

Niklaas Colaert

List of Publications by Year in descending order

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Version: 2024-02-01

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	Improved visualization of protein consensus sequences by iceLogo. <i>Nature Methods</i> , 2009, 6, 786-787.	19.0	664
2	Proteomics analyses reveal the evolutionary conservation and divergence of N-terminal acetyltransferases from yeast and humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 8157-8162.	7.1	472
3	Redox Proteomics of Protein-bound Methionine Oxidation. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.006866.	3.8	117
4	Complementary positional proteomics for screening substrates of endo- and exoproteases. <i>Nature Methods</i> , 2010, 7, 512-515.	19.0	106
5	Analysis of Protein Processing by N-terminal Proteomics Reveals Novel Species-specific Substrate Determinants of Granzyme B Orthologs. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 258-272.	3.8	95
6	Cells Lacking β -Actin are Genetically Reprogrammed and Maintain Conditional Migratory Capacity*. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 255-271.	3.8	93
7	compomics-utilities: an open-source Java library for computational proteomics. <i>BMC Bioinformatics</i> , 2011, 12, 70.	2.6	86
8	In Vitro and in Vivo Protein-bound Tyrosine Nitration Characterized by Diagonal Chromatography. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2642-2652.	3.8	85
9	ms_lim, a simple yet powerful open source laboratory information management system for MS-driven proteomics. <i>Proteomics</i> , 2010, 10, 1261-1264.	2.2	73
10	Analysis of the Resolution Limitations of Peptide Identification Algorithms. <i>Journal of Proteome Research</i> , 2011, 10, 5555-5561.	3.7	60
11	MS-driven protease substrate degradomics. <i>Proteomics</i> , 2010, 10, 1284-1296.	2.2	55
12	The iceLogo web server and SOAP service for determining protein consensus sequences. <i>Nucleic Acids Research</i> , 2015, 43, W543-W546.	14.5	52
13	A Quantitative Proteomics Design for Systematic Identification of Protease Cleavage Events. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2327-2333.	3.8	51
14	Rover: A tool to visualize and validate quantitative proteomics data from different sources. <i>Proteomics</i> , 2010, 10, 1226-1229.	2.2	40
15	thermo-msf-parser: An Open Source Java Library to Parse and Visualize Thermo Proteome Discoverer <i>msf</i> Files. <i>Journal of Proteome Research</i> , 2011, 10, 3840-3843.	3.7	40
16	The substrate specificity profile of human granzyme A. <i>Biological Chemistry</i> , 2010, 391, 983-97.	2.5	37
17	A comparison of MS ² -based label-free quantitative proteomic techniques with regards to accuracy and precision. <i>Proteomics</i> , 2011, 11, 1110-1113.	2.2	22
18	RIBAR and xRIBAR: Methods for Reproducible Relative MS/MS-based Label-Free Protein Quantification. <i>Journal of Proteome Research</i> , 2011, 10, 3183-3189.	3.7	21

#	ARTICLE	IF	CITATIONS
19	Combining quantitative proteomics data processing workflows for greater sensitivity. <i>Nature Methods</i> , 2011, 8, 481-483.	19.0	18
20	The Online Protein Processing Resource (TOPPR): a database and analysis platform for protein processing events. <i>Nucleic Acids Research</i> , 2013, 41, D333-D337.	14.5	17
21	A Case Study on the Comparison of Different Software Tools for Automated Quantification of Peptides. <i>Methods in Molecular Biology</i> , 2011, 753, 373-398.	0.9	14
22	Proteome profiling of the green sulfur bacterium <i>Chlorobaculum tepidum</i> by N-terminal proteomics. <i>Proteomics</i> , 2012, 12, 63-67.	2.2	10
23	A reproducibility-based evaluation procedure for quantifying the differences between MS/MS peak intensity normalization methods. <i>Proteomics</i> , 2011, 11, 1172-1180.	2.2	7