

Debra Dunaway-Mariano

List of Publications by Year in descending order

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times ranked

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#	ARTICLE	IF	CITATIONS
1	Evolutionary Genomics of the HAD Superfamily: Understanding the Structural Adaptations and Catalytic Diversity in a Superfamily of Phosphoesterases and Allied Enzymes. <i>Journal of Molecular Biology</i> , 2006, 361, 1003-1034.	2.0	376
2	The Pentacovalent Phosphorus Intermediate of a Phosphoryl Transfer Reaction. <i>Science</i> , 2003, 299, 2067-2071.	6.0	306
3	Phosphoryl group transfer: evolution of a catalytic scaffold. <i>Trends in Biochemical Sciences</i> , 2004, 29, 495-503.	3.7	249
4	Ancestry of the 4-chlorobenzoate dehalogenase: analysis of amino acid sequence identities among families of acyl:adenyl ligases, enoyl-CoA hydratases/isomerases, and acyl-CoA thioesterases. <i>Biochemistry</i> , 1992, 31, 5594-5604.	1.2	212
5	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
6	The Crystal Structure of <i>Bacillus cereus</i> Phosphonoacetaldehyde Hydrolase: An Insight into Catalysis of Phosphorus Bond Cleavage and Catalytic Diversification within the HAD Enzyme Superfamily. <i>Biochemistry</i> , 2000, 39, 10385-10396.	1.2	136
7	Enzyme Promiscuity: Engine of Evolutionary Innovation. <i>Journal of Biological Chemistry</i> , 2014, 289, 30229-30236.	1.6	125
8	Acyl-Adenylate Motif of the Acyl-Adenylate/Thioester-Forming Enzyme Superfamily: A Site-Directed Mutagenesis Study with the <i>Pseudomonas</i> sp. Strain CBS3 4-Chlorobenzoate:Coenzyme A Ligase. <i>Biochemistry</i> , 1997, 36, 15650-15659.	1.2	120
9	Panoramic view of a superfamily of phosphatases through substrate profiling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1974-83.	3.3	118
10	Caught in the Act: The Structure of Phosphorylated β^2 -Phosphoglucomutase from <i>Lactococcus lactis</i> . <i>Biochemistry</i> , 2002, 41, 8351-8359.	1.2	107
11	Oxaloacetate Hydrolase, the C-C Bond Lyase of Oxalate Secreting Fungi. <i>Journal of Biological Chemistry</i> , 2007, 282, 9581-9590.	1.6	102
12	The Three-dimensional Structure of 4-Hydroxybenzoyl-CoA Thioesterase from <i>Pseudomonas</i> sp. Strain CBS-3. <i>Journal of Biological Chemistry</i> , 1998, 273, 33572-33579.	1.6	101
13	Markers of fitness in a successful enzyme superfamily. <i>Current Opinion in Structural Biology</i> , 2009, 19, 658-665.	2.6	94
14	Analysis of the Substrate Specificity Loop of the HAD Superfamily Cap Domain. <i>Biochemistry</i> , 2004, 43, 2812-2820.	1.2	83
15	Interchange of Catalytic Activity within the 2-Enoyl-Coenzyme A Hydratase/Isomerase Superfamily Based on a Common Active Site Template. <i>Biochemistry</i> , 1999, 38, 7638-7652.	1.2	78
16	HAD Superfamily Phosphotransferase Substrate Diversification: Structure and Function Analysis of HAD Subclass IIB Sugar Phosphatase BT4131. <i>Biochemistry</i> , 2005, 44, 8684-8696.	1.2	75
17	Insights into the Mechanism of Catalysis by the P-C Bond-Cleaving Enzyme Phosphonoacetaldehyde Hydrolase Derived from Gene Sequence Analysis and Mutagenesis. <i>Biochemistry</i> , 1998, 37, 9305-9315.	1.2	71
18	On the origins and functions of the enzymes of the 4-chlorobenzoate to 4-hydroxybenzoate converting pathway. <i>Biodegradation</i> , 1994, 5, 259-276.	1.5	68

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19	The X-ray Crystal Structures of Human $\hat{\iota}$ -Phosphomannomutase 1 Reveal the Structural Basis of Congenital Disorder of Glycosylation Type 1a. <i>Journal of Biological Chemistry</i> , 2006, 281, 14918-14926.	1.6	66
20	Divergence of Function in the Hot Dog Fold Enzyme Superfamily: The Bacterial Thioesterase YciA. <i>Biochemistry</i> , 2008, 47, 2789-2796.	1.2	62
21	Structure, Function, and Mechanism of the Phenylacetate Pathway Hot Dog-fold Thioesterase Paal. <i>Journal of Biological Chemistry</i> , 2006, 281, 11028-11038.	1.6	60
22	The Structure of 4-Hydroxybenzoyl-CoA Thioesterase from <i>Arthrobacter</i> sp. strain SU. <i>Journal of Biological Chemistry</i> , 2003, 278, 43709-43716.	1.6	59
23	Crystal Structures Representing the Michaelis Complex and the Thiuronium Reaction Intermediate of <i>Pseudomonas aeruginosa</i> Arginine Deiminase. <i>Journal of Biological Chemistry</i> , 2005, 280, 34080-34087.	1.6	58
24	Kinetic Analysis of <i>Pseudomonas aeruginosa</i> Arginine Deiminase Mutants and Alternate Substrates Provides Insight into Structural Determinants of Function. <i>Biochemistry</i> , 2006, 45, 1162-1172.	1.2	58
25	Structure and Activity Analyses of <i>Escherichia coli</i> K-12 NagD Provide Insight into the Evolution of Biochemical Function in the Haloalkanoic Acid Dehalogenase Superfamily. <i>Biochemistry</i> , 2006, 45, 1183-1193.	1.2	57
26	Arginine Deiminase Uses an Active-Site Cysteine in Nucleophilic Catalysis of Arginine Hydrolysis. <i>Journal of the American Chemical Society</i> , 2004, 126, 5374-5375.	6.6	56
27	The catalytic scaffold of the haloalkanoic acid dehalogenase enzyme superfamily acts as a mold for the trigonal bipyramidal transition state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 5687-5692.	3.3	56
28	The Mechanisms of Human Hotdog-fold Thioesterase 2 (hTHEM2) Substrate Recognition and Catalysis Illuminated by a Structure and Function Based Analysis. <i>Biochemistry</i> , 2009, 48, 1293-1304.	1.2	54
29	X-ray Crystallographic Analyses of Inhibitor and Substrate Complexes of Wild-type and Mutant 4-Hydroxybenzoyl-CoA Thioesterase. <i>Journal of Biological Chemistry</i> , 2002, 277, 27468-27476.	1.6	53
30	Catalytic Cycling in $\hat{\iota}$ -Phosphoglucomutase: A Kinetic and Structural Analysis. <i>Biochemistry</i> , 2005, 44, 9404-9416.	1.2	51
31	Investigation of the <i>Bacillus cereus</i> phosphonoacetaldehyde hydrolase. Evidence for a Schiff base mechanism and sequence analysis of an active-site peptide containing the catalytic lysine residue. <i>Biochemistry</i> , 1988, 27, 2229-2234.	1.2	48
32	X-ray Crystal Structure of the Hypothetical Phosphotyrosine Phosphatase MDP-1 of the Haloacid Dehalogenase Superfamily. <i>Biochemistry</i> , 2004, 43, 12770-12779.	1.2	47
33	Evidence for electrophilic catalysis in the 4-chlorobenzoyl-CoA dehalogenase reaction: UV, Raman, and ^{13}C -NMR spectral studies of dehalogenase complexes of benzoyl-CoA adducts. <i>Biochemistry</i> , 1995, 34, 13881-13888.	1.2	45
34	Raman Study of the Polarizing Forces Promoting Catalysis in 4-Chlorobenzoate-CoA Dehalogenase. <i>Biochemistry</i> , 1997, 36, 10192-10199.	1.2	45
35	The Phosphonopyruvate Decarboxylase from <i>Bacteroides fragilis</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 41302-41308.	1.6	45
36	Characterization, Kinetics, and Crystal Structures of Fructose-1,6-bisphosphate Aldolase from the Human Parasite, <i>Giardia lamblia</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 4859-4867.	1.6	45

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37	Investigations of the partial reactions catalyzed by pyruvate phosphate dikinase. <i>Biochemistry</i> , 1988, 27, 625-633.	1.2	40
38	Role of Active Site Binding Interactions in 4-Chlorobenzoyl-Coenzyme A Dehalogenase Catalysis. <i>Biochemistry</i> , 2001, 40, 15684-15692.	1.2	38
39	Identification of Active Site Residues Essential to 4-Chlorobenzoyl-Coenzyme A Dehalogenase Catalysis by Chemical Modification and Site Directed Mutagenesis. <i>Biochemistry</i> , 1996, 35, 10879-10885.	1.2	37
40	Inactivation of Microbial Arginine Deiminases by <i>l</i> -Canavanine. <i>Journal of the American Chemical Society</i> , 2008, 130, 1918-1931.	6.6	37
41	The YbgC protein encoded by the ybgC gene of the tol-pal gene cluster of <i>Haemophilus influenzae</i> catalyzes acyl-coenzyme A thioester hydrolysis. <i>FEBS Letters</i> , 2002, 516, 161-163.	1.3	36
42	Divergence of Structure and Function in the Haloacid Dehalogenase Enzyme Superfamily: <i>Bacteroides thetaiotaomicron</i> BT2127 Is an Inorganic Pyrophosphatase. <i>Biochemistry</i> , 2011, 50, 8937-8949.	1.2	36
43	Stereochemical probe for the mechanism of phosphorus-carbon bond cleavage catalyzed by the <i>Bacillus cereus</i> phosphonoacetaldehyde hydrolase. <i>Journal of the American Chemical Society</i> , 1992, 114, 7346-7354.	6.6	35
44	Helix swapping between two β barrels: crystal structure of phosphoenolpyruvate mutase with bound Mg^{2+} -oxalate. <i>Structure</i> , 1999, 7, 539-548.	1.6	35
45	Crystal Structures of 2-Methylisocitrate Lyase in Complex with Product and with Isocitrate Inhibitor Provide Insight into Lyase Substrate Specificity, Catalysis and Evolution. <i>Biochemistry</i> , 2005, 44, 2949-2962.	1.2	35
46	Analysis of the Structural Determinants Underlying Discrimination between Substrate and Solvent in β -Phosphoglucomutase Catalysis. <i>Biochemistry</i> , 2009, 48, 1984-1995.	1.2	35
47	Structural Determinants of Substrate Recognition in the HAD Superfamily Member d-glycero-d-manno-Heptose-1,7-bisphosphate Phosphatase (GmhB). <i>Biochemistry</i> , 2010, 49, 1082-1092.	1.2	35
48	Investigation of Substrate Activation by 4-Chlorobenzoyl-Coenzyme A Dehalogenase. <i>Biochemistry</i> , 1997, 36, 1349-1361.	1.2	34
49	X-ray Crystallographic and Site-directed Mutagenesis Analysis of the Mechanism of Schiff-base Formation in Phosphonoacetaldehyde Hydrolase Catalysis. <i>Journal of Biological Chemistry</i> , 2004, 279, 9353-9361.	1.6	34
50	Response to Comment on "The Pentacovalent Phosphorus Intermediate of a Phosphoryl Transfer Reaction". <i>Science</i> , 2003, 301, 1184d-1184.	6.0	33
51	Characterization of the 4-Hydroxybenzoyl-Coenzyme A Thioesterase from <i>Arthrobacter</i> sp. Strain SU. <i>Applied and Environmental Microbiology</i> , 2003, 69, 2707-2711.	1.4	33
52	Investigation of Metal Ion Binding in Phosphonoacetaldehyde Hydrolase Identifies Sequence Markers for Metal-Activated Enzymes of the HAD Enzyme Superfamily. <i>Biochemistry</i> , 2004, 43, 4990-4997.	1.2	33
53	Diversification of function in the haloacid dehalogenase enzyme superfamily: The role of the cap domain in hydrolytic phosphorus-carbon bond cleavage. <i>Bioorganic Chemistry</i> , 2006, 34, 394-409.	2.0	32
54	Structure of YciA from <i>Haemophilus influenzae</i> (HI0827), a Hexameric Broad Specificity Acyl-Coenzyme A Thioesterase. <i>Biochemistry</i> , 2008, 47, 2797-2805.	1.2	32

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55	Investigation of the substrate binding and catalytic groups of the P _i -C bond cleaving enzyme, phosphonoacetaldehyde hydrolase. <i>Archives of Biochemistry and Biophysics</i> , 1992, 296, 144-151.	1.4	31
56	Structure and Kinetics of Phosphonopyruvate Hydrolase from <i>Vorivora</i> sp. Pal2: A New Insight into the Divergence of Catalysis within the PEP Mutase/Isocitrate Lyase Superfamily. <i>Biochemistry</i> , 2006, 45, 11491-11504.	1.2	31
57	Conformational Cycling in β -Phosphoglucosyltransferase Catalysis: Reorientation of the β -D-Glucose 1,6-(Bis)phosphate Intermediate. <i>Biochemistry</i> , 2006, 45, 7818-7824.	1.2	31
58	Crystal structure of human thioesterase superfamily member 2. <i>Biochemical and Biophysical Research Communications</i> , 2006, 349, 172-177.	1.0	30
59	Mechanisms of catalysis and inhibition operative in the arginine deiminase from the human pathogen <i>Giardia lamblia</i> . <i>Bioorganic Chemistry</i> , 2009, 37, 149-161.	2.0	30
60	Structure of the Trehalose-6-phosphate Phosphatase from <i>Brugia malayi</i> Reveals Key Design Principles for Anthelmintic Drugs. <i>PLoS Pathogens</i> , 2014, 10, e1004245.	2.1	30
61	Insight into the Mechanism of Phosphoenolpyruvate Mutase Catalysis Derived from Site-Directed Mutagenesis Studies of Active Site Residues. <i>Biochemistry</i> , 1999, 38, 14165-14173.	1.2	28
62	Kinetic Evidence for a Substrate-Induced Fit in Phosphonoacetaldehyde Hydrolase Catalysis. <i>Biochemistry</i> , 2002, 41, 13370-13377.	1.2	28
63	Kinetic, Raman, NMR, and Site-Directed Mutagenesis Studies of the <i>Pseudomonas</i> Sp. Strain CBS3 4-Hydroxybenzoyl-CoA Thioesterase Active Site. <i>Biochemistry</i> , 2002, 41, 11152-11160.	1.2	28
64	Diversity of Function in the Isocitrate Lyase Enzyme Superfamily: The <i>Dianthus caryophyllus</i> Petal Death Protein Cleaves β -Keto and β -Hydroxycarboxylic Acids. <i>Biochemistry</i> , 2005, 44, 16365-16376.	1.2	28
65	Structure-Function Analysis of 2-Keto-3-deoxy-D-glycero-D-galactononate-9-phosphate Phosphatase Defines Specificity Elements in Type C0 Haloalkanoate Dehalogenase Family Members. <i>Journal of Biological Chemistry</i> , 2009, 284, 1224-1233.	1.6	27
66	Modulating Electron Density in the Bound Product, 4-Hydroxybenzoyl-CoA, by Mutations in 4-Chlorobenzoyl-CoA Dehalogenase Near the 4-Hydroxy Group. <i>Biochemistry</i> , 1999, 38, 4198-4206.	1.2	26
67	Consequences of domain insertion on sequence-structure divergence in a superfold. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3381-7.	3.3	25
68	Phosphoenolpyruvate Mutase Catalysis of Phosphoryl Transfer in Phosphoenolpyruvate: Kinetics and Mechanism of Phosphorus-Carbon Bond Formation. <i>Biochemistry</i> , 1996, 35, 4628-4635.	1.2	24
69	The Electrostatic Driving Force for Nucleophilic Catalysis in L-Arginine Deiminase: A Combined Experimental and Theoretical Study. <i>Biochemistry</i> , 2008, 47, 4721-4732.	1.2	22
70	In Vitro Kinetic Analysis of Substrate Specificity in Enterobactin Biosynthetic Lower Pathway Enzymes Provides Insight into the Biochemical Function of the Hot Dog-Fold Thioesterase EntH. <i>Biochemistry</i> , 2009, 48, 511-513.	1.2	22
71	The Catalytic Mechanism of the Hotdog-fold Enzyme Superfamily 4-Hydroxybenzoyl-CoA Thioesterase from <i>Arthrobacter</i> sp. Strain SU. <i>Biochemistry</i> , 2012, 51, 7000-7016.	1.2	22
72	Location of the Phosphate Binding Site within <i>Clostridium symbiosum</i> Pyruvate Phosphate Dikinase. <i>Biochemistry</i> , 1998, 37, 13463-13474.	1.2	21

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73	Structure and Function of PA4872 from <i>Pseudomonas aeruginosa</i> , a Novel Class of Oxaloacetate Decarboxylase from the PEP Mutase/Isocitrate Lyase Superfamily. <i>Biochemistry</i> , 2008, 47, 167-182.	1.2	20
74	Structural Basis for the Divergence of Substrate Specificity and Biological Function within HAD Phosphatases in Lipopolysaccharide and Sialic Acid Biosynthesis. <i>Biochemistry</i> , 2013, 52, 5372-5386.	1.2	20
75	The BH1999 Protein of <i>Bacillus halodurans</i> C-125 Is Gentsyl-Coenzyme A Thioesterase. <i>Journal of Bacteriology</i> , 2004, 186, 393-399.	1.0	19
76	The Strength of Dehalogenase's Substrate Hydrogen Bonding Correlates with the Rate of Meisenheimer Intermediate Formation. <i>Biochemistry</i> , 2003, 42, 9482-9490.	1.2	18
77	The Akt C-Terminal Modulator Protein Is an Acyl-CoA Thioesterase of the Hotdog-Fold Family. <i>Biochemistry</i> , 2009, 48, 5507-5509.	1.2	17
78	Catalytic scaffolds for phosphoryl group transfer. <i>Current Opinion in Structural Biology</i> , 2016, 41, 172-179.	2.6	17
79	Human Symbiont <i>Bacteroides thetaiotaomicron</i> Synthesizes 2-Keto-3-Deoxy-D-Glycero-D-Galacto-Nononic Acid (KDN). <i>Chemistry and Biology</i> , 2008, 15, 893-897.	6.2	16
80	Rational design of reversible inhibitors for trehalose 6-phosphate phosphatases. <i>European Journal of Medicinal Chemistry</i> , 2017, 128, 274-286.	2.6	16
81	Crystal Structure of the Petal Death Protein from Carnation Flower. <i>Biochemistry</i> , 2005, 44, 16377-16384.	1.2	14
82	Enzyme Function Discovery. <i>Structure</i> , 2008, 16, 1599-1600.	1.6	14
83	Divergence of Substrate Specificity and Function in the <i>Escherichia coli</i> Hotdog-fold Thioesterase Paralogs Ydil and YdbB. <i>Biochemistry</i> , 2014, 53, 4775-4787.	1.2	14
84	Structure and Function of 2,3-Dimethylmalate Lyase, a PEP Mutase/Isocitrate Lyase Superfamily Member. <i>Journal of Molecular Biology</i> , 2009, 386, 486-503.	2.0	13
85	Raman difference spectroscopic studies of dithiobenzoyl substrate and product analogs binding to the enzyme dehalogenase: π -electron polarization is prevented by the C=O to C=S substitution. <i>Journal of Raman Spectroscopy</i> , 2000, 31, 365-371.	1.2	12
86	Crystallization and preliminary X-ray diffraction studies of β -phosphoglucomutase from <i>Lactococcus lactus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 324-326.	2.5	12
87	Structure and Catalysis in the <i>Escherichia coli</i> Hotdog-fold Thioesterase Paralogs Ydil and YdbB. <i>Biochemistry</i> , 2014, 53, 4788-4805.	1.2	12
88	Rational design of first generation inhibitors for trehalose 6-phosphate phosphatases. <i>Tetrahedron</i> , 2017, 73, 1324-1330.	1.0	12
89	Investigation of the role of the substrate metal ion in the yeast inorganic pyrophosphatase reaction. <i>FEBS Letters</i> , 1984, 165, 251-253.	1.3	11
90	X-ray structure and characterization of carbamate kinase from the human parasite <i>Giardia lamblia</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 386-390.	0.7	11

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91	The X-ray crystallographic structure and specificity profile of HAD superfamily phosphohydrolase BT1666: Comparison of paralogous functions in <i>B. thetaiotaomicron</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 3099-3107.	1.5	11
92	Investigation of the Catalytic Mechanism of the Hotdog-Fold Enzyme Superfamily <i>Pseudomonas</i> sp. Strain CBS3 4-Hydroxybenzoyl-CoA Thioesterase. <i>Biochemistry</i> , 2012, 51, 786-794.	1.2	11
93	Co-evolution of HAD phosphatase and hotdog-fold thioesterase domain function in the menaquinone pathway fusion proteins BF1314 and PG1653. <i>FEBS Letters</i> , 2013, 587, 2851-2859.	1.3	9
94	A thioester substrate binds to the enzyme <i>Arthrobacter</i> thioesterase in two ionization states: evidence from Raman difference spectroscopy. <i>Journal of Raman Spectroscopy</i> , 2012, 43, 65-71.	1.2	8
95	Mechanism of Substrate Recognition and Catalysis of the Haloalkanoic Acid Dehalogenase Family Member \pm -Phosphoglucomutase. <i>Biochemistry</i> , 2018, 57, 4504-4517.	1.2	8
96	Correlation of Structure and Function in the Human Hotdog-fold Enzyme hTHEM4. <i>Biochemistry</i> , 2012, 51, 6490-6492.	1.2	7
97	Structural Basis of the Molecular Switch between Phosphatase and Mutase Functions of Human Phosphomannomutase 1 under Ischemic Conditions. <i>Biochemistry</i> , 2018, 57, 3480-3492.	1.2	7
98	Enzymatic synthesis of radiolabeled phosphonoacetaldehyde. <i>Analytical Biochemistry</i> , 2003, 322, 233-237.	1.1	6
99	W. W. Mo-Cleland: A Catalytic Life. <i>Biochemistry</i> , 2013, 52, 9092-9096.	1.2	6
100	Investigation of the Role of the Domain Linkers in Separate Site Catalysis by <i>Clostridium symbiosum</i> Pyruvate Phosphate Dikinase. <i>Biochemistry</i> , 2001, 40, 13466-13473.	1.2	5
101	The X-ray crystallographic structure and activity analysis of a <i>Pseudomonas</i> specific subfamily of the HAD enzyme superfamily evidences a novel biochemical function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 197-207.	1.5	5
102	Neutron diffraction studies towards deciphering the protonation state of catalytic residues in the bacterial KDN9P phosphatase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1015-1019.	0.7	5
103	Structure-guided approach for detecting large domain inserts in protein sequences as illustrated using the haloacid dehalogenase superfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1896-1906.	1.5	3
104	Raman evidence for product binding to the enzyme W137F 4-chlorobenzoyl-CoA dehalogenase in two conformational states. <i>Journal of Raman Spectroscopy</i> , 2005, 36, 320-325.	1.2	2
105	Structural Analysis of Binding Determinants of <i>Salmonella typhimurium</i> Trehalose-6-phosphate Phosphatase Using Ground-State Complexes. <i>Biochemistry</i> , 2020, 59, 3247-3257.	1.2	2
106	Inhibition and Inactivation of Pyruvate Phosphate Dikinase with Cr(III) Complexes of Adenosine 5-Triphosphate and Inorganic Pyrophosphate. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 1986, 1, 113-125.	0.5	1
107	Catalytic Mechanism of the Hotdog-Fold Thioesterase PA1618 Revealed by X-ray Structure Determination of a Substrate-Bound Oxygen Ester Analogue Complex. <i>ChemBioChem</i> , 2017, 18, 1935-1943.	1.3	0
108	Ligand Binding and Conformational Change Coupling in the HAD Superfamily. <i>FASEB Journal</i> , 2013, 27, 998.8.	0.2	0

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109	The nature of sequence and structure divergence in the Haloalkanoate Dehalogenase SuperFamily (HADSF). FASEB Journal, 2013, 27, 797.2.	0.2	0
110	The structural basis of the secondary function of PMM1 in the presence of IMP. FASEB Journal, 2013, 27, 998.5.	0.2	0
111	Ultra High-throughput Screening Uncovers New Activities in Phosphatases of the Haloalkanoic Acid Dehalogenase Superfamily (HADSF). FASEB Journal, 2013, 27, 571.1.	0.2	0
112	Specificity and Promiscuity in Enzyme Superfamilies. FASEB Journal, 2015, 29, 237.1.	0.2	0