

Hazel M Holden

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	Structure and Function of Enzymes of the Leloir Pathway for Galactose Metabolism. <i>Journal of Biological Chemistry</i> , 2003, 278, 43885-43888.	1.6	417
2	Channeling of Substrates and Intermediates in Enzyme-Catalyzed Reactions. <i>Annual Review of Biochemistry</i> , 2001, 70, 149-180.	5.0	352
3	Structure of Carbamoyl Phosphate Synthetase: A Journey of 96 Å... from Substrate to Product. <i>Biochemistry</i> , 1997, 36, 6305-6316.	1.2	322
4	The structure of GDP-4-keto-6-deoxy-D-mannose-3-dehydratase: A unique coenzyme B6-dependent enzyme. <i>Protein Science</i> , 2006, 15, 2093-2106.	3.1	263
5	Three-Dimensional Structure of Phosphotriesterase: An Enzyme Capable of Detoxifying Organophosphate Nerve Agents. <i>Biochemistry</i> , 1994, 33, 15001-15007.	1.2	206
6	Three-Dimensional Structure of <i>Escherichia coli</i> Asparagine Synthetase B: A Short Journey from Substrate to Product. <i>Biochemistry</i> , 1999, 38, 16146-16157.	1.2	191
7	The Crotonase Superfamily: Divergently Related Enzymes That Catalyze Different Reactions Involving Acyl Coenzyme A Thioesters. <i>Accounts of Chemical Research</i> , 2001, 34, 145-157.	7.6	190
8	Molecular Structure of Dihydroorotase: A Paradigm for Catalysis through the Use of a Binuclear Metal Center. <i>Biochemistry</i> , 2001, 40, 6989-6997.	1.2	189
9	Enzymes with Molecular Tunnels. <i>Accounts of Chemical Research</i> , 2003, 36, 539-548.	7.6	173
10	Structure of 4-Chlorobenzoyl Coenzyme A Dehalogenase Determined to 1.8 Å... Resolution: An Enzyme Catalyst Generated via Adaptive Mutation. <i>Biochemistry</i> , 1996, 35, 8103-8109.	1.2	169
11	Molecular Structure of the NADH/UDP-glucose Abortive Complex of UDP-galactose 4-Epimerase from <i>Escherichia coli</i> : Implications for the Catalytic Mechanism. <i>Biochemistry</i> , 1996, 35, 5137-5144.	1.2	162
12	Crystallographic Evidence for Tyr 157 Functioning as the Active Site Base in Human UDP-Galactose 4-Epimerase. <i>Biochemistry</i> , 2000, 39, 5691-5701.	1.2	155
13	Mechanistic Roles of Tyrosine 149 and Serine 124 in UDP-galactose 4-Epimerase from <i>Escherichia coli</i> . <i>Biochemistry</i> , 1997, 36, 10675-10684.	1.2	151
14	X-ray structure determination of telokin, the C-terminal domain of myosin light chain kinase, at 2.8 Å... resolution. <i>Journal of Molecular Biology</i> , 1992, 227, 840-851.	2.0	149
15	Human UDP-galactose 4-Epimerase. <i>Journal of Biological Chemistry</i> , 2001, 276, 15131-15136.	1.6	116
16	The Amidotransferase Family of Enzymes: Molecular Machines for the Production and Delivery of Ammonia. <i>Biochemistry</i> , 1999, 38, 7891-7899.	1.2	102
17	Dramatic Differences in the Binding of UDP-Galactose and UDP-Glucose to UDP-Galactose 4-Epimerase from <i>Escherichia coli</i> . <i>Biochemistry</i> , 1998, 37, 11469-11477.	1.2	94
18	Molecular Structure of Human Galactokinase. <i>Journal of Biological Chemistry</i> , 2005, 280, 9662-9670.	1.6	94

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19	New Reactions in the Crotonase Superfamily: Structure of Methylmalonyl CoA Decarboxylase from <i>Escherichia coli</i> . <i>Biochemistry</i> , 2000, 39, 4630-4639.	1.2	88
20	High-Resolution X-Ray structure of UDP-galactose 4-epimerase complexed with UDP-phenol. <i>Protein Science</i> , 1996, 5, 2149-2161.	3.1	87
21	The enzymes of biotin dependent CO ₂ metabolism: What structures reveal about their reaction mechanisms. <i>Protein Science</i> , 2012, 21, 1597-1619.	3.1	80
22	Computational Redesign of Acyl-ACP Thioesterase with Improved Selectivity toward Medium-Chain-Length Fatty Acids. <i>ACS Catalysis</i> , 2017, 7, 3837-3849.	5.5	77
23	Three-Dimensional Structure of ATP:Corrinoid Adenosyltransferase from <i>Salmonella typhimurium</i> in Its Free State, Complexed with MgATP, or Complexed with Hydroxycobalamin and MgATP. <i>Biochemistry</i> , 2001, 40, 361-374.	1.2	72
24	The Molecular Architecture of Human N-Acetylgalactosamine Kinase. <i>Journal of Biological Chemistry</i> , 2005, 280, 32784-32791.	1.6	69
25	The Small Subunit of Carbamoyl Phosphate Synthetase: Snapshots along the Reaction Pathway. <i>Biochemistry</i> , 1999, 38, 16158-16166.	1.2	68
26	Structural Analysis of the Y299C Mutant of <i>Escherichia coli</i> UDP-galactose 4-Epimerase. <i>Journal of Biological Chemistry</i> , 2002, 277, 27528-27534.	1.6	67
27	Carbamoyl Phosphate Synthetase: Closure of the B-Domain as a Result of Nucleotide Binding. <i>Biochemistry</i> , 1999, 38, 2347-2357.	1.2	65
28	Structural Analysis of the H166G Site-Directed Mutant of Galactose-1-phosphate Uridyltransferase Complexed with either UDP-glucose or UDP-galactose: Detailed Description of the Nucleotide Sugar Binding Site. <i>Biochemistry</i> , 1997, 36, 1212-1222.	1.2	63
29	Molecular Structure of Galactokinase. <i>Journal of Biological Chemistry</i> , 2003, 278, 33305-33311.	1.6	63
30	Determinants of Function and Substrate Specificity in Human UDP-galactose 4-Epimerase. <i>Journal of Biological Chemistry</i> , 2004, 279, 32796-32803.	1.6	60
31	The molecular architecture of glucose-1-phosphate uridylyltransferase. <i>Protein Science</i> , 2007, 16, 432-440.	3.1	60
32	Molecular Structure of <i>Saccharomyces cerevisiae</i> Gal1p, a Bifunctional Galactokinase and Transcriptional Inducer. <i>Journal of Biological Chemistry</i> , 2005, 280, 36905-36911.	1.6	54
33	High-Resolution X-Ray Structure of Isoaspartyl Dipeptidase from <i>Escherichia coli</i> . <i>Biochemistry</i> , 2003, 42, 4874-4882.	1.2	47
34	Phosphotriesterase: An Enzyme in Search of Its Natural Substrate. <i>Advances in Enzymology and Related Areas of Molecular Biology</i> , 2006, 74, 51-93.	1.3	44
35	The Molecular Architecture of Galactose Mutarotase/UDP-Galactose 4-Epimerase from <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 21900-21907.	1.6	43
36	Molecular Structure of <i>Escherichia coli</i> PurT-Encoded Glycinamide Ribonucleotide Transformylase. <i>Biochemistry</i> , 2000, 39, 8791-8802.	1.2	42

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37	High Resolution X-ray Structure of dTDP-Glucose 4,6-Dehydratase from <i>Streptomyces venezuelae</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 2211-2220.	1.6	41
38	Molecular Structures of the S124A, S124T, and S124V Site-Directed Mutants of UDP-galactose 4-Epimerase from <i>Escherichia coli</i> . <i>Biochemistry</i> , 1997, 36, 10685-10695.	1.2	40
39	Active site geometry of glucose-1-phosphate uridylyltransferase. <i>Protein Science</i> , 2007, 16, 1379-1388.	3.1	40
40	High Resolution X-ray Structure of Galactose Mutarotase from <i>Lactococcus lactis</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 20854-20861.	1.6	38
41	Carbamoyl-phosphate Synthetase. <i>Journal of Biological Chemistry</i> , 2002, 277, 39722-39727.	1.6	35
42	Molecular Architecture of DesL: A Key Enzyme in the Biosynthesis of Desosamine. <i>Biochemistry</i> , 2007, 46, 8999-9006.	1.2	35
43	The catalytic mechanism of galactose mutarotase. <i>Protein Science</i> , 2003, 12, 1051-1059.	3.1	34
44	Molecular Structure of Human Galactose Mutarotase. <i>Journal of Biological Chemistry</i> , 2004, 279, 23431-23437.	1.6	34
45	Molecular architecture of DesV from <i>Streptomyces venezuelae</i> : A PLP-dependent transaminase involved in the biosynthesis of the unusual sugar desosamine. <i>Protein Science</i> , 2007, 16, 887-896.	3.1	34
46	The Binding of Inosine Monophosphate to <i>Escherichia coli</i> Carbamoyl Phosphate Synthetase. <i>Journal of Biological Chemistry</i> , 1999, 274, 22502-22507.	1.6	33
47	X-ray Structure of KijD3, a Key Enzyme Involved in the Biosynthesis of d-Kijanose. <i>Biochemistry</i> , 2010, 49, 3517-3524.	1.2	32
48	Structure of the α 2 homodimer of bacterial luciferase from <i>Vibrio harveyi</i> : X-ray analysis of a kinetic protein folding trap. <i>Protein Science</i> , 1997, 6, 13-23.	3.1	29
49	Structural and Kinetic Studies of Sugar Binding to Galactose Mutarotase from <i>Lactococcus lactis</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 45458-45465.	1.6	28
50	The structure of DesR from <i>Streptomyces venezuelae</i> , a β -glucosidase involved in macrolide activation. <i>Protein Science</i> , 2013, 22, 883-892.	3.1	27
51	Kinetic and Structural Analysis of β -d-Glucose-1-phosphate Cytidylyltransferase from <i>Salmonella typhi</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 10774-10780.	1.6	25
52	Understanding a Transcriptional Paradigm at the Molecular Level. <i>Journal of Biological Chemistry</i> , 2007, 282, 1534-1538.	1.6	25
53	GDP-Perosamine Synthase: Structural Analysis and Production of a Novel Trideoxysugar. <i>Biochemistry</i> , 2008, 47, 2833-2840.	1.2	25
54	Structural and Functional Studies of QdtC: An N-Acetyltransferase Required for the Biosynthesis of dTDP-3-Acetamido-3,6-dideoxy- β -d-glucose. <i>Biochemistry</i> , 2009, 48, 2699-2709.	1.2	24

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55	Discovery of a Glutamine Kinase Required for the Biosynthesis of the <i>O</i> -Methyl Phosphoramidate Modifications Found in the Capsular Polysaccharides of <i>Campylobacter jejuni</i> . <i>Journal of the American Chemical Society</i> , 2017, 139, 9463-9466.	6.6	24
56	Molecular Structure of β -D-Glucose-1-phosphate Cytidyltransferase from <i>Salmonella typhi</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 44023-44029.	1.6	23
57	Structural Analysis of QdtB, an Aminotransferase Required for the Biosynthesis of dTDP-3-acetamido-3,6-dideoxy- β -D-glucose. <i>Biochemistry</i> , 2009, 48, 1553-1561.	1.2	22
58	Combined Structural and Functional Investigation of a C-3 α -Ketoreductase Involved in the Biosynthesis of dTDP- <i>l</i> -Digitoxose. <i>Biochemistry</i> , 2011, 50, 5905-5917.	1.2	22
59	Structural and Biochemical Investigation of PglF from <i>Campylobacter jejuni</i> Reveals a New Mechanism for a Member of the Short Chain Dehydrogenase/Reductase Superfamily. <i>Biochemistry</i> , 2017, 56, 6030-6040.	1.2	22
60	The X-ray Structure of dTDP-4-Keto-6-deoxy-D-glucose-3,4-ketoisomerase. <i>Journal of Biological Chemistry</i> , 2007, 282, 19227-19236.	1.6	21
61	Three-Dimensional Structure of DesVI from <i>Streptomyces venezuelae</i> : A Sugar <i>N,N</i> -Dimethyltransferase Required for dTDP-Desosamine Biosynthesis. <i>Biochemistry</i> , 2008, 47, 3982-3988.	1.2	21
62	Structure of a Sugar <i>N</i> -Formyltransferase from <i>Campylobacter jejuni</i> . <i>Biochemistry</i> , 2013, 52, 6114-6126.	1.2	21
63	Three-dimensional structure of a sugar <i>N</i> -formyltransferase from <i>Francisella tularensis</i> . <i>Protein Science</i> , 2014, 23, 273-283.	3.1	21
64	Biosynthetic enzymes of unusual microbial sugars. <i>Current Opinion in Structural Biology</i> , 2010, 20, 543-550.	2.6	20
65	Molecular Structure of WlbB, a Bacterial N-Acetyltransferase Involved in the Biosynthesis of 2,3-Diacetamido-2,3-dideoxy-d-mannuronic Acid,. <i>Biochemistry</i> , 2010, 49, 4644-4653.	1.2	20
66	New Role for the Ankyrin Repeat Revealed by a Study of the <i>N</i> -Formyltransferase from <i>Providencia alcalifaciens</i> . <i>Biochemistry</i> , 2015, 54, 631-638.	1.2	20
67	Long-range allosteric transitions in carbamoyl phosphate synthetase. <i>Protein Science</i> , 2004, 13, 2398-2405.	3.1	19
68	Structure of CDP-D-glucose 4,6-dehydratase from <i>Salmonella typhi</i> complexed with CDP-D-xylose. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 365-373.	2.5	19
69	Catalytic Mechanism of Perosamine <i>N</i> -Acetyltransferase Revealed by High-Resolution X-ray Crystallographic Studies and Kinetic Analyses. <i>Biochemistry</i> , 2012, 51, 3433-3444.	1.2	19
70	A Structural Study of GDP-4-Keto-6-Deoxy- <i>D</i> -Mannose-3-Dehydratase: Caught in the Act of Geminal Diamine Formation ¹ . <i>Biochemistry</i> , 2007, 46, 14215-14224.	1.2	18
71	Kinetic mechanism of asparagine synthetase from <i>Vibrio cholerae</i> . <i>Bioorganic Chemistry</i> , 2004, 32, 63-75.	2.0	17
72	Accommodation of GDP-Linked Sugars in the Active Site of GDP-Perosamine Synthase ¹ . <i>Biochemistry</i> , 2008, 47, 10685-10693.	1.2	17

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73	Structural and Functional Studies on a 3- α -Epimerase Involved in the Biosynthesis of dTDP-6-deoxy-d-allose. <i>Biochemistry</i> , 2012, 51, 9375-9383.	1.2	17
74	Structural and Functional Studies of WlbA: A Dehydrogenase Involved in the Biosynthesis of 2,3-Diacetamido-2,3-dideoxy-d-mannuronic Acid,. <i>Biochemistry</i> , 2010, 49, 7939-7948.	1.2	16
75	Biochemical and Structural Characterization of WlbA from <i>Bordetella pertussis</i> and <i>Chromobacterium violaceum</i> : Enzymes Required for the Biosynthesis of 2,3-Diacetamido-2,3-dideoxy-d-mannuronic Acid. <i>Biochemistry</i> , 2011, 50, 1483-1491.	1.2	16
76	Active Site Architecture of a Sugar N-Oxygenase. <i>Biochemistry</i> , 2013, 52, 3191-3193.	1.2	16
77	Structure of the external aldimine form of PglE, an aminotransferase required for <i>N</i> -acetylglucosamine biosynthesis. <i>Protein Science</i> , 2015, 24, 1609-1616.	3.1	16
78	Structural and Biochemical Characterization of a Bifunctional Ketoisomerase/ <i>N</i> -Acetyltransferase from <i>Shewanella denitrificans</i> . <i>Biochemistry</i> , 2013, 52, 8374-8385.	1.2	15
79	Biosynthesis of Nucleoside Diphosphoramidates in <i>Campylobacter jejuni</i> . <i>Biochemistry</i> , 2017, 56, 6079-6082.	1.2	15
80	Structural Analysis of Cj1427, an Essential NAD-Dependent Dehydrogenase for the Biosynthesis of the Heptose Residues in the Capsular Polysaccharides of <i>Campylobacter jejuni</i> . <i>Biochemistry</i> , 2020, 59, 1314-1327.	1.2	15
81	Two Site-Directed Mutations Are Required for the Conversion of a Sugar Dehydratase into an Aminotransferase. <i>Biochemistry</i> , 2009, 48, 5246-5253.	1.2	14
82	Molecular Architecture of a <i>C</i> -3-Methyltransferase Involved in the Biosynthesis of d-Tetronitrose. <i>Biochemistry</i> , 2010, 49, 5891-5898.	1.2	14
83	Molecular Architecture of TylM1 from <i>Streptomyces fradiae</i> : An <i>N</i> , <i>N</i> -Dimethyltransferase Involved in the Production of dTDP-d-mycaminose,. <i>Biochemistry</i> , 2011, 50, 780-787.	1.2	14
84	pH-rate profiles support a general base mechanism for galactokinase (<i>Lactococcus lactis</i>). <i>FEBS Letters</i> , 2013, 587, 2876-2881.	1.3	14
85	Molecular structure of an <i>N</i> -formyltransferase from <i>Providencea alcalifaciens</i> . <i>Protein Science</i> , 2015, 24, 976-986.	3.1	14
86	Biosynthesis of d-glycero-l-gluco-Heptose in the Capsular Polysaccharides of <i>Campylobacter jejuni</i> . <i>Biochemistry</i> , 2021, 60, 1552-1563.	1.2	13
87	Mutations of surface residues in <i>Anabaena</i> vegetative and heterocyst ferredoxin that affect thermodynamic stability as determined by guanidine hydrochloride denaturation. <i>Protein Science</i> , 1995, 4, 58-64.	3.1	12
88	Bacterial Sugar 3,4-Ketoisomerases: Structural Insight into Product Stereochemistry. <i>Biochemistry</i> , 2015, 54, 4495-4506.	1.2	12
89	Structural investigation on WlaRG from <i>Campylobacter jejuni</i> : A sugar aminotransferase. <i>Protein Science</i> , 2017, 26, 586-599.	3.1	12
90	Structural and Functional Characterization of YdjI, an Aldolase of Unknown Specificity in <i>Escherichia coli</i> K12. <i>Biochemistry</i> , 2019, 58, 3340-3353.	1.2	12

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91	Structure of the <i>Escherichia coli</i> ArnA N-terminal formyltransferase domain in complex with N ⁵ -methyltetrahydrofolate and UDP-Ara4N. <i>Protein Science</i> , 2016, 25, 1555-1562.	3.1	11
92	GDP-4-Keto-6-deoxy-D-mannose 3-Dehydratase, Accommodating a Sugar Substrate in the Active Site. <i>Journal of Biological Chemistry</i> , 2008, 283, 4295-4303.	1.6	10
93	Structural Studies of AntD: An N-Acyltransferase Involved in the Biosynthesis of <i>ScpD</i> -Anthrose. <i>Biochemistry</i> , 2012, 51, 867-878.	1.2	10
94	Enzymes required for the biosynthesis of N-formylated sugars. <i>Current Opinion in Structural Biology</i> , 2016, 41, 1-9.	2.6	10
95	The three-dimensional structure of NeoB: An aminotransferase involved in the biosynthesis of neomycin. <i>Protein Science</i> , 2018, 27, 945-956.	3.1	9
96	Biochemical analysis of a sugar 4,6-dehydratase from <i>Acanthamoeba polyphaga</i> Mimivirus. <i>Protein Science</i> , 2020, 29, 1148-1159.	3.1	9
97	Molecular architecture of an N-formyltransferase from <i>Salmonella enterica</i> O60. <i>Journal of Structural Biology</i> , 2017, 200, 267-278.	1.3	8
98	Investigation of a sugar N-formyltransferase from the plant pathogen <i>Pantoea ananatis</i> . <i>Protein Science</i> , 2019, 28, 707-716.	3.1	8
99	Biochemical Characterization of WbkC, an N-Formyltransferase from <i>Brucella melitensis</i> . <i>Biochemistry</i> , 2017, 56, 3657-3668.	1.2	7
100	Characterization of the dTDP-Fuc3N and dTDP-Qui3N biosynthetic pathways in <i>Campylobacter jejuni</i> 81116. <i>Glycobiology</i> , 2017, 27, cww136.	1.3	7
101	The structure of RbmB from <i>Streptomyces ribosidificus</i> , an aminotransferase involved in the biosynthesis of ribostamycin. <i>Protein Science</i> , 2017, 26, 1886-1892.	3.1	7
102	Molecular architectures of Pen and Pal: Key enzymes required for CMP-pseudaminic acid biosynthesis in <i>Bacillus thuringiensis</i> . <i>Protein Science</i> , 2018, 27, 738-749.	3.1	7
103	The structure of glucose-1-phosphate thymidyltransferase from <i>Mycobacterium tuberculosis</i> reveals the location of an essential magnesium ion in the RmlA-type enzymes. <i>Protein Science</i> , 2018, 27, 441-450.	3.1	7
104	Characterization of two enzymes from <i>Psychrobacter cryohalolentis</i> that are required for the biosynthesis of an unusual diacetamido-d-sugar. <i>Journal of Biological Chemistry</i> , 2021, 296, 100463.	1.6	7
105	From the Three-Dimensional Structure of Phosphotriesterase. <i>Biochemistry</i> , 2021, 60, 3413-3415.	1.2	7
106	Biochemical studies on WbcA, a sugar epimerase from <i>Yersinia enterocolitica</i> . <i>Protein Science</i> , 2015, 24, 1633-1639.	3.1	6
107	Biochemical Investigation of Rv3404c from <i>Mycobacterium tuberculosis</i> . <i>Biochemistry</i> , 2017, 56, 3818-3825.	1.2	6
108	4-Deoxy-4-fluoro-GalNAz (4FGalNAz) Is a Metabolic Chemical Reporter of O-GlcNAc Modifications, Highlighting the Notable Substrate Flexibility of O-GlcNAc Transferase. <i>ACS Chemical Biology</i> , 2022, 17, 159-170.	1.6	6

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109	Reaction Mechanism and Three-Dimensional Structure of GDP-glycero- β -manno-heptose 4,6-Dehydratase from <i>Campylobacter jejuni</i> . <i>Biochemistry</i> , 2022, 61, 1313-1322.	1.2	6
110	Probing the catalytic mechanism of a C-methyltransferase involved in the biosynthesis of D-tetronitrose. <i>Protein Science</i> , 2012, 21, 876-886.	3.1	5
111	The molecular architecture of QdtA, a sugar 3,4-ketoisomerase from <i>Thermoanaerobacterium thermosaccharolyticum</i> . <i>Protein Science</i> , 2014, 23, 683-692.	3.1	5
112	Production of a Novel N-Monomethylated Dideoxysugar. <i>Biochemistry</i> , 2014, 53, 1105-1107.	1.2	5
113	Structures of KdnB and KdnA from <i>Shewanella oneidensis</i> : Key Enzymes in the Formation of 8-Amino-3,8-Dideoxy-Manno-Octulosonic Acid. <i>Biochemistry</i> , 2016, 55, 4485-4494.	1.2	4
114	Structural Studies on a Glucosamine/Glucosaminide N-Acetyltransferase. <i>Biochemistry</i> , 2016, 55, 4495-4508.	1.2	4
115	Misannotations of the genes encoding sugar N-formyltransferases. <i>Protein Science</i> , 2020, 29, 930-940.	3.1	4
116	Investigation of the enzymes required for the biosynthesis of an unusual formylated sugar in the emerging human pathogen <i>Helicobacter canadensis</i> . <i>Protein Science</i> , 2021, 30, 2144-2160.	3.1	4
117	Biochemical Investigation of an N-acetyltransferase from <i>Helicobacter pullorum</i> . <i>Protein Science</i> , 2021, 30, 2418-2432.	3.1	4
118	The high-resolution structure of a UDP-glucose rhamnose synthase from <i>Acanthamoeba polyphaga</i> Mimivirus. <i>Protein Science</i> , 2020, 29, 2164-2174.	3.1	3
119	Characterization of an aminotransferase from <i>Acanthamoeba polyphaga</i> Mimivirus. <i>Protein Science</i> , 2021, 30, 1882-1894.	3.1	3
120	Structural studies on KijD1, a sugar C-methyltransferase. <i>Protein Science</i> , 2016, 25, 2282-2289.	3.1	2
121	Structural and Functional Investigation of FdhC from <i>Acinetobacter nosocomialis</i> : A Sugar N-Acyltransferase Belonging to the GNAT Superfamily. <i>Biochemistry</i> , 2016, 55, 4509-4518.	1.2	2
122	Structure and function of an N-acetyltransferase from the human pathogen <i>Acinetobacter baumannii</i> isolate BAL_212. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, , .	1.5	2
123	Molecular architecture of KedS8, a sugar N-methyltransferase from <i>S-treptoalloteichus</i> sp. ATCC 53650. <i>Protein Science</i> , 2015, 24, 1593-1599.	3.1	1
124	The <i>Mycobacterium tuberculosis</i> complex has a pathway for the biosynthesis of 4-formamido-4,6-dideoxy-glucose. <i>Protein Science</i> , 2018, 27, 1491-1497.	3.1	1
125	Editorial overview: Catalysis and regulation: Structural features guiding enzyme catalysed processes. <i>Current Opinion in Structural Biology</i> , 2018, 53, iii-v.	2.6	0