

# 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

759233  
12  
h-index

888059  
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. Nature Communications, 2017, 8, 1141.	12.8	145
2	KMT2D regulates p63 target enhancers to coordinate epithelial homeostasis. Genes and Development, 2018, 32, 181-193.	5.9	77
3	H3K27M in Gliomas Causes a One-Step Decrease in H3K27 Methylation and Reduced Spreading within the Constraints of H3K36 Methylation. Cell Reports, 2020, 33, 108390.	6.4	50
4	Analyses of Histone Proteoforms Using Front-end Electron Transfer Dissociation-enabled Orbitrap Instruments. Molecular and Cellular Proteomics, 2016, 15, 975-988.	3.8	43
5	Chromatin dysregulation associated with NSD1 mutation in head and neck squamous cell carcinoma. Cell Reports, 2021, 34, 108769.	6.4	42
6	Accelerating the Field of Epigenetic Histone Modification Through Mass Spectrometry-Based Approaches. Molecular and Cellular Proteomics, 2021, 20, 100006.	3.8	33
7	Metabolic labeling in middle-down proteomics allows for investigation of the dynamics of the histone code. Epigenetics and Chromatin, 2017, 10, 34.	3.9	32
8	A mass spectrometry-based assay using metabolic labeling to rapidly monitor chromatin accessibility of modified histone proteins. Scientific Reports, 2019, 9, 13613.	3.3	32
9	Hydrogen-Deuterium Exchange Coupled to Top- and Middle-Down Mass Spectrometry Reveals Histone Tail Dynamics before and after Nucleosome Assembly. Structure, 2018, 26, 1651-1663.e3.	3.3	30
10	Extensive Characterization of Heavily Modified Histone Tails by 193 nm Ultraviolet Photodissociation Mass Spectrometry via a Middle-Down Strategy. Analytical Chemistry, 2018, 90, 10425-10433.	6.5	26
11	Quantitation of Single and Combinatorial Histone Modifications by Integrated Chromatography of Bottom-up Peptides and Middle-down Polypeptide Tails. Journal of the American Society for Mass Spectrometry, 2019, 30, 2449-2459.	2.8	18
12	Bullet points to evaluate the performance of the middle-down proteomics workflow for histone modification analysis. Methods, 2020, 184, 86-92.	3.8	14
13	Combinatorial Histone H3 Modifications Are Dynamically Altered in Distinct Cell Cycle Phases. Journal of the American Society for Mass Spectrometry, 2021, 32, 1300-1311.	2.8	11
14	A Dynamic and Combinatorial Histone Code Drives Malaria Parasite Asexual and Sexual Development. Molecular and Cellular Proteomics, 2022, 21, 100199.	3.8	11
15	Monitoring proteolytic processing events by quantitative mass spectrometry. Expert Review of Proteomics, 2017, 14, 409-418.	3.0	10
16	Nucleome programming is required for the foundation of totipotency in mammalian germline development. EMBO Journal, 2022, 41, .	7.8	9
17	FGF-2 induces a failure of cell cycle progression in cells harboring amplified K-Ras, revealing new insights into oncogene-induced senescence. Molecular Omics, 2021, 17, 725-739.	2.8	2