

# Lesa J Beamer

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/329711/publications.pdf>

Version: 2024-02-01

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	Structure of the Keap1:Nrf2 interface provides mechanistic insight into Nrf2 signaling. <i>EMBO Journal</i> , 2006, 25, 3605-3617.	7.8	430
2	Refined 1.8 Å... crystal structure of the $\hat{\nu}$ repressor-operator complex. <i>Journal of Molecular Biology</i> , 1992, 227, 177-196.	4.2	308
3	Crystal Structure of the Kelch Domain of Human Keap1. <i>Journal of Biological Chemistry</i> , 2004, 279, 54750-54758.	3.4	193
4	Discovery of a small-molecule inhibitor and cellular probe of Keap1-Nrf2 protein-protein interaction. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2013, 23, 3039-3043.	2.2	167
5	The BPI/LBP family of proteins: A structural analysis of conserved regions. <i>Protein Science</i> , 1998, 7, 906-914.	7.6	125
6	Optimization of Fluorescently Labeled Nrf2 Peptide Probes and the Development of a Fluorescence Polarization Assay for the Discovery of Inhibitors of Keap1-Nrf2 Interaction. <i>Journal of Biomolecular Screening</i> , 2012, 17, 435-447.	2.6	92
7	Evolutionary trace analysis of the $\hat{\pm}$ -D-phosphohexomutase superfamily. <i>Protein Science</i> , 2004, 13, 2130-2138.	7.6	85
8	Structural Basis of Diverse Substrate Recognition by the Enzyme PMM/PGM from <i>P. aeruginosa</i> . <i>Structure</i> , 2004, 12, 55-63.	3.3	77
9	Crystal Structure of PMM/PGM. <i>Structure</i> , 2002, 10, 269-279.	3.3	76
10	Kinetic Analyses of Keap1-Nrf2 Interaction and Determination of the Minimal Nrf2 Peptide Sequence Required for Keap1 Binding Using Surface Plasmon Resonance. <i>Chemical Biology and Drug Design</i> , 2011, 78, 1014-1021.	3.2	74
11	The Metabolic Map into the Pathomechanism and Treatment of PGM1-CDG. <i>American Journal of Human Genetics</i> , 2019, 104, 835-846.	6.2	59
12	The 1.7 Å... crystal structure of BPI: a study of how two dissimilar amino acid sequences can adopt the same fold 1 1 Edited by D. Rees. <i>Journal of Molecular Biology</i> , 2000, 299, 1019-1034.	4.2	50
13	The three-dimensional structure of human bactericidal/permeability-increasing protein. <i>Biochemical Pharmacology</i> , 1999, 57, 225-229.	4.4	47
14	Compromised Catalysis and Potential Folding Defects in in Vitro Studies of Missense Mutants Associated with Hereditary Phosphoglucomutase 1 Deficiency. <i>Journal of Biological Chemistry</i> , 2014, 289, 32010-32019.	3.4	43
15	Defining the Phenotype and Assessing Severity in Phosphoglucomutase-1 Deficiency. <i>Journal of Pediatrics</i> , 2016, 175, 130-136.e8.	1.8	43
16	Structure of human BPI (bactericidal/permeability-increasing protein) and implications for related proteins. <i>Biochemical Society Transactions</i> , 2003, 31, 791-794.	3.4	42
17	The Reaction of Phosphohexomutase from <i>Pseudomonas aeruginosa</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 15564-15571.	3.4	42
18	Detecting distant relatives of mammalian LPS-binding and lipid transport proteins. <i>Protein Science</i> , 1998, 7, 1643-1646.	7.6	40

#	ARTICLE	IF	CITATIONS
19	Mutations in hereditary phosphoglucomutase 1 deficiency map to key regions of enzyme structure and function. <i>Journal of Inherited Metabolic Disease</i> , 2015, 38, 243-256.	3.6	40
20	Conserved solvent and side-chain interactions in the 1.35Å structure of the Kelch domain of Keap1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1335-1342.	2.5	39
21	Crystal Structure of Bacillus anthracis Phosphoglucosamine Mutase, an Enzyme in the Peptidoglycan Biosynthetic Pathway. <i>Journal of Bacteriology</i> , 2011, 193, 4081-4087.	2.2	39
22	Biology, Mechanism, and Structure of Enzymes in the $\alpha$ -D-Phosphohexomutase Superfamily. <i>Advances in Protein Chemistry and Structural Biology</i> , 2017, 109, 265-304.	2.3	38
23	Interallelic Complementation at the Ubiquitous Urease Coding Locus of Soybean. <i>Plant Physiology</i> , 2003, 132, 1801-1810.	4.8	33
24	Roles of Active Site Residues in <i>Pseudomonas aeruginosa</i> Phosphomannomutase/Phosphoglucomutase. <i>Biochemistry</i> , 2003, 42, 9946-9951.	2.5	32
25	Backbone Flexibility, Conformational Change, and Catalysis in a Phosphohexomutase from <i>Pseudomonas aeruginosa</i> . <i>Biochemistry</i> , 2008, 47, 9154-9162.	2.5	32
26	Allosterism and Cooperativity in <i>Pseudomonas aeruginosa</i> GDP-Mannose Dehydrogenase. <i>Biochemistry</i> , 2002, 41, 9637-9645.	2.5	29
27	Crystal structure of a bacterial phosphoglucomutase, an enzyme involved in the virulence of multiple human pathogens. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1215-1229.	2.6	29
28	Domain motion and interdomain hot spots in a multidomain enzyme. <i>Protein Science</i> , 2010, 19, 1662-1672.	7.6	21
29	Induced Structural Disorder as a Molecular Mechanism for Enzyme Dysfunction in Phosphoglucomutase 1 Deficiency. <i>Journal of Molecular Biology</i> , 2016, 428, 1493-1505.	4.2	21
30	Structure and characterization of a class 3B proline utilization A: Ligand-induced dimerization and importance of the C-terminal domain for catalysis. <i>Journal of Biological Chemistry</i> , 2017, 292, 9652-9665.	3.4	21
31	Complexes of the enzyme phosphomannomutase/phosphoglucomutase with a slow substrate and an inhibitor. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 722-726.	0.7	19
32	A Coevolutionary Residue Network at the Site of a Functionally Important Conformational Change in a Phosphohexomutase Enzyme Family. <i>PLoS ONE</i> , 2012, 7, e38114.	2.5	17
33	A Hotspot for Disease-Associated Variants of Human PGM1 Is Associated with Impaired Ligand Binding and Loop Dynamics. <i>Structure</i> , 2018, 26, 1337-1345.e3.	3.3	17
34	Promotion of Enzyme Flexibility by Dephosphorylation and Coupling to the Catalytic Mechanism of a Phosphohexomutase. <i>Journal of Biological Chemistry</i> , 2014, 289, 4674-4682.	3.4	16
35	Sequence-structure relationships, expression profiles, and disease-associated mutations in the paralogs of phosphoglucomutase 1. <i>PLoS ONE</i> , 2017, 12, e0183563.	2.5	16
36	Crystallization and initial crystallographic analysis of phosphomannomutase/phosphoglucomutase from <i>Pseudomonas aeruginosa</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 761-762.	2.5	15

#	ARTICLE	IF	CITATIONS
37	Phosphorylation in the Catalytic Cleft Stabilizes and Attracts Domains of a Phosphohexomutase. <i>Biophysical Journal</i> , 2015, 108, 325-337.	0.5	14
38	Asp263 missense variants perturb the active site of human phosphoglucomutase 1. <i>FEBS Journal</i> , 2017, 284, 937-947.	4.7	14
39	Conservation of Functionally Important Global Motions in an Enzyme Superfamily across Varying Quaternary Structures. <i>Journal of Molecular Biology</i> , 2012, 423, 831-846.	4.2	13
40	Impaired folate binding of serine hydroxymethyltransferase 8 from soybean underlies resistance to the soybean cyst nematode. <i>Journal of Biological Chemistry</i> , 2020, 295, 3708-3718.	3.4	13
41	Crystallization and initial crystallographic analysis of the Kelch domain from human Keap1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2346-2348.	2.5	12
42	Solution NMR of a 463-Residue Phosphohexomutase: Domain 4 Mobility, Substates, and Phosphoryl Transfer Defect. <i>Biochemistry</i> , 2012, 51, 807-819.	2.5	12
43	Identification of an essential active-site residue in the phosphohexomutase enzyme superfamily. <i>FEBS Journal</i> , 2013, 280, 2622-2632.	4.7	12
44	Breaking the covalent connection: Chain connectivity and the catalytic reaction of PMM/PGM. <i>Protein Science</i> , 2010, 19, 1235-1242.	7.6	10
45	Quaternary structure, conformational variability and global motions of phosphoglucomutase. <i>FEBS Journal</i> , 2011, 278, 3298-3307.	4.7	10
46	Synthesis, Derivatization, and Structural Analysis of Phosphorylated Mono-, Di-, and Trifluorinated $\alpha$ -Gluco-heptuloses by Glucokinase: Tunable Phosphoglucomutase Inhibition. <i>ACS Omega</i> , 2019, 4, 7029-7037.	3.5	9
47	Development of a Homogeneous Time-Resolved Fluorescence Resonance Energy Transfer (TR-FRET) Assay for the Inhibition of Keap1-Nrf2 Protein-Protein Interaction. <i>SLAS Discovery</i> , 2021, 26, 100-112.	2.7	9
48	Inhibitory Evaluation of PMM/PGM from <i>Pseudomonas aeruginosa</i> : Chemical Synthesis, Enzyme Kinetics, and Protein Crystallographic Study. <i>Journal of Organic Chemistry</i> , 2019, 84, 9627-9636.	3.2	8
49	Structural and dynamical description of the enzymatic reaction of a phosphohexomutase. <i>Structural Dynamics</i> , 2019, 6, 024703.	2.3	8
50	Multiple Ligand-Bound States of a Phosphohexomutase Revealed by Principal Component Analysis of NMR Peak Shifts. <i>Scientific Reports</i> , 2017, 7, 5343.	3.3	7
51	Crystallization and initial crystallographic analysis of phosphoglucomutase from <i>Bacillus anthracis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 733-735.	0.7	5
52	Data on the phosphorylation state of the catalytic serine of enzymes in the $\alpha$ -D-phosphohexomutase superfamily. <i>Data in Brief</i> , 2017, 10, 398-405.	1.0	5
53	Assessment and Impacts of Phosphorylation on Protein Flexibility of the $\alpha$ -D-Phosphohexomutases. <i>Methods in Enzymology</i> , 2018, 607, 241-267.	1.0	5
54	Enzyme dysfunction at atomic resolution: Disease-associated variants of human phosphoglucomutase-1. <i>Biochimie</i> , 2021, 183, 44-48.	2.6	5

#	ARTICLE	IF	CITATIONS
55	Crystallization of the chaperone protein SecB. <i>Protein Science</i> , 1995, 4, 1651-1653.	7.6	4
56	Chemical shift assignments of domain 4 from the phosphohexomutase from <i>Pseudomonas aeruginosa</i> suggest that freeing perturbs its coevolved domain interface. <i>Biomolecular NMR Assignments</i> , 2014, 8, 329-333.	0.8	4
57	Synchrotron-based macromolecular crystallography module for an undergraduate biochemistry laboratory course. <i>Journal of Applied Crystallography</i> , 2016, 49, 2235-2243.	4.5	4
58	Phosphorylation-Dependent Effects on the Structural Flexibility of Phosphoglucosamine Mutase from <i>Bacillus anthracis</i> . <i>ACS Omega</i> , 2017, 2, 8445-8452.	3.5	4
59	A missense variant remote from the active site impairs stability of human phosphoglucomutase 1. <i>Journal of Inherited Metabolic Disease</i> , 2020, 43, 861-870.	3.6	1
60	Effects of the T337M and G391V disease-related variants on human phosphoglucomutase 1: structural disruptions large and small. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2022, 78, 200-209.	0.8	0