

Karen N Allen

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

126 papers	5,171 citations	41 h-index	68 g-index
183 ext. papers	5,746 ext. citations	6.5 avg, IF	5.43 L-index

#	Paper	IF	Citations
126	The Birth of Genomic Enzymology: Discovery of the Mechanistically Diverse Enolase Superfamily. <i>Biochemistry</i> , 2021 , 60, 3515-3528	3.2	1
125	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	16.4	1
124	The surprising structural and mechanistic dichotomy of membrane-associated phosphoglycosyl transferases. <i>Biochemical Society Transactions</i> , 2021 , 49, 1189-1203	5.1	0
123	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	4.3	2
122	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,	11.5	3
121	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	3.2	4
120	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	6.5	8
119	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	16.4	10
118	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	3.2	11
117	Structural Analysis of Binding Determinants of Trehalose-6-phosphate Phosphatase Using Ground-State Complexes. <i>Biochemistry</i> , 2020 , 59, 3247-3257	3.2	1
116	Catch and Anchor Approach To Combat Both Toxicity and Longevity of Botulinum Toxin A. <i>Journal of Medicinal Chemistry</i> , 2020 , 63, 11100-11120	8.3	10
115	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	3.2	4
114	Structural and mechanistic themes in glycoconjugate biosynthesis at membrane interfaces. <i>Current Opinion in Structural Biology</i> , 2019 , 59, 81-90	8.1	9
113	Monotopic Membrane Proteins Join the Fold. <i>Trends in Biochemical Sciences</i> , 2019 , 44, 7-20	10.3	20
112	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	3.2	4
111	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	11.5	68
110	Using <i>M. marinum</i> T6PP as a Model for <i>M. tuberculosis</i> Inhibitor Design. <i>FASEB Journal</i> , 2018 , 32, 674.160.9		

109	X-ray Fluorescence Nanotomography of Single Bacteria with a Sub-15 nm Beam. <i>Scientific Reports</i> , 2018 , 8, 13415	4.9	19
108	Crystallization of Liganded Phosphatases in the HAD Superfamily. <i>Methods in Enzymology</i> , 2018 , 607, 157-184	1.7	
107	Crystallography Coupled with Kinetic Analysis Provides Mechanistic Underpinnings of a Nicotine-Degrading Enzyme. <i>Biochemistry</i> , 2018 , 57, 3741-3751	3.2	12
106	Membrane association of monotopic phosphoglycosyl transferase underpins function. <i>Nature Chemical Biology</i> , 2018 , 14, 538-541	11.7	19
105	Mechanism of Substrate Recognition and Catalysis of the Haloalkanoic Acid Dehalogenase Family Member Φ Phosphoglucomutase. <i>Biochemistry</i> , 2018 , 57, 4504-4517	3.2	4
104	Construction and Analysis of Two Genome-Scale Deletion Libraries for <i>Bacillus subtilis</i> . <i>Cell Systems</i> , 2017 , 4, 291-305.e7	10.6	245
103	Metal Ions Effectively Ablate the Action of Botulinum Neurotoxin A. <i>Journal of the American Chemical Society</i> , 2017 , 139, 7264-7272	16.4	12
102	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	3	8
101	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	2.8	7
100	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	3.8	
99	Catalytic scaffolds for phosphoryl group transfer. <i>Current Opinion in Structural Biology</i> , 2016 , 41, 172-179	9.1	11
98	Structural Analysis Provides Mechanistic Insight into Nicotine Oxidoreductase from <i>Pseudomonas putida</i> . <i>Biochemistry</i> , 2016 , 55, 6595-6598	3.2	16
97	Substrate Binding Mode and Molecular Basis of a Specificity Switch in Oxalate Decarboxylase. <i>Biochemistry</i> , 2016 , 55, 2163-73	3.2	16
96	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	11.5	47
95	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	11.5	81
94	Enzyme Substrate Specificity Conferred by Distinct Conformational Pathways. <i>Journal of the American Chemical Society</i> , 2015 , 137, 13876-86	16.4	10
93	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, 275-82	3	43
92	Accounting for observed small angle X-ray scattering profile in the protein-protein docking server ClusPro. <i>Journal of Computational Chemistry</i> , 2015 , 36, 1568-72	3.5	22

91	Conservation and Covariance in Small Bacterial Phosphoglycosyltransferases Identify the Functional Catalytic Core. <i>Biochemistry</i> , 2015 , 54, 7326-34	3.2	16
90	Covalent docking predicts substrates for haloalkanoate dehalogenase superfamily phosphatases. <i>Biochemistry</i> , 2015 , 54, 528-37	3.2	20
89	Ligand-Induced Conformational Change Propagates NEMO-Mediated NF- κ B Signaling. <i>FASEB Journal</i> , 2015 , 29, 563.6	0.9	
88	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, 1896-906	4.2	3
87	Enzyme promiscuity: engine of evolutionary innovation. <i>Journal of Biological Chemistry</i> , 2014 , 289, 30229-30236	3.4	107
86	Structure and catalysis in the Escherichia coli hotdog-fold thioesterase paralogs YdiI and YdbB. <i>Biochemistry</i> , 2014 , 53, 4788-805	3.2	12
85	Substrate deconstruction and the nonadditivity of enzyme recognition. <i>Journal of the American Chemical Society</i> , 2014 , 136, 7374-82	16.4	16
84	Divergence of substrate specificity and function in the Escherichia coli hotdog-fold thioesterase paralogs YdiI and YdbB. <i>Biochemistry</i> , 2014 , 53, 4775-87	3.2	12
83	Assigning the EPR fine structure parameters of the Mn(II) centers in Bacillus subtilis oxalate decarboxylase by site-directed mutagenesis and DFT/MM calculations. <i>Journal of the American Chemical Society</i> , 2014 , 136, 2313-23	16.4	17
82	Structure of the trehalose-6-phosphate phosphatase from Brugia malayi reveals key design principles for anthelmintic drugs. <i>PLoS Pathogens</i> , 2014 , 10, e1004245	7.6	29
81	Disulfide-mediated stabilization of the IB kinase binding domain of NF- κ B essential modulator (NEMO). <i>Biochemistry</i> , 2014 , 53, 7929-44	3.2	7
80	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, 2851-9	3.8	8
79	Evaluation of adamantane hydroxamates as botulinum neurotoxin inhibitors: synthesis, crystallography, modeling, kinetic and cellular based studies. <i>Bioorganic and Medicinal Chemistry</i> , 2013 , 21, 1344-8	3.4	41
78	Mutation of nonessential cysteines shows that the NF- κ B essential modulator forms a constitutive noncovalent dimer that binds IB kinase- β with high affinity. <i>Biochemistry</i> , 2013 , 52, 9141-54	3.2	12
77	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, 5372-86	3.2	17
76	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, 1015-9		5
75	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	11.5	19
74	Ligand Binding and Conformational Change Coupling in the HAD Superfamily. <i>FASEB Journal</i> , 2013 , 27, 998.8	0.9	

73	The nature of sequence and structure divergence in the Haloalkanoate Dehalogenase SuperFamily (HADSf). <i>FASEB Journal</i> , 2013 , 27, 797.2	0.9	
72	The structural basis of the secondary function of PMM1 in the presence of IMP. <i>FASEB Journal</i> , 2013 , 27, 998.5	0.9	
71	Ultra High-throughput Screening Uncovers New Activities in Phosphatases of the Haloalkanoic Acid Dehalogenase Superfamily (HADSf). <i>FASEB Journal</i> , 2013 , 27, 571.1	0.9	
70	Tailoring encodable lanthanide-binding tags as MRI contrast agents. <i>ChemBioChem</i> , 2012 , 13, 2567-74	3.8	20
69	A structural element that facilitates proton-coupled electron transfer in oxalate decarboxylase. <i>Biochemistry</i> , 2012 , 51, 2911-20	3.2	20
68	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, 2823-34	16.4	39
67	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, 3099-107	4.2	9
66	Engineering encodable lanthanide-binding tags into loop regions of proteins. <i>Journal of the American Chemical Society</i> , 2011 , 133, 808-19	16.4	118
65	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, 1713-5	5.8	14
64	Binding energy and catalysis by D-xylose isomerase: kinetic, product, and X-ray crystallographic analysis of enzyme-catalyzed isomerization of (R)-glyceraldehyde. <i>Biochemistry</i> , 2011 , 50, 10170-81	3.2	12
63	The Enzyme Function Initiative. <i>Biochemistry</i> , 2011 , 50, 9950-62	3.2	140
62	Homo sapiens dullard protein phosphatase shows a preference for the insulin-dependent phosphorylation site of lipin1. <i>Biochemistry</i> , 2011 , 50, 3045-7	3.2	16
61	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, 8937-49	3.2	30
60	Identifying and negotiating with potential collaborators. <i>FASEB Journal</i> , 2011 , 25, 207.3	0.9	
59	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, 1082-92	3.2	32
58	Chirality holds the key for potent inhibition of the botulinum neurotoxin serotype a protease. <i>Organic Letters</i> , 2010 , 12, 756-9	6.2	27
57	Divergence of biochemical function in the HAD superfamily: D-glycero-D-manno-heptose-1,7-bisphosphate phosphatase (GmhB). <i>Biochemistry</i> , 2010 , 49, 1072-81	3.2	27
56	Lanthanide-tagged proteins--an illuminating partnership. <i>Current Opinion in Chemical Biology</i> , 2010 , 14, 247-54	9.7	91

55	Structure-function analysis of 2-keto-3-deoxy-D-glycero-D-galactonononate-9-phosphate phosphatase defines specificity elements in type C0 haloalkanoate dehalogenase family members. <i>Journal of Biological Chemistry</i> , 2009 , 284, 1224-33	5.4	27
54	Markers of fitness in a successful enzyme superfamily. <i>Current Opinion in Structural Biology</i> , 2009 , 19, 658-65	8.1	77
53	The origin of the electrostatic perturbation in acetoacetate decarboxylase. <i>Nature</i> , 2009 , 459, 393-7	50.4	78
52	Analysis of the structural determinants underlying discrimination between substrate and solvent in beta-phosphoglucosyltransferase catalysis. <i>Biochemistry</i> , 2009 , 48, 1984-95	3.2	30
51	Catalytic features of the botulinum neurotoxin A light chain revealed by high resolution structure of an inhibitory peptide complex. <i>Biochemistry</i> , 2008 , 47, 5736-45	3.2	54
50	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, 5687-92	11.5	52
49	The X-ray crystallographic structure and activity analysis of a Pseudomonas-specific subfamily of the HAD enzyme superfamily evidences a novel biochemical function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 70, 197-207	4.2	5
48	Structure of a rabbit muscle fructose-1,6-bisphosphate aldolase A dimer variant. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008 , 64, 543-50		16
47	Human symbiont Bacteroides thetaiotaomicron synthesizes 2-keto-3-deoxy-D-glycero-D-galacto-nononic acid (KDN). <i>Chemistry and Biology</i> , 2008 , 15, 893-7		15
46	Thermodynamic analysis shows conformational coupling and dynamics confer substrate specificity in fructose-1,6-bisphosphate aldolase. <i>Biochemistry</i> , 2007 , 46, 13010-8	3.2	12
45	Double-lanthanide-binding tags for macromolecular crystallographic structure determination. <i>Journal of the American Chemical Society</i> , 2007 , 129, 7114-20	16.4	74
44	Structures of Clostridium botulinum Neurotoxin Serotype A Light Chain complexed with small-molecule inhibitors highlight active-site flexibility. <i>Chemistry and Biology</i> , 2007 , 14, 533-42		104
43	Double-lanthanide-binding tags: design, photophysical properties, and NMR applications. <i>Journal of the American Chemical Society</i> , 2007 , 129, 7106-13	16.4	129
42	The X-ray crystal structures of human alpha-phosphomannosidase 1 reveal the structural basis of congenital disorder of glycosylation type 1a. <i>Journal of Biological Chemistry</i> , 2006 , 281, 14918-26	5.4	58
41	New superfamily members identified for Schiff-base enzymes based on verification of catalytically essential residues. <i>Biochemistry</i> , 2006 , 45, 8546-55	3.2	21
40	Conformational cycling in beta-phosphoglucosyltransferase catalysis: reorientation of the beta-D-glucose 1,6-(Bis)phosphate intermediate. <i>Biochemistry</i> , 2006 , 45, 7818-24	3.2	30
39	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, 1003-34	6.5	315
38	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	5.1	29

37	Structure and activity analyses of Escherichia coli K-12 NagD provide insight into the evolution of biochemical function in the haloalkanoic acid dehalogenase superfamily. <i>Biochemistry</i> , 2006 , 45, 1183-93 ^{3.2}	48
36	Catalytic cycling in beta-phosphoglucomutase: a kinetic and structural analysis. <i>Biochemistry</i> , 2005 , 44, 9404-16	3.2 49
35	Chemical confirmation of a pentavalent phosphorane in complex with beta-phosphoglucomutase. <i>Journal of the American Chemical Society</i> , 2005 , 127, 5298-9	16.4 54
34	HAD superfamily phosphotransferase substrate diversification: structure and function analysis of HAD subclass IIB sugar phosphatase BT4131. <i>Biochemistry</i> , 2005 , 44, 8684-96	3.2 66
33	Structure of the thermolabile mutant aldolase B, A149P: molecular basis of hereditary fructose intolerance. <i>Journal of Molecular Biology</i> , 2005 , 347, 135-44	6.5 32
32	Design of a heterospecific, tetrameric, 21-residue miniprotein with mixed alpha/beta structure. <i>Structure</i> , 2005 , 13, 225-34	5.2 33
31	Structure of human brain fructose 1,6-(bis)phosphate aldolase: linking isozyme structure with function. <i>Protein Science</i> , 2004 , 13, 3077-84	6.3 42
30	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, 12183-8	11.5 18
29	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, 9353-61	5.4 30
28	Phosphoryl group transfer: evolution of a catalytic scaffold. <i>Trends in Biochemical Sciences</i> , 2004 , 29, 495-503	10.3 229
27	Structural origin of the high affinity of a chemically evolved lanthanide-binding peptide. <i>Angewandte Chemie - International Edition</i> , 2004 , 43, 3682-5	16.4 139
26	Structural Origin of the High Affinity of a Chemically Evolved Lanthanide-Binding Peptide. <i>Angewandte Chemie</i> , 2004 , 116, 3768-3771	3.6 19
25	Analysis of the substrate specificity loop of the HAD superfamily cap domain. <i>Biochemistry</i> , 2004 , 43, 2812-20	3.2 78
24	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, 4990-7	3.2 31
23	X-ray crystal structure of the hypothetical phosphotyrosine phosphatase MDP-1 of the haloacid dehalogenase superfamily. <i>Biochemistry</i> , 2004 , 43, 12770-9	3.2 42
22	Intein-mediated purification of a recombinantly expressed peptide. <i>Chemical Communications</i> , 2004 , 2412-3	5.8 13
21	Enzymatic synthesis of radiolabeled phosphonoacetaldehyde. <i>Analytical Biochemistry</i> , 2003 , 322, 233-7	3.1 6
20	The pentacovalent phosphorus intermediate of a phosphoryl transfer reaction. <i>Science</i> , 2003 , 299, 2067-71	3.1 291

19	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, 17307-13	5.4	23
18	Chemical-modification rescue assessed by mass spectrometry demonstrates that gamma-thia-lysine yields the same activity as lysine in aldolase. <i>Protein Science</i> , 2002 , 11, 1591-9	6.3	29
17	Crystallization and preliminary X-ray diffraction studies of beta-phosphoglucomutase from <i>Lactococcus lactus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 324-6		12
16	Caught in the act: the structure of phosphorylated beta-phosphoglucomutase from <i>Lactococcus lactis</i> . <i>Biochemistry</i> , 2002 , 41, 8351-9	3.2	100
15	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, 13861-7	3.2	119
14	Kinetic evidence for a substrate-induced fit in phosphonoacetaldehyde hydrolase catalysis. <i>Biochemistry</i> , 2002 , 41, 13370-7	3.2	25
13	Snapshots of catalysis: the structure of fructose-1,6-(bis)phosphate aldolase covalently bound to the substrate dihydroxyacetone phosphate. <i>Biochemistry</i> , 2001 , 40, 13868-75	3.2	71
12	Crystallization and preliminary crystallographic analysis of phosphonoacetaldehyde hydrolase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 206-9		3
11	The crystal structure of <i>Bacillus cereus</i> phosphonoacetaldehyde hydrolase: insight into catalysis of phosphorus bond cleavage and catalytic diversification within the HAD enzyme superfamily. <i>Biochemistry</i> , 2000 , 39, 10385-96	3.2	124
10	The 2.1 Å structure of a cysteine protease with proline specificity from ginger rhizome, <i>Zingiber officinale</i> . <i>Biochemistry</i> , 1999 , 38, 11624-33	3.2	54
9	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, 12655-64	3.2	49
8	An Experimental Approach to Mapping the Binding Surfaces of Crystalline Proteins. <i>The Journal of Physical Chemistry</i> , 1996 , 100, 2605-2611		167
7	Aspirin--now we can see it. <i>Nature Medicine</i> , 1995 , 1, 882-3	50.5	6
6	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, 3742-9	3.2	56
5	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, 1488-94	3.2	69
4	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, 5469-80	3.2	108
3	Isotopic exchange plus substrate and inhibition kinetics of D-xylose isomerase do not support a proton-transfer mechanism. <i>Biochemistry</i> , 1994 , 33, 1481-7	3.2	70
2	Inhibition of pig liver esterase by trifluoromethyl ketones: modulators of the catalytic reaction alter inhibition kinetics. <i>Biochemistry</i> , 1989 , 28, 135-40	3.2	19

- 1 Inhibition kinetics of acetylcholinesterase with fluoromethyl ketones. *Biochemistry*, **1989**, 28, 8466-73 3.2 54