Christina Ludwig

List of Publications by Year
in descending order

28 papers	2,518 citations	394421 19 h-index	501196 28 g-index
36 all docs	36 docs citations	36 times ranked	4500 citing authors

#	Article	IF	Citations
1	Spotlight on alternative frame coding: Two long overlapping genes in Pseudomonas aeruginosa are translated and under purifying selection. IScience, 2022, 25, 103844.	4.1	13
2	RGIâ€GOLVEN signaling promotes cell surface immune receptor abundance to regulate plant immunity. EMBO Reports, 2022, 23, e53281.	4.5	20
3	Proteomic Analysis Reveals Enzymes for Î²-D-Glucan Formation and Degradation in Levilactobacillus brevis TMW 1.2112. International Journal of Molecular Sciences, 2022, 23, 3393.	4.1	2
4	Dietary intervention improves health metrics and life expectancy of the genetically obese Titan mouse. Communications Biology, 2022, 5, 408.	4.4	4
5	A tailored phosphoaspartate probe unravels CprR as a response regulator in *Pseudomonas aeruginosa* interkingdom signaling. Chemical Science, 2021, 12, 4763-4770.	7.4	10
6	From coarse to fine: the absolute *Escherichia coli* proteome under diverse growth conditions. Molecular Systems Biology, 2021, 17, e9536.	7.2	82
7	Dissecting the sequence determinants for dephosphorylation by the catalytic subunits of phosphatases PP1 and PP2A. Nature Communications, 2020, 11, 3583.	12.8	38
8	Living the Sweet Life: How Liquorilactobacillus hordei TMW 1.1822 Changes Its Behavior in the Presence of Sucrose in Comparison to Glucose. Foods, 2020, 9, 1150.	4.3	8
9	Identification of Isopeptides Between Human Tissue Transglutaminase and Wheat, Rye, and Barley Gluten Peptides. Scientific Reports, 2020, 10, 7426.	3.3	11
10	Data, Reagents, Assays and Merits of Proteomics for SARS-CoV-2 Research and Testing. Molecular and Cellular Proteomics, 2020, 19, 1503-1522.	3.8	78
11	Dynamically evolving novel overlapping gene as a factor in the SARS-CoV-2 pandemic. ELife, 2020, 9, .	6.0	74
12	Comprehensive Detection of Isopeptides between Human Tissue Transglutaminase and Gluten Peptides. Nutrients, 2019, 11, 2263.	4.1	11
13	Label-free quantitative proteomic analysis reveals the lifestyle of Lactobacillus hordei in the presence of Sacchromyces cerevisiae. International Journal of Food Microbiology, 2019, 294, 18-26.	4.7	26
14	Proteomic Analysis of Lactobacillus nagelii in the Presence of Saccharomyces cerevisiae Isolated From Water Kefir and Comparison With Lactobacillus hordei. Frontiers in Microbiology, 2019, 10, 325.	3.5	23
15	Panorama Public: A Public Repository for Quantitative Data Sets Processed in Skyline. Molecular and Cellular Proteomics, 2018, 17, 1239-1244.	3.8	177
16	Sucrose-Induced Proteomic Response and Carbohydrate Utilization of Lactobacillus sakei TMW 1.411 During Dextran Formation. Frontiers in Microbiology, 2018, 9, 2796.	3.5	21
17	Dataâ€independent acquisitionâ€based SWATH â€•MS for quantitative proteomics: a tutorial. Molecular Systems Biology, 2018, 14, e8126.	7.2	701
18	Increased Pancreatic Protease Activity in Response to Antibiotics Impairs Gut Barrier and Triggers Colitis. Cellular and Molecular Gastroenterology and Hepatology, 2018, 6, 370-388.e3.	4.5	22

#	Article	IF	Citations
19	Inference and quantification of peptidoforms in large sample cohorts by SWATH-MS. Nature Biotechnology, 2017, 35, 781-788.	17.5	122
20	Attenuation of pattern recognition receptor signaling is mediated by a <scp>MAP</scp> kinase kinase kinase. EMBO Reports, 2016, 17, 441-454.	4.5	50
21	Inferring causal metabolic signals that regulate the dynamic <scp>TORC</scp>1â€dependent transcriptome. Molecular Systems Biology, 2015, 11, 802.	7.2	49
22	Absolute Proteome Composition and Dynamics during Dormancy and Resuscitation of Mycobacterium tuberculosis. Cell Host and Microbe, 2015, 18, 96-108.	11.0	229
23	Dynamic phosphoproteomics reveals TORC1-dependent regulation of yeast nucleotide and amino acid biosynthesis. Science Signaling, 2015, 8, rs4.	3.6	64
24	aLFQ: an R-package for estimating absolute protein quantities from label-free LC-MS/MS proteomics data. Bioinformatics, 2014, 30, 2511-2513.	4.1	63
25	Getting Absolute: Determining Absolute Protein Quantities via Selected Reaction Monitoring Mass Spectrometry. New Developments in Mass Spectrometry, 2014, , 80-109.	0.2	17
26	The Mtb Proteome Library: A Resource of Assays to Quantify the Complete Proteome of Mycobacterium tuberculosis. Cell Host and Microbe, 2013, 13, 602-612.	11.0	165
27	Large-Scale Quantitative Assessment of Different In-Solution Protein Digestion Protocols Reveals Superior Cleavage Efficiency of Tandem Lys-C/Trypsin Proteolysis over Trypsin Digestion. Journal of Proteome Research, 2012, 11, 5145-5156.	3.7	298
28	Estimation of Absolute Protein Quantities of Unlabeled Samples by Selected Reaction Monitoring Mass Spectrometry. Molecular and Cellular Proteomics, 2012, 11, M111.013987.	3.8	117