

Fredrik Levander

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2735211/publications.pdf>

Version: 2024-02-01

76
papers

3,460
citations

136950

32
h-index

149698

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. Molecular and Cellular Proteomics, 2011, 10, R110.000133. | 3.8 | 555 |
| 2 | Normalyzer: A Tool for Rapid Evaluation of Normalization Methods for Omics Data Sets. Journal of Proteome Research, 2014, 13, 3114-3120. | 3.7 | 218 |
| 3 | Human Proteinpedia enables sharing of human protein data. Nature Biotechnology, 2008, 26, 164-167. | 17.5 | 155 |
| 4 | Enhanced Exopolysaccharide Production by Metabolic Engineering of Streptococcus thermophilus. Applied and Environmental Microbiology, 2002, 68, 784-790. | 3.1 | 154 |
| 5 | NormalyzerDE: Online Tool for Improved Normalization of Omics Expression Data and High-Sensitivity Differential Expression Analysis. Journal of Proteome Research, 2019, 18, 732-740. | 3.7 | 137 |
| 6 | DIANAâ€”algorithmic improvements for analysis of data-independent acquisition MS data. Bioinformatics, 2015, 31, 555-562. | 4.1 | 95 |
| 7 | The Proteios Software Environment: An Extensible Multiuser Platform for Management and Analysis of Proteomics Data. Journal of Proteome Research, 2009, 8, 3037-3043. | 3.7 | 88 |
| 8 | Requirement for Phosphoglucomutase in Exopolysaccharide Biosynthesis in Glucose- and Lactose-Utilizing Streptococcus thermophilus. Applied and Environmental Microbiology, 2001, 67, 2734-2738. | 3.1 | 86 |
| 9 | Phosphite-induced changes of the transcriptome and secretome in Solanum tuberosum leading to resistance against Phytophthora infestans. BMC Plant Biology, 2014, 14, 254. | 3.6 | 77 |
| 10 | Quantitative proteomics and transcriptomics of potato in response to Phytophthora infestans in compatible and incompatible interactions. BMC Genomics, 2014, 15, 497. | 2.8 | 77 |
| 11 | The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat009-bat009. | 3.0 | 76 |
| 12 | Modular, scriptable and automated analysis tools for high-throughput peptide mass fingerprinting. Bioinformatics, 2004, 20, 3628-3635. | 4.1 | 74 |
| 13 | 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. | 3.4 | 71 |
| 14 | Dinosaur: A Refined Open-Source Peptide MS Feature Detector. Journal of Proteome Research, 2016, 15, 2143-2151. | 3.7 | 70 |
| 15 | Towards a standardized bioinformatics infrastructure for N- and O-glycomics. Nature Communications, 2019, 10, 3275. | 12.8 | 70 |
| 16 | Proteomics and transcriptomics of the BABA-induced resistance response in potato using a novel functional annotation approach. BMC Genomics, 2014, 15, 315. | 2.8 | 67 |
| 17 | Starch-hydrolyzing bacteria from Ethiopian soda lakes. Extremophiles, 2001, 5, 135-144. | 2.3 | 65 |
| 18 | TraMLâ€”A Standard Format for Exchange of Selected Reaction Monitoring Transition Lists. Molecular and Cellular Proteomics, 2012, 11, R111.015040. | 3.8 | 65 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 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. | 2.2 | 61 |
| 20 | Numerical Compression Schemes for Proteomics Mass Spectrometry Data. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1537-1542. | 3.8 | 53 |
| 21 | Is label-free LC-MS/MS ready for biomarker discovery?. <i>Proteomics - Clinical Applications</i> , 2015, 9, 289-294. | 1.6 | 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. | 2.3 | 50 |
| 23 | Targeted Proteomics Approach for Precision Plant Breeding. <i>Journal of Proteome Research</i> , 2016, 15, 638-646. | 3.7 | 44 |
| 24 | Paranoid potato. <i>Plant Signaling and Behavior</i> , 2012, 7, 400-408. | 2.4 | 43 |
| 25 | Physiological Role of β -Phosphoglucosyltransferase in <i>Lactococcus lactis</i> . <i>Applied and Environmental Microbiology</i> , 2001, 67, 4546-4553. | 3.1 | 42 |
| 26 | Patient-Derived Xenograft Models Reveal Intratumor Heterogeneity and Temporal Stability in Neuroblastoma. <i>Cancer Research</i> , 2018, 78, 5958-5969. | 0.9 | 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. | 6.5 | 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. | 2.3 | 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. | 2.9 | 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. | 2.2 | 38 |
| 31 | Automated methods for improved protein identification by peptide mass fingerprinting. <i>Proteomics</i> , 2004, 4, 2594-2601. | 2.2 | 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. | 3.1 | 35 |
| 33 | Antibody Heavy Chain Variable Domains of Different Germline Gene Origins Diversify through Different Paths. <i>Frontiers in Immunology</i> , 2017, 8, 1433. | 4.8 | 34 |
| 34 | An Adaptive Alignment Algorithm for Quality-controlled Label-free LC-MS. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1407-1420. | 3.8 | 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. | 3.7 | 33 |
| 36 | Proteome analysis of the xylose-fermenting mutant yeast strain TMB 3400. <i>Yeast</i> , 2009, 26, 371-382. | 1.7 | 31 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 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. | 3.8 | 31 |
| 38 | Automated reporting from gel-based proteomics experiments using the open source Proteios database application. <i>Proteomics</i> , 2007, 7, 668-674. | 2.2 | 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. | 3.3 | 28 |
| 40 | Generic workflow for quality assessment of quantitative label-free LC-MS analysis. <i>Proteomics</i> , 2011, 11, 1114-1124. | 2.2 | 28 |
| 41 | Automated Selected Reaction Monitoring Software for Accurate Label-Free Protein Quantification. <i>Journal of Proteome Research</i> , 2012, 11, 3766-3773. | 3.7 | 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. | 2.4 | 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. | 3.7 | 26 |
| 44 | BEX1 acts as a tumor suppressor in acute myeloid leukemia. <i>Oncotarget</i> , 2015, 6, 21395-21405. | 1.8 | 25 |
| 45 | Critical Comparison of Multidimensional Separation Methods for Increasing Protein Expression Coverage. <i>Journal of Proteome Research</i> , 2012, 11, 2644-2652. | 3.7 | 22 |
| 46 | Acidic proteome of growing and resting <i>Lactococcus lactis</i> metabolizing maltose. <i>Proteomics</i> , 2004, 4, 3881-3898. | 2.2 | 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. | 3.7 | 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. | 3.7 | 19 |
| 49 | Getting a grip on proteomics data – Proteomics Data Collection (ProDaC). <i>Proteomics</i> , 2009, 9, 3928-3933. | 2.2 | 15 |
| 50 | Data on haplotype-supported immunoglobulin germline gene inference. <i>Data in Brief</i> , 2017, 13, 620-640. | 1.0 | 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. | 3.7 | 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. | 1.6 | 13 |
| 54 | In Vitro Evolution of Antibodies Inspired by In Vivo Evolution. <i>Frontiers in Immunology</i> , 2018, 9, 1391. | 4.8 | 13 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 55 | The Protein Expression of <i>Streptococcus pyogenes</i> Is Significantly Influenced by Human Plasma. <i>Journal of Proteome Research</i> , 2005, 4, 2302-2311. | 3.7 | 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. | 2.4 | 12 |
| 57 | High-Resolution Proteomic Profiling Shows Sexual Dimorphism in Zebrafish Heart-Associated Proteins. <i>Journal of Proteome Research</i> , 2021, 20, 4075-4088. | 3.7 | 12 |
| 58 | Quantification of Membrane Proteins Using Nonspecific Protease Digestions. <i>Journal of Proteome Research</i> , 2009, 8, 5666-5673. | 3.7 | 11 |
| 59 | Comparative Membrane-Associated Proteomics of Three Different Immune Reactions in Potato. <i>International Journal of Molecular Sciences</i> , 2018, 19, 538. | 4.1 | 11 |
| 60 | Proteomics of PTI and Two ETI Immune Reactions in Potato Leaves. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4726. | 4.1 | 11 |
| 61 | Representation of selected reaction monitoring data in the mzQuantML data standard. <i>Proteomics</i> , 2015, 15, 2592-2596. | 2.2 | 7 |
| 62 | Proteomic changes after fertilization and before first cleavage in rainbow trout <i>Oncorhynchus mykiss</i> . <i>Aquaculture</i> , 2020, 520, 734951. | 3.5 | 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. | 2.4 | 6 |
| 64 | Multimodel Pathway Enrichment Methods for Functional Evaluation of Expression Regulation. <i>Journal of Proteome Research</i> , 2012, 11, 2955-2967. | 3.7 | 5 |
| 65 | Automated quality control system for LC-SRM setups. <i>Journal of Proteomics</i> , 2013, 95, 77-83. | 2.4 | 5 |
| 66 | OmicLoupe: facilitating biological discovery by interactive exploration of multiple omic datasets and statistical comparisons. <i>BMC Bioinformatics</i> , 2021, 22, 107. | 2.6 | 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. | 3.7 | 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. | 0.9 | 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. | 3.7 | 3 |
| 71 | Proteomics Data Collection – ProDaC Workshop 15 August 2008, Amsterdam, The Netherlands. <i>Proteomics</i> , 2009, 9, 218-222. | 2.2 | 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. | 4.1 | 1 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 73 | Chapter 9 Mass spectrometry for protein identification. Comprehensive Analytical Chemistry, 2005, 46, 429-447. | 1.3 | 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. | 1.4 | 0 |