

# Kyle M Stiers

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/259103/publications.pdf>

Version: 2024-02-01

21  
papers

312  
citations

933447

10  
h-index

888059

17  
g-index

21  
all docs

21  
docs citations

21  
times ranked

419  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	Biology, Mechanism, and Structure of Enzymes in the $\hat{1}\pm$ -d-Phosphohexomutase Superfamily. <i>Advances in Protein Chemistry and Structural Biology</i> , 2017, 109, 265-304.	2.3	38
4	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
5	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
6	Structure, biochemistry, and gene expression patterns of the proline biosynthetic enzyme pyrroline-5-carboxylate reductase (PYCR), an emerging cancer therapy target. <i>Amino Acids</i> , 2021, 53, 1817-1834.	2.7	20
7	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
8	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
9	Asp263 missense variants perturb the active site of human phosphoglucomutase 1. <i>FEBS Journal</i> , 2017, 284, 937-947.	4.7	14
10	Trapping conformational states of a flavin-dependent N-monooxygenase in crystallo reveals protein and flavin dynamics. <i>Journal of Biological Chemistry</i> , 2020, 295, 13239-13249.	3.4	13
11	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
12	Inhibitory Evaluation of $\hat{1}\pm$ 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
13	Structural and dynamical description of the enzymatic reaction of a phosphohexomutase. <i>Structural Dynamics</i> , 2019, 6, 024703.	2.3	8
14	Cautionary Tale of Using Tris(alkyl)phosphine Reducing Agents with NAD <sup>+</sup> -Dependent Enzymes. <i>Biochemistry</i> , 2020, 59, 3285-3289.	2.5	7
15	Assessment and Impacts of Phosphorylation on Protein Flexibility of the $\hat{1}\pm$ -d-Phosphohexomutases. <i>Methods in Enzymology</i> , 2018, 607, 241-267.	1.0	5
16	Synchrotron-based macromolecular crystallography module for an undergraduate biochemistry laboratory course. <i>Journal of Applied Crystallography</i> , 2016, 49, 2235-2243.	4.5	4
17	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
18	Structural basis for the stereospecific inhibition of the dual proline/hydroxyproline catabolic enzyme ALDH4A1 by trans- $\alpha$ -hydroxyproline. <i>Protein Science</i> , 2021, 30, 1714-1722.	7.6	4

#	ARTICLE	IF	CITATIONS
19	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
20	Kinetics of human pyrroline-5-carboxylate reductase in l-thioproline metabolism. <i>Amino Acids</i> , 2021, 53, 1863-1874.	2.7	0
21	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