Ruth Hüttenhain

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2824169/publications.pdf

Version: 2024-02-01

26 papers 7,396

304368 22 h-index 26 g-index

30 all docs

30 docs citations

30 times ranked

14890 citing authors

#	Article	IF	Citations
1	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. Nature, 2020, 583, 459-468.	13.7	3,542
2	The Global Phosphorylation Landscape of SARS-CoV-2 Infection. Cell, 2020, 182, 685-712.e19.	13.5	825
3	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. Science, 2020, 370, .	6.0	508
4	An Approach to Spatiotemporally Resolve Protein Interaction Networks in Living Cells. Cell, 2017, 169, 350-360.e12.	13.5	322
5	On the Development of Plasma Protein Biomarkers. Journal of Proteome Research, 2011, 10, 5-16.	1.8	289
6	Comparative Flavivirus-Host Protein Interaction Mapping Reveals Mechanisms of Dengue and Zika Virus Pathogenesis. Cell, 2018, 175, 1931-1945.e18.	13.5	252
7	Reproducible Quantification of Cancer-Associated Proteins in Body Fluids Using Targeted Proteomics. Science Translational Medicine, 2012, 4, 142ra94.	5.8	236
8	<pre><scp>PASSEL</scp>: The <scp>P</scp>eptide<scp>A</scp>tlas <scp>SRM</scp>experiment library. Proteomics, 2012, 12, 1170-1175.</pre>	1.3	200
9	Perspectives of targeted mass spectrometry for protein biomarker verification. Current Opinion in Chemical Biology, 2009, 13, 518-525.	2.8	165
10	Tau interactome maps synaptic and mitochondrial processes associated with neurodegeneration. Cell, 2022, 185, 712-728.e14.	13.5	114
11	The Psychiatric Cell Map Initiative: A Convergent Systems Biological Approach to Illuminating Key Molecular Pathways in Neuropsychiatric Disorders. Cell, 2018, 174, 505-520.	13.5	108
12	Prediction of colorectal cancer diagnosis based onÂcirculating plasma proteins. EMBO Molecular Medicine, 2015, 7, 1166-1178.	3.3	80
13	A systems approach to infectious disease. Nature Reviews Genetics, 2020, 21, 339-354.	7.7	72
14	MassIVE.quant: a community resource of quantitative mass spectrometry–based proteomics datasets. Nature Methods, 2020, 17, 981-984.	9.0	66
15	Enterovirus pathogenesis requires the host methyltransferase SETD3. Nature Microbiology, 2019, 4, 2523-2537.	5.9	51
16	N-Glycoprotein SRMAtlas. Molecular and Cellular Proteomics, 2013, 12, 1005-1016.	2.5	48
17	A Targeted Mass Spectrometry Strategy for Developing Proteomic Biomarkers: A Case Study of Epithelial Ovarian Cancer. Molecular and Cellular Proteomics, 2019, 18, 1836-1850.	2.5	42
18	ARIH2 Is a Vif-Dependent Regulator of CUL5-Mediated APOBEC3G Degradation in HIV Infection. Cell Host and Microbe, 2019, 26, 86-99.e7.	5.1	42

#	Article	IF	CITATION
19	Smoothened transduces Hedgehog signals via activity-dependent sequestration of PKA catalytic subunits. PLoS Biology, 2021, 19, e3001191.	2.6	40
20	Transcription factor protein interactomes reveal genetic determinants in heart disease. Cell, 2022, 185, 794-814.e30.	13.5	39
21	Similarities and Differences of Blood N-Glycoproteins in Five Solid Carcinomas at Localized Clinical Stage Analyzed by SWATH-MS. Cell Reports, 2018, 23, 2819-2831.e5.	2.9	36
22	Proteomic Approaches to Study SARS-CoV-2 Biology and COVID-19 Pathology. Journal of Proteome Research, 2021, 20, 1133-1152.	1.8	27
23	Genetic interaction mapping informs integrative structure determination of protein complexes. Science, 2020, 370, .	6.0	24
24	CRL4 ^{AMBRA1} targets Elongin C for ubiquitination and degradation to modulate CRL5 signaling. EMBO Journal, 2018, 37, .	3.5	13
25	Global post-translational modification profiling of HIV-1-infected cells reveals mechanisms of host cellular pathway remodeling. Cell Reports, 2022, 39, 110690.	2.9	12
26	A combined topâ€down and bottomâ€up MS approach for the characterization of hemoglobin variants in Rhesus monkeys. Proteomics, 2010, 10, 3657-3668.	1.3	7