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	MD Simulations Revealing Special Activation Mechanism of Cannabinoid Receptor 1. Frontiers in Molecular Biosciences, 2022, 9, 860035.	3.5	4
2	Identification and Characterization of the Biosynthetic Pathway of the Sulfonolipid Capnine. Biochemistry, 2022, 61, 2861-2869.	2.5	4
3	The unconventional activation of the muscarinic acetylcholine receptor M4R by diverse ligands. Nature Communications, 2022, 13, .	12.8	13
4	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
5	H2B Lys34 Ubiquitination Induces Nucleosome Distortion to Stimulate Dot1L Activity. Nature Chemical Biology, 2022, 18, 972-980.	8.0	38
6	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
7	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
8	A widespread pathway for substitution of adenine by diaminopurine in phage genomes. Science, 2021, 372, 512-516.	12.6	55
9	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
10	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
11	Ligands of Adrenergic Receptors: A Structural Point of View. Biomolecules, 2021, 11, 936.	4.0	40
12	Rational Remodeling of Atypical Scaffolds for the Design of Photoswitchable Cannabinoid Receptor Tools. Journal of Medicinal Chemistry, 2021, 64, 13752-13765.	6.4	9
13	Structures of the human cholecystokinin receptors bound to agonists and antagonists. Nature Chemical Biology, 2021, 17, 1230-1237.	8.0	27
14	Elucidation of Distinct Modular Assemblies of Smoothened Receptor by Bitopic Ligand Measurement. Journal of Medicinal Chemistry, 2021, 64, 13830-13840.	6.4	3
15	G protein-coupled receptors: structure- and function-based drug discovery. Signal Transduction and Targeted Therapy, 2021, 6, 7.	17.1	241
16	Structureâ€Activity Relationship Studies of Hydantoinâ€Cored Ligands for Smoothened Receptor. ChemistryOpen, 2021, 10, 1028-1032.	1.9	0
17	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
18	Programmable adenine deamination in bacteria using a Cas9â€“adenine-deaminase fusion. Chemical Science, 2020, 11, 1657-1664.	7.4	21

#	Article	IF	Citations
19	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
20	Identification of a Small Probe That Can Be Conjugated to Proteins by Proximity Labeling. ACS Chemical Biology, 2020, 15, 39-43.	3.4	8
21	Structural basis for activation of the growth hormone-releasing hormone receptor. Nature Communications, 2020, 11, 5205.	12.8	57
22	A unique hormonal recognition feature of the human glucagon-like peptide-2 receptor. Cell Research, 2020, 30, 1098-1108.	12.0	52
23	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
24	Structural basis of CXC chemokine receptor 2 activation and signalling. Nature, 2020, 585, 135-140.	27.8	128
25	Catalytic-state structure and engineering of Streptococcus thermophilus Cas9. Nature Catalysis, 2020, 3, 813-823.	34.4	23
26	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
27	Activation and Signaling Mechanism Revealed by Cannabinoid Receptor-Gi Complex Structures. Cell, 2020, 180, 655-665.e18.	28.9	212
28	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
29	Determination of the melanocortin-4 receptor structure identifies Ca ²⁺ as a cofactor for ligand binding. Science, 2020, 368, 428-433.	12.6	89
30	Metabolic Reprogramming in Cancer Is Induced to Increase Proton Production. Cancer Research, 2020, 80, 1143-1155.	0.9	43
31	Structural basis of ligand recognition and self-activation of orphan GPR52. Nature, 2020, 579, 152-157.	27.8	97
32	The structural study of mutation-induced inactivation of human muscarinic receptor M4. IUCrJ, 2020, 7, 294-305.	2.2	9
33	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
34	Disulfideâ€Containing Detergents (DCDs) for the Structural Biology of Membrane Proteins. Chemistry - A European Journal, 2019, 25, 11635-11640.	3.3	5
35	The structure-based traceless specific fluorescence labeling of the smoothened receptor. Organic and Biomolecular Chemistry, 2019, 17, 6136-6142.	2.8	5
36	Molecular Mechanism of Acetate Transport through the Acetate Channel SatP. Journal of Chemical Information and Modeling, 2019, 59, 2374-2382.	5.4	7

#	Article	IF	Citations
37	Structural Basis of the Diversity of Adrenergic Receptors. Cell Reports, 2019, 29, 2929-2935.e4.	6.4	30
38	Examination of the Deubiquitylation Site Selectivity of USP51 by Using Chemically Synthesized Ubiquitylated Histones. ChemBioChem, 2019, 20, 221-229.	2.6	26
39	Crystal Structure of the Human Cannabinoid Receptor CB2. Cell, 2019, 176, 459-467.e13.	28.9	268
40	GPCR Allosteric Modulator Discovery. Advances in Experimental Medicine and Biology, 2019, 1163, 225-251.	1.6	29
41	Common activation mechanism of class A GPCRs. ELife, 2019, 8, .	6.0	339
42	High-throughput identification of G protein-coupled receptor modulators through affinity mass spectrometry screening. Chemical Science, 2018, 9, 3192-3199.	7.4	33
43	5-HT2C Receptor Structures Reveal the Structural Basis of GPCR Polypharmacology. Cell, 2018, 172, 719-730.e14.	28.9	185
44	Succinate-acetate permease from Citrobacter koseri is an anion channel that unidirectionally translocates acetate. Cell Research, 2018, 28, 644-654.	12.0	15
45	Identification of natural products as novel ligands for the human 5-HT2C receptor. Biophysics Reports, 2018, 4, 50-61.	0.8	23
46	Indoleacetate decarboxylase is a glycyl radical enzyme catalysing the formation of malodorant skatole. Nature Communications, 2018, 9, 4224.	12.8	37
47	Salvianolic acids from antithrombotic Traditional Chinese Medicine Danshen are antagonists of human P2Y1 and P2Y12 receptors. Scientific Reports, 2018, 8, 8084.	3.3	20
48	Prediction of enzymatic pathways by integrative pathway mapping. ELife, 2018, 7, .	6.0	30
49	Molecular Basis for the Final Oxidative Rearrangement Steps in Chartreusin Biosynthesis. Journal of the American Chemical Society, 2018, 140, 10909-10914.	13.7	26
50	Crystal structure of the Frizzled 4 receptor in a ligand-free state. Nature, 2018, 560, 666-670.	27.8	77
51	A structurally guided dissection-then-evolution strategy for ligand optimization of smoothened receptor. MedChemComm, 2017, 8, 1332-1336.	3.4	9
52	Human GLP-1 receptor transmembrane domain structure in complex with allosteric modulators. Nature, 2017, 546, 312-315.	27.8	192
53	Crystal structure of a multi-domain human smoothened receptor in complex with a super stabilizing ligand. Nature Communications, 2017, 8, 15383.	12.8	81
54	Structural Basis for Apelin Control of the Human Apelin Receptor. Structure, 2017, 25, 858-866.e4.	3.3	96

#	Article	IF	Citations
55	Structural insights into the committed step of bacterial phospholipid biosynthesis. Nature Communications, 2017, 8, 1691.	12.8	33
56	Crystal structures of agonist-bound human cannabinoid receptor CB1. Nature, 2017, 547, 468-471.	27.8	379
57	A Novel Lid-Covering Peptide Inhibitor of Nicotinic Acetylcholine Receptors Derived from Î±D-Conotoxin GeXXA. Marine Drugs, 2017, 15, 164.	4.6	11
58	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
59	Crystal Structure of the Human Cannabinoid Receptor CB1. Cell, 2016, 167, 750-762.e14.	28.9	468
60	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
61	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
62	Prediction and Biochemical Demonstration of a Catabolic Pathway for the Osmoprotectant Proline Betaine. MBio, 2014, 5, e00933-13.	4.1	19
63	Leveraging structure for enzyme function prediction: methods, opportunities, and challenges. Trends in Biochemical Sciences, 2014, 39, 363-371.	7.5	31
64	Prediction and characterization of enzymatic activities guided by sequence similarity and genome neighborhood networks. ELife, 2014, 3, .	6.0	81
65	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
66	Discovery of new enzymes and metabolic pathways by using structure and genome context. Nature, 2013, 502, 698-702.	27.8	124
67	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
68	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
69	Progress in super long loop prediction. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2920-2935.	2.6	40
70	Toward better refinement of comparative models: Predicting loops in inexact environments. Proteins: Structure, Function and Bioinformatics, 2008, 72, 959-971.	2.6	80
71	Long loop prediction using the protein local optimization program. Proteins: Structure, Function and Bioinformatics, 2006, 65, 438-452.	2.6	110
72	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