

Zhi-Jie Liu

List of Publications by Year in descending order

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155
papers

7,939
citations

57758

44
h-index

58581

82
g-index

164
all docs

164
docs citations

164
times ranked

10290
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal Structure of the Human Cannabinoid Receptor CB1. <i>Cell</i> , 2016, 167, 750-762.e14.	28.9	468
2	Crystal structures of agonist-bound human cannabinoid receptor CB1. <i>Nature</i> , 2017, 547, 468-471.	27.8	379
3	Curved EFC/F-BAR-Domain Dimers Are Joined End to End into a Filament for Membrane Invagination in Endocytosis. <i>Cell</i> , 2007, 129, 761-772.	28.9	366
4	The helicase DDX41 recognizes the bacterial secondary messengers cyclic di-GMP and cyclic di-AMP to activate a type I interferon immune response. <i>Nature Immunology</i> , 2012, 13, 1155-1161.	14.5	363
5	Common activation mechanism of class A GPCRs. <i>ELife</i> , 2019, 8, .	6.0	339
6	The first structure of an aldehyde dehydrogenase reveals novel interactions between NAD and the Rossmann fold. <i>Nature Structural Biology</i> , 1997, 4, 317-326.	9.7	289
7	Structural Analysis of the STING Adaptor Protein Reveals a Hydrophobic Dimer Interface and Mode of Cyclic di-GMP Binding. <i>Immunity</i> , 2012, 36, 1073-1086.	14.3	282
8	Crystal Structure of the Human Cannabinoid Receptor CB2. <i>Cell</i> , 2019, 176, 459-467.e13.	28.9	268
9	NLRC3, a Member of the NLR Family of Proteins, Is a Negative Regulator of Innate Immune Signaling Induced by the DNA Sensor STING. <i>Immunity</i> , 2014, 40, 329-341.	14.3	245
10	Activation and Signaling Mechanism Revealed by Cannabinoid Receptor-Gi Complex Structures. <i>Cell</i> , 2020, 180, 655-665.e18.	28.9	212
11	Human GLP-1 receptor transmembrane domain structure in complex with allosteric modulators. <i>Nature</i> , 2017, 546, 312-315.	27.8	192
12	5-HT _{2C} Receptor Structures Reveal the Structural Basis of GPCR Polypharmacology. <i>Cell</i> , 2018, 172, 719-730.e14.	28.9	185
13	Structure of the Ca ²⁺ -regulated photoprotein obelin at 1.7 Å... resolution determined directly from its sulfur substructure. <i>Protein Science</i> , 2000, 9, 2085-2093.	7.6	170
14	Inhibition mechanism of SARS-CoV-2 main protease by ebiselen and its derivatives. <i>Nature Communications</i> , 2021, 12, 3061.	12.8	149
15	Structural basis of CXC chemokine receptor 2 activation and signalling. <i>Nature</i> , 2020, 585, 135-140.	27.8	128
16	Mechanism of Class 1 (Glycosylhydrolase Family 47) Î±-Mannosidases Involved in N-Glycan Processing and Endoplasmic Reticulum Quality Control. <i>Journal of Biological Chemistry</i> , 2005, 280, 16197-16207.	3.4	106
17	Native phasing of x-ray free-electron laser data for a G protein-coupled receptor. <i>Science Advances</i> , 2016, 2, e1600292.	10.3	97
18	Crystal Structure of the Cytoskeleton-associated Protein Glycine-rich (CAP-Gly) Domain. <i>Journal of Biological Chemistry</i> , 2002, 277, 48596-48601.	3.4	88

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19	Structural analysis of asparaginyl endopeptidase reveals the activation mechanism and a reversible intermediate maturation stage. <i>Cell Research</i> , 2014, 24, 344-358.	12.0	86
20	All three Ca ²⁺ -binding loops of photoproteins bind calcium ions: The crystal structures of calcium-loaded apo-aequorin and apo-obelin. <i>Protein Science</i> , 2005, 14, 663-675.	7.6	85
21	Structural and Biochemical Characterization Reveals LysGH15 as an Unprecedented α -EF-Hand-Like Calcium-Binding Phage Lysin. <i>PLoS Pathogens</i> , 2014, 10, e1004109.	4.7	85
22	Crystal structure of obelin after Ca ²⁺ -triggered bioluminescence suggests neutral coelenteramide as the primary excited state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2570-2575.	7.1	84
23	Elucidating the active μ -opioid receptor crystal structure with peptide and small-molecule agonists. <i>Science Advances</i> , 2019, 5, eaax9115.	10.3	81
24	Life in the fast lane for protein crystallization and X-ray crystallography. <i>Progress in Biophysics and Molecular Biology</i> , 2005, 88, 359-386.	2.9	77
25	X-ray Crystal Structures of Reduced Rubrerythrin and Its Azide Adduct: A Structure-Based Mechanism for a Non-Heme Diiron Peroxidase. <i>Journal of the American Chemical Society</i> , 2002, 124, 9845-9855.	13.7	76
26	The multifunctional human p100 protein 'hooks' methylated ligands. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 779-784.	8.2	72
27	The emerging roles of the DDX41 protein in immunity and diseases. <i>Protein and Cell</i> , 2017, 8, 83-89.	11.0	72
28	Structure of Severe Fever with Thrombocytopenia Syndrome Virus Nucleocapsid Protein in Complex with Suramin Reveals Therapeutic Potential. <i>Journal of Virology</i> , 2013, 87, 6829-6839.	3.4	67
29	Crystal structure of an aerobic FMN-dependent azoreductase (AzoA) from <i>Enterococcus faecalis</i> . <i>Archives of Biochemistry and Biophysics</i> , 2007, 463, 68-77.	3.0	66
30	Computational design of thermostabilizing point mutations for G protein-coupled receptors. <i>ELife</i> , 2018, 7, .	6.0	60
31	Structure of the Leanyer orthobunyavirus nucleoprotein-RNA complex reveals unique architecture for RNA encapsidation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 9054-9059.	7.1	59
32	Violet Bioluminescence and Fast Kinetics from W92F Obelin: Structure-Based Proposals for the Bioluminescence Triggering and the Identification of the Emitting Species. <i>Biochemistry</i> , 2003, 42, 6013-6024.	2.5	57
33	Atomic resolution structure of obelin: soaking with calcium enhances electron density of the second oxygen atom substituted at the C2-position of coelenterazine. <i>Biochemical and Biophysical Research Communications</i> , 2003, 311, 433-439.	2.1	56
34	Functionality-Independent DNA Encoding of Complex Natural Products. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 9254-9261.	13.8	54
35	In vitro expression and analysis of the 826 human G protein-coupled receptors. <i>Protein and Cell</i> , 2016, 7, 325-337.	11.0	53
36	Structural Basis and Catalytic Mechanism for the Dual Functional Endo- β -N-Acetylglucosaminidase A. <i>PLoS ONE</i> , 2009, 4, e4658.	2.5	52

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37	Crystal Structure of a Ca ²⁺ -discharged Photoprotein. <i>Journal of Biological Chemistry</i> , 2004, 279, 33647-33652.	3.4	51
38	Combination Therapy of LysGH15 and Apigenin as a New Strategy for Treating Pneumonia Caused by <i>Staphylococcus aureus</i> . <i>Applied and Environmental Microbiology</i> , 2016, 82, 87-94.	3.1	51
39	Structural features of activated GPCR signaling complexes. <i>Current Opinion in Structural Biology</i> , 2020, 63, 82-89.	5.7	50
40	Structure of Mouse Golgi α -Mannosidase IA Reveals the Molecular Basis for Substrate Specificity among Class 1 (Family 47 Glycosylhydrolase) α 1,2-Mannosidases. <i>Journal of Biological Chemistry</i> , 2004, 279, 29774-29786.	3.4	48
41	New insights into the structural basis of DNA recognition by HINa and HINb domains of IFI16. <i>Journal of Molecular Cell Biology</i> , 2016, 8, 51-61.	3.3	48
42	NMR-derived Topology of a GFP-photoprotein Energy Transfer Complex*. <i>Journal of Biological Chemistry</i> , 2010, 285, 40891-40900.	3.4	47
43	Aldehyde Dehydrogenase Catalytic Mechanism. <i>Advances in Experimental Medicine and Biology</i> , 1999, 463, 53-59.	1.6	47
44	Novel dimerization mode of the human Bcl-2 family protein Bak, a mitochondrial apoptosis regulator. <i>Journal of Structural Biology</i> , 2009, 166, 32-37.	2.8	46
45	Structural and functional analyses of human tryptophan 2,3-dioxygenase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 3210-3216.	2.6	46
46	Structural basis for DNA recognition by STAT6. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13015-13020.	7.1	46
47	A test of enhancing model accuracy in high-throughput crystallography. <i>Journal of Structural and Functional Genomics</i> , 2005, 6, 1-11.	1.2	45
48	Structural insight into acute intermittent porphyria. <i>FASEB Journal</i> , 2009, 23, 396-404.	0.5	45
49	Structural basis for the emission of violet bioluminescence from a W92F obelin mutant. <i>FEBS Letters</i> , 2001, 506, 281-285.	2.8	44
50	A Genetically Encoded F-19 NMR Probe Reveals the Allosteric Modulation Mechanism of Cannabinoid Receptor 1. <i>Journal of the American Chemical Society</i> , 2021, 143, 16320-16325.	13.7	44
51	Structures of an unliganded neurophysin and its vasopressin complex: Implications for binding and allosteric mechanisms. <i>Protein Science</i> , 2001, 10, 1869-1880.	7.6	42
52	Structure-function analysis of human l-prostaglandin D synthase bound with fatty acid molecules. <i>FASEB Journal</i> , 2010, 24, 4668-4677.	0.5	40
53	Structural and Functional Insights into Cannabinoid Receptors. <i>Trends in Pharmacological Sciences</i> , 2020, 41, 665-677.	8.7	40
54	Structural basis for termination of AIM2-mediated signaling by p202. <i>Cell Research</i> , 2013, 23, 855-858.	12.0	38

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55	Exploring a new ligand binding site of G protein-coupled receptors. <i>Chemical Science</i> , 2018, 9, 6480-6489.	7.4	37
56	Role of the HIN Domain in Regulation of Innate Immune Responses. <i>Molecular and Cellular Biology</i> , 2014, 34, 2-15.	2.3	36
57	The Hyperthermophile Protein Sso10a is a Dimer of Winged Helix DNA-binding Domains Linked by an Antiparallel Coiled Coil Rod. <i>Journal of Molecular Biology</i> , 2004, 341, 73-91.	4.2	35
58	The crystal structures of <i>Phascolopsis gouldii</i> wild type and L98Y methemerythrins: structural and functional alterations of the O ₂ binding pocket. <i>Journal of Biological Inorganic Chemistry</i> , 2001, 6, 418-429.	2.6	34
59	Structure of the Conserved Transcriptional Repressor Enhancer of Rudimentary Homolog. <i>Biochemistry</i> , 2005, 44, 5017-5023.	2.5	34
60	High-throughput identification of G protein-coupled receptor modulators through affinity mass spectrometry screening. <i>Chemical Science</i> , 2018, 9, 3192-3199.	7.4	33
61	The First Agmatine/Cadaverine Aminopropyl Transferase: Biochemical and Structural Characterization of an Enzyme Involved in Polyamine Biosynthesis in the Hyperthermophilic Archaeon <i>Pyrococcus furiosus</i> . <i>Journal of Bacteriology</i> , 2007, 189, 6057-6067.	2.2	31
62	Crystal structure of coelenterazine-binding protein from <i>Renilla muelleri</i> at 1.7 Å.: Why it is not a calcium-regulated photoprotein. <i>Photochemical and Photobiological Sciences</i> , 2008, 7, 442.	2.9	31
63	Crystal structure of human esterase D: a potential genetic marker of retinoblastoma. <i>FASEB Journal</i> , 2009, 23, 1441-1446.	0.5	31
64	Oxygen Activation of Apo-Obelin-Coelenterazine Complex. <i>ChemBioChem</i> , 2013, 14, 739-745.	2.6	31
65	Structural Basis of the Diversity of Adrenergic Receptors. <i>Cell Reports</i> , 2019, 29, 2929-2935.e4.	6.4	30
66	Characterization of a corrinoid protein involved in the C1 metabolism of strict anaerobic bacterium <i>Moorella thermoacetica</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 167-176.	2.6	28
67	Conversion of ribulose 5-phosphate to D-xylulose 5-phosphate: new insights from structural and biochemical studies on human RPE. <i>FASEB Journal</i> , 2011, 25, 497-504.	0.5	28
68	Preparation and X-ray crystallographic analysis of recombinant obelin crystals diffracting to beyond 1.1 Å. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1919-1921.	2.5	27
69	Crystal Structures of Tyrosyl-tRNA Synthetases from Archaea. <i>Journal of Molecular Biology</i> , 2006, 355, 395-408.	4.2	27
70	Structure of dNTP-inducible dNTP triphosphohydrolase: insight into broad specificity for dNTPs and triphosphohydrolase-type hydrolysis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 230-239.	2.5	27
71	Mechanism of the Rpn13-induced activation of Uch37. <i>Protein and Cell</i> , 2014, 5, 616-630.	11.0	27
72	Crystal structures of the F88Y obelin mutant before and after bioluminescence provide molecular insight into spectral tuning among hydromedusan photoproteins. <i>FEBS Journal</i> , 2014, 281, 1432-1445.	4.7	26

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73	Parameter-space screening: a powerful tool for high-throughput crystal structure determination. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 520-527.	2.5	25
74	Crystal Structures of the Lytic Transglycosylase MltA from <i>N.gonorrhoeae</i> and <i>E.coli</i> : Insights into Interdomain Movements and Substrate Binding. <i>Journal of Molecular Biology</i> , 2006, 359, 122-136.	4.2	25
75	A multi-dataset data-collection strategy produces better diffraction data. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2011, 67, 544-549.	0.3	25
76	Structural insights into a human anti-IFN antibody exerting therapeutic potential for systemic lupus erythematosus. <i>Journal of Molecular Medicine</i> , 2012, 90, 837-846.	3.9	25
77	Spatial structure of the novel light-sensitive photoprotein berovin from the ctenophore <i>Beroë abyssicola</i> in the Ca ²⁺ -loaded apoprotein conformation state. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 2139-2146.	2.3	25
78	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.	11.3	25
79	S-SAD phasing study of death receptor 6 and its solution conformation revealed by SAXS. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 521-530.	2.5	24
80	Structures of the Ca ²⁺ -regulated photoprotein obelin Y138F mutant before and after bioluminescence support the catalytic function of a water molecule in the reaction. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 720-732.	2.5	23
81	Identification of natural products as novel ligands for the human 5-HT _{2C} receptor. <i>Biophysics Reports</i> , 2018, 4, 50-61.	0.8	23
82	The high-throughput protein-to-structure pipeline at SECSG. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 679-684.	2.5	22
83	Structure of acostatin, a dimeric disintegrin from Southern copperhead (<i>Agkistrodon contortrix</i>) Tj ETQq1 1 0.784314 rgBT /Overl 2008, 64, 466-470.	2.5	20
84	Protein-protein complexation in bioluminescence. <i>Protein and Cell</i> , 2011, 2, 957-972.	11.0	20
85	Structural and functional analyses of human DDX41 DEAD domain. <i>Protein and Cell</i> , 2017, 8, 72-76.	11.0	20
86	Displacement of iron by zinc at the diiron site of <i>Desulfovibrio vulgaris</i> rubrerythrin: X-ray crystal structure and anomalous scattering analysis. <i>Journal of Inorganic Biochemistry</i> , 2004, 98, 786-796.	3.5	19
87	Structure determination of fibrillarlin from the hyperthermophilic archaeon <i>Pyrococcus furiosus</i> . <i>Biochemical and Biophysical Research Communications</i> , 2004, 315, 726-732.	2.1	19
88	Structure based mechanism of the Ca ²⁺ -induced release of coelenterazine from the <i>Renilla</i> binding protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 583-593.	2.6	19
89	Structural insights into the activation initiation of full-length mGlu1. <i>Protein and Cell</i> , 2021, 12, 662-667.	11.0	19
90	Structural genomics of <i>Pyrococcus furiosus</i> : X-ray crystallography reveals 3D domain swapping in rubrerythrin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 878-882.	2.6	18

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91	Binding of bacterial secondary messenger molecule c di-GMP is a STING operation. <i>Protein and Cell</i> , 2013, 4, 117-129.	11.0	18
92	A primase subunit essential for efficient primer synthesis by an archaeal eukaryotic-type primase. <i>Nature Communications</i> , 2015, 6, 7300.	12.8	18
93	Mitrocomin from the jellyfish <i>Mitrocoma cellularia</i> with deleted C-terminal tyrosine reveals a higher bioluminescence activity compared to wild type photoprotein. <i>Journal of Photochemistry and Photobiology B: Biology</i> , 2016, 162, 286-297.	3.8	18
94	Organized cannabinoid receptor distribution in neurons revealed by super-resolution fluorescence imaging. <i>Nature Communications</i> , 2020, 11, 5699.	12.8	18
95	Self-capping of nucleoprotein filaments protects the Newcastle disease virus genome. <i>ELife</i> , 2019, 8, .	6.0	18
96	On increasing protein-crystallization throughput for X-ray diffraction studies. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 123-129.	2.5	17
97	(NZ)CH...O Contacts assist crystallization of a ParB-like nuclease. <i>BMC Structural Biology</i> , 2007, 7, 46.	2.3	17
98	Studies of Human 2,4-Dienoyl CoA Reductase Shed New Light on Peroxisomal \hat{I}^2 -Oxidation of Unsaturated Fatty Acids. <i>Journal of Biological Chemistry</i> , 2012, 287, 28956-28965.	3.4	17
99	Structural biology study of human TNF receptor associated factor 4 TRAF domain. <i>Protein and Cell</i> , 2013, 4, 687-694.	11.0	17
100	Structure and Function of a C \hat{C} Bond Cleaving Oxygenase in Atypical Angucycline Biosynthesis. <i>ACS Chemical Biology</i> , 2017, 12, 142-152.	3.4	17
101	Molecular Mechanism for Ligand Recognition and Subtype Selectivity of \hat{I}^2 Adrenergic Receptor. <i>Cell Reports</i> , 2019, 29, 2936-2943.e4.	6.4	17
102	Cryo-EM analysis of the HCoV-229E spike glycoprotein reveals dynamic prefusion conformational changes. <i>Nature Communications</i> , 2021, 12, 141.	12.8	17
103	Structure of the human Tim44 C-terminal domain in complex with pentaethylene glycol: ligand-bound form. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 1225-1234.	2.5	16
104	Structural Basis for the Inhibition of Human 5,10-Methenyltetrahydrofolate Synthetase by N10-Substituted Folate Analogues. <i>Cancer Research</i> , 2009, 69, 7294-7301.	0.9	16
105	aKMT Catalyzes Extensive Protein Lysine Methylation in the Hyperthermophilic Archaeon <i>Sulfolobus islandicus</i> but is Dispensable for the Growth of the Organism. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2908-2923.	3.8	16
106	All Ca $^{2+}$ -binding loops of light-sensitive ctenophore photoprotein berovin bind magnesium ions: The spatial structure of Mg $^{2+}$ -loaded apo-berovin. <i>Journal of Photochemistry and Photobiology B: Biology</i> , 2016, 154, 57-66.	3.8	16
107	X-ray Crystal Structure of <i>Desulfovibrio vulgaris</i> Rubrerythrin with Zinc Substituted into the [Fe(SCys) 4] Site and Alternative Diron Site Structures. <i>Biochemistry</i> , 2004, 43, 3204-3213.	2.5	14
108	Protein Production and Crystallization at SECSG – An Overview. <i>Journal of Structural and Functional Genomics</i> , 2005, 6, 233-243.	1.2	14

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109	Altered architecture of substrate binding region defines the unique specificity of UDP-GalNAc 4-epimerases. <i>Protein Science</i> , 2011, 20, 856-866.	7.6	14
110	Protein crystal quality oriented disulfide bond engineering. <i>Protein and Cell</i> , 2018, 9, 659-663.	11.0	14
111	Crystal Structure of ATP-Bound Human ABCF1 Demonstrates a Unique Conformation of ABC Proteins. <i>Structure</i> , 2018, 26, 1259-1265.e3.	3.3	14
112	Crystal structure of a novel non-Pfam protein PF2046 solved using low resolution B-factor sharpening and multi-crystal averaging methods. <i>Protein and Cell</i> , 2010, 1, 453-458.	11.0	13
113	Structural and functional characterization of the C-terminal catalytic domain of SSV1 integrase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 659-670.	2.5	13
114	Molecular insights into ligand recognition and G protein coupling of the neuromodulatory orphan receptor GPR139. <i>Cell Research</i> , 2022, 32, 210-213.	12.0	13
115	Three-dimensional structure of GlcNAc 1-4Gal releasing Endo- β -Galactosidase from <i>Clostridium perfringens</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 141-144.	2.6	12
116	Crystal structure of the N-terminal methyltransferase-like domain of anamorsin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1066-1071.	2.6	12
117	Crystal Structure of a Class 3 Aldehyde Dehydrogenase at 2.6Å... Resolution. <i>Advances in Experimental Medicine and Biology</i> , 1996, 414, 1-7.	1.6	12
118	Conserved Residues in the Aldehyde Dehydrogenase Family. <i>Advances in Experimental Medicine and Biology</i> , 1996, 414, 9-13.	1.6	12
119	Away from the edge II: in-house Se-SAS phasing with chromium radiation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 960-966.	2.5	10
120	High-resolution crystal structure of the catalytic domain of human dual-specificity phosphatase 26. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1160-1170.	2.5	10
121	Rational Remodeling of Atypical Scaffolds for the Design of Photoswitchable Cannabinoid Receptor Tools. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 13752-13765.	6.4	9
122	Procedure for reductive methylation of protein to improve crystallizability. <i>Protocol Exchange</i> , 0, , .	0.3	9
123	The structural study of mutation-induced inactivation of human muscarinic receptor M4. <i>IUCr</i> , 2020, 7, 294-305.	2.2	9
124	Crystallization and preliminary X-ray diffraction analysis of lectin-1 from <i>Pseudomonas aeruginosa</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1241-1242.	2.5	8
125	Isolation, crystallization and preliminary X-ray analysis of a methanol-induced corrinoid protein from <i>Moorella thermoacetica</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 537-540.	0.7	8
126	Crystal structure of a novel non-Pfam protein AF1514 from <i>Archeoglobus fulgidus</i> DSM 4304 solved by SAD using a Cr X-ray source. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 2109-2113.	2.6	8

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127	Novel Functionalized Cannabinoid Receptor Probes: Development of Exceptionally Potent Agonists. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 3870-3884.	6.4	8
128	Preparation and X-ray crystallographic analysis of the Ca ²⁺ -discharged photoprotein obelin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 512-514.	2.5	7
129	Crystal structure solution of a ParB-like nuclease at atomic resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 263-267.	2.6	7
130	Ligand identification of the adenosine A _{2A} receptor in self-assembled nanodiscs by affinity mass spectrometry. <i>Analytical Methods</i> , 2017, 9, 5851-5858.	2.7	7
131	Structural insights into the activation of chemokine receptor CXCR2. <i>FEBS Journal</i> , 2022, 289, 386-393.	4.7	7
132	Structure of the hypothetical protein PF0899 from <i>Pyrococcus furiosus</i> at 1.85 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 549-552.	0.7	6
133	Biochemical features of the adhesion G protein-coupled receptor CD97 related to its auto-proteolysis and HeLa cell attachment activities. <i>Acta Pharmacologica Sinica</i> , 2017, 38, 56-68.	6.1	6
134	A Chemical Strategy for Amphiphile Replacement in Membrane Protein Research. <i>Langmuir</i> , 2019, 35, 4319-4327.	3.5	6
135	Preparation and preliminary study of crystals of the recombinant calcium-regulated photoprotein obelin from the bioluminescent hydroid <i>Obelia longissima</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1965-1966.	2.5	5
136	Disulfide-Containing Detergents (DCDs) for the Structural Biology of Membrane Proteins. <i>Chemistry - A European Journal</i> , 2019, 25, 11635-11640.	3.3	5
137	Crystallization and preliminary crystallographic analysis of molybdenum-cofactor biosynthesis protein C from <i>Thermus thermophilus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 27-29.	0.7	4
138	Probing the CB ₁ Cannabinoid Receptor Binding Pocket with AM6538, a High-Affinity Irreversible Antagonist. <i>Molecular Pharmacology</i> , 2019, 96, 619-628.	2.3	4
139	Crystal structure of semisynthetic obelin. <i>Protein Science</i> , 2021, , .	7.6	4
140	MD Simulations Revealing Special Activation Mechanism of Cannabinoid Receptor 1. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 860035.	3.5	4
141	Structural basis of CoA recognition by the <i>Pyrococcus</i> single-domain CoA-binding proteins. <i>Journal of Structural and Functional Genomics</i> , 2007, 7, 119-129.	1.2	3
142	Low-salt crystallization of T7 RNA polymerase: a first step towards the transcription bubble complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1188-1192.	2.5	2
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