

Mahavir Singh

List of Publications by Year in descending order

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Version: 2024-02-01

14
papers

249
citations

1307594

7
h-index

1058476

14
g-index

16
all docs

16
docs citations

16
times ranked

441
citing authors

#	ARTICLE	IF	CITATIONS
1	RGG-box in hnRNPA1 specifically recognizes the telomere G-quadruplex DNA and enhances the G-quadruplex unfolding ability of UP1 domain. <i>Nucleic Acids Research</i> , 2018, 46, 10246-10261.	14.5	58
2	SIRT2 regulates oxidative stress-induced cell death through deacetylation of c-Jun NH2-terminal kinase. <i>Cell Death and Differentiation</i> , 2018, 25, 1638-1656.	11.2	43
3	SIRT2 deacetylase regulates the activity of GSK3 isoforms independent of inhibitory phosphorylation. <i>ELife</i> , 2018, 7, .	6.0	40
4	SIRT6 transcriptionally regulates global protein synthesis through transcription factor Sp1 independent of its deacetylase activity. <i>Nucleic Acids Research</i> , 2019, 47, 9115-9131.	14.5	36
5	Structure specific recognition of telomeric repeats containing RNA by the RGG-box of hnRNPA1. <i>Nucleic Acids Research</i> , 2020, 48, 4492-4506.	14.5	20
6	Domain architecture of BAF250a reveals the ARID and ARM-repeat domains with implication in function and assembly of the BAF remodeling complex. <i>PLoS ONE</i> , 2018, 13, e0205267.	2.5	19
7	2.09 Å Resolution structure of <i>E. coli</i> HigBA toxin-antitoxin complex reveals an ordered DNA-binding domain and intrinsic dynamics in antitoxin. <i>Biochemical Journal</i> , 2020, 477, 4001-4019.	3.7	8
8	Molecular determinants of complex formation between DNA and the AT-rich interaction domain of BAF 250a. <i>FEBS Letters</i> , 2019, 593, 2716-2729.	2.8	7
9	Signatures of Specific DNA Binding by the AT-Rich Interaction Domain of BAF250a. <i>Biochemistry</i> , 2020, 59, 100-113.	2.5	6
10	Identification, functional characterization, assembly and structure of ToxIN type III toxin-antitoxin complex from <i>E. coli</i> . <i>Nucleic Acids Research</i> , 2022, 50, 1687-1700.	14.5	4
11	Mechanistic Insights into the Differential Catalysis by RheB and Its Mutants: Y35A and Y35A-D65A. <i>ACS Omega</i> , 2017, 2, 6691-6702.	3.5	2
12	Sequential backbone resonance assignment of AT-rich interaction domain of human BAF200. <i>Biomolecular NMR Assignments</i> , 2019, 13, 115-119.	0.8	2
13	Resonance assignment and secondary structure of the tandem harmonin homology domains of human RTEL1. <i>Biomolecular NMR Assignments</i> , 2022, 16, 159-164.	0.8	2
14	Structure and DNA binding analysis of AT-rich interaction domain present in human BAF-specific subunit BAF250b. <i>Protein Science</i> , 2022, 31, e4294.	7.6	1