

Stefka Tyanova

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11345960/publications.pdf>

Version: 2024-02-01

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