

Ruchi Anand

List of Publications by Year in descending order

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45
papers

1,162
citations

471061

17
h-index

395343

33
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48
all docs

48
docs citations

48
times ranked

1682
citing authors

#	ARTICLE	IF	CITATIONS
1	Mechanism of Coordinated Gating and Signal Transduction in Purine Biosynthetic Enzyme Formylglycinamide Synthetase. <i>ACS Catalysis</i> , 2022, 12, 1930-1944.	5.5	5
2	Decoding the Mechanism of Specific RNA Targeting by Ribosomal Methyltransferases. <i>ACS Chemical Biology</i> , 2022, 17, 829-839.	1.6	3
3	Harnessing the Potential of Biological Recognition Elements for Water Pollution Monitoring. <i>ACS Sensors</i> , 2022, 7, 704-715.	4.0	13
4	Identification of allosteric hotspots regulating the ribosomal RNA binding by antibiotic resistance-conferring Erm methyltransferases. <i>Journal of Biological Chemistry</i> , 2022, 298, 102208.	1.6	4
5	Deciphering protein microenvironment by using a cysteine specific switch-ON fluorescent probe. <i>Organic and Biomolecular Chemistry</i> , 2021, 19, 5161-5168.	1.5	3
6	Tunable Multiplexed Whole-Cell Biosensors as Environmental Diagnostics for ppb-Level Detection of Aromatic Pollutants. <i>ACS Sensors</i> , 2021, 6, 1933-1939.	4.0	26
7	Insights into the Dual Shuttle Catalytic Mechanism of Guanine Deaminase. <i>Journal of Physical Chemistry B</i> , 2021, 125, 8814-8826.	1.2	4
8	Structure guided mutagenesis reveals the substrate determinants of guanine deaminase. <i>Journal of Structural Biology</i> , 2021, 213, 107747.	1.3	3
9	The Coenzyme A Level Modulator Hopantenate (HoPan) Inhibits Phosphopantotenoylcysteine Synthetase Activity. <i>ACS Chemical Biology</i> , 2021, 16, 2401-2414.	1.6	7
10	Tunnel Architectures in Enzyme Systems that Transport Gaseous Substrates. <i>ACS Omega</i> , 2021, 6, 33274-33283.	1.6	4
11	Role of allosteric switches and adaptor domains in long-distance cross-talk and transient tunnel formation. <i>Science Advances</i> , 2020, 6, eaay7919.	4.7	10
12	Structural basis for differentiation between two classes of thiolase: Degradative vs biosynthetic thiolase. <i>Journal of Structural Biology: X</i> , 2020, 4, 100018.	0.7	8
13	A combinatorial approach involving <i>E. coli</i> cytosine deaminase and 5-fluorocytosine-nanoparticles as an enzyme-prodrug therapeutic method for highly substrate selective in situ generation of 5-fluorouracil. <i>Journal of Drug Delivery Science and Technology</i> , 2020, 58, 101799.	1.4	4
14	Use of 6-Methylisoxanthopterin, a Fluorescent Guanine Analog, to Probe Fob1-Mediated Dynamics at the Stalling Fork Barrier DNA Sequences. <i>Chemistry - an Asian Journal</i> , 2019, 14, 4760-4766.	1.7	1
15	Deciphering Determinants in Ribosomal Methyltransferases That Confer Antimicrobial Resistance. <i>Journal of the American Chemical Society</i> , 2019, 141, 1425-1429.	6.6	18
16	Fluorescence Quenching Studies of β -Butyrolactone-Binding Protein (CprB) from <i>Streptomyces coelicolor</i> A3(2). <i>Methods in Molecular Biology</i> , 2018, 1673, 131-143.	0.4	1
17	Nucleobase deaminases: a potential enzyme system for new therapies. <i>RSC Advances</i> , 2018, 8, 23567-23577.	1.7	10
18	Design of Protein-Based Biosensors for Selective Detection of Benzene Groups of Pollutants. <i>ACS Sensors</i> , 2018, 3, 1632-1638.	4.0	27

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19	Design of Ultrasensitive Protein Biosensor Strips for Selective Detection of Aromatic Contaminants in Environmental Wastewater. <i>Analytical Chemistry</i> , 2018, 90, 8960-8968.	3.2	17
20	Structure Guided Design of Protein Biosensors for Phenolic Pollutants. <i>ACS Sensors</i> , 2017, 2, 411-418.	4.0	25
21	TetR Regulators: A Structural and Functional Perspective. <i>Journal of the Indian Institute of Science</i> , 2017, 97, 245-259.	0.9	13
22	Rassf Proteins as Modulators of Mst1 Kinase Activity. <i>Scientific Reports</i> , 2017, 7, 45020.	1.6	26
23	Structural and dynamics studies of the TetR family protein, CprB from <i>Streptomyces coelicolor</i> in complex with its biological operator sequence. <i>Journal of Structural Biology</i> , 2017, 198, 134-146.	1.3	11
24	Site-Specific Fluorescence Dynamics To Probe Polar Arrest by Fob1 in Replication Fork Barrier Sequences. <i>ACS Omega</i> , 2017, 2, 7389-7399.	1.6	4
25	Selective Deamination of Mutagens by a Mycobacterial Enzyme. <i>Journal of the American Chemical Society</i> , 2017, 139, 10762-10768.	6.6	5
26	Functional insights into the mode of DNA and ligand binding of the TetR family regulator TylP from <i>Streptomyces fradiae</i> . <i>Journal of Biological Chemistry</i> , 2017, 292, 15301-15311.	1.6	12
27	Structural Basis of Selective Aromatic Pollutant Sensing by the Effector Binding Domain of MopR, an NtrC Family Transcriptional Regulator. <i>ACS Chemical Biology</i> , 2016, 11, 2357-2365.	1.6	35
28	Determination of the Formylglycinamide Ribonucleotide Amidotransferase Ammonia Pathway by Combining 3D-RISM Theory with Experiment. <i>ACS Chemical Biology</i> , 2015, 10, 698-704.	1.6	11
29	Mode of DNA binding with \hat{I}^3 -butyrolactone receptor protein CprB from <i>Streptomyces coelicolor</i> revealed by site-specific fluorescence dynamics. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2015, 1850, 2283-2292.	1.1	3
30	Structural and functional basis of transcriptional regulation by TetR family protein CprB from <i>S. coelicolor</i> A3(2). <i>Nucleic Acids Research</i> , 2014, 42, 10122-10133.	6.5	49
31	Fluorescence Quenching Studies of \hat{I}^3 -Butyrolactone Binding Protein (CprB) from <i>Streptomyces coelicolor</i> A3(2). <i>Journal of Physical Chemistry B</i> , 2014, 118, 10035-10042.	1.2	18
32	Identification of Function and Mechanistic Insights of Guanine Deaminase from <i>Nitrosomonas europaea</i> : Role of the C-Terminal Loop in Catalysis. <i>Biochemistry</i> , 2013, 52, 3512-3522.	1.2	11
33	Structural Basis of the Substrate Specificity of Cytidine Deaminase Superfamily Guanine Deaminase. <i>Biochemistry</i> , 2013, 52, 8106-8114.	1.2	14
34	Importance of Hydrophobic Cavities in Allosteric Regulation of Formylglycinamide Synthetase: Insight from Xenon Trapping and Statistical Coupling Analysis. <i>PLoS ONE</i> , 2013, 8, e77781.	1.1	20
35	Formylglycinamide ribonucleotide amidotransferase from <i>Salmonella typhimurium</i> : role of ATP complexation and the glutaminase domain in catalytic coupling. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 627-636.	2.5	7
36	Toward the Development of a Potent and Selective Organoruthenium Mammalian Sterile 20 Kinase Inhibitor. <i>Journal of Medicinal Chemistry</i> , 2009, 52, 1602-1611.	2.9	74

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37	Structural Basis for DNA Recognition by FoxO1 and Its Regulation by Posttranslational Modification. <i>Structure</i> , 2008, 16, 1407-1416.	1.6	172
38	Structure and Mechanism of Lysine-specific Demethylase Enzymes. <i>Journal of Biological Chemistry</i> , 2007, 282, 35425-35429.	1.6	114
39	Complexed Structures of Formylglycinamide Ribonucleotide Amidotransferase from <i>Thermotoga maritima</i> Describe a Novel ATP Binding Protein Superfamily. <i>Biochemistry</i> , 2006, 45, 14880-14895.	1.2	26
40	A Model for the <i>Bacillus subtilis</i> Formylglycinamide Ribonucleotide Amidotransferase Multiprotein Complex. <i>Biochemistry</i> , 2004, 43, 10343-10352.	1.2	26
41	The Formylglycinamide Ribonucleotide Amidotransferase Complex from <i>Bacillus subtilis</i> : A Metabolite-Mediated Complex Formation. <i>Biochemistry</i> , 2004, 43, 10314-10327.	1.2	29
42	Domain Organization of <i>Salmonella typhimurium</i> Formylglycinamide Ribonucleotide Amidotransferase Revealed by X-ray Crystallography. <i>Biochemistry</i> , 2004, 43, 10328-10342.	1.2	59
43	Structures of Purine 2-Deoxyribosyltransferase, Substrate Complexes, and the Ribosylated Enzyme Intermediate at 2.0 Å... Resolution. <i>Biochemistry</i> , 2004, 43, 2384-2393.	1.2	42
44	Designer Gene Therapy Using an <i>Escherichia coli</i> Purine Nucleoside Phosphorylase/Prodrug System. <i>Chemistry and Biology</i> , 2003, 10, 1173-1181.	6.2	43
45	Structure of Oxalate Decarboxylase from <i>Bacillus subtilis</i> at 1.75 Å... Resolution. <i>Biochemistry</i> , 2002, 41, 7659-7669.	1.2	144