

Zanlin Yu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1620189/publications.pdf>

Version: 2024-02-01

102
papers

18,361
citations

50566

48
h-index

40945

97
g-index

113
all docs

113
docs citations

113
times ranked

24228
citing authors

#	ARTICLE	IF	CITATIONS
1	Selective G protein signaling driven by substance Pâ€“neurokinin receptor dynamics. <i>Nature Chemical Biology</i> , 2022, 18, 109-115.	3.9	40
2	Sensory TRP Channels in Three Dimensions. <i>Annual Review of Biochemistry</i> , 2022, 91, 629-649.	5.0	22
3	TRPV1 and Piezo: the 2021 Nobel Prize in Physiology or Medicine. <i>IUCr</i> , 2022, 9, 4-5.	1.0	4
4	Allostery Modulates Interactions between Proteasome Core Particles and Regulatory Particles. <i>Biomolecules</i> , 2022, 12, 764.	1.8	3
5	Viral E protein neutralizes BET protein-mediated post-entry antagonism of SARS-CoV-2. <i>Cell Reports</i> , 2022, 40, 111088.	2.9	15
6	Molecular goniometers for single-particle cryo-electron microscopy of DNA-binding proteins. <i>Nature Biotechnology</i> , 2021, 39, 378-386.	9.4	26
7	Structure of the radial spoke head and insights into its role in mechanoregulation of ciliary beating. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 20-28.	3.6	39
8	A tumor-specific mechanism of T _{reg} enrichment mediated by the integrin Î±vÎ²8. <i>Science Immunology</i> , 2021, 6, .	5.6	17
9	Identification of recombinant Fabs for structural and functional characterization of HIV-host factor complexes. <i>PLoS ONE</i> , 2021, 16, e0250318.	1.1	0
10	High-power near-concentric Fabryâ€“Perot cavity for phase contrast electron microscopy. <i>Review of Scientific Instruments</i> , 2021, 92, 053005.	0.6	24
11	Structural insight into SARS-CoV-2 neutralizing antibodies and modulation of syncytia. <i>Cell</i> , 2021, 184, 3192-3204.e16.	13.5	68
12	Practical considerations for using K3 cameras in CDS mode for high-resolution and high-throughput single particle cryo-EM. <i>Journal of Structural Biology</i> , 2021, 213, 107745.	1.3	33
13	Structural snapshots of TRPV1 reveal mechanism of polymodal functionality. <i>Cell</i> , 2021, 184, 5138-5150.e12.	13.5	101
14	Classifying Liganded States in Heterogeneous Single-Particle Cryo-EM Datasets. <i>Microscopy (Oxford,)</i> Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.7	0
15	Dispatched uses Na ⁺ flux to power release of lipid-modified Hedgehog. <i>Nature</i> , 2021, 599, 320-324.	13.7	16
16	Amino and PEG-amino graphene oxide grids enrich and protect samples for high-resolution single particle cryo-electron microscopy. <i>Journal of Structural Biology</i> , 2020, 209, 107437.	1.3	45
17	Structure of hepcidin-bound ferroportin reveals iron homeostatic mechanisms. <i>Nature</i> , 2020, 586, 807-811.	13.7	172
18	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. <i>Science</i> , 2020, 370, .	6.0	508

#	ARTICLE	IF	CITATIONS
19	Protein nanoribbons template enamel mineralization. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 19201-19208.	3.3	46
20	The application of deep learning based diagnostic system to cervical squamous intraepithelial lesions recognition in colposcopy images. Scientific Reports, 2020, 10, 11639.	1.6	54
21	Targeting Phosphotyrosine in Native Proteins with Conditional, Bispecific Antibody Traps. Journal of the American Chemical Society, 2020, 142, 17703-17713.	6.6	7
22	Allosteric coupling between $\hat{\pm}$ -rings of the 20S proteasome. Nature Communications, 2020, 11, 4580.	5.8	16
23	Stoichiometry of Nucleotide Binding to Proteasome AAA+ ATPase Hexamer Established by Native Mass Spectrometry. Molecular and Cellular Proteomics, 2020, 19, 1997-2015.	2.5	2
24	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.	3.3	71
25	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.	3.3	22
26	Ion transport and regulation in a synaptic vesicle glutamate transporter. Science, 2020, 368, 893-897.	6.0	53
27	Irritant-evoked activation and calcium modulation of the TRPA1 receptor. Nature, 2020, 585, 141-145.	13.7	93
28	Exploring long-range cooperativity in the 20S proteasome core particle from <i>Thermoplasma acidophilum</i> using methyl-TROSY-based NMR. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 5298-5309.	3.3	16
29	Cryo-EM Reveals Integrin-Mediated TGF- $\hat{1}^2$ Activation without Release from Latent TGF- $\hat{1}^2$. Cell, 2020, 180, 490-501.e16.	13.5	102
30	High-resolution structures of transient receptor potential vanilloid channels: Unveiling a functionally diverse group of ion channels. Protein Science, 2020, 29, 1569-1580.	3.1	20
31	Enhancing the signal-to-noise ratio and generating contrast for cryo-EM images with convolutional neural networks. IUCr, 2020, 7, 1142-1150.	1.0	24
32	Cryo-EM Studies of TMEM16F Calcium-Activated Ion Channel Suggest Features Important for Lipid Scrambling. Cell Reports, 2019, 28, 567-579.e4.	2.9	76
33	Membrane mimetic systems in CryoEM: keeping membrane proteins in their native environment. Current Opinion in Structural Biology, 2019, 58, 259-268.	2.6	60
34	Structural Studies $\hat{\pm}$ $\hat{1}^2$ Integrin by Single Particle Cryo-EM. Microscopy and Microanalysis, 2019, 25, 1312-1313.	0.2	0
35	Single-particle cryo-EM: beyond the resolution. National Science Review, 2019, 6, 864-866.	4.6	9
36	Antibody-Drug Conjugates Targeting the Urokinase Receptor (uPAR) as a Possible Treatment of Aggressive Breast Cancer. Antibodies, 2019, 8, 54.	1.2	16

#	ARTICLE	IF	CITATIONS
37	Structural insights into TRPM8 inhibition and desensitization. <i>Science</i> , 2019, 365, 1434-1440.	6.0	118
38	Why recombinant antibodies are benefits and applications. <i>Current Opinion in Biotechnology</i> , 2019, 60, 153-158.	3.3	44
39	Structural insight into TRPV5 channel function and modulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 8869-8878.	3.3	78
40	Cohesin cleavage by separase is enhanced by a substrate motif distinct from the cleavage site. <i>Nature Communications</i> , 2019, 10, 5189.	5.8	23
41	Cryo-EM of multiple cage architectures reveals a universal mode of clathrin self-assembly. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 890-898.	3.6	56
42	A Nucleosome Bridging Mechanism for Activation of a Maintenance DNA Methyltransferase. <i>Molecular Cell</i> , 2019, 73, 73-83.e6.	4.5	33
43	Cryo-EM structures of remodeler-nucleosome intermediates suggest allosteric control through the nucleosome. <i>ELife</i> , 2019, 8, .	2.8	70
44	Structure of the human TRPM4 ion channel in a lipid nanodisc. <i>Science</i> , 2018, 359, 228-232.	6.0	219
45	Structural Basis for Cholesterol Transport-like Activity of the Hedgehog Receptor Patched. <i>Cell</i> , 2018, 175, 1352-1364.e14.	13.5	197
46	Membrane protein structural biology in the era of single particle cryo-EM. <i>Current Opinion in Structural Biology</i> , 2018, 52, 58-63.	2.6	122
47	Structural basis for activation of voltage sensor domains in an ion channel TPC1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E9095-E9104.	3.3	40
48	Single-particle cryo-EM—How did it get here and where will it go. <i>Science</i> , 2018, 361, 876-880.	6.0	291
49	Cryo-EM structure of the $\alpha 2 \beta 8$ integrin reveals a mechanism for stabilizing integrin extension. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 698-704.	3.6	40
50	Cryo-EM structure of a fungal mitochondrial calcium uniporter. <i>Nature</i> , 2018, 559, 570-574.	13.7	125
51	A simple and robust procedure for preparing graphene-oxide cryo-EM grids. <i>Journal of Structural Biology</i> , 2018, 204, 80-84.	1.3	101
52	The first single particle analysis Map Challenge: A summary of the assessments. <i>Journal of Structural Biology</i> , 2018, 204, 291-300.	1.3	17
53	K3 - A First Look at The New Direct Electron Detection Camera from Gatan Company. <i>Microscopy and Microanalysis</i> , 2018, 24, 890-891.	0.2	6
54	Fab-based inhibitors reveal ubiquitin independent functions for HIV Vif neutralization of APOBEC3 restriction factors. <i>PLoS Pathogens</i> , 2018, 14, e1006830.	2.1	17

#	ARTICLE	IF	CITATIONS
55	Visualizing small molecule binding in membrane protein by single particle cryo-EM. Proceedings for Annual Meeting of the Japanese Pharmacological Society, 2018, WCP2018, SY16-3.	0.0	0
56	MotionCor2: anisotropic correction of beam-induced motion for improved cryo-electron microscopy. Nature Methods, 2017, 14, 331-332.	9.0	6,166
57	Regulation of Rvb1/Rvb2 by a Domain within the INO80 Chromatin Remodeling Complex Implicates the Yeast Rvbs as Protein Assembly Chaperones. Cell Reports, 2017, 19, 2033-2044.	2.9	43
58	Controlling Styrene Maleic Acid Lipid Particles through RAFT. Biomacromolecules, 2017, 18, 3706-3713.	2.6	44
59	Ion Channel in Lipid Nanodisc By Single Particle Cryo-EM - Pushing The Technology Limit. Microscopy and Microanalysis, 2017, 23, 822-823.	0.2	2
60	Cryo-EM structures of the TMEM16A calcium-activated chloride channel. Nature, 2017, 552, 426-429.	13.7	274
61	How Cryo-EM Became so Hot. Cell, 2017, 171, 1229-1231.	13.5	60
62	Electron cryo-microscopy structure of the mechanotransduction channel NOMPC. Nature, 2017, 547, 118-122.	13.7	198
63	TRPV1 structures in nanodiscs reveal mechanisms of ligand and lipid action. Nature, 2016, 534, 347-351.	13.7	702
64	Single-particle cryo-EM data acquisition by using direct electron detection camera. Microscopy (Oxford, England), 2016, 65, 35-41.	0.7	46
65	The Special Issue of Microscopy on single-particle cryo-electron microscopy. Microscopy (Oxford, England), 2016, 65, 35-41.	0.7	46
66	A saposin-lipoprotein nanoparticle system for membrane proteins. Nature Methods, 2016, 13, 345-351.	9.0	209
67	Automated structure refinement of macromolecular assemblies from cryo-EM maps using Rosetta. ELife, 2016, 5, .	2.8	407
68	Evaluation of super-resolution performance of the K2 electron-counting camera using 2D crystals of aquaporin-0. Journal of Structural Biology, 2015, 192, 163-173.	1.3	26
69	Rqc2p and 60S ribosomal subunits mediate mRNA-independent elongation of nascent chains. Science, 2015, 347, 75-78.	6.0	245
70	Disassembly of Lys11 and Mixed Linkage Polyubiquitin Conjugates Provides Insights into Function of Proteasomal Deubiquitinases Rpn11 and Ubp6. Journal of Biological Chemistry, 2015, 290, 4688-4704.	1.6	42
71	Alignment of direct detection device micrographs using a robust Optical Flow approach. Journal of Structural Biology, 2015, 189, 163-176.	1.3	59
72	Mechanistic insights into the recycling machine of the SNARE complex. Nature, 2015, 518, 61-67.	13.7	216

#	ARTICLE	IF	CITATIONS
73	De novo protein structure determination from near-atomic-resolution cryo-EM maps. <i>Nature Methods</i> , 2015, 12, 335-338.	9.0	172
74	A Primer to Single-Particle Cryo-Electron Microscopy. <i>Cell</i> , 2015, 161, 438-449.	13.5	478
75	Single-Particle Cryo-EM at Crystallographic Resolution. <i>Cell</i> , 2015, 161, 450-457.	13.5	481
76	Substrates Control Multimerization and Activation of the Multi-Domain ATPase Motor of Type VII Secretion. <i>Cell</i> , 2015, 161, 501-512.	13.5	124
77	Atomic-accuracy models from 4.5-Å... cryo-electron microscopy data with density-guided iterative local refinement. <i>Nature Methods</i> , 2015, 12, 361-365.	9.0	313
78	Structure of the TRPA1 ion channel suggests regulatory mechanisms. <i>Nature</i> , 2015, 520, 511-517.	13.7	522
79	Asynchronous data acquisition and on-the-fly analysis of dose fractionated cryoEM images by UCSFImage. <i>Journal of Structural Biology</i> , 2015, 192, 174-178.	1.3	92
80	EMRinger: side chain-directed model and map validation for 3D cryo-electron microscopy. <i>Nature Methods</i> , 2015, 12, 943-946.	9.0	799
81	Crystals of a toxic core. <i>Nature</i> , 2015, 525, 458-459.	13.7	6
82	Glycine receptor mechanism elucidated by electron cryo-microscopy. <i>Nature</i> , 2015, 526, 224-229.	13.7	370
83	Subnanometre-resolution electron cryomicroscopy structure of a heterodimeric ABC exporter. <i>Nature</i> , 2015, 517, 396-400.	13.7	114
84	Selective Targeting of TGF- β 2 Activation to Treat Fibroinflammatory Airway Disease. <i>Science Translational Medicine</i> , 2014, 6, 241ra79.	5.8	79
85	Allosteric Communication in the Dynein Motor Domain. <i>Cell</i> , 2014, 159, 857-868.	13.5	97
86	CTER-Rapid estimation of CTF parameters with error assessment. <i>Ultramicroscopy</i> , 2014, 140, 9-19.	0.8	65
87	Single particle electron cryo-microscopy of a mammalian ion channel. <i>Current Opinion in Structural Biology</i> , 2014, 27, 1-7.	2.6	79
88	The export receptor Crm1 forms a dimer to promote nuclear export of HIV RNA. <i>ELife</i> , 2014, 3, e04121.	2.8	58
89	Acetylation-Mediated Proteasomal Degradation of Core Histones during DNA Repair and Spermatogenesis. <i>Cell</i> , 2013, 153, 1012-1024.	13.5	272
90	Mechanistic Analysis of HP1 heterochromatin assembly. <i>FASEB Journal</i> , 2013, 27, 456.3.	0.2	0

#	ARTICLE	IF	CITATIONS
91	Self-Assembly of Filamentous Amelogenin Requires Calcium and Phosphate: From Dimers via Nanoribbons to Fibrils. <i>Biomacromolecules</i> , 2012, 13, 3494-3502.	2.6	42
92	Fabs Enable Single Particle cryoEM Studies of Small Proteins. <i>Structure</i> , 2012, 20, 582-592.	1.6	154
93	Self-assembly of amelogenin proteins at the water-oil interface. <i>European Journal of Oral Sciences</i> , 2011, 119, 75-82.	0.7	20
94	Interactions of PAN's C-termini with archaeal 20S proteasome and implications for the eukaryotic proteasome-ATPase interactions. <i>EMBO Journal</i> , 2010, 29, 692-702.	3.5	100
95	Toward an atomic model of the 26S proteasome. <i>Current Opinion in Structural Biology</i> , 2009, 19, 203-208.	2.6	33
96	The Advent of Near-Atomic Resolution in Single-Particle Electron Microscopy. <i>Annual Review of Biochemistry</i> , 2009, 78, 723-742.	5.0	46
97	Mechanisms of ATP-dependent Chromatin Remodeling Enzymes. <i>FASEB Journal</i> , 2009, 23, 325.2.	0.2	0
98	Mechanism of Gate Opening in the 20S Proteasome by the Proteasomal ATPases. <i>Molecular Cell</i> , 2008, 30, 360-368.	4.5	334
99	Reconstructing the Endocytotic Machinery. <i>Methods in Cell Biology</i> , 2007, 79, 463-487.	0.5	3
100	Docking of the Proteasomal ATPases' Carboxyl Termini in the 20S Proteasome's Î± Ring Opens the Gate for Substrate Entry. <i>Molecular Cell</i> , 2007, 27, 731-744.	4.5	460
101	ATP Binding to PAN or the 26S ATPases Causes Association with the 20S Proteasome, Gate Opening, and Translocation of Unfolded Proteins. <i>Molecular Cell</i> , 2005, 20, 687-698.	4.5	230
102	Negative staining and image classification "powerful tools in modern electron microscopy. <i>Biological Procedures Online</i> , 2004, 6, 23-34.	1.4	598