

Sanchita Hati

List of Publications by Year in descending order

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Version: 2024-02-01

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papers

624
citations

840776

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713466

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22
times ranked

905
citing authors

#	ARTICLE	IF	CITATIONS
1	Role of Oxidative Stress on SARS-CoV (SARS) and SARS-CoV-2 (COVID-19) Infection: A Review. Protein Journal, 2020, 39, 644-656.	1.6	213
2	Impact of Thiol-Disulfide Balance on the Binding of Covid-19 Spike Protein with Angiotensin-Converting Enzyme 2 Receptor. ACS Omega, 2020, 5, 16292-16298.	3.5	140
3	Pre-transfer Editing by Class II Prolyl-tRNA Synthetase. Journal of Biological Chemistry, 2006, 281, 27862-27872.	3.4	54
4	Interplay of Flavin's Redox States and Protein Dynamics: An Insight from QM/MM Simulations of Dihyronicotinamide Riboside Quinone Oxidoreductase 2. Journal of Physical Chemistry B, 2011, 115, 3632-3641.	2.6	26
5	Evolutionary Basis for the Coupled-domain Motions in Thermus thermophilus Leucyl-tRNA Synthetase. Journal of Biological Chemistry, 2009, 284, 10088-10099.	3.4	20
6	Vitamin D and COVID-19: A review on the role of vitamin D in preventing and reducing the severity of COVID-19 infection. Protein Science, 2021, 30, 2206-2220.	7.6	20
7	Strictly Conserved Lysine of Prolyl-tRNA Synthetase Editing Domain Facilitates Binding and Positioning of Misacylated tRNA ^{Pro} . Biochemistry, 2014, 53, 1059-1068.	2.5	19
8	Role of Coupled Dynamics in the Catalytic Activity of Prokaryotic-like Prolyl-tRNA Synthetases. Biochemistry, 2012, 51, 2146-2156.	2.5	17
9	Multiple Pathways Promote Dynamical Coupling between Catalytic Domains in <i>Escherichia coli</i> Prolyl-tRNA Synthetase. Biochemistry, 2013, 52, 4399-4412.	2.5	16
10	Incorporating modeling and simulations in undergraduate biophysical chemistry course to promote understanding of structure-dynamics-function relationships in proteins. Biochemistry and Molecular Biology Education, 2016, 44, 140-159.	1.2	14
11	Probing the global and local dynamics of aminoacyl-tRNA synthetases using all-atom and coarse-grained simulations. Journal of Molecular Modeling, 2014, 20, 2245.	1.8	13
12	Crowder-Induced Conformational Ensemble Shift in Escherichia coli Prolyl-tRNA Synthetase. Biophysical Journal, 2019, 117, 1269-1284.	0.5	12
13	Comparison of the Intrinsic Dynamics of Aminoacyl-tRNA Synthetases. Protein Journal, 2014, 33, 184-198.	1.6	11
14	Pre-Existing Oxidative Stress Creates a Docking-Ready Conformation of the SARS-CoV-2 Receptor-Binding Domain. ACS Bio & Med Chem Au, 2022, 2, 84-93.	3.7	11
15	Comparison of intrinsic dynamics of cytochrome p450 proteins using normal mode analysis. Protein Science, 2015, 24, 1495-1507.	7.6	9
16	Cyclic Changes in Active Site Polarization and Dynamics Drive the "Ping-pong" Kinetics in NRH:Quinone Oxidoreductase 2: An Insight from QM/MM Simulations. ACS Catalysis, 2018, 8, 12015-12029.	11.2	7
17	Effects of Distal Mutations on Prolyl-Adenylate Formation of Escherichia coli Prolyl-tRNA Synthetase. Protein Journal, 2020, 39, 542-553.	1.6	5
18	Investigation of intrinsic dynamics of enzymes involved in metabolic pathways using coarse-grained normal mode analysis. Cogent Biology, 2017, 3, 1291877.	1.7	4

#	ARTICLE	IF	CITATIONS
19	Insight into the kinetics and thermodynamics of the hydride transfer reactions between quinones and lumiflavin: a density functional theory study. <i>Journal of Molecular Modeling</i> , 2016, 22, 199.	1.8	3
20	Integrating Research into the Curriculum: A Low-Cost Strategy for Promoting Undergraduate Research. <i>ACS Symposium Series</i> , 2018, , 119-141.	0.5	2
21	Editing Domain Motions Preorganize the Synthetic Active Site of Prolyl-tRNA Synthetase. <i>ACS Catalysis</i> , 2020, 10, 10229-10242.	11.2	2