

# Johan A Malmström

## List of Publications by Year in descending order

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123  
papers

6,815  
citations

101384

36  
h-index

66788

78  
g-index

139  
all docs

139  
docs citations

139  
times ranked

10013  
citing authors

#	ARTICLE	IF	CITATIONS
1	OpenSWATH enables automated, targeted analysis of data-independent acquisition MS data. <i>Nature Biotechnology</i> , 2014, 32, 219-223.	9.4	692
2	The quantitative proteome of a human cell line. <i>Molecular Systems Biology</i> , 2011, 7, 549.	3.2	691
3	Proteome-wide cellular protein concentrations of the human pathogen <i>Leptospira interrogans</i> . <i>Nature</i> , 2009, 460, 762-765.	13.7	402
4	A High-Confidence Human Plasma Proteome Reference Set with Estimated Concentrations in PeptideAtlas. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.006353.	2.5	381
5	Simian Virus 40 Depends on ER Protein Folding and Quality Control Factors for Entry into Host Cells. <i>Cell</i> , 2007, 131, 516-529.	13.5	285
6	A high-quality catalog of the <i>Drosophila melanogaster</i> proteome. <i>Nature Biotechnology</i> , 2007, 25, 576-583.	9.4	247
7	Comparative Functional Analysis of the <i>Caenorhabditis elegans</i> and <i>Drosophila melanogaster</i> Proteomes. <i>PLoS Biology</i> , 2009, 7, e1000048.	2.6	208
8	Targeted Quantitative Analysis of <i>Streptococcus pyogenes</i> Virulence Factors by Multiple Reaction Monitoring. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1489-1500.	2.5	189
9	PhosphoPep <sup>®</sup> a phosphoproteome resource for systems biology research in <i>Drosophila</i> Kc167 cells. <i>Molecular Systems Biology</i> , 2007, 3, 139.	3.2	168
10	Perspectives of targeted mass spectrometry for protein biomarker verification. <i>Current Opinion in Chemical Biology</i> , 2009, 13, 518-525.	2.8	165
11	Visual proteomics of the human pathogen <i>Leptospira interrogans</i> . <i>Nature Methods</i> , 2009, 6, 817-823.	9.0	142
12	Biosynthesis of Dermatan Sulfate. <i>Journal of Biological Chemistry</i> , 2006, 281, 11560-11568.	1.6	120
13	Antibody orientation at bacterial surfaces is related to invasive infection. <i>Journal of Experimental Medicine</i> , 2012, 209, 2367-2381.	4.2	104
14	Transforming Growth Factor- $\beta$ 1 Specifically Induce Proteins Involved in the Myofibroblast Contractile Apparatus. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 466-477.	2.5	97
15	Advances in proteomic workflows for systems biology. <i>Current Opinion in Biotechnology</i> , 2007, 18, 378-384.	3.3	95
16	DIANA <sup>®</sup> algorithmic improvements for analysis of data-independent acquisition MS data. <i>Bioinformatics</i> , 2015, 31, 555-562.	1.8	95
17	Rtt101 and Mms1 in budding yeast form a CUL4 <sup>DDB1</sup> -like ubiquitin ligase that promotes replication through damaged DNA. <i>EMBO Reports</i> , 2008, 9, 1034-1040.	2.0	91
18	Absolute quantification of microbial proteomes at different states by directed mass spectrometry. <i>Molecular Systems Biology</i> , 2011, 7, 510.	3.2	91

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19	Complete Removal of Extracellular IgG Antibodies in a Randomized Dose-Escalation Phase I Study with the Bacterial Enzyme IdeS – A Novel Therapeutic Opportunity. <i>PLoS ONE</i> , 2015, 10, e0132011.	1.1	91
20	Optimized Peptide Separation and Identification for Mass Spectrometry Based Proteomics via Free-Flow Electrophoresis. <i>Journal of Proteome Research</i> , 2006, 5, 2241-2249.	1.8	88
21	Large-scale inference of protein tissue origin in gram-positive sepsis plasma using quantitative targeted proteomics. <i>Nature Communications</i> , 2016, 7, 10261.	5.8	88
22	Proteins of novel lactic acid bacteria from <i>Apis mellifera mellifera</i> : an insight into the production of known extra-cellular proteins during microbial stress. <i>BMC Microbiology</i> , 2013, 13, 235.	1.3	78
23	Neutrophil extracellular traps in the central nervous system hinder bacterial clearance during pneumococcal meningitis. <i>Nature Communications</i> , 2019, 10, 1667.	5.8	77
24	Interaction with the host: the role of fibronectin and extracellular matrix proteins in the adhesion of Gram-negative bacteria. <i>Medical Microbiology and Immunology</i> , 2020, 209, 277-299.	2.6	73
25	On-chip microextraction for proteomic sample preparation of in-gel digests. <i>Proteomics</i> , 2002, 2, 413.	1.3	72
26	Dinosaur: A Refined Open-Source Peptide MS Feature Detector. <i>Journal of Proteome Research</i> , 2016, 15, 2143-2151.	1.8	70
27	Proteome-wide selected reaction monitoring assays for the human pathogen <i>Streptococcus pyogenes</i> . <i>Nature Communications</i> , 2012, 3, 1301.	5.8	63
28	Quantitative proteomic characterization of the lung extracellular matrix in chronic obstructive pulmonary disease and idiopathic pulmonary fibrosis. <i>Journal of Proteomics</i> , 2018, 189, 23-33.	1.2	61
29	Numerical Compression Schemes for Proteomics Mass Spectrometry Data. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1537-1542.	2.5	53
30	Proteome Profiling of Recombinant DNase Therapy in Reducing NETs and Aiding Recovery in COVID-19 Patients. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100113.	2.5	51
31	Presence of Activated Mobile Fibroblasts in Bronchoalveolar Lavage from Patients with Mild Asthma. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2004, 170, 1049-1056.	2.5	50
32	Data processing methods and quality control strategies for label-free LC-MS protein quantification. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 29-41.	1.1	50
33	Rapid determination of quaternary protein structures in complex biological samples. <i>Nature Communications</i> , 2019, 10, 192.	5.8	47
34	Functional and phenotypical comparison of myofibroblasts derived from biopsies and bronchoalveolar lavage in mild asthma and scleroderma. <i>Respiratory Research</i> , 2006, 7, 11.	1.4	44
35	Quantifying extracellular matrix turnover in human lung scaffold cultures. <i>Scientific Reports</i> , 2018, 8, 5409.	1.6	44
36	A Systems View of the Heparan Sulfate Interactome. <i>Journal of Histochemistry and Cytochemistry</i> , 2021, 69, 105-119.	1.3	44

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37	Proteoglycan and proteome profiling of central human pulmonary fibrotic tissue utilizing miniaturized sample preparation: A feasibility study. <i>Proteomics</i> , 2002, 2, 394.	1.3	41
38	A Novel Role for Pro-Coagulant Microvesicles in the Early Host Defense against <i>Streptococcus pyogenes</i> . <i>PLoS Pathogens</i> , 2013, 9, e1003529.	2.1	40
39	Stimulation of blood mononuclear cells with bacterial virulence factors leads to the release of pro-coagulant and pro-inflammatory microparticles. <i>Cellular Microbiology</i> , 2012, 14, 107-119.	1.1	39
40	Protein Expression Changes in Ovarian Cancer during the Transition from Benign to Malignant. <i>Journal of Proteome Research</i> , 2012, 11, 2876-2889.	1.8	39
41	Two-dimensional separation of human plasma proteins using iterative free-flow electrophoresis. <i>Proteomics</i> , 2007, 7, 4218-4227.	1.3	37
42	A proteomic approach to mimic fibrosis disease evolution by an in vitro cell line. <i>Electrophoresis</i> , 2001, 22, 1776-1784.	1.3	36
43	A quantitative <i>Streptococcus pyogenes</i> -human protein-protein interaction map reveals localization of opsonizing antibodies. <i>Nature Communications</i> , 2019, 10, 2727.	5.8	36
44	Proteomics – the protein expression technology to study connective tissue biology. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2001, 24, 815-824.	1.4	35
45	<i>Streptococcus pyogenes</i> in Human Plasma. <i>Journal of Biological Chemistry</i> , 2012, 287, 1415-1425.	1.6	35
46	Matrisome Properties of Scaffolds Direct Fibroblasts in Idiopathic Pulmonary Fibrosis. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4013.	1.8	35
47	Activation of platelet-derived growth factor pathway in human asthmatic pulmonary-derived mesenchymal cells. <i>Electrophoresis</i> , 2003, 24, 276-285.	1.3	34
48	Development of Large-scale Cross-linking Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1055-1066.	2.5	34
49	A Combined Shotgun and Targeted Mass Spectrometry Strategy for Breast Cancer Biomarker Discovery. <i>Journal of Proteome Research</i> , 2015, 14, 2807-2818.	1.8	33
50	Data Processing Has Major Impact on the Outcome of Quantitative Label-Free LC-MS Analysis. <i>Journal of Proteome Research</i> , 2015, 14, 676-687.	1.8	33
51	Quantitative proteomic characterization of lung-MSC and bone marrow-MSC using DIA-mass spectrometry. <i>Scientific Reports</i> , 2017, 7, 9316.	1.6	33
52	Biglycan isoforms with differences in polysaccharide substitution and core protein in human lung fibroblasts. <i>FEBS Journal</i> , 2002, 269, 3688-3696.	0.2	32
53	Proteome Annotations and Identifications of the Human Pulmonary Fibroblast. <i>Journal of Proteome Research</i> , 2004, 3, 525-537.	1.8	31
54	A comprehensive analysis of the <i>Streptococcus pyogenes</i> and human plasma protein interaction network. <i>Molecular BioSystems</i> , 2014, 10, 1698-1708.	2.9	28

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55	Quantitative proteogenomics of human pathogens using DIA-MS. <i>Journal of Proteomics</i> , 2015, 129, 98-107.	1.2	28
56	Automated Selected Reaction Monitoring Software for Accurate Label-Free Protein Quantification. <i>Journal of Proteome Research</i> , 2012, 11, 3766-3773.	1.8	27
57	The Human Salivary Antimicrobial Peptide Profile according to the Oral Microbiota in Health, Periodontitis and Smoking. <i>Journal of Innate Immunity</i> , 2019, 11, 432-444.	1.8	27
58	Nanocapillary liquid chromatography interfaced to tandem matrix-assisted laser desorption/ionization and electrospray ionization-mass spectrometry: Mapping the nuclear proteome of human fibroblasts. <i>Electrophoresis</i> , 2003, 24, 3806-3814.	1.3	26
59	Targeting hepatocytes from liver tissue by laser capture microdissection and proteomics expression profiling. <i>Electrophoresis</i> , 2003, 24, 3800-3805.	1.3	26
60	Exploring the Context of the Lung Proteome within the Airway Mucosa Following Allergen Challenge. <i>Journal of Proteome Research</i> , 2004, 3, 307-320.	1.8	25
61	Comprehensive Proteomic Characterization of Ontogenic Changes in Hematopoietic Stem and Progenitor Cells. <i>Cell Reports</i> , 2017, 21, 3285-3297.	2.9	25
62	Quantitative proteomics of microbes: Principles and applications to virulence. <i>Proteomics</i> , 2011, 11, 2947-2956.	1.3	24
63	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. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2012, 1820, 1366-1372.	1.1	24
64	<i>Streptococcus pyogenes</i> evades adaptive immunity through specific IgG glycan hydrolysis. <i>Journal of Experimental Medicine</i> , 2019, 216, 1615-1629.	4.2	24
65	Targeted Proteomics and Absolute Protein Quantification for the Construction of a Stoichiometric Host-Pathogen Surface Density Model. <i>Molecular and Cellular Proteomics</i> , 2017, 16, S29-S41.	2.5	23
66	The TLR2 Antagonist Staphylococcal Superantigen-Like Protein 3 Acts as a Virulence Factor to Promote Bacterial Pathogenicity in vivo. <i>Journal of Innate Immunity</i> , 2017, 9, 561-573.	1.8	22
67	2DDB - a bioinformatics solution for analysis of quantitative proteomics data. <i>BMC Bioinformatics</i> , 2006, 7, 158.	1.2	20
68	Automated Workflow for Large-Scale Selected Reaction Monitoring Experiments. <i>Journal of Proteome Research</i> , 2012, 11, 1644-1653.	1.8	20
69	Improvements in Mass Spectrometry Assay Library Generation for Targeted Proteomics. <i>Journal of Proteome Research</i> , 2017, 16, 2384-2392.	1.8	20
70	Heparan sulfate upregulates platelet-derived growth factor receptors on human lung fibroblasts. <i>Glycobiology</i> , 1998, 8, 1149-1155.	1.3	19
71	Proteomic 2DE Database for Spot Selection, Automated Annotation, and Data Analysis. <i>Journal of Proteome Research</i> , 2002, 1, 135-138.	1.8	19
72	Glycoproteomic identification of galectin-3 and -8 ligands in bronchoalveolar lavage of mild asthmatics and healthy subjects. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2012, 1820, 1429-1436.	1.1	19

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73	Multinodal Acoustic Trapping Enables High Capacity and High Throughput Enrichment of Extracellular Vesicles and Microparticles in miRNA and MS Proteomics Studies. <i>Analytical Chemistry</i> , 2021, 93, 3929-3937.	3.2	19
74	<i>Streptococcus pyogenes</i> Infection and the Human Proteome with a Special Focus on the Immunoglobulin G-cleaving Enzyme IdeS. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1097-1111.	2.5	18
75	Splicosomal and serine and arginine-rich splicing factors as targets for TGF- $\beta$ 2. <i>Fibrogenesis and Tissue Repair</i> , 2012, 5, 6.	3.4	16
76	Proteomic analysis identifies candidate proteins associated with distant recurrences in breast cancer after adjuvant chemotherapy. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2007, 43, 1086-1093.	1.4	15
77	Complement Activation Occurs at the Surface of Platelets Activated by Streptococcal M1 Protein and This Results in Phagocytosis of Platelets. <i>Journal of Immunology</i> , 2019, 202, 503-513.	0.4	14
78	Proteogenomic Workflow Reveals Molecular Phenotypes Related to Breast Cancer Mammographic Appearance. <i>Journal of Proteome Research</i> , 2021, 20, 2983-3001.	1.8	14
79	Quantitative Mass Spectrometry To Study Inflammatory Cartilage Degradation and Resulting Interactions with the Complement System. <i>Journal of Immunology</i> , 2016, 197, 3415-3424.	0.4	13
80	Structural proteomics, electron cryo-microscopy and structural modeling approaches in bacteria-human protein interactions. <i>Medical Microbiology and Immunology</i> , 2020, 209, 265-275.	2.6	13
81	Cerebrospinal fluid proteome maps detect pathogen-specific host response patterns in meningitis. <i>ELife</i> , 2021, 10, .	2.8	13
82	<i>Streptococcus pyogenes</i> Forms Serotype- and Local Environment-Dependent Interspecies Protein Complexes. <i>MSystems</i> , 2021, 6, e0027121.	1.7	13
83	Saliva-Induced Clotting Captures Streptococci: Novel Roles for Coagulation and Fibrinolysis in Host Defense and Immune Evasion. <i>Infection and Immunity</i> , 2016, 84, 2813-2823.	1.0	12
84	Structural determination of <i>Streptococcus pyogenes</i> M1 protein interactions with human immunoglobulin G using integrative structural biology. <i>PLoS Computational Biology</i> , 2021, 17, e1008169.	1.5	12
85	Effective protein extraction combined with data independent acquisition analysis reveals a comprehensive and quantifiable insight into the proteomes of articular cartilage and subchondral bone. <i>Osteoarthritis and Cartilage</i> , 2022, 30, 137-146.	0.6	11
86	Targeted mass spectrometry analysis of neutrophil-derived proteins released during sepsis progression. <i>Thrombosis and Haemostasis</i> , 2014, 112, 1230-1243.	1.8	9
87	Cancer associated proteins in blood plasma: Determining normal variation. <i>Proteomics</i> , 2016, 16, 1928-1937.	1.3	9
88	Citrullination of extracellular histone H3.1 reduces antibacterial activity and exacerbates its proteolytic degradation. <i>Journal of Cystic Fibrosis</i> , 2021, 20, 346-355.	0.3	9
89	Long-Read Sequencing Reveals Genetic Adaptation of <i>Bartonella Adhesin A</i> Among Different <i>Bartonella henselae</i> Isolates. <i>Frontiers in Microbiology</i> , 2022, 13, 838267.	1.5	9
90	Differential compartmentalization of <i>Streptococcus pyogenes</i> virulence factors and host protein binding properties as a mechanism for host adaptation. <i>International Journal of Medical Microbiology</i> , 2016, 306, 504-516.	1.5	8

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91	Comprehensive Mass Spectrometric Survey of <i>Streptococcus pyogenes</i> Subcellular Proteomes. <i>Journal of Proteome Research</i> , 2018, 17, 600-617.	1.8	8
92	Quantitative proteomic analysis of human peripheral nerves from subjects with type 2 diabetes. <i>Diabetic Medicine</i> , 2021, 38, e14658.	1.2	8
93	Endothelial Heparan Sulfate Mediates Hepatic Neutrophil Trafficking and Injury during <i>Staphylococcus aureus</i> Sepsis. <i>MBio</i> , 2021, 12, e0118121.	1.8	8
94	Landscape of surfaceome and endocytome in human glioma is divergent and depends on cellular spatial organization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	8
95	In vivo Cross-Linking MS of the Complement System MAC Assembled on Live Gram-Positive Bacteria. <i>Frontiers in Genetics</i> , 2020, 11, 612475.	1.1	7
96	Functional and Structural Properties of a Novel Protein and Virulence Factor (Protein sHIP) in <i>Streptococcus pyogenes</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 18175-18188.	1.6	6
97	Targeted mass spectrometry for Serum Amyloid A (SAA) isoform profiling in sequential blood samples from experimentally <i>Staphylococcus aureus</i> infected pigs. <i>Journal of Proteomics</i> , 2020, 227, 103904.	1.2	6
98	Extending the Proteomic Characterization of <i>Candida albicans</i> Exposed to Stress and Apoptotic Inducers through Data-Independent Acquisition Mass Spectrometry. <i>MSystems</i> , 2021, 6, e0094621.	1.7	6
99	Proteomics: A new research area for the biomedical field. <i>Journal of Organ Dysfunction</i> , 2005, 1, 83-94.	0.3	5
100	Galectin-8 in IgA Nephritis: Decreased Binding of IgA by Galectin-8 Affinity Chromatography and Associated Increased Binding in Non-IgA Serum Glycoproteins. <i>Journal of Clinical Immunology</i> , 2012, 32, 246-255.	2.0	5
101	Automated quality control system for LC-SRM setups. <i>Journal of Proteomics</i> , 2013, 95, 77-83.	1.2	5
102	Development of Phage-Based Antibody Fragment Reagents for Affinity Enrichment of Bacterial Immunoglobulin G Binding Proteins. <i>Journal of Proteome Research</i> , 2015, 14, 4704-4713.	1.8	5
103	Host-Pathogen Adhesion as the Basis of Innovative Diagnostics for Emerging Pathogens. <i>Diagnostics</i> , 2021, 11, 1259.	1.3	5
104	Quantitative proteomic analysis of fibroblast nuclear proteins after stimulation with mitogen activated protein kinase inhibiting heparan sulfate. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2005, 815, 333-342.	1.2	4
105	Greedy de novo motif discovery to construct motif repositories for bacterial proteomes. <i>BMC Bioinformatics</i> , 2019, 20, 141.	1.2	4
106	Distinct Serotypes of Streptococcal M Proteins Mediate Fibrinogen-Dependent Platelet Activation and Proinflammatory Effects. <i>Infection and Immunity</i> , 2022, 90, IA10046221.	1.0	4
107	Interaction of <i>Bartonella henselae</i> with Fibronectin Represents the Molecular Basis for Adhesion to Host Cells. <i>Microbiology Spectrum</i> , 2022, 10, e0059822.	1.2	4
108	Identification of two abundant <i>Aerococcus urinae</i> cell wall-anchored proteins. <i>International Journal of Medical Microbiology</i> , 2019, 309, 151325.	1.5	3

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109	The structure of human dermatan sulfate epimerase 1 emphasizes the importance of C5-epimerization of glucuronic acid in higher organisms. <i>Chemical Science</i> , 2021, 12, 1869-1885.	3.7	3
110	Protein Signatures of Remodeled Airways in Transplanted Lungs with Bronchiolitis Obliterans Syndrome Obtained Using Laser-Capture Microdissection. <i>American Journal of Pathology</i> , 2021, 191, 1398-1411.	1.9	3
111	Business intelligence strategies enables rapid analysis of quantitative proteomics data. <i>Journal of Proteome Science and Computational Biology</i> , 2012, 1, 5.	1.0	3
112	Surface proteins of group G <i>Streptococcus</i> in different phases of growth: patterns of production and implications for the host-bacteria relationship. <i>Microbiology (United Kingdom)</i> , 2014, 160, 279-286.	0.7	2
113	Analysis of Bacterial Surface Interactions with Mass Spectrometry-Based Proteomics. <i>Methods in Molecular Biology</i> , 2017, 1535, 17-24.	0.4	2
114	Leucocyte recruitment and molecular fortification of keratinocytes triggered by streptococcal M1 protein. <i>Cellular Microbiology</i> , 2018, 20, e12792.	1.1	2
115	Antiproliferative heparan sulfate inhibiting hyaluronan and transforming growth factor- $\beta^2$ expression in human lung fibroblast cells. <i>Clinical Proteomics</i> , 2004, 1, 271-284.	1.1	1
116	Characterization of Released Polypeptides During an Interferon- $\beta^3$ -Dependent Antibacterial Response in Airway Epithelial Cells. <i>Journal of Interferon and Cytokine Research</i> , 2012, 32, 524-533.	0.5	1
117	Targeted Selected Reaction Monitoring Verifies Histology Specific Peptide Signatures in Epithelial Ovarian Cancer. <i>Cancers</i> , 2021, 13, 5713.	1.7	1
118	Chapter 14 Proteomics and remodeling of extracellular matrix in lung diseases. <i>Comprehensive Analytical Chemistry</i> , 2005, 46, 535-556.	0.7	0
119	Deciphering the interactions of <i>Streptococcus pyogenes</i> and the complement system using a novel mouse infection model. <i>Immunobiology</i> , 2012, 217, 1163.	0.8	0
120	Structure and Interactions of a Dimeric Variant of sHIP, a Novel Virulence Determinant of <i>Streptococcus pyogenes</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 95.	1.5	0
121	Cheetah-MS: a web server to model protein complexes using tandem cross-linking mass spectrometry data. <i>Bioinformatics</i> , 2021, 37, 4871-4872.	1.8	0
122	LATE-BREAKING ABSTRACT: Do mesenchymal stromal cells provide an organ-specific tissue niche? A proteomic matrisome characterization. , 2016, , .		0
123	Proteome turnover analysis in human lung scaffold cultures with stable isotope labelling. , 2017, , .		0