Suwen Zhao

List of Publications by Year
in descending order

72 papers	5,198 citations	159585 30 h-index	95266 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. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2794-2812.	2.6	773
2	Crystal Structure of the Human Cannabinoid Receptor CB1. Cell, 2016, 167, 750-762.e14.	28.9	468
3	Crystal structures of agonist-bound human cannabinoid receptor CB1. Nature, 2017, 547, 468-471.	27.8	379
4	Common activation mechanism of class A GPCRs. ELife, 2019, 8, .	6.0	339
5	Crystal Structure of the Human Cannabinoid Receptor CB2. Cell, 2019, 176, 459-467.e13.	28.9	268
6	G protein-coupled receptors: structure- and function-based drug discovery. Signal Transduction and Targeted Therapy, 2021, 6, 7.	17.1	241
7	Activation and Signaling Mechanism Revealed by Cannabinoid Receptor-Gi Complex Structures. Cell, 2020, 180, 655-665.e18.	28.9	212
8	Human GLP-1 receptor transmembrane domain structure in complex with allosteric modulators. Nature, 2017, 546, 312-315.	27.8	192
9	5-HT2C Receptor Structures Reveal the Structural Basis of GPCR Polypharmacology. Cell, 2018, 172, 719-730.e14.	28.9	185
10	Structural basis of CXC chemokine receptor 2 activation and signalling. Nature, 2020, 585, 135-140.	27.8	128
11	Discovery of new enzymes and metabolic pathways by using structure and genome context. Nature, 2013, 502, 698-702.	27.8	124
12	Long loop prediction using the protein local optimization program. Proteins: Structure, Function and Bioinformatics, 2006, 65, 438-452.	2.6	110
13	Structural basis of ligand recognition and self-activation of orphan GPR52. Nature, 2020, 579, 152-157.	27.8	97
14	Structural Basis for Apelin Control of the Human Apelin Receptor. Structure, 2017, 25, 858-866.e4.	3.3	96
15	Experimental Strategies for Functional Annotation and Metabolism Discovery: Targeted Screening of Solute Binding Proteins and Unbiased Panning of Metabolomes. Biochemistry, 2015, 54, 909-931.	2.5	95
16	Determination of the melanocortin-4 receptor structure identifies Ca ²⁺ as a cofactor for ligand binding. Science, 2020, 368, 428-433.	12.6	89
17	Crystal structure of a multi-domain human smoothened receptor in complex with a super stabilizing ligand. Nature Communications, 2017, 8, 15383.	12.8	81
18	Prediction and characterization of enzymatic activities guided by sequence similarity and genome neighborhood networks. ELife, 2014, 3, .	6.0	81

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19	Toward better refinement of comparative models: Predicting loops in inexact environments. Proteins: Structure, Function and Bioinformatics, 2008, 72, 959-971.	2.6	80
20	Crystal structure of the Frizzled 4 receptor in a ligand-free state. Nature, 2018, 560, 666-670.	27.8	77
21	Structural basis for activation of the growth hormone-releasing hormone receptor. Nature Communications, 2020, 11, 5205.	12.8	57
22	A widespread pathway for substitution of adenine by diaminopurine in phage genomes. Science, 2021, 372, 512-516.	12.6	55
23	A unique hormonal recognition feature of the human glucagon-like peptide-2 receptor. Cell Research, 2020, 30, 1098-1108.	12.0	52
24	Assignment of function to a domain of unknown function: DUF1537 is a new kinase family in catabolic pathways for acid sugars. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4161-9.	7.1	46
25	Metabolic Reprogramming in Cancer Is Induced to Increase Proton Production. Cancer Research, 2020, 80, 1143-1155.	0.9	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. Proteins: Structure, Function and Bioinformatics, 2006, 66, 824-837.	2.6	40
27	Progress in super long loop prediction. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2920-2935.	2.6	40
28	Ligands of Adrenergic Receptors: A Structural Point of View. Biomolecules, 2021, 11, 936.	4.0	40
29	H2B Lys34 Ubiquitination Induces Nucleosome Distortion to Stimulate Dot1L Activity. Nature Chemical Biology, 2022, 18, 972-980.	8.0	38
30	Indoleacetate decarboxylase is a glycyl radical enzyme catalysing the formation of malodorant skatole. Nature Communications, 2018, 9, 4224.	12.8	37
31	Structural insights into the committed step of bacterial phospholipid biosynthesis. Nature Communications, 2017, 8, 1691.	12.8	33
32	High-throughput identification of G protein-coupled receptor modulators through affinity mass spectrometry screening. Chemical Science, 2018, 9, 3192-3199.	7.4	33
33	Leveraging structure for enzyme function prediction: methods, opportunities, and challenges. Trends in Biochemical Sciences, 2014, 39, 363-371.	7.5	31
34	Prediction of enzymatic pathways by integrative pathway mapping. ELife, 2018, 7, .	6.0	30
35	Structural Basis of the Diversity of Adrenergic Receptors. Cell Reports, 2019, 29, 2929-2935.e4.	6.4	30
36	GPCR Allosteric Modulator Discovery. Advances in Experimental Medicine and Biology, 2019, 1163, 225-251.	1.6	29

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37	Structures of the human cholecystokinin receptors bound to agonists and antagonists. Nature Chemical Biology, 2021, 17, 1230-1237.	8.0	27
38	Molecular Basis for the Final Oxidative Rearrangement Steps in Chartreusin Biosynthesis. Journal of the American Chemical Society, 2018, 140, 10909-10914.	13.7	26
39	Examination of the Deubiquitylation Site Selectivity of USP51 by Using Chemically Synthesized Ubiquitylated Histones. ChemBioChem, 2019, 20, 221-229.	2.6	26
40	A Novel G Protein-Biased and Subtype-Selective Agonist for a G Protein-Coupled Receptor Discovered from Screening Herbal Extracts. ACS Central Science, 2020, 6, 213-225.	11.3	25
41	Identification of natural products as novel ligands for the human 5-HT2C receptor. Biophysics Reports, 2018, 4, 50-61.	0.8	23
42	Catalytic-state structure and engineering of Streptococcus thermophilus Cas9. Nature Catalysis, 2020, 3, 813-823.	34.4	23
43	Programmable adenine deamination in bacteria using a Cas9â€“adenine-deaminase fusion. Chemical Science, 2020, 11, 1657-1664.	7.4	21
44	Salvianolic acids from antithrombotic Traditional Chinese Medicine Danshen are antagonists of human P2Y1 and P2Y12 receptors. Scientific Reports, 2018, 8, 8084.	3.3	20
45	Prediction and Biochemical Demonstration of a Catabolic Pathway for the Osmoprotectant Proline Betaine. MBio, 2014, 5, e00933-13.	4.1	19
46	Large-Scale Analysis of Bioactive Ligand Conformational Strain Energy by Ab Initio Calculation. Journal of Chemical Information and Modeling, 2021, 61, 1180-1192.	5.4	16
47	Structure-Based Design of Dual-Acting Compounds Targeting Adenosine A_{2A} Receptor and Histone Deacetylase as Novel Tumor Immunotherapeutic Agents. Journal of Medicinal Chemistry, 2021, 64, 16573-16597.	6.4	16
48	Succinate-acetate permease from Citrobacter koseri is an anion channel that unidirectionally translocates acetate. Cell Research, 2018, 28, 644-654.	12.0	15
49	Design and Synthesis of Bitopic 2-Phenylcyclopropylmethylamine (PCPMA) Derivatives as Selective Dopamine D3 Receptor Ligands. Journal of Medicinal Chemistry, 2020, 63, 4579-4602.	6.4	15
50	Affinity Mass Spectrometry-Based Fragment Screening Identified a New Negative Allosteric Modulator of the Adenosine A_{2A} Receptor Targeting the Sodium Ion Pocket. ACS Chemical Biology, 2021, 16, 991-1002.	3.4	15
51	A Unique cis-3-Hydroxy-<scp>l</scp>-proline Dehydratase in the Enolase Superfamily. Journal of the American Chemical Society, 2015, 137, 1388-1391.	13.7	13
52	The unconventional activation of the muscarinic acetylcholine receptor M4R by diverse ligands. Nature Communications, 2022, 13, .	12.8	13
53	Structure-Based Design of Melanocortin 4 Receptor Ligands Based on the SHU-9119-hMC4R Cocrystal Structure. Journal of Medicinal Chemistry, 2021, 64, 357-369.	6.4	12
54	A Novel Lid-Covering Peptide Inhibitor of Nicotinic Acetylcholine Receptors Derived from Î±D-Conotoxin GeXXA. Marine Drugs, 2017, 15, 164.	4.6	11

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55	Prediction of Long Loops with Embedded Secondary Structure Using the Protein Local Optimization Program. Journal of Chemical Theory and Computation, 2013, 9, 1846-1864.	5.3	9
56	A structurally guided dissection-then-evolution strategy for ligand optimization of smoothened receptor. MedChemComm, 2017, 8, 1332-1336.	3.4	9
57	Rational Remodeling of Atypical Scaffolds for the Design of Photoswitchable Cannabinoid Receptor Tools. Journal of Medicinal Chemistry, 2021, 64, 13752-13765.	6.4	9
58	The structural study of mutation-induced inactivation of human muscarinic receptor M4. IUCrJ, 2020, 7, 294-305.	2.2	9
59	Identification of a Small Probe That Can Be Conjugated to Proteins by Proximity Labeling. ACS Chemical Biology, 2020, 15, 39-43.	3.4	8
60	Targeted Proteomics Combined with Affinity Mass Spectrometry Analysis Reveals Antagonist E7 Acts As an Intracellular Covalent Ligand of Orphan Receptor GPR52. ACS Chemical Biology, 2020, 15, 3275-3284.	3.4	8
61	Molecular Mechanism of Acetate Transport through the Acetate Channel SatP. Journal of Chemical Information and Modeling, 2019, 59, 2374-2382.	5.4	7
62	Evaluation of chemical cross-linkers for in-depth structural analysis of G protein-coupled receptors through cross-linking mass spectrometry. Analytica Chimica Acta, 2020, 1102, 53-62.	5.4	7
63	Discovery of Novel Allosteric Modulators Targeting an Extra-Helical Binding Site of GLP-1R Using Structure- and Ligand-Based Virtual Screening. Biomolecules, 2021, 11, 929.	4.0	7
64	Predicting Enzymeâ€“Substrate Specificity with QM/MM Methods: A Case Study of the Stereospecificity of <scp>d</scp>-Glucarate Dehydratase. Biochemistry, 2013, 52, 5511-5513.	2.5	6
65	Colocalization Strategy Unveils an Underside Binding Site in the Transmembrane Domain of Smoothened Receptor. Journal of Medicinal Chemistry, 2019, 62, 9983-9989.	6.4	5
66	Disulfideâ€Containing Detergents (DCDs) for the Structural Biology of Membrane Proteins. Chemistry - A European Journal, 2019, 25, 11635-11640.	3.3	5
67	The structure-based traceless specific fluorescence labeling of the smoothened receptor. Organic and Biomolecular Chemistry, 2019, 17, 6136-6142.	2.8	5
68	Building the Chordata Olfactory Receptor Database using more than 400,000 receptors annotated by Genome2OR. Science China Life Sciences, 2022, 65, 2539-2551.	4.9	5
69	MD Simulations Revealing Special Activation Mechanism of Cannabinoid Receptor 1. Frontiers in Molecular Biosciences, 2022, 9, 860035.	3.5	4
70	Identification and Characterization of the Biosynthetic Pathway of the Sulfonolipid Capnine. Biochemistry, 2022, 61, 2861-2869.	2.5	4
71	Elucidation of Distinct Modular Assemblies of Smoothened Receptor by Bitopic Ligand Measurement. Journal of Medicinal Chemistry, 2021, 64, 13830-13840.	6.4	3
72	Structureâ€Activity Relationship Studies of Hydantoinâ€Cored Ligands for Smoothened Receptor. ChemistryOpen, 2021, 10, 1028-1032.	1.9	0