

Ruth HÃ¼ttenhain

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

7,396
citations

304743

22
h-index

552781

26
g-index

30
all docs

30
docs citations

30
times ranked

14890
citing authors

#	ARTICLE	IF	CITATIONS
1	Tau interactome maps synaptic and mitochondrial processes associated with neurodegeneration. <i>Cell</i> , 2022, 185, 712-728.e14.	28.9	114
2	Transcription factor protein interactomes reveal genetic determinants in heart disease. <i>Cell</i> , 2022, 185, 794-814.e30.	28.9	39
3	Global post-translational modification profiling of HIV-1-infected cells reveals mechanisms of host cellular pathway remodeling. <i>Cell Reports</i> , 2022, 39, 110690.	6.4	12
4	Proteomic Approaches to Study SARS-CoV-2 Biology and COVID-19 Pathology. <i>Journal of Proteome Research</i> , 2021, 20, 1133-1152.	3.7	27
5	Smoothed transduces Hedgehog signals via activity-dependent sequestration of PKA catalytic subunits. <i>PLoS Biology</i> , 2021, 19, e3001191.	5.6	40
6	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. <i>Science</i> , 2020, 370, .	12.6	508
7	MassIVE.quant: a community resource of quantitative mass spectrometry-based proteomics datasets. <i>Nature Methods</i> , 2020, 17, 981-984.	19.0	66
8	Genetic interaction mapping informs integrative structure determination of protein complexes. <i>Science</i> , 2020, 370, .	12.6	24
9	The Global Phosphorylation Landscape of SARS-CoV-2 Infection. <i>Cell</i> , 2020, 182, 685-712.e19.	28.9	825
10	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. <i>Nature</i> , 2020, 583, 459-468.	27.8	3,542
11	A systems approach to infectious disease. <i>Nature Reviews Genetics</i> , 2020, 21, 339-354.	16.3	72
12	A Targeted Mass Spectrometry Strategy for Developing Proteomic Biomarkers: A Case Study of Epithelial Ovarian Cancer. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1836-1850.	3.8	42
13	ARIH2 Is a Vif-Dependent Regulator of CUL5-Mediated APOBEC3G Degradation in HIV Infection. <i>Cell Host and Microbe</i> , 2019, 26, 86-99.e7.	11.0	42
14	Enterovirus pathogenesis requires the host methyltransferase SETD3. <i>Nature Microbiology</i> , 2019, 4, 2523-2537.	13.3	51
15	Comparative Flavivirus-Host Protein Interaction Mapping Reveals Mechanisms of Dengue and Zika Virus Pathogenesis. <i>Cell</i> , 2018, 175, 1931-1945.e18.	28.9	252
16	CRL4 ^{AMBRA1} targets Elongin C for ubiquitination and degradation to modulate CRL5 signaling. <i>EMBO Journal</i> , 2018, 37, .	7.8	13
17	Similarities and Differences of Blood N-Glycoproteins in Five Solid Carcinomas at Localized Clinical Stage Analyzed by SWATH-MS. <i>Cell Reports</i> , 2018, 23, 2819-2831.e5.	6.4	36
18	The Psychiatric Cell Map Initiative: A Convergent Systems Biological Approach to Illuminating Key Molecular Pathways in Neuropsychiatric Disorders. <i>Cell</i> , 2018, 174, 505-520.	28.9	108

#	ARTICLE	IF	CITATIONS
19	An Approach to Spatiotemporally Resolve Protein Interaction Networks in Living Cells. <i>Cell</i> , 2017, 169, 350-360.e12.	28.9	322
20	Prediction of colorectal cancer diagnosis based on circulating plasma proteins. <i>EMBO Molecular Medicine</i> , 2015, 7, 1166-1178.	6.9	80
21	N-Glycoprotein SRMAtlas. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1005-1016.	3.8	48
22	Reproducible Quantification of Cancer-Associated Proteins in Body Fluids Using Targeted Proteomics. <i>Science Translational Medicine</i> , 2012, 4, 142ra94.	12.4	236
23	<scp>PASSEL</scp>: The <scp>P</scp>eptide<scp>A</scp>tlas <scp>SRM</scp>experiment library. <i>Proteomics</i> , 2012, 12, 1170-1175.	2.2	200
24	On the Development of Plasma Protein Biomarkers. <i>Journal of Proteome Research</i> , 2011, 10, 5-16.	3.7	289
25	A combined top-down and bottom-up MS approach for the characterization of hemoglobin variants in Rhesus monkeys. <i>Proteomics</i> , 2010, 10, 3657-3668.	2.2	7
26	Perspectives of targeted mass spectrometry for protein biomarker verification. <i>Current Opinion in Chemical Biology</i> , 2009, 13, 518-525.	6.1	165