Johan A MalmstrÃ¶m

List of Publications by Year
in descending order

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123	6,815	101384 36	66788 78
papers	citations	h-index	g-index

139	139	139	10013
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Effective protein extraction combined with data independent acquisition analysis reveals a comprehensive and quantifiable insight into the proteomes of articular cartilage and subchondral bone. Osteoarthritis and Cartilage, 2022, 30, 137-146.	0.6	11
2	Long-Read Sequencing Reveals Genetic Adaptation of Bartonella Adhesin A Among Different Bartonella henselae Isolates. Frontiers in Microbiology, 2022, 13, 838267.	1.5	9
3	Distinct Serotypes of Streptococcal M Proteins Mediate Fibrinogen-Dependent Platelet Activation and Proinflammatory Effects. Infection and Immunity, 2022, 90, IAI0046221.	1.0	4
4	Landscape of surfaceome and endocytome in human glioma is divergent and depends on cellular spatial organization. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	8
5	Interaction of Bartonella henselae with Fibronectin Represents the Molecular Basis for Adhesion to Host Cells. Microbiology Spectrum, 2022, 10, e0059822.	1.2	4
6	Citrullination of extracellular histone H3.1 reduces antibacterial activity and exacerbates its proteolytic degradation. Journal of Cystic Fibrosis, 2021, 20, 346-355.	0.3	9
7	The structure of human dermatan sulfate epimerase 1 emphasizes the importance of C5-epimerization of glucuronic acid in higher organisms. Chemical Science, 2021, 12, 1869-1885.	3.7	3
8	Proteome Profiling of Recombinant DNase Therapy in Reducing NETs and Aiding Recovery in COVID-19 Patients. Molecular and Cellular Proteomics, 2021, 20, 100113.	2.5	51
9	A Systems View of the Heparan Sulfate Interactome. Journal of Histochemistry and Cytochemistry, 2021, 69, 105-119.	1.3	44
10	Structural determination of Streptococcus pyogenes M1 protein interactions with human immunoglobulin G using integrative structural biology. PLoS Computational Biology, 2021, 17, e1008169.	1.5	12
11	Multinodal Acoustic Trapping Enables High Capacity and High Throughput Enrichment of Extracellular Vesicles and Microparticles in miRNA and MS Proteomics Studies. Analytical Chemistry, 2021, 93, 3929-3937.	3.2	19
12	Cerebrospinal fluid proteome maps detect pathogen-specific host response patterns in meningitis. ELife, 2021, 10, .	2.8	13
13	Proteogenomic Workflow Reveals Molecular Phenotypes Related to Breast Cancer Mammographic Appearance. Journal of Proteome Research, 2021, 20, 2983-3001.	1.8	14
14	Protein Signatures of Remodeled Airways in Transplanted Lungs with Bronchiolitis Obliterans Syndrome Obtained Using Laser-Capture Microdissection. American Journal of Pathology, 2021, 191, 1398-1411.	1.9	3
15	Cheetah-MS: a web server to model protein complexes using tandem cross-linking mass spectrometry data. Bioinformatics, 2021, 37, 4871-4872.	1.8	0
16	Host-Pathogen Adhesion as the Basis of Innovative Diagnostics for Emerging Pathogens. Diagnostics, 2021, 11, 1259.	1.3	5
17	Quantitative proteomic analysis of human peripheral nerves from subjects with type 2 diabetes. Diabetic Medicine, 2021, 38, e14658.	1.2	8
18	Endothelial Heparan Sulfate Mediates Hepatic Neutrophil Trafficking and Injury during Staphylococcus aureus Sepsis. MBio, 2021, 12, e0118121.	1.8	8

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19	Streptococcus pyogenes Forms Serotype- and Local Environment-Dependent Interspecies Protein Complexes. MSystems, 2021, 6, e0027121.	1.7	13
20	Extending the Proteomic Characterization of Candida albicans Exposed to Stress and Apoptotic Inducers through Data-Independent Acquisition Mass Spectrometry. MSystems, 2021, 6, e0094621.	1.7	6
21	Targeted Selected Reaction Monitoring Verifies Histology Specific Peptide Signatures in Epithelial Ovarian Cancer. Cancers, 2021, 13, 5713.	1.7	1
22	Interaction with the host: the role of fibronectin and extracellular matrix proteins in the adhesion of Gram-negative bacteria. Medical Microbiology and Immunology, 2020, 209, 277-299.	2.6	73
23	Targeted mass spectrometry for Serum Amyloid A (SAA) isoform profiling in sequential blood samples from experimentally Staphylococcus aureus infected pigs. Journal of Proteomics, 2020, 227, 103904.	1.2	6
24	Structural proteomics, electron cryo-microscopy and structural modeling approaches in bacteriaâ€“human protein interactions. Medical Microbiology and Immunology, 2020, 209, 265-275.	2.6	13
25	In vivo Cross-Linking MS of the Complement System MAC Assembled on Live Gram-Positive Bacteria. Frontiers in Genetics, 2020, 11, 612475.	1.1	7
26	Matrisome Properties of Scaffolds Direct Fibroblasts in Idiopathic Pulmonary Fibrosis. International Journal of Molecular Sciences, 2019, 20, 4013.	1.8	35
27	A quantitative Streptococcus pyogenesâ€“human proteinâ€“protein interaction map reveals localization of opsonizing antibodies. Nature Communications, 2019, 10, 2727.	5.8	36
28	Identification of two abundant Aerococcus urinae cell wall-anchored proteins. International Journal of Medical Microbiology, 2019, 309, 151325.	1.5	3
29	Greedy de novo motif discovery to construct motif repositories for bacterial proteomes. BMC Bioinformatics, 2019, 20, 141.	1.2	4
30	<i>Streptococcus pyogenes</i> evades adaptive immunity through specific IgG glycan hydrolysis. Journal of Experimental Medicine, 2019, 216, 1615-1629.	4.2	24
31	Neutrophil extracellular traps in the central nervous system hinder bacterial clearance during pneumococcal meningitis. Nature Communications, 2019, 10, 1667.	5.8	77
32	Rapid determination of quaternary protein structures in complex biological samples. Nature Communications, 2019, 10, 192.	5.8	47
33	Complement Activation Occurs at the Surface of Platelets Activated by Streptococcal M1 Protein and This Results in Phagocytosis of Platelets. Journal of Immunology, 2019, 202, 503-513.	0.4	14
34	The Human Salivary Antimicrobial Peptide Profile according to the Oral Microbiota in Health, Periodontitis and Smoking. Journal of Innate Immunity, 2019, 11, 432-444.	1.8	27
35	Streptococcus pyogenes Infection and the Human Proteome with a Special Focus on the Immunoglobulin G-cleaving Enzyme IdeS. Molecular and Cellular Proteomics, 2018, 17, 1097-1111.	2.5	18
36	Quantifying extracellular matrix turnover in human lung scaffold cultures. Scientific Reports, 2018, 8, 5409.	1.6	44

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37	Quantitative proteomic characterization of the lung extracellular matrix in chronic obstructive pulmonary disease and idiopathic pulmonary fibrosis. Journal of Proteomics, 2018, 189, 23-33.	1.2	61
38	Development of Large-scale Cross-linking Mass Spectrometry. Molecular and Cellular Proteomics, 2018, 17, 1055-1066.	2.5	34
39	Leucocyte recruitment and molecular fortification of keratinocytes triggered by streptococcal M1 protein. Cellular Microbiology, 2018, 20, e12792.	1.1	2
40	Comprehensive Mass Spectrometric Survey of <i>Streptococcus pyogenes</i> Subcellular Proteomes. Journal of Proteome Research, 2018, 17, 600-617.	1.8	8
41	Targeted Proteomics and Absolute Protein Quantification for the Construction of a Stoichiometric Host-Pathogen Surface Density Model. Molecular and Cellular Proteomics, 2017, 16, S29-S41.	2.5	23
42	Analysis of Bacterial Surface Interactions with Mass Spectrometry-Based Proteomics. Methods in Molecular Biology, 2017, 1535, 17-24.	0.4	2
43	Improvements in Mass Spectrometry Assay Library Generation for Targeted Proteomics. Journal of Proteome Research, 2017, 16, 2384-2392.	1.8	20
44	Quantitative proteomic characterization of lung-MSC and bone marrow-MSC using DIA-mass spectrometry. Scientific Reports, 2017, 7, 9316.	1.6	33
45	The TLR2 Antagonist Staphylococcal Superantigen-Like Protein 3 Acts as a Virulence Factor to Promote Bacterial Pathogenicity in vivo. Journal of Innate Immunity, 2017, 9, 561-573.	1.8	22
46	Comprehensive Proteomic Characterization of Ontogenic Changes in Hematopoietic Stem and Progenitor Cells. Cell Reports, 2017, 21, 3285-3297.	2.9	25
47	Proteome turnover analysis in human lung scaffold cultures with stable isotope labelling. , 2017, , .		0
48	Structure and Interactions of a Dimeric Variant of sHIP, a Novel Virulence Determinant of Streptococcus pyogenes. Frontiers in Microbiology, 2016, 7, 95.	1.5	0
49	Cancer associated proteins in blood plasma: Determining normal variation. Proteomics, 2016, 16, 1928-1937.	1.3	9
50	Dinosaur: A Refined Open-Source Peptide MS Feature Detector. Journal of Proteome Research, 2016, 15, 2143-2151.	1.8	70
51	Quantitative Mass Spectrometry To Study Inflammatory Cartilage Degradation and Resulting Interactions with the Complement System. Journal of Immunology, 2016, 197, 3415-3424.	0.4	13
52	Differential compartmentalization of Streptococcus pyogenes virulence factors and host protein binding properties as a mechanism for host adaptation. International Journal of Medical Microbiology, 2016, 306, 504-516.	1.5	8
53	Saliva-Induced Clotting Captures Streptococci: Novel Roles for Coagulation and Fibrinolysis in Host Defense and Immune Evasion. Infection and Immunity, 2016, 84, 2813-2823.	1.0	12
54	Large-scale inference of protein tissue origin in gram-positive sepsis plasma using quantitative targeted proteomics. Nature Communications, 2016, 7, 10261.	5.8	88

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55	LATE-BREAKING ABSTRACT: Do mesenchymal stromal cells provide an organ-specific tissue niche? â€“ A proteomic matrisome characterization. , 2016, , .		0
56	Complete Removal of Extracellular IgG Antibodies in a Randomized Dose-Escalation Phase I Study with the Bacterial Enzyme IdeS â€“ A Novel Therapeutic Opportunity. PLoS ONE, 2015, 10, e0132011.	1.1	91
57	A Combined Shotgun and Targeted Mass Spectrometry Strategy for Breast Cancer Biomarker Discovery. Journal of Proteome Research, 2015, 14, 2807-2818.	1.8	33
58	Quantitative proteogenomics of human pathogens using DIA-MS. Journal of Proteomics, 2015, 129, 98-107.	1.2	28
59	Development of Phage-Based Antibody Fragment Reagents for Affinity Enrichment of Bacterial Immunoglobulin G Binding Proteins. Journal of Proteome Research, 2015, 14, 4704-4713.	1.8	5
60	Data Processing Has Major Impact on the Outcome of Quantitative Label-Free LC-MS Analysis. Journal of Proteome Research, 2015, 14, 676-687.	1.8	33
61	DIANAâ€”algorithmic improvements for analysis of data-independent acquisition MS data. Bioinformatics, 2015, 31, 555-562.	1.8	95
62	Targeted mass spectrometry analysis of neutrophil-derived proteins released during sepsis progression. Thrombosis and Haemostasis, 2014, 112, 1230-1243.	1.8	9
63	Surface proteins of group G Streptococcus in different phases of growth: patterns of production and implications for the hostâ€“bacteria relationship. Microbiology (United Kingdom), 2014, 160, 279-286.	0.7	2
64	A comprehensive analysis of the Streptococcus pyogenes and human plasma protein interaction network. Molecular BioSystems, 2014, 10, 1698-1708.	2.9	28
65	Numerical Compression Schemes for Proteomics Mass Spectrometry Data. Molecular and Cellular Proteomics, 2014, 13, 1537-1542.	2.5	53
66	OpenSWATH enables automated, targeted analysis of data-independent acquisition MS data. Nature Biotechnology, 2014, 32, 219-223.	9.4	692
67	Functional and Structural Properties of a Novel Protein and Virulence Factor (Protein sHIP) in Streptococcus pyogenes. Journal of Biological Chemistry, 2014, 289, 18175-18188.	1.6	6
68	Data processing methods and quality control strategies for label-free LCâ€“MS protein quantification. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 29-41.	1.1	50
69	Automated quality control system for LC-SRM setups. Journal of Proteomics, 2013, 95, 77-83.	1.2	5
70	Proteins of novel lactic acid bacteria from Apis mellifera mellifera: an insight into the production of known extra-cellular proteins during microbial stress. BMC Microbiology, 2013, 13, 235.	1.3	78
71	A Novel Role for Pro-Coagulant Microvesicles in the Early Host Defense against Streptococcus pyogenes. PLoS Pathogens, 2013, 9, e1003529.	2.1	40
72	Characterization of Released Polypeptides During an Interferon-Î³-Dependent Antibacterial Response in Airway Epithelial Cells. Journal of Interferon and Cytokine Research, 2012, 32, 524-533.	0.5	1

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73	Streptococcus pyogenes in Human Plasma. Journal of Biological Chemistry, 2012, 287, 1415-1425.	1.6	35
74	Antibody orientation at bacterial surfaces is related to invasive infection. Journal of Experimental Medicine, 2012, 209, 2367-2381.	4.2	104
75	Stimulation of blood mononuclear cells with bacterial virulence factors leads to the release of pro-coagulant and pro-inflammatory microparticles. Cellular Microbiology, 2012, 14, 107-119.	1.1	39
76	Deciphering the interactions of Streptococcus pyogenes and the complement system using a novel mouse infection model. Immunobiology, 2012, 217, 1163.	0.8	0
77	Protein Expression Changes in Ovarian Cancer during the Transition from Benign to Malignant. Journal of Proteome Research, 2012, 11, 2876-2889.	1.8	39
78	Glycoproteomic identification of galectin-3 and -8 ligands in bronchoalveolar lavage of mild asthmatics and healthy subjects. Biochimica Et Biophysica Acta - General Subjects, 2012, 1820, 1429-1436.	1.1	19
79	Different fractions of human serum glycoproteins bind galectin-1 or galectin-8, and their ratio may provide a refined biomarker for pathophysiological conditions in cancer and inflammatory disease. Biochimica Et Biophysica Acta - General Subjects, 2012, 1820, 1366-1372.	1.1	24
80	Splicosomal and serine and arginine-rich splicing factors as targets for TGF-Î². Fibrogenesis and Tissue Repair, 2012, 5, 6.	3.4	16
81	Proteome-wide selected reaction monitoring assays for the human pathogen Streptococcus pyogenes. Nature Communications, 2012, 3, 1301.	5.8	63
82	Automated Selected Reaction Monitoring Software for Accurate Label-Free Protein Quantification. Journal of Proteome Research, 2012, 11, 3766-3773.	1.8	27
83	Automated Workflow for Large-Scale Selected Reaction Monitoring Experiments. Journal of Proteome Research, 2012, 11, 1644-1653.	1.8	20
84	Galectin-8 in IgA Nephritis: Decreased Binding of IgA by Galectin-8 Affinity Chromatography and Associated Increased Binding in Non-IgA Serum Glycoproteins. Journal of Clinical Immunology, 2012, 32, 246-255.	2.0	5
85	Business intelligence strategies enables rapid analysis of quantitative proteomics data. Journal of Proteome Science and Computational Biology, 2012, 1, 5.	1.0	3
86	Absolute quantification of microbial proteomes at different states by directed mass spectrometry. Molecular Systems Biology, 2011, 7, 510.	3.2	91
87	A High-Confidence Human Plasma Proteome Reference Set with Estimated Concentrations in PeptideAtlas. Molecular and Cellular Proteomics, 2011, 10, M110.006353.	2.5	381
88	Quantitative proteomics of microbes: Principles and applications to virulence. Proteomics, 2011, 11, 2947-2956.	1.3	24
89	The quantitative proteome of a human cell line. Molecular Systems Biology, 2011, 7, 549.	3.2	691
90	Proteome-wide cellular protein concentrations of the human pathogen Leptospira interrogans. Nature, 2009, 460, 762-765.	13.7	402

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91	Visual proteomics of the human pathogen Leptospira interrogans. Nature Methods, 2009, 6, 817-823.	9.0	142
92	Perspectives of targeted mass spectrometry for protein biomarker verification. Current Opinion in Chemical Biology, 2009, 13, 518-525.	2.8	165
93	Comparative Functional Analysis of the Caenorhabditis elegans and Drosophila melanogaster Proteomes. PLoS Biology, 2009, 7, e1000048.	2.6	208
94	Rtt101 and Mms1 in budding yeast form a CUL4^{DDB1}â€like ubiquitin ligase that promotes replication through damaged DNA. EMBO Reports, 2008, 9, 1034-1040.	2.0	91
95	Targeted Quantitative Analysis of Streptococcus pyogenes Virulence Factors by Multiple Reaction Monitoring. Molecular and Cellular Proteomics, 2008, 7, 1489-1500.	2.5	189
96	Simian Virus 40 Depends on ER Protein Folding and Quality Control Factors for Entry into Host Cells. Cell, 2007, 131, 516-529.	13.5	285
97	Proteomic analysis identifies candidate proteins associated with distant recurrences in breast cancer after adjuvant chemotherapy. Journal of Pharmaceutical and Biomedical Analysis, 2007, 43, 1086-1093.	1.4	15
98	Twoâ€dimensional separation of human plasma proteins using iterative freeâ€flow electrophoresis. Proteomics, 2007, 7, 4218-4227.	1.3	37
99	A high-quality catalog of the Drosophila melanogaster proteome. Nature Biotechnology, 2007, 25, 576-583.	9.4	247
100	PhosphoPepâ€"a phosphoproteome resource for systems biology research in <i>Drosophila</i> Kc167 cells. Molecular Systems Biology, 2007, 3, 139.	3.2	168
101	Advances in proteomic workflows for systems biology. Current Opinion in Biotechnology, 2007, 18, 378-384.	3.3	95
102	Functional and phenotypical comparison of myofibroblasts derived from biopsies and bronchoalveolar lavage in mild asthma and scleroderma. Respiratory Research, 2006, 7, 11.	1.4	44
103	Optimized Peptide Separation and Identification for Mass Spectrometry Based Proteomics via Free-Flow Electrophoresis. Journal of Proteome Research, 2006, 5, 2241-2249.	1.8	88
104	2DDB - a bioinformatics solution for analysis of quantitative proteomics data. BMC Bioinformatics, 2006, 7, 158.	1.2	20
105	Biosynthesis of Dermatan Sulfate. Journal of Biological Chemistry, 2006, 281, 11560-11568.	1.6	120
106	Quantitative proteomic analysis of fibroblast nuclear proteins after stimulation with mitogen activated protein kinase inhibiting heparan sulfate. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2005, 815, 333-342.	1.2	4
107	Proteomics: A new research area for the biomedical field. Journal of Organ Dysfunction, 2005, 1, 83-94.	0.3	5
108	Chapter 14 Proteomics and remodeling of extracellular matrix in lung diseases. Comprehensive Analytical Chemistry, 2005, 46, 535-556.	0.7	0

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109	Presence of Activated Mobile Fibroblasts in Bronchoalveolar Lavage from Patients with Mild Asthma. American Journal of Respiratory and Critical Care Medicine, 2004, 170, 1049-1056.	2.5	50
110	Transforming Growth Factor-Î²1 Specifically Induce Proteins Involved in the Myofibroblast Contractile Apparatus. Molecular and Cellular Proteomics, 2004, 3, 466-477.	2.5	97
111	Antiproliferative heparan sulfate inhibiting hyaluronan and transforming growth factor-Î² expression in human lung fibroblast cells. Clinical Proteomics, 2004, 1, 271-284.	1.1	1
112	Exploring the Context of the Lung Proteome within the Airway Mucosa Following Allergen Challenge. Journal of Proteome Research, 2004, 3, 307-320.	1.8	25
113	Proteome Annotations and Identifications of the Human Pulmonary Fibroblast. Journal of Proteome Research, 2004, 3, 525-537.	1.8	31
114	Nanocapillary liquid chromatography interfaced to tandem matrix-assisted laser desorption/ionization and electrospray ionization-mass spectrometry: Mapping the nuclear proteome of human fibroblasts. Electrophoresis, 2003, 24, 3806-3814.	1.3	26
115	Targeting hepatocytes from liver tissue by laser capture microdissection and proteomics expression profiling. Electrophoresis, 2003, 24, 3800-3805.	1.3	26
116	Activation of platelet-derived growth factor pathway in human asthmatic pulmonary-derived mesenchymal cells. Electrophoresis, 2003, 24, 276-285.	1.3	34
117	Proteomic 2DE Database for Spot Selection, Automated Annotation, and Data Analysis. Journal of Proteome Research, 2002, 1, 135-138.	1.8	19
118	Proteoglycan and proteome profiling of central human pulmonary fibrotic tissue utilizing miniaturized sample preparation: A feasibility study. Proteomics, 2002, 2, 394.	1.3	41
119	On-chip microextraction for proteomic sample preparation of in-gel digests. Proteomics, 2002, 2, 413.	1.3	72
120	Biglycan isoforms with differences in polysaccharide substitution and core protein in human lung fibroblasts. FEBS Journal, 2002, 269, 3688-3696.	0.2	32
121	Proteomics â€" the protein expression technology to study connective tissue biology. Journal of Pharmaceutical and Biomedical Analysis, 2001, 24, 815-824.	1.4	35
122	A proteomic approach to mimic fibrosis disease evolvement by anin vitro cell line. Electrophoresis, 2001, 22, 1776-1784.	1.3	36
123	Heparan sulfate upregulates platelet-derived growth factor receptors on human lung fibroblasts. Glycobiology, 1998, 8, 1149-1155.	1.3	19