Brian G Miller

List of Publications by Year
in descending order

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38 papers	1,269 citations	331538 21 h-index	360920 35 g-index
39 all docs	39 docs citations	39 times ranked	1660 citing authors

#	Article	IF	Citations
1	Catalytic Proficiency: The Unusual Case of OMP Decarboxylase. Annual Review of Biochemistry, 2002, 71, 847-885.	5.0	266
2	Cooperativity in monomeric enzymes with single ligand-binding sites. Bioorganic Chemistry, 2012, 43, 44-50.	2.0	90
3	Molecular and cellular regulation of human glucokinase. Archives of Biochemistry and Biophysics, 2019, 663, 199-213.	1.4	89
4	Identifying Latent Enzyme Activities:Â Substrate Ambiguity within Modern Bacterial Sugar Kinasesâ€. Biochemistry, 2004, 43, 6387-6392.	1.2	86
5	Orderâ€“Disorder Transitions Govern Kinetic Cooperativity and Allostery of Monomeric Human Glucokinase. PLoS Biology, 2012, 10, e1001452.	2.6	51
6	Dissecting a Charged Network at the Active Site of Orotidine-5â€²-phosphate Decarboxylase. Journal of Biological Chemistry, 2001, 276, 15174-15176.	1.6	50
7	Enantioselective synthesis of tatanans Aâ€“C and reinvestigation of their glucokinase-activating properties. Nature Chemistry, 2013, 5, 410-416.	6.6	48
8	Dual allosteric activation mechanisms in monomeric human glucokinase. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11553-11558.	3.3	46
9	Reconstitution of a Defunct Glycolytic Pathway via Recruitment of Ambiguous Sugar Kinasesâ€. Biochemistry, 2005, 44, 10776-10783.	1.2	42
10	Structural Basis for Regulation of Human Glucokinase by Glucokinase Regulatory Protein. Biochemistry, 2013, 52, 6232-6239.	1.2	41
11	Evolutionary Bases of Carbohydrate Recognition and Substrate Discrimination in the ROK Protein Family. Journal of Molecular Evolution, 2010, 70, 545-556.	0.8	40
12	Homotropic allosteric regulation in monomeric mammalian glucokinase. Archives of Biochemistry and Biophysics, 2012, 519, 103-111.	1.4	35
13	Divergent Evolution of Function in the ROK Sugar Kinase Superfamily:â€‰ Role of Enzyme Loops in Substrate Specificity. Biochemistry, 2007, 46, 13564-13572.	1.2	30
14	OMP decarboxylaseâ€”An enigma persists. Bioorganic Chemistry, 2007, 35, 465-469.	2.0	29
15	Direct Evidence of Conformational Heterogeneity in Human Pancreatic Glucokinase from High-Resolution Nuclear Magnetic Resonance. Biochemistry, 2010, 49, 7969-7971.	1.2	29
16	Kinetic Cooperativity in Human Pancreatic Glucokinase Originates from Millisecond Dynamics of the Small Domain. Angewandte Chemie - International Edition, 2015, 54, 8129-8132.	7.2	29
17	Short Total Synthesis of [¹⁵N₅]-Cylindrospermopsins from ¹⁵NH₄Cl Enables Precise Quantification of Freshwater Cyanobacterial Contamination. Journal of the American Chemical Society, 2018, 140, 6027-6032.	6.6	28
18	Activating Mutations in the Human Glucokinase Gene Revealed by Genetic Selection. Biochemistry, 2009, 48, 814-816.	1.2	25

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19	Small-Molecule Allosteric Activation of Human Glucokinase in the Absence of Glucose. ACS Medicinal Chemistry Letters, 2013, 4, 580-584.	1.3	24
20	A Metabolic Bypass of the Triosephosphate Isomerase Reaction. Biochemistry, 2008, 47, 7983-7985.	1.2	23
21	23-Residue C-Terminal Î±-Helix Governs Kinetic Cooperativity in Monomeric Human Glucokinase. Biochemistry, 2009, 48, 6157-6165.	1.2	23
22	Global Fit Analysis of Glucose Binding Curves Reveals a Minimal Model for Kinetic Cooperativity in Human Glucokinase. Biochemistry, 2010, 49, 8902-8911.	1.2	23
23	Biliverdin Reductase B Dynamics Are Coupled to Coenzyme Binding. Journal of Molecular Biology, 2018, 430, 3234-3250.	2.0	22
24	Role of connecting loop I in catalysis and allosteric regulation of human glucokinase. Protein Science, 2014, 23, 915-922.	3.1	11
25	Mechanistic Origins of Enzyme Activation in Human Glucokinase Variants Associated with Congenital Hyperinsulinism. Biochemistry, 2018, 57, 1632-1639.	1.2	11
26	Analysis of Interactions Stabilized by Fusicoccin A Reveals an Expanded Suite of Potential 14â€“3â€“3 Binding Partners. ACS Chemical Biology, 2020, 15, 305-310.	1.6	11
27	The mutability of enzyme activeâ€site shape determinants. Protein Science, 2007, 16, 1965-1968.	3.1	10
28	Conformational heterogeneity and intrinsic disorder in enzyme regulation: Glucokinase as a case study. Intrinsically Disordered Proteins, 2015, 3, e1011008.	1.9	10
29	Probing the 14-3-3 Isoform-Specificity Profile of Proteinâ€“Protein Interactions Stabilized by Fusicoccin A. ACS Omega, 2020, 5, 25029-25035.	1.6	8
30	Selenolysine: A New Tool for Traceless Isopeptide Bond Formation. Chemistry - A European Journal, 2020, 26, 4952-4957.	1.7	8
31	Kinetic Cooperativity in Human Pancreatic Glucokinase Originates from Millisecond Dynamics of the Small Domain. Angewandte Chemie, 2015, 127, 8247-8250.	1.6	7
32	Nanosecond-Timescale Dynamics and Conformational Heterogeneity in Human GCK Regulation and Disease. Biophysical Journal, 2020, 118, 1109-1118.	0.2	7
33	Biochemical and biophysical investigations of the interaction between human glucokinase and pro-apoptotic BAD. PLoS ONE, 2017, 12, e0171587.	1.1	6
34	Antidiabetic Disruptors of the Glucokinaseâ”Glucokinase Regulatory Protein Complex Reorganize a Coulombic Interface. Biochemistry, 2017, 56, 3150-3157.	1.2	5
35	Kinetic Basis of Carbohydrate-Mediated Inhibition of Human Glucokinase by the Glucokinase Regulatory Protein. Biochemistry, 2016, 55, 2899-2902.	1.2	4
36	l-Glyceraldehyde 3-phosphate reductase from Escherichia coli is a heme binding protein. Bioorganic Chemistry, 2010, 38, 37-41.	2.0	1

#	Article	IF	Citations
37	Vertical Investigations of Enzyme Evolution Using Ancestral Sequence Reconstruction. , 2020, , 640-653.		1
38	Enzyme recruitment and the evolution of new metabolic potential. FASEB Journal, 2013, 27, 203.2.	0.2	0