

Lukas Kl

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

66

papers

8,411

citations

34

h-index

81

g-index

81

ext. papers

10,576

ext. citations

7.2

avg, IF

6.18

L-index

#	Paper	IF	Citations
66	A combined transmembrane topology and signal peptide prediction method. <i>Journal of Molecular Biology</i> , 2004 , 338, 1027-36	6.5	1669
65	Semi-supervised learning for peptide identification from shotgun proteomics datasets. <i>Nature Methods</i> , 2007 , 4, 923-5	21.6	1362
64	Advantages of combined transmembrane topology and signal peptide prediction--the Phobius web server. <i>Nucleic Acids Research</i> , 2007 , 35, W429-32	20.1	1033
63	The TOPCONS web server for consensus prediction of membrane protein topology and signal peptides. <i>Nucleic Acids Research</i> , 2015 , 43, W401-7	20.1	492
62	Assigning significance to peptides identified by tandem mass spectrometry using decoy databases. <i>Journal of Proteome Research</i> , 2008 , 7, 29-34	5.6	449
61	An HMM posterior decoder for sequence feature prediction that includes homology information. <i>Bioinformatics</i> , 2005 , 21 Suppl 1, i251-7	7.2	246
60	Gene-specific correlation of RNA and protein levels in human cells and tissues. <i>Molecular Systems Biology</i> , 2016 , 12, 883	12.2	230
59	Posterior error probabilities and false discovery rates: two sides of the same coin. <i>Journal of Proteome Research</i> , 2008 , 7, 40-4	5.6	218
58	Improvements to the percolator algorithm for Peptide identification from shotgun proteomics data sets. <i>Journal of Proteome Research</i> , 2009 , 8, 3737-45	5.6	197
57	Transmembrane topology and signal peptide prediction using dynamic bayesian networks. <i>PLoS Computational Biology</i> , 2008 , 4, e1000213	5	175
56	HiRIEF LC-MS enables deep proteome coverage and unbiased proteogenomics. <i>Nature Methods</i> , 2014 , 11, 59-62	21.6	171
55	Membrane topology of the Drosophila OR83b odorant receptor. <i>FEBS Letters</i> , 2007 , 581, 5601-4	3.8	165
54	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	3.5	158
53	Rapid and accurate peptide identification from tandem mass spectra. <i>Journal of Proteome Research</i> , 2008 , 7, 3022-7	5.6	144
52	A general model of G protein-coupled receptor sequences and its application to detect remote homologs. <i>Protein Science</i> , 2006 , 15, 509-21	6.3	139
51	Peptide-Centric Proteome Analysis: An Alternative Strategy for the Analysis of Tandem Mass Spectrometry Data. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 2301-7	7.6	104
50	Crux: rapid open source protein tandem mass spectrometry analysis. <i>Journal of Proteome Research</i> , 2014 , 13, 4488-91	5.6	93

49	Multi-omic data analysis using Galaxy. <i>Nature Biotechnology</i> , 2015 , 33, 137-9	44.5	93
48	Non-parametric estimation of posterior error probabilities associated with peptides identified by tandem mass spectrometry. <i>Bioinformatics</i> , 2008 , 24, i42-8	7.2	84
47	QUALITY: non-parametric estimation of q-values and posterior error probabilities. <i>Bioinformatics</i> , 2009 , 25, 964-6	7.2	76
46	Training, selection, and robust calibration of retention time models for targeted proteomics. <i>Journal of Proteome Research</i> , 2010 , 9, 5209-16	5.6	69
45	Use of shotgun proteomics for the identification, confirmation, and correction of <i>C. elegans</i> gene annotations. <i>Genome Research</i> , 2008 , 18, 1660-9	9.7	69
44	Fast and accurate database searches with MS-GF+Percolator. <i>Journal of Proteome Research</i> , 2014 , 13, 890-7	5.6	62
43	Reliability of transmembrane predictions in whole-genome data. <i>FEBS Letters</i> , 2002 , 532, 415-8	3.8	58
42	DeMix-Q: Quantification-Centered Data Processing Workflow. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 1467-78	7.6	50
41	Growth of Cyanobacteria Is Constrained by the Abundance of Light and Carbon Assimilation Proteins. <i>Cell Reports</i> , 2018 , 25, 478-486.e8	10.6	50
40	Peptide retention time prediction. <i>Mass Spectrometry Reviews</i> , 2017 , 36, 615-623	11	47
39	Computational mass spectrometry-based proteomics. <i>PLoS Computational Biology</i> , 2011 , 7, e1002277	5	47
38	A novel transmembrane topology of presenilin based on reconciling experimental and computational evidence. <i>FEBS Journal</i> , 2005 , 272, 2727-33	5.7	43
37	Solution to Statistical Challenges in Proteomics Is More Statistics, Not Less. <i>Journal of Proteome Research</i> , 2015 , 14, 4099-103	5.6	38
36	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, 2671-8	5.6	38
35	Chromatographic retention time prediction for posttranslationally modified peptides. <i>Proteomics</i> , 2012 , 12, 1151-9	4.8	37
34	Covariation of Peptide Abundances Accurately Reflects Protein Concentration Differences. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 936-948	7.6	36
33	How to talk about protein-level false discovery rates in shotgun proteomics. <i>Proteomics</i> , 2016 , 16, 2461-2.8	4.8	36
32	Quality assessments of peptide-spectrum matches in shotgun proteomics. <i>Proteomics</i> , 2011 , 11, 1086-93.8	4.8	33

31	Determining the calibration of confidence estimation procedures for unique peptides in shotgun proteomics. <i>Journal of Proteomics</i> , 2013 , 80, 123-31	3.9	32
30	Optimized nonlinear gradients for reversed-phase liquid chromatography in shotgun proteomics. <i>Analytical Chemistry</i> , 2013 , 85, 7777-85	7.8	30
29	Enhanced peptide identification by electron transfer dissociation using an improved Mascot Percolator. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 478-91	7.6	30
28	Recognizing uncertainty increases robustness and reproducibility of mass spectrometry-based protein inferences. <i>Journal of Proteome Research</i> , 2012 , 11, 5586-91	5.6	29
27	IPeak: An open source tool to combine results from multiple MS/MS search engines. <i>Proteomics</i> , 2015 , 15, 2916-20	4.8	26
26	MaRaCluster: A Fragment Rarity Metric for Clustering Fragment Spectra in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2016 , 15, 713-20	5.6	26
25	A guideline to proteome-wide helical membrane protein topology predictions. <i>Proteomics</i> , 2012 , 12, 2282-94	4.8	26
24	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018 , 17, 4051-4066	6.6	26
23	A cross-validation scheme for machine learning algorithms in shotgun proteomics. <i>BMC Bioinformatics</i> , 2012 , 13 Suppl 16, S3	3.6	22
22	Nonparametric Bayesian evaluation of differential protein quantification. <i>Journal of Proteome Research</i> , 2013 , 12, 4556-65	5.6	20
21	Integrated Identification and Quantification Error Probabilities for Shotgun Proteomics. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 561-570	7.6	18
20	Focus on the spectra that matter by clustering of quantification data in shotgun proteomics. <i>Nature Communications</i> , 2020 , 11, 3234	17.4	13
19	A Protein Standard That Emulates Homology for the Characterization of Protein Inference Algorithms. <i>Journal of Proteome Research</i> , 2018 , 17, 1879-1886	5.6	12
18	Mass fingerprinting of complex mixtures: protein inference from high-resolution peptide masses and predicted retention times. <i>Journal of Proteome Research</i> , 2013 , 12, 5730-41	5.6	12
17	Uncertainty estimation of predictions of peptides chromatographic retention times in shotgun proteomics. <i>Bioinformatics</i> , 2017 , 33, 508-513	7.2	10
16	Membrane protein shaving with thermolysin can be used to evaluate topology predictors. <i>Proteomics</i> , 2013 , 13, 1467-80	4.8	9
15	Response to "Comparison and Evaluation of Clustering Algorithms for Tandem Mass Spectra". <i>Journal of Proteome Research</i> , 2018 , 17, 1993-1996	5.6	7
14	Prediction of transmembrane topology and signal peptide given a protein's amino acid sequence. <i>Methods in Molecular Biology</i> , 2010 , 673, 53-62	1.4	6

13	The one-carbon pool controls mitochondrial energy metabolism via complex I and iron-sulfur clusters. <i>Science Advances</i> , 2021 , 7,	14.3	6
12	CoExpresso: assess the quantitative behavior of protein complexes in human cells. <i>BMC Bioinformatics</i> , 2019 , 20, 17	3.6	5
11	Speeding Up Percolator. <i>Journal of Proteome Research</i> , 2019 , 18, 3353-3359	5.6	5
10	GradientOptimizer: an open-source graphical environment for calculating optimized gradients in reversed-phase liquid chromatography. <i>Proteomics</i> , 2014 , 14, 1464-6	4.8	4
9	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	1.1	4
8	Triqler for MaxQuant: Enhancing Results from MaxQuant by Bayesian Error Propagation and Integration. <i>Journal of Proteome Research</i> , 2021 , 20, 2062-2068	5.6	3
7	A simple null model for inferences from network enrichment analysis. <i>PLoS ONE</i> , 2018 , 13, e0206864	3.7	3
6	Putting Humpty Dumpty Back Together Again: What Does Protein Quantification Mean in Bottom-Up Proteomics?. <i>Journal of Proteome Research</i> , 2022 ,	5.6	3
5	Focus on the spectra that matter by clustering of quantification data in shotgun proteomics		2
4	A protein standard that emulates homology for the characterization of protein inference algorithms		1
3	Parallelized calculation of permutation tests. <i>Bioinformatics</i> , 2021 , 36, 5392-5397	7.2	1
2	Survival analysis of pathway activity as a prognostic determinant in breast cancer.. <i>PLoS Computational Biology</i> , 2022 , 18, e1010020	5	0
1	Performing Selection on a Monotonic Function in Lieu of Sorting Using Layer-Ordered Heaps. <i>Journal of Proteome Research</i> , 2021 , 20, 1849-1854	5.6	