

Lars Malmström

List of Publications by Year in descending order

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Version: 2024-02-01

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	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.	7.4	3
2	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.	3.2	12
3	Cerebrospinal fluid proteome maps detect pathogen-specific host response patterns in meningitis. <i>ELife</i> , 2021, 10, .	6.0	13
4	Proteogenomic Workflow Reveals Molecular Phenotypes Related to Breast Cancer Mammographic Appearance. <i>Journal of Proteome Research</i> , 2021, 20, 2983-3001.	3.7	14
5	Cheetah-MS: a web server to model protein complexes using tandem cross-linking mass spectrometry data. <i>Bioinformatics</i> , 2021, 37, 4871-4872.	4.1	0
6	<i>Streptococcus pyogenes</i> Forms Serotype- and Local Environment-Dependent Interspecies Protein Complexes. <i>MSystems</i> , 2021, 6, e0027121.	3.8	13
7	Quaternary Structure Modeling Through Chemical Cross-Linking Mass Spectrometry: Extending TX-MS Jupyter Reports. <i>Journal of Visualized Experiments</i> , 2021, , .	0.3	0
8	Spike-Dependent Opsonization Indicates Both Dose-Dependent Inhibition of Phagocytosis and That Non-Neutralizing Antibodies Can Confer Protection to SARS-CoV-2. <i>Frontiers in Immunology</i> , 2021, 12, 808932.	4.8	34
9	Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020, 17, 665-680.	19.0	513
10	Extracellular Vesicle-Contained microRNA of <i>C. elegans</i> as a Tool to Decipher the Molecular Basis of Nematode Parasitism. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 217.	3.9	14
11	Structural proteomics, electron cryo-microscopy and structural modeling approaches in bacteria-human protein interactions. <i>Medical Microbiology and Immunology</i> , 2020, 209, 265-275.	4.8	13
12	In vivo Cross-Linking MS of the Complement System MAC Assembled on Live Gram-Positive Bacteria. <i>Frontiers in Genetics</i> , 2020, 11, 612475.	2.3	7
13	A quantitative <i>Streptococcus pyogenes</i> -human protein-protein interaction map reveals localization of opsonizing antibodies. <i>Nature Communications</i> , 2019, 10, 2727.	12.8	36
14	Greedy de novo motif discovery to construct motif repositories for bacterial proteomes. <i>BMC Bioinformatics</i> , 2019, 20, 141.	2.6	4
15	Computational Proteomics with Jupyter and Python. <i>Methods in Molecular Biology</i> , 2019, 1977, 237-248.	0.9	3
16	Rapid determination of quaternary protein structures in complex biological samples. <i>Nature Communications</i> , 2019, 10, 192.	12.8	47
17	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.	2.4	61
18	Comprehensive ADP-ribosylome analysis identifies tyrosine as an ADP-ribose acceptor site. <i>EMBO Reports</i> , 2018, 19, .	4.5	75

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19	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.	3.8	23
20	Inference and quantification of peptidofoms in large sample cohorts by SWATH-MS. <i>Nature Biotechnology</i> , 2017, 35, 781-788.	17.5	122
21	FAIRDOMHub: a repository and collaboration environment for sharing systems biology research. <i>Nucleic Acids Research</i> , 2017, 45, D404-D407.	14.5	98
22	An objective comparison of cell-tracking algorithms. <i>Nature Methods</i> , 2017, 14, 1141-1152.	19.0	399
23	TRIC: an automated alignment strategy for reproducible protein quantification in targeted proteomics. <i>Nature Methods</i> , 2016, 13, 777-783.	19.0	173
24	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. <i>Nature Methods</i> , 2016, 13, 741-748.	19.0	537
25	Deciphering the mode of action of the processive polysaccharide modifying enzyme dermatan sulfate epimerase 1 by hydrogenâ€“deuterium exchange mass spectrometry. <i>Chemical Science</i> , 2016, 7, 1447-1456.	7.4	16
26	The SIB Swiss Institute of Bioinformaticsâ€™ resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016, 44, D27-D37.	14.5	64
27	Large-scale inference of protein tissue origin in gram-positive sepsis plasma using quantitative targeted proteomics. <i>Nature Communications</i> , 2016, 7, 10261.	12.8	88
28	A Combined Shotgun and Targeted Mass Spectrometry Strategy for Breast Cancer Biomarker Discovery. <i>Journal of Proteome Research</i> , 2015, 14, 2807-2818.	3.7	33
29	Efficient visualization of high-throughput targeted proteomics experiments: TAPIR. <i>Bioinformatics</i> , 2015, 31, 2415-2417.	4.1	14
30	Quantitative proteogenomics of human pathogens using DIA-MS. <i>Journal of Proteomics</i> , 2015, 129, 98-107.	2.4	28
31	Identification of a Set of Conserved Eukaryotic Internal Retention Time Standards for Data-independent Acquisition Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2800-2813.	3.8	76
32	xTract: software for characterizing conformational changes of protein complexes by quantitative cross-linking mass spectrometry. <i>Nature Methods</i> , 2015, 12, 1185-1190.	19.0	83
33	Reproducible quantitative proteotype data matrices for systems biology. <i>Molecular Biology of the Cell</i> , 2015, 26, 3926-3931.	2.1	46
34	iPortal: the swiss grid proteomics portal: Requirements and new features based on experience and usability considerations. <i>Concurrency Computation Practice and Experience</i> , 2015, 27, 433-445.	2.2	54
35	DIANAâ€™ algorithmic improvements for analysis of data-independent acquisition MS data. <i>Bioinformatics</i> , 2015, 31, 555-562.	4.1	95
36	Fast and Efficient XML Data Access for Next-Generation Mass Spectrometry. <i>PLoS ONE</i> , 2015, 10, e0125108.	2.5	17

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37	A divergent <i>Pseudomonas aeruginosa</i> palmitoyltransferase essential for cystic fibrosis-specific lipid A. <i>Molecular Microbiology</i> , 2014, 91, 158-174.	2.5	42
38	aLFQ: an R-package for estimating absolute protein quantities from label-free LC-MS/MS proteomics data. <i>Bioinformatics</i> , 2014, 30, 2511-2513.	4.1	63
39	pyOpenMS: A Python-based interface to the OpenMS mass spectrometry algorithm library. <i>Proteomics</i> , 2014, 14, 74-77.	2.2	109
40	Numerical Compression Schemes for Proteomics Mass Spectrometry Data. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1537-1542.	3.8	53
41	OpenSWATH enables automated, targeted analysis of data-independent acquisition MS data. <i>Nature Biotechnology</i> , 2014, 32, 219-223.	17.5	692
42	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.	3.4	6
43	Using synthetic peptides to benchmark peptide identification software and search parameters for MS/MS data analysis. <i>EuPA Open Proteomics</i> , 2014, 5, 21-31.	2.5	8
44	An Automated Pipeline for High-Throughput Label-Free Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2013, 12, 1628-1644.	3.7	146
45	Cross-Link Guided Molecular Modeling with ROSETTA. <i>PLoS ONE</i> , 2013, 8, e73411.	2.5	144
46	Proteome Analysis Pipeline. , 2013, , 1792-1794.		0
47	A Computational Tool to Detect and Avoid Redundancy in Selected Reaction Monitoring. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 540-549.	3.8	90
48	<i>Streptococcus pyogenes</i> in Human Plasma. <i>Journal of Biological Chemistry</i> , 2012, 287, 1415-1425.	3.4	35
49	Bioinformatic Challenges in Targeted Proteomics. <i>Journal of Proteome Research</i> , 2012, 11, 4393-4402.	3.7	20
50	Structural Probing of a Protein Phosphatase 2A Network by Chemical Cross-Linking and Mass Spectrometry. <i>Science</i> , 2012, 337, 1348-1352.	12.6	357
51	Splicosomal and serine and arginine-rich splicing factors as targets for TGF- β ² . <i>Fibrogenesis and Tissue Repair</i> , 2012, 5, 6.	3.4	16
52	Proteome-wide selected reaction monitoring assays for the human pathogen <i>Streptococcus pyogenes</i> . <i>Nature Communications</i> , 2012, 3, 1301.	12.8	63
53	Automated Workflow for Large-Scale Selected Reaction Monitoring Experiments. <i>Journal of Proteome Research</i> , 2012, 11, 1644-1653.	3.7	20
54	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

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55	openBIS: a flexible framework for managing and analyzing complex data in biology research. BMC Bioinformatics, 2011, 12, 468.	2.6	114
56	Quantitative proteomics of microbes: Principles and applications to virulence. Proteomics, 2011, 11, 2947-2956.	2.2	24
57	The Proteome Folding Project: Proteome-scale prediction of structure and function. Genome Research, 2011, 21, 1981-1994.	5.5	40
58	Accelerating 3D Protein Modeling Using Cloud Computing: Using Rosetta as a Service on the IBM SmartCloud., 2011, , .		2
59	Xwalk: computing and visualizing distances in cross-linking experiments. Bioinformatics, 2011, 27, 2163-2164.	4.1	130
60	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
61	Protein Structure Modeling. Methods in Molecular Biology, 2010, 673, 63-72.	0.9	6
62	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
63	On the use of hydrogen/deuterium exchange mass spectrometry data to improve <i>de novo</i> protein structure prediction. Rapid Communications in Mass Spectrometry, 2009, 23, 459-461.	1.5	4
64	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
65	Identification of secreted glycoproteins of human prostate and bladder stromal cells by comparative quantitative proteomics. Prostate, 2009, 69, 49-61.	2.3	24
66	Deciphering diatom biochemical pathways via whole-cell proteomics. Aquatic Microbial Ecology, 2009, 55, 241-253.	1.8	48
67	Superfamily Assignments for the Yeast Proteome through Integration of Structure Prediction with the Gene Ontology. PLoS Biology, 2007, 5, e76.	5.6	48
68	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
69	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
70	2DDB - a bioinformatics solution for analysis of quantitative proteomics data. BMC Bioinformatics, 2006, 7, 158.	2.6	20
71	Free modeling with Rosetta in CASP6. Proteins: Structure, Function and Bioinformatics, 2005, 61, 128-134.	2.6	131
72	Prediction of CASP6 structures using automated rosetta protocols. Proteins: Structure, Function and Bioinformatics, 2005, 61, 157-166.	2.6	124

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73	Automated prediction of domain boundaries in CASP6 targets using Ginzu and RosettaDOM. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 193-200.	2.6	85
74	Proteomics: A new research area for the biomedical field. <i>Journal of Organ Dysfunction</i> , 2005, 1, 83-94.	0.3	5
75	The Yeast Resource Center Public Data Repository. <i>Nucleic Acids Research</i> , 2004, 33, D378-D382.	14.5	25
76	Proteome Annotations and Identifications of the Human Pulmonary Fibroblast. <i>Journal of Proteome Research</i> , 2004, 3, 525-537.	3.7	31
77	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.	2.4	26
78	Automated prediction of CASP-5 structures using the Robetta server. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 524-533.	2.6	261
79	Assigning Function to Yeast Proteins by Integration of Technologies. <i>Molecular Cell</i> , 2003, 12, 1353-1365.	9.7	248
80	Proteomic 2DE Database for Spot Selection, Automated Annotation, and Data Analysis. <i>Journal of Proteome Research</i> , 2002, 1, 135-138.	3.7	19
81	De Novo Prediction of Three-dimensional Structures for Major Protein Families. <i>Journal of Molecular Biology</i> , 2002, 322, 65-78.	4.2	237
82	Quality Assessment of Low Free-Energy Protein Structure Predictions. , 0, , .		0