

# X Edward Zhou

## List of Publications by Year in descending order

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Version: 2024-02-01

35  
papers

3,635  
citations

257450

24  
h-index

345221

36  
g-index

36  
all docs

36  
docs citations

36  
times ranked

4828  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Structural insights into the human D1 and D2 dopamine receptor signaling complexes. <i>Cell</i> , 2021, 184, 931-942.e18.  | 28.9 | 140       |
| 2  | Mechanism of dopamine binding and allosteric modulation of the human D1 dopamine receptor. <i>Cell Research</i> , 2021, 31, 593-596.   | 12.0 | 48        |
| 3  | Structures of the human dopamine D3 receptor-Gi complexes. <i>Molecular Cell</i> , 2021, 81, 1147-1159.e4.   | 9.7  | 51        |
| 4  | Structural insights into the lipid and ligand regulation of serotonin receptors. <i>Nature</i> , 2021, 592, 469-473.   | 27.8 | 138       |
| 5  | Structure of an AMPK complex in an inactive, ATP-bound state. <i>Science</i> , 2021, 373, 413-419.   | 12.6 | 42        |
| 6  | Structural basis of binding and inhibition of ornithine decarboxylase by 1-amino-oxy-3-aminopropane. <i>Biochemical Journal</i> , 2021, 478, 4137-4149.  | 3.7  | 4         |
| 7  | Crystal structure of heliorhodopsin 48C12. <i>Cell Research</i> , 2020, 30, 88-90.   | 12.0 | 25        |
| 8  | Structure of nucleosome-bound DNA methyltransferases DNMT3A and DNMT3B. <i>Nature</i> , 2020, 586, 151-155.  | 27.8 | 61        |
| 9  | Cryo-EM structure of an activated VIP1 receptor-G protein complex revealed by a NanoBIT tethering strategy. <i>Nature Communications</i> , 2020, 11, 4121.   | 12.8 | 136       |
| 10 | Identification and structural insight of an effective PPAR $\beta$ modulator with improved therapeutic index for anti-diabetic drug discovery. <i>Chemical Science</i> , 2020, 11, 2260-2268.                        | 7.4  | 15        |
| 11 | Structural basis of Fusarium myosin I inhibition by phenamacril. <i>PLoS Pathogens</i> , 2020, 16, e1008323.   | 4.7  | 27        |
| 12 | Structure of formylpeptide receptor 2-Gi complex reveals insights into ligand recognition and signaling. <i>Nature Communications</i> , 2020, 11, 885.   | 12.8 | 85        |
| 13 | Cryo-EM Structure of the Human Cannabinoid Receptor CB2-Gi Signaling Complex. <i>Cell</i> , 2020, 180, 645-654.e13.  | 28.9 | 167       |
| 14 | Molecular Basis for Hormone Recognition and Activation of Corticotropin-Releasing Factor Receptors. <i>Molecular Cell</i> , 2020, 77, 669-680.e4.  | 9.7  | 70        |
| 15 | Structural biology of G protein-coupled receptor signaling complexes. <i>Protein Science</i> , 2019, 28, 487-501.  | 7.6  | 41        |
| 16 | Structure and dynamics of the active human parathyroid hormone receptor-1. <i>Science</i> , 2019, 364, 148-153.  | 12.6 | 185       |
| 17 | A complex structure of arrestin-2 bound to a G protein-coupled receptor. <i>Cell Research</i> , 2019, 29, 971-983.   | 12.0 | 155       |
| 18 | Structures of AMP-activated protein kinase bound to novel pharmacological activators in phosphorylated, non-phosphorylated, and nucleotide-free states. <i>Journal of Biological Chemistry</i> , 2019, 294, 953-967. | 3.4  | 29        |

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|----|---|------|-----------|
| 19 | Structure and Physiological Regulation of AMPK. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3534.  | 4.1  | 136       |
| 20 | Conformational heterogeneity of the allosteric drug and metabolite (ADaM) site in AMP-activated protein kinase (AMPK). <i>Journal of Biological Chemistry</i> , 2018, 293, 16994-17007. | 3.4  | 13        |
| 21 | Cryo-EM structure of human rhodopsin bound to an inhibitory G protein. <i>Nature</i> , 2018, 558, 553-558.  | 27.8 | 230       |
| 22 | Identification of a novel selective PPAR $\beta$ ligand with a unique binding mode and improved therapeutic profile in vitro. <i>Scientific Reports</i> , 2017, 7, 41487.               | 3.3  | 15        |
| 23 | Crystal structure of TBC1D15 GTPase-activating protein (GAP) domain and its activity on Rab GTPases. <i>Protein Science</i> , 2017, 26, 834-846.  | 7.6  | 6         |
| 24 | Structural Basis of TPR-Mediated Oligomerization and Activation of Oncogenic Fusion Kinases. <i>Structure</i> , 2017, 25, 867-877.e3.   | 3.3  | 14        |
| 25 | Functional role of the three conserved cysteines in the N domain of visual arrestin-1. <i>Journal of Biological Chemistry</i> , 2017, 292, 12496-12502.                                 | 3.4  | 7         |
| 26 | Combining chemical and genetic approaches to increase drought resistance in plants. <i>Nature Communications</i> , 2017, 8, 1183.   | 12.8 | 108       |
| 27 | Structure determination and activity manipulation of the turfgrass ABA receptor FePYR1. <i>Scientific Reports</i> , 2017, 7, 14022.   | 3.3  | 16        |
| 28 | Identification of Phosphorylation Codes for Arrestin Recruitment by G Protein-Coupled Receptors. <i>Cell</i> , 2017, 170, 457-469.e13.  | 28.9 | 344       |
| 29 | A structural snapshot of the rhodopsin-arrestin complex. <i>FEBS Journal</i> , 2016, 283, 816-821.  | 4.7  | 16        |
| 30 | An intrinsic agonist mechanism for activation of glucagon-like peptide-1 receptor by its extracellular domain. <i>Cell Discovery</i> , 2016, 2, 16042.                                  | 6.7  | 28        |
| 31 | X-ray laser diffraction for structure determination of the rhodopsin-arrestin complex. <i>Scientific Data</i> , 2016, 3, 160021.  | 5.3  | 51        |
| 32 | Crystal structure of rhodopsin bound to arrestin by femtosecond X-ray laser. <i>Nature</i> , 2015, 523, 561-567.  | 27.8 | 683       |
| 33 | Destabilization of strigolactone receptor DWARF14 by binding of ligand and E3-ligase signaling effector DWARF3. <i>Cell Research</i> , 2015, 25, 1219-1236.                             | 12.0 | 152       |
| 34 | Structural basis of JAZ repression of MYC transcription factors in jasmonate signalling. <i>Nature</i> , 2015, 525, 269-273.  | 27.8 | 248       |
| 35 | Structural basis of AMPK regulation by adenine nucleotides and glycogen. <i>Cell Research</i> , 2015, 25, 50-66.  | 12.0 | 147       |