Lukas Käll

List of Publications by Year
in descending order

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	A Combined Transmembrane Topology and Signal Peptide Prediction Method. Journal of Molecular Biology, 2004, 338, 1027-1036.	2.0	2,145
2	Semi-supervised learning for peptide identification from shotgun proteomics datasets. Nature Methods, 2007, 4, 923-925.	9.0	2,010
3	Advantages of combined transmembrane topology and signal peptide prediction--the Phobius web server. Nucleic Acids Research, 2007, 35, W429-W432.	6.5	1,461
4	The TOPCONS web server for consensus prediction of membrane protein topology and signal peptides. Nucleic Acids Research, 2015, 43, W401-W407.	6.5	776
5	Assigning Significance to Peptides Identified by Tandem Mass Spectrometry Using Decoy Databases. Journal of Proteome Research, 2008, 7, 29-34.	1.8	551
6	Gene‐specific correlation of <scp>RNA</scp> and protein levels in human cells and tissues. Molecular Systems Biology, 2016, 12, 883.	3.2	347
7	Fast and Accurate Protein False Discovery Rates on Large-Scale Proteomics Data Sets with Percolator 3.0. Journal of the American Society for Mass Spectrometry, 2016, 27, 1719-1727.	1.2	311
8	An HMM posterior decoder for sequence feature prediction that includes homology information. Bioinformatics, 2005, 21, i251-i257.	1.8	292
9	Posterior Error Probabilities and False Discovery Rates: Two Sides of the Same Coin. Journal of Proteome Research, 2008, 7, 40-44.	1.8	264
10	Improvements to the Percolator Algorithm for Peptide Identification from Shotgun Proteomics Data Sets. Journal of Proteome Research, 2009, 8, 3737-3745.	1.8	251
11	Transmembrane Topology and Signal Peptide Prediction Using Dynamic Bayesian Networks. PLoS Computational Biology, 2008, 4, e1000213.	1.5	232
12	HiRIEF LC-MS enables deep proteome coverage and unbiased proteogenomics. Nature Methods, 2014, 11, 59-62.	9.0	222
13	Membrane topology of the <i>Drosophila</i> OR83b odorant receptor. FEBS Letters, 2007, 581, 5601-5604.	1.3	194
14	Rapid and Accurate Peptide Identification from Tandem Mass Spectra. Journal of Proteome Research, 2008, 7, 3022-3027.	1.8	181
15	A general model of G protein-coupled receptor sequences and its application to detect remote homologs. Protein Science, 2006, 15, 509-521.	3.1	158
16	Non-parametric estimation of posterior error probabilities associated with peptides identified by tandem mass spectrometry. Bioinformatics, 2008, 24, i42-i48.	1.8	147
17	Peptide-Centric Proteome Analysis: An Alternative Strategy for the Analysis of Tandem Mass Spectrometry Data. Molecular and Cellular Proteomics, 2015, 14, 2301-2307.	2.5	146
18	Multi-omic data analysis using Galaxy. Nature Biotechnology, 2015, 33, 137-139.	9.4	140

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19	Crux: Rapid Open Source Protein Tandem Mass Spectrometry Analysis. Journal of Proteome Research, 2014, 13, 4488-4491.	1.8	130
20	<scp>qvality</scp>: non-parametric estimation of <i>q</i>-values and posterior error probabilities. Bioinformatics, 2009, 25, 964-966.	1.8	107
21	Growth of Cyanobacteria Is Constrained by the Abundance of Light and Carbon Assimilation Proteins. Cell Reports, 2018, 25, 478-486.e8.	2.9	97
22	Training, Selection, and Robust Calibration of Retention Time Models for Targeted Proteomics. Journal of Proteome Research, 2010, 9, 5209-5216.	1.8	93
23	Fast and Accurate Database Searches with MS-GF+Percolator. Journal of Proteome Research, 2014, 13, 890-897.	1.8	89
24	Use of shotgun proteomics for the identification, confirmation, and correction of <i>C. elegans</i> gene annotations. Genome Research, 2008, 18, 1660-1669.	2.4	75
25	Reliability of transmembrane predictions in whole€genome data. FEBS Letters, 2002, 532, 415-418.	1.3	70
26	Peptide retention time prediction. Mass Spectrometry Reviews, 2017, 36, 615-623.	2.8	66
27	Covariation of Peptide Abundances Accurately Reflects Protein Concentration Differences. Molecular and Cellular Proteomics, 2017, 16, 936-948.	2.5	64
28	DeMix-Q: Quantification-Centered Data Processing Workflow. Molecular and Cellular Proteomics, 2016, 15, 1467-1478.	2.5	63
29	Computational Mass Spectrometry€"Based Proteomics. PLoS Computational Biology, 2011, 7, e1002277.	1.5	55
30	On Using Samples of Known Protein Content to Assess the Statistical Calibration of Scores Assigned to Peptide-Spectrum Matches in Shotgun Proteomics. Journal of Proteome Research, 2011, 10, 2671-2678.	1.8	52
31	Chromatographic retention time prediction for posttranslationally modified peptides. Proteomics, 2012, 12, 1151-1159.	1.3	49
32	Determining the calibration of confidence estimation procedures for unique peptides in shotgun proteomics. Journal of Proteomics, 2013, 80, 123-131.	1.2	49
33	Expanding the Use of Spectral Libraries in Proteomics. Journal of Proteome Research, 2018, 17, 4051-4060.	1.8	47
34	A novel transmembrane topology of presenilin based on reconciling experimental and computational evidence. FEBS Journal, 2005, 272, 2727-2733.	2.2	45
35	How to talk about protein€level false discovery rates in shotgun proteomics. Proteomics, 2016, 16, 2461-2469.	1.3	45
36	Solution to Statistical Challenges in Proteomics Is More Statistics, Not Less. Journal of Proteome Research, 2015, 14, 4099-4103.	1.8	44

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37	Optimized Nonlinear Gradients for Reversed-Phase Liquid Chromatography in Shotgun Proteomics. Analytical Chemistry, 2013, 85, 7777-7785.	3.2	39
38	Quality assessments of peptide–spectrum matches in shotgun proteomics. Proteomics, 2011, 11, 1086-1093.	1.3	38
39	MaRaCluster: A Fragment Rarity Metric for Clustering Fragment Spectra in Shotgun Proteomics. Journal of Proteome Research, 2016, 15, 713-720.	1.8	37
40	Recognizing Uncertainty Increases Robustness and Reproducibility of Mass Spectrometry-based Protein Inferences. Journal of Proteome Research, 2012, 11, 5586-5591.	1.8	36
41	Putting Humpty Dumpty Back Together Again: What Does Protein Quantification Mean in Bottom-Up Proteomics?. Journal of Proteome Research, 2022, 21, 891-898.	1.8	35
42	Enhanced Peptide Identification by Electron Transfer Dissociation Using an Improved Mascot Percolator. Molecular and Cellular Proteomics, 2012, 11, 478-491.	2.5	34
43	A cross-validation scheme for machine learning algorithms in shotgun proteomics. BMC Bioinformatics, 2012, 13, S3.	1.2	34
44	IPeak: An open source tool to combine results from multiple MS/MS search engines. Proteomics, 2015, 15, 2916-2920.	1.3	33
45	Integrated Identification and Quantification Error Probabilities for Shotgun Proteomics. Molecular and Cellular Proteomics, 2019, 18, 561-570.	2.5	32
46	A guideline to proteome–wide α–helical membrane protein topology predictions. Proteomics, 2012, 12, 2282-2294.	1.3	29
47	The one-carbon pool controls mitochondrial energy metabolism via complex I and iron-sulfur clusters. Science Advances, 2021, 7, .	4.7	23
48	Nonparametric Bayesian Evaluation of Differential Protein Quantification. Journal of Proteome Research, 2013, 12, 4556-4565.	1.8	22
49	A Protein Standard That Emulates Homology for the Characterization of Protein Inference Algorithms. Journal of Proteome Research, 2018, 17, 1879-1886.	1.8	22
50	Focus on the spectra that matter by clustering of quantification data in shotgun proteomics. Nature Communications, 2020, 11, 3234.	5.8	19
51	Uncertainty estimation of predictions of peptides' chromatographic retention times in shotgun proteomics. Bioinformatics, 2017, 33, 508-513.	1.8	17
52	Mass Fingerprinting of Complex Mixtures: Protein Inference from High-Resolution Peptide Masses and Predicted Retention Times. Journal of Proteome Research, 2013, 12, 5730-5741.	1.8	15
53	Membrane protein shaving with thermolysin can be used to evaluate topology predictors. Proteomics, 2013, 13, 1467-1480.	1.3	10
54	Prosit Transformer: A transformer for Prediction of MS2 Spectrum Intensities. Journal of Proteome Research, 2022, 21, 1359-1364.	1.8	10

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55	Response to â€œComparison and Evaluation of Clustering Algorithms for Tandem Mass Spectraâ€. Journal of Proteome Research, 2018, 17, 1993-1996.	1.8	9
56	CoExpresso: assess the quantitative behavior of protein complexes in human cells. BMC Bioinformatics, 2019, 20, 17.	1.2	9
57	Speeding Up Percolator. Journal of Proteome Research, 2019, 18, 3353-3359.	1.8	8
58	Interpretation of the DOME Recommendations for Machine Learning in Proteomics and Metabolomics. Journal of Proteome Research, 2022, 21, 1204-1207.	1.8	7
59	A simple null model for inferences from network enrichment analysis. PLoS ONE, 2018, 13, e0206864.	1.1	6
60	ABRF Proteome Informatics Research Group (iPRG) 2016 Study: Inferring Proteoforms from Bottom-up Proteomics Data. Journal of Biomolecular Techniques, 2018, 29, 39-45.	0.8	6
61	Triqler for MaxQuant: Enhancing Results from MaxQuant by Bayesian Error Propagation and Integration. Journal of Proteome Research, 2021, 20, 2062-2068.	1.8	6
62	Prediction of Transmembrane Topology and Signal Peptide Given a Proteinâ€™s Amino Acid Sequence. Methods in Molecular Biology, 2010, 673, 53-62.	0.4	6
63	GradientOptimizer: An openâ€source graphical environment for calculating optimized gradients in reversedâ€phase liquid chromatography. Proteomics, 2014, 14, 1464-1466.	1.3	5
64	Parallelized calculation of permutation tests. Bioinformatics, 2021, 36, 5392-5397.	1.8	4
65	Survival analysis of pathway activity as a prognostic determinant in breast cancer. PLoS Computational Biology, 2022, 18, e1010020.	1.5	4
66	On Using Samples of Known Protein Content to Assess the Statistical Calibration of Scores Assigned to Peptide-Spectrum Matches in Shotgun Proteomics. Journal of Proteome Research, 2011, 10, 3844-3844.	1.8	3
67	A Comprehensive Evaluation of Consensus Spectrum Generation Methods in Proteomics. Journal of Proteome Research, 2022, 21, 1566-1574.	1.8	2
68	Performing Selection on a Monotonic Function in Lieu of Sorting Using Layer-Ordered Heaps. Journal of Proteome Research, 2021, 20, 1849-1854.	1.8	0