

Jorge Babul

List of Publications by Year in descending order

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40
papers

959
citations

623734

14
h-index

434195

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41
all docs

41
docs citations

41
times ranked

604
citing authors

#	ARTICLE	IF	CITATIONS
1	Human FoxP Transcription Factors as Tractable Models of the Evolution and Functional Outcomes of Three-Dimensional Domain Swapping. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10296.	4.1	2
2	Single-molecule optical tweezers reveals folding steps of the domain swapping mechanism of α -protein. <i>Biophysical Journal</i> , 2021, 120, 4809-4818.	0.5	2
3	Intrinsically Disordered Regions of the DNA-Binding Domain of Human FoxP1 Facilitate Domain Swapping. <i>Journal of Molecular Biology</i> , 2020, 432, 5411-5429.	4.2	12
4	Characterization of hydroxymethylpyrimidine phosphate kinase from mesophilic and thermophilic bacteria and structural insights into their differential thermal stability. <i>Archives of Biochemistry and Biophysics</i> , 2020, 688, 108389.	3.0	6
5	Studying the phosphoryl transfer mechanism of the <i>E. coli</i> phosphofructokinase-2: from X-ray structure to quantum mechanics/molecular mechanics simulations. <i>Chemical Science</i> , 2019, 10, 2882-2892.	7.4	15
6	The protonation state of an evolutionarily conserved histidine modulates domain swapping stability of FoxP1. <i>Scientific Reports</i> , 2019, 9, 5441.	3.3	15
7	Unusual dimerization of a Bc Csp mutant leads to reduced conformational dynamics. <i>FEBS Journal</i> , 2017, 284, 1882-1896.	4.7	2
8	New visible and selective DNA staining method in gels with tetrazolium salts. <i>Analytical Biochemistry</i> , 2017, 517, 31-35.	2.4	4
9	Regulatory network of the allosteric ATP inhibition of <i>E. coli</i> phosphofructokinase-2 studied by hybrid dimers. <i>Biochimie</i> , 2016, 128-129, 209-216.	2.6	2
10	Three-Dimensional Domain Swapping Changes the Folding Mechanism of the Forkhead Domain of FoxP1. <i>Biophysical Journal</i> , 2016, 110, 2349-2360.	0.5	29
11	Role of monovalent and divalent metal cations in human ribokinase catalysis and regulation. <i>BioMetals</i> , 2015, 28, 401-413.	4.1	12
12	The Folding Unit of Phosphofructokinase-2 as Defined by the Biophysical Properties of a Monomeric Mutant. <i>Biophysical Journal</i> , 2015, 108, 2350-2361.	0.5	8
13	Observation of Solvent Penetration during Cold Denaturation of <i>E. coli</i> Phosphofructokinase-2. <i>Biophysical Journal</i> , 2013, 104, 2254-2263.	0.5	11
14	A Ribokinase Family Conserved Monovalent Cation Binding Site Enhances the MgATP-induced Inhibition in <i>E. coli</i> Phosphofructokinase-2. <i>Biophysical Journal</i> , 2013, 105, 185-193.	0.5	11
15	Expanded Monomeric Intermediate upon Cold and Heat Unfolding of Phosphofructokinase-2 from <i>Escherichia coli</i> . <i>Biophysical Journal</i> , 2012, 103, 2187-2194.	0.5	8
16	Divalent metal cation requirements of phosphofructokinase-2 from <i>E. coli</i> . Evidence for a high affinity binding site for Mn ²⁺ . <i>Archives of Biochemistry and Biophysics</i> , 2011, 505, 60-66.	3.0	10
17	Folding kinetic pathway of phosphofructokinase-2 from <i>Escherichia coli</i> : A homodimeric enzyme with a complex domain organization. <i>FEBS Letters</i> , 2011, 585, 2158-2164.	2.8	6
18	The Crystal Complex of Phosphofructokinase-2 of <i>Escherichia coli</i> with Fructose-6-phosphate. <i>Journal of Biological Chemistry</i> , 2011, 286, 5774-5783.	3.4	26

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19	Ribokinase family evolution and the role of conserved residues at the active site of the PfkB subfamily representative, Pfk-2 from <i>Escherichia coli</i> . <i>Archives of Biochemistry and Biophysics</i> , 2010, 502, 23-30.	3.0	32
20	Reversible unfolding of dimeric phosphofructokinase-2 from <i>Escherichia coli</i> reveals a dominant role of inter-subunit contacts for stability. <i>FEBS Letters</i> , 2009, 583, 2054-2060.	2.8	9
21	Uncoupling the MgATP-induced inhibition and aggregation of <i>Escherichia coli</i> phosphofructokinase-2 by C-terminal mutations. <i>FEBS Letters</i> , 2008, 582, 1907-1912.	2.8	7
22	Crystallographic Structure of Phosphofructokinase-2 from <i>Escherichia coli</i> in Complex with Two ATP Molecules. Implications for Substrate Inhibition. <i>Journal of Molecular Biology</i> , 2008, 383, 588-602.	4.2	26
23	Unfolding Pathway of the Dimeric and Tetrameric Forms of Phosphofructokinase-2 from <i>Escherichia coli</i> . <i>Biochemistry</i> , 2007, 46, 6141-6148.	2.5	12
24	Role of Cys-295 on subunit interactions and allosteric regulation of phosphofructokinase-2 from <i>Escherichia coli</i> . <i>FEBS Letters</i> , 2005, 579, 2313-2318.	2.8	11
25	Domain Motions and Quaternary Packing of Phosphofructokinase-2 from <i>Escherichia coli</i> Studied by Small Angle X-ray Scattering and Homology Modeling. <i>Journal of Biological Chemistry</i> , 2003, 278, 12913-12919.	3.4	13
26	Structural and functional roles of Cys-238 and Cys-295 in <i>Escherichia coli</i> phosphofructokinase-2. <i>Biochemical Journal</i> , 2003, 376, 277-283.	3.7	2
27	Ligand-dependent structural changes and limited proteolysis of <i>Escherichia coli</i> phosphofructokinase-2. <i>Archives of Biochemistry and Biophysics</i> , 2002, 406, 289-295.	3.0	8
28	Ligand-Induced Conformational Transitions in <i>Escherichia coli</i> Phosphofructokinase 2: Evidence for an Allosteric Site for MgATP. <i>Biochemistry</i> , 1998, 37, 13269-13275.	2.5	29
29	A mutant phosphofructokinase produces a futile cycle during gluconeogenesis in <i>Escherichia coli</i> . <i>Biochemical Journal</i> , 1997, 327, 675-684.	3.7	37
30	An in vitro model showing different rates of substrate cycle for phosphofructokinases of <i>Escherichia coli</i> with different kinetic properties. <i>FEBS Journal</i> , 1991, 200, 471-476.	0.2	4
31	Determination of the molecular weight of proteins by electrophoresis in slab gels with a transverse pore gradient of crosslinked polyacrylamide in the absence of denaturing agents. <i>Analytical Biochemistry</i> , 1988, 175, 544-547.	2.4	15
32	Influence of ligands on the aggregation of the normal and mutant forms of phosphofructokinase 2 of <i>Escherichia coli</i> . <i>Archives of Biochemistry and Biophysics</i> , 1988, 264, 519-524.	3.0	21
33	Phosphate modification of fructose-1,6-bisphosphate aldolase in <i>Escherichia coli</i> . <i>Biochemical and Biophysical Research Communications</i> , 1988, 151, 1033-1038.	2.1	7
34	Fructose bisphosphatase from <i>Escherichia coli</i> . Purification and characterization. <i>Archives of Biochemistry and Biophysics</i> , 1983, 225, 944-949.	3.0	42
35	An Alteration in Phosphofructokinase 2 of <i>Escherichia coli</i> which Impairs Gluconeogenic Growth and Improves Growth on Sugars. <i>FEBS Journal</i> , 1982, 126, 373-379.	0.2	26
36	An examination of the involvement of proline peptide isomerization in protein folding. <i>Journal of Molecular Biology</i> , 1978, 126, 117-121.	4.2	20

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37	Are the Aerobic and Anaerobic Phosphofructokinases of Escherichia coli Different?. FEBS Journal, 1977, 74, 533-537.	0.2	11
38	Rat Liver Hexokinases during Development. Enzyme, 1975, 20, 334-348.	0.7	22
39	The structure of hemopeptide 1â€“65 from cytochrome c. Archives of Biochemistry and Biophysics, 1972, 148, 141-147.	3.0	16
40	Measurement of protein concentration with interferences optics. Analytical Biochemistry, 1969, 28, 216-221.	2.4	407