Fredrik Levander

List of Publications by Year
in descending order

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	OmicLoupe: facilitating biological discovery by interactive exploration of multiple omic datasets and statistical comparisons. BMC Bioinformatics, 2021, 22, 107.	1.2	5
2	High-Resolution Proteomic Profiling Shows Sexual Dimorphism in Zebrafish Heart-Associated Proteins. Journal of Proteome Research, 2021, 20, 4075-4088.	1.8	12
3	Leaf Apoplast of Field-Grown Potato Analyzed by Quantitative Proteomics and Activity-Based Protein Profiling. International Journal of Molecular Sciences, 2021, 22, 12033.	1.8	1
4	Interactive proteogenomic exploration of response to Fusarium head blight in oat varieties with different resistance. Journal of Proteomics, 2020, 218, 103688.	1.2	6
5	Proteomic changes after fertilization and before first cleavage in rainbow trout Oncorhynchus mykiss. Aquaculture, 2020, 520, 734951.	1.7	7
6	An integrated transcriptomic- and proteomic-based approach to evaluate the human skin sensitization potential of glyphosate and its commercial agrochemical formulations. Journal of Proteomics, 2020, 217, 103647.	1.2	12
7	Towards a standardized bioinformatics infrastructure for N- and O-glycomics. Nature Communications, 2019, 10, 3275.	5.8	70
8	Proteomics of PTI and Two ETI Immune Reactions in Potato Leaves. International Journal of Molecular Sciences, 2019, 20, 4726.	1.8	11
9	NormalyzerDE: Online Tool for Improved Normalization of Omics Expression Data and High-Sensitivity Differential Expression Analysis. Journal of Proteome Research, 2019, 18, 732-740.	1.8	137
10	Patient-Derived Xenograft Models Reveal Intratumor Heterogeneity and Temporal Stability in Neuroblastoma. Cancer Research, 2018, 78, 5958-5969.	0.4	40
11	In Vitro Evolution of Antibodies Inspired by In Vivo Evolution. Frontiers in Immunology, 2018, 9, 1391.	2.2	13
12	Comparative Membrane-Associated Proteomics of Three Different Immune Reactions in Potato. International Journal of Molecular Sciences, 2018, 19, 538.	1.8	11
13	Parallel antibody germline gene and haplotype analyses support the validity of immunoglobulin germline gene inference and discovery. Molecular Immunology, 2017, 87, 12-22.	1.0	38
14	Proteomic Analysis of Phytophthora infestans Reveals the Importance of Cell Wall Proteins in Pathogenicity. Molecular and Cellular Proteomics, 2017, 16, 1958-1971.	2.5	31
15	Data on haplotype-supported immunoglobulin germline gene inference. Data in Brief, 2017, 13, 620-640.	0.5	15
16	Antibody-encoding repertoires of bone marrow and peripheral blood—a focus on IgE. Journal of Allergy and Clinical Immunology, 2017, 139, 1026-1030.	1.5	39
17	Antibody Heavy Chain Variable Domains of Different Germline Gene Origins Diversify through Different Paths. Frontiers in Immunology, 2017, 8, 1433.	2.2	34
18	Dinosaur: A Refined Open-Source Peptide MS Feature Detector. Journal of Proteome Research, 2016, 15, 2143-2151.	1.8	70

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19	Targeted Proteomics Approach for Precision Plant Breeding. Journal of Proteome Research, 2016, 15, 638-646.	1.8	44
20	Representation of selected‐reaction monitoring data in the mzQuantML data standard. Proteomics, 2015, 15, 2592-2596.	1.3	7
21	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
22	Pathway-centric analysis of the DNA damage response to chemotherapeutic agents in two breast cell lines. EuPA Open Proteomics, 2015, 8, 128-136.	2.5	4
23	Is label‐free LC‐MS/MS ready for biomarker discovery?. Proteomics - Clinical Applications, 2015, 9, 289-294.	0.8	51
24	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
25	DIANA—algorithmic improvements for analysis of data-independent acquisition MS data. Bioinformatics, 2015, 31, 555-562.	1.8	95
26	BEX1 acts as a tumor suppressor in acute myeloid leukemia. Oncotarget, 2015, 6, 21395-21405.	0.8	25
27	Aberrant Activation of the PI3K/mTOR Pathway Promotes Resistance to Sorafenib in AML. Blood, 2015, 126, 2472-2472.	0.6	0
28	Phosphite-induced changes of the transcriptome and secretome in Solanum tuberosum leading to resistance against Phytophthora infestans. BMC Plant Biology, 2014, 14, 254.	1.6	77
29	Normalyzer: A Tool for Rapid Evaluation of Normalization Methods for Omics Data Sets. Journal of Proteome Research, 2014, 13, 3114-3120.	1.8	218
30	Quantitative Label-Free Phosphoproteomics of Six Different Life Stages of the Late Blight Pathogen *Phytophthora infestans* Reveals Abundant Phosphorylation of Members of the CRN Effector Family. Journal of Proteome Research, 2014, 13, 1848-1859.	1.8	26
31	Numerical Compression Schemes for Proteomics Mass Spectrometry Data. Molecular and Cellular Proteomics, 2014, 13, 1537-1542.	2.5	53
32	Quantitative proteomics and transcriptomics of potato in response to Phytophthora infestans in compatible and incompatible interactions. BMC Genomics, 2014, 15, 497.	1.2	77
33	Proteomics and transcriptomics of the BABA-induced resistance response in potato using a novel functional annotation approach. BMC Genomics, 2014, 15, 315.	1.2	67
34	Data processing methods and quality control strategies for label-free LC‐MS protein quantification. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 29-41.	1.1	50
35	Automated quality control system for LC-SRM setups. Journal of Proteomics, 2013, 95, 77-83.	1.2	5
36	An Adaptive Alignment Algorithm for Quality-controlled Label-free LC-MS. Molecular and Cellular Proteomics, 2013, 12, 1407-1420.	2.5	33

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37	Proteome of the Nematode-Trapping Cells of the Fungus Monacrosporium haptotylum. Applied and Environmental Microbiology, 2013, 79, 4993-5004.	1.4	35
38	The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat009-bat009.	1.4	76
39	Paranoid potato. Plant Signaling and Behavior, 2012, 7, 400-408.	1.2	43
40	TraMLâ€"A Standard Format for Exchange of Selected Reaction Monitoring Transition Lists. Molecular and Cellular Proteomics, 2012, 11, R111.015040.	2.5	65
41	Multimodel Pathway Enrichment Methods for Functional Evaluation of Expression Regulation. Journal of Proteome Research, 2012, 11, 2955-2967.	1.8	5
42	Critical Comparison of Multidimensional Separation Methods for Increasing Protein Expression Coverage. Journal of Proteome Research, 2012, 11, 2644-2652.	1.8	22
43	Automated Selected Reaction Monitoring Software for Accurate Label-Free Protein Quantification. Journal of Proteome Research, 2012, 11, 3766-3773.	1.8	27
44	Relative Quantification of Membrane Proteins in Wild-Type and Prion Protein (PrP)-Knockout Cerebellar Granule Neurons. Journal of Proteome Research, 2012, 11, 523-536.	1.8	19
45	Hunting for Protein Markers of Hypoxia by Combining Plasma Membrane Enrichment with a New Approach to Membrane Protein Analysis. Journal of Proteome Research, 2011, 10, 1645-1656.	1.8	4
46	Generic workflow for quality assessment of quantitative labelâ€free LCâ€MS analysis. Proteomics, 2011, 11, 1114-1124.	1.3	28
47	mzMLâ€"a Community Standard for Mass Spectrometry Data. Molecular and Cellular Proteomics, 2011, 10, R110.000133.	2.5	555
48	Laboratory Data and Sample Management for Proteomics. Methods in Molecular Biology, 2011, 696, 79-92.	0.4	4
49	Improved Label-Free LC-MS Analysis by Wavelet-Based Noise Rejection. Journal of Biomedicine and Biotechnology, 2010, 2010, 1-9.	3.0	14
50	Proteome analysis of the xyloseâ€fermenting mutant yeast strain TMB 3400. Yeast, 2009, 26, 371-382.	0.8	31
51	Proteomics Data Collection â€" 4th ProDaC Workshop 15 August 2008, Amsterdam, The Netherlands. Proteomics, 2009, 9, 218-222.	1.3	3
52	Getting a grip on proteomics data â€" Proteomics Data Collection (ProDaC). Proteomics, 2009, 9, 3928-3933.	1.3	15
53	Proteomic expression analysis and comparison of protein and mRNA expression profiles in human malignant gliomas. Proteomics - Clinical Applications, 2009, 3, 83-94.	0.8	13
54	A label-free nano-liquid chromatographyâ€"mass spectrometry approach for quantitative serum peptidomics in Crohn's disease patients. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2009, 877, 3127-3136.	1.2	39

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55	Differential proteomic analysis of HT29 Cl.16E and intestinal epithelial cells by LC ESI/QTOF mass spectrometry. Journal of Proteomics, 2009, 72, 865-873.	1.2	26
56	The Proteios Software Environment: An Extensible Multiuser Platform for Management and Analysis of Proteomics Data. Journal of Proteome Research, 2009, 8, 3037-3043.	1.8	88
57	Quantification of Membrane Proteins Using Nonspecific Protease Digestions. Journal of Proteome Research, 2009, 8, 5666-5673.	1.8	11
58	Human Proteinpedia enables sharing of human protein data. Nature Biotechnology, 2008, 26, 164-167.	9.4	155
59	Wavelet-Based Method for Noise Characterization and Rejection in High-Performance Liquid Chromatography Coupled to Mass Spectrometry. Analytical Chemistry, 2008, 80, 4960-4968.	3.2	39
60	Membrane Protein Identification: N-Terminal Labeling of Nontryptic Membrane Protein Peptides Facilitates Database Searching. Journal of Proteome Research, 2008, 7, 659-665.	1.8	19
61	Development of Reagents for Differential Protein Quantitation by Subtractive Parent (Precursor) Ion Scanning. Journal of Proteome Research, 2007, 6, 1101-1113.	1.8	3
62	Automated reporting from gel-based proteomics experiments using the open source Proteios database application. Proteomics, 2007, 7, 668-674.	1.3	30
63	Tutorial on protein fingerprinting. , 2006, , .		0
64	Chemical derivatization of phosphoserine and phosphothreonine containing peptides to increase sensitivity for MALDI-based analysis and for selectivity of MS/MS analysis. Proteomics, 2006, 6, 757-766.	1.3	61
65	Automated Protein Identification by the Combination of MALDI MS and MS/MS Spectra from Different Instruments. Journal of Proteome Research, 2005, 4, 71-74.	1.8	13
66	The Protein Expression ofStreptococcuspyogenesIs Significantly Influenced by Human Plasma. Journal of Proteome Research, 2005, 4, 2302-2311.	1.8	12
67	Chapter 9 Mass spectrometry for protein identification. Comprehensive Analytical Chemistry, 2005, 46, 429-447.	0.7	0
68	Modular, scriptable and automated analysis tools for high-throughput peptide mass fingerprinting. Bioinformatics, 2004, 20, 3628-3635.	1.8	74
69	Automated methods for improved protein identification by peptide mass fingerprinting. Proteomics, 2004, 4, 2594-2601.	1.3	36
70	Acidic proteome of growing and restingLactococcus lactismetabolizing maltose. Proteomics, 2004, 4, 3881-3898.	1.3	19
71	Enhanced Exopolysaccharide Production by Metabolic Engineering of Streptococcus thermophilus. Applied and Environmental Microbiology, 2002, 68, 784-790.	1.4	154
72	Starch-hydrolyzing bacteria from Ethiopian soda lakes. Extremophiles, 2001, 5, 135-144.	0.9	65

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73	Small-scale analysis of exopolysaccharides from Streptococcus thermophilus grown in a semi-defined medium. BMC Microbiology, 2001, 1, 23.	1.3	28
74	Requirement for Phosphoglucomutase in Exopolysaccharide Biosynthesis in Glucose- and Lactose-Utilizing Streptococcus thermophilus. Applied and Environmental Microbiology, 2001, 67, 2734-2738.	1.4	86
75	Trehalose-6-phosphate Phosphorylase Is Part of a Novel Metabolic Pathway for Trehalose Utilization in Lactococcus lactis. Journal of Biological Chemistry, 2001, 276, 42707-42713.	1.6	71
76	Physiological Role of Î²-Phosphoglucomutase in Lactococcus lactis. Applied and Environmental Microbiology, 2001, 67, 4546-4553.	1.4	42