Lesa J Beamer

List of Publications by Year
in descending order

60 papers	2,655 citations	218677 26 h-index	189892 50 g-index
61 all docs	61 docs citations	61 times ranked	2876 citing authors

#	Article	IF	Citations
1	Effects of the T337M and G391V disease-related variants on human phosphoglucomutase 1: structural disruptions large and small. Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 200-209.	0.8	0
2	Development of a Homogeneous Time-Resolved Fluorescence Resonance Energy Transfer (TR-FRET) Assay for the Inhibition of Keap1â€“Nrf2 Proteinâ€“Protein Interaction. SLAS Discovery, 2021, 26, 100-112.	2.7	9
3	Enzyme dysfunction at atomic resolution: Disease-associated variants of human phosphoglucomutase-1. Biochimie, 2021, 183, 44-48.	2.6	5
4	A missense variant remote from the active site impairs stability of human phosphoglucomutase 1. Journal of Inherited Metabolic Disease, 2020, 43, 861-870.	3.6	1
5	Impaired folate binding of serine hydroxymethyltransferase 8 from soybean underlies resistance to the soybean cyst nematode. Journal of Biological Chemistry, 2020, 295, 3708-3718.	3.4	13
6	Inhibitory Evaluation of Î±PMM/PGM from Pseudomonas aeruginosa: Chemical Synthesis, Enzyme Kinetics, and Protein Crystallographic Study. Journal of Organic Chemistry, 2019, 84, 9627-9636.	3.2	8
7	Synthesis, Derivatization, and Structural Analysis of Phosphorylated Mono-, Di-, and Trifluorinated <scp>d</scp>-Gluco-heptuloses by Glucokinase: Tunable Phosphoglucomutase Inhibition. ACS Omega, 2019, 4, 7029-7037.	3.5	9
8	The Metabolic Map into the Pathomechanism and Treatment of PGM1-CDG. American Journal of Human Genetics, 2019, 104, 835-846.	6.2	59
9	Structural and dynamical description of the enzymatic reaction of a phosphohexomutase. Structural Dynamics, 2019, 6, 024703.	2.3	8
10	Assessment and Impacts of Phosphorylation on Protein Flexibility of the Î±-d-Phosphohexomutases. Methods in Enzymology, 2018, 607, 241-267.	1.0	5
11	A Hotspot for Disease-Associated Variants of Human PGM1 Is Associated with Impaired Ligand Binding and Loop Dynamics. Structure, 2018, 26, 1337-1345.e3.	3.3	17
12	Data on the phosphorylation state of the catalytic serine of enzymes in the Î±-D-phosphohexomutase superfamily. Data in Brief, 2017, 10, 398-405.	1.0	5
13	Asp263 missense variants perturb the active site of human phosphoglucomutase 1. FEBS Journal, 2017, 284, 937-947.	4.7	14
14	Structure and characterization of a class 3B proline utilization A: Ligand-induced dimerization and importance of the C-terminal domain for catalysis. Journal of Biological Chemistry, 2017, 292, 9652-9665.	3.4	21
15	Multiple Ligand-Bound States of a Phosphohexomutase Revealed by Principal Component Analysis of NMR Peak Shifts. Scientific Reports, 2017, 7, 5343.	3.3	7
16	Phosphorylation-Dependent Effects on the Structural Flexibility of Phosphoglucosamine Mutase from Bacillus anthracis. ACS Omega, 2017, 2, 8445-8452.	3.5	4
17	Biology, Mechanism, and Structure of Enzymes in the Î±- d -Phosphohexomutase Superfamily. Advances in Protein Chemistry and Structural Biology, 2017, 109, 265-304.	2.3	38
18	Sequence-structure relationships, expression profiles, and disease-associated mutations in the paralogs of phosphoglucomutase 1. PLoS ONE, 2017, 12, e0183563.	2.5	16

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19	Synchrotron-based macromolecular crystallography module for an undergraduate biochemistry laboratory course. Journal of Applied Crystallography, 2016, 49, 2235-2243.	4.5	4
20	Defining the Phenotype and Assessing Severity in Phosphoglucomutase-1ÂDeficiency. Journal of Pediatrics, 2016, 175, 130-136.e8.	1.8	43
21	Induced Structural Disorder as a Molecular Mechanism for Enzyme Dysfunction in Phosphoglucomutase 1 Deficiency. Journal of Molecular Biology, 2016, 428, 1493-1505.	4.2	21
22	Mutations in hereditary phosphoglucomutase 1 deficiency map to key regions of enzyme structure and function. Journal of Inherited Metabolic Disease, 2015, 38, 243-256.	3.6	40
23	Phosphorylation in the Catalytic Cleft Stabilizes and Attracts Domains of a Phosphohexomutase. Biophysical Journal, 2015, 108, 325-337.	0.5	14
24	Promotion of Enzyme Flexibility by Dephosphorylation and Coupling to the Catalytic Mechanism of a Phosphohexomutase. Journal of Biological Chemistry, 2014, 289, 4674-4682.	3.4	16
25	Chemical shift assignments of domain 4 from the phosphohexomutase from Pseudomonas aeruginosa suggest that freeing perturbs its coevolved domain interface. Biomolecular NMR Assignments, 2014, 8, 329-333.	0.8	4
26	Compromised Catalysis and Potential Folding Defects in in Vitro Studies of Missense Mutants Associated with Hereditary Phosphoglucomutase 1 Deficiency. Journal of Biological Chemistry, 2014, 289, 32010-32019.	3.4	43
27	Identification of an essential activeâ€site residue in the Î±â€<scp>d</scp>â€phosphohexomutase enzyme superfamily. FEBS Journal, 2013, 280, 2622-2632.	4.7	12
28	Discovery of a small-molecule inhibitor and cellular probe of Keap1â€“Nrf2 proteinâ€“protein interaction. Bioorganic and Medicinal Chemistry Letters, 2013, 23, 3039-3043.	2.2	167
29	Optimization of Fluorescently Labeled Nrf2 Peptide Probes and the Development of a Fluorescence Polarization Assay for the Discovery of Inhibitors of Keap1-Nrf2 Interaction. Journal of Biomolecular Screening, 2012, 17, 435-447.	2.6	92
30	Solution NMR of a 463-Residue Phosphohexomutase: Domain 4 Mobility, Substates, and Phosphoryl Transfer Defect. Biochemistry, 2012, 51, 807-819.	2.5	12
31	Conservation of Functionally Important Global Motions in an Enzyme Superfamily across Varying Quaternary Structures. Journal of Molecular Biology, 2012, 423, 831-846.	4.2	13
32	A Coevolutionary Residue Network at the Site of a Functionally Important Conformational Change in a Phosphohexomutase Enzyme Family. PLoS ONE, 2012, 7, e38114.	2.5	17
33	Quaternary structure, conformational variability and global motions of phosphoglucosamine mutase. FEBS Journal, 2011, 278, 3298-3307.	4.7	10
34	Kinetic Analyses of Keap1â€“Nrf2 Interaction and Determination of the Minimal Nrf2 Peptide Sequence Required for Keap1 Binding Using Surface Plasmon Resonance. Chemical Biology and Drug Design, 2011, 78, 1014-1021.	3.2	74
35	Crystal structure of a bacterial phosphoglucomutase, an enzyme involved in the virulence of multiple human pathogens. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1215-1229.	2.6	29
36	Crystal Structure of Bacillus anthracis Phosphoglucosamine Mutase, an Enzyme in the Peptidoglycan Biosynthetic Pathway. Journal of Bacteriology, 2011, 193, 4081-4087.	2.2	39

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37	Breaking the covalent connection: Chain connectivity and the catalytic reaction of PMM/PGM. Protein Science, 2010, 19, 1235-1242.	7.6	10
38	Domain motion and interdomain hot spots in a multidomain enzyme. Protein Science, 2010, 19, 1662-1672.	7.6	21
39	Crystallization and initial crystallographic analysis of phosphoglucosamine mutase fromBacillus anthracis. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 733-735.	0.7	5
40	Backbone Flexibility, Conformational Change, and Catalysis in a Phosphohexomutase from Pseudomonas aeruginosa. Biochemistry, 2008, 47, 9154-9162.	2.5	32
41	Complexes of the enzyme phosphomannomutase/phosphoglucomutase with a slow substrate and an inhibitor. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 722-726.	0.7	19
42	Structure of the Keap1:Nrf2 interface provides mechanistic insight into Nrf2 signaling. EMBO Journal, 2006, 25, 3605-3617.	7.8	430
43	The Reaction of Phosphohexomutase from Pseudomonas aeruginosa. Journal of Biological Chemistry, 2006, 281, 15564-15571.	3.4	42
44	Conserved solvent and side-chain interactions in the 1.35â€...Ã... structure of the Kelch domain of Keap1. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 1335-1342.	2.5	39
45	Crystal Structure of the Kelch Domain of Human Keap1. Journal of Biological Chemistry, 2004, 279, 54750-54758.	3.4	193
46	Structural Basis of Diverse Substrate Recognition by the Enzyme PMM/PGM from P. aeruginosa. Structure, 2004, 12, 55-63.	3.3	77
47	Evolutionary trace analysis of the Î±-D-phosphohexomutase superfamily. Protein Science, 2004, 13, 2130-2138.	7.6	85
48	Crystallization and initial crystallographic analysis of the Kelch domain from human Keap1. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2346-2348.	2.5	12
49	Roles of Active Site Residues inPseudomonas aeruginosaPhosphomannomutase/Phosphoglucomutaseâ€. Biochemistry, 2003, 42, 9946-9951.	2.5	32
50	Interallelic Complementation at the Ubiquitous Urease Coding Locus of Soybean. Plant Physiology, 2003, 132, 1801-1810.	4.8	33
51	Structure of human BPI (bactericidal/permeability-increasing protein) and implications for related proteins. Biochemical Society Transactions, 2003, 31, 791-794.	3.4	42
52	Allosterism and Cooperativity inPseudomonas aeruginosaGDP-Mannose Dehydrogenaseâ€. Biochemistry, 2002, 41, 9637-9645.	2.5	29
53	Crystal Structure of PMM/PGM. Structure, 2002, 10, 269-279.	3.3	76
54	Crystallization and initial crystallographic analysis of phosphomannomutase/phosphoglucomutase fromPseudomonas aeruginosa. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 761-762.	2.5	15

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55	The 1.7 Ã… crystal structure of BPI: a study of how two dissimilar amino acid sequences can adopt the same fold 1 1Edited by D. Rees. Journal of Molecular Biology, 2000, 299, 1019-1034.	4.2	50
56	The three-dimensional structure of human bactericidal/permeability-increasing protein. Biochemical Pharmacology, 1999, 57, 225-229.	4.4	47
57	The BPI/LBP family of proteins: A structural analysis of conserved regions. Protein Science, 1998, 7, 906-914.	7.6	125
58	Detecting distant relatives of mammalian LPSâ€binding and lipid transport proteins. Protein Science, 1998, 7, 1643-1646.	7.6	40
59	Crystallization of the chaperone protein SecB. Protein Science, 1995, 4, 1651-1653.	7.6	4
60	Refined 1.8 Ã… crystal structure of the Î» repressor-operator complex. Journal of Molecular Biology, 1992, 227, 177-196.	4.2	308