

# Lennart Martens

## List of Publications by Year in descending order

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255  
papers

19,282  
citations

22548

61  
h-index

17373

126  
g-index

310  
all docs

310  
docs citations

310  
times ranked

26520  
citing authors

#	ARTICLE	IF	CITATIONS
1	PDBe-KB: collaboratively defining the biological context of structural data. <i>Nucleic Acids Research</i> , 2022, 50, D534-D542.	6.5	46
2	Orthogonal proteomics methods to unravel the HOTAIR interactome. <i>Scientific Reports</i> , 2022, 12, 1513.	1.6	3
3	<i>Pout2Prot</i>: An Efficient Tool to Create Protein (Sub)groups from Percolator Output Files. <i>Journal of Proteome Research</i> , 2022, 21, 1175-1180.	1.8	4
4	A comprehensive LFQ benchmark dataset on modern day acquisition strategies in proteomics. <i>Scientific Data</i> , 2022, 9, 126.	2.4	20
5	Sensitive and Specific Spectral Library Searching with CompOmics Spectral Library Searching Tool and Percolator. <i>Journal of Proteome Research</i> , 2022, 21, 1365-1370.	1.8	6
6	MS2Rescore: Data-Driven Rescoring Dramatically Boosts Immunopeptide Identification Rates. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100266.	2.5	34
7	Unipept Desktop: A Faster, More Powerful Metaproteomics Results Analysis Tool. <i>Journal of Proteome Research</i> , 2021, 20, 2005-2009.	1.8	17
8	Data Management of Sensitive Human Proteomics Data: Current Practices, Recommendations, and Perspectives for the Future. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100071.	2.5	25
9	MegaGO: A Fast Yet Powerful Approach to Assess Functional Gene Ontology Similarity across Meta-Omics Data Sets. <i>Journal of Proteome Research</i> , 2021, 20, 2083-2088.	1.8	8
10	Personalized Proteome: Comparing Proteogenomics and Open Variant Search Approaches for Single Amino Acid Variant Detection. <i>Journal of Proteome Research</i> , 2021, 20, 3353-3364.	1.8	10
11	The RNA landscape of the human placenta in health and disease. <i>Nature Communications</i> , 2021, 12, 2639.	5.8	75
12	Cov-MS: A Community-Based Template Assay for Mass-Spectrometry-Based Protein Detection in SARS-CoV-2 Patients. <i>Jacs Au</i> , 2021, 1, 750-765.	3.6	29
13	Unipept Visualizations: an interactive visualization library for biological data. <i>Bioinformatics</i> , 2021, , .	1.8	1
14	Spectral Prediction Features as a Solution for the Search Space Size Problem in Proteogenomics. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100076.	2.5	31
15	DeepLC can predict retention times for peptides that carry as-yet unseen modifications. <i>Nature Methods</i> , 2021, 18, 1363-1369.	9.0	95
16	Massively parallel interrogation of protein fragment secretability using SECRIFY reveals features influencing secretory system transit. <i>Nature Communications</i> , 2021, 12, 6414.	5.8	5
17	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. <i>Nature Communications</i> , 2021, 12, 7305.	5.8	34
18	Anatomy and evolution of database search enginesâ€”a central component of mass spectrometry based proteomic workflows. <i>Mass Spectrometry Reviews</i> , 2020, 39, 292-306.	2.8	97

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19	ThermoRawFileParser: Modular, Scalable, and Cross-Platform RAW File Conversion. <i>Journal of Proteome Research</i> , 2020, 19, 537-542.	1.8	144
20	Precursor Intensity-Based Label-Free Quantification Software Tools for Proteomic and Multi-Omic Analysis within the Galaxy Platform. <i>Proteomes</i> , 2020, 8, 15.	1.7	9
21	Removing the Hidden Data Dependency of DIA with Predicted Spectral Libraries. <i>Proteomics</i> , 2020, 20, e1900306.	1.3	38
22	Community standards for open cell migration data. <i>GigaScience</i> , 2020, 9, .	3.3	12
23	Connecting MetaProteomeAnalyzer and PeptideShaker to Unipept for Seamless End-to-End Metaproteomics Data Analysis. <i>Journal of Proteome Research</i> , 2020, 19, 3562-3566.	1.8	11
24	COSS: A Fast and User-Friendly Tool for Spectral Library Searching. <i>Journal of Proteome Research</i> , 2020, 19, 2786-2793.	1.8	18
25	Unipept CLI 2.0: adding support for visualizations and functional annotations. <i>Bioinformatics</i> , 2020, 36, 4220-4221.	1.8	9
26	The CEP5 Peptide Promotes Abiotic Stress Tolerance, As Revealed by Quantitative Proteomics, and Attenuates the AUX/IAA Equilibrium in Arabidopsis. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1248-1262.	2.5	35
27	Scop3P: A Comprehensive Resource of Human Phosphosites within Their Full Context. <i>Journal of Proteome Research</i> , 2020, 19, 3478-3486.	1.8	19
28	Simple Peptide Quantification Approach for MS-Based Proteomics Quality Control. <i>ACS Omega</i> , 2020, 5, 6754-6762.	1.6	26
29	MSqRob Takes the Missing Hurdle: Uniting Intensity- and Count-Based Proteomics. <i>Analytical Chemistry</i> , 2020, 92, 6278-6287.	3.2	34
30	The Age of Data-Driven Proteomics: How Machine Learning Enables Novel Workflows. <i>Proteomics</i> , 2020, 20, e1900351.	1.3	34
31	Generalized Calibration Across Liquid Chromatography Setups for Generic Prediction of Small-Molecule Retention Times. <i>Analytical Chemistry</i> , 2020, 92, 6571-6578.	3.2	26
32	Robust Summarization and Inference in Proteome-wide Label-free Quantification. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1209-1219.	2.5	37
33	DoRes within CellMissy: dose-response analysis on cell migration and related data. <i>Bioinformatics</i> , 2019, 35, 696-697.	1.8	1
34	Comprehensive and Empirical Evaluation of Machine Learning Algorithms for Small Molecule LC Retention Time Prediction. <i>Analytical Chemistry</i> , 2019, 91, 3694-3703.	3.2	64
35	A comparison of collision cross section values obtained via travelling wave ion mobility-mass spectrometry and ultra high performance liquid chromatography-ion mobility-mass spectrometry: Application to the characterisation of metabolites in rat urine. <i>Journal of Chromatography A</i> , 2019, 1602, 386-396.	1.8	34
36	Updated MS <sup>2</sup> PIP web server delivers fast and accurate MS <sup>2</sup> peak intensity prediction for multiple fragmentation methods, instruments and labeling techniques. <i>Nucleic Acids Research</i> , 2019, 47, W295-W299.	6.5	77

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37	Accurate peptide fragmentation predictions allow data driven approaches to replace and improve upon proteomics search engine scoring functions. <i>Bioinformatics</i> , 2019, 35, 5243-5248.	1.8	52
38	Challenges and promise at the interface of metaproteomics and genomics: an overview of recent progress in metaproteogenomic data analysis. <i>Expert Review of Proteomics</i> , 2019, 16, 375-390.	1.3	86
39	Bcl-2 and IP3 compete for the ligand-binding domain of IP3Rs modulating Ca <sup>2+</sup> signaling output. <i>Cellular and Molecular Life Sciences</i> , 2019, 76, 3843-3859.	2.4	31
40	Unipept 4.0: Functional Analysis of Metaproteome Data. <i>Journal of Proteome Research</i> , 2019, 18, 606-615.	1.8	112
41	LNCipedia 5: towards a reference set of human long non-coding RNAs. <i>Nucleic Acids Research</i> , 2019, 47, D135-D139.	6.5	403
42	Scop3D: Online Visualization of Mutation Rates on Protein Structure. <i>Journal of Proteome Research</i> , 2019, 18, 765-769.	1.8	2
43	Update on the moFF Algorithm for Label-Free Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2019, 18, 728-731.	1.8	13
44	SQANTI: extensive characterization of long-read transcript sequences for quality control in full-length transcriptome identification and quantification. <i>Genome Research</i> , 2018, 28, 396-411.	2.4	299
45	Analysis of Invasion Dynamics of Matrix-Embedded Cells in a Multisample Format. <i>Methods in Molecular Biology</i> , 2018, 1749, 79-117.	0.4	4
46	Cross-linked peptide identification: A computational forest of algorithms. <i>Mass Spectrometry Reviews</i> , 2018, 37, 738-749.	2.8	27
47	High-throughput metaproteomics data analysis with Unipept: A tutorial. <i>Journal of Proteomics</i> , 2018, 171, 11-22.	1.2	65
48	The online Tabloid Proteome: an annotated database of protein associations. <i>Nucleic Acids Research</i> , 2018, 46, D581-D585.	6.5	6
49	MPA Portable: A Stand-Alone Software Package for Analyzing Metaproteome Samples on the Go. <i>Analytical Chemistry</i> , 2018, 90, 685-689.	3.2	65
50	Quality control in mass spectrometry-based proteomics. <i>Mass Spectrometry Reviews</i> , 2018, 37, 697-711.	2.8	82
51	Surveillance of Myelodysplastic Syndrome via Migration Analyses of Blood Neutrophils: A Potential Prognostic Tool. <i>Journal of Immunology</i> , 2018, 201, 3546-3557.	0.4	17
52	The study of degradation mechanisms of glyco-engineered plant produced anti-rabies monoclonal antibodies E559 and 62-71-3. <i>PLoS ONE</i> , 2018, 13, e0209373.	1.1	3
53	Data-Driven Rescoring of Metabolite Annotations Significantly Improves Sensitivity. <i>Analytical Chemistry</i> , 2018, 90, 11636-11642.	3.2	8
54	Differences in antigenic sites and other functional regions between genotype A and G mumps virus surface proteins. <i>Scientific Reports</i> , 2018, 8, 13337.	1.6	22

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55	The mutational landscape of <i>MYCN</i> , <i>Lin28b</i> and <i>ALK</i> <i>F1174L</i> driven murine neuroblastoma mimics human disease. <i>Oncotarget</i> , 2018, 9, 8334-8349.	0.8	6
56	Protein complex analysis: From raw protein lists to protein interaction networks. <i>Mass Spectrometry Reviews</i> , 2017, 36, 600-614.	2.8	22
57	A Golden Age for Working with Public Proteomics Data. <i>Trends in Biochemical Sciences</i> , 2017, 42, 333-341.	3.7	92
58	An end-to-end software solution for the analysis of high-throughput single-cell migration data. <i>Scientific Reports</i> , 2017, 7, 42383.	1.6	30
59	N-terminal Proteomics Assisted Profiling of the Unexplored Translation Initiation Landscape in <i>Arabidopsis thaliana</i> . <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1064-1080.	2.5	54
60	Unbiased Protein Association Study on the Public Human Proteome Reveals Biological Connections between Co-Occurring Protein Pairs. <i>Journal of Proteome Research</i> , 2017, 16, 2204-2212.	1.8	3
61	Noncoding after All: Biases in Proteomics Data Do Not Explain Observed Absence of lncRNA Translation Products. <i>Journal of Proteome Research</i> , 2017, 16, 2508-2515.	1.8	44
62	Methods to Calculate Spectrum Similarity. <i>Methods in Molecular Biology</i> , 2017, 1549, 75-100.	0.4	18
63	An Accessible Proteogenomics Informatics Resource for Cancer Researchers. <i>Cancer Research</i> , 2017, 77, e43-e46.	0.4	27
64	Mass spectrometrists should search for all peptides, but assess only the ones they care about. <i>Nature Methods</i> , 2017, 14, 643-644.	9.0	42
65	Computational quality control tools for mass spectrometry proteomics. <i>Proteomics</i> , 2017, 17, 1600159.	1.3	34
66	MAPPI-DAT: data management and analysis for protein-protein interaction data from the high-throughput MAPPIT cell microarray platform. <i>Bioinformatics</i> , 2017, 33, 1424-1425.	1.8	2
67	A community proposal to integrate proteomics activities in ELIXIR. <i>F1000Research</i> , 2017, 6, 875.	0.8	13
68	Identification of Quantitative Proteomic Differences between <i>Mycobacterium tuberculosis</i> Lineages with Altered Virulence. <i>Frontiers in Microbiology</i> , 2016, 7, 813.	1.5	34
69	Metaproteomic data analysis at a glance: advances in computational microbial community proteomics. <i>Expert Review of Proteomics</i> , 2016, 13, 757-769.	1.3	67
70	moFF: a robust and automated approach to extract peptide ion intensities. <i>Nature Methods</i> , 2016, 13, 964-966.	9.0	56
71	The impact of sequence database choice on metaproteomic results in gut microbiota studies. <i>Microbiome</i> , 2016, 4, 51.	4.9	124
72	Database Search Engines: Paradigms, Challenges and Solutions. <i>Advances in Experimental Medicine and Biology</i> , 2016, 919, 147-156.	0.8	18

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73	Designing biomedical proteomics experiments: state-of-the-art and future perspectives. <i>Expert Review of Proteomics</i> , 2016, 13, 495-511.	1.3	13
74	Public proteomics data: How the field has evolved from sceptical inquiry to the promise of in silico proteomics. <i>EuPA Open Proteomics</i> , 2016, 11, 42-44.	2.5	6
75	A Pipeline for Differential Proteomics in Unsequenced Species. <i>Journal of Proteome Research</i> , 2016, 15, 1963-1970.	1.8	10
76	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. <i>Journal of Proteome Research</i> , 2016, 15, 3961-3970.	1.8	158
77	Xilmass: A New Approach toward the Identification of Cross-Linked Peptides. <i>Analytical Chemistry</i> , 2016, 88, 9949-9957.	3.2	25
78	Up-to-Date Workflow for Plant (Phospho)proteomics Identifies Differential Drought-Responsive Phosphorylation Events in Maize Leaves. <i>Journal of Proteome Research</i> , 2016, 15, 4304-4317.	1.8	50
79	The Lyssavirus glycoprotein: A key to cross-immunity. <i>Virology</i> , 2016, 498, 250-256.	1.1	11
80	Proteome-scale Binary Interactomics in Human Cells. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3624-3639.	2.5	23
81	An extra dimension in protein tagging by quantifying universal proteotypic peptides using targeted proteomics. <i>Scientific Reports</i> , 2016, 6, 27220.	1.6	15
82	Resolution of protein structure by mass spectrometry. <i>Mass Spectrometry Reviews</i> , 2016, 35, 653-665.	2.8	15
83	Taking Aim at Moving Targets in Computational Cell Migration. <i>Trends in Cell Biology</i> , 2016, 26, 88-110.	3.6	100
84	Unsupervised Quality Assessment of Mass Spectrometry Proteomics Experiments by Multivariate Quality Control Metrics. <i>Journal of Proteome Research</i> , 2016, 15, 1300-1307.	1.8	15
85	Exploring the potential of public proteomics data. <i>Proteomics</i> , 2016, 16, 214-225.	1.3	72
86	sORFs.org: a repository of small ORFs identified by ribosome profiling. <i>Nucleic Acids Research</i> , 2016, 44, D324-D329.	6.5	123
87	The challenge of metaproteomic analysis in human samples. <i>Expert Review of Proteomics</i> , 2016, 13, 135-138.	1.3	20
88	SFINX: Straightforward Filtering Index for Affinity Purificationâ€“Mass Spectrometry Data Analysis. <i>Journal of Proteome Research</i> , 2016, 15, 332-338.	1.8	20
89	Pladipus Enables Universal Distributed Computing in Proteomics Bioinformatics. <i>Journal of Proteome Research</i> , 2016, 15, 707-712.	1.8	11
90	Ariadneâ€™s Thread: A Robust Software Solution Leading to Automated Absolute and Relative Quantification of SRM Data. <i>Journal of Proteome Research</i> , 2015, 14, 3779-3792.	1.8	4

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91	Ryanodine receptors are targeted by anti-apoptotic Bcl-XL involving its BH4 domain and Lys87 from its BH3 domain. <i>Scientific Reports</i> , 2015, 5, 9641.	1.6	30
92	Colonic metaproteomic signatures of active bacteria and the host in obesity. <i>Proteomics</i> , 2015, 15, 3544-3552.	1.3	70
93	Summarization vs Peptide-Based Models in Label-Free Quantitative Proteomics: Performance, Pitfalls, and Data Analysis Guidelines. <i>Journal of Proteome Research</i> , 2015, 14, 2457-2465.	1.8	44
94	Phospho-iTRAQ data article: Assessing isobaric labels for the large-scale study of phosphopeptide stoichiometry. <i>Data in Brief</i> , 2015, 4, 60-65.	0.5	16
95	MS <sup>2</sup> PIP prediction server: compute and visualize MS <sup>2</sup> peak intensity predictions for CID and HCD fragmentation. <i>Nucleic Acids Research</i> , 2015, 43, W326-W330.	6.5	63
96	Phospho-iTRAQ: Assessing Isobaric Labels for the Large-Scale Study Of Phosphopeptide Stoichiometry. <i>Journal of Proteome Research</i> , 2015, 14, 839-849.	1.8	15
97	An open data ecosystem for cell migration research. <i>Trends in Cell Biology</i> , 2015, 25, 55-58.	3.6	26
98	The MetaProteomeAnalyzer: A Powerful Open-Source Software Suite for Metaproteomics Data Analysis and Interpretation. <i>Journal of Proteome Research</i> , 2015, 14, 1557-1565.	1.8	169
99	Scop3D: Three-dimensional visualization of sequence conservation. <i>Proteomics</i> , 2015, 15, 1448-1452.	1.3	11
100	PeptideShaker enables reanalysis of MS-derived proteomics data sets. <i>Nature Biotechnology</i> , 2015, 33, 22-24.	9.4	460
101	A Decoy-Free Approach to the Identification of Peptides. <i>Journal of Proteome Research</i> , 2015, 14, 1792-1798.	1.8	35
102	An update on LNCipedia: a database for annotated human lncRNA sequences. <i>Nucleic Acids Research</i> , 2015, 43, D174-D180.	6.5	298
103	iMonDB: Mass Spectrometry Quality Control through Instrument Monitoring. <i>Journal of Proteome Research</i> , 2015, 14, 2360-2366.	1.8	21
104	Navigating through metaproteomics data: A logbook of database searching. <i>Proteomics</i> , 2015, 15, 3439-3453.	1.3	128
105	The iceLogo web server and SOAP service for determining protein consensus sequences. <i>Nucleic Acids Research</i> , 2015, 43, W543-W546.	6.5	52
106	PepShell: Visualization of Conformational Proteomics Data. <i>Journal of Proteome Research</i> , 2015, 14, 1987-1990.	1.8	2
107	Managing Expectations When Publishing Tools and Methods for Computational Proteomics. <i>Journal of Proteome Research</i> , 2015, 14, 2002-2004.	1.8	5
108	Ten years of public proteomics data: How things have evolved, and where the next ten years should lead us. <i>EuPA Open Proteomics</i> , 2015, 8, 28-35.	2.5	4

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109	Open-Source, Platform-Independent Library and Online Scripting Environment for Accessing Thermo Scientific RAW Files. <i>Journal of Proteome Research</i> , 2015, 14, 4940-4943.	1.8	3
110	Limited Proteolysis Combined with Stable Isotope Labeling Reveals Conformational Changes in Protein (Pseudo)kinases upon Binding Small Molecules. <i>Journal of Proteome Research</i> , 2015, 14, 4179-4193.	1.8	7
111	Viewing the proteome: How to visualize proteomics data?. <i>Proteomics</i> , 2015, 15, 1341-1355.	1.3	32
112	An improved toolbox to unravel the plant cellular machinery by tandem affinity purification of Arabidopsis protein complexes. <i>Nature Protocols</i> , 2015, 10, 169-187.	5.5	160
113	JSparklines: Making tabular proteomics data come alive. <i>Proteomics</i> , 2015, 15, 1428-1431.	1.3	7
114	jqcML: An Open-Source Java API for Mass Spectrometry Quality Control Data in the qcML Format. <i>Journal of Proteome Research</i> , 2014, 13, 3484-3487.	1.8	9
115	Machine learning applications in proteomics research: How the past can boost the future. <i>Proteomics</i> , 2014, 14, 353-366.	1.3	52
116	Distributed computing and data storage in proteomics: Many hands make light work, and a stronger memory. <i>Proteomics</i> , 2014, 14, 367-377.	1.3	21
117	qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1905-1913.	2.5	42
118	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , 2014, 32, 223-226.	9.4	2,505
119	Introduction to opportunities and pitfalls in functional mass spectrometry based proteomics. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 12-20.	1.1	27
120	DeNovoGUI: An Open Source Graphical User Interface for <i>de Novo</i> Sequencing of Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2014, 13, 1143-1146.	1.8	73
121	Shedding light on black boxes in protein identification. <i>Proteomics</i> , 2014, 14, 1001-1005.	1.3	20
122	Toward More Transparent and Reproducible Omics Studies Through a Common Metadata Checklist and Data Publications. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 10-14.	1.0	54
123	Time-resolved characterization of cAMP/PKA-dependent signaling reveals that platelet inhibition is a concerted process involving multiple signaling pathways. <i>Blood</i> , 2014, 123, e1-e10.	0.6	80
124	Bioinformatics for Proteomics: Opportunities at the Interface Between the Scientists, Their Experiments, and the Community. <i>Methods in Molecular Biology</i> , 2014, 1156, 239-248.	0.4	0
125	Crowdsourcing in proteomics: public resources lead to better experiments. <i>Amino Acids</i> , 2013, 44, 1129-1137.	1.2	26
126	Asn <sub>3</sub> , a Reliable, Robust, and Universal Lock Mass for Improved Accuracy in LC-MS and LC-MS/MS. <i>Analytical Chemistry</i> , 2013, 85, 11054-11060.	3.2	13



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127	MS2PIP: a tool for MS/MS peak intensity prediction. <i>Bioinformatics</i> , 2013, 29, 3199-3203.	1.8	108
128	In praise of open research measures. <i>Nature</i> , 2013, 498, 170-170.	13.7	11
129	Searching for a needle in a stack of needles: challenges in metaproteomics data analysis. <i>Molecular BioSystems</i> , 2013, 9, 578-585.	2.9	93
130	ProteoCloud: A full-featured open source proteomics cloud computing pipeline. <i>Journal of Proteomics</i> , 2013, 88, 104-108.	1.2	34
131	Protein structure as a means to triage proposed <sc>PTM</sc> sites. <i>Proteomics</i> , 2013, 13, 1028-1035.	1.3	31
132	Pride-asap: Automatic fragment ion annotation of identified PRIDE spectra. <i>Journal of Proteomics</i> , 2013, 95, 89-92.	1.2	17
133	Computational proteomics pitfalls and challenges: HavanaBioinfo 2012 Workshop report. <i>Journal of Proteomics</i> , 2013, 87, 134-138.	1.2	19
134	Predicting Tryptic Cleavage from Proteomics Data Using Decision Tree Ensembles. <i>Journal of Proteome Research</i> , 2013, 12, 2253-2259.	1.8	48
135	Getting intimate with trypsin, the leading protease in proteomics. <i>Mass Spectrometry Reviews</i> , 2013, 32, 453-465.	2.8	164
136	Bringing proteomics into the clinic: The need for the field to finally take itself seriously. <i>Proteomics - Clinical Applications</i> , 2013, 7, 388-391.	0.8	13
137	About Dice, Boulderling, and Team Empowerment: Running the CompOmics Group at VIB and Ghent University, Belgium. <i>PLoS Computational Biology</i> , 2013, 9, e1003332.	1.5	1
138	CellMissy: a tool for management, storage and analysis of cell migration data produced in wound healing-like assays. <i>Bioinformatics</i> , 2013, 29, 2661-2663.	1.8	12
139	Proteome-derived Peptide Libraries to Study the Substrate Specificity Profiles of Carboxypeptidases. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2096-2110.	2.5	40
140	The Online Protein Processing Resource (TOPPR): a database and analysis platform for protein processing events. <i>Nucleic Acids Research</i> , 2013, 41, D333-D337.	6.5	17
141	LNCipedia: a database for annotated human lncRNA transcript sequences and structures. <i>Nucleic Acids Research</i> , 2013, 41, D246-D251.	6.5	488
142	Resilience in the proteomics data ecosystem: How the field cares for its data. <i>Proteomics</i> , 2013, 13, 1548-1550.	1.3	5
143	Toward More Transparent and Reproducible Omics Studies Through a Common Metadata Checklist and Data Publications. <i>Big Data</i> , 2013, 1, 196-201.	2.1	5
144	Delsa Workshop IV: Launching the Quantified Human Initiative. <i>Big Data</i> , 2013, 1, 187-190.	2.1	4

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145	<sc>D</sc>â€score: A search engine independent <sc>MD</sc>â€score. Proteomics, 2013, 13, 1036-1041.	1.3	46
146	The PRoteomics IDentification (PRIDE) Converter 2 Framework: An Improved Suite of Tools to Facilitate Data Submission to the PRIDE Database and the ProteomeXchange Consortium. Molecular and Cellular Proteomics, 2012, 11, 1682-1689.	2.5	105
147	Enabling Computational Proteomics by Public and Local Data Management Systems. Circulation: Cardiovascular Genetics, 2012, 5, 266-266.	5.1	1
148	TraMLâ€”A Standard Format for Exchange of Selected Reaction Monitoring Transition Lists. Molecular and Cellular Proteomics, 2012, 11, R111.015040.	2.5	65
149	Current methods for global proteome identification. Expert Review of Proteomics, 2012, 9, 519-532.	1.3	43
150	The Effect of Peptide Identification Search Algorithms on MS2-Based Label-Free Protein Quantification. OMICS A Journal of Integrative Biology, 2012, 16, 443-448.	1.0	3
151	The first comprehensive and quantitative analysis of human platelet protein composition allows the comparative analysis of structural and functional pathways. Blood, 2012, 120, e73-e82.	0.6	623
152	iTRAQ Data Interpretation. Methods in Molecular Biology, 2012, 893, 501-509.	0.4	4
153	A Complex Standard for Protein Identification, Designed by Evolution. Journal of Proteome Research, 2012, 11, 5065-5071.	1.8	51
154	Integral Quantification Accuracy Estimation for Reporter Ion-based Quantitative Proteomics (iQuARI). Journal of Proteome Research, 2012, 11, 5072-5080.	1.8	25
155	Towards a human proteomics atlas. Analytical and Bioanalytical Chemistry, 2012, 404, 1069-1077.	1.9	12
156	The HUPO initiative on Model Organism Proteomes, iMOP. Proteomics, 2012, 12, 340-345.	1.3	9
157	Chromatographic retention time prediction for posttranslationally modified peptides. Proteomics, 2012, 12, 1151-1159.	1.3	49
158	Sigpep: Calculating unique peptide signature transition sets in a complete proteome background. Proteomics, 2012, 12, 1142-1146.	1.3	9
159	PRIDE Inspector: a tool to visualize and validate MS proteomics data. Nature Biotechnology, 2012, 30, 135-137.	9.4	109
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