

Christian Dahl Kelstrup

List of Publications by Year in descending order

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36
papers

5,583
citations

201674

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345221

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39
all docs

39
docs citations

39
times ranked

9827
citing authors

#	ARTICLE	IF	CITATIONS
1	GHB analogs confer neuroprotection through specific interaction with the CaMKII β hub domain. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	31
2	ProAlanase is an Effective Alternative to Trypsin for Proteomics Applications and Disulfide Bond Mapping. Molecular and Cellular Proteomics, 2020, 19, 2139-2157.	3.8	27
3	Rapid and site-specific deep phosphoproteome profiling by data-independent acquisition without the need for spectral libraries. Nature Communications, 2020, 11, 787.	12.8	251
4	Early Pleistocene enamel proteome from Dmanisi resolves Stephanorhinus phylogeny. Nature, 2019, 574, 103-107.	27.8	135
5	Oncogenic Mutations Rewire Signaling Pathways by Switching Protein Recruitment to Phosphotyrosine Sites. Cell, 2019, 179, 543-560.e26.	28.9	65
6	Benchmarking common quantification strategies for large-scale phosphoproteomics. Nature Communications, 2018, 9, 1045.	12.8	232
7	Performance Evaluation of the Q Exactive HF-X for Shotgun Proteomics. Journal of Proteome Research, 2018, 17, 727-738.	3.7	221
8	Quantitative metaproteomics of medieval dental calculus reveals individual oral health status. Nature Communications, 2018, 9, 4744.	12.8	63
9	Limits for Resolving Isobaric Tandem Mass Tag Reporter Ions Using Phase-Constrained Spectrum Deconvolution. Journal of Proteome Research, 2018, 17, 4008-4016.	3.7	29
10	UbiSite approach for comprehensive mapping of lysine and N-terminal ubiquitination sites. Nature Structural and Molecular Biology, 2018, 25, 631-640.	8.2	341
11	Generic Workflow for Mapping of Complex Disulfide Bonds Using In-Source Reduction and Extracted Ion Chromatograms from Data-Dependent Mass Spectrometry. Analytical Chemistry, 2018, 90, 8202-8210.	6.5	15
12	Complete Mapping of Complex Disulfide Patterns with Closely-Spaced Cysteines by In-Source Reduction and Data-Dependent Mass Spectrometry. Analytical Chemistry, 2017, 89, 5949-5957.	6.5	27
13	An Optimized Shotgun Strategy for the Rapid Generation of Comprehensive Human Proteomes. Cell Systems, 2017, 4, 587-599.e4.	6.2	413
14	Analytic framework for peptidomics applied to large-scale neuropeptide identification. Nature Communications, 2016, 7, 11436.	12.8	92
15	Ancient proteins resolve the evolutionary history of Darwin's South American ungulates. Nature, 2015, 522, 81-84.	27.8	273
16	Molecular evidence of use of hide glue in 4th millennium BC Europe. Journal of Archaeological Science, 2015, 63, 65-71.	2.4	32
17	Analytical Utility of Mass Spectral Binning in Proteomic Experiments by Spectral Immonium Ion Detection (SPIID). Molecular and Cellular Proteomics, 2014, 13, 1914-1924.	3.8	22
18	Rapid and Deep Proteomes by Faster Sequencing on a Benchtop Quadrupole Ultra-High-Field Orbitrap Mass Spectrometer. Journal of Proteome Research, 2014, 13, 6187-6195.	3.7	168

#	ARTICLE	IF	CITATIONS
19	qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1905-1913.	3.8	42
20	Pathogens and host immunity in the ancient human oral cavity. <i>Nature Genetics</i> , 2014, 46, 336-344.	21.4	482
21	Uncovering SUMOylation Dynamics during Cell-Cycle Progression Reveals FoxM1 as a Key Mitotic SUMO Target Protein. <i>Molecular Cell</i> , 2014, 53, 1053-1066.	9.7	153
22	Resolution of the type material of the Asian elephant, <i>Elephas maximus</i> Linnaeus, 1758 (Proboscidea, Elephantidae). <i>Zoological Journal of the Linnean Society</i> , 2014, 170, 222-232.	2.3	31
23	Resolution of the type material of the Asian elephant, <i>Elephas maximus</i> Linnaeus, 1758 (Proboscidea, Tj ETQq1 1 0,784314 rgBT /Over	2.3	22
24	Comprehensive Identification of SUMO2/3 Targets and Their Dynamics during Mitosis. <i>PLoS ONE</i> , 2014, 9, e100692.	2.5	19
25	Species Identification of Archaeological Skin Objects from Danish Bogs: Comparison between Mass Spectrometry-Based Peptide Sequencing and Microscopy-Based Methods. <i>PLoS ONE</i> , 2014, 9, e106875.	2.5	70
26	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013, 499, 74-78.	27.8	717
27	In Vivo Phosphoproteomics Analysis Reveals the Cardiac Targets of β -Adrenergic Receptor Signaling. <i>Science Signaling</i> , 2013, 6, rs11.	3.6	164
28	The Ndc80 internal loop is required for recruitment of the Ska complex to establish end-on microtubule attachment to kinetochores.. <i>Journal of Cell Science</i> , 2012, 125, 3243-53.	2.0	62
29	Proteomic Analyses Reveal Divergent Ubiquitylation Site Patterns in Murine Tissues. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1578-1585.	3.8	244
30	Proteomic Analysis of Lysine Acetylation Sites in Rat Tissues Reveals Organ Specificity and Subcellular Patterns. <i>Cell Reports</i> , 2012, 2, 419-431.	6.4	493
31	Optimized Fast and Sensitive Acquisition Methods for Shotgun Proteomics on a Quadrupole Orbitrap Mass Spectrometer. <i>Journal of Proteome Research</i> , 2012, 11, 3487-3497.	3.7	270
32	Comprehensive profiling of proteome changes upon sequential deletion of deubiquitylating enzymes. <i>Journal of Proteomics</i> , 2012, 75, 3886-3897.	2.4	18
33	Pinpointing Phosphorylation Sites: Quantitative Filtering and a Novel Site-specific x-Ion Fragment. <i>Journal of Proteome Research</i> , 2011, 10, 2937-2948.	3.7	27
34	Global Phosphoproteome Profiling Reveals Unanticipated Networks Responsive to Cisplatin Treatment of Embryonic Stem Cells. <i>Molecular and Cellular Biology</i> , 2011, 31, 4964-4977.	2.3	56
35	Quantitative Phosphoproteomics Dissection of Seven-transmembrane Receptor Signaling Using Full and Biased Agonists. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1540-1553.	3.8	135
36	Global analysis of the yeast osmotic stress response by quantitative proteomics. <i>Molecular BioSystems</i> , 2009, 5, 1337.	2.9	128