

Ulrike Kusebauch

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

2,206
citations

361413

20
h-index

552781

26
g-index

35
all docs

35
docs citations

35
times ranked

4559
citing authors

#	ARTICLE	IF	CITATIONS
1	Non-responder phenotype reveals apparent microbiome-wide antibiotic tolerance in the murine gut. <i>Communications Biology</i> , 2021, 4, 316.	4.4	2
2	Hallstatt miners consumed blue cheese and beer during the Iron Age and retained a non-Westernized gut microbiome until the Baroque period. <i>Current Biology</i> , 2021, 31, 5149-5162.e6.	3.9	22
3	<i>Plasmodium falciparum</i> Calcium-Dependent Protein Kinase 4 is Critical for Male Gametogenesis and Transmission to the Mosquito Vector. <i>MBio</i> , 2021, 12, e0257521.	4.1	26
4	A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , 2020, 11, 5301.	12.8	152
5	DIALib-QC an assessment tool for spectral libraries in data-independent acquisition proteomics. <i>Nature Communications</i> , 2020, 11, 5251.	12.8	32
6	A comprehensive spectral assay library to quantify the <i>Escherichia coli</i> proteome by DIA/SWATH-MS. <i>Scientific Data</i> , 2020, 7, 389.	5.3	28
7	Selective Translation of Low Abundance and Upregulated Transcripts in <i>Halobacterium salinarum</i> . <i>MSystems</i> , 2020, 5, .	3.8	10
8	Insights from the First Phosphopeptide Challenge of the MS Resource Pillar of the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2020, 19, 4754-4765.	3.7	7
9	Luminal calcification and microvasculopathy in fetuin-A-deficient mice lead to multiple organ morbidity. <i>PLoS ONE</i> , 2020, 15, e0228503.	2.5	35
10	Title is missing!. , 2020, 15, e0228503.		0
11	Title is missing!. , 2020, 15, e0228503.		0
12	Title is missing!. , 2020, 15, e0228503.		0
13	Title is missing!. , 2020, 15, e0228503.		0
14	PTMProphet: Fast and Accurate Mass Modification Localization for the Trans-Proteomic Pipeline. <i>Journal of Proteome Research</i> , 2019, 18, 4262-4272.	3.7	80
15	Selected reaction monitoring mass spectrometry of mastitis milk reveals pathogen-specific regulation of bovine host response proteins. <i>Journal of Dairy Science</i> , 2018, 101, 6532-6541.	3.4	25
16	The Iceman's Last Meal Consisted of Fat, Wild Meat, and Cereals. <i>Current Biology</i> , 2018, 28, 2348-2355.e9.	3.9	39
17	Building ProteomeTools based on a complete synthetic human proteome. <i>Nature Methods</i> , 2017, 14, 259-262.	19.0	182
18	A global <i>Staphylococcus aureus</i> proteome resource applied to the in vivo characterization of host-pathogen interactions. <i>Scientific Reports</i> , 2017, 7, 9718.	3.3	42

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19	A wellness study of 108 individuals using personal, dense, dynamic data clouds. <i>Nature Biotechnology</i> , 2017, 35, 747-756.	17.5	340
20	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. <i>Journal of Proteome Research</i> , 2016, 15, 3961-3970.	3.7	158
21	An activated form of ADAM10 is tumor selective and regulates cancer stem-like cells and tumor growth. <i>Journal of Experimental Medicine</i> , 2016, 213, 1741-1757.	8.5	55
22	Identification of Organ-Enriched Protein Biomarkers of Acute Liver Injury by Targeted Quantitative Proteomics of Blood in Acetaminophen- and Carbon-Tetrachloride-Treated Mouse Models and Acetaminophen Overdose Patients. <i>Journal of Proteome Research</i> , 2016, 15, 3724-3740.	3.7	28
23	Human SRMATlas: A Resource of Targeted Assays to Quantify the Complete Human Proteome. <i>Cell</i> , 2016, 166, 766-778.	28.9	295
24	Recommendations for the Generation, Quantification, Storage, and Handling of Peptides Used for Mass Spectrometry-Based Assays. <i>Clinical Chemistry</i> , 2016, 62, 48-69.	3.2	187
25	The 5300-year-old <i>Helicobacter pylori</i> genome of the Iceman. <i>Science</i> , 2016, 351, 162-165.	12.6	200
26	RNA Sequencing Identifies Novel Translational Biomarkers of Kidney Fibrosis. <i>Journal of the American Society of Nephrology: JASN</i> , 2016, 27, 1702-1713.	6.1	53
27	State of the Human Proteome in 2014/2015 As Viewed through PeptideAtlas: Enhancing Accuracy and Coverage through the AtlasProphet. <i>Journal of Proteome Research</i> , 2015, 14, 3461-3473.	3.7	72
28	Decreased Gap Width in a Cylindrical High-Field Asymmetric Waveform Ion Mobility Spectrometry Device Improves Protein Discovery. <i>Analytical Chemistry</i> , 2015, 87, 12230-12237.	6.5	10
29	<i>Mycobacterium tuberculosis</i> supports protein tyrosine phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9265-9270.	7.1	67
30	Using PeptideAtlas, SRMATlas, and PASSEL: Comprehensive Resources for Discovery and Targeted Proteomics. <i>Current Protocols in Bioinformatics</i> , 2014, 46, 13.25.1-28.	25.8	51
31	Engineered SH2 Domains for Targeted Phosphoproteomics. <i>ACS Chemical Biology</i> , 0, , .	3.4	6