

Christian K Frese

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

2,495
citations

394421

19
h-index

434195

31
g-index

33
all docs

33
docs citations

33
times ranked

4284
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive Identification of RNA-Binding Domains in Human Cells. <i>Molecular Cell</i> , 2016, 63, 696-710.	9.7	493
2	Improved Peptide Identification by Targeted Fragmentation Using CID, HCD and ETD on an LTQ-Orbitrap Velos. <i>Journal of Proteome Research</i> , 2011, 10, 2377-2388.	3.7	277
3	Toward Full Peptide Sequence Coverage by Dual Fragmentation Combining Electron-Transfer and Higher-Energy Collision Dissociation Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2012, 84, 9668-9673.	6.5	246
4	Expanding the detectable HLA peptide repertoire using electron-transfer/higher-energy collision dissociation (EThcD). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4507-4512.	7.1	189
5	Unambiguous Phosphosite Localization using Electron-Transfer/Higher-Energy Collision Dissociation (EThcD). <i>Journal of Proteome Research</i> , 2013, 12, 1520-1525.	3.7	145
6	Global changes of the RNA-bound proteome during the maternal-to-zygotic transition in <i>Drosophila</i> . <i>Nature Communications</i> , 2016, 7, 12128.	12.8	134
7	The Cardiomyocyte RNA-Binding Proteome: Links to Intermediary Metabolism and Heart Disease. <i>Cell Reports</i> , 2016, 16, 1456-1469.	6.4	128
8	The quantitative proteomes of human-induced pluripotent stem cells and embryonic stem cells. <i>Molecular Systems Biology</i> , 2011, 7, 550.	7.2	125
9	<i>De novo</i> discovery of phenotypic intratumour heterogeneity using imaging mass spectrometry. <i>Journal of Pathology</i> , 2015, 235, 3-13.	4.5	116
10	Benchmarking stable isotope labeling based quantitative proteomics. <i>Journal of Proteomics</i> , 2013, 88, 14-26.	2.4	112
11	The cytosolic DNA sensor cGAS recognizes neutrophil extracellular traps. <i>Science Signaling</i> , 2021, 14, .	3.6	87
12	The alarmones (p)ppGpp are part of the heat shock response of <i>Bacillus subtilis</i> . <i>PLoS Genetics</i> , 2020, 16, e1008275.	3.5	52
13	Single-nephron proteomes connect morphology and function in proteinuric kidney disease. <i>Kidney International</i> , 2018, 93, 1308-1319.	5.2	49
14	Alterations of redox and iron metabolism accompany the development of HIV latency. <i>EMBO Journal</i> , 2020, 39, e102209.	7.8	37
15	CASC3 promotes transcriptome-wide activation of nonsense-mediated decay by the exon junction complex. <i>Nucleic Acids Research</i> , 2020, 48, 8626-8644.	14.5	35
16	Identification of RNA-binding domains of RNA-binding proteins in cultured cells on a system-wide scale with RBDmap. <i>Nature Protocols</i> , 2017, 12, 2447-2464.	12.0	32
17	Expanding the Depth and Sensitivity of Cross-Link Identification by Differential Ion Mobility Using High-Field Asymmetric Waveform Ion Mobility Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 10495-10503.	6.5	32
18	Profiling of Diet-Induced Neuropeptide Changes in Rat Brain by Quantitative Mass Spectrometry. <i>Analytical Chemistry</i> , 2013, 85, 4594-4604.	6.5	24

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19	Imaging Mass Spectrometry-based Molecular Histology Differentiates Microscopically Identical and Heterogeneous Tumors. <i>Journal of Proteome Research</i> , 2013, 12, 1847-1855.	3.7	24
20	Analytical Utility of Mass Spectral Binning in Proteomic Experiments by Spectral Immonium Ion Detection (SPIID). <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1914-1924.	3.8	22
21	Mechanism suppressing H3K9 trimethylation in pluripotent stem cells and its demise by polyQ-expanded huntingtin mutations. <i>Human Molecular Genetics</i> , 2018, 27, 4117-4134.	2.9	21
22	A protein-RNA interaction atlas of the ribosome biogenesis factor AATF. <i>Scientific Reports</i> , 2019, 9, 11071.	3.3	19
23	<i>Corynebacterium glutamicum</i> exhibits a membrane-related response to a small ferrocene-conjugated antimicrobial peptide. <i>Journal of Biological Inorganic Chemistry</i> , 2010, 15, 1293-1303.	2.6	18
24	Maternal exercise conveys protection against NAFLD in the offspring via hepatic metabolic programming. <i>Scientific Reports</i> , 2020, 10, 15424.	3.3	18
25	The RNA-Protein Interactome of Differentiated Kidney Tubular Epithelial Cells. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 564-576.	6.1	16
26	Automated Phosphopeptide Enrichment for Gram-Positive Bacteria. <i>Journal of Proteome Research</i> , 2021, 20, 4886-4892.	3.7	10
27	Diet-Induced Neuropeptide Expression: Feasibility of Quantifying Extended and Highly Charged Endogenous Peptide Sequences by Selected Reaction Monitoring. <i>Analytical Chemistry</i> , 2015, 87, 9966-9973.	6.5	8
28	Role of Premycofactocin Synthase in Growth, Microaerophilic Adaptation, and Metabolism of <i>Mycobacterium tuberculosis</i> . <i>MBio</i> , 2021, 12, e0166521.	4.1	7
29	Time-Resolved Proteome Analysis of <i>Listeria monocytogenes</i> during Infection Reveals the Role of the AAA+ Chaperone ClpC for Host Cell Adaptation. <i>MSystems</i> , 2021, 6, e0021521.	3.8	6
30	<i>Escherichia coli</i> exhibits a membrane-related response to a small arginine- and tryptophan-rich antimicrobial peptide. <i>Proteomics</i> , 2012, 12, 2319-2330.	2.2	5
31	Characterization of Electron Transfer Dissociation in the Orbitrap Velos HCD Cell. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 1663-1670.	2.8	5