

Stephen Tate

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/242954/publications.pdf>

Version: 2024-02-01

21
papers

4,159
citations

567281

15
h-index

752698

20
g-index

23
all docs

23
docs citations

23
times ranked

6533
citing authors

#	ARTICLE	IF	CITATIONS
1	A comprehensive LFQ benchmark dataset on modern day acquisition strategies in proteomics. <i>Scientific Data</i> , 2022, 9, 126.	5.3	20
2	Ultra-fast proteomics with Scanning SWATH. <i>Nature Biotechnology</i> , 2021, 39, 846-854.	17.5	173
3	A comprehensive CHO SWATH-MS spectral library for robust quantitative profiling of 10,000 proteins. <i>Scientific Data</i> , 2020, 7, 263.	5.3	17
4	MetaboKit: a comprehensive data extraction tool for untargeted metabolomics. <i>Molecular Omics</i> , 2020, 16, 436-447.	2.8	12
5	Tracking genome-editing and associated molecular perturbations by SWATH mass spectrometry. <i>Scientific Reports</i> , 2019, 9, 15240.	3.3	10
6	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 4051-4060.	3.7	47
7	SWATH-ID: An instrument method which combines identification and quantification in a single analysis. <i>Proteomics</i> , 2017, 17, e1500522.	2.2	17
8	Statistical control of peptide and protein error rates in large-scale targeted data-independent acquisition analyses. <i>Nature Methods</i> , 2017, 14, 921-927.	19.0	189
9	Albumin Decrease Is Associated with Spontaneous Preterm Delivery within 48 h in Women with Threatened Preterm Labor. <i>Journal of Proteome Research</i> , 2015, 14, 457-466.	3.7	9
10	MSPLIT-DIA: sensitive peptide identification for data-independent acquisition. <i>Nature Methods</i> , 2015, 12, 1106-1108.	19.0	113
11	A repository of assays to quantify 10,000 human proteins by SWATH-MS. <i>Scientific Data</i> , 2014, 1, 140031.	5.3	370
12	Mapping differential interactomes by affinity purification coupled with data-independent mass spectrometry acquisition. <i>Nature Methods</i> , 2013, 10, 1239-1245.	19.0	277
13	Label-free quantitative proteomics trends for protein-protein interactions. <i>Journal of Proteomics</i> , 2013, 81, 91-101.	2.4	55
14	Targeted Data Extraction of the MS/MS Spectra Generated by Data-independent Acquisition: A New Concept for Consistent and Accurate Proteome Analysis. <i>Molecular and Cellular Proteomics</i> , 2012, 11, O111.016717.	3.8	2,285
15	Pyruvate kinase is a dosage-dependent regulator of cellular amino acid homeostasis. <i>Oncotarget</i> , 2012, 3, 1356-1369.	1.8	25
16	A cost-benefit analysis of multidimensional fractionation of affinity purification-mass spectrometry samples. <i>Proteomics</i> , 2011, 11, 2603-2612.	2.2	29
17	Structure-Function Analysis of Core STRIPAK Proteins. <i>Journal of Biological Chemistry</i> , 2011, 286, 25065-25075.	3.4	136
18	Methodological considerations in the development of HPLC-MS methods for the analysis of rodent plasma for metabolomic studies. <i>Molecular BioSystems</i> , 2009, 6, 108-120.	2.9	45

#	ARTICLE	IF	CITATIONS
19	Instrumental and experimental effects in LC-MS-based metabolomics. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2008, 871, 227-235.	2.3	60
20	Proteomics Analysis of Rat Brain Postsynaptic Density. Journal of Biological Chemistry, 2004, 279, 987-1002.	3.4	245
21	Optimization of Microflow LC Coupled with Scanning SWATH and Its Application in Hepatocellular Carcinoma Tissues. Journal of Proteome Research, 0, , .	3.7	5