

Kyung-Min Noh

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2734152/publications.pdf>

Version: 2024-02-01

21
papers

3,688
citations

516710

16
h-index

713466

21
g-index

27
all docs

27
docs citations

27
times ranked

5503
citing authors

#	ARTICLE	IF	CITATIONS
1	High-throughput functional characterization of protein phosphorylation sites in yeast. <i>Nature Biotechnology</i> , 2022, 40, 382-390.	17.5	24
2	Multi-omic profiling of histone variant H3.3 lysine 27 methylation reveals a distinct role from canonical H3 in stem cell differentiation. <i>Molecular Omics</i> , 2022, 18, 296-314.	2.8	2
3	Donor cell memory confers a metastable state of directly converted cells. <i>Cell Stem Cell</i> , 2021, 28, 1291-1306.e10.	11.1	5
4	The functional landscape of the human phosphoproteome. <i>Nature Biotechnology</i> , 2020, 38, 365-373.	17.5	273
5	Histone Variant H3.3 Mutations in Defining the Chromatin Function in Mammals. <i>Cells</i> , 2020, 9, 2716.	4.1	10
6	Genomic Rewiring of SOX2 Chromatin Interaction Network during Differentiation of ESCs to Postmitotic Neurons. <i>Cell Systems</i> , 2020, 10, 480-494.e8.	6.2	25
7	Lysine 4 of histone H3.3 is required for embryonic stem cell differentiation, histone enrichment at regulatory regions and transcription accuracy. <i>Nature Genetics</i> , 2020, 52, 273-282.	21.4	37
8	Systematic analysis of protein turnover in primary cells. <i>Nature Communications</i> , 2018, 9, 689.	12.8	280
9	Haploinsufficiency of the intellectual disability gene SETD5 disturbs developmental gene expression and cognition. <i>Nature Neuroscience</i> , 2018, 21, 1717-1727.	14.8	65
10	Intragenic CpG islands play important roles in bivalent chromatin assembly of developmental genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1885-E1894.	7.1	27
11	Elsässer et al. reply. <i>Nature</i> , 2017, 548, E7-E9.	27.8	7
12	CTCF-Mediated Chromatin Loops between Promoter and Gene Body Regulate Alternative Splicing across Individuals. <i>Cell Systems</i> , 2017, 5, 628-637.e6.	6.2	80
13	Reading between the Lines: Adding Histone and DNA Methylation Marks toward a New Epigenetic Sumo. <i>ACS Chemical Biology</i> , 2016, 11, 554-563.	3.4	20
14	Engineering of a Histone-Recognition Domain in Dnmt3a Alters the Epigenetic Landscape and Phenotypic Features of Mouse ESCs. <i>Molecular Cell</i> , 2015, 59, 89-103.	9.7	76
15	ATRX tolerates activity-dependent histone H3 methyl/phos switching to maintain repetitive element silencing in neurons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6820-6827.	7.1	49
16	Critical Role of Histone Turnover in Neuronal Transcription and Plasticity. <i>Neuron</i> , 2015, 87, 77-94.	8.1	257
17	Histone H3.3 is required for endogenous retroviral element silencing in embryonic stem cells. <i>Nature</i> , 2015, 522, 240-244.	27.8	303
18	Every amino acid matters: essential contributions of histone variants to mammalian development and disease. <i>Nature Reviews Genetics</i> , 2014, 15, 259-271.	16.3	285

#	ARTICLE	IF	CITATIONS
19	Histone variant H3.3 is an essential maternal factor for oocyte reprogramming. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7325-7330.	7.1	95
20	Daxx is an H3.3-specific histone chaperone and cooperates with ATRX in replication-independent chromatin assembly at telomeres. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 14075-14080.	7.1	685
21	Distinct Factors Control Histone Variant H3.3 Localization at Specific Genomic Regions. Cell, 2010, 140, 678-691.	28.9	1,069