

# Suwen Zhao

## List of Publications by Year in descending order

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72  
papers

5,198  
citations

159358

30  
h-index

95083

68  
g-index

84  
all docs

84  
docs citations

84  
times ranked

6367  
citing authors

#	ARTICLE	IF	CITATIONS
1	The VSGB 2.0 model: A next generation energy model for high resolution protein structure modeling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2794-2812.	1.5	773
2	Crystal Structure of the Human Cannabinoid Receptor CB1. <i>Cell</i> , 2016, 167, 750-762.e14.	13.5	468
3	Crystal structures of agonist-bound human cannabinoid receptor CB1. <i>Nature</i> , 2017, 547, 468-471.	13.7	379
4	Common activation mechanism of class A GPCRs. <i>ELife</i> , 2019, 8, .	2.8	339
5	Crystal Structure of the Human Cannabinoid Receptor CB2. <i>Cell</i> , 2019, 176, 459-467.e13.	13.5	268
6	G protein-coupled receptors: structure- and function-based drug discovery. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 7.	7.1	241
7	Activation and Signaling Mechanism Revealed by Cannabinoid Receptor-Gi Complex Structures. <i>Cell</i> , 2020, 180, 655-665.e18.	13.5	212
8	Human GLP-1 receptor transmembrane domain structure in complex with allosteric modulators. <i>Nature</i> , 2017, 546, 312-315.	13.7	192
9	5-HT <sub>2C</sub> Receptor Structures Reveal the Structural Basis of GPCR Polypharmacology. <i>Cell</i> , 2018, 172, 719-730.e14.	13.5	185
10	Structural basis of CXC chemokine receptor 2 activation and signalling. <i>Nature</i> , 2020, 585, 135-140.	13.7	128
11	Discovery of new enzymes and metabolic pathways by using structure and genome context. <i>Nature</i> , 2013, 502, 698-702.	13.7	124
12	Long loop prediction using the protein local optimization program. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 438-452.	1.5	110
13	Structural basis of ligand recognition and self-activation of orphan GPR52. <i>Nature</i> , 2020, 579, 152-157.	13.7	97
14	Structural Basis for Apelin Control of the Human Apelin Receptor. <i>Structure</i> , 2017, 25, 858-866.e4.	1.6	96
15	Experimental Strategies for Functional Annotation and Metabolism Discovery: Targeted Screening of Solute Binding Proteins and Unbiased Panning of Metabolomes. <i>Biochemistry</i> , 2015, 54, 909-931.	1.2	95
16	Determination of the melanocortin-4 receptor structure identifies Ca <sup>2+</sup> as a cofactor for ligand binding. <i>Science</i> , 2020, 368, 428-433.	6.0	89
17	Crystal structure of a multi-domain human smoothed receptor in complex with a super stabilizing ligand. <i>Nature Communications</i> , 2017, 8, 15383.	5.8	81
18	Prediction and characterization of enzymatic activities guided by sequence similarity and genome neighborhood networks. <i>ELife</i> , 2014, 3, .	2.8	81

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19	Toward better refinement of comparative models: Predicting loops in inexact environments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 959-971.	1.5	80
20	Crystal structure of the Frizzled 4 receptor in a ligand-free state. <i>Nature</i> , 2018, 560, 666-670.	13.7	77
21	Structural basis for activation of the growth hormone-releasing hormone receptor. <i>Nature Communications</i> , 2020, 11, 5205.	5.8	57
22	A widespread pathway for substitution of adenine by diaminopurine in phage genomes. <i>Science</i> , 2021, 372, 512-516.	6.0	55
23	A unique hormonal recognition feature of the human glucagon-like peptide-2 receptor. <i>Cell Research</i> , 2020, 30, 1098-1108.	5.7	52
24	Assignment of function to a domain of unknown function: DUF1537 is a new kinase family in catabolic pathways for acid sugars. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4161-9.	3.3	46
25	Metabolic Reprogramming in Cancer Is Induced to Increase Proton Production. <i>Cancer Research</i> , 2020, 80, 1143-1155.	0.4	43
26	Assignment of polar states for protein amino acid residues using an interaction cluster decomposition algorithm and its application to high resolution protein structure modeling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 66, 824-837.	1.5	40
27	Progress in super long loop prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2920-2935.	1.5	40
28	Ligands of Adrenergic Receptors: A Structural Point of View. <i>Biomolecules</i> , 2021, 11, 936.	1.8	40
29	H2B Lys34 Ubiquitination Induces Nucleosome Distortion to Stimulate Dot1L Activity. <i>Nature Chemical Biology</i> , 2022, 18, 972-980.	3.9	38
30	Indoleacetate decarboxylase is a glycol radical enzyme catalysing the formation of malodorous skatole. <i>Nature Communications</i> , 2018, 9, 4224.	5.8	37
31	Structural insights into the committed step of bacterial phospholipid biosynthesis. <i>Nature Communications</i> , 2017, 8, 1691.	5.8	33
32	High-throughput identification of G protein-coupled receptor modulators through affinity mass spectrometry screening. <i>Chemical Science</i> , 2018, 9, 3192-3199.	3.7	33
33	Leveraging structure for enzyme function prediction: methods, opportunities, and challenges. <i>Trends in Biochemical Sciences</i> , 2014, 39, 363-371.	3.7	31
34	Prediction of enzymatic pathways by integrative pathway mapping. <i>ELife</i> , 2018, 7, .	2.8	30
35	Structural Basis of the Diversity of Adrenergic Receptors. <i>Cell Reports</i> , 2019, 29, 2929-2935.e4.	2.9	30
36	GPCR Allosteric Modulator Discovery. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1163, 225-251.	0.8	29

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37	Structures of the human cholecystokinin receptors bound to agonists and antagonists. <i>Nature Chemical Biology</i> , 2021, 17, 1230-1237.	3.9	27
38	Molecular Basis for the Final Oxidative Rearrangement Steps in Chartreusin Biosynthesis. <i>Journal of the American Chemical Society</i> , 2018, 140, 10909-10914.	6.6	26
39	Examination of the Deubiquitylation Site Selectivity of USP51 by Using Chemically Synthesized Ubiquitylated Histones. <i>ChemBioChem</i> , 2019, 20, 221-229.	1.3	26
40	A Novel G Protein-Biased and Subtype-Selective Agonist for a G Protein-Coupled Receptor Discovered from Screening Herbal Extracts. <i>ACS Central Science</i> , 2020, 6, 213-225.	5.3	25
41	Identification of natural products as novel ligands for the human 5-HT <sub>2C</sub> receptor. <i>Biophysics Reports</i> , 2018, 4, 50-61.	0.2	23
42	Catalytic-state structure and engineering of <i>Streptococcus thermophilus</i> Cas9. <i>Nature Catalysis</i> , 2020, 3, 813-823.	16.1	23
43	Programmable adenine deamination in bacteria using a Cas9-adenine-deaminase fusion. <i>Chemical Science</i> , 2020, 11, 1657-1664.	3.7	21
44	Salvianolic acids from antithrombotic Traditional Chinese Medicine Danshen are antagonists of human P2Y <sub>1</sub> and P2Y <sub>12</sub> receptors. <i>Scientific Reports</i> , 2018, 8, 8084.	1.6	20
45	Prediction and Biochemical Demonstration of a Catabolic Pathway for the Osmoprotectant Proline Betaine. <i>MBio</i> , 2014, 5, e00933-13.	1.8	19
46	Large-Scale Analysis of Bioactive Ligand Conformational Strain Energy by <i>Ab Initio</i> Calculation. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 1180-1192.	2.5	16
47	Structure-Based Design of Dual-Acting Compounds Targeting Adenosine A <sub>2A</sub> Receptor and Histone Deacetylase as Novel Tumor Immunotherapeutic Agents. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 16573-16597.	2.9	16
48	Succinate-acetate permease from <i>Citrobacter koseri</i> is an anion channel that unidirectionally translocates acetate. <i>Cell Research</i> , 2018, 28, 644-654.	5.7	15
49	Design and Synthesis of Bitopic 2-Phenylcyclopropylmethylamine (PCPMA) Derivatives as Selective Dopamine D <sub>3</sub> Receptor Ligands. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 4579-4602.	2.9	15
50	Affinity Mass Spectrometry-Based Fragment Screening Identified a New Negative Allosteric Modulator of the Adenosine A <sub>2A</sub> Receptor Targeting the Sodium Ion Pocket. <i>ACS Chemical Biology</i> , 2021, 16, 991-1002.	1.6	15
51	A Unique <i>cis</i> -3-Hydroxy- <i>l</i> -proline Dehydratase in the Enolase Superfamily. <i>Journal of the American Chemical Society</i> , 2015, 137, 1388-1391.	6.6	13
52	The unconventional activation of the muscarinic acetylcholine receptor M4R by diverse ligands. <i>Nature Communications</i> , 2022, 13, .	5.8	13
53	Structure-Based Design of Melanocortin 4 Receptor Ligands Based on the SHU-9119-hMC4R Cocrystal Structure. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 357-369.	2.9	12
54	A Novel Lid-Covering Peptide Inhibitor of Nicotinic Acetylcholine Receptors Derived from $\hat{1}\pm$ D-Conotoxin GeXXA. <i>Marine Drugs</i> , 2017, 15, 164.	2.2	11

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55	Prediction of Long Loops with Embedded Secondary Structure Using the Protein Local Optimization Program. <i>Journal of Chemical Theory and Computation</i> , 2013, 9, 1846-1864.	2.3	9
56	A structurally guided dissection-then-evolution strategy for ligand optimization of smoothed receptor. <i>MedChemComm</i> , 2017, 8, 1332-1336.	3.5	9
57	Rational Remodeling of Atypical Scaffolds for the Design of Photoswitchable Cannabinoid Receptor Tools. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 13752-13765.	2.9	9
58	The structural study of mutation-induced inactivation of human muscarinic receptor M4. <i>IUCr</i> , 2020, 7, 294-305.	1.0	9
59	Identification of a Small Probe That Can Be Conjugated to Proteins by Proximity Labeling. <i>ACS Chemical Biology</i> , 2020, 15, 39-43.	1.6	8
60	Targeted Proteomics Combined with Affinity Mass Spectrometry Analysis Reveals Antagonist E7 Acts As an Intracellular Covalent Ligand of Orphan Receptor GPR52. <i>ACS Chemical Biology</i> , 2020, 15, 3275-3284.	1.6	8
61	Molecular Mechanism of Acetate Transport through the Acetate Channel SatP. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 2374-2382.	2.5	7
62	Evaluation of chemical cross-linkers for in-depth structural analysis of G protein-coupled receptors through cross-linking mass spectrometry. <i>Analytica Chimica Acta</i> , 2020, 1102, 53-62.	2.6	7
63	Discovery of Novel Allosteric Modulators Targeting an Extra-Helical Binding Site of GLP-1R Using Structure- and Ligand-Based Virtual Screening. <i>Biomolecules</i> , 2021, 11, 929.	1.8	7
64	Predicting Enzyme's Substrate Specificity with QM/MM Methods: A Case Study of the Stereospecificity of <i>α</i> -Glucarate Dehydratase. <i>Biochemistry</i> , 2013, 52, 5511-5513.	1.2	6
65	Colocalization Strategy Unveils an Underside Binding Site in the Transmembrane Domain of Smoothed Receptor. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 9983-9989.	2.9	5
66	Disulfide-Containing Detergents (DCDs) for the Structural Biology of Membrane Proteins. <i>Chemistry - A European Journal</i> , 2019, 25, 11635-11640.	1.7	5
67	The structure-based traceless specific fluorescence labeling of the smoothed receptor. <i>Organic and Biomolecular Chemistry</i> , 2019, 17, 6136-6142.	1.5	5
68	Building the Chordata Olfactory Receptor Database using more than 400,000 receptors annotated by Genome2OR. <i>Science China Life Sciences</i> , 2022, 65, 2539-2551.	2.3	5
69	MD Simulations Revealing Special Activation Mechanism of Cannabinoid Receptor 1. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 860035.	1.6	4
70	Identification and Characterization of the Biosynthetic Pathway of the Sulfonolipid Capnine. <i>Biochemistry</i> , 2022, 61, 2861-2869.	1.2	4
71	Elucidation of Distinct Modular Assemblies of Smoothed Receptor by Bitopic Ligand Measurement. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 13830-13840.	2.9	3
72	Structure-Activity Relationship Studies of Hydantoin-Cored Ligands for Smoothed Receptor. <i>ChemistryOpen</i> , 2021, 10, 1028-1032.	0.9	0