

Andreas-David Brunner

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

19
papers

892
citations

12
h-index

25
g-index

25
ext. papers

1,756
ext. citations

17.4
avg, IF

4.24
L-index

#	Paper	IF	Citations
19	Online Parallel Accumulation-Serial Fragmentation (PASEF) with a Novel Trapped Ion Mobility Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 2534-2545	7.6	280
18	Pervasive functional translation of noncanonical human open reading frames. <i>Science</i> , 2020 , 367, 1140-1146	33.9	168
17	diaPASEF: parallel accumulation-serial fragmentation combined with data-independent acquisition. <i>Nature Methods</i> , 2020 , 17, 1229-1236	21.6	85
16	Trapped ion mobility spectrometry and PASEF enable in-depth lipidomics from minimal sample amounts. <i>Nature Communications</i> , 2020 , 11, 331	17.4	78
15	Site-specific ubiquitylation and SUMOylation using genetic-code expansion and sortase. <i>Nature Chemical Biology</i> , 2019 , 15, 276-284	11.7	55
14	MaxQuant.Live Enables Global Targeting of More Than 25,000 Peptides. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 982-994	7.6	54
13	Ultra-high sensitivity mass spectrometry quantifies single-cell proteome changes upon perturbation		46
12	Ultra-high sensitivity mass spectrometry quantifies single-cell proteome changes upon perturbation.. <i>Molecular Systems Biology</i> , 2022 , 18, e10798	12.2	24
11	Deep learning the collisional cross sections of the peptide universe from a million experimental values. <i>Nature Communications</i> , 2021 , 12, 1185	17.4	21
10	Parallel accumulation Serial fragmentation combined with data-independent acquisition (diaPASEF): Bottom-up proteomics with near optimal ion usage		18
9	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	14.6	13
8	AI-driven Deep Visual Proteomics defines cell identity and heterogeneity		12
7	OpenCell: Endogenous tagging for the cartography of human cellular organization.. <i>Science</i> , 2022 , 375, eabi6983	33.3	9
6	OpenCell: proteome-scale endogenous tagging enables the cartography of human cellular organization		4
5	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	5.8	3
4	AlphaMap: an open-source python package for the visual annotation of proteomics data with sequence specific knowledge. <i>Bioinformatics</i> , 2021 ,	7.2	3
3	Deep learning the collisional cross sections of the peptide universe from a million training samples		2

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| 2 | AlphaMap: An open-source Python package for the visual annotation of proteomics data with sequence specific knowledge | 1 |
| 1 | Reply to "Quality control requirements for the correct annotation of lipidomics data". <i>Nature Communications</i> , 2021 , 12, 4772 | 17.4 1 |