

# Lukas KÄll

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/330058/publications.pdf>

Version: 2024-02-01

68  
papers

11,644  
citations

101496

36  
h-index

95218

68  
g-index

81  
all docs

81  
docs citations

81  
times ranked

18009  
citing authors

#	ARTICLE	IF	CITATIONS
1	Interpretation of the DOME Recommendations for Machine Learning in Proteomics and Metabolomics. <i>Journal of Proteome Research</i> , 2022, 21, 1204-1207.	1.8	7
2	Putting Humpty Dumpty Back Together Again: What Does Protein Quantification Mean in Bottom-Up Proteomics?. <i>Journal of Proteome Research</i> , 2022, 21, 891-898.	1.8	35
3	Survival analysis of pathway activity as a prognostic determinant in breast cancer. <i>PLoS Computational Biology</i> , 2022, 18, e1010020.	1.5	4
4	Prosit Transformer: A transformer for Prediction of MS2 Spectrum Intensities. <i>Journal of Proteome Research</i> , 2022, 21, 1359-1364.	1.8	10
5	A Comprehensive Evaluation of Consensus Spectrum Generation Methods in Proteomics. <i>Journal of Proteome Research</i> , 2022, 21, 1566-1574.	1.8	2
6	Performing Selection on a Monotonic Function in Lieu of Sorting Using Layer-Ordered Heaps. <i>Journal of Proteome Research</i> , 2021, 20, 1849-1854.	1.8	0
7	The one-carbon pool controls mitochondrial energy metabolism via complex I and iron-sulfur clusters. <i>Science Advances</i> , 2021, 7, .	4.7	23
8	Triqler for MaxQuant: Enhancing Results from MaxQuant by Bayesian Error Propagation and Integration. <i>Journal of Proteome Research</i> , 2021, 20, 2062-2068.	1.8	6
9	Parallelized calculation of permutation tests. <i>Bioinformatics</i> , 2021, 36, 5392-5397.	1.8	4
10	Focus on the spectra that matter by clustering of quantification data in shotgun proteomics. <i>Nature Communications</i> , 2020, 11, 3234.	5.8	19
11	Speeding Up Percolator. <i>Journal of Proteome Research</i> , 2019, 18, 3353-3359.	1.8	8
12	CoExpresso: assess the quantitative behavior of protein complexes in human cells. <i>BMC Bioinformatics</i> , 2019, 20, 17.	1.2	9
13	Integrated Identification and Quantification Error Probabilities for Shotgun Proteomics. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 561-570.	2.5	32
14	Response to "Comparison and Evaluation of Clustering Algorithms for Tandem Mass Spectra". <i>Journal of Proteome Research</i> , 2018, 17, 1993-1996.	1.8	9
15	A Protein Standard That Emulates Homology for the Characterization of Protein Inference Algorithms. <i>Journal of Proteome Research</i> , 2018, 17, 1879-1886.	1.8	22
16	A simple null model for inferences from network enrichment analysis. <i>PLoS ONE</i> , 2018, 13, e0206864.	1.1	6
17	Growth of Cyanobacteria Is Constrained by the Abundance of Light and Carbon Assimilation Proteins. <i>Cell Reports</i> , 2018, 25, 478-486.e8.	2.9	97
18	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 4051-4060.	1.8	47

#	ARTICLE	IF	CITATIONS
19	ABRF Proteome Informatics Research Group (iPRG) 2016 Study: Inferring Proteoforms from Bottom-up Proteomics Data. <i>Journal of Biomolecular Techniques</i> , 2018, 29, 39-45.	0.8	6
20	Uncertainty estimation of predictions of peptides' chromatographic retention times in shotgun proteomics. <i>Bioinformatics</i> , 2017, 33, 508-513.	1.8	17
21	Peptide retention time prediction. <i>Mass Spectrometry Reviews</i> , 2017, 36, 615-623.	2.8	66
22	Covariation of Peptide Abundances Accurately Reflects Protein Concentration Differences. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 936-948.	2.5	64
23	Gene-specific correlation of <i>scnRNA</i> and protein levels in human cells and tissues. <i>Molecular Systems Biology</i> , 2016, 12, 883.	3.2	347
24	DeMix-Q: Quantification-Centered Data Processing Workflow. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1467-1478.	2.5	63
25	Fast and Accurate Protein False Discovery Rates on Large-Scale Proteomics Data Sets with Percolator 3.0. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 1719-1727.	1.2	311
26	How to talk about protein-level false discovery rates in shotgun proteomics. <i>Proteomics</i> , 2016, 16, 2461-2469.	1.3	45
27	MaRaCluster: A Fragment Rarity Metric for Clustering Fragment Spectra in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2016, 15, 713-720.	1.8	37
28	The TOPCONS web server for consensus prediction of membrane protein topology and signal peptides. <i>Nucleic Acids Research</i> , 2015, 43, W401-W407.	6.5	776
29	Multi-omic data analysis using Galaxy. <i>Nature Biotechnology</i> , 2015, 33, 137-139.	9.4	140
30	lPeak: An open source tool to combine results from multiple MS/MS search engines. <i>Proteomics</i> , 2015, 15, 2916-2920.	1.3	33
31	Solution to Statistical Challenges in Proteomics Is More Statistics, Not Less. <i>Journal of Proteome Research</i> , 2015, 14, 4099-4103.	1.8	44
32	Peptide-Centric Proteome Analysis: An Alternative Strategy for the Analysis of Tandem Mass Spectrometry Data. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2301-2307.	2.5	146
33	GradientOptimizer: An open-source graphical environment for calculating optimized gradients in reversed-phase liquid chromatography. <i>Proteomics</i> , 2014, 14, 1464-1466.	1.3	5
34	HiRIEF LC-MS enables deep proteome coverage and unbiased proteogenomics. <i>Nature Methods</i> , 2014, 11, 59-62.	9.0	222
35	Fast and Accurate Database Searches with MS-GF+Percolator. <i>Journal of Proteome Research</i> , 2014, 13, 890-897.	1.8	89
36	Crux: Rapid Open Source Protein Tandem Mass Spectrometry Analysis. <i>Journal of Proteome Research</i> , 2014, 13, 4488-4491.	1.8	130

#	ARTICLE	IF	CITATIONS
37	Optimized Nonlinear Gradients for Reversed-Phase Liquid Chromatography in Shotgun Proteomics. <i>Analytical Chemistry</i> , 2013, 85, 7777-7785.	3.2	39
38	Nonparametric Bayesian Evaluation of Differential Protein Quantification. <i>Journal of Proteome Research</i> , 2013, 12, 4556-4565.	1.8	22
39	Determining the calibration of confidence estimation procedures for unique peptides in shotgun proteomics. <i>Journal of Proteomics</i> , 2013, 80, 123-131.	1.2	49
40	Membrane protein shaving with thermolysin can be used to evaluate topology predictors. <i>Proteomics</i> , 2013, 13, 1467-1480.	1.3	10
41	Mass Fingerprinting of Complex Mixtures: Protein Inference from High-Resolution Peptide Masses and Predicted Retention Times. <i>Journal of Proteome Research</i> , 2013, 12, 5730-5741.	1.8	15
42	Enhanced Peptide Identification by Electron Transfer Dissociation Using an Improved Mascot Percolator. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 478-491.	2.5	34
43	Recognizing Uncertainty Increases Robustness and Reproducibility of Mass Spectrometry-based Protein Inferences. <i>Journal of Proteome Research</i> , 2012, 11, 5586-5591.	1.8	36
44	A guideline to proteome-wide $\pm$ helical membrane protein topology predictions. <i>Proteomics</i> , 2012, 12, 2282-2294.	1.3	29
45	A cross-validation scheme for machine learning algorithms in shotgun proteomics. <i>BMC Bioinformatics</i> , 2012, 13, S3.	1.2	34
46	Chromatographic retention time prediction for posttranslationally modified peptides. <i>Proteomics</i> , 2012, 12, 1151-1159.	1.3	49
47	On Using Samples of Known Protein Content to Assess the Statistical Calibration of Scores Assigned to Peptide-Spectrum Matches in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2011, 10, 3844-3844.	1.8	3
48	On Using Samples of Known Protein Content to Assess the Statistical Calibration of Scores Assigned to Peptide-Spectrum Matches in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2011, 10, 2671-2678.	1.8	52
49	Quality assessments of peptide-spectrum matches in shotgun proteomics. <i>Proteomics</i> , 2011, 11, 1086-1093.	1.3	38
50	Computational Mass Spectrometry-Based Proteomics. <i>PLoS Computational Biology</i> , 2011, 7, e1002277.	1.5	55
51	Training, Selection, and Robust Calibration of Retention Time Models for Targeted Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 5209-5216.	1.8	93
52	Prediction of Transmembrane Topology and Signal Peptide Given a Protein's Amino Acid Sequence. <i>Methods in Molecular Biology</i> , 2010, 673, 53-62.	0.4	6
53	<scp>quality</scp>: non-parametric estimation of $\langle i \rangle q \langle /i \rangle$ -values and posterior error probabilities. <i>Bioinformatics</i> , 2009, 25, 964-966.	1.8	107
54	Improvements to the Percolator Algorithm for Peptide Identification from Shotgun Proteomics Data Sets. <i>Journal of Proteome Research</i> , 2009, 8, 3737-3745.	1.8	251

#	ARTICLE	IF	CITATIONS
55	Rapid and Accurate Peptide Identification from Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2008, 7, 3022-3027.	1.8	181
56	Assigning Significance to Peptides Identified by Tandem Mass Spectrometry Using Decoy Databases. <i>Journal of Proteome Research</i> , 2008, 7, 29-34.	1.8	551
57	Posterior Error Probabilities and False Discovery Rates: Two Sides of the Same Coin. <i>Journal of Proteome Research</i> , 2008, 7, 40-44.	1.8	264
58	Non-parametric estimation of posterior error probabilities associated with peptides identified by tandem mass spectrometry. <i>Bioinformatics</i> , 2008, 24, i42-i48.	1.8	147
59	Transmembrane Topology and Signal Peptide Prediction Using Dynamic Bayesian Networks. <i>PLoS Computational Biology</i> , 2008, 4, e1000213.	1.5	232
60	Use of shotgun proteomics for the identification, confirmation, and correction of <i>C. elegans</i> gene annotations. <i>Genome Research</i> , 2008, 18, 1660-1669.	2.4	75
61	Membrane topology of the <i>Drosophila</i> OR83b odorant receptor. <i>FEBS Letters</i> , 2007, 581, 5601-5604.	1.3	194
62	Advantages of combined transmembrane topology and signal peptide prediction—the Phobius web server. <i>Nucleic Acids Research</i> , 2007, 35, W429-W432.	6.5	1,461
63	Semi-supervised learning for peptide identification from shotgun proteomics datasets. <i>Nature Methods</i> , 2007, 4, 923-925.	9.0	2,010
64	A general model of G protein-coupled receptor sequences and its application to detect remote homologs. <i>Protein Science</i> , 2006, 15, 509-521.	3.1	158
65	A novel transmembrane topology of presenilin based on reconciling experimental and computational evidence. <i>FEBS Journal</i> , 2005, 272, 2727-2733.	2.2	45
66	An HMM posterior decoder for sequence feature prediction that includes homology information. <i>Bioinformatics</i> , 2005, 21, i251-i257.	1.8	292
67	A Combined Transmembrane Topology and Signal Peptide Prediction Method. <i>Journal of Molecular Biology</i> , 2004, 338, 1027-1036.	2.0	2,145
68	Reliability of transmembrane predictions in whole-genome data. <i>FEBS Letters</i> , 2002, 532, 415-418.	1.3	70