

Sarvind M Tripathi

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

33
papers

735
citations

16
h-index

26
g-index

46
ext. papers

1,034
ext. citations

11.9
avg, IF

4.1
L-index

#	Paper	IF	Citations
33	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	17.4	0
32	Cross-HLA targeting of intracellular oncoproteins with peptide-centric CARs. <i>Nature</i> , 2021 , 599, 477-484	50.4	14
31	Reconstitution of an intact clock reveals mechanisms of circadian timekeeping. <i>Science</i> , 2021 , 374, eabd4453	44.53	12
30	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	3.4	2
29	A long lost key opens an ancient lock: Myb causes a synthetic multivulval phenotype in nematodes. <i>Biology Open</i> , 2020 , 9,	2.2	3
28	Casein kinase 1 dynamics underlie substrate selectivity and the PER2 circadian phosphoswitch. <i>ELife</i> , 2020 , 9,	8.9	26
27	Dynamics at the serine loop underlie differential affinity of cryptochromes for CLOCK:BMAL1 to control circadian timing. <i>ELife</i> , 2020 , 9,	8.9	27
26	A tyrosine phosphoregulatory system controls exopolysaccharide biosynthesis and biofilm formation in <i>Vibrio cholerae</i> . <i>PLoS Pathogens</i> , 2020 , 16, e1008745	7.6	4
25	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	16.4	15
24	p27 allosterically activates cyclin-dependent kinase 4 and antagonizes palbociclib inhibition. <i>Science</i> , 2019 , 366,	33.3	52
23	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	11.5	24
22	Testing the N-Terminal Velcro Model of CoxA Carbon Monoxide Activation. <i>Biochemistry</i> , 2018 , 57, 3059-3064	32.64	4
21	A Recurrent Mutation in Anaplastic Lymphoma Kinase with Distinct Neoepitope Conformations. <i>Frontiers in Immunology</i> , 2018 , 9, 99	8.4	16
20	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	11.5	14
19	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	11.5	56
18	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	11.5	19
17	Dissecting binding of a β barrel membrane protein by phage display. <i>Molecular BioSystems</i> , 2017 , 13, 1438-1447		2

16	Structural basis of the day-night transition in a bacterial circadian clock. <i>Science</i> , 2017 , 355, 1174-1180	33.3	99
15	Structural basis of divergent cyclin-dependent kinase activation by Spy1/RINGO proteins. <i>EMBO Journal</i> , 2017 , 36, 2251-2262	13	23
14	Structural basis for LIN54 recognition of CHR elements in cell cycle-regulated promoters. <i>Nature Communications</i> , 2016 , 7, 12301	17.4	36
13	Structural, Mechanistic, and Antigenic Characterization of the Human Astrovirus Capsid. <i>Journal of Virology</i> , 2015 , 90, 2254-63	6.6	24
12	Mutational analysis of Mycobacterium tuberculosis lysine ε-aminotransferase and inhibitor co-crystal structures, reveals distinct binding modes. <i>Biochemical and Biophysical Research Communications</i> , 2015 , 463, 154-60	3.4	2
11	Enzymatic Mechanism of Leishmania major Peroxidase and the Critical Role of Specific Ionic Interactions. <i>Biochemistry</i> , 2015 , 54, 3328-36	3.2	6
10	Crystal structure of cindoxin, the P450cin redox partner. <i>Biochemistry</i> , 2014 , 53, 1435-46	3.2	16
9	Crystal structure of the Pseudomonas aeruginosa cytoplasmic heme binding protein, Apo-PhuS. <i>Journal of Inorganic Biochemistry</i> , 2013 , 128, 131-6	4.2	11
8	Structural basis for effector control and redox partner recognition in cytochrome P450. <i>Science</i> , 2013 , 340, 1227-30	33.3	138
7	Crystal structures of substrate-free and nitrosyl cytochrome P450cin: implications for O ₂ activation. <i>Biochemistry</i> , 2012 , 51, 6623-31	3.2	14
6	Identification of in vitro inhibitors of Mycobacterium tuberculosis Lysine ε-aminotransferase by pharmacophore mapping and three-dimensional flexible searches. <i>Medicinal Chemistry Research</i> , 2008 , 17, 182-188	2.2	7
5	Overexpression, purification, crystallization and preliminary X-ray analysis of Rv2780 from Mycobacterium tuberculosis H37Rv. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 367-70		4
4	Crystal structures of the Mycobacterium tuberculosis 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, 1089-95	4.2	20
3	Direct evidence for a glutamate switch necessary for substrate recognition: crystal structures of lysine ε-aminotransferase (Rv3290c) from Mycobacterium tuberculosis H37Rv. <i>Journal of Molecular Biology</i> , 2006 , 362, 877-86	6.5	22
2	Overexpression, purification and crystallization of lysine ε-aminotransferase (Rv3290c) from Mycobacterium tuberculosis H37Rv. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006 , 62, 572-5		16
1	Structural mimicry confers robustness in the cyanobacterial circadian clock		4