

Fredrik Levander

List of Publications by Year in descending order

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76
papers

3,460
citations

136740

32
h-index

149479

56
g-index

80
all docs

80
docs citations

80
times ranked

5230
citing authors

#	ARTICLE	IF	CITATIONS
1	mzMLâ€”a Community Standard for Mass Spectrometry Data. <i>Molecular and Cellular Proteomics</i> , 2011, 10, R110.000133.	2.5	555
2	Normalyzer: A Tool for Rapid Evaluation of Normalization Methods for Omics Data Sets. <i>Journal of Proteome Research</i> , 2014, 13, 3114-3120.	1.8	218
3	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008, 26, 164-167.	9.4	155
4	Enhanced Exopolysaccharide Production by Metabolic Engineering of <i>Streptococcus thermophilus</i> . <i>Applied and Environmental Microbiology</i> , 2002, 68, 784-790.	1.4	154
5	NormalyzerDE: Online Tool for Improved Normalization of Omics Expression Data and High-Sensitivity Differential Expression Analysis. <i>Journal of Proteome Research</i> , 2019, 18, 732-740.	1.8	137
6	DIANAâ€”algorithmic improvements for analysis of data-independent acquisition MS data. <i>Bioinformatics</i> , 2015, 31, 555-562.	1.8	95
7	The Proteios Software Environment: An Extensible Multiuser Platform for Management and Analysis of Proteomics Data. <i>Journal of Proteome Research</i> , 2009, 8, 3037-3043.	1.8	88
8	Requirement for Phosphoglucomutase in Exopolysaccharide Biosynthesis in Glucose- and Lactose-Utilizing <i>Streptococcus thermophilus</i> . <i>Applied and Environmental Microbiology</i> , 2001, 67, 2734-2738.	1.4	86
9	Phosphite-induced changes of the transcriptome and secretome in <i>Solanum tuberosum</i> leading to resistance against <i>Phytophthora infestans</i> . <i>BMC Plant Biology</i> , 2014, 14, 254.	1.6	77
10	Quantitative proteomics and transcriptomics of potato in response to <i>Phytophthora infestans</i> in compatible and incompatible interactions. <i>BMC Genomics</i> , 2014, 15, 497.	1.2	77
11	The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. Database: the <i>Journal of Biological Databases and Curation</i> , 2013, 2013, bat009-bat009.	1.4	76
12	Modular, scriptable and automated analysis tools for high-throughput peptide mass fingerprinting. <i>Bioinformatics</i> , 2004, 20, 3628-3635.	1.8	74
13	Trehalose-6-phosphate Phosphorylase Is Part of a Novel Metabolic Pathway for Trehalose Utilization in <i>Lactococcus lactis</i> . <i>Journal of Biological Chemistry</i> , 2001, 276, 42707-42713.	1.6	71
14	Dinosaur: A Refined Open-Source Peptide MS Feature Detector. <i>Journal of Proteome Research</i> , 2016, 15, 2143-2151.	1.8	70
15	Towards a standardized bioinformatics infrastructure for N- and O-glycomics. <i>Nature Communications</i> , 2019, 10, 3275.	5.8	70
16	Proteomics and transcriptomics of the BABA-induced resistance response in potato using a novel functional annotation approach. <i>BMC Genomics</i> , 2014, 15, 315.	1.2	67
17	Starch-hydrolyzing bacteria from Ethiopian soda lakes. <i>Extremophiles</i> , 2001, 5, 135-144.	0.9	65
18	TraMLâ€”A Standard Format for Exchange of Selected Reaction Monitoring Transition Lists. <i>Molecular and Cellular Proteomics</i> , 2012, 11, R111.015040.	2.5	65

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19	Chemical derivatization of phosphoserine and phosphothreonine containing peptides to increase sensitivity for MALDI-based analysis and for selectivity of MS/MS analysis. <i>Proteomics</i> , 2006, 6, 757-766.	1.3	61
20	Numerical Compression Schemes for Proteomics Mass Spectrometry Data. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1537-1542.	2.5	53
21	Is label-free LC-MS/MS ready for biomarker discovery?. <i>Proteomics - Clinical Applications</i> , 2015, 9, 289-294.	0.8	51
22	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
23	Targeted Proteomics Approach for Precision Plant Breeding. <i>Journal of Proteome Research</i> , 2016, 15, 638-646.	1.8	44
24	Paranoid potato. <i>Plant Signaling and Behavior</i> , 2012, 7, 400-408.	1.2	43
25	Physiological Role of Î ² -Phosphoglucosyltransferase in <i>Lactococcus lactis</i> . <i>Applied and Environmental Microbiology</i> , 2001, 67, 4546-4553.	1.4	42
26	Patient-Derived Xenograft Models Reveal Intratumor Heterogeneity and Temporal Stability in Neuroblastoma. <i>Cancer Research</i> , 2018, 78, 5958-5969.	0.4	40
27	Wavelet-Based Method for Noise Characterization and Rejection in High-Performance Liquid Chromatography Coupled to Mass Spectrometry. <i>Analytical Chemistry</i> , 2008, 80, 4960-4968.	3.2	39
28	A label-free nano-liquid chromatography-mass spectrometry approach for quantitative serum peptidomics in Crohn's disease patients. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2009, 877, 3127-3136.	1.2	39
29	Antibody-encoding repertoires of bone marrow and peripheral blood—a focus on IgE. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 1026-1030.	1.5	39
30	Parallel antibody germline gene and haplotype analyses support the validity of immunoglobulin germline gene inference and discovery. <i>Molecular Immunology</i> , 2017, 87, 12-22.	1.0	38
31	Automated methods for improved protein identification by peptide mass fingerprinting. <i>Proteomics</i> , 2004, 4, 2594-2601.	1.3	36
32	Proteome of the Nematode-Trapping Cells of the Fungus <i>Monacrosporium haptotylum</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 4993-5004.	1.4	35
33	Antibody Heavy Chain Variable Domains of Different Germline Gene Origins Diversify through Different Paths. <i>Frontiers in Immunology</i> , 2017, 8, 1433.	2.2	34
34	An Adaptive Alignment Algorithm for Quality-controlled Label-free LC-MS. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1407-1420.	2.5	33
35	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
36	Proteome analysis of the xylose-fermenting mutant yeast strain TMB 3400. <i>Yeast</i> , 2009, 26, 371-382.	0.8	31

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37	Proteomic Analysis of <i>Phytophthora infestans</i> Reveals the Importance of Cell Wall Proteins in Pathogenicity. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1958-1971.	2.5	31
38	Automated reporting from gel-based proteomics experiments using the open source Proteios database application. <i>Proteomics</i> , 2007, 7, 668-674.	1.3	30
39	Small-scale analysis of exopolysaccharides from <i>Streptococcus thermophilus</i> grown in a semi-defined medium. <i>BMC Microbiology</i> , 2001, 1, 23.	1.3	28
40	Generic workflow for quality assessment of quantitative label-free LC-MS analysis. <i>Proteomics</i> , 2011, 11, 1114-1124.	1.3	28
41	Automated Selected Reaction Monitoring Software for Accurate Label-Free Protein Quantification. <i>Journal of Proteome Research</i> , 2012, 11, 3766-3773.	1.8	27
42	Differential proteomic analysis of HT29 Cl.16E and intestinal epithelial cells by LC ESI/QTOF mass spectrometry. <i>Journal of Proteomics</i> , 2009, 72, 865-873.	1.2	26
43	Quantitative Label-Free Phosphoproteomics of Six Different Life Stages of the Late Blight Pathogen <i>Phytophthora infestans</i> Reveals Abundant Phosphorylation of Members of the CRN Effector Family. <i>Journal of Proteome Research</i> , 2014, 13, 1848-1859.	1.8	26
44	BEX1 acts as a tumor suppressor in acute myeloid leukemia. <i>Oncotarget</i> , 2015, 6, 21395-21405.	0.8	25
45	Critical Comparison of Multidimensional Separation Methods for Increasing Protein Expression Coverage. <i>Journal of Proteome Research</i> , 2012, 11, 2644-2652.	1.8	22
46	Acidic proteome of growing and resting <i>Lactococcus lactis</i> metabolizing maltose. <i>Proteomics</i> , 2004, 4, 3881-3898.	1.3	19
47	Membrane Protein Identification: N-Terminal Labeling of Nontryptic Membrane Protein Peptides Facilitates Database Searching. <i>Journal of Proteome Research</i> , 2008, 7, 659-665.	1.8	19
48	Relative Quantification of Membrane Proteins in Wild-Type and Prion Protein (PrP)-Knockout Cerebellar Granule Neurons. <i>Journal of Proteome Research</i> , 2012, 11, 523-536.	1.8	19
49	Getting a grip on proteomics data – Proteomics Data Collection (ProDaC). <i>Proteomics</i> , 2009, 9, 3928-3933.	1.3	15
50	Data on haplotype-supported immunoglobulin germline gene inference. <i>Data in Brief</i> , 2017, 13, 620-640.	0.5	15
51	Improved Label-Free LC-MS Analysis by Wavelet-Based Noise Rejection. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-9.	3.0	14
52	Automated Protein Identification by the Combination of MALDI MS and MS/MS Spectra from Different Instruments. <i>Journal of Proteome Research</i> , 2005, 4, 71-74.	1.8	13
53	Proteomic expression analysis and comparison of protein and mRNA expression profiles in human malignant gliomas. <i>Proteomics - Clinical Applications</i> , 2009, 3, 83-94.	0.8	13
54	In Vitro Evolution of Antibodies Inspired by In Vivo Evolution. <i>Frontiers in Immunology</i> , 2018, 9, 1391.	2.2	13

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55	The Protein Expression of <i>Streptococcus pyogenes</i> Significantly Influenced by Human Plasma. <i>Journal of Proteome Research</i> , 2005, 4, 2302-2311.	1.8	12
56	An integrated transcriptomic- and proteomic-based approach to evaluate the human skin sensitization potential of glyphosate and its commercial agrochemical formulations. <i>Journal of Proteomics</i> , 2020, 217, 103647.	1.2	12
57	High-Resolution Proteomic Profiling Shows Sexual Dimorphism in Zebrafish Heart-Associated Proteins. <i>Journal of Proteome Research</i> , 2021, 20, 4075-4088.	1.8	12
58	Quantification of Membrane Proteins Using Nonspecific Protease Digestions. <i>Journal of Proteome Research</i> , 2009, 8, 5666-5673.	1.8	11
59	Comparative Membrane-Associated Proteomics of Three Different Immune Reactions in Potato. <i>International Journal of Molecular Sciences</i> , 2018, 19, 538.	1.8	11
60	Proteomics of PTI and Two ETI Immune Reactions in Potato Leaves. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4726.	1.8	11
61	Representation of selected reaction monitoring data in the mzQuantML data standard. <i>Proteomics</i> , 2015, 15, 2592-2596.	1.3	7
62	Proteomic changes after fertilization and before first cleavage in rainbow trout <i>Oncorhynchus mykiss</i> . <i>Aquaculture</i> , 2020, 520, 734951.	1.7	7
63	Interactive proteogenomic exploration of response to <i>Fusarium</i> head blight in oat varieties with different resistance. <i>Journal of Proteomics</i> , 2020, 218, 103688.	1.2	6
64	Multimodel Pathway Enrichment Methods for Functional Evaluation of Expression Regulation. <i>Journal of Proteome Research</i> , 2012, 11, 2955-2967.	1.8	5
65	Automated quality control system for LC-SRM setups. <i>Journal of Proteomics</i> , 2013, 95, 77-83.	1.2	5
66	OmicLoupe: facilitating biological discovery by interactive exploration of multiple omic datasets and statistical comparisons. <i>BMC Bioinformatics</i> , 2021, 22, 107.	1.2	5
67	Hunting for Protein Markers of Hypoxia by Combining Plasma Membrane Enrichment with a New Approach to Membrane Protein Analysis. <i>Journal of Proteome Research</i> , 2011, 10, 1645-1656.	1.8	4
68	Pathway-centric analysis of the DNA damage response to chemotherapeutic agents in two breast cell lines. <i>EuPA Open Proteomics</i> , 2015, 8, 128-136.	2.5	4
69	Laboratory Data and Sample Management for Proteomics. <i>Methods in Molecular Biology</i> , 2011, 696, 79-92.	0.4	4
70	Development of Reagents for Differential Protein Quantitation by Subtractive Parent (Precursor) Ion Scanning. <i>Journal of Proteome Research</i> , 2007, 6, 1101-1113.	1.8	3
71	Proteomics Data Collection – ProDaC Workshop 15 August 2008, Amsterdam, The Netherlands. <i>Proteomics</i> , 2009, 9, 218-222.	1.3	3
72	Leaf Apoplast of Field-Grown Potato Analyzed by Quantitative Proteomics and Activity-Based Protein Profiling. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12033.	1.8	1

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73	Chapter 9 Mass spectrometry for protein identification. Comprehensive Analytical Chemistry, 2005, 46, 429-447.	0.7	0
74	Tutorial on protein fingerprinting. , 2006, , .		0
75	A Breast Cell Atlas: Organelle analysis of the MDA-MB-231 cell line by density-gradient fractionation using isotopic marking and label-free analysis. EuPA Open Proteomics, 2015, 8, 68-77.	2.5	0
76	Aberrant Activation of the PI3K/mTOR Pathway Promotes Resistance to Sorafenib in AML. Blood, 2015, 126, 2472-2472.	0.6	0