

James Henderson Naismith

List of Publications by Year in descending order

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279
papers

18,715
citations

9234

74
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17055

122
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303
all docs

303
docs citations

303
times ranked

21005
citing authors

#	ARTICLE	IF	CITATIONS
1	An efficient one-step site-directed deletion, insertion, single and multiple-site plasmid mutagenesis protocol. <i>BMC Biotechnology</i> , 2008, 8, 91.	1.7	876
2	TNF α and the TNF receptor superfamily: Structure-function relationship(s). <i>Microscopy Research and Technique</i> , 2000, 50, 184-195.	1.2	790
3	Polymeric Chains of SUMO-2 and SUMO-3 Are Conjugated to Protein Substrates by SAE1/SAE2 and Ubc9. <i>Journal of Biological Chemistry</i> , 2001, 276, 35368-35374.	1.6	690
4	Structure of the DNA Repair Helicase XPD. <i>Cell</i> , 2008, 133, 801-812.	13.5	490
5	Structure of a RING E3 ligase and ubiquitin-loaded E2 primed for catalysis. <i>Nature</i> , 2012, 489, 115-120.	13.7	437
6	Neutralizing nanobodies bind SARS-CoV-2 spike RBD and block interaction with ACE2. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 846-854.	3.6	434
7	Tryptophan 7-Halogenase (PrnA) Structure Suggests a Mechanism for Regioselective Chlorination. <i>Science</i> , 2005, 309, 2216-2219.	6.0	338
8	Wza the translocon for E. coli capsular polysaccharides defines a new class of membrane protein. <i>Nature</i> , 2006, 444, 226-229.	13.7	321
9	Crystal structure and mechanism of a bacterial fluorinating enzyme. <i>Nature</i> , 2004, 427, 561-565.	13.7	306
10	Structure and Mechanism of the CMR Complex for CRISPR-Mediated Antiviral Immunity. <i>Molecular Cell</i> , 2012, 45, 303-313.	4.5	279
11	Structural Basis of Trimannoside Recognition by Concanavalin A. <i>Journal of Biological Chemistry</i> , 1996, 271, 972-976.	1.6	272
12	Structural basis for the neutralization of SARS-CoV-2 by an antibody from a convalescent patient. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 950-958.	3.6	268
13	Pivotal Roles of the Outer Membrane Polysaccharide Export and Polysaccharide Copolymerase Protein Families in Export of Extracellular Polysaccharides in Gram-Negative Bacteria. <i>Microbiology and Molecular Biology Reviews</i> , 2009, 73, 155-177.	2.9	249
14	On the Meaning of Affinity: Å Cluster Glycoside Effects and Concanavalin A. <i>Journal of the American Chemical Society</i> , 1999, 121, 10286-10296.	6.6	227
15	Porins and small-molecule translocation across the outer membrane of Gram-negative bacteria. <i>Nature Reviews Microbiology</i> , 2020, 18, 164-176.	13.6	225
16	Modularity in the TNF-receptor family. <i>Trends in Biochemical Sciences</i> , 1998, 23, 74-79.	3.7	208
17	The rhamnose pathway. <i>Current Opinion in Structural Biology</i> , 2000, 10, 687-696.	2.6	205
18	MtsslWizard: In Silico Spin-Labeling and Generation of Distance Distributions in PyMOL. <i>Applied Magnetic Resonance</i> , 2012, 42, 377-391.	0.6	196

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19	The Structure of an Open Form of an <i>E. coli</i> Mechanosensitive Channel at 3.45 Å... Resolution. <i>Science</i> , 2008, 321, 1179-1183.	6.0	194
20	Structural and Functional Characterization of an Archaeal Clustered Regularly Interspaced Short Palindromic Repeat (CRISPR)-associated Complex for Antiviral Defense (CASCADE). <i>Journal of Biological Chemistry</i> , 2011, 286, 21643-21656.	1.6	183
21	The structural basis of the catalytic mechanism and regulation of glucose-1-phosphate thymidyltransferase (RmlA). <i>EMBO Journal</i> , 2000, 19, 6652-6663.	3.5	177
22	Crystallographic Evidence for Dimerization of Unliganded Tumor Necrosis Factor Receptor. <i>Journal of Biological Chemistry</i> , 1995, 270, 13303-13307.	1.6	168
23	YcaO-Dependent Posttranslational Amide Activation: Biosynthesis, Structure, and Function. <i>Chemical Reviews</i> , 2017, 117, 5389-5456.	23.0	166
24	The role of lipids in mechanosensation. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 991-998.	3.6	160
25	Mechanism of ubiquitylation by dimeric RING ligase RNF4. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1052-1059.	3.6	157
26	Structural analysis of leader peptide binding enables leader-free cyanobactin processing. <i>Nature Chemical Biology</i> , 2015, 11, 558-563.	3.9	155
27	Novel inhibitors of an emerging target in <i>Mycobacterium tuberculosis</i> ; substituted thiazolidinones as inhibitors of dTDP-rhamnose synthesis. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2003, 13, 3227-3230.	1.0	151
28	Structures of the extracellular domain of the type I tumor necrosis factor receptor. <i>Structure</i> , 1996, 4, 1251-1262.	1.6	146
29	The 3D structure of a periplasm-spanning platform required for assembly of group 1 capsular polysaccharides in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 2390-2395.	3.3	139
30	UDP-galactopyranose mutase has a novel structure and mechanism. <i>Nature Structural Biology</i> , 2001, 8, 858-863.	9.7	138
31	The mechanism of patellamide macrocyclization revealed by the characterization of the PatG macrocyclase domain. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 767-772.	3.6	136
32	Adenylate-forming enzymes. <i>Current Opinion in Structural Biology</i> , 2009, 19, 666-671.	2.6	132
33	The Structure of Serine Palmitoyltransferase; Gateway to Sphingolipid Biosynthesis. <i>Journal of Molecular Biology</i> , 2007, 370, 870-886.	2.0	124
34	The crystal structure of dTDP-d-glucose 4,6-dehydratase (RmlB) from <i>Salmonella enterica</i> serovar typhimurium, the second enzyme in the dTDP-l-rhamnose pathway. <i>Journal of Molecular Biology</i> , 2001, 307, 283-295.	2.0	123
35	Insights into ssDNA recognition by the OB fold from a structural and thermodynamic study of <i>Sulfolobus</i> SSB protein. <i>EMBO Journal</i> , 2003, 22, 2561-2570.	3.5	122
36	Structural Insights into Regioselectivity in the Enzymatic Chlorination of Tryptophan. <i>Journal of Molecular Biology</i> , 2009, 391, 74-85.	2.0	122

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37	Refined structure of concanavalin A complexed with methyl α -D-mannopyranoside at 2.0 Å... resolution and comparison with the saccharide-free structure. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1994, 50, 847-858.	2.5	121
38	The structure of SENP1-SUMO-2 complex suggests a structural basis for discrimination between SUMO paralogues during processing. <i>Biochemical Journal</i> , 2006, 397, 279-288.	1.7	121
39	Structural aspects of non-ribosomal peptide biosynthesis. <i>Current Opinion in Structural Biology</i> , 2004, 14, 748-756.	2.6	120
40	Extensive DNA mimicry by the ArdA anti-restriction protein and its role in the spread of antibiotic resistance. <i>Nucleic Acids Research</i> , 2009, 37, 4887-4897.	6.5	117
41	Getting Drugs into Gram-Negative Bacteria: Rational Rules for Permeation through General Porins. <i>ACS Infectious Diseases</i> , 2018, 4, 1487-1498.	1.8	117
42	CRISPR interference: a structural perspective. <i>Biochemical Journal</i> , 2013, 453, 155-166.	1.7	113
43	The crystal structure of a class II fructose-1,6-bisphosphate aldolase shows a novel binuclear metal-binding active site embedded in a familiar fold. <i>Structure</i> , 1996, 4, 1303-1315.	1.6	112
44	SUMO protease SENP1 induces isomerization of the scissile peptide bond. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 1069-1077.	3.6	110
45	New Insights into the Mechanism of Enzymatic Chlorination of Tryptophan. <i>Angewandte Chemie - International Edition</i> , 2008, 47, 9533-9536.	7.2	110
46	A simple and efficient expression and purification system using two newly constructed vectors. <i>Protein Expression and Purification</i> , 2009, 63, 102-111.	0.6	110
47	RmlC, the third enzyme of dTDP-L-rhamnose pathway, is a new class of epimerase. <i>Nature Structural Biology</i> , 2000, 7, 398-402.	9.7	107
48	The Scottish Structural Proteomics Facility: targets, methods and outputs. <i>Journal of Structural and Functional Genomics</i> , 2010, 11, 167-180.	1.2	107
49	Structural basis of NEDD8 ubiquitin discrimination by the deNEDDylating enzyme NEDP1. <i>EMBO Journal</i> , 2005, 24, 1341-1351.	3.5	103
50	Mechanism of Enzymatic Fluorination in <i>Streptomyces cattleya</i> . <i>Journal of the American Chemical Society</i> , 2007, 129, 14597-14604.	6.6	102
51	A potent SARS-CoV-2 neutralising nanobody shows therapeutic efficacy in the Syrian golden hamster model of COVID-19. <i>Nature Communications</i> , 2021, 12, 5469.	5.8	102
52	Structural basis for the RING-catalyzed synthesis of K63-linked ubiquitin chains. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 597-602.	3.6	99
53	The Fluorinase from <i>Streptomyces cattleya</i> Is Also a Chlorinase. <i>Angewandte Chemie - International Edition</i> , 2006, 45, 759-762.	7.2	98
54	Altered Antibiotic Transport in OmpC Mutants Isolated from a Series of Clinical Strains of Multi-Drug Resistant <i>E. coli</i> . <i>PLoS ONE</i> , 2011, 6, e25825.	1.1	98

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55	The Chemical Basis of Serine Palmitoyltransferase Inhibition by Myriocin. <i>Journal of the American Chemical Society</i> , 2013, 135, 14276-14285.	6.6	98
56	Identification of Fluorinases from <i>Streptomyces</i> sp MA37, <i>Norcardia brasiliensis</i> , and <i>Actinoplanes</i> sp N902 by Genome Mining. <i>ChemBioChem</i> , 2014, 15, 364-368.	1.3	97
57	Carbohydrate-Protein Recognition: Molecular Dynamics Simulations and Free Energy Analysis of Oligosaccharide Binding to Concanavalin A. <i>Biophysical Journal</i> , 2001, 81, 1373-1388.	0.2	96
58	TonB-Dependent Receptor Repertoire of <i>Pseudomonas aeruginosa</i> for Uptake of Siderophore-Drug Conjugates. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	95
59	Toward a Structural Understanding of the Dehydratase Mechanism. <i>Structure</i> , 2002, 10, 81-92.	1.6	94
60	Bacterial Mechanosensitive Channels—MscS: Evolution's Solution to Creating Sensitivity in Function. <i>Annual Review of Biophysics</i> , 2012, 41, 157-177.	4.5	93
61	The Cyanobactin Heterocyclase Enzyme: A Processive Adenylase That Operates with a Defined Order of Reaction. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 13991-13996.	7.2	93
62	Conformational state of the MscS mechanosensitive channel in solution revealed by pulsed electron double resonance (PELDOR) spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E2675-82.	3.3	92
63	Epimerases: structure, function and mechanism. <i>Cellular and Molecular Life Sciences</i> , 2001, 58, 1650-1665.	2.4	89
64	A flavin-dependent tryptophan 6-halogenase and its use in modification of pyrrolnitrin biosynthesis. <i>Biocatalysis and Biotransformation</i> , 2006, 24, 401-408.	1.1	89
65	NMR Spectroscopic and Theoretical Analysis of a Spontaneously Formed Lys-Asp Isopeptide Bond. <i>Angewandte Chemie - International Edition</i> , 2010, 49, 8421-8425.	7.2	88
66	Structure and Function of GDP-Mannose-5-Epimerase: An Enzyme which Performs Three Chemical Reactions at the Same Active Site. <i>Journal of the American Chemical Society</i> , 2005, 127, 18309-18320.	6.6	86
67	Pironetin reacts covalently with cysteine-316 of β -tubulin to destabilize microtubule. <i>Nature Communications</i> , 2016, 7, 12103.	5.8	83
68	Crystal Structures of <i>Mycobacteria tuberculosis</i> and <i>Klebsiella pneumoniae</i> UDP-Galactopyranose Mutase in the Oxidised State and <i>Klebsiella pneumoniae</i> UDP-Galactopyranose Mutase in the (Active) Reduced State. <i>Journal of Molecular Biology</i> , 2005, 348, 971-982.	2.0	81
69	Structure of the DNA Repair Helicase Hel308 Reveals DNA Binding and Autoinhibitory Domains. <i>Journal of Biological Chemistry</i> , 2008, 283, 5118-5126.	1.6	81
70	Translocation of Group 1 Capsular Polysaccharide in <i>Escherichia coli</i> Serotype K30. <i>Journal of Biological Chemistry</i> , 2003, 278, 49763-49772.	1.6	80
71	Structural, mechanistic and regulatory studies of serine palmitoyltransferase. <i>Biochemical Society Transactions</i> , 2012, 40, 547-554.	1.6	80
72	A Novel Outer Membrane Protein, Wzi, Is Involved in Surface Assembly of the <i>Escherichia coli</i> K30 Group 1 Capsule. <i>Journal of Bacteriology</i> , 2003, 185, 5882-5890.	1.0	79

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73	TarO: a target optimisation system for structural biology. <i>Nucleic Acids Research</i> , 2008, 36, W190-W196.	6.5	79
74	Megabodies expand the nanobody toolkit for protein structure determination by single-particle cryo-EM. <i>Nature Methods</i> , 2021, 18, 60-68.	9.0	79
75	The chemical nature of amavadin. <i>Journal of the American Chemical Society</i> , 1993, 115, 807-808.	6.6	78
76	Concanavalin A distorts the α -GlcNAc-(1 \rightarrow 2)-Man linkage of α -GlcNAc-(1 \rightarrow 2)- α -Man-(1 \rightarrow 3)-[α -GlcNAc-(1 \rightarrow 2)- α -Man-(1 \rightarrow 6)]-Man upon binding. <i>Glycobiology</i> , 1998, 8, 173-181.	1.3	78
77	Structure and Function of the PiuA and PirA Siderophore-Drug Receptors from <i>Pseudomonas aeruginosa</i> and <i>Acinetobacter baumannii</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	78
78	Changing the Regioselectivity of the Tryptophan 7 α -Halogenase PrnA by Site α -Directed Mutagenesis. <i>Angewandte Chemie - International Edition</i> , 2011, 50, 2951-2953.	7.2	76
79	Directed Evolution of a New Catalytic Site in 2-Keto-3-Deoxy-6-Phosphogluconate Aldolase from <i>Escherichia coli</i> . <i>Structure</i> , 2001, 9, 1-9.	1.6	70
80	Variation on a Theme of SDR. <i>Structure</i> , 2002, 10, 773-786.	1.6	69
81	Crystal Structures of Wzb of <i>Escherichia coli</i> and CpsB of <i>Streptococcus pneumoniae</i> , Representatives of Two Families of Tyrosine Phosphatases that Regulate Capsule Assembly. <i>Journal of Molecular Biology</i> , 2009, 392, 678-688.	2.0	69
82	The role of polar interactions in the molecular recognition of CD40L with its receptor CD40. <i>Protein Science</i> , 1998, 7, 1124-1135.	3.1	67
83	AcsD catalyzes enantioselective citrate desymmetrization in siderophore biosynthesis. <i>Nature Chemical Biology</i> , 2009, 5, 174-182.	3.9	67
84	RmlC, a C3 α and C5 α Carbohydrate Epimerase, Appears to Operate via an Intermediate with an Unusual Twist Boat Conformation. <i>Journal of Molecular Biology</i> , 2007, 365, 146-159.	2.0	65
85	Molecular Basis of Filtering Carbapenems by Porins from β -Lactam-resistant Clinical Strains of <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 2837-2847.	1.6	65
86	A marine viral halogenase that iodinated diverse substrates. <i>Nature Chemistry</i> , 2019, 11, 1091-1097.	6.6	65
87	PELDOR Spectroscopy Distance Fingerprinting of the Octameric Outer α -Membrane Protein Wza from <i>Escherichia coli</i> . <i>Angewandte Chemie - International Edition</i> , 2009, 48, 2904-2906.	7.2	63
88	Wzi Is an Outer Membrane Lectin that Underpins Group 1 Capsule Assembly in <i>Escherichia coli</i> . <i>Structure</i> , 2013, 21, 844-853.	1.6	63
89	The complex of ferric-enterobactin with its transporter from <i>Pseudomonas aeruginosa</i> suggests a two-site model. <i>Nature Communications</i> , 2019, 10, 3673.	5.8	62
90	Man α 1-2 Man α -OMe-concanavalin A complex reveals a balance of forces involved in carbohydrate recognition. <i>Glycobiology</i> , 1999, 9, 539-545.	1.3	61

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91	Structure of the heterotrimeric PCNA from <i>Sulfolobus solfataricus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 944-948.	0.7	61
92	Biological Halogenation has Moved far Beyond Haloperoxidases. <i>Advances in Applied Microbiology</i> , 2006, 59, 127-157.	1.3	61
93	Periplasmic Protein-Protein Contacts in the Inner Membrane Protein Wzc Form a Tetrameric Complex Required for the Assembly of <i>Escherichia coli</i> Group 1 Capsules. <i>Journal of Biological Chemistry</i> , 2006, 281, 2144-2150.	1.6	61
94	Potentiometric Analysis of UDP-Galactopyranose Mutase: Stabilization of the Flavosemiquinone by Substrate. <i>Biochemistry</i> , 2003, 42, 2104-2109.	1.2	57
95	Structure and Function of Both Domains of ArnA, a Dual Function Decarboxylase and a Formyltransferase, Involved in 4-Amino-4-deoxy-L-arabinose Biosynthesis. <i>Journal of Biological Chemistry</i> , 2005, 280, 23000-23008.	1.6	57
96	The External Aldimine Form of Serine Palmitoyltransferase. <i>Journal of Biological Chemistry</i> , 2009, 284, 17328-17339.	1.6	57
97	Three-dimensional Structure of Wza, the Protein Required for Translocation of Group 1 Capsular Polysaccharide across the Outer Membrane of <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 28227-28232.	1.6	55
98	A coiled-coil domain acts as a molecular ruler to regulate O-antigen chain length in lipopolysaccharide. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 50-56.	3.6	55
99	Structure of Ubiquitin-Conjugating Enzyme 9 Displays Significant Differences with Other Ubiquitin-Conjugating Enzymes Which May Reflect its Specificity for Sumo Rather Than Ubiquitin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 891-898.	2.5	54
100	Mechanism of the Class I KDPG aldolase. <i>Bioorganic and Medicinal Chemistry</i> , 2006, 14, 3002-3010.	1.4	53
101	An Efficient Method for the In Vitro Production of Azol(in)e-Based Cyclic Peptides. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 14171-14174.	7.2	53
102	Adenovirus DNA Replication. <i>Current Topics in Microbiology and Immunology</i> , 2003, 272, 131-164.	0.7	52
103	The Structure of NADH in the Enzyme dTDP-d-glucose Dehydratase (RmlB). <i>Journal of the American Chemical Society</i> , 2003, 125, 11872-11878.	6.6	51
104	Crystal structure and silica condensing activities of silicatein Î± cathepsin L chimeras. <i>Chemical Communications</i> , 2008, , 1765.	2.2	51
105	Halomethane Biosynthesis: Structure of a SAM-Dependent Halide Methyltransferase from <i>Arabidopsis thaliana</i> . <i>Angewandte Chemie - International Edition</i> , 2010, 49, 3646-3648.	7.2	50
106	Overexpression, purification, crystallization and preliminary structural study of dTDP-6-deoxy-L-lyxo-4-hexulose reductase (RmlD), the fourth enzyme of the dTDP-L-rhamnose synthesis pathway, from <i>Salmonella enterica</i> serovar Typhimurium. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 2043-2046.	2.5	49
107	The Discovery of New Cyanobactins from <i>Cyanothece</i> PCC 7425 Defines a New Signature for Processing of Patellamides. <i>ChemBioChem</i> , 2012, 13, 2683-2689.	1.3	49
108	A Unique Tryptophan Prenyltransferase from the Kawaguchi-peptin Biosynthetic Pathway. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 3596-3599.	7.2	49

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109	Probing the Structure of the Mechanosensitive Channel of Small Conductance in Lipid Bilayers with Pulsed Electron-Electron Double Resonance. <i>Biophysical Journal</i> , 2014, 106, 834-842.	0.2	48
110	A Localized Tolerance in the Substrate Specificity of the Fluorinase Enzyme enables a Stepwise Fluorination of a RGD Peptide under Ambient Aqueous Conditions. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 8913-8918.	7.2	48
111	Enzymatic Macrocyclization of 1,2,3-Triazole Peptide Mimetics. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 5842-5845.	7.2	48
112	A molecular mechanism for the enzymatic methylation of nitrogen atoms within peptide bonds. <i>Science Advances</i> , 2018, 4, eaat2720.	4.7	48
113	Hydrophobic recognition allows the glycosyltransferase UGT76G1 to catalyze its substrate in two orientations. <i>Nature Communications</i> , 2019, 10, 3214.	5.8	47
114	The Structural Basis of Chain Length Control in Rv1086. <i>Journal of Molecular Biology</i> , 2008, 381, 129-140.	2.0	46
115	Structural and Functional Characterisation of a Conserved Archaeal RadA Paralog with Antirecombinase Activity. <i>Journal of Molecular Biology</i> , 2009, 389, 661-673.	2.0	45
116	The Respiratory Arsenite Oxidase: Structure and the Role of Residues Surrounding the Rieske Cluster. <i>PLoS ONE</i> , 2013, 8, e72535.	1.1	45
117	The 1.2 Å resolution structure of the con A-dimannose complex. <i>Journal of Molecular Biology</i> , 2001, 310, 875-884.	2.0	44
118	Trapped translocation intermediates establish the route for export of capsular polysaccharides across <i>Escherichia coli</i> outer membranes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8203-8208.	3.3	44
119	Low Resolution Structure of a Bacterial SLC26 Transporter Reveals Dimeric Stoichiometry and Mobile Intracellular Domains. <i>Journal of Biological Chemistry</i> , 2011, 286, 27058-27067.	1.6	42
120	Preacinetobactin not acinetobactin is essential for iron uptake by the BauA transporter of the pathogen <i>Acinetobacter baumannii</i> . <i>ELife</i> , 2018, 7, .	2.8	41
121	A structural perspective on the enzymes that convert dTDP-d-glucose into dTDP-l-rhamnose. <i>Biochemical Society Transactions</i> , 2003, 31, 532-536.	1.6	40
122	Structural and Kinetic Characterization of Quinolate Phosphoribosyltransferase (hQPRTase) from <i>Homo sapiens</i> . <i>Journal of Molecular Biology</i> , 2007, 373, 755-763.	2.0	40
123	Accurate Extraction of Nanometer Distances in Multimers by Pulse EPR. <i>Chemistry - A European Journal</i> , 2016, 22, 4700-4703.	1.7	40
124	Sugar nucleotide recognition by <i>Klebsiella pneumoniae</i> UDP-d-galactopyranose mutase: Fluorinated substrates, kinetics and equilibria. <i>Organic and Biomolecular Chemistry</i> , 2009, 7, 1009.	1.5	39
125	Inhibition of the PLP-dependent enzyme serine palmitoyltransferase by cycloserine: evidence for a novel decarboxylative mechanism of inactivation. <i>Molecular BioSystems</i> , 2010, 6, 1682.	2.9	39
126	Allosteric Competitive Inhibitors of the Glucose-1-phosphate Thymidyltransferase (RmlA) from <i>Pseudomonas aeruginosa</i> . <i>ACS Chemical Biology</i> , 2013, 8, 387-396.	1.6	39

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127	The structural biology of patellamide biosynthesis. <i>Current Opinion in Structural Biology</i> , 2014, 29, 112-121.	2.6	39
128	Discovery of an Allosteric Inhibitor Binding Site in 3-Oxo-acyl-ACP Reductase from <i>Pseudomonas aeruginosa</i> . <i>ACS Chemical Biology</i> , 2013, 8, 2518-2527.	1.6	38
129	A snapshot of carnitine acetyltransferase. <i>Trends in Biochemical Sciences</i> , 2003, 28, 343-346.	3.7	37
130	High-Resolution Structures of RmlC from <i>Streptococcus suis</i> in Complex with Substrate Analogs Locate the Active Site of This Class of Enzyme. <i>Structure</i> , 2003, 11, 715-723.	1.6	37
131	The serine palmitoyltransferase from <i>Sphingomonas wittichii</i> RW1: An interesting link to an unusual acyl carrier protein. <i>Biopolymers</i> , 2010, 93, 811-822.	1.2	37
132	Mechanism of DNA loading by the DNA repair helicase XPD. <i>Nucleic Acids Research</i> , 2016, 44, 2806-2815.	6.5	37
133	Spectator no more, the role of the membrane in regulating ion channel function. <i>Current Opinion in Structural Biology</i> , 2017, 45, 59-66.	2.6	37
134	A Dimeric Rep Protein Initiates Replication of a Linear Archaeal Virus Genome: Implications for the Rep Mechanism and Viral Replication. <i>Journal of Virology</i> , 2011, 85, 925-931.	1.5	36
135	Enzymatic Macrocyclization of 1,2,3-Triazole Peptide Mimetics. <i>Angewandte Chemie</i> , 2016, 128, 5936-5939.	1.6	36
136	MOMP from <i>Campylobacter jejuni</i> Is a Trimer of 18-Stranded β -Barrel Monomers with a Ca ²⁺ Ion Bound at the Constriction Zone. <i>Journal of Molecular Biology</i> , 2016, 428, 4528-4543.	2.0	36
137	Structural and Mechanistic Basis of Bacterial Sugar Nucleotide-Modifying Enzymes. <i>Biochemistry</i> , 2003, 42, 7637-7647.	1.2	35
138	Substrate specificity in enzymatic fluorination. The fluorinase from <i>Streptomyces cattleya</i> accepts 2'-deoxyadenosine substrates. <i>Organic and Biomolecular Chemistry</i> , 2006, 4, 1458.	1.5	35
139	Displacement of the canonical single-stranded DNA-binding protein in the Thermoproteales. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E398-405.	3.3	34
140	PELDOR in rotationally symmetric homo-oligomers. <i>Molecular Physics</i> , 2013, 111, 2845-2854.	0.8	34
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