

Sarvind M Tripathi

List of Publications by Year in descending order

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35
papers

1,241
citations

430442

18
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414034

32
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46
all docs

46
docs citations

46
times ranked

1771
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural Basis for Effector Control and Redox Partner Recognition in Cytochrome P450. <i>Science</i> , 2013, 340, 1227-1230.	6.0	160
2	Structural basis of the day-night transition in a bacterial circadian clock. <i>Science</i> , 2017, 355, 1174-1180.	6.0	144
3	p27 allosterically activates cyclin-dependent kinase 4 and antagonizes palbociclib inhibition. <i>Science</i> , 2019, 366, .	6.0	132
4	Formation of a repressive complex in the mammalian circadian clock is mediated by the secondary pocket of CRY1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1560-1565.	3.3	92
5	Structural basis for LIN54 recognition of CHR elements in cell cycle-regulated promoters. <i>Nature Communications</i> , 2016, 7, 12301.	5.8	52
6	Casein kinase 1 dynamics underlie substrate selectivity and the PER2 circadian phosphoswitch. <i>ELife</i> , 2020, 9, .	2.8	52
7	Dynamics at the serine loop underlie differential affinity of cryptochromes for CLOCK:BMAL1 to control circadian timing. <i>ELife</i> , 2020, 9, .	2.8	50
8	Molecular determinants of chaperone interactions on MHC-I for folding and antigen repertoire selection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25602-25613.	3.3	43
9	Structural basis of divergent cyclin-dependent kinase activation by Spy1/RINGO proteins. <i>EMBO Journal</i> , 2017, 36, 2251-2262.	3.5	40
10	A Recurrent Mutation in Anaplastic Lymphoma Kinase with Distinct Neoepitope Conformations. <i>Frontiers in Immunology</i> , 2018, 9, 99.	2.2	35
11	Conservation and divergence of C-terminal domain structure in the retinoblastoma protein family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4942-4947.	3.3	33
12	Reconstitution of an intact clock reveals mechanisms of circadian timekeeping. <i>Science</i> , 2021, 374, eabd4453.	6.0	32
13	Crystal structures of the <i>Mycobacterium tuberculosis</i> secretory antigen alanine dehydrogenase (Rv2780) in apo and ternary complex forms captures "open" and "closed" enzyme conformations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 1089-1095.	1.5	30
14	Structural, Mechanistic, and Antigenic Characterization of the Human Astrovirus Capsid. <i>Journal of Virology</i> , 2016, 90, 2254-2263.	1.5	30
15	Structural mechanism of Myb-MuvB assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10016-10021.	3.3	30
16	Direct Evidence for a Glutamate Switch Necessary for Substrate Recognition: Crystal Structures of Lysine μ -Aminotransferase (Rv3290c) from <i>Mycobacterium tuberculosis</i> H37Rv. <i>Journal of Molecular Biology</i> , 2006, 362, 877-886.	2.0	26
17	Ligand and Redox Partner Binding Generates a New Conformational State in Cytochrome P450cam (CYP101A1). <i>Journal of the American Chemical Society</i> , 2019, 141, 2678-2683.	6.6	23
18	Crystal Structure of Cindoxin, the P450cin Redox Partner. <i>Biochemistry</i> , 2014, 53, 1435-1446.	1.2	19

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19	Overexpression, purification and crystallization of lysine α -aminotransferase (Rv3290c) from <i>Mycobacterium tuberculosis</i> H37Rv. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 572-575.	0.7	17
20	Crystal Structures of Substrate-Free and Nitrosyl Cytochrome P450cin: Implications for O ₂ Activation. <i>Biochemistry</i> , 2012, 51, 6623-6631.	1.2	15
21	Crystal structure of the <i>Pseudomonas aeruginosa</i> cytoplasmic heme binding protein, Apo-PhuS. <i>Journal of Inorganic Biochemistry</i> , 2013, 128, 131-136.	1.5	14
22	The MuvB complex binds and stabilizes nucleosomes downstream of the transcription start site of cell-cycle dependent genes. <i>Nature Communications</i> , 2022, 13, 526.	5.8	12
23	A tyrosine phosphoregulatory system controls exopolysaccharide biosynthesis and biofilm formation in <i>Vibrio cholerae</i> . <i>PLoS Pathogens</i> , 2020, 16, e1008745.	2.1	10
24	Identification of in vitro inhibitors of <i>Mycobacterium tuberculosis</i> Lysine μ -aminotransferase by pharmacophore mapping and three-dimensional flexible searches. <i>Medicinal Chemistry Research</i> , 2008, 17, 182-188.	1.1	9
25	Enzymatic Mechanism of <i>Leishmania major</i> Peroxidase and the Critical Role of Specific Ionic Interactions. <i>Biochemistry</i> , 2015, 54, 3328-3336.	1.2	9
26	Docking and mutagenesis studies lead to improved inhibitor development of ML355 for human platelet 12-lipoxygenase. <i>Bioorganic and Medicinal Chemistry</i> , 2021, 46, 116347.	1.4	9
27	A long lost key opens an ancient lock: <i>Drosophila</i> Myb causes a synthetic multivulval phenotype in nematodes. <i>Biology Open</i> , 2020, 9, .	0.6	8
28	Testing the N-Terminal Velcro Model of CoaA Carbon Monoxide Activation. <i>Biochemistry</i> , 2018, 57, 3059-3064.	1.2	6
29	Structural basis for tunable affinity and specificity of LxCxE-dependent protein interactions with the retinoblastoma protein family. <i>Structure</i> , 2022, 30, 1340-1353.e3.	1.6	6
30	Overexpression, purification, crystallization and preliminary X-ray analysis of Rv2780 from <i>Mycobacterium tuberculosis</i> H37Rv. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 367-370.	0.7	4
31	Mutational analysis of <i>Mycobacterium tuberculosis</i> lysine ϵ -aminotransferase and inhibitor co-crystal structures, reveals distinct binding modes. <i>Biochemical and Biophysical Research Communications</i> , 2015, 463, 154-160.	1.0	3
32	Structural Insights on the Conversion of Cytochrome P450 to P420. <i>ACS Omega</i> , 2022, 7, 18481-18485.	1.6	3
33	Dissecting binding of a β -barrel membrane protein by phage display. <i>Molecular BioSystems</i> , 2017, 13, 1438-1447.	2.9	2
34	Abstract 4891: Identification of recurrent high-affinity MHC class I restricted neo-epitopes in neuroblastoma using ProTECT. , 2017, , .		0
35	Abstract B02: Distinct CD8+ T-cell recognition profiles driven by conformational plasticity of recurrent neuroblastoma neoepitopes. , 2018, , .		0