

Karen N Allen

List of Publications by Year in descending order

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128
papers

6,244
citations

66315

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73
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all docs

183
docs citations

183
times ranked

6420
citing authors

#	ARTICLE	IF	CITATIONS
1	Construction and Analysis of Two Genome-Scale Deletion Libraries for <i>Bacillus subtilis</i> . <i>Cell Systems</i> , 2017, 4, 291-305.e7.	2.9	457
2	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
3	The Pentacovalent Phosphorus Intermediate of a Phosphoryl Transfer Reaction. <i>Science</i> , 2003, 299, 2067-2071.	6.0	306
4	Phosphoryl group transfer: evolution of a catalytic scaffold. <i>Trends in Biochemical Sciences</i> , 2004, 29, 495-503.	3.7	249
5	An Experimental Approach to Mapping the Binding Surfaces of Crystalline Proteins. <i>The Journal of Physical Chemistry</i> , 1996, 100, 2605-2611.	2.9	179
6	The Enzyme Function Initiative. <i>Biochemistry</i> , 2011, 50, 9950-9962.	1.2	169
7	Structural Origin of the High Affinity of a Chemically Evolved Lanthanide-Binding Peptide. <i>Angewandte Chemie - International Edition</i> , 2004, 43, 3682-3685.	7.2	158
8	Double-Lanthanide-Binding Tags: Design, Photophysical Properties, and NMR Applications. <i>Journal of the American Chemical Society</i> , 2007, 129, 7106-7113.	6.6	142
9	The Crystal Structure of <i>Bacillus cereus</i> Phosphonoacetaldehyde Hydrolase: A 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
10	Engineering Encodable Lanthanide-Binding Tags into Loop Regions of Proteins. <i>Journal of the American Chemical Society</i> , 2011, 133, 808-819.	6.6	132
11	The 2.1 Å... Structure of <i>Torpedo californica</i> Creatine Kinase Complexed with the ADP-Mg ²⁺ -NO ₃ ⁻ Creatine Transition-State Analogue Complex. <i>Biochemistry</i> , 2002, 41, 13861-13867.	1.2	129
12	Enzyme Promiscuity: Engine of Evolutionary Innovation. <i>Journal of Biological Chemistry</i> , 2014, 289, 30229-30236.	1.6	125
13	X-ray Crystallographic Structures of D-Xylose Isomerase-Substrate Complexes Position the Substrate and Provide Evidence for Metal Movement during Catalysis. <i>Biochemistry</i> , 1994, 33, 5469-5480.	1.2	124
14	Structures of <i>Clostridium botulinum</i> Neurotoxin Serotype A Light Chain Complexed with Small-Molecule Inhibitors Highlight Active-Site Flexibility. <i>Chemistry and Biology</i> , 2007, 14, 533-542.	6.2	119
15	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
16	Lanthanide-tagged proteins: an illuminating partnership. <i>Current Opinion in Chemical Biology</i> , 2010, 14, 247-254.	2.8	110
17	Caught in the Act: The Structure of Phosphorylated ² -Phosphoglucomutase from <i>Lactococcus lactis</i> . <i>Biochemistry</i> , 2002, 41, 8351-8359.	1.2	107
18	Exploring the structural origins of cryptic sites on proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3416-E3425.	3.3	96

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19	Markers of fitness in a successful enzyme superfamily. <i>Current Opinion in Structural Biology</i> , 2009, 19, 658-665.	2.6	94
20	The origin of the electrostatic perturbation in acetoacetate decarboxylase. <i>Nature</i> , 2009, 459, 393-397.	13.7	86
21	Analysis of the Substrate Specificity Loop of the HAD Superfamily Cap Domain. <i>Biochemistry</i> , 2004, 43, 2812-2820.	1.2	83
22	Snapshots of Catalysis: the Structure of Fructose-1,6-(bis)phosphate Aldolase Covalently Bound to the Substrate Dihydroxyacetone Phosphate. <i>Biochemistry</i> , 2001, 40, 13868-13875.	1.2	79
23	Isotopic Exchange plus Substrate and Inhibition Kinetics of D-Xylose Isomerase Do Not Support a Proton-Transfer Mechanism. <i>Biochemistry</i> , 1994, 33, 1481-1487.	1.2	78
24	Double-Lanthanide-Binding Tags for Macromolecular Crystallographic Structure Determination. <i>Journal of the American Chemical Society</i> , 2007, 129, 7114-7120.	6.6	78
25	Role of the Divalent Metal Ion in Sugar Binding, Ring Opening, and Isomerization by D-Xylose Isomerase: Replacement of a Catalytic Metal by an Amino Acid. <i>Biochemistry</i> , 1994, 33, 1488-1494.	1.2	76
26	HAD Superfamily Phosphotransferase Substrate Diversification: A Structure and Function Analysis of HAD Subclass IIB Sugar Phosphatase BT4131. <i>Biochemistry</i> , 2005, 44, 8684-8696.	1.2	75
27	The X-ray Crystal Structures of Human α -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
28	Inhibition kinetics of acetylcholinesterase with fluoromethyl ketones. <i>Biochemistry</i> , 1989, 28, 8466-8473.	1.2	64
29	Design, Synthesis, and Characterization of a Potent Xylose Isomerase Inhibitor, D-Threono-hydroxamic Acid, and High-Resolution X-ray Crystallographic Structure of the Enzyme-Inhibitor Complex. <i>Biochemistry</i> , 1995, 34, 3742-3749.	1.2	63
30	Ligand deconstruction: Why some fragment binding positions are conserved and others are not. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2585-94.	3.3	61
31	The 2.1 Å... Structure of a Cysteine Protease with Proline Specificity from Ginger Rhizome, <i>Zingiber officinale</i> . <i>Biochemistry</i> , 1999, 38, 11624-11633.	1.2	59
32	Catalytic Features of the Botulinum Neurotoxin A Light Chain Revealed by High Resolution Structure of an Inhibitory Peptide Complex. <i>Biochemistry</i> , 2008, 47, 5736-5745.	1.2	59
33	Structure of a Fructose-1,6-bis(phosphate) Aldolase Liganded to Its Natural Substrate in a Cleavage-Defective Mutant at 2.3 Å. <i>Biochemistry</i> , 1999, 38, 12655-12664.	1.2	57
34	Chemical Confirmation of a Pentavalent Phosphorane in Complex with α -Phosphoglucomutase. <i>Journal of the American Chemical Society</i> , 2005, 127, 5298-5299.	6.6	57
35	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
36	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

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37	Structure of human brain fructose 1,6-(bis)phosphate aldolase: Linking isozyme structure with function. <i>Protein Science</i> , 2009, 13, 3077-3084.	3.1	54
38	Evaluation of adamantane hydroxamates as botulinum neurotoxin inhibitors: Synthesis, crystallography, modeling, kinetic and cellular based studies. <i>Bioorganic and Medicinal Chemistry</i> , 2013, 21, 1344-1348.	1.4	53
39	Catalytic Cycling in $\hat{1}^2$ -Phosphoglucomutase: A Kinetic and Structural Analysis. <i>Biochemistry</i> , 2005, 44, 9404-9416.	1.2	51
40	Quaternary Ammonium Oxidative Demethylation: X-ray Crystallographic, Resonance Raman, and UV-Visible Spectroscopic Analysis of a Rieske-Type Demethylase. <i>Journal of the American Chemical Society</i> , 2012, 134, 2823-2834.	6.6	48
41	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
42	Monotopic Membrane Proteins Join the Fold. <i>Trends in Biochemical Sciences</i> , 2019, 44, 7-20.	3.7	47
43	Encoded loop-lanthanide-binding tags for long-range distance measurements in proteins by NMR and EPR spectroscopy. <i>Journal of Biomolecular NMR</i> , 2015, 63, 275-282.	1.6	44
44	Membrane association of monotopic phosphoglycosyl transferase underpins function. <i>Nature Chemical Biology</i> , 2018, 14, 538-541.	3.9	39
45	Structure of the Thermolabile Mutant Aldolase B, A149P: Molecular Basis of Hereditary Fructose Intolerance. <i>Journal of Molecular Biology</i> , 2005, 347, 135-144.	2.0	38
46	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
47	Analysis of the Structural Determinants Underlying Discrimination between Substrate and Solvent in $\hat{1}^2$ -Phosphoglucomutase Catalysis. <i>Biochemistry</i> , 2009, 48, 1984-1995.	1.2	35
48	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
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	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
51	Design of a Heterospecific, Tetrameric, 21-Residue Mini-protein with Mixed $\hat{1}^{\pm}/\hat{1}^2$ Structure. <i>Structure</i> , 2005, 13, 225-234.	1.6	33
52	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
53	Divergence of Biochemical Function in the HAD Superfamily: d-glycero-d-manno-Heptose-1,7-bisphosphate Phosphatase (GmhB). <i>Biochemistry</i> , 2010, 49, 1072-1081.	1.2	32
54	Conformational Cycling in $\hat{1}^2$ -Phosphoglucomutase Catalysis: Reorientation of the $\hat{1}^2$ -d-Glucose 1,6-(Bis)phosphate Intermediate. <i>Biochemistry</i> , 2006, 45, 7818-7824.	1.2	31

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55	Chemical-modification rescue assessed by mass spectrometry demonstrates that $\hat{1}^3$ -thia-lysine yields the same activity as lysine in aldolase. <i>Protein Science</i> , 2009, 11, 1591-1599.	3.1	30
56	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
57	Conservation and Covariance in Small Bacterial Phosphoglycosyltransferases Identify the Functional Catalytic Core. <i>Biochemistry</i> , 2015, 54, 7326-7334.	1.2	30
58	Kinetic Evidence for a Substrate-Induced Fit in Phosphonoacetaldehyde Hydrolase Catalysis. <i>Biochemistry</i> , 2002, 41, 13370-13377.	1.2	28
59	Chirality Holds the Key for Potent Inhibition of the Botulinum Neurotoxin Serotype A Protease. <i>Organic Letters</i> , 2010, 12, 756-759.	2.4	28
60	X-ray Fluorescence Nanotomography of Single Bacteria with a Sub-15-nm Beam. <i>Scientific Reports</i> , 2018, 8, 13415.	1.6	28
61	Interaction Energetics and Druggability of the Protein-Protein Interaction between Kelch-like ECH-Associated Protein 1 (KEAP1) and Nuclear Factor Erythroid 2 Like 2 (Nrf2). <i>Biochemistry</i> , 2020, 59, 563-581.	1.2	28
62	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
63	Accounting for observed small angle X-ray scattering profile in the protein-protein docking server cluspro. <i>Journal of Computational Chemistry</i> , 2015, 36, 1568-1572.	1.5	27
64	Lanthanide-Binding Tags for 3D X-ray Imaging of Proteins in Cells at Nanoscale Resolution. <i>Journal of the American Chemical Society</i> , 2020, 142, 2145-2149.	6.6	27
65	Spatial Clustering of Isozyme-specific Residues Reveals Unlikely Determinants of Isozyme Specificity in Fructose-1,6-bisphosphate Aldolase. <i>Journal of Biological Chemistry</i> , 2003, 278, 17307-17313.	1.6	26
66	Covalent Docking Predicts Substrates for Haloalkanoate Dehalogenase Superfamily Phosphatases. <i>Biochemistry</i> , 2015, 54, 528-537.	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	New Superfamily Members Identified for Schiff-Base Enzymes Based on Verification of Catalytically Essential Residues. <i>Biochemistry</i> , 2006, 45, 8546-8555.	1.2	23
69	Structural and mechanistic themes in glycoconjugate biosynthesis at membrane interfaces. <i>Current Opinion in Structural Biology</i> , 2019, 59, 81-90.	2.6	23
70	Inhibition of pig liver esterase by trifluoromethyl ketones: modulators of the catalytic reaction alter inhibition kinetics. <i>Biochemistry</i> , 1989, 28, 135-140.	1.2	22
71	<i>Homo sapiens</i> Dullard Protein Phosphatase Shows a Preference for the Insulin-Dependent Phosphorylation Site of Lipin1. <i>Biochemistry</i> , 2011, 50, 3045-3047.	1.2	22
72	Tailoring Encodable Lanthanide-Binding Tags as MRI Contrast Agents. <i>ChemBioChem</i> , 2012, 13, 2567-2574.	1.3	22

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73	A Structural Element That Facilitates Proton-Coupled Electron Transfer in Oxalate Decarboxylase. <i>Biochemistry</i> , 2012, 51, 2911-2920.	1.2	22
74	Bioinformatic Analysis of the Flavin-Dependent Amine Oxidase Superfamily: Adaptations for Substrate Specificity and Catalytic Diversity. <i>Journal of Molecular Biology</i> , 2020, 432, 3269-3288.	2.0	21
75	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
76	Substrate Deconstruction and the Nonadditivity of Enzyme Recognition. <i>Journal of the American Chemical Society</i> , 2014, 136, 7374-7382.	6.6	20
77	Structure of a rabbit muscle fructose-1,6-bisphosphate aldolase A dimer variant. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 543-550.	2.5	19
78	Structural Analysis Provides Mechanistic Insight into Nicotine Oxidoreductase from <i>Pseudomonas putida</i> . <i>Biochemistry</i> , 2016, 55, 6595-6598.	1.2	19
79	X-ray structure analysis of a designed oligomeric miniprotein reveals a discrete quaternary architecture. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12183-12188.	3.3	18
80	A cross-over inhibitor of the botulinum neurotoxin light chain B: a natural product implicating an exosite mechanism of action. <i>Chemical Communications</i> , 2011, 47, 1713.	2.2	18
81	Assigning the EPR Fine Structure Parameters of the Mn(II) Centers in <i>Bacillus subtilis</i> Oxalate Decarboxylase by Site-Directed Mutagenesis and DFT/MM Calculations. <i>Journal of the American Chemical Society</i> , 2014, 136, 2313-2323.	6.6	17
82	Enzyme Substrate Specificity Conferred by Distinct Conformational Pathways. <i>Journal of the American Chemical Society</i> , 2015, 137, 13876-13886.	6.6	17
83	Catalytic scaffolds for phosphoryl group transfer. <i>Current Opinion in Structural Biology</i> , 2016, 41, 172-179.	2.6	17
84	Glycoconjugate pathway connections revealed by sequence similarity network analysis of the monotopic phosphoglycosyl transferases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	17
85	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
86	Substrate Binding Mode and Molecular Basis of a Specificity Switch in Oxalate Decarboxylase. <i>Biochemistry</i> , 2016, 55, 2163-2173.	1.2	16
87	Crystallography Coupled with Kinetic Analysis Provides Mechanistic Underpinnings of a Nicotine-Degrading Enzyme. <i>Biochemistry</i> , 2018, 57, 3741-3751.	1.2	16
88	Thermodynamic Analysis Shows Conformational Coupling and Dynamics Confer Substrate Specificity in Fructose-1,6-bisphosphate Aldolase. <i>Biochemistry</i> , 2007, 46, 13010-13018.	1.2	15
89	Binding Energy and Catalysis by <i>Xylose Isomerase</i> : Kinetic, Product, and X-ray Crystallographic Analysis of Enzyme-Catalyzed Isomerization of <i>D-Glyceraldehyde</i> . <i>Biochemistry</i> , 2011, 50, 10170-10181.	1.2	15
90	Metal Ions Effectively Ablate the Action of Botulinum Neurotoxin A. <i>Journal of the American Chemical Society</i> , 2017, 139, 7264-7272.	6.6	15

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91	Recapitulating the Binding Affinity of Nrf2 for KEAP1 in a Cyclic Heptapeptide, Guided by NMR, X-ray Crystallography, and Machine Learning. <i>Journal of the American Chemical Society</i> , 2021, 143, 3779-3793.	6.6	15
92	Mutation of Nonessential Cysteines Shows That the NF- κ B Essential Modulator Forms a Constitutive Noncovalent Dimer That Binds I κ B Kinase- β with High Affinity. <i>Biochemistry</i> , 2013, 52, 9141-9154.	1.2	14
93	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
94	Intein-mediated purification of a recombinantly expressed peptide. <i>Chemical Communications</i> , 2004, , 2412.	2.2	13
95	Catch and Anchor Approach To Combat Both Toxicity and Longevity of Botulinum Toxin A. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 11100-11120.	2.9	13
96	Crystallization and preliminary X-ray diffraction studies of I κ B-phosphoglucomutase from <i>Lactococcus lactus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 324-326.	2.5	12
97	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
98	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
99	Disulfide-Mediated Stabilization of the I κ B Kinase Binding Domain of NF- κ B Essential Modulator (NEMO). <i>Biochemistry</i> , 2014, 53, 7929-7944.	1.2	11
100	The surprising structural and mechanistic dichotomy of membrane-associated phosphoglycosyl transferases. <i>Biochemical Society Transactions</i> , 2021, 49, 1189-1203.	1.6	11
101	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
102	Small molecule metalloprotease inhibitor with in vitro, ex vivo and in vivo efficacy against botulinum neurotoxin serotype A. <i>Toxicon</i> , 2017, 137, 36-47.	0.8	9
103	Conformational dynamics and alignment properties of loop lanthanide-binding-tags (LBTs) studied in interleukin-1 β . <i>Journal of Biomolecular NMR</i> , 2017, 68, 187-194.	1.6	8
104	Mechanism of Substrate Recognition and Catalysis of the Haloalkanoic Acid Dehalogenase Family Member I κ B-Phosphoglucomutase. <i>Biochemistry</i> , 2018, 57, 4504-4517.	1.2	8
105	Fast Kinetics Reveals Rate-Limiting Oxidation and the Role of the Aromatic Cage in the Mechanism of the Nicotine-Degrading Enzyme NicA2. <i>Biochemistry</i> , 2021, 60, 259-273.	1.2	8
106	Aspirin – now we can see it. <i>Nature Medicine</i> , 1995, 1, 882-883.	15.2	7
107	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
108	A Central Region of NF- κ B Essential Modulator Is Required for IKK β -Induced Conformational Change and for Signal Propagation. <i>Biochemistry</i> , 2019, 58, 2906-2920.	1.2	7

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109	Enzymatic synthesis of radiolabeled phosphonoacetaldehyde. <i>Analytical Biochemistry</i> , 2003, 322, 233-237.	1.1	6
110	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
111	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
112	The Birth of Genomic Enzymology: Discovery of the Mechanistically Diverse Enolase Superfamily. <i>Biochemistry</i> , 2021, 60, 3515-3528.	1.2	5
113	Crystallization and preliminary crystallographic analysis of phosphonoacetaldehyde hydrolase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 206-209.	2.5	4
114	Form finds function. <i>Nature Chemical Biology</i> , 2007, 3, 452-453.	3.9	3
115	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
116	Use of Crystallography and Molecular Modeling for the Inhibition of the Botulinum Neurotoxin A Protease. <i>ACS Medicinal Chemistry Letters</i> , 2021, 12, 1318-1324.	1.3	3
117	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
118	Crystallization of Liganded Phosphatases in the HAD Superfamily. <i>Methods in Enzymology</i> , 2018, 607, 157-184.	0.4	1
119	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
120	Preface. <i>Methods in Enzymology</i> , 2018, 607, xv-xviii.	0.4	0
121	Structural Enzymology in the Haloalkanoic Acid Dehalogenase Superfamily. <i>FASEB Journal</i> , 2007, 21, .	0.2	0
122	Identifying and negotiating with potential collaborators. <i>FASEB Journal</i> , 2011, 25, 207.3.	0.2	0
123	Ligand Binding and Conformational Change Coupling in the HAD Superfamily. <i>FASEB Journal</i> , 2013, 27, 998.8.	0.2	0
124	The nature of sequence and structure divergence in the Haloalkanoate Dehalogenase SuperFamily (HADSF). <i>FASEB Journal</i> , 2013, 27, 797.2.	0.2	0
125	The structural basis of the secondary function of PMM1 in the presence of IMP. <i>FASEB Journal</i> , 2013, 27, 998.5.	0.2	0
126	Ultra High-throughput Screening Uncovers New Activities in Phosphatases of the Haloalkanoic Acid Dehalogenase Superfamily (HADSF). <i>FASEB Journal</i> , 2013, 27, 571.1.	0.2	0

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127	Ligand-Induced Conformational Change Propagates NEMO-Mediated NF- κ B Signaling. FASEB Journal, 2015, 29, 563.6.	0.2	0
128	Using M. marinum T6PP as a Model for M. tuberculosis Inhibitor Design. FASEB Journal, 2018, 32, 674.16.	0.2	0