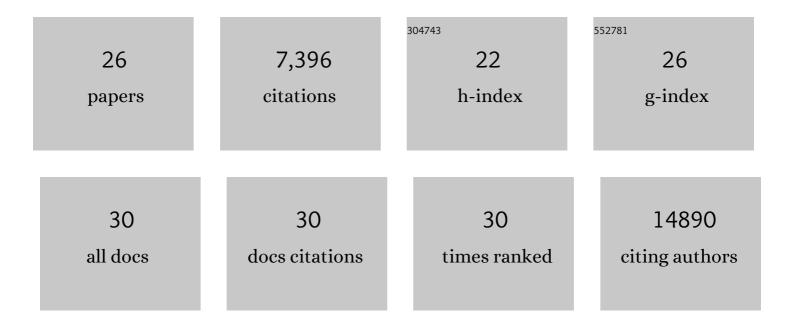
## Ruth Hüttenhain

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2824169/publications.pdf Version: 2024-02-01



<u>Ριιτή Ηδιάττενιμαίν</u>

#	Article	IF	CITATIONS
1	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. Nature, 2020, 583, 459-468.	27.8	3,542
2	The Global Phosphorylation Landscape of SARS-CoV-2 Infection. Cell, 2020, 182, 685-712.e19.	28.9	825
3	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. Science, 2020, 370, .	12.6	508
4	An Approach to Spatiotemporally Resolve Protein Interaction Networks in Living Cells. Cell, 2017, 169, 350-360.e12.	28.9	322
5	On the Development of Plasma Protein Biomarkers. Journal of Proteome Research, 2011, 10, 5-16.	3.7	289
6	Comparative Flavivirus-Host Protein Interaction Mapping Reveals Mechanisms of Dengue and Zika Virus Pathogenesis. Cell, 2018, 175, 1931-1945.e18.	28.9	252
7	Reproducible Quantification of Cancer-Associated Proteins in Body Fluids Using Targeted Proteomics. Science Translational Medicine, 2012, 4, 142ra94.	12.4	236
8	<scp>PASSEL</scp> : The <scp>P</scp> eptide <scp>A</scp> tlas <scp>SRM</scp> experiment library. Proteomics, 2012, 12, 1170-1175.	2.2	200
9	Perspectives of targeted mass spectrometry for protein biomarker verification. Current Opinion in Chemical Biology, 2009, 13, 518-525.	6.1	165
10	Tau interactome maps synaptic and mitochondrial processes associated with neurodegeneration. Cell, 2022, 185, 712-728.e14.	28.9	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.	28.9	108
12	Prediction of colorectal cancer diagnosis based onÂcirculating plasma proteins. EMBO Molecular Medicine, 2015, 7, 1166-1178.	6.9	80
13	A systems approach to infectious disease. Nature Reviews Genetics, 2020, 21, 339-354.	16.3	72
14	MassIVE.quant: a community resource of quantitative mass spectrometry–based proteomics datasets. Nature Methods, 2020, 17, 981-984.	19.0	66
15	Enterovirus pathogenesis requires the host methyltransferase SETD3. Nature Microbiology, 2019, 4, 2523-2537.	13.3	51
16	N-Glycoprotein SRMAtlas. Molecular and Cellular Proteomics, 2013, 12, 1005-1016.	3.8	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.	3.8	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.	11.0	42

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#	Article	IF	CITATIONS
19	Smoothened transduces Hedgehog signals via activity-dependent sequestration of PKA catalytic subunits. PLoS Biology, 2021, 19, e3001191.	5.6	40
20	Transcription factor protein interactomes reveal genetic determinants in heart disease. Cell, 2022, 185, 794-814.e30.	28.9	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.	6.4	36
22	Proteomic Approaches to Study SARS-CoV-2 Biology and COVID-19 Pathology. Journal of Proteome Research, 2021, 20, 1133-1152.	3.7	27
23	Genetic interaction mapping informs integrative structure determination of protein complexes. Science, 2020, 370, .	12.6	24
24	CRL4 <sup>AMBRA1</sup> targets Elongin C for ubiquitination and degradation to modulate CRL5 signaling. EMBO Journal, 2018, 37, .	7.8	13
25	Clobal post-translational modification profiling of HIV-1-infected cells reveals mechanisms of host cellular pathway remodeling. Cell Reports, 2022, 39, 110690.	6.4	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.	2.2	7