Lars MalmstrÃ¶m

List of Publications by Year
in descending order

82 papers	**6,650** citations	94433 **37** h-index	71685 **76** g-index
91 all docs	**91** docs citations	**91** times ranked	**9761** citing authors

#	Article	IF	Citations
1	OpenSWATH enables automated, targeted analysis of data-independent acquisition MS data. Nature Biotechnology, 2014, 32, 219-223.	17.5	692
2	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. Nature Methods, 2016, 13, 741-748.	19.0	537
3	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	19.0	513
4	An objective comparison of cell-tracking algorithms. Nature Methods, 2017, 14, 1141-1152.	19.0	399
5	Structural Probing of a Protein Phosphatase 2A Network by Chemical Cross-Linking and Mass Spectrometry. Science, 2012, 337, 1348-1352.	12.6	357
6	Automated prediction of CASP-5 structures using the Robetta server. Proteins: Structure, Function and Bioinformatics, 2003, 53, 524-533.	2.6	261
7	Assigning Function to Yeast Proteins by Integration of Technologies. Molecular Cell, 2003, 12, 1353-1365.	9.7	248
8	De Novo Prediction of Three-dimensional Structures for Major Protein Families. Journal of Molecular Biology, 2002, 322, 65-78.	4.2	237
9	Structure prediction for CASP7 targets using extensive all-atom refinement with Rosetta@home. Proteins: Structure, Function and Bioinformatics, 2007, 69, 118-128.	2.6	178
10	TRIC: an automated alignment strategy for reproducible protein quantification in targeted proteomics. Nature Methods, 2016, 13, 777-783.	19.0	173
11	An Automated Pipeline for High-Throughput Label-Free Quantitative Proteomics. Journal of Proteome Research, 2013, 12, 1628-1644.	3.7	146
12	Cross-Link Guided Molecular Modeling with ROSETTA. PLoS ONE, 2013, 8, e73411.	2.5	144
13	Free modeling with Rosetta in CASP6. Proteins: Structure, Function and Bioinformatics, 2005, 61, 128-134.	2.6	131
14	Xwalk: computing and visualizing distances in cross-linking experiments. Bioinformatics, 2011, 27, 2163-2164.	4.1	130
15	Prediction of CASP6 structures using automated robetta protocols. Proteins: Structure, Function and Bioinformatics, 2005, 61, 157-166.	2.6	124
16	Inference and quantification of peptidoforms in large sample cohorts by SWATH-MS. Nature Biotechnology, 2017, 35, 781-788.	17.5	122
17	openBIS: a flexible framework for managing and analyzing complex data in biology research. BMC Bioinformatics, 2011, 12, 468.	2.6	114
18	pyOpenMS: A Python€based interface to the OpenMS mass€spectrometry algorithm library. Proteomics, 2014, 14, 74-77.	2.2	109

#	Article	IF	Citations
19	FAIRDOMHub: a repository and collaboration environment for sharing systems biology research. Nucleic Acids Research, 2017, 45, D404-D407.	14.5	98
20	DIANAâ€"algorithmic improvements for analysis of data-independent acquisition MS data. Bioinformatics, 2015, 31, 555-562.	4.1	95
21	A Computational Tool to Detect and Avoid Redundancy in Selected Reaction Monitoring. Molecular and Cellular Proteomics, 2012, 11, 540-549.	3.8	90
22	Large-scale inference of protein tissue origin in gram-positive sepsis plasma using quantitative targeted proteomics. Nature Communications, 2016, 7, 10261.	12.8	88
23	Automated prediction of domain boundaries in CASP6 targets using Ginzu and RosettaDOM. Proteins: Structure, Function and Bioinformatics, 2005, 61, 193-200.	2.6	85
24	xTract: software for characterizing conformational changes of protein complexes by quantitative cross-linking mass spectrometry. Nature Methods, 2015, 12, 1185-1190.	19.0	83
25	Identification of a Set of Conserved Eukaryotic Internal Retention Time Standards for Data-independent Acquisition Mass Spectrometry. Molecular and Cellular Proteomics, 2015, 14, 2800-2813.	3.8	76
26	Comprehensive ADPâ€‘ribosylome analysis identifies tyrosine as an ADPâ€‘ribose acceptor site. EMBO Reports, 2018, 19, .	4.5	75
27	The SIB Swiss Institute of Bioinformaticsâ€™ resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37.	14.5	64
28	Proteome-wide selected reaction monitoring assays for the human pathogen Streptococcus pyogenes. Nature Communications, 2012, 3, 1301.	12.8	63
29	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
30	Quantitative proteomic characterization of the lung extracellular matrix in chronic obstructive pulmonary disease and idiopathic pulmonary fibrosis. Journal of Proteomics, 2018, 189, 23-33.	2.4	61
31	The importance of fibroblasts in remodelling of the human uterine cervix during pregnancy and parturition. Molecular Human Reproduction, 2007, 13, 333-341.	2.8	60
32	iPortal: the swiss grid proteomics portal: Requirements and new features based on experience and usability considerations. Concurrency Computation Practice and Experience, 2015, 27, 433-445.	2.2	54
33	Numerical Compression Schemes for Proteomics Mass Spectrometry Data. Molecular and Cellular Proteomics, 2014, 13, 1537-1542.	3.8	53
34	Superfamily Assignments for the Yeast Proteome through Integration of Structure Prediction with the Gene Ontology. PLoS Biology, 2007, 5, e76.	5.6	48
35	Deciphering diatom biochemical pathways via whole-cell proteomics. Aquatic Microbial Ecology, 2009, 55, 241-253.	1.8	48
36	Rapid determination of quaternary protein structures in complex biological samples. Nature Communications, 2019, 10, 192.	12.8	47

#	Article	IF	Citations
37	Reproducible quantitative proteotype data matrices for systems biology. Molecular Biology of the Cell, 2015, 26, 3926-3931.	2.1	46
38	A divergent <i><scp>P</scp>seudomonas aeruginosa</i> palmitoyltransferase essential for cystic fibrosisâ€‘specific lipid <scp>A</scp>. Molecular Microbiology, 2014, 91, 158-174.	2.5	42
39	The Proteome Folding Project: Proteome-scale prediction of structure and function. Genome Research, 2011, 21, 1981-1994.	5.5	40
40	A quantitative Streptococcus pyogenesâ€“human proteinâ€“protein interaction map reveals localization of opsonizing antibodies. Nature Communications, 2019, 10, 2727.	12.8	36
41	Streptococcus pyogenes in Human Plasma. Journal of Biological Chemistry, 2012, 287, 1415-1425.	3.4	35
42	Spike-Dependent Opsonization Indicates Both Dose-Dependent Inhibition of Phagocytosis and That Non-Neutralizing Antibodies Can Confer Protection to SARS-CoV-2. Frontiers in Immunology, 2021, 12, 808932.	4.8	34
43	A Combined Shotgun and Targeted Mass Spectrometry Strategy for Breast Cancer Biomarker Discovery. Journal of Proteome Research, 2015, 14, 2807-2818.	3.7	33
44	Proteome Annotations and Identifications of the Human Pulmonary Fibroblast. Journal of Proteome Research, 2004, 3, 525-537.	3.7	31
45	Quantitative proteogenomics of human pathogens using DIA-MS. Journal of Proteomics, 2015, 129, 98-107.	2.4	28
46	Identification of the Active Site of DS-epimerase 1 and Requirement of N-Glycosylation for Enzyme Function. Journal of Biological Chemistry, 2009, 284, 1741-1747.	3.4	27
47	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.	2.4	26
48	The Yeast Resource Center Public Data Repository. Nucleic Acids Research, 2004, 33, D378-D382.	14.5	25
49	Identification of secreted glycoproteins of human prostate and bladder stromal cells by comparative quantitative proteomics. Prostate, 2009, 69, 49-61.	2.3	24
50	Quantitative proteomics of microbes: Principles and applications to virulence. Proteomics, 2011, 11, 2947-2956.	2.2	24
51	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.	3.8	23
52	The path to preservation: Using proteomics to decipher the fate of diatom proteins during microbial degradation. Limnology and Oceanography, 2010, 55, 1790-1804.	3.1	22
53	2DDB - a bioinformatics solution for analysis of quantitative proteomics data. BMC Bioinformatics, 2006, 7, 158.	2.6	20
54	Bioinformatic Challenges in Targeted Proteomics. Journal of Proteome Research, 2012, 11, 4393-4402.	3.7	20

#	ARTICLE	IF	CITATIONS
55	Automated Workflow for Large-Scale Selected Reaction Monitoring Experiments. Journal of Proteome Research, 2012, 11, 1644-1653.	3.7	20
56	Proteomic 2DE Database for Spot Selection, Automated Annotation, and Data Analysis. Journal of Proteome Research, 2002, 1, 135-138.	3.7	19
57	Fast and Efficient XML Data Access for Next-Generation Mass Spectrometry. PLoS ONE, 2015, 10, e0125108.	2.5	17
58	Splicosomal and serine and arginine-rich splicing factors as targets for TGF-Î². Fibrogenesis and Tissue Repair, 2012, 5, 6.	3.4	16
59	Deciphering the mode of action of the processive polysaccharide modifying enzyme dermatan sulfate epimerase 1 by hydrogenâ€"deuterium exchange mass spectrometry. Chemical Science, 2016, 7, 1447-1456.	7.4	16
60	Efficient visualization of high-throughput targeted proteomics experiments: TAPIR. Bioinformatics, 2015, 31, 2415-2417.	4.1	14
61	Extracellular Vesicle-Contained microRNA of C. elegans as a Tool to Decipher the Molecular Basis of Nematode Parasitism. Frontiers in Cellular and Infection Microbiology, 2020, 10, 217.	3.9	14
62	Proteogenomic Workflow Reveals Molecular Phenotypes Related to Breast Cancer Mammographic Appearance. Journal of Proteome Research, 2021, 20, 2983-3001.	3.7	14
63	Structural proteomics, electron cryo-microscopy and structural modeling approaches in bacteriaâ€"human protein interactions. Medical Microbiology and Immunology, 2020, 209, 265-275.	4.8	13
64	Cerebrospinal fluid proteome maps detect pathogen-specific host response patterns in meningitis. ELife, 2021, 10, .	6.0	13
65	Streptococcus pyogenes Forms Serotype- and Local Environment-Dependent Interspecies Protein Complexes. MSystems, 2021, 6, e0027121.	3.8	13
66	Structural determination of Streptococcus pyogenes M1 protein interactions with human immunoglobulin G using integrative structural biology. PLoS Computational Biology, 2021, 17, e1008169.	3.2	12
67	Using synthetic peptides to benchmark peptide identification software and search parameters for MS/MS data analysis. EuPA Open Proteomics, 2014, 5, 21-31.	2.5	8
68	In vivo Cross-Linking MS of the Complement System MAC Assembled on Live Gram-Positive Bacteria. Frontiers in Genetics, 2020, 11, 612475.	2.3	7
69	Functional and Structural Properties of a Novel Protein and Virulence Factor (Protein sHIP) in Streptococcus pyogenes. Journal of Biological Chemistry, 2014, 289, 18175-18188.	3.4	6
70	Protein Structure Modeling. Methods in Molecular Biology, 2010, 673, 63-72.	0.9	6
71	Proteomics: A new research area for the biomedical field. Journal of Organ Dysfunction, 2005, 1, 83-94.	0.3	5
72	On the use of hydrogen/deuterium exchange mass spectrometry data to improve *de novo* protein structure prediction. Rapid Communications in Mass Spectrometry, 2009, 23, 459-461.	1.5	4

#	Article	IF	Citations
73	Greedy de novo motif discovery to construct motif repositories for bacterial proteomes. BMC Bioinformatics, 2019, 20, 141.	2.6	4
74	Proteomics analysis of liver pathological calcification suggests a role for the IQ motif containing GTPase activating protein 1 in myofibroblast function. Proteomics - Clinical Applications, 2009, 3, 307-321.	1.6	3
75	Computational Proteomics with Jupyter and Python. Methods in Molecular Biology, 2019, 1977, 237-248.	0.9	3
76	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.	7.4	3
77	Business intelligence strategies enables rapid analysis of quantitative proteomics data. Journal of Proteome Science and Computational Biology, 2012, 1, 5.	1.0	3
78	Accelerating 3D Protein Modeling Using Cloud Computing: Using Rosetta as a Service on the IBM SmartCloud. , 2011, , .		2
79	Quality Assessment of Low Free-Energy Protein Structure Predictions. , 0, , .		0
80	Cheetah-MS: a web server to model protein complexes using tandem cross-linking mass spectrometry data. Bioinformatics, 2021, 37, 4871-4872.	4.1	0
81	Proteome Analysis Pipeline. , 2013, , 1792-1794.		0
82	Quaternary Structure Modeling Through Chemical Cross-Linking Mass Spectrometry: Extending TX-MS Jupyter Reports. Journal of Visualized Experiments, 2021, , .	0.3	0