

Hongda Huang

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

1,580
citations

623734

14
h-index

839539

18
g-index

19
all docs

19
docs citations

19
times ranked

2483
citing authors

#	ARTICLE	IF	CITATIONS
1	NASP maintains histone H3â€“H4 homeostasis through two distinct H3 binding modes. <i>Nucleic Acids Research</i> , 2022, 50, 5349-5368.	14.5	21
2	Structural basis for histone H3 recognition by NASP in <i>Arabidopsis</i> . <i>Journal of Integrative Plant Biology</i> , 2022, , .	8.5	2
3	MARK4 controls ischaemic heart failure through microtubule detyrosination. <i>Nature</i> , 2021, 594, 560-565.	27.8	52
4	DNAJC9 integrates heat shock molecular chaperones into the histone chaperone network. <i>Molecular Cell</i> , 2021, 81, 2533-2548.e9.	9.7	31
5	Structural basis for anti-CRISPR repression mediated by bacterial operon proteins Aca1 and Aca2. <i>Journal of Biological Chemistry</i> , 2021, 297, 101357.	3.4	7
6	Molecular basis of abasic site sensing in single-stranded DNA by the SRAP domain of <i>E. coli</i> yedK. <i>Nucleic Acids Research</i> , 2019, 47, 10388-10399.	14.5	22
7	Structural basis of tubulin detyrosination by the vasohibinâ€“SVBP enzyme complex. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 571-582.	8.2	42
8	Molecular basis of vasohibins-mediated detyrosination and its impact on spindle function and mitosis. <i>Cell Research</i> , 2019, 29, 533-547.	12.0	56
9	Histone chaperone networks shaping chromatin function. <i>Nature Reviews Molecular Cell Biology</i> , 2017, 18, 141-158.	37.0	401
10	Structural and mechanistic insights into ATRX-dependent and -independent functions of the histone chaperone DAXX. <i>Nature Communications</i> , 2017, 8, 1193.	12.8	84
11	Structural basis underlying viral hijacking of a histone chaperone complex. <i>Nature Communications</i> , 2016, 7, 12707.	12.8	27
12	H4K20me0 marks post-replicative chromatin and recruits the TONSLâ€“MMS22L DNA repair complex. <i>Nature</i> , 2016, 534, 714-718.	27.8	172
13	The CENP-T/W complex is a binding partner of the histone chaperone FACT. <i>Genes and Development</i> , 2016, 30, 1313-1326.	5.9	45
14	Structureâ€“function studies of histone H3/H4 tetramer maintenance during transcription by chaperone Spt2. <i>Genes and Development</i> , 2015, 29, 1326-1340.	5.9	46
15	A unique binding mode enables MCM2 to chaperone histones H3â€“H4 at replication forks. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 618-626.	8.2	192
16	DAXX envelops a histone H3.3â€“H4 dimer for H3.3-specific recognition. <i>Nature</i> , 2012, 491, 560-565.	27.8	220
17	Structure of a CENP-Aâ€“histone H4 heterodimer in complex with chaperone HJURP. <i>Genes and Development</i> , 2011, 25, 901-906.	5.9	157