Hemalatha Balaram

List of Publications by Year
in descending order

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46	672	567281 15	642732 23
papers	citations	h-index	g-index

51	51	51	889
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Tertiary and Quaternary Structure Organization in GMP Synthetases: Implications for Catalysis. Biomolecules, 2022, 12, 871.	4.0	2
2	Structural basis for the hyperthermostability of an archaeal enzyme induced by succinimide formation. Biophysical Journal, 2021, 120, 3732-3746.	0.5	5
3	Toward Developing Intuitive Rules for Protein Variant Effect Prediction Using Deep Mutational Scanning Data. ACS Omega, 2020, 5, 29667-29677.	3.5	9
4	Helices on Interdomain Interface Couple Catalysis in the ATPPase Domain with Allostery in Plasmodium falciparum GMP Synthetase. ChemBioChem, 2020, 21, 2805-2817.	2.6	7
5	Structure and catalytic regulation of Plasmodium falciparum IMP specific nucleotidase. Nature Communications, 2020, 11, 3228.	12.8	4
6	How a purine salvage enzyme singles out the right base. Journal of Biological Chemistry, 2019, 294, 11992-11993.	3.4	0
7	Phosphoglycolate phosphatase is a metabolic proofreading enzyme essential for cellular function in Plasmodium berghei. Journal of Biological Chemistry, 2019, 294, 4997-5007.	3.4	3
8	Biochemical and physiological investigations on adenosine 5Ê¹ monophosphate deaminase from Plasmodium spp.. Molecular Microbiology, 2019, 112, 699-717.	2.5	1
9	Biochemical characterization and essentiality of fumarate hydratase. Journal of Biological Chemistry, 2018, 293, 5878-5894.	3.4	16
10	Connecting Activeâ€Site Loop Conformations and Catalysis in Triosephosphate Isomerase: Insights from a Rare Variation at Residueâ€...96 in the Plasmodial Enzyme. ChemBioChem, 2016, 17, 620-629.	2.6	9
11	Role of W181 in modulating kinetic properties of Plasmodium falciparum hypoxanthine guanine xanthine phosphoribosyltransferase. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1658-1669.	2.6	2
12	Product Release Pathways in Human and Plasmodium falciparum Phosphoribosyltransferase. Journal of Chemical Information and Modeling, 2016, 56, 1528-1538.	5.4	4
13	Unexpected functional implication of a stable succinimide in the structural stability of Methanocaldococcus jannaschii glutaminase. Nature Communications, 2016, 7, 12798.	12.8	22
14	Exquisite Modulation of the Active Site of Methanocaldococcus jannaschii Adenylosuccinate Synthetase in Forward Reaction Complexes. Biochemistry, 2016, 55, 2491-2499.	2.5	0
15	Structural and dynamical correlations in PfHGXPRT oligomers: A molecular dynamics simulation study. Journal of Biomolecular Structure and Dynamics, 2016, 34, 1590-1605.	3.5	3
16	Active site coupling in Plasmodium falciparum GMP synthetase is triggered by domain rotation. Nature Communications, 2015, 6, 8930.	12.8	24
17	Differential Distortion of Purine Substrates by Human and Plasmodium falciparum Hypoxanthineâ€Guanine Phosphoribosyltransferase to Catalyse the Formation of Mononucleotides. ChemPhysChem, 2015, 16, 2172-2181.	2.1	8
18	Probing the role of highly conserved residues in triosephosphate isomeraseÂâ€“Âanalysis of site specific mutants at positions 64 and 75 in the Plasmodial enzyme. FEBS Journal, 2015, 282, 3863-3882.	4.7	4

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19	Kinetic mechanism of Plasmodium falciparum hypoxanthine-guanine-xanthine phosphoribosyltransferase. Molecular and Biochemical Parasitology, 2015, 204, 111-120.	1.1	14
20	Prediction of substrate specificity and preliminary kinetic characterization of the hypothetical protein PVX_123945 from Plasmodium vivax. Experimental Parasitology, 2015, 151-152, 56-63.	1.2	8
21	Slow ligand-induced conformational switch increases the catalytic rate in Plasmodium falciparum hypoxanthine guanine xanthine phosphoribosyltransferase. Molecular BioSystems, 2015, 11, 1410-1424.	2.9	10
22	Deciphering Differential Distortion of Purine Substrates by Human and Plasmodium falciparum HGPRT. FASEB Journal, 2015, 29, 721.19.	0.5	0
23	A Histidine Aspartate Ionic Lock Gates the Iron Passage in Miniferritins from Mycobacterium smegmatis. Journal of Biological Chemistry, 2014, 289, 11042-11058.	3.4	17
24	Allosteric regulation and substrate activation in cytosolic nucleotidase <scp>II</scp> from <scp>L</scp>egionellaÂpneumophila. FEBS Journal, 2014, 281, 1613-1628.	4.7	29
25	Solution Nuclear Magnetic Resonance Structure of the GATase Subunit and Structural Basis of the Interaction between GATase and ATPPase Subunits in a two-subunit-type GMPS from Methanocaldococcus jannaschii. Biochemistry, 2013, 52, 4308-4323.	2.5	8
26	Mutational analysis of cysteine 328 and cysteine 368 at the interface of Plasmodium falciparum adenylosuccinate synthetase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2012, 1824, 589-597.	2.3	2
27	Hypoxanthine Guanine Phosphoribosyltransferase Distorts the Purine Ring of Nucleotide Substrates and Perturbs the pK_a of Bound Xanthosine Monophosphate. Biochemistry, 2011, 50, 4184-4193.	2.5	10
28	Ammonia Channeling in Plasmodium falciparum GMP Synthetase: Investigation by NMR Spectroscopy and Biochemical Assays. Biochemistry, 2011, 50, 3346-3356.	2.5	16
29	Mechanism of growth inhibition of intraerythrocytic stages of Plasmodium falciparum by 5-aminoimidazole-4-carboxamide ribonucleoside (AICAR). Molecular and Biochemical Parasitology, 2011, 177, 1-11.	1.1	8
30	Metabolic Fate of Fumarate, a Side Product of the Purine Salvage Pathway in the Intraerythrocytic Stages of Plasmodium falciparum. Journal of Biological Chemistry, 2011, 286, 9236-9245.	3.4	57
31	Reversible binding of zinc in Plasmodium falciparum Sir2: Structure and activity of the apoenzyme. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2010, 1804, 1743-1750.	2.3	25
32	Studies on active site mutants of P. falciparum adenylosuccinate synthetase: Insights into enzyme catalysis and activation. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2010, 1804, 1996-2002.	2.3	4
33	Elucidation of the substrate specificity, kinetic and catalytic mechanism of adenylosuccinate lyase from Plasmodium falciparum. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2009, 1794, 642-654.	2.3	40
34	Crystal structure of a chimera of human and plasmodium falciparum hypoxanthine guanine phosphoribosyltransferases provides insights into oligomerization. Proteins: Structure, Function and Bioinformatics, 2008, 73, 1010-1020.	2.6	5
35	Biochemical characterization of Plasmodium falciparum Sir2, a NAD+-dependent deacetylase. Molecular and Biochemical Parasitology, 2008, 158, 139-151.	1.1	42
36	Kinetic and biochemical characterization ofPlasmodium falciparumGMP synthetase. Biochemical Journal, 2008, 409, 263-273.	3.7	38

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37	Application of HPLC to study the kinetics of a branched bi-enzyme system consisting of hypoxanthine-guanine phosphoribosyltransferase and xanthine oxidaseâ€"an important biochemical system to evaluate the efficiency of the anticancer drug 6-mercaptopurine in ALL cell line. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2007, 850, 7-14.	2.3	10
38	ISN1 nucleotidases and HAD superfamily protein fold: in silico sequence and structure analysis. In Silico Biology, 2007, 7, 187-93.	0.9	9
39	Plasmodiumâ€ƒfalciparum hypoxanthine guanine phosphoribosyltransferase. FEBS Journal, 2005, 272, 1900-1911.	4.7	17
40	Unique kinetic mechanism of Plasmodium falciparum adenylosuccinate synthetase. Molecular and Biochemical Parasitology, 2004, 138, 1-8.	1.1	27
41	A non-active site mutation in human hypoxanthine guanine phosphoribosyltransferase expands substrate specificity. Archives of Biochemistry and Biophysics, 2004, 427, 116-122.	3.0	13
42	Purification and Characterization of Recombinant Plasmodium falciparum Adenylosuccinate Synthetase Expressed in Escherichia coli. Protein Expression and Purification, 2002, 25, 65-72.	1.3	32
43	A point mutation at the subunit interface of hypoxanthine-guanine-xanthine phosphoribosyltransferase impairs activity: role of oligomerization in catalysis. FEBS Letters, 2002, 521, 72-76.	2.8	12
44	Synthetic peptides as inactivators of multimeric enzymes: inhibition ofPlasmodium falciparumtriosephosphate isomerase by interface peptides. FEBS Letters, 2001, 501, 19-23.	2.8	48
45	Unusual Substrate Specificity of a Chimeric Hypoxanthineâ€"Guanine Phosphoribosyltransferase Containing Segments from the Plasmodium falciparum and Human Enzymes. Biochemical and Biophysical Research Communications, 2000, 272, 596-602.	2.1	27
46	Evidence for Multiple Active States of Plasmodium falciparum Hypoxanthineâ€"Guanineâ€"Xanthine Phosphoribosyltransferase. Biochemical and Biophysical Research Communications, 2000, 279, 433-437.	2.1	21