

Mariel Coradin

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8885372/publications.pdf>

Version: 2024-02-01

17
papers

585
citations

758635

12
h-index

887659

17
g-index

19
all docs

19
docs citations

19
times ranked

952
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of histone acylations links chromatin modifications with metabolism. <i>Nature Communications</i> , 2017, 8, 1141.	5.8	145
2	KMT2D regulates p63 target enhancers to coordinate epithelial homeostasis. <i>Genes and Development</i> , 2018, 32, 181-193.	2.7	77
3	H3K27M in Gliomas Causes a One-Step Decrease in H3K27 Methylation and Reduced Spreading within the Constraints of H3K36 Methylation. <i>Cell Reports</i> , 2020, 33, 108390.	2.9	50
4	Analyses of Histone Proteoforms Using Front-end Electron Transfer Dissociation-enabled Orbitrap Instruments. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 975-988.	2.5	43
5	Chromatin dysregulation associated with NSD1 mutation in head and neck squamous cell carcinoma. <i>Cell Reports</i> , 2021, 34, 108769.	2.9	42
6	Accelerating the Field of Epigenetic Histone Modification Through Mass Spectrometry-Based Approaches. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100006.	2.5	33
7	Metabolic labeling in middle-down proteomics allows for investigation of the dynamics of the histone code. <i>Epigenetics and Chromatin</i> , 2017, 10, 34.	1.8	32
8	A mass spectrometry-based assay using metabolic labeling to rapidly monitor chromatin accessibility of modified histone proteins. <i>Scientific Reports</i> , 2019, 9, 13613.	1.6	32
9	Hydrogen-Deuterium Exchange Coupled to Top- and Middle-Down Mass Spectrometry Reveals Histone Tail Dynamics before and after Nucleosome Assembly. <i>Structure</i> , 2018, 26, 1651-1663.e3.	1.6	30
10	Extensive Characterization of Heavily Modified Histone Tails by 193 nm Ultraviolet Photodissociation Mass Spectrometry via a Middle-Down Strategy. <i>Analytical Chemistry</i> , 2018, 90, 10425-10433.	3.2	26
11	Quantitation of Single and Combinatorial Histone Modifications by Integrated Chromatography of Bottom-up Peptides and Middle-down Polypeptide Tails. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 2449-2459.	1.2	18
12	Bullet points to evaluate the performance of the middle-down proteomics workflow for histone modification analysis. <i>Methods</i> , 2020, 184, 86-92.	1.9	14
13	Combinatorial Histone H3 Modifications Are Dynamically Altered in Distinct Cell Cycle Phases. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1300-1311.	1.2	11
14	A Dynamic and Combinatorial Histone Code Drives Malaria Parasite Asexual and Sexual Development. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100199.	2.5	11
15	Monitoring proteolytic processing events by quantitative mass spectrometry. <i>Expert Review of Proteomics</i> , 2017, 14, 409-418.	1.3	10
16	Nucleome programming is required for the foundation of totipotency in mammalian germline development. <i>EMBO Journal</i> , 2022, 41, .	3.5	9
17	FGF-2 induces a failure of cell cycle progression in cells harboring amplified K-Ras, revealing new insights into oncogene-induced senescence. <i>Molecular Omics</i> , 2021, 17, 725-739.	1.4	2