

Zanlin Yu

List of Publications by Year in descending order

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Version: 2024-02-01

102
papers

18,361
citations

44066

48
h-index

36025

97
g-index

113
all docs

113
docs citations

113
times ranked

22019
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Selective G protein signaling driven by substance Pâ€“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 | Viral E protein neutralizes BET protein-mediated post-entry antagonism of SARS-CoV-2. Cell Reports, 2022, 40, 111088. | 6.4 | 15 |
| 6 | Molecular goniometers for single-particle cryo-electron microscopy of DNA-binding proteins. Nature Biotechnology, 2021, 39, 378-386. | 17.5 | 26 |
| 7 | Structure of the radial spoke head and insights into its role in mechanoregulation of ciliary beating. Nature Structural and Molecular Biology, 2021, 28, 20-28. | 8.2 | 39 |
| 8 | A tumor-specific mechanism of T _{reg} enrichment mediated by the integrin Î±vÎ²8. Science Immunology, 2021, 6, . | 11.9 | 17 |
| 9 | Identification of recombinant Fabs for structural and functional characterization of HIV-host factor complexes. PLoS ONE, 2021, 16, e0250318. | 2.5 | 0 |
| 10 | High-power near-concentric Fabryâ€“Perot cavity for phase contrast electron microscopy. Review of Scientific Instruments, 2021, 92, 053005. | 1.3 | 24 |
| 11 | Structural insight into SARS-CoV-2 neutralizing antibodies and modulation of syncytia. Cell, 2021, 184, 3192-3204.e16. | 28.9 | 68 |
| 12 | Practical considerations for using K3 cameras in CDS mode for high-resolution and high-throughput single particle cryo-EM. Journal of Structural Biology, 2021, 213, 107745. | 2.8 | 33 |
| 13 | Structural snapshots of TRPV1 reveal mechanism of polymodal functionality. Cell, 2021, 184, 5138-5150.e12. | 28.9 | 101 |
| 14 | Classifying Liganded States in Heterogeneous Single-Particle Cryo-EM Datasets. Microscopy (Oxford,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf | 1.5 | 0 |
| 15 | Dispatched uses Na ⁺ flux to power release of lipid-modified Hedgehog. Nature, 2021, 599, 320-324. | 27.8 | 16 |
| 16 | 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 |
| 17 | Structure of hepcidin-bound ferroportin reveals iron homeostatic mechanisms. Nature, 2020, 586, 807-811. | 27.8 | 172 |
| 18 | Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. Science, 2020, 370, . | 12.6 | 508 |

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|----|--|------|-----------|
| 19 | 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 |
| 20 | The application of deep learning based diagnostic system to cervical squamous intraepithelial lesions recognition in colposcopy images. Scientific Reports, 2020, 10, 11639. | 3.3 | 54 |
| 21 | Targeting Phosphotyrosine in Native Proteins with Conditional, Bispecific Antibody Traps. Journal of the American Chemical Society, 2020, 142, 17703-17713. | 13.7 | 7 |
| 22 | Allosteric coupling between $\hat{\pm}$ -rings of the 20S proteasome. Nature Communications, 2020, 11, 4580. | 12.8 | 16 |
| 23 | Stoichiometry of Nucleotide Binding to Proteasome AAA+ ATPase Hexamer Established by Native Mass Spectrometry. Molecular and Cellular Proteomics, 2020, 19, 1997-2015. | 3.8 | 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. | 7.1 | 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. | 7.1 | 22 |
| 26 | Ion transport and regulation in a synaptic vesicle glutamate transporter. Science, 2020, 368, 893-897. | 12.6 | 53 |
| 27 | Irritant-evoked activation and calcium modulation of the TRPA1 receptor. Nature, 2020, 585, 141-145. | 27.8 | 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. | 7.1 | 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. | 28.9 | 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. | 7.6 | 20 |
| 31 | Enhancing the signal-to-noise ratio and generating contrast for cryo-EM images with convolutional neural networks. IUCr, 2020, 7, 1142-1150. | 2.2 | 24 |
| 32 | Cryo-EM Studies of TMEM16F Calcium-Activated Ion Channel Suggest Features Important for Lipid Scrambling. Cell Reports, 2019, 28, 567-579.e4. | 6.4 | 76 |
| 33 | Membrane mimetic systems in CryoEM: keeping membrane proteins in their native environment. Current Opinion in Structural Biology, 2019, 58, 259-268. | 5.7 | 60 |
| 34 | Structural Studies $\hat{1}^2$ Integrin by Single Particle Cryo-EM. Microscopy and Microanalysis, 2019, 25, 1312-1313. | 0.4 | 0 |
| 35 | Single-particle cryo-EM: beyond the resolution. National Science Review, 2019, 6, 864-866. | 9.5 | 9 |
| 36 | Antibody-Drug Conjugates Targeting the Urokinase Receptor (uPAR) as a Possible Treatment of Aggressive Breast Cancer. Antibodies, 2019, 8, 54. | 2.5 | 16 |

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|----|--|------|-----------|
| 37 | Structural insights into TRPM8 inhibition and desensitization. <i>Science</i> , 2019, 365, 1434-1440. | 12.6 | 118 |
| 38 | Why recombinant antibodies â€” benefits and applications. <i>Current Opinion in Biotechnology</i> , 2019, 60, 153-158. | 6.6 | 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. | 7.1 | 78 |
| 40 | Cohesin cleavage by separase is enhanced by a substrate motif distinct from the cleavage site. <i>Nature Communications</i> , 2019, 10, 5189. | 12.8 | 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. | 8.2 | 56 |
| 42 | A Nucleosome Bridging Mechanism for Activation of a Maintenance DNA Methyltransferase. <i>Molecular Cell</i> , 2019, 73, 73-83.e6. | 9.7 | 33 |
| 43 | Cryo-EM structures of remodeler-nucleosome intermediates suggest allosteric control through the nucleosome. <i>ELife</i> , 2019, 8, . | 6.0 | 70 |
| 44 | Structure of the human TRPM4 ion channel in a lipid nanodisc. <i>Science</i> , 2018, 359, 228-232. | 12.6 | 219 |
| 45 | Structural Basis for Cholesterol Transport-like Activity of the Hedgehog Receptor Patched. <i>Cell</i> , 2018, 175, 1352-1364.e14. | 28.9 | 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. | 5.7 | 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. | 7.1 | 40 |
| 48 | Single-particle cryo-EMâ€”How did it get here and where will it go. <i>Science</i> , 2018, 361, 876-880. | 12.6 | 291 |
| 49 | Cryo-EM structure of the Î±vÎ²8 integrin reveals a mechanism for stabilizing integrin extension. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 698-704. | 8.2 | 40 |
| 50 | Cryo-EM structure of a fungal mitochondrial calcium uniporter. <i>Nature</i> , 2018, 559, 570-574. | 27.8 | 125 |
| 51 | A simple and robust procedure for preparing graphene-oxide cryo-EM grids. <i>Journal of Structural Biology</i> , 2018, 204, 80-84. | 2.8 | 101 |
| 52 | The first single particle analysis Map Challenge: A summary of the assessments. <i>Journal of Structural Biology</i> , 2018, 204, 291-300. | 2.8 | 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. | 0.4 | 6 |
| 54 | Fab-based inhibitors reveal ubiquitin independent functions for HIV Vif neutralization of APOBEC3 restriction factors. <i>PLoS Pathogens</i> , 2018, 14, e1006830. | 4.7 | 17 |

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|----|---|------|-----------|
| 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. | 19.0 | 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. | 6.4 | 43 |
| 58 | Controlling Styrene Maleic Acid Lipid Particles through RAFT. Biomacromolecules, 2017, 18, 3706-3713. | 5.4 | 44 |
| 59 | Ion Channel in Lipid Nanodisc By Single Particle Cryo-EM - Pushing The Technology Limit. Microscopy and Microanalysis, 2017, 23, 822-823. | 0.4 | 2 |
| 60 | Cryo-EM structures of the TMEM16A calcium-activated chloride channel. Nature, 2017, 552, 426-429. | 27.8 | 274 |
| 61 | How Cryo-EM Became so Hot. Cell, 2017, 171, 1229-1231. | 28.9 | 60 |
| 62 | Electron cryo-microscopy structure of the mechanotransduction channel NOMPC. Nature, 2017, 547, 118-122. | 27.8 | 198 |
| 63 | TRPV1 structures in nanodiscs reveal mechanisms of ligand and lipid action. Nature, 2016, 534, 347-351. | 27.8 | 702 |
| 64 | Single-particle cryo-EM data acquisition by using direct electron detection camera. Microscopy (Oxford, England), 2016, 65, 35-41. | 1.5 | 46 |
| 65 | The Special Issue of Microscopy on single-particle cryo-electron microscopy. Microscopy (Oxford, England), 2016, 65, 1-4. | 1.5 | 4 |
| 66 | A saposin-lipoprotein nanoparticle system for membrane proteins. Nature Methods, 2016, 13, 345-351. | 19.0 | 209 |
| 67 | Automated structure refinement of macromolecular assemblies from cryo-EM maps using Rosetta. ELife, 2016, 5, . | 6.0 | 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. | 2.8 | 26 |
| 69 | Rqc2p and 60S ribosomal subunits mediate mRNA-independent elongation of nascent chains. Science, 2015, 347, 75-78. | 12.6 | 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. | 3.4 | 42 |
| 71 | Alignment of direct detection device micrographs using a robust Optical Flow approach. Journal of Structural Biology, 2015, 189, 163-176. | 2.8 | 59 |
| 72 | Mechanistic insights into the recycling machine of the SNARE complex. Nature, 2015, 518, 61-67. | 27.8 | 216 |

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|----|---|------|-----------|
| 73 | De novo protein structure determination from near-atomic-resolution cryo-EM maps. <i>Nature Methods</i> , 2015, 12, 335-338. | 19.0 | 172 |
| 74 | A Primer to Single-Particle Cryo-Electron Microscopy. <i>Cell</i> , 2015, 161, 438-449. | 28.9 | 478 |
| 75 | Single-Particle Cryo-EM at Crystallographic Resolution. <i>Cell</i> , 2015, 161, 450-457. | 28.9 | 481 |
| 76 | Substrates Control Multimerization and Activation of the Multi-Domain ATPase Motor of Type VII Secretion. <i>Cell</i> , 2015, 161, 501-512. | 28.9 | 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. | 19.0 | 313 |
| 78 | Structure of the TRPA1 ion channel suggests regulatory mechanisms. <i>Nature</i> , 2015, 520, 511-517. | 27.8 | 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. | 2.8 | 92 |
| 80 | EMRinger: side chainâ€‘directed model and map validation for 3D cryo-electron microscopy. <i>Nature Methods</i> , 2015, 12, 943-946. | 19.0 | 799 |
| 81 | Crystals of a toxic core. <i>Nature</i> , 2015, 525, 458-459. | 27.8 | 6 |
| 82 | Glycine receptor mechanism elucidated by electron cryo-microscopy. <i>Nature</i> , 2015, 526, 224-229. | 27.8 | 370 |
| 83 | Subnanometre-resolution electron cryomicroscopy structure of a heterodimeric ABC exporter. <i>Nature</i> , 2015, 517, 396-400. | 27.8 | 114 |
| 84 | Selective Targeting of TGF-Î² Activation to Treat Fibroinflammatory Airway Disease. <i>Science Translational Medicine</i> , 2014, 6, 241ra79. | 12.4 | 79 |
| 85 | Allosteric Communication in the Dynein Motor Domain. <i>Cell</i> , 2014, 159, 857-868. | 28.9 | 97 |
| 86 | CTERâ€‘Rapid estimation of CTF parameters with error assessment. <i>Ultramicroscopy</i> , 2014, 140, 9-19. | 1.9 | 65 |
| 87 | Single particle electron cryo-microscopy of a mammalian ion channel. <i>Current Opinion in Structural Biology</i> , 2014, 27, 1-7. | 5.7 | 79 |
| 88 | The export receptor Crm1 forms a dimer to promote nuclear export of HIV RNA. <i>ELife</i> , 2014, 3, e04121. | 6.0 | 58 |
| 89 | Acetylation-Mediated Proteasomal Degradation of Core Histones during DNA Repair and Spermatogenesis. <i>Cell</i> , 2013, 153, 1012-1024. | 28.9 | 272 |
| 90 | Mechanistic Analysis of HP1 heterochromatin assembly. <i>FASEB Journal</i> , 2013, 27, 456.3. | 0.5 | 0 |

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|-----|--|------|-----------|
| 91 | Self-Assembly of Filamentous Amelogenin Requires Calcium and Phosphate: From Dimers via Nanoribbons to Fibrils. <i>Biomacromolecules</i> , 2012, 13, 3494-3502. | 5.4 | 42 |
| 92 | Fabs Enable Single Particle cryoEM Studies of Small Proteins. <i>Structure</i> , 2012, 20, 582-592. | 3.3 | 154 |
| 93 | Self-Assembly of amelogenin proteins at the water-oil interface. <i>European Journal of Oral Sciences</i> , 2011, 119, 75-82. | 1.5 | 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. | 7.8 | 100 |
| 95 | Toward an atomic model of the 26S proteasome. <i>Current Opinion in Structural Biology</i> , 2009, 19, 203-208. | 5.7 | 33 |
| 96 | The Advent of Near-Atomic Resolution in Single-Particle Electron Microscopy. <i>Annual Review of Biochemistry</i> , 2009, 78, 723-742. | 11.1 | 46 |
| 97 | Mechanisms of ATP-dependent Chromatin Remodeling Enzymes. <i>FASEB Journal</i> , 2009, 23, 325.2. | 0.5 | 0 |
| 98 | Mechanism of Gate Opening in the 20S Proteasome by the Proteasomal ATPases. <i>Molecular Cell</i> , 2008, 30, 360-368. | 9.7 | 334 |
| 99 | Reconstructing the Endocytotic Machinery. <i>Methods in Cell Biology</i> , 2007, 79, 463-487. | 1.1 | 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. | 9.7 | 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. | 9.7 | 230 |
| 102 | Negative staining and image classification "powerful tools in modern electron microscopy. <i>Biological Procedures Online</i> , 2004, 6, 23-34. | 2.9 | 598 |