

Qiang Zhou

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

10,370
citations

147801

31
h-index

189892

50
g-index

58
all docs

58
docs citations

58
times ranked

19218
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Structural basis for the recognition of SARS-CoV-2 by full-length human ACE2. <i>Science</i> , 2020, 367, 1444-1448. | 12.6 | 4,319 |
| 2 | A neutralizing human antibody binds to the N-terminal domain of the Spike protein of SARS-CoV-2. <i>Science</i> , 2020, 369, 650-655. | 12.6 | 1,292 |
| 3 | Structure of the voltage-gated calcium channel Cav1.1 at 3.6Å resolution. <i>Nature</i> , 2016, 537, 191-196. | 27.8 | 398 |
| 4 | AXL is a candidate receptor for SARS-CoV-2 that promotes infection of pulmonary and bronchial epithelial cells. <i>Cell Research</i> , 2021, 31, 126-140. | 12.0 | 356 |
| 5 | Structure of a eukaryotic voltage-gated sodium channel at near-atomic resolution. <i>Science</i> , 2017, 355, . | 12.6 | 351 |
| 6 | Structure of the human voltage-gated sodium channel Nav1.4 in complex with β 1. <i>Science</i> , 2018, 362, . | 12.6 | 333 |
| 7 | Structural and biochemical basis for induced self-propagation of NLRC4. <i>Science</i> , 2015, 350, 399-404. | 12.6 | 282 |
| 8 | Structure of the Nav1.4- β 1 Complex from Electric Eel. <i>Cell</i> , 2017, 170, 470-482.e11. | 28.9 | 272 |
| 9 | Structural Insights into the Niemann-Pick C1 (NPC1)-Mediated Cholesterol Transfer and Ebola Infection. <i>Cell</i> , 2016, 165, 1467-1478. | 28.9 | 266 |
| 10 | Recognition of the amyloid precursor protein by human β -secretase. <i>Science</i> , 2019, 363, . | 12.6 | 229 |
| 11 | Structure of the human LAT1-4F2hc heteromeric amino acid transporter complex. <i>Nature</i> , 2019, 568, 127-130. | 27.8 | 217 |
| 12 | Structural basis for the modulation of voltage-gated sodium channels by animal toxins. <i>Science</i> , 2018, 362, . | 12.6 | 200 |
| 13 | Structural basis of Notch recognition by human β -secretase. <i>Nature</i> , 2019, 565, 192-197. | 27.8 | 194 |
| 14 | Structural basis for the recognition of Sonic Hedgehog by human Patched1. <i>Science</i> , 2018, 361, . | 12.6 | 168 |
| 15 | SARS-CoV-2 exacerbates proinflammatory responses in myeloid cells through C-type lectin receptors and TWEET family member 2. <i>Immunity</i> , 2021, 54, 1304-1319.e9. | 14.3 | 115 |
| 16 | Modulation of cardiac ryanodine receptor 2 by calmodulin. <i>Nature</i> , 2019, 572, 347-351. | 27.8 | 110 |
| 17 | The cryo-EM structure of the SF3b spliceosome complex bound to a splicing modulator reveals a pre-mRNA substrate competitive mechanism of action. <i>Genes and Development</i> , 2018, 32, 309-320. | 5.9 | 89 |
| 18 | Structural basis for the different states of the spike protein of SARS-CoV-2 in complex with ACE2. <i>Cell Research</i> , 2021, 31, 717-719. | 12.0 | 77 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | Engineered trimeric ACE2 binds viral spike protein and locks it in a "Three-up" conformation to potently inhibit SARS-CoV-2 infection. <i>Cell Research</i> , 2021, 31, 98-100. | 12.0 | 76 |
| 20 | Structure of the human plasma membrane Ca ²⁺ -ATPase 1 in complex with its obligatory subunit neuroplastin. <i>Nature Communications</i> , 2018, 9, 3623. | 12.8 | 71 |
| 21 | Neutralization mechanism of a human antibody with pan-coronavirus reactivity including SARS-CoV-2. <i>Nature Microbiology</i> , 2022, 7, 1063-1074. | 13.3 | 63 |
| 22 | Structural basis for bivalent binding and inhibition of SARS-CoV-2 infection by human potent neutralizing antibodies. <i>Cell Research</i> , 2021, 31, 517-525. | 12.0 | 54 |
| 23 | ACE2-targeting monoclonal antibody as potent and broad-spectrum coronavirus blocker. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 315. | 17.1 | 53 |
| 24 | Molecular architecture of the luminal ring of the <i>Xenopus laevis</i> nuclear pore complex. <i>Cell Research</i> , 2020, 30, 532-540. | 12.0 | 51 |
| 25 | Structure of the cytoplasmic ring of the <i>Xenopus laevis</i> nuclear pore complex by cryo-electron microscopy single particle analysis. <i>Cell Research</i> , 2020, 30, 520-531. | 12.0 | 51 |
| 26 | Structural mechanism of phospholipids translocation by MlaFEDB complex. <i>Cell Research</i> , 2020, 30, 1127-1135. | 12.0 | 49 |
| 27 | The structure of erastin-bound xCT ^{4F2hc} complex reveals molecular mechanisms underlying erastin-induced ferroptosis. <i>Cell Research</i> , 2022, 32, 687-690. | 12.0 | 48 |
| 28 | Structural and Functional Characterization of Ryanodine Receptor-Natratin Toxin Interaction. <i>Biophysical Journal</i> , 2008, 95, 4289-4299. | 0.5 | 46 |
| 29 | A structure of human Scap bound to Insig-2 suggests how their interaction is regulated by sterols. <i>Science</i> , 2021, 371, . | 12.6 | 44 |
| 30 | Structure of the cytoplasmic ring of the <i>Xenopus laevis</i> nuclear pore complex. <i>Science</i> , 2022, 376, . | 12.6 | 44 |
| 31 | Cryo-EM structure of SNAP-SNARE assembly in 20S particle. <i>Cell Research</i> , 2015, 25, 551-560. | 12.0 | 42 |
| 32 | Mechanism of substrate transport and inhibition of the human LAT1-4F2hc amino acid transporter. <i>Cell Discovery</i> , 2021, 7, 16. | 6.7 | 40 |
| 33 | Cryo-EM structures of the full-length human KCC2 and KCC3 cation-chloride cotransporters. <i>Cell Research</i> , 2021, 31, 482-484. | 12.0 | 31 |
| 34 | Cryo-EM structure of the human heteromeric amino acid transporter b ^{0,+} AT-rBAT. <i>Science Advances</i> , 2020, 6, eaay6379. | 10.3 | 27 |
| 35 | Mechanistic insights into the SNARE complex disassembly. <i>Science Advances</i> , 2019, 5, eaau8164. | 10.3 | 25 |
| 36 | Cryo-EM structures of <i>Acinetobacter baumannii</i> glycerophospholipid transporter. <i>Cell Discovery</i> , 2020, 6, 86. | 6.7 | 23 |

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|----|---|------|-----------|
| 37 | Novel sarbecovirus bispecific neutralizing antibodies with exceptional breadth and potency against currently circulating SARS-CoV-2 variants and sarbecoviruses. <i>Cell Discovery</i> , 2022, 8, 36. | 6.7 | 22 |
| 38 | Cryo-EM structure of human Wntless in complex with Wnt3a. <i>Nature Communications</i> , 2021, 12, 4541. | 12.8 | 20 |
| 39 | Structural biology in the fight against COVID-19. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 2-7. | 8.2 | 20 |
| 40 | Cryo-EM structure of the nuclear ring from <i>Xenopus laevis</i> nuclear pore complex. <i>Cell Research</i> , 2022, 32, 349-358. | 12.0 | 19 |
| 41 | Broad ultra-potent neutralization of SARS-CoV-2 variants by monoclonal antibodies specific to the tip of RBD. <i>Cell Discovery</i> , 2022, 8, 16. | 6.7 | 18 |
| 42 | Cryo-EM structure of the inner ring from the <i>Xenopus laevis</i> nuclear pore complex. <i>Cell Research</i> , 2022, 32, 451-460. | 12.0 | 15 |
| 43 | Broadly neutralizing antibodies against Omicron-included SARS-CoV-2 variants induced by vaccination. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 139. | 17.1 | 14 |
| 44 | Structural insight into the substrate recognition and transport mechanism of the human LAT2 α 4F2hc complex. <i>Cell Discovery</i> , 2020, 6, 82. | 6.7 | 13 |
| 45 | ACE2, BOAT1, and SARS-CoV-2 spike protein: Structural and functional implications. <i>Current Opinion in Structural Biology</i> , 2022, 74, 102388. | 5.7 | 10 |
| 46 | Cryo-EM structures of recombinant human sodium-potassium pump determined in three different states. <i>Nature Communications</i> , 2022, 13, . | 12.8 | 10 |
| 47 | Particle segmentation algorithm for flexible single particle reconstruction. <i>Biophysics Reports</i> , 2017, 3, 43-55. | 0.8 | 9 |
| 48 | Structural Characterization of the Complex of SecB and Metallothionein-Labeled proOmpA by Cryo-Electron Microscopy. <i>PLoS ONE</i> , 2012, 7, e47015. | 2.5 | 6 |
| 49 | Cryo-EM structure of L-fucokinase/GDP-fucose pyrophosphorylase (FKP) in <i>Bacteroides fragilis</i> . <i>Protein and Cell</i> , 2019, 10, 365-369. | 11.0 | 6 |