

# Robert M Stroud

## List of Publications by Year in descending order

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213  
papers

22,094  
citations

10986

71  
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9861

141  
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224  
all docs

224  
docs citations

224  
times ranked

26707  
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular basis of multistep voltage activation in plant two-pore channel 1. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	12
2	Symmetry Reduction in a Hyperpolarization-Activated Homotetrameric Ion Channel. Biochemistry, 2022, 61, 2177-2181.	2.5	5
3	Diversity of function and mechanism in a family of organic anion transporters. Current Opinion in Structural Biology, 2022, 75, 102399.	5.7	6
4	Bi-paratopic and multivalent VH domains block ACE2 binding and neutralize SARS-CoV-2. Nature Chemical Biology, 2021, 17, 113-121.	8.0	78
5	Highlighting membrane protein structure and function: A celebration of the Protein Data Bank. Journal of Biological Chemistry, 2021, 296, 100557.	3.4	42
6	Caught in Action: X-ray Structure of Thymidylate Synthase with Noncovalent Intermediate Analog. Biochemistry, 2021, 60, 1243-1247.	2.5	1
7	Structural basis for <i>Clostridium perfringens</i> enterotoxin targeting of claudins at tight junctions in mammalian gut. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	22
8	Molecular and Structural Basis Underlying Selective Targeting of Claudins by Clostridium perfringens Enterotoxin in Mammalian Gut. FASEB Journal, 2021, 35, .	0.5	0
9	Key computational findings reveal proton transfer as driving the functional cycle in the phosphate transporter PiPT. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	10
10	Allosteric Inhibition of a Vesicular Glutamate Transporter by an Isoform-Specific Antibody. Biochemistry, 2021, 60, 2463-2470.	2.5	1
11	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. Science, 2020, 370, .	12.6	508
12	An ultrapotent synthetic nanobody neutralizes SARS-CoV-2 by stabilizing inactive Spike. Science, 2020, 370, 1473-1479.	12.6	336
13	Diversity in kinetics correlated with structure in nano body-stabilized LacY. PLoS ONE, 2020, 15, e0232846.	2.5	3
14	Ion transport and regulation in a synaptic vesicle glutamate transporter. Science, 2020, 368, 893-897.	12.6	53
15	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. Nature, 2020, 583, 459-468.	27.8	3,542
16	Resting state structure of the hyperdepolarization activated two-pore channel 3. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1988-1993.	7.1	14
17	Structural and mechanistic basis of the EMC-dependent biogenesis of distinct transmembrane clients. ELife, 2020, 9, .	6.0	66
18	Diversity in kinetics correlated with structure in nano body-stabilized LacY. , 2020, 15, e0232846.		0

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19	Diversity in kinetics correlated with structure in nano body-stabilized LacY. , 2020, 15, e0232846.		0
20	Diversity in kinetics correlated with structure in nano body-stabilized LacY. , 2020, 15, e0232846.		0
21	Diversity in kinetics correlated with structure in nano body-stabilized LacY. , 2020, 15, e0232846.		0
22	High-Throughput Nano-Scale Characterization of Membrane Proteins Using Fluorescence-Detection Size-Exclusion Chromatography. <i>Methods in Molecular Biology</i> , 2019, 2025, 361-388.	0.9	0
23	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
24	Structures suggest a mechanism for energy coupling by a family of organic anion transporters. <i>PLoS Biology</i> , 2019, 17, e3000260.	5.6	40
25	Ceapins block the unfolded protein response sensor ATF6 $\beta$ by inducing a neomorphic inter-organelle tether. <i>ELife</i> , 2019, 8, .	6.0	46
26	Structural basis for human claudin $\beta$ 9 ion selectivity and tight junction dissociation by a bacterial toxin. <i>FASEB Journal</i> , 2019, 33, 656.14.	0.5	0
27	A Single Mutation Traps a Half-Sites Reactive Enzyme in Midstream, Explaining Asymmetry in Hydride Transfer. <i>Biochemistry</i> , 2018, 57, 2786-2795.	2.5	9
28	On the structure and mechanism of two $\beta$ pore channels. <i>FEBS Journal</i> , 2018, 285, 233-243.	4.7	38
29	Structure and Mechanisms of Selectivity Gating, Inhibition and Activation in an Ion Channel. <i>Biophysical Journal</i> , 2018, 114, 34a-35a.	0.5	0
30	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
31	Crystal Structure of a ligand-bound LacY $\beta$ -Nanobody Complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 8769-8774.	7.1	32
32	Crystal structure and mechanistic basis of a functional homolog of the antigen transporter TAP. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E438-E447.	7.1	67
33	The impact of task performance scoring and tracking on second language engagement. <i>System</i> , 2017, 69, 121-132.	3.4	33
34	Mechanism of inhibition of human glucose transporter GLUT1 is conserved between cytochalasin B and phenylalanine amides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 4711-4716.	7.1	170
35	Modulation of P2X3 and P2X2/3 Receptors by Monoclonal Antibodies. <i>Journal of Biological Chemistry</i> , 2016, 291, 12254-12270.	3.4	26
36	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

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37	The Preserved HTH-Docking Cleft of HIV-1 Integrase Is Functionally Critical. <i>Structure</i> , 2016, 24, 1936-1946.	3.3	4
38	Integral Membrane Protein Expression in <i>Saccharomyces cerevisiae</i> . <i>Methods in Molecular Biology</i> , 2016, 1432, 163-186.	0.9	3
39	Small-Scale Screening to Large-Scale Over-Expression of Human Membrane Proteins for Structural Studies. <i>Methods in Molecular Biology</i> , 2016, 1432, 203-221.	0.9	4
40	Structure, inhibition and regulation of two-pore channel TPC1 from <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2016, 531, 258-264.	27.8	155
41	Fungal association and utilization of phosphate by plants: success, limitations, and future prospects. <i>Frontiers in Microbiology</i> , 2015, 6, 984.	3.5	96
42	Crystal Structure of the Human tRNA m1A58 Methyltransferase-tRNA <sup>Lys</sup> Complex: Refolding of Substrate tRNA Allows Access to the Methylation Target. <i>Journal of Molecular Biology</i> , 2015, 427, 3862-3876.	4.2	48
43	Alanine Mutants of the Interface Residues of Human Thymidylate Synthase Decode Key Features of the Binding Mode of Allosteric Anticancer Peptides. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 1012-1018.	6.4	9
44	Structure of LacY with an $\alpha$ -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
45	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
46	Hotspots in an Obligate Homodimeric Anticancer Target. Structural and Functional Effects of Interfacial Mutations in Human Thymidylate Synthase. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 3572-3581.	6.4	21
47	Subnanometre-resolution electron cryomicroscopy structure of a heterodimeric ABC exporter. <i>Nature</i> , 2015, 517, 396-400.	27.8	114
48	Architecture of a single membrane spanning cytochrome P450 suggests constraints that orient the catalytic domain relative to a bilayer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 3865-3870.	7.1	231
49	General qPCR and Plate Reader Methods for Rapid Optimization of Membrane Protein Purification and Crystallization Using Thermostability Assays. <i>Current Protocols in Protein Science</i> , 2014, 77, 29.11.1-29.11.14.	2.8	15
50	The mechanism of pseudouridine synthases from a covalent complex with RNA, and alternate specificity for U2605 versus U2604 between close homologs. <i>Nucleic Acids Research</i> , 2014, 42, 2037-2048.	14.5	19
51	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
52	Tetra Detector Analysis of Membrane Proteins. <i>Current Protocols in Protein Science</i> , 2014, 77, 29.10.1-29.10.30.	2.8	4
53	Structure of a new DNA-binding domain which regulates pathogenesis in a wide variety of fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 10404-10410.	7.1	18
54	Coordinating the impact of structural genomics on the human $\alpha$ -helical transmembrane proteome. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 135-138.	8.2	64

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55	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
56	Crystal structure of a eukaryotic phosphate transporter. <i>Nature</i> , 2013, 496, 533-536.	27.8	202
57	Development and Binding Mode Assessment of <i>N</i> -[4-[2-Propyn-1-yl]-(6 <i>S</i> )-4,6,7,8-tetrahydro-2-(hydroxymethyl)-4-oxo-3 <i>H</i> -cyclopenta[ <i>g</i> ]quinazolin-6-yl]amide Acid (BGC 945), a Novel Thymidylate Synthase Inhibitor That Targets Tumor Cells. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 5446-5455.	6.4	15
58	Mg <sup>2+</sup> 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
59	Structural basis for alternating access of a eukaryotic calcium/proton exchanger. <i>Nature</i> , 2013, 499, 107-110.	27.8	87
60	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
61	Inhibitor of Ovarian Cancer Cells Growth by Virtual Screening: A New Thiazole Derivative Targeting Human Thymidylate Synthase. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 10272-10276.	6.4	20
62	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
63	LpxI structures reveal how a lipid A precursor is synthesized. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1132-1138.	8.2	21
64	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
65	Overexpressing human membrane proteins in stably transfected and clonal human embryonic kidney 293S cells. <i>Nature Protocols</i> , 2012, 7, 453-466.	12.0	69
66	Insights into the Mechanism of Bovine CD38/NAD <sup>+</sup> Glycohydrolase from the X-Ray Structures of Its Michaelis Complex and Covalently-Trapped Intermediates. <i>PLoS ONE</i> , 2012, 7, e34918.	2.5	21
67	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
68	Fabs Enable Single Particle cryoEM Studies of Small Proteins. <i>Structure</i> , 2012, 20, 582-592.	3.3	154
69	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
70	Rapid identification of recombinant Fabs that bind to membrane proteins. <i>Methods</i> , 2011, 55, 303-309.	3.8	31
71	Comparison of human solute carriers. <i>Protein Science</i> , 2010, 19, 412-428.	7.6	99
72	Function of human Rh based on structure of RhCG at 2.1 Å. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 9638-9643.	7.1	178

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73	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
74	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
75	Overexpression and Purification of Integral Membrane Proteins in Yeast. Methods in Enzymology, 2010, 470, 695-707.	1.0	27
76	Tandem Facial Amphiphiles for Membrane Protein Stabilization. Journal of the American Chemical Society, 2010, 132, 16750-16752.	13.7	85
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	Immunodominant T Cell Determinants of Aquaporin-4, the Autoantigen Associated with Neuromyelitis Optica. PLoS ONE, 2010, 5, e15050.	2.5	42
79	Discovery, characterization, and structural determination of a novel UDP-2,3-diacylglucosamine hydrolase. FASEB Journal, 2010, 24, 509.1.	0.5	1
80	Catalytically-active complex of HIV-1 integrase with a viral DNA substrate binds anti-integrase drugs. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 8192-8197.	7.1	33
81	Ratiocinative screen of eukaryotic integral membrane protein expression and solubilization for structure determination. Journal of Structural and Functional Genomics, 2009, 10, 9-16.	1.2	9
82	2007 Annual progress report synopsis of the Center for Structures of Membrane Proteins. Journal of Structural and Functional Genomics, 2009, 10, 193-208.	1.2	17
83	A survey of integral $\alpha$ -helical membrane proteins. Journal of Structural and Functional Genomics, 2009, 10, 269-280.	1.2	12
84	The unfolded protein response signals through high-order assembly of Ire1. Nature, 2009, 457, 687-693.	27.8	565
85	A general protocol for the crystallization of membrane proteins for X-ray structural investigation. Nature Protocols, 2009, 4, 619-637.	12.0	116
86	Crystal structure of human aquaporin 4 at 1.8 Å and its mechanism of conductance. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 7437-7442.	7.1	297
87	Selecting Optimum Eukaryotic Integral Membrane Proteins for Structure Determination by Rapid Expression and Solubilization Screening. Journal of Molecular Biology, 2009, 385, 820-830.	4.2	53
88	Crystal Structure of an RluF-RNA Complex: A Base-Pair Rearrangement Is the Key to Selectivity of RluF for U2604 of the Ribosome. Journal of Molecular Biology, 2009, 388, 785-800.	4.2	19
89	Michael A. Raftery (1936-2007)-the first enzyme mechanism, sequential cooperativity, and the nicotinic acetylcholine receptor defined. Protein Science, 2008, 17, 1864-1866.	7.6	0
90	Crystal structure of the aquaglyceroporin PfAQP from the malarial parasite Plasmodium falciparum. Nature Structural and Molecular Biology, 2008, 15, 619-625.	8.2	143

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91	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
92	Structure of a TrmA-RNA complex: A consensus RNA fold contributes to substrate selectivity and catalysis in m <sup>5</sup> C methyltransferases. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6876-6881.	7.1	75
93	Crystal structure of bovine mitochondrial factor B at 0.96-A resolution. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 13379-13384.	7.1	16
94	The Structure of G1pF, A Glycerol Conducting Channel. Novartis Foundation Symposium, 2008, , 51-65.	1.1	14
95	Structures of SRP54 and SRP19, the Two Proteins that Organize the Ribonucleic Core of the Signal Recognition Particle from Pyrococcus furiosus. PLoS ONE, 2008, 3, e3528.	2.5	21
96	Structures of the Signal Recognition Particle Receptor from the Archaeon Pyrococcus furiosus: Implications for the Targeting Step at the Membrane. PLoS ONE, 2008, 3, e3619.	2.5	21
97	Inhibitory complex of the transmembrane ammonia channel, AmtB, and the cytosolic regulatory protein, GlnK, at 1.96 A. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 42-47.	7.1	124
98	Transmembrane transporters: An open and closed case. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1445-1446.	7.1	10
99	TARP Auxiliary Subunits Switch AMPA Receptor Antagonists into Partial Agonists. Science, 2007, 318, 815-817.	12.6	144
100	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 A resolution. Nucleic Acids Research, 2007, 35, 2651-2660.	14.5	32
101	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. Rna, 2007, 13, 1043-1051.	3.5	50
102	The Crystal Structure of E. coli rRNA Pseudouridine Synthase RluE. Journal of Molecular Biology, 2007, 367, 1459-1470.	4.2	10
103	Structural Basis of Aquaporin Inhibition by Mercury. Journal of Molecular Biology, 2007, 368, 607-617.	4.2	127
104	How U38, 39, and 40 of Many tRNAs Become the Targets for Pseudouridylation by TruA. Molecular Cell, 2007, 26, 189-203.	9.7	71
105	The role of tryptophan cation-pi interactions on ammonia transport through the AmtB ammonia channel. International Congress Series, 2007, 1304, 15-21.	0.2	1
106	Cell-free complements in vivo expression of the E. coli membrane proteome. Protein Science, 2007, 16, 966-976.	7.6	50
107	X-ray Structures of the Signal Recognition Particle Receptor Reveal Targeting Cycle Intermediates. PLoS ONE, 2007, 2, e607.	2.5	20
108	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

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109	The Structure of a Ketoreductase Determines the Organization of the Î²-Carbon Processing Enzymes of Modular Polyketide Synthases. <i>Structure</i> , 2006, 14, 737-748.	3.3	197
110	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
111	Targeting proteins to membranes: structure of the signal recognition particle. <i>Current Opinion in Structural Biology</i> , 2005, 15, 213-220.	5.7	206
112	The structure of <i>Cryptococcus neoformans</i> thymidylate synthase suggests strategies for using target dynamics for species-specific inhibition. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1320-1334.	2.5	10
113	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
114	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
115	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
116	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
117	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
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	Mechanistic Diversity of Cytokine Receptor Signaling Across Cell Membranes. <i>Science Signaling</i> , 2004, 2004, re7-re7.	3.6	84
120	Unraveling the interface of signal recognition particle and its receptor by using chemical cross-linking and tandem mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 16454-16459.	7.1	72
121	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
122	Mechanism of Association and Reciprocal Activation of Two GTPases. <i>PLoS Biology</i> , 2004, 2, e320.	5.6	94
123	An antibiotic factory caught in action. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 888-893.	8.2	162
124	Substrate twinning activates the signal recognition particle and its receptor. <i>Nature</i> , 2004, 427, 215-221.	27.8	270
125	Crystal Structure of RumA, an Iron-Sulfur Cluster Containing <i>E. coli</i> Ribosomal RNA 5-Methyluridine Methyltransferase. <i>Structure</i> , 2004, 12, 397-407.	3.3	40
126	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



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127	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
128	Glycerol facilitator GlpF and the associated aquaporin family of channels. <i>Current Opinion in Structural Biology</i> , 2003, 13, 424-431.	5.7	71
129	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
130	The First Structure of an RNA m <sup>5</sup> C Methyltransferase, Fmu, Provides Insight into Catalytic Mechanism and Specific Binding of RNA Substrate. <i>Structure</i> , 2003, 11, 1609-1620.	3.3	57
131	Crystal Structure and Molecular Modeling of 17-DMAG in Complex with Human Hsp90. <i>Chemistry and Biology</i> , 2003, 10, 361-368.	6.0	183
132	Conformational Dynamics along an Enzymatic Reaction Pathway: Thymidylate Synthase, the Movie. <i>Biochemistry</i> , 2003, 42, 239-247.	2.5	96
133	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
134	Selectivity and conductance among the glycerol and water conducting aquaporin family of channels. <i>FEBS Letters</i> , 2003, 555, 79-84.	2.8	52
135	Phylogenetic Classification of Protozoa Based on the Structure of the Linker Domain in the Bifunctional Enzyme, Dihydrofolate Reductase-Thymidylate Synthase. <i>Journal of Biological Chemistry</i> , 2003, 278, 52980-52987.	3.4	62
136	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
137	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
138	Architecture and Selectivity in Aquaporins: 2.5 Å... X-Ray Structure of Aquaporin Z. <i>PLoS Biology</i> , 2003, 1, e72.	5.6	248
139	Characterization of the 23 S Ribosomal RNA m <sup>5</sup> U1939 Methyltransferase from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 8835-8840.	3.4	68
140	Structural Basis for Mobility in the 1.1 Å... Crystal Structure of the NG Domain of <i>Thermus aquaticus</i> Ffh. <i>Journal of Molecular Biology</i> , 2002, 320, 783-799.	4.2	35
141	Encoding Selectivity of a Transmembrane Channel. <i>Scientific World Journal</i> , The, 2002, 2, 111-111.	2.1	0
142	Crystal Structure of the Priming $\hat{1}^2$ -Ketosynthase from the R1128 Polyketide Biosynthetic Pathway. <i>Structure</i> , 2002, 10, 1559-1568.	3.3	75
143	Control of the Selectivity of the Aquaporin Water Channel Family by Global Orientational Tuning. <i>Science</i> , 2002, 296, 525-530.	12.6	833
144	The Signal Recognition Particle. <i>Annual Review of Biochemistry</i> , 2001, 70, 755-775.	11.1	541

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145	Multi-targeted antifolates aimed at avoiding drug resistance form covalent closed inhibitory complexes with human and Escherichia coli thymidylate synthases. <i>Journal of Molecular Biology</i> , 2001, 313, 813-829.	4.2	57
146	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
147	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: 1JCO.. <i>Chemistry and Biology</i> , 2001, 8, 981-995.	6.0	28
148	Approaches to solving the rigid receptor problem by identifying a minimal set of flexible residues during ligand docking11PDB coordinates have been deposited with the RSCB with accession ID: 1F28.. <i>Chemistry and Biology</i> , 2001, 8, 445-457.	6.0	71
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