

# Marie Locard-Paulet

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8560082/publications.pdf>

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