Stefka Tyanova

List of Publications by Year
in descending order

17 papers	**13,149** citations	516710 **16** h-index	888059 **17** g-index
18 all docs	**18** docs citations	**18** times ranked	**23472** citing authors

#	ARTICLE	IF	CITATIONS
1	SILAC-based quantitative mass spectrometry-based proteomics quantifies endoplasmic reticulum stress in whole HeLa cells. DMM Disease Models and Mechanisms, 2019, 12, .	2.4	10
2	Perseus: A Bioinformatics Platform for Integrative Analysis of Proteomics Data in Cancer Research. Methods in Molecular Biology, 2018, 1711, 133-148.	0.9	389
3	Multiplexed proteome analysis with neutron-encoded stable isotope labeling in cells and mice. Nature Protocols, 2018, 13, 293-306.	12.0	35
4	The Proteome of Prostate Cancer Bone Metastasis Reveals Heterogeneity with Prognostic Implications. Clinical Cancer Research, 2018, 24, 5433-5444.	7.0	68
5	A Mass Spectrometry-Based Approach for Mapping Protein Subcellular Localization Reveals the Spatial Proteome of Mouse Primary Neurons. Cell Reports, 2017, 20, 2706-2718.	6.4	105
6	Global, quantitative and dynamic mapping of protein subcellular localization. ELife, 2016, 5, .	6.0	469
7	Proteomics reveals the effects of sustained weight loss on the human plasma proteome. Molecular Systems Biology, 2016, 12, 901.	7.2	188
8	The MaxQuant computational platform for mass spectrometry-based shotgun proteomics. Nature Protocols, 2016, 11, 2301-2319.	12.0	3,353
9	The Perseus computational platform for comprehensive analysis of (prote)omics data. Nature Methods, 2016, 13, 731-740.	19.0	6,181
10	The Proteome of Primary Prostate Cancer. European Urology, 2016, 69, 942-952.	1.9	122
11	Proteomic maps of breast cancer subtypes. Nature Communications, 2016, 7, 10259.	12.8	256
12	Visualization of LCâ€MS/MS proteomics data in MaxQuant. Proteomics, 2015, 15, 1453-1456.	2.2	248
13	Machine Learning-based Classification of Diffuse Large B-cell Lymphoma Patients by Their Protein Expression Profiles. Molecular and Cellular Proteomics, 2015, 14, 2947-2960.	3.8	73
14	Cell typeâ€" and brain regionâ€"resolved mouse brain proteome. Nature Neuroscience, 2015, 18, 1819-1831.	14.8	672
15	Ultradeep Human Phosphoproteome Reveals a Distinct Regulatory Nature of Tyr and Ser/Thr-Based Signaling. Cell Reports, 2014, 8, 1583-1594.	6.4	839
16	MaxQuant for In-Depth Analysis of Large SILAC Datasets. Methods in Molecular Biology, 2014, 1188, 351-364.	0.9	79
17	Phosphorylation Variation during the Cell Cycle Scales with Structural Propensities of Proteins. PLoS Computational Biology, 2013, 9, e1002842.	3.2	54