Zhibin Ning

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/8160513/publications.pdf

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49	1,929	279487	315357
papers	citations	23 h-index	38 g-index

58	58	58	2585
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Metaproteomics reveals associations between microbiome and intestinal extracellular vesicle proteins in pediatric inflammatory bowel disease. Nature Communications, 2018, 9, 2873.	5.8	209
2	RapidAIM: a culture- and metaproteomics-based Rapid Assay of Individual Microbiome responses to drugs. Microbiome, 2020, 8, 33.	4.9	209
3	MetaPro-IQ: a universal metaproteomic approach to studying human and mouse gut microbiota. Microbiome, 2016, 4, 31.	4.9	154
4	MetaLab: an automated pipeline for metaproteomic data analysis. Microbiome, 2017, 5, 157.	4.9	128
5	Assessing the impact of protein extraction methods for human gut metaproteomics. Journal of Proteomics, 2018, 180, 120-127.	1.2	115
6	Deep Metaproteomics Approach for the Study of Human Microbiomes. Analytical Chemistry, 2017, 89, 9407-9415.	3.2	83
7	An in vitro model maintaining taxon-specific functional activities of the gut microbiome. Nature Communications, 2019, 10, 4146.	5.8	70
8	Proteomic analysis of ascending colon biopsies from a paediatric inflammatory bowel disease inception cohort identifies protein biomarkers that differentiate Crohn's disease from UC. Gut, 2017, 66, 1573-1583.	6.1	69
9	iMetaLab 1.0: a web platform for metaproteomics data analysis. Bioinformatics, 2018, 34, 3954-3956.	1.8	64
10	The Proteomic Landscape of the Suprachiasmatic Nucleus Clock Reveals Large-Scale Coordination of Key Biological Processes. PLoS Genetics, 2014, 10, e1004695.	1.5	63
11	Quantitative site-specific ADP-ribosylation profiling of DNA-dependent PARPs. DNA Repair, 2015, 30, 68-79.	1.3	56
12	Bottom-Up Proteomics (2013â€“2015): Keeping up in the Era of Systems Biology. Analytical Chemistry, 2016, 88, 95-121.	3.2	52
13	Proteomic and Metaproteomic Approaches to Understand Hostâ€“Microbe Interactions. Analytical Chemistry, 2018, 90, 86-109.	3.2	44
14	Evaluating in Vitro Culture Medium of Gut Microbiome with Orthogonal Experimental Design and a Metaproteomics Approach. Journal of Proteome Research, 2018, 17, 154-163.	1.8	41
15	In Vitro Metabolic Labeling of Intestinal Microbiota for Quantitative Metaproteomics. Analytical Chemistry, 2016, 88, 6120-6125.	3.2	40
16	Phosphoproteome Profiling Reveals Circadian Clock Regulation of Posttranslational Modifications in the Murine Hippocampus. Frontiers in Neurology, 2017, 8, 110.	1.1	35
17	Discovery of Substrates for a SET Domain Lysine Methyltransferase Predicted by Multistate Computational Protein Design. Structure, 2015, 23, 206-215.	1.6	34
18	Quantitative proteomic analysis of Dunaliella salina upon acute arsenate exposure. Chemosphere, 2016, 145, 112-118.	4.2	31

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19	A charge-suppressing strategy for probing protein methylation. Chemical Communications, 2016, 52, 5474-5477.	2.2	30
20	Berberine and its structural analogs have differing effects on functional profiles of individual gut microbiomes. Gut Microbes, 2020, 11, 1348-1361.	4.3	30
21	Analytical Aspects of Proteomics: 2009â€“2010. Analytical Chemistry, 2011, 83, 4407-4426.	3.2	28
22	From Cells to Peptides: â€œOne-Stopâ€•Integrated Proteomic Processing Using Amphipols. Journal of Proteome Research, 2013, 12, 1512-1519.	1.8	28
23	Metaproteomic and Metabolomic Approaches for Characterizing the Gut Microbiome. Proteomics, 2019, 19, e1800363.	1.3	28
24	High throughput solid phase microextraction: A new alternative for analysis of cellular lipidome?. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2017, 1043, 12-19.	1.2	26
25	Open: Mucosal-luminal interface proteomics reveals biomarkers of pediatric inflammatory bowel disease-associated colitis. American Journal of Gastroenterology, 2018, 113, 713-724.	0.2	23
26	MetaLab 2.0 Enables Accurate Post-Translational Modifications Profiling in Metaproteomics. Journal of the American Society for Mass Spectrometry, 2020, 31, 1473-1482.	1.2	21
27	APols-Aided Protein Precipitation: A Rapid Method for Concentrating Proteins for Proteomic Analysis. Journal of Membrane Biology, 2014, 247, 941-947.	1.0	17
28	Quantitative phosphoproteomics reveals involvement of multiple signaling pathways in early phagocytosis by the retinal pigmented epithelium. Journal of Biological Chemistry, 2017, 292, 19826-19839.	1.6	17
29	A functional ecological network based on metaproteomics responses of individual gut microbiomes to resistant starches. Computational and Structural Biotechnology Journal, 2020, 18, 3833-3842.	1.9	15
30	Proteomic Analysis of Cerebellum in Common Marmoset Exposed to Methylmercury. Toxicological Sciences, 2015, 146, 43-51.	1.4	14
31	N-Glycopeptide Reduction with Exoglycosidases Enables Accurate Characterization of Site-Specific N-Glycosylation. Analytical Chemistry, 2016, 88, 11837-11843.	3.2	14
32	Peptide-Centric Approaches Provide an Alternative Perspective To Re-Examine Quantitative Proteomic Data. Analytical Chemistry, 2016, 88, 1973-1978.	3.2	14
33	Associations Between Soluble LDLR and Lipoproteins in a White Cohort and the Effect of PCSK9 Loss-of-Function. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 3486-3495.	1.8	14
34	Proteome profiling reveals regional protein alteration in cerebrum of common marmoset (Callithrix) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.0	11
35	Chemoenzymatic Method for Glycoproteomic N-Glycan Type Quantitation. Analytical Chemistry, 2020, 92, 1618-1627.	3.2	11
36	Detecting Proteinâ€“Protein Interactions/Complex Components Using Mass Spectrometry Coupled Techniques. Methods in Molecular Biology, 2014, 1164, 1-13.	0.4	9

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37	Differential proteomic analysis of synovial fluid from hip arthroplasty patients with a pseudotumor vs. Periprosthetic osteolysis. Journal of Orthopaedic Research, 2018, 36, 1849-1859.	1.2	7
38	pepFunk: a tool for peptide-centric functional analysis of metaproteomic human gut microbiome studies. Bioinformatics, 2020, 36, 4171-4179.	1.8	7
39	Metaproteomics Reveals Growth Phase-Dependent Responses of an In Vitro Gut Microbiota to Metformin. Journal of the American Society for Mass Spectrometry, 2020, 31, 1448-1458.	1.2	7
40	Evaluating live microbiota biobanking using an ex vivo microbiome assay and metaproteomics. Gut Microbes, 2022, 14, 2035658.	4.3	7
41	Activityâ€based profiling of the proteasome pathway during hepatitis C virus infection. Proteomics, 2015, 15, 3815-3825.	1.3	6
42	Exploring the Microbiome-Wide Lysine Acetylation, Succinylation, and Propionylation in Human Gut Microbiota. Analytical Chemistry, 2021, 93, 6594-6598.	3.2	6
43	Studying the Temporal Dynamics of the Gut Microbiota Using Metabolic Stable Isotope Labeling and Metaproteomics. Analytical Chemistry, 2020, 92, 15711-15718.	3.2	5
44	MealTime-MS: A Machine Learning-Guided Real-Time Mass Spectrometry Analysis for Protein Identification and Efficient Dynamic Exclusion. Journal of the American Society for Mass Spectrometry, 2020, 31, 1459-1472.	1.2	5
45	Examining the Effects of an Anti-Salmonella Bacteriophage Preparation, BAFASALÂ®, on Ex-Vivo Human Gut Microbiome Composition and Function Using a Multi-Omics Approach. Viruses, 2021, 13, 1734.	1.5	5
46	Structural analysis of Atopobium parvulum SufS cysteine desulfurase linked to Crohn's disease. FEBS Letters, 2022, 596, 898-909.	1.3	5
47	Differential Lysis Approach Enables Selective Extraction of Taxon-Specific Proteins for Gut Metaproteomics. Analytical Chemistry, 2020, 92, 5379-5386.	3.2	4
48	Elevated colonic microbiota-associated paucimannosidic and truncated N-glycans in pediatric ulcerative colitis. Journal of Proteomics, 2021, 249, 104369.	1.2	4
49	Comprehensive Assessment of Functional Effects of Commonly Used Sugar Substitute Sweeteners on Ex Vivo Human Gut Microbiome. Microbiology Spectrum, 2022, 10, .	1.2	3