

# Jörg Kuharev

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2261620/publications.pdf>

Version: 2024-02-01

16  
papers

5,000  
citations

567144

15  
h-index

996849

15  
g-index

16  
all docs

16  
docs citations

16  
times ranked

8870  
citing authors

#	ARTICLE	IF	CITATIONS
1	Rapid formation of plasma protein corona critically affects nanoparticle pathophysiology. <i>Nature Nanotechnology</i> , 2013, 8, 772-781.	15.6	1,817
2	Nanoparticle Size Is a Critical Physicochemical Determinant of the Human Blood Plasma Corona: A Comprehensive Quantitative Proteomic Analysis. <i>ACS Nano</i> , 2011, 5, 7155-7167.	7.3	749
3	Protein Corona of Nanoparticles: Distinct Proteins Regulate the Cellular Uptake. <i>Biomacromolecules</i> , 2015, 16, 1311-1321.	2.6	497
4	Drift time-specific collision energies enable deep-coverage data-independent acquisition proteomics. <i>Nature Methods</i> , 2014, 11, 167-170.	9.0	411
5	A multicenter study benchmarks software tools for label-free proteome quantification. <i>Nature Biotechnology</i> , 2016, 34, 1130-1136.	9.4	321
6	Label-free quantification in ion mobility-enhanced data-independent acquisition proteomics. <i>Nature Protocols</i> , 2016, 11, 795-812.	5.5	258
7	Evaluation of FASP, SP3, and iST Protocols for Proteomic Sample Preparation in the Low Microgram Range. <i>Journal of Proteome Research</i> , 2017, 16, 4060-4072.	1.8	227
8	Quantitative profiling of the protein coronas that form around nanoparticles. <i>Nature Protocols</i> , 2014, 9, 2030-2044.	5.5	200
9	Quantitative and Integrative Proteome Analysis of Peripheral Nerve Myelin Identifies Novel Myelin Proteins and Candidate Neuropathy Loci. <i>Journal of Neuroscience</i> , 2011, 31, 16369-16386.	1.7	164
10	In-depth protein profiling of the postsynaptic density from mouse hippocampus using data-independent acquisition proteomics. <i>Proteomics</i> , 2014, 14, 2607-2613.	1.3	103
11	A Systems Level Analysis Reveals Transcriptomic and Proteomic Complexity in <i>Ixodes Ricinus</i> Midgut and Salivary Glands During Early Attachment and Feeding. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2725-2735.	2.5	73
12	In-depth evaluation of software tools for data-independent acquisition based label-free quantification. <i>Proteomics</i> , 2015, 15, 3140-3151.	1.3	66
13	Proteome-Wide Characterization of the RNA-Binding Protein RALY-Interactome Using the in Vivo-Biotinylation-Pulldown-Quant (iBioPQ) Approach. <i>Journal of Proteome Research</i> , 2013, 12, 2869-2884.	1.8	49
14	Mast Cell-deficient <i>Kit<sup>W-sh</sup></i> $\alpha$ -Sash <sup>+</sup> Mutant Mice Display Aberrant Myelopoiesis Leading to the Accumulation of Splenocytes That Act as Myeloid-Derived Suppressor Cells. <i>Journal of Immunology</i> , 2013, 190, 5534-5544.	0.4	36
15	Biomedical applications of ion mobility-enhanced data-independent acquisition-based label-free quantitative proteomics. <i>Expert Review of Proteomics</i> , 2014, 11, 675-684.	1.3	29
16	Data-independent acquisition strategies for quantitative proteomics. , 2013, , 51-54.		0