

P Lynne Howell

List of Publications by Year in descending order

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139
papers

8,003
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47006

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docs citations

153
times ranked

7789
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#	ARTICLE	IF	CITATIONS
1	The <i>Pseudomonas aeruginosa</i> homeostasis enzyme AlgL clears the periplasmic space of accumulated alginate during polymer biosynthesis. <i>Journal of Biological Chemistry</i> , 2022, 298, 101560.	3.4	8
2	Termination of Poly- <i>N</i> -acetylglucosamine (PNAG) Polymerization with <i>N</i> -Acetylglucosamine Analogues. <i>ACS Chemical Biology</i> , 2022, 17, 3036-3046.	3.4	4
3	Co-Operative Biofilm Interactions between <i>Aspergillus fumigatus</i> and <i>Pseudomonas aeruginosa</i> through Secreted Galactosaminogalactan Exopolysaccharide. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 336.	3.5	6
4	The Pel polysaccharide is predominantly composed of a dimeric repeat of $\hat{1}\pm$ -1,4 linked galactosamine and N-acetylglactosamine. <i>Communications Biology</i> , 2022, 5, .	4.4	20
5	Preclinical Evaluation of Recombinant Microbial Glycoside Hydrolases as Antibiofilm Agents in Acute Pulmonary <i>Pseudomonas aeruginosa</i> Infection. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, .	3.2	5
6	The Matrix Revisited: Opening Night for the Pel Polysaccharide Across Eubacterial Kingdoms. <i>Microbiology Insights</i> , 2021, 14, 117863612098858.	2.0	9
7	<i>Pseudomonas aeruginosa</i> Uses c-di-GMP Phosphodiesterases RmcA and MorA To Regulate Biofilm Maintenance. <i>MBio</i> , 2021, 12, .	4.1	25
8	A phage-encoded anti-activator inhibits quorum sensing in <i>Pseudomonas aeruginosa</i> . <i>Molecular Cell</i> , 2021, 81, 571-583.e6.	9.7	80
9	Protective Liquid Crystal Nanoparticles for Targeted Delivery of PslG: A Biofilm Dispersing Enzyme. <i>ACS Infectious Diseases</i> , 2021, 7, 2102-2115.	3.8	18
10	CryoEM map of <i>Pseudomonas aeruginosa</i> PilQ enables structural characterization of TsaP. <i>Structure</i> , 2021, 29, 457-466.e4.	3.3	9
11	Enhancing the therapeutic use of biofilm-dispersing enzymes with smart drug delivery systems. <i>Advanced Drug Delivery Reviews</i> , 2021, 179, 113916.	13.7	32
12	The role of Psl in the failure to eradicate <i>Pseudomonas aeruginosa</i> biofilms in children with cystic fibrosis. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 63.	6.4	18
13	Preclinical Evaluation of Recombinant Microbial Glycoside Hydrolases in the Prevention of Experimental Invasive Aspergillosis. <i>MBio</i> , 2021, 12, e0244621.	4.1	8
14	Preventing <i>Pseudomonas aeruginosa</i> Biofilms on Indwelling Catheters by Surface-Bound Enzymes. <i>ACS Applied Bio Materials</i> , 2021, 4, 8248-8258.	4.6	16
15	Structural basis for the O-acetyltransferase function of the extracytoplasmic domain of OatA from <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2020, 295, 8204-8213.	3.4	11
16	Structural and biochemical characterization of the exopolysaccharide deacetylase Agd3 required for <i>Aspergillus fumigatus</i> biofilm formation. <i>Nature Communications</i> , 2020, 11, 2450.	12.8	38
17	Methylation deficiency disrupts biological rhythms from bacteria to humans. <i>Communications Biology</i> , 2020, 3, 211.	4.4	17
18	Reducing <i>Aspergillus fumigatus</i> Virulence through Targeted Dysregulation of the Conidiation Pathway. <i>MBio</i> , 2020, 11, .	4.1	18

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19	PelX is a UDP-N-acetylglucosamine C4-epimerase involved in Pel polysaccharide-dependent biofilm formation. <i>Journal of Biological Chemistry</i> , 2020, 295, 11949-11962.	3.4	10
20	A systematic pipeline for classifying bacterial operons reveals the evolutionary landscape of biofilm machineries. <i>PLoS Computational Biology</i> , 2020, 16, e1007721.	3.2	28
21	Discovery and characterization of a Gram-positive Pel polysaccharide biosynthetic gene cluster. <i>PLoS Pathogens</i> , 2020, 16, e1008281.	4.7	30
22	Pel Polysaccharide Biosynthesis Requires an Inner Membrane Complex Comprised of PelD, PelE, PelF, and PelG. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	29
23	Title is missing!. , 2020, 16, e1007721.		0
24	Title is missing!. , 2020, 16, e1007721.		0
25	Title is missing!. , 2020, 16, e1007721.		0
26	Title is missing!. , 2020, 16, e1007721.		0
27	Ega3 from the fungal pathogen <i>Aspergillus fumigatus</i> is an endo-1,4-galactosaminidase that disrupts microbial biofilms. <i>Journal of Biological Chemistry</i> , 2019, 294, 13833-13849.	3.4	35
28	Galactosaminogalactan (GAG) and its multiple roles in <i>Aspergillus</i> pathogenesis. <i>Virulence</i> , 2019, 10, 976-983.	4.4	52
29	Molecular mechanism of <i>Aspergillus fumigatus</i> biofilm disruption by fungal and bacterial glycoside hydrolases. <i>Journal of Biological Chemistry</i> , 2019, 294, 10760-10772.	3.4	50
30	Treatment with the <i>Pseudomonas aeruginosa</i> Glycoside Hydrolase PslG Combats Wound Infection by Improving Antibiotic Efficacy and Host Innate Immune Activity. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	61
31	The Dynamic Structures of the Type IV Pilus. <i>Microbiology Spectrum</i> , 2019, 7, .	3.0	34
32	Multiple conformations facilitate PilT function in the type IV pilus. <i>Nature Communications</i> , 2019, 10, 5198.	12.8	16
33	The Dynamic Structures of the Type IV Pilus. , 2019, , 113-128.		2
34	Synthesis of defined mono-de-N-acetylated 2-(1 \rightarrow 6)-N-acetyl-d-glucosamine oligosaccharides to characterize PgaB hydrolase activity. <i>Organic and Biomolecular Chemistry</i> , 2019, 17, 9456-9466.	2.8	11
35	Molecular Basis for the Attachment of S-Layer Proteins to the Cell Wall of <i>Bacillus anthracis</i> . <i>Biochemistry</i> , 2018, 57, 1949-1953.	2.5	21
36	Hoisted by their own petard: do microbial enzymes hold the solution to treating and preventing biofilm infections?. <i>Future Microbiology</i> , 2018, 13, 395-398.	2.0	1

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37	Non-eluting, surface-bound enzymes disrupt surface attachment of bacteria by continuous biofilm polysaccharide degradation. <i>Biomaterials</i> , 2018, 167, 168-176.	11.4	41
38	PatB1 is an O-acetyltransferase that decorates secondary cell wall polysaccharides. <i>Nature Chemical Biology</i> , 2018, 14, 79-85.	8.0	37
39	Deacetylated microbial biofilm exopolysaccharides: It pays to be positive. <i>PLoS Pathogens</i> , 2018, 14, e1007411.	4.7	32
40	Gram-negative synthase-dependent exopolysaccharide biosynthetic machines. <i>Current Opinion in Structural Biology</i> , 2018, 53, 32-44.	5.7	53
41	PgaB orthologues contain a glycoside hydrolase domain that cleaves deacetylated poly- β -(1,6)-N-acetylglucosamine and can disrupt bacterial biofilms. <i>PLoS Pathogens</i> , 2018, 14, e1006998.	4.7	59
42	Oligomeric lipoprotein PelC guides Pel polysaccharide export across the outer membrane of <i>Pseudomonas aeruginosa</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 2892-2897.	7.1	31
43	The Type IVa Pilus Machinery Is Recruited to Sites of Future Cell Division. <i>MBio</i> , 2017, 8, .	4.1	35
44	The molecular mechanism of the type IVa pilus motors. <i>Nature Communications</i> , 2017, 8, 15091.	12.8	108
45	Microbial glycoside hydrolases as antibiofilm agents with cross-kingdom activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7124-7129.	7.1	88
46	Cyclic AMP-Independent Control of Twitching Motility in <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2017, 199, .	2.2	28
47	<i>Pseudomonas aeruginosa</i> Alginate Overproduction Promotes Coexistence with <i>Staphylococcus aureus</i> in a Model of Cystic Fibrosis Respiratory Infection. <i>MBio</i> , 2017, 8, .	4.1	124
48	PelA and PelB proteins form a modification and secretion complex essential for Pel polysaccharide-dependent biofilm formation in <i>Pseudomonas aeruginosa</i> . <i>Journal of Biological Chemistry</i> , 2017, 292, 19411-19422.	3.4	47
49	Chemical synthesis of guanosine diphosphate mannuronic acid (GDP-ManA) and its C-4-O-methyl and C-4-deoxy congeners. <i>Carbohydrate Research</i> , 2017, 450, 12-18.	2.3	11
50	In vitro characterization of the antivirulence target of Gram-positive pathogens, peptidoglycan O-acetyltransferase A (OatA). <i>PLoS Pathogens</i> , 2017, 13, e1006667.	4.7	35
51	Biofilm Exopolysaccharides of Pathogenic Fungi: Lessons from Bacteria. <i>Journal of Biological Chemistry</i> , 2016, 291, 12529-12537.	3.4	105
52	PilN Binding Modulates the Structure and Binding Partners of the <i>Pseudomonas aeruginosa</i> Type IVa Pilus Protein PilM. <i>Journal of Biological Chemistry</i> , 2016, 291, 11003-11015.	3.4	53
53	Structure of the <i>Pseudomonas aeruginosa</i> Type IVa Pilus Secretin at 7.4 Å. <i>Structure</i> , 2016, 24, 1778-1787.	3.3	47
54	The Conserved Tetratricopeptide Repeat-Containing C-Terminal Domain of <i>Pseudomonas aeruginosa</i> FimV Is Required for Its Cyclic AMP-Dependent and -Independent Functions. <i>Journal of Bacteriology</i> , 2016, 198, 2263-2274.	2.2	23

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55	Type IV Pilus Alignment Subcomplex Proteins PilN and PilO Form Homo- and Heterodimers in Vivo. <i>Journal of Biological Chemistry</i> , 2016, 291, 19923-19938.	3.4	28
56	Adhesive Bacterial Exopolysaccharides. , 2016, , 1-24.		1
57	Exopolysaccharide biosynthetic glycoside hydrolases can be utilized to disrupt and prevent <i>Pseudomonas aeruginosa</i> biofilms. <i>Science Advances</i> , 2016, 2, e1501632.	10.3	201
58	Deacetylation of Fungal Exopolysaccharide Mediates Adhesion and Biofilm Formation. <i>MBio</i> , 2016, 7, e00252-16.	4.1	91
59	Enzymatic modifications of exopolysaccharides enhance bacterial persistence. <i>Frontiers in Microbiology</i> , 2015, 6, 471.	3.5	100
60	Novel Role for PilNO in Type IV Pilus Retraction Revealed by Alignment Subcomplex Mutations. <i>Journal of Bacteriology</i> , 2015, 197, 2229-2238.	2.2	45
61	Dimeric c-di-GMP Is Required for Post-translational Regulation of Alginate Production in <i>Pseudomonas aeruginosa</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 12451-12462.	3.4	75
62	Sph3 Is a Glycoside Hydrolase Required for the Biosynthesis of Galactosaminogalactan in <i>Aspergillus fumigatus</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 27438-27450.	3.4	77
63	Identification of Poly-N-acetylglucosamine as a Major Polysaccharide Component of the <i>Bacillus subtilis</i> Biofilm Matrix. <i>Journal of Biological Chemistry</i> , 2015, 290, 19261-19272.	3.4	118
64	Biogenesis of <i>Pseudomonas aeruginosa</i> type IV pili and regulation of their function. <i>Environmental Microbiology</i> , 2015, 17, 4148-4163.	3.8	88
65	Direct Staudinger Phosphonite Reaction Provides Methylphosphonamidates as Inhibitors of CE4 Deacetylases. <i>ChemBioChem</i> , 2015, 16, 1350-1356.	2.6	11
66	Precision-engineering the <i>Pseudomonas aeruginosa</i> genome with two-step allelic exchange. <i>Nature Protocols</i> , 2015, 10, 1820-1841.	12.0	381
67	Characterization of the <i>Pseudomonas aeruginosa</i> Glycoside Hydrolase PslG Reveals That Its Levels Are Critical for Psl Polysaccharide Biosynthesis and Biofilm Formation. <i>Journal of Biological Chemistry</i> , 2015, 290, 28374-28387.	3.4	68
68	Pel is a cationic exopolysaccharide that cross-links extracellular DNA in the <i>Pseudomonas aeruginosa</i> biofilm matrix. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11353-11358.	7.1	485
69	The Protein BpsB Is a Poly- β -1,6-N-acetyl-d-glucosamine Deacetylase Required for Biofilm Formation in <i>Bordetella bronchiseptica</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 22827-22840.	3.4	31
70	<i>P. aeruginosa</i> SGNH Hydrolase-Like Proteins AlgJ and AlgX Have Similar Topology but Separate and Distinct Roles in Alginate Acetylation. <i>PLoS Pathogens</i> , 2014, 10, e1004334.	4.7	54
71	Structural Basis for the De-N-acetylation of Poly- β -1,6-N-acetyl-d-glucosamine in Gram-positive Bacteria. <i>Journal of Biological Chemistry</i> , 2014, 289, 35907-35917.	3.4	24
72	A conformational landscape for alginate secretion across the outer membrane of <i>Pseudomonas aeruginosa</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2054-2068.	2.5	46

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73	Catalytic Mechanism and Mode of Action of the Periplasmic Alginate Epimerase AlgG. <i>Journal of Biological Chemistry</i> , 2014, 289, 6006-6019.	3.4	39
74	Modification and periplasmic translocation of the biofilm exopolysaccharide poly- β -1,6- <i>N</i> -acetyl- <i>D</i> -glucosamine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11013-11018.	7.1	48
75	Structural and Functional Characterization of <i>Pseudomonas aeruginosa</i> AlgX. <i>Journal of Biological Chemistry</i> , 2013, 288, 22299-22314.	3.4	48
76	Functional Mapping of PilF and PilQ in the <i>Pseudomonas aeruginosa</i> Type IV Pilus System. <i>Biochemistry</i> , 2013, 52, 2914-2923.	2.5	42
77	PilMNOPQ from the <i>Pseudomonas aeruginosa</i> Type IV Pilus System Form a Transenvelope Protein Interaction Network That Interacts with PilA. <i>Journal of Bacteriology</i> , 2013, 195, 2126-2135.	2.2	113
78	Functional Characterization of <i>Staphylococcus epidermidis</i> IcaB, a De- <i>N</i> -acetylase Important for Biofilm Formation. <i>Biochemistry</i> , 2013, 52, 5463-5471.	2.5	32
79	The Platform Protein Is Essential for Type IV Pilus Biogenesis. <i>Journal of Biological Chemistry</i> , 2013, 288, 9721-9728.	3.4	103
80	Structural Insights into the Regulation of Foreign Genes in <i>Salmonella</i> by the Hha/H-NS Complex. <i>Journal of Biological Chemistry</i> , 2013, 288, 13356-13369.	3.4	61
81	PelA Deacetylase Activity Is Required for Pel Polysaccharide Synthesis in <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2013, 195, 2329-2339.	2.2	90
82	Structure of the Cytoplasmic Region of PelD, a Degenerate Diguanylate Cyclase Receptor That Regulates Exopolysaccharide Production in <i>Pseudomonas aeruginosa</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 23582-23593.	3.4	101
83	The Structure- and Metal-dependent Activity of <i>Escherichia coli</i> PgaB Provides Insight into the Partial De- <i>N</i> -acetylation of Poly- β -1,6- <i>N</i> -acetyl- <i>D</i> -glucosamine. <i>Journal of Biological Chemistry</i> , 2012, 287, 31126-31137.	3.4	65
84	Synthesis and evaluation of inhibitors of <i>E. coli</i> PgaB, a polysaccharide de- <i>N</i> -acetylase involved in biofilm formation. <i>Organic and Biomolecular Chemistry</i> , 2012, 10, 7103.	2.8	22
85	Expression, purification, crystallization and preliminary X-ray analysis of <i>Pseudomonas aeruginosa</i> PelD. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 181-184.	0.7	11
86	Decoding the roles of pilotins and accessory proteins in secretin escort services. <i>FEMS Microbiology Letters</i> , 2012, 328, 1-12.	1.8	60
87	Modular Evolution and the Origins of Symmetry: Reconstruction of a Three-Fold Symmetric Globular Protein. <i>Structure</i> , 2012, 20, 161-171.	3.3	97
88	Expression, purification, crystallization and preliminary X-ray analysis of <i>Pseudomonas aeruginosa</i> AlgL. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 584-587.	0.7	11
89	Combining <i>in situ</i> proteolysis and mass spectrometry to crystallize <i>Escherichia coli</i> PgaB. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 842-845.	0.7	14
90	The Pel and Psl polysaccharides provide <i>Pseudomonas aeruginosa</i> structural redundancy within the biofilm matrix. <i>Environmental Microbiology</i> , 2012, 14, 1913-1928.	3.8	447

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91	Biosynthesis of the <i>Pseudomonas aeruginosa</i> Extracellular Polysaccharides, Alginate, Pel, and Psl. <i>Frontiers in Microbiology</i> , 2011, 2, 167.	3.5	432
92	Mechanism of substrate specificity in 5- ϵ -methylthioadenosine/S-adenosylhomocysteine nucleosidases. <i>Journal of Structural Biology</i> , 2011, 173, 86-98.	2.8	21
93	The Peptidoglycan-Binding Protein FimV Promotes Assembly of the <i>Pseudomonas aeruginosa</i> Type IV Pilus Secretin. <i>Journal of Bacteriology</i> , 2011, 193, 540-550.	2.2	70
94	Structural basis for alginate secretion across the bacterial outer membrane. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13083-13088.	7.1	81
95	AlgK Is a TPR-Containing Protein and the Periplasmic Component of a Novel Exopolysaccharide Secretin. <i>Structure</i> , 2010, 18, 265-273.	3.3	98
96	Architecture of the type II secretion and type IV pilus machineries. <i>Future Microbiology</i> , 2010, 5, 1203-1218.	2.0	115
97	The Solution Structure of the C-Terminal Ig-like Domain of the Bacteriophage ϕ Tail Tube Protein. <i>Journal of Molecular Biology</i> , 2010, 403, 468-479.	4.2	46
98	The phage ϕ major tail protein structure reveals a common evolution for long-tailed phages and the type VI bacterial secretion system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4160-4165.	7.1	243
99	The X-Ray Crystal Structure of the Phage ϕ Tail Terminator Protein Reveals the Biologically Relevant Hexameric Ring Structure and Demonstrates a Conserved Mechanism of Tail Termination among Diverse Long-Tailed Phages. <i>Journal of Molecular Biology</i> , 2009, 389, 938-951.	4.2	55
100	PilM/N/O/P Proteins Form an Inner Membrane Complex That Affects the Stability of the <i>Pseudomonas aeruginosa</i> Type IV Pilus Secretin. <i>Journal of Molecular Biology</i> , 2009, 394, 128-142.	4.2	137
101	Modulation of activity by Arg407: structure of a fungal α -1,2-mannosidase in complex with a substrate analogue. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 227-236.	2.5	4
102	Structure of <i>Staphylococcus aureus</i> 5- ϵ -methylthioadenosine/S-adenosylhomocysteine nucleosidase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 343-350.	0.7	33
103	Molecular Determinants of Substrate Specificity in Plant 5- ϵ -Methylthioadenosine Nucleosidases. <i>Journal of Molecular Biology</i> , 2008, 378, 112-128.	4.2	16
104	Theoretical and experimental demonstration of the importance of specific nonnative interactions in protein folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 9999-10004.	7.1	120
105	PilF Is an Outer Membrane Lipoprotein Required for Multimerization and Localization of the <i>Pseudomonas aeruginosa</i> Type IV Pilus Secretin. <i>Journal of Bacteriology</i> , 2008, 190, 6961-6969.	2.2	97
106	Functional role of conserved residues in the characteristic secretion NTPase motifs of the <i>Pseudomonas aeruginosa</i> type IV pilus motor proteins PilB, PilT and PilU. <i>Microbiology (United Kingdom)</i> , 2008, 162, 1097-1107.	10.5	50
107	Structures of 5-Methylthioribose Kinase Reveal Substrate Specificity and Unusual Mode of Nucleotide Binding. <i>Journal of Biological Chemistry</i> , 2007, 282, 22195-22206.	3.4	15
108	Substrate and Product Complexes of <i>Escherichia coli</i> Adenylosuccinate Lyase Provide New Insights into the Enzymatic Mechanism. <i>Journal of Molecular Biology</i> , 2007, 370, 541-554.	4.2	44

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109	ADP-2Ho as a phasing tool for nucleotide-containing proteins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 493-499.	2.5	5
110	Distributed Replica Sampling. <i>Journal of Chemical Theory and Computation</i> , 2006, 2, 725-731.	5.3	26
111	Structure of <i>Escherichia coli</i> tryptophanase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 814-823.	2.5	32
112	Femtomolar Transition State Analogue Inhibitors of 5-Methylthioadenosine/S-Adenosylhomocysteine Nucleosidase from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 18265-18273.	3.4	122
113	Structural Rationale for the Affinity of Pico- and Femtomolar Transition State Analogues of <i>Escherichia coli</i> 5-Methylthioadenosine/S-Adenosylhomocysteine Nucleosidase. <i>Journal of Biological Chemistry</i> , 2005, 280, 18274-18282.	3.4	71
114	Mutational Analysis of a Nucleosidase Involved in Quorum-Sensing Autoinducer-2 Biosynthesis. <i>Biochemistry</i> , 2005, 44, 11049-11057.	2.5	29
115	Structural Snapshots of MTA/AdoHcy Nucleosidase Along the Reaction Coordinate Provide Insights into Enzyme and Nucleoside Flexibility During Catalysis. <i>Journal of Molecular Biology</i> , 2005, 352, 559-574.	4.2	33
116	Structure of Kre2p/Mnt1p. <i>Journal of Biological Chemistry</i> , 2004, 279, 17921-17931.	3.4	61
117	Disruption of a Salt Bridge Dramatically Accelerates Subunit Exchange in Duck Î2 Crystallin. <i>Journal of Biological Chemistry</i> , 2004, 279, 40972-40979.	3.4	11
118	Crystallization and preliminary X-ray analysis of 5-methylthioribose kinase from <i>Bacillus subtilis</i> and <i>Arabidopsis thaliana</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 116-119.	2.5	10
119	Catalytic Strategy of S-Adenosyl-L-homocysteine Hydrolase: A Transition-State Stabilization and the Avoidance of Abortive Reactions. <i>Biochemistry</i> , 2003, 42, 1900-1909.	2.5	74
120	Structure of <i>Escherichia coli</i> 5-Methylthioadenosine/ S-Adenosylhomocysteine Nucleosidase Inhibitor Complexes Provide Insight into the Conformational Changes Required for Substrate Binding and Catalysis. <i>Journal of Biological Chemistry</i> , 2003, 278, 8761-8770.	3.4	51
121	Structure of <i>Penicillium citrinum</i> Î±1,2-Mannosidase Reveals the Basis for Differences in Specificity of the Endoplasmic Reticulum and Golgi Class I Enzymes. <i>Journal of Biological Chemistry</i> , 2002, 277, 5620-5630.	3.4	45
122	Substrate Induced Conformational Changes in Argininosuccinate Synthetase. <i>Journal of Biological Chemistry</i> , 2002, 277, 13074-13081.	3.4	22
123	Mutational Analysis of Duck Î2 Crystallin and the Structure of an Inactive Mutant with Bound Substrate Provide Insight into the Enzymatic Mechanism of Argininosuccinate Lyase. <i>Journal of Biological Chemistry</i> , 2002, 277, 4166-4175.	3.4	33
124	S-SAD, Se-SAD and S/Se-SIRAS using Cu K α radiation: why wait for synchrotron time?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 2096-2101.	2.5	14
125	Three-Dimensional Structure of the Argininosuccinate Lyase Frequently Complementing Allele Q286R. <i>Biochemistry</i> , 2001, 40, 15570-15580.	2.5	36
126	Mechanisms for Intragenic Complementation at the Human Argininosuccinate Lyase Locus. <i>Biochemistry</i> , 2001, 40, 15581-15590.	2.5	22

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127	Expression, purification, crystallization and preliminary X-ray analysis of Escherichia coli 5-methylthioadenosine/S-adenosylhomocysteine nucleosidase. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 150-152.	2.5	24
128	Optimizing DREAR and SnB parameters for determining Se-atom substructures. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 604-617.	2.5	16
129	Structure and Function of S-Adenosylhomocysteine Hydrolase. Cell Biochemistry and Biophysics, 2000, 33, 101-125.	1.8	148
130	Structural Basis for Catalysis and Inhibition of N-Glycan Processing Class I α 1,2-Mannosidases. Journal of Biological Chemistry, 2000, 275, 41287-41298.	3.4	141
131	Purification, crystallization and preliminary X-ray crystallographic analysis of recombinant murine Golgi mannosidase IA, a class I α 1-mannosidase involved in Asn-linked oligosaccharide maturation. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 571-573.	2.5	4
132	Expression, purification, crystallization and preliminary X-ray analysis of Escherichia coli argininosuccinate synthetase. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 2028-2030.	2.5	6
133	Domain exchange experiments in duck α crystallins: Functional and evolutionary implications. Protein Science, 1999, 8, 529-537.	7.6	5
134	Structure determination of selenomethionyl S-adenosylhomocysteine hydrolase using data at a single wavelength. Nature Structural Biology, 1998, 5, 369-376.	9.7	111
135	Intragenic Complementation at the Human Argininosuccinate Lyase Locus. Journal of Biological Chemistry, 1997, 272, 6777-6783.	3.4	22
136	Crystallization and preliminary X-ray analysis of aldehyde dehydrogenase from <i>Vibrio harveyi</i> . Protein Science, 1996, 5, 2130-2132.	7.6	4
137	Four new adenosine deaminase mutations, altering a zinc-binding histidine, two conserved alanines, and a splice site. Human Mutation, 1995, 5, 243-250.	2.5	18
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