

Shveta Bisht

List of Publications by Year in descending order

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Version: 2024-02-01

15
papers

1,219
citations

840119

11
h-index

1058022

14
g-index

17
all docs

17
docs citations

17
times ranked

1304
citing authors

#	ARTICLE	IF	CITATIONS
1	Real-time imaging of DNA loop extrusion by condensin. <i>Science</i> , 2018, 360, 102-105.	6.0	624
2	The condensin complex is a mechanochemical motor that translocates along DNA. <i>Science</i> , 2017, 358, 672-676.	6.0	266
3	Structural Basis for a Safety-Belt Mechanism That Anchors Condensin to Chromosomes. <i>Cell</i> , 2017, 171, 588-600.e24.	13.5	144
4	Real-time detection of condensin-driven DNA compaction reveals a multistep binding mechanism. <i>EMBO Journal</i> , 2017, 36, 3448-3457.	3.5	71
5	Electrospray mass spectrometric characterization of hemoglobin Q (Hb Q-India) and a double mutant hemoglobin S/D in clinical samples. <i>Clinical Biochemistry</i> , 2008, 41, 75-81.	0.8	21
6	Crystal Structure of Escherichia coli Diaminopropionate Ammonia-lyase Reveals Mechanism of Enzyme Activation and Catalysis. <i>Journal of Biological Chemistry</i> , 2012, 287, 20369-20381.	1.6	15
7	Structural and Mutational Studies on Substrate Specificity and Catalysis of Salmonella typhimurium D-Cysteine Desulphydrase. <i>PLoS ONE</i> , 2012, 7, e36267.	1.1	15
8	Structural and functional studies of Bacillus stearothermophilus serine hydroxymethyltransferase: the role of Asn341, Tyr60 and Phe351 in tetrahydrofolate binding. <i>Biochemical Journal</i> , 2009, 418, 635-642.	1.7	14
9	Mechanistic Insights into the Neutralization of Cytotoxic Abrin by the Monoclonal Antibody D6F10. <i>PLoS ONE</i> , 2013, 8, e70273.	1.1	13
10	Crystal structures of open and closed forms of serine deaminase from Salmonella typhimurium implications on substrate specificity and catalysis. <i>FEBS Journal</i> , 2011, 278, 2879-2891.	2.2	12
11	Importance of tyrosine residues of Bacillus stearothermophilus serine hydroxymethyltransferase in cofactor binding and allo-Thr cleavage. <i>FEBS Journal</i> , 2008, 275, 4606-4619.	2.2	11
12	Modeling of DNA binding to the condensin hinge domain using molecular dynamics simulations guided by atomic force microscopy. <i>PLoS Computational Biology</i> , 2021, 17, e1009265.	1.5	4
13	Identification of key amino acid residues in the catalytic mechanism of diaminopropionate ammonialyase from Salmonella typhimurium. <i>FEBS Journal</i> , 2013, 280, 5039-5051.	2.2	3
14	Twist to disentangle. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 252-253.	3.6	1
15	Prediction of Protein-Protein Interactions Between Human Host and Two Mycobacterial Organisms. <i>International Journal of Knowledge Discovery in Bioinformatics</i> , 2010, 1, 1-13.	0.8	0