

Marie Locard-Paulet

List of Publications by Year in descending order

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Version: 2024-02-01

16
papers

294
citations

933447

10
h-index

996975

15
g-index

23
all docs

23
docs citations

23
times ranked

538
citing authors

#	ARTICLE	IF	CITATIONS
1	A proteomics sample metadata representation for multiomics integration and big data analysis. Nature Communications, 2021, 12, 5854.	12.8	45
2	Phosphoproteomic analysis of interacting tumor and endothelial cells identifies regulatory mechanisms of transendothelial migration. Science Signaling, 2016, 9, ra15.	3.6	34
3	Comparing 22 Popular Phosphoproteomics Pipelines for Peptide Identification and Site Localization. Journal of Proteome Research, 2020, 19, 1338-1345.	3.7	30
4	Conformational maps of human 20S proteasomes reveal PA28- and immuno-dependent inter-ring crosstalks. Nature Communications, 2020, 11, 6140.	12.8	23
5	HDX-Viewer: interactive 3D visualization of hydrogen-deuterium exchange data. Bioinformatics, 2019, 35, 5331-5333.	4.1	19
6	Proteomic Analysis of Regulatory T Cells Reveals the Importance of Themis1 in the Control of Their Suppressive Function. Molecular and Cellular Proteomics, 2017, 16, 1416-1432.	3.8	16
7	The protein kinase PknB negatively regulates biosynthesis and trafficking of mycolic acids in mycobacteria. Journal of Lipid Research, 2020, 61, 1180-1191.	4.2	15
8	A time-resolved multi-omics atlas of Acanthamoeba castellanii encystment. Nature Communications, 2022, 13, .	12.8	14
9	LymphoAtlas: a dynamic and integrated phosphoproteomic resource of <scp>TCR</scp> signaling in primary T cells reveals <scp>ITSN</scp> 2 as a regulator of effector functions. Molecular Systems Biology, 2020, 16, e9524.	7.2	13
10	Analysing signalling networks by mass spectrometry. Amino Acids, 2012, 43, 1061-1074.	2.7	12
11	Clinical implications of recent advances in proteogenomics. Expert Review of Proteomics, 2016, 13, 185-199.	3.0	12
12	VisioProt-MS: interactive 2D maps from intact protein mass spectrometry. Bioinformatics, 2019, 35, 679-681.	4.1	9
13	Phosphorylation of SHP2 at Tyr62 Enables Acquired Resistance to SHP2 Allosteric Inhibitors in FLT3-ITD-Driven AML. Cancer Research, 2022, 82, 2141-2155.	0.9	8
14	Top-Down and Intact Protein Mass Spectrometry Data Visualization for Proteoform Analysis Using VisioProt-MS. Bioinformatics and Biology Insights, 2019, 13, 117793221986822.	2.0	7
15	The final assembly of trehalose polyphleates takes place within the outer layer of the mycobacterial cell envelope. Journal of Biological Chemistry, 2020, 295, 11184-11194.	3.4	6
16	The European Bioinformatics Community for Mass Spectrometry (EuBIC-MS): an open community for bioinformatics training and research. Rapid Communications in Mass Spectrometry, 2021, , e9087.	1.5	3