers for single-particle cryo-electron microscopy of DNA-binding proteins. Nature Biotechnology, 2021, 39, 378-386.	17.5	26
61	High-power near-concentric Fabryâ€“Perot cavity for phase contrast electron microscopy. Review of Scientific Instruments, 2021, 92, 053005.	1.3	24
62	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
63	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
64	Sensory TRP Channels in Three Dimensions. Annual Review of Biochemistry, 2022, 91, 629-649.	11.1	22
65	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
66	The first single particle analysis Map Challenge: A summary of the assessments. Journal of Structural Biology, 2018, 204, 291-300.	2.8	17
67	A tumor-specific mechanism of T _{reg} enrichment mediated by the integrin Î±vÎ²8. Science Immunology, 2021, 6, .	11.9	17
68	Fab-based inhibitors reveal ubiquitin independent functions for HIV Vif neutralization of APOBEC3 restriction factors. PLoS Pathogens, 2018, 14, e1006830.	4.7	17
69	Antibody-Drug Conjugates Targeting the Urokinase Receptor (uPAR) as a Possible Treatment of Aggressive Breast Cancer. Antibodies, 2019, 8, 54.	2.5	16
70	Allosteric coupling between Î±-rings of the 20S proteasome. Nature Communications, 2020, 11, 4580.	12.8	16
71	Dispatched uses Na+ flux to power release of lipid-modified Hedgehog. Nature, 2021, 599, 320-324.	27.8	16
72	Single-particle cryo-EM: beyond the resolution. National Science Review, 2019, 6, 864-866.	9.5	9

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73	TRPV1 and Piezo: the 2021 Nobel Prize in Physiology or Medicine. IUCrJ, 2022, 9, 4-5.	2.2	4
74	Allostery Modulates Interactions between Proteasome Core Particles and Regulatory Particles. Biomolecules, 2022, 12, 764.	4.0	3
75	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
76	Structural Studies Î±vÎ²8 Integrin by Single Particle Cryo-EM. Microscopy and Microanalysis, 2019, 25, 1312-1313.	0.4	0
77	Identification of recombinant Fabs for structural and functional characterization of HIV-host factor complexes. PLoS ONE, 2021, 16, e0250318.	2.5	0
78	Classifying Liganded States in Heterogeneous Single-Particle Cryo-EM Datasets. Microscopy (Oxford,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.5	0