

Magnus Ã. Arntzen

List of Publications by Year in descending order

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74
papers

2,627
citations

172386

29
h-index

223716

46
g-index

85
all docs

85
docs citations

85
times ranked

4097
citing authors

#	ARTICLE	IF	CITATIONS
1	The human gut Firmicute <i>Roseburia intestinalis</i> is a primary degrader of dietary β -mannans. <i>Nature Communications</i> , 2019, 10, 905.	5.8	202
2	Identification of Nuclear Phosphatidylinositol 4,5-Bisphosphate-Interacting Proteins by Neomycin Extraction. <i>Molecular and Cellular Proteomics</i> , 2011, 10, S1-S15.	2.5	107
3	Denitrification as an N ₂ O sink. <i>Water Research</i> , 2019, 151, 381-387.	5.3	101
4	Different binding motifs of the celiac disease-associated HLA molecules DQ2.5, DQ2.2, and DQ7.5 revealed by relative quantitative proteomics of endogenous peptide repertoires. <i>Immunogenetics</i> , 2015, 67, 73-84.	1.2	94
5	Simultaneous analysis of C1 and C4 oxidized oligosaccharides, the products of lytic polysaccharide monoxygenases acting on cellulose. <i>Journal of Chromatography A</i> , 2016, 1445, 46-54.	1.8	90
6	The Preferred Substrates for Transglutaminase 2 in a Complex Wheat Gluten Digest Are Peptide Fragments Harboring Celiac Disease T-Cell Epitopes. <i>PLoS ONE</i> , 2010, 5, e14056.	1.1	88
7	MiR-133b Targets Antiapoptotic Genes and Enhances Death Receptor-Induced Apoptosis. <i>PLoS ONE</i> , 2012, 7, e35345.	1.1	87
8	IsobariQ: Software for Isobaric Quantitative Proteomics using IPTL, iTRAQ, and TMT. <i>Journal of Proteome Research</i> , 2011, 10, 913-920.	1.8	84
9	Multipoint Precision Binding of Substrate Protects Lytic Polysaccharide Monoxygenases from Self-Destructive Off-Pathway Processes. <i>Biochemistry</i> , 2018, 57, 4114-4124.	1.2	78
10	Extracellular Identification of a Processed Type II ComR/ComS Pheromone of <i>Streptococcus mutans</i> . <i>Journal of Bacteriology</i> , 2012, 194, 3781-3788.	1.0	69
11	Quantitative Metaproteomics Highlight the Metabolic Contributions of Uncultured Phylotypes in a Thermophilic Anaerobic Digester. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	67
12	Proteogenomic Analysis of Polymorphisms and Gene Annotation Divergences in Prokaryotes using a Clustered Mass Spectrometry-Friendly Database. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.002527.	2.5	62
13	Proteome analysis of xylose metabolism in <i>Rhodotorula toruloides</i> during lipid production. <i>Biotechnology for Biofuels</i> , 2019, 12, 137.	6.2	61
14	Butyrate Levels in the Transition from an Infant- to an Adult-Like Gut Microbiota Correlate with Bacterial Networks Associated with <i>Eubacterium Rectale</i> and <i>Ruminococcus Gnavus</i> . <i>Genes</i> , 2020, 11, 1245.	1.0	58
15	The lytic polysaccharide monoxygenase CbpD promotes <i>Pseudomonas aeruginosa</i> virulence in systemic infection. <i>Nature Communications</i> , 2021, 12, 1230.	5.8	57
16	Outer membrane vesicles from <i>Fibrobacter succinogenes</i> S85 contain an array of carbohydrate-active enzymes with versatile polysaccharide-degrading capacity. <i>Environmental Microbiology</i> , 2017, 19, 2701-2714.	1.8	55
17	Microbiota-directed fibre activates both targeted and secondary metabolic shifts in the distal gut. <i>Nature Communications</i> , 2020, 11, 5773.	5.8	55
18	Quantitative comparison of the biomass-degrading enzyme repertoires of five filamentous fungi. <i>Scientific Reports</i> , 2020, 10, 20267.	1.6	51

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19	Isobaric Peptide Termini Labeling Utilizing Site-Specific N-Terminal Succinylation. <i>Analytical Chemistry</i> , 2011, 83, 4775-4781.	3.2	50
20	Membrane and membrane-associated proteins in Triton X-114 extracts of <i>Mycobacterium bovis</i> BCG identified using a combination of gel-based and gel-free fractionation strategies. <i>Proteomics</i> , 2008, 8, 1859-1870.	1.3	46
21	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber. <i>ISME Journal</i> , 2021, 15, 421-434.	4.4	46
22	Lytic polysaccharide monooxygenases and other oxidative enzymes are abundantly secreted by <i>Aspergillus nidulans</i> grown on different starches. <i>Biotechnology for Biofuels</i> , 2016, 9, 187.	6.2	42
23	An Approach for Triplex-Isobaric Peptide Termini Labeling (Triplex-IPTL). <i>Analytical Chemistry</i> , 2013, 85, 2478-2485.	3.2	40
24	The Metaproteomics Initiative: a coordinated approach for propelling the functional characterization of microbiomes. <i>Microbiome</i> , 2021, 9, 243.	4.9	36
25	MSMSpddb: providing protein databases of closely related organisms to improve proteomic characterization of prokaryotic microbes. <i>Bioinformatics</i> , 2010, 26, 698-699.	1.8	34
26	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. <i>Nature Communications</i> , 2021, 12, 7305.	5.8	34
27	Down-stream processing of baker's yeast (<i>Saccharomyces cerevisiae</i>) – Effect on nutrient digestibility and immune response in Atlantic salmon (<i>Salmo salar</i>). <i>Aquaculture</i> , 2021, 530, 735707.	1.7	33
28	<i>Candidatus Paraporphyromonas polyenzymogenes</i> encodes multi-modular cellulases linked to the type IX secretion system. <i>Microbiome</i> , 2018, 6, 44.	4.9	32
29	Production, Characterization, and Application of an Alginate Lyase, AMOR_PL7A, from Hot Vents in the Arctic Mid-Ocean Ridge. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 2936-2945.	2.4	31
30	ApoptoProteomics, an Integrated Database for Analysis of Proteomics Data Obtained from Apoptotic Cells. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.010447.	2.5	30
31	Novel Syntrophic Populations Dominate an Ammonia-Tolerant Methanogenic Microbiome. <i>MSystems</i> , 2016, 1, .	1.7	30
32	From proteins to polysaccharides: lifestyle and genetic evolution of <i>Coprothermobacter proteolyticus</i> . <i>ISME Journal</i> , 2019, 13, 603-617.	4.4	30
33	Proteomic Dissection of the Cellulolytic Machineries Used by Soil-Dwelling <i>Bacteroidetes</i> . <i>MSystems</i> , 2018, 3, .	1.7	29
34	Proteomic investigation of the secretome of <i>Cellvibrio japonicus</i> during growth on chitin. <i>Proteomics</i> , 2016, 16, 1904-1914.	1.3	28
35	Genomic, proteomic and biochemical analysis of the chitinolytic machinery of <i>Serratia marcescens</i> BJL200. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 414-421.	1.1	28
36	High-fiber rapeseed co-product diet for Norwegian Landrace pigs: Effect on digestibility. <i>Livestock Science</i> , 2017, 203, 1-9.	0.6	28

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37	Integration of absolute multi-omics reveals dynamic protein-to-RNA ratios and metabolic interplay within mixed-domain microbiomes. <i>Nature Communications</i> , 2020, 11, 4708.	5.8	28
38	The Farmed Atlantic Salmon (<i>Salmo salar</i>) Skin Mucus Proteome and Its Nutrient Potential for the Resident Bacterial Community. <i>Genes</i> , 2019, 10, 515.	1.0	26
39	Metaproteomics: Sample Preparation and Methodological Considerations. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1073, 187-215.	0.8	26
40	Spruce sugars and poultry hydrolysate as growth medium in repeated fed-batch fermentation processes for production of yeast biomass. <i>Bioprocess and Biosystems Engineering</i> , 2020, 43, 723-736.	1.7	26
41	Competition for electrons favours N_2O reduction in denitrifying <i>Bradyrhizobium</i> isolates. <i>Environmental Microbiology</i> , 2021, 23, 2244-2259.	1.8	24
42	Proteomic Investigation of the Response of <i>Enterococcus faecalis</i> V583 when Cultivated in Urine. <i>PLoS ONE</i> , 2015, 10, e0126694.	1.1	23
43	A novel proteomics sample preparation method for secretome analysis of <i>Hypocrea jecorina</i> growing on insoluble substrates. <i>Journal of Proteomics</i> , 2016, 131, 104-112.	1.2	23
44	Analyzing Activities of Lytic Polysaccharide Monooxygenases by Liquid Chromatography and Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2017, 1588, 71-92.	0.4	23
45	Hypoxia Strongly Affects Mitochondrial Ribosomal Proteins and Translocases, as Shown by Quantitative Proteomics of HeLa Cells. <i>International Journal of Proteomics</i> , 2015, 2015, 1-9.	2.0	22
46	Cell Death Proteomics Database: Consolidating Proteomics Data on Cell Death. <i>Journal of Proteome Research</i> , 2013, 12, 2206-2213.	1.8	21
47	Rumen metaproteomics: Closer to linking rumen microbial function to animal productivity traits. <i>Methods</i> , 2021, 186, 42-51.	1.9	21
48	A novel analytical method for d-glucosamine quantification and its application in the analysis of chitosan degradation by a minimal enzyme cocktail. <i>Carbohydrate Research</i> , 2016, 433, 18-24.	1.1	18
49	Gluten-specific antibodies of celiac disease gut plasma cells recognize long proteolytic fragments that typically harbor T-cell epitopes. <i>Scientific Reports</i> , 2016, 6, 25565.	1.6	18
50	Alginate Degradation: Insights Obtained through Characterization of a Thermophilic Exolytic Alginate Lyase. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	17
51	Consolidation of proteomics data in the Cancer Proteomics database. <i>Proteomics</i> , 2015, 15, 3765-3771.	1.3	16
52	Nitrous oxide respiring bacteria in biogas digestates for reduced agricultural emissions. <i>ISME Journal</i> , 2022, 16, 580-590.	4.4	16
53	Yeast as a novel protein source - Effect of species and autolysis on protein and amino acid digestibility in Atlantic salmon (<i>Salmo salar</i>). <i>Aquaculture</i> , 2022, 546, 737312.	1.7	16
54	Quantitative profiling of tyrosine phosphorylation revealed changes in the activity of the T cell receptor signaling pathway upon cisplatin-induced apoptosis. <i>Journal of Proteomics</i> , 2013, 91, 344-357.	1.2	14

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55	Impact of down-stream processing on functional properties of yeasts and the implications on gut health of Atlantic salmon (<i>Salmo salar</i>). <i>Scientific Reports</i> , 2021, 11, 4496.	1.6	14
56	Quantitative Proteome Analysis Using Isobaric Peptide Termini Labeling (IPTL). <i>Methods in Molecular Biology</i> , 2011, 753, 65-76.	0.4	12
57	Synthesis of glycoconjugates utilizing the regioselectivity of a lytic polysaccharide monooxygenase. <i>Scientific Reports</i> , 2020, 10, 13197.	1.6	12
58	Assessing high affinity binding to HLA-DQ2.5 by a novel peptide library based approach. <i>Bioorganic and Medicinal Chemistry</i> , 2011, 19, 2470-2477.	1.4	10
59	The impact of carbon-13 and deuterium on relative quantification of proteins using stable isotope diethyl labeling. <i>Rapid Communications in Mass Spectrometry</i> , 2015, 29, 830-836.	0.7	9
60	Isolation and Characterization of Extracellular Vesicles Secreted In Vitro by Porcine Microbiota. <i>Microorganisms</i> , 2020, 8, 983.	1.6	9
61	Experimental and computational analysis of the secretome of the hyperthermophilic archaeon <i>Pyrococcus furiosus</i> . <i>Extremophiles</i> , 2013, 17, 921-930.	0.9	8
62	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. <i>F1000Research</i> , 2021, 10, 103.	0.8	8
63	The Fish Pathogen <i>Aliivibrio salmonicida</i> LFI1238 Can Degrade and Metabolize Chitin despite Gene Disruption in the Chitinolytic Pathway. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0052921.	1.4	8
64	Comparison of data analysis parameters and MS/MS fragmentation techniques for quantitative proteome analysis using isobaric peptide termini labeling (IPTL). <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 1103-1114.	1.9	7
65	Endozoicomonadaceae symbiont in gills of <i>Acesta</i> clam encodes genes for essential nutrients and polysaccharide degradation. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	7
66	Chromatographic analysis of oxidized cello-oligomers generated by lytic polysaccharide monooxygenases using dual electrolytic eluent generation. <i>Journal of Chromatography A</i> , 2022, 1662, 462691.	1.8	7
67	Sjögren syndrome/scleroderma autoantigen 1 is a direct Tankyrase binding partner in cancer cells. <i>Communications Biology</i> , 2020, 3, 123.	2.0	5
68	Updates on metaQuantome Software for Quantitative Metaproteomics. <i>Journal of Proteome Research</i> , 2021, 20, 2130-2137.	1.8	5
69	POSTMan (POSTranslational modification analysis), a software application for PTM discovery. <i>Proteomics</i> , 2009, 9, 1400-1406.	1.3	4
70	Proteomic Detection of Carbohydrate-Active Enzymes (CAZymes) in Microbial Secretomes. <i>Methods in Molecular Biology</i> , 2019, 1871, 159-177.	0.4	3
71	Genomic and Proteomic Study of <i>Andreprevotia ripae</i> Isolated from an Anthill Reveals an Extensive Repertoire of Chitinolytic Enzymes. <i>Journal of Proteome Research</i> , 2021, 20, 4041-4052.	1.8	3
72	Effects of Yeast Species and Processing on Intestinal Health and Transcriptomic Profiles of Atlantic Salmon (<i>Salmo salar</i>) Fed Soybean Meal-Based Diets in Seawater. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1675.	1.8	3

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73	A Rapid Approach for Isobaric Peptide Termini Labeling. <i>Methods in Molecular Biology</i> , 2012, 893, 129-141.	0.4	2
74	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. <i>F1000Research</i> , 2021, 10, 103.	0.8	1