

Robert M Stroud

List of Publications by Year in descending order

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213
papers

22,094
citations

10986

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224
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224
docs citations

224
times ranked

26707
citing authors

#	ARTICLE	IF	CITATIONS
1	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. <i>Nature</i> , 2020, 583, 459-468.	27.8	3,542
2	Structure of a Glycerol-Conducting Channel and the Basis for Its Selectivity. <i>Science</i> , 2000, 290, 481-486.	12.6	938
3	Control of the Selectivity of the Aquaporin Water Channel Family by Global Orientational Tuning. <i>Science</i> , 2002, 296, 525-530.	12.6	833
4	Mechanism of Ammonia Transport by Amt/MEP/Rh: Structure of AmtB at 1.35 Å. <i>Science</i> , 2004, 305, 1587-1594.	12.6	605
5	The unfolded protein response signals through high-order assembly of Ire1. <i>Nature</i> , 2009, 457, 687-693.	27.8	565
6	Efficiency of signalling through cytokine receptors depends critically on receptor orientation. <i>Nature</i> , 1998, 395, 511-516.	27.8	545
7	The Signal Recognition Particle. <i>Annual Review of Biochemistry</i> , 2001, 70, 755-775.	11.1	541
8	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. <i>Science</i> , 2020, 370, .	12.6	508
9	On the mechanism of sensing unfolded protein in the endoplasmic reticulum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18773-18784.	7.1	465
10	An ultrapotent synthetic nanobody neutralizes SARS-CoV-2 by stabilizing inactive Spike. <i>Science</i> , 2020, 370, 1473-1479.	12.6	336
11	Crystal structure of human aquaporin 4 at 1.8 Å and its mechanism of conductance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 7437-7442.	7.1	297
12	The structure of bovine trypsin : Electron density maps of the inhibited enzyme at 5 Å and at 2.7 Å resolution. <i>Journal of Molecular Biology</i> , 1974, 83, 185-208.	4.2	292
13	Aquaporin 4-specific T cells in neuromyelitis optica exhibit a Th17 bias and recognize <i>Clostridium</i> ABC transporter. <i>Annals of Neurology</i> , 2012, 72, 53-64.	5.3	281
14	Crystal Structure of the Signal Sequence Binding Subunit of the Signal Recognition Particle. <i>Cell</i> , 1998, 94, 181-191.	28.9	277
15	Substrate twinning activates the signal recognition particle and its receptor. <i>Nature</i> , 2004, 427, 215-221.	27.8	270
16	Crystal structure of colicin Ia. <i>Nature</i> , 1997, 385, 461-464.	27.8	250
17	The channel architecture of aquaporin 0 at a 2.2-Å resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 14045-14050.	7.1	248
18	Architecture and Selectivity in Aquaporins: 2.5 Å X-Ray Structure of Aquaporin Z. <i>PLoS Biology</i> , 2003, 1, e72.	5.6	248

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19	Architecture of a single membrane spanning cytochrome P450 suggests constraints that orient the catalytic domain relative to a bilayer. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 3865-3870.	7.1	231
20	Structure of the conserved GTPase domain of the signal recognition particle. Nature, 1997, 385, 361-364.	27.8	228
21	Targeting proteins to membranes: structure of the signal recognition particle. Current Opinion in Structural Biology, 2005, 15, 213-220.	5.7	206
22	Pyrrrolidine Carboxamides as a Novel Class of Inhibitors of Enoyl Acyl Carrier Protein Reductase from Mycobacterium tuberculosis. Journal of Medicinal Chemistry, 2006, 49, 6308-6323.	6.4	205
23	Crystal structure of a eukaryotic phosphate transporter. Nature, 2013, 496, 533-536.	27.8	202
24	The Structure of a Ketoreductase Determines the Organization of the β^2 -Carbon Processing Enzymes of Modular Polyketide Synthases. Structure, 2006, 14, 737-748.	3.3	197
25	Family of G protein β chains: amphipathic analysis and predicted structure of functional domains. Protein Engineering, Design and Selection, 1986, 1, 47-54.	2.1	187
26	Crystal Structure and Molecular Modeling of 17-DMAG in Complex with Human Hsp90. Chemistry and Biology, 2003, 10, 361-368.	6.0	183
27	Structural studies of a membrane-bound acetylcholine receptor from Torpedo californica. Journal of Molecular Biology, 1977, 116, 635-659.	4.2	181
28	Function of human Rh based on structure of RhCG at 2.1 Å. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9638-9643.	7.1	178
29	Acetylcholine Receptor Structure, Function, and Evolution. Annual Review of Cell Biology, 1985, 1, 317-351.	26.1	172
30	Mechanism of inhibition of human glucose transporter GLUT1 is conserved between cytochalasin B and phenylalanine amides. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 4711-4716.	7.1	170
31	Design of potent selective zinc-mediated serine protease inhibitors. Nature, 1998, 391, 608-612.	27.8	164
32	An antibiotic factory caught in action. Nature Structural and Molecular Biology, 2004, 11, 888-893.	8.2	162
33	The crystal structure of β -bungarotoxin at 2.5 Å resolution: relation to solution structure and binding to acetylcholine receptor. Protein Engineering, Design and Selection, 1986, 1, 37-46.	2.1	157
34	A Family of Protein-Cutting Proteins. Scientific American, 1974, 231, 74-88.	1.0	156
35	Lateral opening of a translocon upon entry of protein suggests the mechanism of insertion into membranes. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 17182-17187.	7.1	155
36	Structure, inhibition and regulation of two-pore channel TPC1 from Arabidopsis thaliana. Nature, 2016, 531, 258-264.	27.8	155

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37	Plastic adaptation toward mutations in proteins: Structural comparison of thymidylate synthases. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990, 8, 315-333.	2.6	154
38	Fabs Enable Single Particle cryoEM Studies of Small Proteins. <i>Structure</i> , 2012, 20, 582-592.	3.3	154
39	Immunospecific identification and three-dimensional structure of a membrane-bound acetylcholine receptor from <i>Torpedo californica</i> . <i>Journal of Molecular Biology</i> , 1979, 128, 319-334.	4.2	151
40	Structural basis for conductance by the archaeal aquaporin AqpM at 1.68 Å. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18932-18937.	7.1	146
41	TARP Auxiliary Subunits Switch AMPA Receptor Antagonists into Partial Agonists. <i>Science</i> , 2007, 318, 815-817.	12.6	144
42	Crystal structure of the aquaglyceroporin PfAQP from the malarial parasite <i>Plasmodium falciparum</i> . <i>Nature Structural and Molecular Biology</i> , 2008, 15, 619-625.	8.2	143
43	Structural Basis of Aquaporin Inhibition by Mercury. <i>Journal of Molecular Biology</i> , 2007, 368, 607-617.	4.2	127
44	Projected structure of purple membrane determined to 3.7 Å resolution by low temperature electron microscopy. <i>Journal of Molecular Biology</i> , 1981, 151, 491-517.	4.2	126
45	Catalysis, Specificity, and ACP Docking Site of <i>Streptomyces coelicolor</i> Malonyl-CoA:ACP Transacylase. <i>Structure</i> , 2003, 11, 147-154.	3.3	125
46	Inhibitory complex of the transmembrane ammonia channel, AmtB, and the cytosolic regulatory protein, GlnK, at 1.96 Å. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 42-47.	7.1	124
47	Substrates Control Multimerization and Activation of the Multi-Domain ATPase Motor of Type VII Secretion. <i>Cell</i> , 2015, 161, 501-512.	28.9	124
48	A designed four helix bundle protein with native-like structure. <i>Nature Structural Biology</i> , 1997, 4, 1039-1046.	9.7	119
49	Structure of tRNA pseudouridine synthase TruB and its RNA complex: RNA recognition through a combination of rigid docking and induced fit. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12648-12653.	7.1	117
50	A general protocol for the crystallization of membrane proteins for X-ray structural investigation. <i>Nature Protocols</i> , 2009, 4, 619-637.	12.0	116
51	Subnanometre-resolution electron cryomicroscopy structure of a heterodimeric ABC exporter. <i>Nature</i> , 2015, 517, 396-400.	27.8	114
52	Domain Flexibility in Retroviral Proteases: Structural Implications for Drug Resistant Mutations. <i>Biochemistry</i> , 1998, 37, 2607-2621.	2.5	112
53	Structure of sugar-bound LacY. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1784-1788.	7.1	111
54	Solvent structure in crystals of trypsin determined by X-ray and neutron diffraction. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992, 12, 203-222.	2.6	102

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55	A Unique RNA Fold in the RumA-RNA-Cofactor Ternary Complex Contributes to Substrate Selectivity and Enzymatic Function. <i>Cell</i> , 2005, 120, 599-611.	28.9	99
56	Comparison of human solute carriers. <i>Protein Science</i> , 2010, 19, 412-428.	7.6	99
57	LINKING REGIONS BETWEEN HELICES IN BACTERIORHODOPSIN REVEALED. <i>Biophysical Journal</i> , 1982, 37, 589-602.	0.5	97
58	Conformational Dynamics along an Enzymatic Reaction Pathway: Thymidylate Synthase, the Movie. <i>Biochemistry</i> , 2003, 42, 239-247.	2.5	96
59	Fungal association and utilization of phosphate by plants: success, limitations, and future prospects. <i>Frontiers in Microbiology</i> , 2015, 6, 984.	3.5	96
60	Mechanism of Association and Reciprocal Activation of Two GTPases. <i>PLoS Biology</i> , 2004, 2, e320.	5.6	94
61	Structural basis for alternating access of a eukaryotic calcium/proton exchanger. <i>Nature</i> , 2013, 499, 107-110.	27.8	87
62	Refined Structures of Substrate-bound and Phosphate-bound Thymidylate Synthase from <i>Lactobacillus casei</i> . <i>Journal of Molecular Biology</i> , 1993, 232, 1101-1116.	4.2	85
63	Tandem Facial Amphiphiles for Membrane Protein Stabilization. <i>Journal of the American Chemical Society</i> , 2010, 132, 16750-16752.	13.7	85
64	Mechanistic Diversity of Cytokine Receptor Signaling Across Cell Membranes. <i>Science Signaling</i> , 2004, 2004, re7-re7.	3.6	84
65	Functional changes in the structure of the SRP GTPase on binding GDP and Mg ²⁺ +GDP. <i>Nature Structural Biology</i> , 1999, 6, 793-801.	9.7	83
66	Structure of Bor1 supports an elevator transport mechanism for SLC4 anion exchangers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10542-10546.	7.1	83
67	Effects of detergent environments on the photocycle of purified monomeric bacteriorhodopsin. <i>Biochemistry</i> , 1991, 30, 1751-1761.	2.5	81
68	The structural basis for tRNA recognition and pseudouridine formation by pseudouridine synthase I. <i>Nature Structural Biology</i> , 2000, 7, 23-27.	9.7	79
69	Bi-paratopic and multivalent VH domains block ACE2 binding and neutralize SARS-CoV-2. <i>Nature Chemical Biology</i> , 2021, 17, 113-121.	8.0	78
70	The Structural Mechanism for Half-the-Sites Reactivity in an Enzyme, Thymidylate Synthase, Involves a Relay of Changes between Subunits. <i>Biochemistry</i> , 1999, 38, 13829-13836.	2.5	77
71	Protein Structure Prediction with a Combined Solvation Free Energy-Molecular Mechanics Force Field. <i>Molecular Simulation</i> , 1993, 10, 121-149.	2.0	76
72	Crystal Structure of the Priming β^2 -Ketosynthase from the R1128 Polyketide Biosynthetic Pathway. <i>Structure</i> , 2002, 10, 1559-1568.	3.3	75

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73	Structure of a TrmA-RNA complex: A consensus RNA fold contributes to substrate selectivity and catalysis in m ⁵ C-U methyltransferases. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6876-6881.	7.1	75
74	The additivity of substrate fragments in enzyme-ligand binding. Structure, 1998, 6, 839-848.	3.3	74
75	Structural and biochemical insights into the dicing mechanism of mouse Dicer: A conserved lysine is critical for dsRNA cleavage. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2391-2396.	7.1	74
76	Structural context shapes the aquaporin selectivity filter. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 17164-17169.	7.1	74
77	Metal-induced conformational changes in ZneB suggest an active role of membrane fusion proteins in efflux resistance systems. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 11038-11043.	7.1	74
78	Unraveling the interface of signal recognition particle and its receptor by using chemical cross-linking and tandem mass spectrometry. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 16454-16459.	7.1	72
79	Approaches to solving the rigid receptor problem by identifying a minimal set of flexible residues during ligand docking. 11 PDB coordinates have been deposited with the RSCB with accession ID: 1F28.. Chemistry and Biology, 2001, 8, 445-457.	6.0	71
80	Glycerol facilitator GlpF and the associated aquaporin family of channels. Current Opinion in Structural Biology, 2003, 13, 424-431.	5.7	71
81	How U38, 39, and 40 of Many tRNAs Become the Targets for Pseudouridylation by TruA. Molecular Cell, 2007, 26, 189-203.	9.7	71
82	Overexpressing human membrane proteins in stably transfected and clonal human embryonic kidney 293S cells. Nature Protocols, 2012, 7, 453-466.	12.0	69
83	Characterization of the 23 S Ribosomal RNA m ⁵ U1939 Methyltransferase from Escherichia coli. Journal of Biological Chemistry, 2002, 277, 8835-8840.	3.4	68
84	Crystal structure and mechanistic basis of a functional homolog of the antigen transporter TAP. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E438-E447.	7.1	67
85	Structural and mechanistic basis of the EMC-dependent biogenesis of distinct transmembrane clients. ELife, 2020, 9, .	6.0	66
86	Coordinating the impact of structural genomics on the human α -helical transmembrane proteome. Nature Structural and Molecular Biology, 2013, 20, 135-138.	8.2	64
87	Phylogenetic Classification of Protozoa Based on the Structure of the Linker Domain in the Bifunctional Enzyme, Dihydrofolate Reductase-Thymidylate Synthase. Journal of Biological Chemistry, 2003, 278, 52980-52987.	3.4	62
88	Binding of the anticancer drug ZD1694 to E. coli thymidylate synthase: assessing specificity and affinity. Structure, 1996, 4, 1317-1324.	3.3	59
89	Multi-targeted antifolates aimed at avoiding drug resistance form covalent closed inhibitory complexes with human and Escherichia coli thymidylate synthases. Journal of Molecular Biology, 2001, 313, 813-829.	4.2	57
90	The First Structure of an RNA m ⁵ C Methyltransferase, Fmu, Provides Insight into Catalytic Mechanism and Specific Binding of RNA Substrate. Structure, 2003, 11, 1609-1620.	3.3	57

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91	Inclusion of solvation free energy with molecular mechanics energy: Alanine dipeptide as a test case. <i>Protein Science</i> , 1992, 1, 396-400.	7.6	56
92	Crystal Structure of the First KH Domain of Human Poly(C)-binding Protein-2 in Complex with a C-rich Strand of Human Telomeric DNA at 1.7 Å.... <i>Journal of Biological Chemistry</i> , 2005, 280, 38823-38830.	3.4	54
93	Selecting Optimum Eukaryotic Integral Membrane Proteins for Structure Determination by Rapid Expression and Solubilization Screening. <i>Journal of Molecular Biology</i> , 2009, 385, 820-830.	4.2	53
94	Ion transport and regulation in a synaptic vesicle glutamate transporter. <i>Science</i> , 2020, 368, 893-897.	12.6	53
95	Selectivity and conductance among the glycerol and water conducting aquaporin family of channels. <i>FEBS Letters</i> , 2003, 555, 79-84.	2.8	52
96	X-ray crystallographic and NMR studies of protein-protein and protein-nucleic acid interactions involving the KH domains from human poly(C)-binding protein-2. <i>Rna</i> , 2007, 13, 1043-1051.	3.5	50
97	Cell-free complements in vivo expression of the E. coli membrane proteome. <i>Protein Science</i> , 2007, 16, 966-976.	7.6	50
98	Structures of intermediate transport states of ZneA, a Zn(II)/proton antiporter. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 18484-18489.	7.1	49
99	Crystal Structure of the Human tRNA m1A58 Methyltransferase-tRNA ³ Lys Complex: Refolding of Substrate tRNA Allows Access to the Methylation Target. <i>Journal of Molecular Biology</i> , 2015, 427, 3862-3876.	4.2	48
100	Prediction of homologous protein structures based on conformational searches and energetics. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990, 8, 30-43.	2.6	46
101	Ceapins block the unfolded protein response sensor ATF6 ^{1±} by inducing a neomorphic inter-organelle tether. <i>ELife</i> , 2019, 8, .	6.0	46
102	Structure of LacY with an 1±-substituted galactoside: Connecting the binding site to the protonation site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9004-9009.	7.1	45
103	Significance of structural changes in proteins: Expected errors in refined protein structures. <i>Protein Science</i> , 1995, 4, 2392-2404.	7.6	43
104	Claudin-9 structures reveal mechanism for toxin-induced gut barrier breakdown. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17817-17824.	7.1	43
105	A Remote Mutation Affects the Hydride Transfer by Disrupting Concerted Protein Motions in Thymidylate Synthase. <i>Journal of the American Chemical Society</i> , 2012, 134, 17722-17730.	13.7	42
106	Highlighting membrane protein structure and function: A celebration of the Protein Data Bank. <i>Journal of Biological Chemistry</i> , 2021, 296, 100557.	3.4	42
107	Immunodominant T Cell Determinants of Aquaporin-4, the Autoantigen Associated with Neuromyelitis Optica. <i>PLoS ONE</i> , 2010, 5, e15050.	2.5	42
108	Stereochemistry of a multistep/bipartite methyl transfer reaction: thymidylate synthase. <i>FASEB Journal</i> , 1993, 7, 671-677.	0.5	40

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109	Crystal Structure of RumA, an Iron-Sulfur Cluster Containing E. coli Ribosomal RNA 5-Methyluridine Methyltransferase. <i>Structure</i> , 2004, 12, 397-407.	3.3	40
110	Structural basis for activation of voltage sensor domains in an ion channel TPC1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E9095-E9104.	7.1	40
111	Structures suggest a mechanism for energy coupling by a family of organic anion transporters. <i>PLoS Biology</i> , 2019, 17, e3000260.	5.6	40
112	1.59 Å... structure of trypsin at 120 K: Comparison of low temperature and room temperature structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991, 10, 171-187.	2.6	39
113	The complex of the anti-cancer therapeutic, BW1843U89, with thymidylate synthase at 2.0 Å resolution: implications for a new mode of inhibition. <i>Structure</i> , 1996, 4, 67-77.	3.3	38
114	On the structure and mechanism of two pore channels. <i>FEBS Journal</i> , 2018, 285, 233-243.	4.7	38
115	Atomic structure of a glycerol channel and implications for substrate permeation in aqua(glycero)porins. <i>FEBS Letters</i> , 2001, 504, 112-117.	2.8	37
116	An electrostatic highway. <i>Nature Structural Biology</i> , 1994, 1, 131-134.	9.7	36
117	Enzyme-catalyzed therapeutic agent (ECTA) design: activation of the antibiotic ECTA compound NB1011 by thymidylate synthase Abbreviations: BVdU, (E)-5-(2-bromovinyl)-2'-deoxyuridine; BVdUMP, (E)-5-(2-bromovinyl)-2'-deoxyuridine 5'-monophosphate; NB1011, (E)-5-(2-bromovinyl)-2'-deoxy-5-uridy] phenyl l-methoxyalaninylphosphoramidate; COSY, correlated spectroscopy; DCI, direct current ionization; DMF, N,N-dimethylformamide; dUMP, 2'-deoxyuridine 5'-monophosphate; ECTA, enzyme-catalyzed therapeutic agent; 5-FU, <i>Biochemical Pharmacology</i> , 2001, 61, 179-189.	4.4	36
118	Redox Reactions of the Iron-Sulfur Cluster in a Ribosomal RNA Methyltransferase, RumA. <i>Journal of Biological Chemistry</i> , 2004, 279, 34123-34129.	3.4	36
119	Structural Basis for Mobility in the 1.1 Å... Crystal Structure of the NG Domain of Thermus aquaticus Ffh. <i>Journal of Molecular Biology</i> , 2002, 320, 783-799.	4.2	35
120	Crystal Structure of an Acyl-ACP Dehydrogenase from the FK520 Polyketide Biosynthetic Pathway: Insights into Extender Unit Biosynthesis. <i>Journal of Molecular Biology</i> , 2003, 334, 435-444.	4.2	35
121	Catalytically-active complex of HIV-1 integrase with a viral DNA substrate binds anti-integrase drugs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 8192-8197.	7.1	33
122	EspR, a key regulator of <i>Mycobacterium tuberculosis</i> virulence, adopts a unique dimeric structure among helix-turn-helix proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13450-13455.	7.1	33
123	The impact of task performance scoring and tracking on second language engagement. <i>System</i> , 2017, 69, 121-132.	3.4	33
124	The domain structure of the ion channel-forming protein colicin Ia. <i>Nature Structural and Molecular Biology</i> , 1994, 1, 597-604.	8.2	32
125	Crystal structure of the third KH domain of human poly(C)-binding protein-2 in complex with a C-rich strand of human telomeric DNA at 1.6 Å resolution. <i>Nucleic Acids Research</i> , 2007, 35, 2651-2660.	14.5	32
126	Crystal Structure of a ligand-bound LacY-Nanobody Complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 8769-8774.	7.1	32

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127	Location of terbium binding sites on acetylcholine receptor-enriched membranes. <i>Journal of Molecular Biology</i> , 1986, 189, 673-680.	4.2	31
128	Substrate Recognition by RNA 5-Methyluridine Methyltransferases and Pseudouridine Synthases: A Structural Perspective. <i>Journal of Biological Chemistry</i> , 2006, 281, 38969-38973.	3.4	31
129	Rapid identification of recombinant Fabs that bind to membrane proteins. <i>Methods</i> , 2011, 55, 303-309.	3.8	31
130	Active site water molecules revealed in the 2.1 Å... resolution structure of a site-directed mutant of isocitrate dehydrogenase 1 Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 2000, 295, 377-385.	4.2	30
131	A new class of HIV-1 protease inhibitor: The crystallographic structure, inhibition and chemical synthesis of an aminimide peptide isostere. <i>Bioorganic and Medicinal Chemistry</i> , 1996, 4, 1545-1558.	3.0	28
132	Predicting and harnessing protein flexibility in the design of species-specific inhibitors of thymidylate synthase1,21Escherichia coli thymidylate synthase numbering is used unless otherwise noted.2PDB coordinates have been deposited with the RCSB with accession ID: 1JG0.. <i>Chemistry and Biology</i> , 2001, 8, 981-995.	6.0	28
133	The structure of <i>Enterococcus faecalis</i> thymidylate synthase provides clues about folate bacterial metabolism. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1232-1241.	2.5	28
134	Water and glycerol permeation through the glycerol channel GlpF and the aquaporin family. <i>Journal of Synchrotron Radiation</i> , 2004, 11, 86-88.	2.4	27
135	Overexpression and Purification of Integral Membrane Proteins in Yeast. <i>Methods in Enzymology</i> , 2010, 470, 695-707.	1.0	27
136	In Human Pseudouridine Synthase 1 (hPus1), a C-Terminal Helical Insert Blocks tRNA from Binding in the Same Orientation as in the Pus1 Bacterial Homologue TruA, Consistent with Their Different Target Selectivities. <i>Journal of Molecular Biology</i> , 2013, 425, 3875-3887.	4.2	27
137	Modulation of P2X3 and P2X2/3 Receptors by Monoclonal Antibodies. <i>Journal of Biological Chemistry</i> , 2016, 291, 12254-12270.	3.4	26
138	Entropy in Bi-substrate Enzymes: Proposed Role of an Alternate Site in Chaperoning Substrate into, and Products out of, Thymidylate Synthase. <i>Journal of Molecular Biology</i> , 1996, 255, 522-535.	4.2	25
139	De novo design of an IL-4 antagonist and its structure at 1.9 Å. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1889-1894.	7.1	25
140	Balancing ATP in the cell. <i>Nature Structural Biology</i> , 1996, 3, 567-569.	9.7	24
141	Phthalein Derivatives as a New Tool for Selectivity in Thymidylate Synthase Inhibition. <i>Journal of Medicinal Chemistry</i> , 1999, 42, 2112-2124.	6.4	23
142	The crystal structure of thymidylate synthase from <i>Pneumocystis carinii</i> reveals a fungal insert important for drug design. <i>Journal of Molecular Biology</i> , 2000, 297, 645-657.	4.2	23
143	The glycerol facilitator GlpF, its aquaporin family of channels, and their selectivity. <i>Advances in Protein Chemistry</i> , 2003, 63, 291-316.	4.4	22
144	Structural basis for <i>Clostridium perfringens</i> enterotoxin targeting of claudins at tight junctions in mammalian gut. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	22

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145	Reversible dissociation and unfolding of the dimeric protein thymidylate synthase. <i>Protein Science</i> , 1992, 1, 796-800.	7.6	21
146	LpxI structures reveal how a lipid A precursor is synthesized. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1132-1138.	8.2	21
147	Insights into the Mechanism of Bovine CD38/NAD ⁺ Glycohydrolase from the X-Ray Structures of Its Michaelis Complex and Covalently-Trapped Intermediates. <i>PLoS ONE</i> , 2012, 7, e34918.	2.5	21
148	Mg ²⁺ Binds to the Surface of Thymidylate Synthase and Affects Hydride Transfer at the Interior Active Site. <i>Journal of the American Chemical Society</i> , 2013, 135, 7583-7592.	13.7	21
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