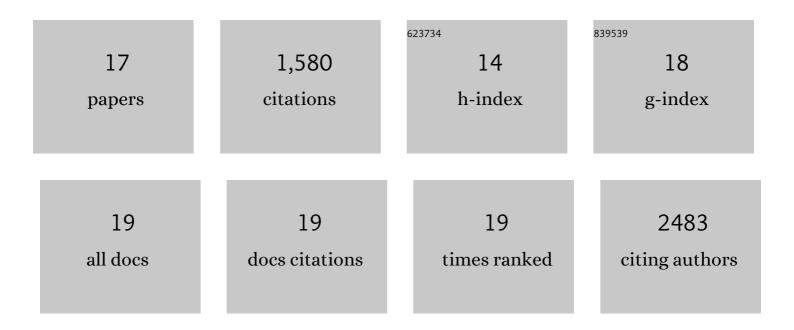
Hongda Huang

List of Publications by Year in descending order

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ΗΟΝΟΡΑ ΗΠΑΝΟ

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