Niklaas Colaert

List of Publications by Year
in descending order

23 papers	2,235 citations	430874 18 h-index	642732 23 g-index
24 all docs	24 docs citations	24 times ranked	3742 citing authors

#	Article	IF	Citations
1	The iceLogo web server and SOAP service for determining protein consensus sequences. Nucleic Acids Research, 2015, 43, W543-W546.	14.5	52
2	The Online Protein Processing Resource (TOPPR): a database and analysis platform for protein processing events. Nucleic Acids Research, 2013, 41, D333-D337.	14.5	17
3	Cells Lacking Î²-Actin are Genetically Reprogrammed and Maintain Conditional Migratory Capacity*. Molecular and Cellular Proteomics, 2012, 11, 255-271.	3.8	93
4	Proteome profiling of the green sulfur bacterium *Chlorobaculum tepidum* by Nâ€terminal proteomics. Proteomics, 2012, 12, 63-67.	2.2	10
5	thermo-msf-parser: An Open Source Java Library to Parse and Visualize Thermo Proteome Discoverer *msf* Files. Journal of Proteome Research, 2011, 10, 3840-3843.	3.7	40
6	A Case Study on the Comparison of Different Software Tools for Automated Quantification of Peptides. Methods in Molecular Biology, 2011, 753, 373-398.	0.9	14
7	RIBAR and xRIBAR: Methods for Reproducible Relative MS/MS-based Label-Free Protein Quantification. Journal of Proteome Research, 2011, 10, 3183-3189.	3.7	21
8	Analysis of the Resolution Limitations of Peptide Identification Algorithms. Journal of Proteome Research, 2011, 10, 5555-5561.	3.7	60
9	Combining quantitative proteomics data processing workflows for greater sensitivity. Nature Methods, 2011, 8, 481-483.	19.0	18
10	compomics-utilities: an open-source Java library for computational proteomics. BMC Bioinformatics, 2011, 12, 70.	2.6	86
11	A comparison of MS2â€based labelâ€free quantitative proteomic techniques with regards to accuracy and precision. Proteomics, 2011, 11, 1110-1113.	2.2	22
12	A reproducibilityâ€based evaluation procedure for quantifying the differences between MS/MS peak intensity normalization methods. Proteomics, 2011, 11, 1172-1180.	2.2	7
13	Redox Proteomics of Protein-bound Methionine Oxidation. Molecular and Cellular Proteomics, 2011, 10, M110.006866.	3.8	117
14	Rover: A tool to visualize and validate quantitative proteomics data from different sources. Proteomics, 2010, 10, 1226-1229.	2.2	40
15	ms_lims, a simple yet powerful open source laboratory information management system for MSâ€driven proteomics. Proteomics, 2010, 10, 1261-1264.	2.2	73
16	MSâ€driven protease substrate degradomics. Proteomics, 2010, 10, 1284-1296.	2.2	55
17	Complementary positional proteomics for screening substrates of endo- and exoproteases. Nature Methods, 2010, 7, 512-515.	19.0	106
18	The substrate specificity profile of human granzyme A. Biological Chemistry, 2010, 391, 983-97.	2.5	37

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19	A Quantitative Proteomics Design for Systematic Identification of Protease Cleavage Events. Molecular and Cellular Proteomics, 2010, 9, 2327-2333.	3.8	51
20	Proteomics analyses reveal the evolutionary conservation and divergence of N-terminal acetyltransferases from yeast and humans. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 8157-8162.	7.1	472
21	In Vitro and in Vivo Protein-bound Tyrosine Nitration Characterized by Diagonal Chromatography. Molecular and Cellular Proteomics, 2009, 8, 2642-2652.	3.8	85
22	Analysis of Protein Processing by N-terminal Proteomics Reveals Novel Species-specific Substrate Determinants of Granzyme B Orthologs. Molecular and Cellular Proteomics, 2009, 8, 258-272.	3.8	95
23	Improved visualization of protein consensus sequences by iceLogo. Nature Methods, 2009, 6, 786-787.	19.0	664