

Dorte Breinholdt Bekker-Jensen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6191314/publications.pdf>

Version: 2024-02-01

16
papers

2,422
citations

623734

14
h-index

940533

16
g-index

18
all docs

18
docs citations

18
times ranked

3858
citing authors

#	ARTICLE	IF	CITATIONS
1	Data Processing and Analysis for DIA-Based Phosphoproteomics Using Spectronaut. <i>Methods in Molecular Biology</i> , 2021, 2361, 95-107.	0.9	21
2	Proteomic investigation of Cbl and Cbl-b in neuroblastoma cell differentiation highlights roles for SHP-2 and CDK16. <i>IScience</i> , 2021, 24, 102321.	4.1	8
3	Regulation of the Golgi Apparatus by p38 and JNK Kinases during Cellular Stress Responses. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9595.	4.1	6
4	Causal integration of multi-omics data with prior knowledge to generate mechanistic hypotheses. <i>Molecular Systems Biology</i> , 2021, 17, e9730.	7.2	78
5	Spatial-proteomics reveals phospho-signaling dynamics at subcellular resolution. <i>Nature Communications</i> , 2021, 12, 7113.	12.8	38
6	Rapid and site-specific deep phosphoproteome profiling by data-independent acquisition without the need for spectral libraries. <i>Nature Communications</i> , 2020, 11, 787.	12.8	251
7	A Compact Quadrupole-Orbitrap Mass Spectrometer with FAIMS Interface Improves Proteome Coverage in Short LC Gradients. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 716-729.	3.8	284
8	ZAK1± Recognizes Stalled Ribosomes through Partially Redundant Sensor Domains. <i>Molecular Cell</i> , 2020, 78, 700-713.e7.	9.7	90
9	Oncogenic Mutations Rewire Signaling Pathways by Switching Protein Recruitment to Phosphotyrosine Sites. <i>Cell</i> , 2019, 179, 543-560.e26.	28.9	65
10	Benchmarking common quantification strategies for large-scale phosphoproteomics. <i>Nature Communications</i> , 2018, 9, 1045.	12.8	232
11	Performance Evaluation of the Q Exactive HF-X for Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 727-738.	3.7	221
12	Integrated proximal proteomics reveals IRS2 as a determinant of cell survival in ALK-driven neuroblastoma. <i>Science Signaling</i> , 2018, 11, .	3.6	33
13	UbiSite approach for comprehensive mapping of lysine and N-terminal ubiquitination sites. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 631-640.	8.2	341
14	A Novel LC System Embeds Analytes in Pre-formed Gradients for Rapid, Ultra-robust Proteomics. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2284-2296.	3.8	270
15	An Optimized Shotgun Strategy for the Rapid Generation of Comprehensive Human Proteomes. <i>Cell Systems</i> , 2017, 4, 587-599.e4.	6.2	413
16	Temporal proteomics of NGF-TrkA signaling identifies an inhibitory role for the E3 ligase Cbl-b in neuroblastoma cell differentiation. <i>Science Signaling</i> , 2015, 8, ra40.	3.6	64