

# Moritz Heusel

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6466242/publications.pdf>

Version: 2024-02-01

12  
papers

1,003  
citations

840776

11  
h-index

1199594

12  
g-index

15  
all docs

15  
docs citations

15  
times ranked

1849  
citing authors

#	ARTICLE	IF	CITATIONS
1	A repository of assays to quantify 10,000 human proteins by SWATH-MS. <i>Scientific Data</i> , 2014, 1, 140031.	5.3	370
2	Statistical control of peptide and protein error rates in large-scale targeted data-independent acquisition analyses. <i>Nature Methods</i> , 2017, 14, 921-927.	19.0	189
3	Complex-centric proteome profiling by <scp>SEC</scp> â€•<scp>SWATH</scp> â€•<scp>MS</scp>. <i>Molecular Systems Biology</i> , 2019, 15, e8438.	7.2	109
4	The interactome of <scp>KRAB</scp> zinc finger proteins reveals the evolutionary history of their functional diversification. <i>EMBO Journal</i> , 2019, 38, e101220.	7.8	67
5	A Global Screen for Assembly State Changes of the Mitotic Proteome by SEC-SWATH-MS. <i>Cell Systems</i> , 2020, 10, 133-155.e6.	6.2	57
6	SWATH2stats: An R/Bioconductor Package to Process and Convert Quantitative SWATH-MS Proteomics Data for Downstream Analysis Tools. <i>PLoS ONE</i> , 2016, 11, e0153160.	2.5	40
7	Systematic detection of functional proteoform groups from bottom-up proteomic datasets. <i>Nature Communications</i> , 2021, 12, 3810.	12.8	40
8	Complex-centric proteome profiling by SEC-SWATH-MS for the parallel detection of hundreds of protein complexes. <i>Nature Protocols</i> , 2020, 15, 2341-2386.	12.0	34
9	PCprophet: a framework for protein complex prediction and differential analysis using proteomic data. <i>Nature Methods</i> , 2021, 18, 520-527.	19.0	32
10	Precise Temporal Profiling of Signaling Complexes in Primary Cells Using SWATH Mass Spectrometry. <i>Cell Reports</i> , 2017, 18, 3219-3226.	6.4	28
11	SECAT: Quantifying Protein Complex Dynamics across Cell States by Network-Centric Analysis of SEC-SWATH-MS Profiles. <i>Cell Systems</i> , 2020, 11, 589-607.e8.	6.2	26
12	MSLibrarian: Optimized Predicted Spectral Libraries for Data-Independent Acquisition Proteomics. <i>Journal of Proteome Research</i> , 2022, 21, 535-546.	3.7	9