

Andreas-David Brunner

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3704487/publications.pdf>

Version: 2024-02-01

15
papers

2,748
citations

759233

12
h-index

996975

15
g-index

25
all docs

25
docs citations

25
times ranked

3104
citing authors

#	ARTICLE	IF	CITATIONS
1	AlphaMap: an open-source Python package for the visual annotation of proteomics data with sequence-specific knowledge. <i>Bioinformatics</i> , 2022, 38, 849-852.	4.1	12
2	Ultra-high sensitivity mass spectrometry quantifies single-cell proteome changes upon perturbation. <i>Molecular Systems Biology</i> , 2022, 18, e10798.	7.2	261
3	OpenCell: Endogenous tagging for the cartography of human cellular organization. <i>Science</i> , 2022, 375, eabi6983.	12.6	174
4	Deep Visual Proteomics defines single-cell identity and heterogeneity. <i>Nature Biotechnology</i> , 2022, 40, 1231-1240.	17.5	160
5	Unbiased spatial proteomics with single-cell resolution in tissues. <i>Molecular Cell</i> , 2022, 82, 2335-2349.	9.7	85
6	Deep learning the collisional cross sections of the peptide universe from a million experimental values. <i>Nature Communications</i> , 2021, 12, 1185.	12.8	81
7	The Swiss Primary Hypersomnolence and Narcolepsy Cohort study (SPHYNCS): Study protocol for a prospective, multicentre cohort observational study. <i>Journal of Sleep Research</i> , 2021, 30, e13296.	3.2	12
8	Multi-omics profiling of living human pancreatic islet donors reveals heterogeneous beta cell trajectories towards type 2 diabetes. <i>Nature Metabolism</i> , 2021, 3, 1017-1031.	11.9	76
9	Reply to "Quality control requirements for the correct annotation of lipidomics data". <i>Nature Communications</i> , 2021, 12, 4772.	12.8	2
10	diaPASEF: parallel accumulation-serial fragmentation combined with data-independent acquisition. <i>Nature Methods</i> , 2020, 17, 1229-1236.	19.0	387
11	Pervasive functional translation of noncanonical human open reading frames. <i>Science</i> , 2020, 367, 1140-1146.	12.6	400
12	Trapped ion mobility spectrometry and PASEF enable in-depth lipidomics from minimal sample amounts. <i>Nature Communications</i> , 2020, 11, 331.	12.8	138
13	MaxQuant.Live Enables Global Targeting of More Than 25,000 Peptides. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 982a-994.	3.8	91
14	Site-specific ubiquitylation and SUMOylation using genetic-code expansion and sortase. <i>Nature Chemical Biology</i> , 2019, 15, 276-284.	8.0	96
15	Online Parallel Accumulation-Serial Fragmentation (PASEF) with a Novel Trapped Ion Mobility Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2534-2545.	3.8	602