CURRICULUM VITAE

Prof. Dr. Lennart MARTENS

Ghent University and VIB, Ghent, Belgium

Last update: 6 March 2024

NAME	MARTENS
FIRST NAME	Lennart
NATIONALITY	Belgian
PROFESSIONAL ADDRESS	Technologiepark-Zwijnaarde 75 B-9052 Gent Belgium e-mail: lennart.martens@UGent.be
ACADEMIC TITLES	- **Candidature Biology** (*Bachelor degree*) July 1998, Limburgs Universitair Centrum (LUC – *now Hasselt University*), Belgium. - **Licentiate Biotechnology** (*Master in Science degree*) July 2000, Ghent University, Belgium. - **Doctorate (Ph.D.) in Sciences: Biotechnology** 15 June 2006, Ghent University, Belgium.
TITLE OF MASTER'S THESIS	"The development of novel algorithms for the identification of proteins via MALDI-PSD mass spectrometry"
TITLE OF PH. D. THESIS	"Novel bioinformatics tools assisting targeted peptide-centric proteomics and global proteomics data dissemination"
PROFESSIONAL TITLES	Sun Certified Programmer for the Java 2 Platform (score of 93%).
PRESENT APPOINTMENTS	Senior Full Professor of Systems Biology in the Department of Biochemistry, Faculty of Medicine and Health Sciences, Ghent University, Ghent, Belgium. *(Career progression: tenured Associate Professor in October 2009; Full Professor in October 2014; Senior Full Professor in September 2022).* Associate Director (since September 2016) and Group Leader (since October 2009), Computational Omics and Systems Biology Group, VIB-UGent Center for Medical Biotechnology, VIB, Ghent, Belgium. Visiting Researcher (since October 2009), European Molecular Biology Laboratory's European Bioinformatics Institute (EMBL-EBI), Cambridge, United Kingdom.

PAST APPOINTMENTS

- October 2017 to October 2020: Visiting Group Leader, European Molecular Biology Laboratory's European Bioinformatics Institute (EMBL-EBI), Cambridge, United Kingdom.
- July 2006 to October 2009: PRIDE Group Coordinator at the European Bioinformatics Institute (EBI), European Molecular Biology Laboratory (EMBL) outstation, Hinxton, Cambridge, United Kingdom.
- October 2002 to July 2006: Research Assistant of the Fund for Scientific Research, Flanders, Belgium (FWO Vlaanderen).
- March 2002 to October 2002: Predoctoral researcher of the Flanders Interuniversitary Institute for Biotechnology (VIB).
- September 2000 to February 2002: Developer at Sydney-Tristar DC, Hasselt, Belgium; J2EE (Java 2 Enterprise Edition) architecture, design and development: component-based development (EJBs – Enterprise JavaBeans) in a distributed (multitiered) environment.

TEACHING

Professional courses

- Java 2, Sydney-Tristar DC, Hasselt, Belgium
- Enterprise Java Beans & J2EE, Sydney-Tristar DC, Hasselt, Belgium
- A complete overview of the J2EE framework: introduction, JDBC, EJB, .Net and application servers, I.T. Works, Ghent, Belgium.
- Several custom-built, on-site Java, object-orientation and J2EE courses for (a.o.) Securex (Brussels, Belgium), Associated Weavers (Kortrijk, Belgium), ANWB (The Hague, The Netherlands), Telenet (Mechelen, Belgium), and Johnson & Johnson Belgium (Beerse, Belgium).

Online courses

- YouTube lecture series on Mass Spectrometry Basics: http://tinyurl.com/msbasics
- YouTube lecture on Proteomics Informatics: www.youtube.com/watch?v=ZgwNWRuI98o

University courses at Ghent University

- Responsible lecturer, Scientific Literature and Public Databases, 1st Bachelor Biomedical Sciences, Ghent University, Belgium (2015-2020).
- Responsible lecturer, Metabolism, 3rd Bachelor Biomedical Sciences, Ghent University, Belgium (2010-present).
- Responsible lecturer, Bio-informatics, 3rd Bachelor Biomedical Sciences, Ghent University, Belgium (2010-present).
- Lecturer, Specialised Bioinformatics, 1st Master Biomedical Sciences, Ghent University, Belgium (responsible lecturer: 2013-2016; co-lecturer: 2017-present).
- Responsible lecturer, Major in Systems Biology, 1st and 2nd Master Biomedical Sciences, Ghent University, Belgium (2011-present).
- Lecturer, Systems Biology, 2nd Master Biomedical Sciences, 2nd Master Biomedical Sciences, Ghent University, Belgium (responsible lecturer: 2014-2020; co-lecturer: 2021-present).

PUBLICATIONS

H-index of 72, i-10 index of 241, 23466 citations, 9693 since 2019.

Note that I frequently allow my postdocs to take the senior author position(s).

Google Scholar link: https://scholar.google.com/citations?user=B5fWD38AAAAJ
PubMed link: https://pubmed.ncbi.nlm.nih.gov/?term=Lennart+Martens&sort=date

1. Gevaert K, Demol H, **Martens L**, Hoorelbeke B, Puype M, Goethals M, Van Damme J, De Boeck S and Vandekerckhove J (2001), 'Protein identification based on matrix-assisted laser desorption/ionization-post-source decay-mass spectrometry', *Electrophoresis* **22**, 1645-1651 (IF: 4.282).
2. Gevaert K, Van Damme J, Goethals M, Thomas GR, Hoorelbeke B, Demol H, **Martens L**, Puype M, Staes A and Vandekerckhove J (2002), 'Chromatographic isolation of methionine-containing peptides for gel-free proteome analysis – Identification of more than 800 Escherichia coli proteins', *Mol. Cell. Proteomics* **1**, 896-903 (IF: 8.316).
3. Gevaert K, Goethals M, **Martens L**, Van Damme J, Staes A, Thomas GR and Vandekerckhove J (2003), 'Exploring proteomes and analyzing protein processing by mass spectrometric identification of sorted N-terminal peptides', *Nat. Biotechnol.* **21**, 566-569 (IF: 11.310).
4. Vandekerckhove J, Van Damme J, **Martens L**, Thomas G, Staes A, Goethals M, et al. (2003), IL-29 'Is proteomics heading towards medicine?', *Pigment Cell Research*. 2003;16(5):586–586 (IF: 2.919).
5. Gevaert K, Ghesquière B, Staes A, **Martens L**, Van Damme J, Thomas GR and Vandekerckhove J (2004), 'Reversible labeling of cysteine-containing peptides allows their chromatographic isolation for non-gel proteome studies', *Proteomics* **4**, 897-908 (IF: 5.766).
6. Staes A, Demol H, Van Damme J, **Martens L**, Vandekerckhove J and Gevaert K (2004), 'Global differential non-gel proteomics by quantitative and stable labeling of tryptic peptides with oxygen-18', *J. Proteome Res.*, **3**, 786- 791 (IF: 6.917).
7. **Martens L,** Van Damme P, Van Damme J, Staes A, Timmerman E, Ghesquière B, Thomas GR, Vandekerckhove J and Gevaert K (2005), 'The human platelet proteome mapped by peptide-centric proteomics: a functional protein profile', *Proteomics*, **5**, 3193-3204 (IF: 6.088).
8. Gevaert K, Van Damme P, **Martens L** and Vandekerckhove J (2005), 'Diagonal reverse-phase chromatography applications in peptide-centric proteomics; ahead of catalogue-omics?', *Anal. Biochem.*, **345**, 18-29 (IF: 2.370).
9. Adamski M, Blackwell T, Menon R, **Martens L**, Hermjakob H, Taylor C, Omenn GS and States DJ (2005), 'Data Management in the Pilot Phase of the HUPO Plasma Proteome Project', *Proteomics*, **5**, 3246-3261 (IF: 6.088).
10. **Martens L**, Nesvizhskii AI, Hermjakob H, Adamski M, Omenn GS, Vandekerckhove J and Gevaert K (2005), 'Do we want our data raw? Including binary mass-spectrometry data in public proteomics data repositories', *Proteomics*, **5**, 3501-3505 (IF: 6.088).
11. **Martens L**, Hermjakob H, Jones P, Adamski M, Taylor C, States D, Gevaert K, Vandekerckhove J and Apweiler R (2005), 'PRIDE: The PRoteomics IDEntifications database', *Proteomics*, **5**, 3537-3545 (IF: 6.088).
12. Gevaert K, Staes A, Van Damme J, De Groot S, Hugelier K, Demol H, **Martens L**, Goethals M and Vandekerckhove J (2005), 'Global phosphoproteome analysis on human HepG2 hepatocytes using reversed-phase diagonal LC', *Proteomics*, **5**, 3589-3599 (IF: 6.088).
13. **Martens L**, Vandekerckhove J and Gevaert K (2005), 'DBToolkit: processing

sequence databases for enhanced peptide identification in peptide-centric proteome analyses', *Bioinformatics*, **21**, 3584-3585 (IF: 6.019).

14. Stephan C, Hamacher M, Bluggel M, Korting G, Chamrad D, Scheer C, Marcus K, Reidegeld KA, Lohaus C, Schafer H, **Martens L**, Jones P, Muller M, Auyeung K, Taylor C, Binz PA, Thiele H, Parkinson D, Meyer HE and Apweiler R (2005), '5(th) HUPO BPP Bioinformatics Meeting at the European Bioinformatics Institute in Hinxton, UK - Setting the Analysis Frame', *Proteomics*, **5**, 3560-3562 (IF: 6.088).
15. Van Damme P, **Martens L**, Van Damme J, Hugelier K, Staes A, Vandekerckhove J and Gevaert K (2005), 'Caspase-specific and nonspecific *in vivo* protein processing during Fas-induced apoptosis', *Nature Methods*, **2**, 771-777 (IF: 6.741).
16. Jones P, Côté RG, **Martens L**, Quinn AF, Taylor CF, Derache W, Hermjakob H and Apweiler R (2006), 'PRIDE: A Public Repository of Protein and Peptide Identifications for the Proteomics Community', *Nucleic Acids Res.*, **34** (database issue), D659-D663 (IF: 6.317).
17. Reidegeld KA, Hamacher M, Meyer HE, Stephan C, Blüggel M, Körting G, Chamrad D, Scheer C, Thiele H, Taylor C, Müller M, Apweiler R, Jones P and **Martens L** (2006), 'The HUPO Brain Proteome Project', *European Pharmaceutical Review*, **1**, 33-38.
18. **Martens L**, Flikka K, Gevaert K, Vandekerckhove J and Eidhammer I (2006), 'Improving the Reliability and Throughput of Mass Spectrometry Based Proteomics by Spectrum Quality Filtering', *Proteomics*, **6**, 2086-2094 (IF: 5.735).
19. Hamacher M, Stephan C, Bluggel M, Chamrad D, Korting G, **Martens L**, Muller M, Hermjakob H, Parkinson D, Dowsey A, Reidegeld KA, Marcus K, Dunn MJ, Meyer HE and Apweiler R (2006), 'The HUPO Brain Proteome Project Jamboree: Centralised summary of the pilot studies', *Proteomics*, **6**, 1719-1721 (IF: 5.735).
20. Gevaert K, Pinxteren J, Demol H, Hugelier K, Staes A, Van Damme J, **Martens L** and Vandekerckhove J (2006), 'Four Stage Liquid Chromatographic Selection of Methionyl Peptides for Peptide-Centric Proteome Analysis: The Proteome of Human Multipotent Adult Progenitor Cells', *Journal of Proteome Research*, **5**, 1415-1428 (IF: 5.151).
21. **Martens L**, Monsieur G, Ampe C, Gevaert K and Vandekerckhove J (2006), 'Cell_motility: a cross-platform, open source application for the study of cell motion paths', *BMC Bioinformatics*, **7**, 289 (IF: 3.617).
22. Ghesquière B, Van Damme J, **Martens L**, Vandekerckhove J and Gevaert K (2006) 'Proteome-wide characterization of N-glycosylation events by diagonal chromatography', *Journal of Proteome Research*, **5**, 2438-2447 (IF: 5.151).
23. Hamacher M, Apweiler R, Arnold G, Becker A, Blüggel M, Carrette O, Colvis C, Dunn MJ, Fröhlich T, Fountoulakis M, van Hall A, Herberg F, Ji J, Kretzschmar H, Lewczuk P, Lubec G, Marcus K, **Martens L**, Palacios Bustamante N, Park YM, Pennington SR, Robben J, Stühler K, Reidegeld KA, Riederer P, Rossier J, Sanchez JC, Schrader M, Stephan C, Tagle D, Thiele H, Wang J, Wiltfang J, Yoo JS, Zhang C, Klose J and Meyer HE (2006) 'HUPO Brain Proteome Project: Summary of the pilot phase and introduction of a comprehensive data reprocessing strategy', *Proteomics*, **6**, 4890-4898 (IF: 5.735).
24. Reidegeld KA, Müller M, Stephan C, Blüggel M, Hamacher M, **Martens L**, Körting G, Chamrad D, Parkinson D, Apweiler R, Meyer HE and Marcus K (2006) 'The Power of Cooperative Investigation: Summary and Comparison of the HUPO Brain Proteome Project Pilot Studies Results', *Proteomics*, **6**, 4997-5014 (IF: 5.735).
25. Stephan C, Reidegeld KA, Hamacher M, van Hall A, Marcus K, Taylor C, Jones P, Müller M, Apweiler R, **Martens L**, Körting G, Chamrad DC, Thiele H, Blüggel M, Parkinson D, Binz PA, Lyall A and Meyer HE (2006) 'Automated reprocessing pipeline for searching heterogeneous mass spectrometric data of the HUPO Brain Proteome Project pilot phase', *Proteomics*, **6**, 5015-5029 (IF: 5.735).
26. Mueller M, **Martens L**, Reidegeld KA, Hamacher M, Stephan C, Blüggel M, Körting G, Chamrad D, Scheer C, Marcus K, Meyer HE and Apweiler R (2006) 'Functional

annotation of proteins identified in human brain samples during the HUPO Brain Proteome Project pilot study', *Proteomics*, **6**, 5059-5075 (IF: 5.735).

27. **Martens L**, Mueller M, Stephan C, Hamacher M, Reidegeld KA, Meyer HA, Blüggel M, Vandekerckhove J, Gevaert K and Apweiler R (2006) 'A comparison of the HUPO Brain Proteome Project pilot with other proteomics studies', *Proteomics*, **6**, 5076-5086 (IF: 5.735).
28. Hanoulle X, Van Damme J, Staes A, **Martens L**, Goethals M, Vandekerckhove J and Gevaert K (2006) 'A new functional, chemical proteomics technology to identify purine nucleotide binding sites in complex proteomes', *Journal of Proteome Research*, **5**, 3438-3445 (IF: 5.735).
29. **Martens L**, Helsens K, Vandekerckhove J and Gevaert K (2007) 'MascotDatfile: an open-source library to fully parse and analyze Mascot MS/MS search results', *Proteomics*, **7**, 364-366 (IF: 5.479).
30. Hamacher M, Stephan C, Eisenacher M, van Hall A, Marcus K, **Martens L**, Park YM, Gutstein HB, Herberg F and Meyer HE (2007) 'Proteomics for everyday use: Activities of the HUPO Brain Proteome Project during the 5(th) HUPO World Congress', *Proteomics*, **7**, 1012-1015 (IF: 5.479).
31. **Martens L**, Mueller M and Apweiler R (2007) 'Annotating the human proteome: Beyond establishing a parts list', *Biochimica Et Biophysica Acta - Proteins And Proteomics*, **1774**, 175-191 (IF: 3.078).
32. Aivaliotis M, Gevaert K, Falb M, Tebbe A, Konstantinidis K, Bisle B, Klein C, **Martens L**, Staes A, Timmerman E, Van Damme J, Siedler F, Pfeiffer F, Vandekerckhove J and Oesterhelt D (2007) 'Large scale identification of N-terminal peptides in the halophilic archaea Halobacterium salinarum and Natronomonas pharaonis', *Journal of Proteome Research*, **6**, 2195-2204 (IF: 5.675).
33. **Martens L**, Vizcaíno JA, Hermjakob H, Julian RK and Paton NW (2007) 'The PSI formal document process and its implementation on the PSI website', *Proteomics*, **7**, 2355-2357 (IF: 5.479).
34. Hamacher M, Stephan C, Eisenacher M, Lewczuk P, Wiltfang J, **Martens L**, Vizcaíno JA, Kwon KH, Yoo JS, Park YM, Beckers J, Horsch M, de Angelis MH, Cho ZH, Apweiler R and Meyer HE (2007) 'High Performance Proteomics: 7(th) HUPO Brain Proteome Project Workshop', *Proteomics*, **7**, 2490-2496 (IF: 5.479).
35. Gevaert K, Van Damme P, Ghesquière B, Impens F, **Martens L**, Helsens K and Vandekerckhove J (2007) 'A la carte proteomics with an emphasis on gel-free techniques', *Proteomics*, **7**, 2698-2718 (IF: 5.479).
36. **Martens L** and Hermjakob H (2007) 'Proteomics data validation: why all must provide data', *Molecular BioSystems,* **3**, 518-522 (IF: 4.121).
37. Eisenacher M, Hardt T, Hamacher M, **Martens L**, Hakkinen J, Levander F, Apweiler R, Meyer HE and Stephan C (2007) 'The 1(st) ProDaC workshop 26 April 2007 Ecole Normale Superieur, Lyon, France', *Proteomics*, **7**, 3034-3037 (IF: 5.479).
38. Taylor CF, Paton NW, Lilley KS, Binz PA, Julian RK Jr, Jones AR, Zhu W, Apweiler R, Aebersold R, Deutsch EW, Dunn MJ, Heck AJ, Leitner A, Macht M, Mann M, **Martens L**, Neubert TA, Patterson SD, Ping P, Seymour SL, Souda P, Tsugita A, Vandekerckhove J, Vondriska TM, Whitelegge JP, Wilkins MR, Xenarios I, Yates JR 3rd and Hermjakob H (2007) 'The minimum information about a proteomics experiment (MIAPE)', *Nature Biotechnology*, **25**, 887-893 (IF: 22.848).
39. Flikka K, Meukens J, Helsens K, Vandekerckhove J, Eidhammer I, Gevaert K and **Martens L** (2007) 'Implementation and application of a versatile clustering tool for tandem mass spectrometry data', *Proteomics*, **7**, 3245-3258 (IF: 5.479).
40. **Martens L**, Orchard S, Apweiler R and Hermjakob H (2007) 'Human Proteome Organization Proteomics Standards Initiative: Data Standardization, a View on Developments and Policy', *Molecular & Cellular Proteomics*, **6**, 1666-1667 (IF: 9.425).
41. Côté RG, Jones P, **Martens L**, Kerrien S, Reisinger F, Lin Q, Leinonen R, Apweiler R

and Hermjakob H (2007), ‘The Protein Identifier Cross-Referencing (PICR) service: reconciling protein identifiers across multiple source databases’, *BMC Bioinformatics*, **8**, 401 (IF: 3.493).

42. Mueller M, Vizcaíno JA, Jones P, Côté R, Thorneycroft D, Apweiler R, Hermjakob H and **Martens L** (2008), ‘Analysis of the experimental detection of central nervous system related genes in human brain and cerebrospinal fluid datasets’, *Proteomics*, **8**, 1138-1148 (IF: 5.479).
43. Eisenacher M, Hardt T, Hamacher M, **Martens L**, Häkkinen J, Levander F, Apweiler R, Meyer HE and Stephan C (2008) ‘Proteomics Data Collection - 2nd ProDaC Workshop 5 October 2007, Seoul, South Korea.’ *Proteomics* **8**, 1326-1330 (IF: 5.479).
44. **Martens L**, Klie S, Vizcaíno JA, Côté R, Jones P, Apweiler R, Hinneburg A and Hermjakob H (2008) ‘Analyzing large-scale proteomics projects with latent semantic indexing’, *Journal of Proteome Research*, **7**, 182-191 (IF: 5.684).
45. Jones P, Côté R, Cho SY, Klie S, **Martens L**, Quinn A, Thorneycroft D and Hermjakob H (2008) 'PRIDE: New Developments and New Datasets', *Nucleic Acids Research* **36** (database issue), D878-D883 (IF: 6.878).
46. Orchard S, **Martens L**, Tasman J, Binz PA, Albar JP and Hermjakob H (2008) ‘6th HUPO Annual World Congress - Proteomics Standards Initiative Workshop 6-10 October 2007, Seoul, South Korea.’ *Proteomics* **8**, 1331-1333 (IF: 4.586).
47. Mathivanan S, Ahmed M, Ahn NG, Alexandre H, Amanchy R, Andrews PC, …, Mann M, **Martens L**, Martinez-Heredia J, … and Pandey A (2008) 'Human Proteinpedia enables sharing of human protein data.', *Nature Biotech.*, **26**, 164-167 (IF: 22.297).
48. Hamacher M, Eisenacher M, Tribl F, Stephan C, Marcus K, Hardt T, Wiltfang J, **Martens L**, Desiderio D, Gutstein H, Park YM and Meyer HE (2008) 'The HUPO Brain Proteome project wish list.' *Proteomics* **8**, 2160-2164 (IF: 4.586).
49. **Martens L**, Tharakan R, Van Eyk J and Graham D (2008) ‘OMSSAGUI: an open-source user interface component to configure and run the OMSSA search engine.’, *Proteomics* **8**, 2376-2378 (IF: 4.586).
50. Côté RG, Jones P, **Martens L**, Apweiler R and Hermjakob H (2008) 'The Ontology Lookup Service: more data and better tools for controlled vocabulary queries', *Nucleic Acids Research* **36**, W25-W29 (IF: 6.878).
51. Eisenacher M, Hardt T, **Martens L**, Häkkinen J, Apweiler R, Hamacher M, Meyer HE and Stephan C (2008) ‘Proteomics Data Collection - 3rd ProDaC Workshop April 22nd 2008, Toledo, Spain.’, *Proteomics* **8**, 4163-4167 (IF: 4.586).
52. Helsens K, Timmerman E, Vandekerckhove J, Gevaert K and **Martens L** (2008) 'Peptizer: a tool for assessing false positive peptide identifications and manually validating selected results', *Molecular & Cellular Proteomics* **7**, 2364-2372. (IF: 8.834).
53. Eisenacher M, Kohl M, **Martens L**, Barsnes H, Hardt T, Levander F, Häkkinen J, Apweiler R, Meyer HE, Stephan C (2009) ‘Proteomics data collection--4th ProDaC workshop 15 August 2008, Amsterdam, The Netherlands.’, *Proteomics* **9**, 218-222 (IF: 4.426).
54. Vizcaíno JA, Mueller M, Hermjakob H and **Martens L** (2009) ‘Charting online OMICS resources: a navigational chart for clinical researchers’, *Proteomics Clinical Applications* **3**, 18–29 (IF: 1.875).
55. Taylor CF and **Martens L** (2009) ‘Progress by the Proteomics Standards Initiative’, *European Pharmaceutical Review* **1/09**, 33-37 (IF: *N/A*).
56. **Martens L**, Eisenacher M, Hardt T, Kohl M, Barsnes H, Helsens K, Häkkinen J, Levander F, Aebersold R, Vandekerckhove J, Dunn MJ, Lisacek F, Siepen JA, Hubbard SJ, Binz PA, Blüggel M Thiele H, Cottrell J, Meyer HE, Apweiler R and Stephan C (2009) ‘Getting a Grip on Proteomics Data – Proteomics Data Collection (ProDaC)’, *Proteomics*, **9**, 1-6 (IF: 4.426).
57. Barsnes H, Huber S, Sickmann A, Eidhammer I and **Martens L** (2009) ‘OMSSA Parser: An open-source library to parse and extract data from OMSSA MS/MS search

results', *Proteomics*, **9**, 3772-3774 (IF: 4.426).

58. Bell AW, Deutsch EW, Au CE, Kearney RE, Beavis R, Sechi S, Nilsson T, Bergeron JJM, **Martens L** and the HUPO Test Sample Working Group (2009), 'A HUPO test sample study reveals common problems in mass spectrometry–based proteomics', *Nature Methods*, **6**, 423 - 430 (IF: 16.874).
59. Eisenacher M, **Martens L**, Barsnes H, Hardt T, Kohl M, Häkkinen J, Apweiler R, Meyer HE and Stephan C (2009) "Proteomics Data Collection - 5th ProDaC Workshop: 4 March 2009, Kolympari, Crete, Greece.", *Proteomics*, **9**, 3626-3629 (IF: 4.426).
60. Barsnes H, Vizcaíno JA, Eidhammer I and **Martens L** (2009), 'PRIDE Converter: Making Proteomics Data Sharing Easy', *Nature Biotechnology*, **27**, 598-599 (IF: 29.495).
61. Vizcaíno JA, Côté R, Reisinger F, Foster J, Mueller M, Rameseder J, Hermjakob H and **Martens L** (2009), 'A guide to the PRIDE proteomics data repository', *Proteomics*, **9**, 4276-4283 (IF: 4.426).
62. Reisinger F and **Martens L** (2009), 'Database on Demand – an online tool for the custom generation of FASTA formatted sequence databases', *Proteomics*, **9**, 4421-4424 (IF: 4.426).
63. Montecchi-Palazzi L, Kerrien S, Reisinger F, Aranda B, Jones AR, **Martens L** and Hermjakob H (2009), 'The PSI semantic validator: A framework to check MIAPE compliance of proteomics data', *Proteomics*, **9**, 5112-5119 (IF: 4.426).
64. Muth T, Keller D, Puetz SM, **Martens L**, Sickmann A and Boehm AM (2009), 'jTraqX: a free, platform independent tool for isobaric tag quantitation at the protein level', *Proteomics*, **10**, 1223-1225 (IF: 4.426).
65. Kim YH, Marcus K, Grinberg LT, Goehler H, Wiltfang J, Stephan C, Eisenacher M, Hardt T, **Martens L**, Dunn MJ, Park YM and Meyer HE (2009) 'Toward a Successful Clinical Neuroproteomics', *Proteomics Clinical Applications*, **3**, 1012-1016 (IF: 1.875).
66. Colaert N, Helsens K, **Martens L**, Vandekerckhove J and Gevaert K (2009), 'Improved visualization of protein consensus sequences by iceLogo', *Nature Methods*, **6**, 786-787 (IF: 16.874).
67. Vizcaíno JA, Côté R, Reisinger F, Barsnes H, Foster J, Rameseder J, Hermjakob H and **Martens L** (2010), 'The Proteomics Identifications (PRIDE) database: 2010 update', *Nucleic Acids Research*, **38** (database issue), D736-D742 (IF: 7.836).
68. Helsens K, Colaert N, Barsnes H, Muth T, Flikka K, Staes A, Timmerman E, Wortelkamp S, Sickmann A, Vandekerckhove J, Gevaert K and **Martens L** (2010), 'ms_lims, a simple yet powerful open source LIMS for mass spectrometry-driven proteomics', *Proteomics*, **10**, 1261-1264 (IF: 4.426).
69. Vaudel M, Sickmann A and **Martens L** (2010), 'Peptide and Protein Quantification: a Map of the Minefield', *Proteomics*, **10**, 650-670 (IF: 4.815).
70. Barsnes H, Eidhammer I and **Martens L** (2010), 'FragmentationAnalyzer: An open-source tool to analyze MS/MS fragmentation data', *Proteomics*, **10**, 1087-1090 (IF: 4.815).
71. Muth T, Vaudel M, Barsnes H, **Martens L** and Sickmann A (2010), 'XTandem Parser: An open-source library to parse and analyse X!Tandem MS/MS search results', *Proteomics*, **10**, 1522-1524 (IF: 4.815).
72. Côté RG, Reisinger F and **Martens L** (2010), 'jmzML, an open-source Java API for mzML, the PSI standard for mass spectrometry data', *Proteomics*, **10**, 1332-1335 (IF: 4.815).
73. Barsnes H, Côté RG, Eidhammer I and **Martens L** (2010), 'OLS Dialog: an open-source front end to the Ontology Lookup Service', *BMC Bioinformatics*, **11**, 34 (IF: 3.028).
74. Côté R, Reisinger F, **Martens L**, Barsnes H, Vizcaino JA, Hermjakob H (2010), 'The Ontology Lookup Service: Bigger and Better.', *Nucleic Acids Research*, **38**, W155-W160 (IF: 7.836).

75. **Martens L** (2010), ‘A report on the ESF workshop on quality control in proteomics’, *Molecular BioSystems*, **6**, 935-938 (IF: 3.825).
76. Vizcaíno JA, Foster JM and **Martens L** (2010), 'Proteomics data repositories: providing a safe haven for your data and acting as a springboard for further research', *Journal of Proteomics*, **78**, 2136-2146 (IF: 5.074).
77. **Martens L**, Chambers M, Sturm M, Kessner D, Levander F, Shofstahl J, Tang WH, Rompp A, Neumann S, Pizarro AD, Montecchi-Palazzi L, Tasman N, Coleman M, Reisinger F, Souda P, Hermjakob H, Binz PA and Deutsch EW (2011), 'mzML - a Community Standard for Mass Spectrometry Data', *Molecular & Cellular Proteomics*, **10**, R110.000133 (IF: 7.398).
78. **Martens L**, Vizcaíno JA and Banks R (2011) 'Quality control in proteomics', *Proteomics*, **11**, 1015-1016 (IF: 4.505).
79. Colaert N, Vandekerckhove J, Gevaert K and **Martens L** (2011) 'A comparison of MS2 based label-free quantitative proteomics techniques with regards to accuracy and precision.', *Proteomics*, **11**, 1110-1113 (IF: 4.505).
80. Barsnes H, Eidhammer I and **Martens L** (2011), 'A global analysis of peptide fragmentation variability', *Proteomics*, **11**, 1181-1188 (IF: 4.505).
81. Vaudel M, Barsnes H, Berven F, Sickmann A and **Martens L** (2011), 'SearchGUI: An open-source graphical user interface for simultaneous OMSSA and X!Tandem searches', *Proteomics*, **11**, 996-999 (IF: 4.505).
82. Burkhart JM, Vaudel M, Zahedi RP, **Martens L** and Sickmann A (2011), 'iTRAQ protein quantification: a quality controlled workflow', *Proteomics*, **11**, 1125-1134 (IF: 4.505).
83. Degroeve S, Colaert N, Vandekerckhove J, Gevaert K and **Martens L** (2011), 'Quantifying the differences between MS/MS peak intensity normalization methods', *Proteomics*, **11**, 1172-1180 (IF: 4.505).
84. Barsnes H, Vaudel M, Colaert N, Helsens K, Sickmann A, Berven FS and **Martens L** (2011), 'compomics-utilities: an open-source Java library for computational proteomics', *BMC Bioinformatics*, **12**, 70 (IF: 2.751).
85. Abrahams JP, Apweiler R, Balling R, Bertero MG, Bujnicki JM, Chayen NE, Chène P, Corthals GL, Dyląg T, Förster F, Heck AJ, Henderson PJ, Herwig R, Jehenson P, Kokalj SJ, Laue E, Legrain P, **Martens L**, Migliorini C, Musacchio A, Podobnik M, Schertler GF, Schreiber G, Sixma TK, Smit AB, Stuart D, Svergun DI and Taussig MJ (2011), ‘4D Biology for health and disease workshop report’, *N Biotechnol.*, **28**, 291-293 (IF: 2.756)
86. Vaudel M, Burkhart JM, Sickmann A, **Martens L** and Zahedi RP (2011), 'Peptide Identification Quality Control', *Proteomics*, **11**, 2105-2114 (IF: 4.505).
87. Foster JM, Degroeve S, Gatto L, Visser M, Wang R, Griss J, Apweiler R and **Martens L** (2011), ‘A posteriori quality control for the curation and reuse of public proteomics data’, *Proteomics*, **11**, 2182-2194 (IF: 4.505).
88. Colaert N, Van Huele C, Degroeve S, Staes A, Vandekerckhove J, Gevaert K and **Martens L** (2011), 'Combining quantitative proteomics data processing workflows for greater sensitivity', *Nature Methods*, **8**, 481–483 (IF: 19.276).
89. Colaert N, Gevaert K and **Martens L** (2011), 'RIBAR and xRIBAR: methods for reproducible relative MS/MS based label-free protein quantification', *Journal of Proteome Research*, **10**, 3183-3189 (IF: 5.113).
90. Helsens K, Van Damme P, Degroeve S, **Martens L**, Arnesen T, Vandekerckhove J and Gevaert K (2011), 'Bioinformatics analysis of a Saccharomyces cerevisiae N-terminal proteome provides evidence of alternative translation initiation and post-translational N-terminal acetylation', *Journal of Proteome Research*, **10**, 3578-3589 (IF: 5.113).
91. Colaert N, Barsnes H, Vaudel M, Helsens K, Timmerman E, Sickmann A, Gevaert K and **Martens L** (2011), 'Thermo-msf-parser: an open source Java library to parse and

visualize Thermo Proteome Discoverer msf files', *Journal of Proteome Research*, **10**, 3840-3843 (IF: 5.113).

92. Helsens K, Brusniak MY, Deutsch E, Moritz RL and **Martens L** (2011), 'jTraML: An open source java API for TraML, the PSI standard for sharing SRM transitions', *Journal of Proteome Research*, **10**, 5260-5263 (IF: 5.113).
93. Colaert N, Degroeve S, Helsens K and **Martens L** (2011), 'An analysis of the resolution limitations of peptide identification algorithms', *Journal of Proteome Research*, **10**, 5555-5561 (IF: 5.113).
94. Deutsch EW, Chambers M, Neumann S, Levander F, Binz PA, Shofstahl J, Campbell DS, Mendoza L, Ovelleiro D, Helsens K, **Martens L**, Aebersold R, Moritz RL and Brusniak MY (2011) 'TraML: a standard format for exchange of selected reaction monitoring transition lists' *Molecular & Cellular Proteomics*, **10**, R111.015040 (IF: 7.398).
95. Jones AM, Aebersold R, Ahrens CH, Apweiler R, Baerenfaller K, Baker M, Bendixen E, Briggs S, Brownridge P, Brunner E, Daube M, Deutsch EW, Grossniklaus U, Heazlewood J, Hengartner MO, Hermjakob H, Jovanovic M, Lawless C, Lochnit G, **Martens L**, Ravnsborg C, Schrimpf SP, Shim YH, Subasic D, Tholey A, van Wijk K, von Mering C, Weiss M and Zheng X (2012) 'The HUPO initiative on Model Organism Proteomes, iMOP.', *Proteomics*, **12**, 340-345 (IF: 4.505).
96. Helsens K and **Martens L** (2012) ‘Enabling computational proteomics by public and local data management systems’, *Circulation: Cardiovascular Genetics*, **5**, 266 (IF: 6.105).
97. Wang R, Fabregat A, Ríos D, Ovelleiro D, Foster JM, Côté RG, Griss J, Csordas A, Pérez-Riverol Y, Reisinger F, Hermjakob H, **Martens L** and Vizcaíno JA (2012) ‘PRIDE Inspector: a tool to visualize and validate MS proteomics data’, *Nature Biotechnology*, **30**, 135-137 (IF: 32.438).
98. Moruz L, Staes A, Foster J, Hatzou M, Timmerman E, **Martens L** and Käll L (2012) 'Chromatographic Retention Time Prediction for Post-translationally Modified Peptides', *Proteomics*, **12**, 1151-1159 (IF: 4.505).
99. Helsens K, Mueller M, Hulstaert N and **Martens L** (2012) 'Sigpep: calculating unique peptide signature transition sets in a complete proteome background', *Proteomics*, **12**, 1142-1146 (IF: 4.505).
100. Degroeve S, Staes A, De Bock PJ and **Martens L** (2012) ‘The effect of peptide identification search algorithms on MS2-based label-free protein quantification’, *OMICS*, **16**, 443-448 (IF: 2.441).
101. Gonnelli G, Hulstaert N, Degroeve S and **Martens L** (2012) ‘Towards a human proteomics atlas’, *Analytical and Bioanalytical Chemistry*, 4, 1069-1077 (IF: 3.778).
102. Vaudel M, Burkhart JM, Daniela B, Zahedi RP, Sickmann A and **Martens L** (2012) ‘A complex standard for protein identification, designed by evolution’, *Journal of Proteome Research*, **11**, 5065-5071 (IF: 5.113).
103. Burkhart JM, Vaudel M, Gambaryan S, Radau S, Walter U, **Martens L**, Geiger J, Sickmann A, Zahedi RP (2012) 'The first comprehensive and quantitative analysis of human platelet protein composition allows the comparative analysis of structural and functional pathways', *Blood*, **120**, e73-e82 (IF: 9.898).
104. Vaudel M, Sickmann A and **Martens L** (2012) ‘Current methods for global proteome identification’, *Expert Review in Proteomics*, **9**, 519-532 (IF: 3.685).
105. Vaudel M, Burkhart JM, Radau S, Zahedi RP, **Martens L** and Sickmann A (2012) 'Integral Quantification Accuracy estimation for Reporter Ion based quantitative proteomics (iQuARI)', *Journal of Proteome Research*, **11**, 5072-5080 (IF: 5.113).
106. Côté RG, Griss J, Dianes JA, Wang R, Wright JC, van den Toorn HWP, van Breukelen B, Hulstaert N, **Martens L**, Reisinger F, Csordas A, Ovelleiro D, Perez-Rivevol Y, Barsnes H, Hermjakob H and Vizcaíno JA (2012) ‘The PRIDE Converter 2 Framework: An Improved Suite of Tools to Facilitate Data Submission to the PRIDE Database and

the ProteomeXchange Consortium', *Molecular & Cellular Proteomics*, **11**, 1682-1689 (IF: 7.398).

107. Vandermarliere E and **Martens L** (2013) 'Protein structure as a means to triage proposed post-translational modification sites', *Proteomics*, **13**, 1028-1035 (IF: 3.973).
108. Volders P-J, Helsens K, Wang X, **Martens L**, Gevaert K, Vandesompele J and Mestdagh P (2013) 'lncipedia: a database for annotated human lncRNA transcript sequences and structures', *Nucleic Acids Research*, **41**, D246-D251 (IF: 8.808).
109. Colaert N, Maddelein D, Impens F, Van Damme P, Plasman K, Helsens K, Hulstaert N, Vandekerckhove J, Gevaert K and **Martens L** (2013) 'The Online Protein Processing Resource (TOPPR): a database and analysis platform for protein processing events', *Nucleic Acids Research*, **41**, D333-D337 (IF: 8.808).
110. Muth T, Benndorf D, Reichl U, Rapp E and **Martens L** (2013) 'Searching for a needle in a stack of needles: challenges in metaproteomics data analysis', *Molecular BioSystems*, **9**, 578-585 (IF: 3.183).
111. Vaudel M, Breiter D, Beck F, Rahnenführer J, **Martens L** and Zahedi RP (2013) 'D-score: a search engine independent MD-score', *Proteomics*, **13**, 1036-1041 (IF: 3.973).
112. Muth T, Peters J, Blackburn J, Rapp E and **Martens L** (2013) 'ProteoCloud: a full-featured open source proteomics cloud computing pipeline', *Journal of Proteomics*, **88**, 104-108 (IF: 3.929).
113. Barsnes H and **Martens L** (2013) 'Crowdsourcing in proteomics: public resources lead to better experiments', *Amino Acids*, **44**, 1129-1137 (IF: 3.653).
114. Perez-Riverol Y, Hermjakob H, Kohlbacher O, **Martens L**, Creasy D, Cox J, Leprevost F, Shan BP, Pérez-Nueno VI, Blazejczyk M, Punta M, Vierlinger K, Valiente P, Leon K, Chinea G, Guirola O, Bringas R, Cabrera G, Guillen G, Padron G, Gonzalez LJ, Besada V (2013) 'Computational Proteomics Pitfalls and Challenges: HavanaBioinfo 2012 Workshop Report', *Journal of Proteomics*, **87**, 134-138 (IF: 3.929).
115. Vandermarliere E, Mueller M, and **Martens L** (2013) 'Getting intimate with trypsin, the leading protease in proteomics', *Mass Spectrometry Reviews*, **32**, 453-465 (IF: 8.053).
116. Fannes T, Vandermarliere E, Schietgat L, Degroeve S, **Martens L** and Ramon J (2013) 'Predicting tryptic cleavage from proteomics data using decision tree ensembles', *Journal of Proteome Research*, **12**, 2253-2259 (IF: 5.001).
117. **Martens L** (2013) 'Bringing proteomics into the clinic: the need for the field to finally take itself seriously', *Proteomics - Clinical Applications*, **7**, 388-391(IF: 2.683).
118. **Martens L** (2013) 'Resilience in the proteomics data ecosystem: how the field cares for its data', *Proteomics*, **13**, 1548-1550 (IF: 3.973).
119. Hulstaert N, Reisinger F, Rameseder J, Barsnes H, Vizcaíno JA and **Martens L** (2013) 'pride-asap: automatic fragment ion annotation of identified PRIDE spectra', *Journal of Proteomics*, **95**, 89-92 (IF: 3.929).
120. Tanco S, Lorenzo J, Garcia-Pardo J, Degroeve S, **Martens L**, Aviles FX, Gevaert K and Van Damme P (2013) 'Proteome-derived peptide libraries to study the substrate specificity profiles of carboxypeptidases', *Molecular & Cellular Proteomics*, **12**, 2096-2110 (IF: 7.254).
121. Kolker E, Altintas I, Bourne P, Faris J, Fox G, Frishman D, Geraci C, Hancock W, Lin B, Lancet D, Lisitsa A, Knight R, **Martens L**, Mesirov J, Özdemir V, Schultes E, Smith T, Snyder M, Srivastava S, Toppo S and Wilmes P (2013) 'Reproducibility: In praise of open research measures', *Nature*, **498**, 170 (IF: 42.351).
122. **Martens L** (2013) 'About Dice, Bouldering and Team Empowerment: Running the CompOmics Group at VIB and Ghent University, Belgium', *PLoS Computational Biology*, **9**, e1003332 (IF: 4.829).
123. Masuzzo P, Hulstaert N, Huyck L, Ampe C, Van Troys M and **Martens L** (2013) 'CellMissy: a tool for management, storage and analysis of cell migration data produced in wound healing-like assays', *Bioinformatics*, **29**, 2661-2663 (IF: 4.621).
124. Degroeve S and **Martens L** (2013) 'MS2PIP: a tool for MS/MS peak intensity

prediction', *Bioinformatics*, **29**, 3199-3203 (IF: 4.621).

125. De Antonellis P, Carotenuto M, De Vita G, Vandenbussche J, Medaglia C, Vandesompele J, Mestdagh P, **Martens L**, An S, Moens K, Cinalli G, Gevaert K & Zollo M (2013) "Early targets of miR-34a in neuroblastoma.", *Pediatric Blood & Cancer,* **60**, 116 (IF: 2.303).
126. Staes A, Vandenbussche J, Demol H, Goethals M, Yilmaz S, Hulstaert N, Degroeve S, Kelchtermans P, **Martens L** and Gevaert K (2013) 'Asn3, a reliable, robust and universal lock mass for improved accuracy in LC-MS and LCMS/MS', *Analytical Chemistry*, **85**, 11054-11060 (IF: 5.825).
127. Beck F, Geiger J, Gambaryan S, Veit J, Vaudel M, Nollau P, Kohlbacher O, **Martens L**, Walter U, Sickmann A, and Zahedi RP (2013) 'Time-resolved characterization of cAMP/PKA-dependant signaling reveals that platelet inhibition is a concerted process involving multiple signaling pathways', *Blood*, 123, e1-e10 (IF: 9.775).
128. Muth T, Weilnböck L, Rapp E, Huber C, **Martens L**, Vaudel M and Barsnes H (2013) 'DeNovoGUI: an open source graphical user interface for de novo sequencing of tandem mass spectra.', *Journal of Proteome Research*, **13**, 1143-1146 (IF: 5.001).
129. Stewart E, Smith T, De Souza A, Faris J, **Martens L**, Mohin S, et al. (2013) 'Delsa workshop IV: launching the Quantified Human Initiative', *Big Data*. 2013;1(3):187–90.
130. Vaudel M, Sickmann A and **Martens L** (2014) 'Introduction to Opportunities and Pitfalls in Functional Mass Spectrometry Based Proteomics', *BBA - Proteins and Proteomics*, **1844**, 12-20 (IF 3.191).
131. Verheggen K, Barsnes H and **Martens L** (2014) 'Distributed computing and data storage in proteomics: many hands make light work, and a stronger memory', *Proteomics*, **14**, 367-377 (IF: 3.973).
132. Kelchtermans P, Bittremieux W, De Grave K, Degroeve S, Ramon J, Laukens K, Valkenborg D, Barsnes H and **Martens L** (2014) 'Machine learning applications in proteomics research: how the past can boost the future.', *Proteomics*, **14**, 353-366 (IF: 3.973).
133. Vizcaíno JA, Deutsch EW, Wang R, Csordas A, Reisinger F, Ríos D, Dianes JA, Sun Z, Farrah T, Bandeira N, Binz PA, Xenarios I, Eisenacher M, Gatto L, Campos A, Chalkley RJ, Kraus HJ, Albar JP, Omenn GS, **Martens L**, Jones AR and Hermjakob H (2014) 'ProteomeXchange: globally co-ordinated proteomics data submission and dissemination', *Nature Biotechnology*, **32**, 223-226 (IF: 39.080).
134. Vaudel M, Venne AS, Berven FS, Zahedi RP, **Martens L** and Barsnes H (2014) 'Shedding light on black boxes in protein identification', *Proteomics*, **14**, 1001-1005 (IF: 3.973).
135. Kolker E, Ozdemir V, **Martens L**, Hancock W, Anderson G, Anderson N, Aynacioglu S, Baranova A, Campagna SR, Chen R, Choiniere J, Dearth SP, Feng WC, Ferguson L, Fox G, Frishman D, Grossman R, Heath A, Higdon R, Hutz MH, Janko I, Jiang L, Joshi S, Kel A, Kemnitz JW, Kohane IS, Kolker N, Lancet D, Lee E, Li W, Lisitsa A, Llerena A, Macnealy-Koch C, Marshall JC, Masuzzo P, May A, Mias G, Monroe M, Montague E, Mooney S, Nesvizhskii A, Noronha S, Omenn G, Rajasimha H, Ramamoorthy P, Sheehan J, Smarr L, Smith CV, Smith T, Snyder M, Rapole S, Srivastava S, Stanberry L, Stewart E, Toppo S, Uetz P, Verheggen K, Voy BH, Warnich L, Wilhelm SW and Yandl G (2014) 'Toward more transparent and reproducible omics studies through a common metadata checklist and data publications.', *OMICS*, **18**, 10-14 (IF: 2.730).
136. Vandermarliere E, Ghesquière B, Jonckheere V, Gevaert K and **Martens L** (2014) 'Unraveling the specificities of the different human methionine sulfoxide reductases', *Proteomics*, **14**, 1990-1998 (IF: 3.973).
137. Walzer M, Pernas LE, Nasso S, Bittremieux W, Nahnsen S, Kelchtermans P, Pichler P, van den Toorn HW, Staes A, Vandenbussche J, Mazanek M, Taus T, Scheltema RA, Kelstrup CD, Gatto L, van Breukelen B, Aiche S, Valkenborg D, Laukens K, Lilley KS, Olsen JV, Heck AJ, Mechtler K, Aebersold R, Gevaert K, Vizcaino JA, Hermjakob

H, Kohlbacher O and **Martens L** (2014) ‘qcML: an exchange format for quality control metrics from mass spectrometry experiments’, *Molecular & Cellular Proteomics*, **13**, 1905-1913 (IF: 7.254).

138. Bittremieux W, Kelchtermans P, Valkenborg D, **Martens L** and Laukens K (2014) 'jqcML: an open-source Java API for mass spectrometry quality control data in the qcML format', *Journal of Proteome Research*, **13**, 3484-3487 (IF: 5.001).
139. Van Leene J, Eeckhout D, Canoot B, De Winne N, Persiau G, Van De Slijke E, Vercruysse L, Dedecker M, Verkest A, Vandepoele K, **Martens L**, Witters E, Gevaert K and De Jaeger G (2014) 'Tandem affinity purification on Arabidopsis seedlings and cell cultures: an improved toolbox to unravel the plant cellular machinery', *Nature Protocols*, **10**,169-187 (IF: 7.782).
140. Barsnes H, Vaudel M and **Martens L** (2014) 'JSparklines: Making Tabular Proteomics Data Come Alive', *Proteomics*, **15**, 1428-1431 (IF: 3.973).
141. Vaudel M, Burkhart JM, Zahedi RP, Oveland E, Berven FS, Sickmann A, **Martens L** and Barsnes H (2015) 'PeptideShaker enables reanalysis of mass spectrometry-derived proteomics datasets', *Nature Biotechnology*, **33**, 22-24 (IF: 39.080).
142. Volders PJ, Verheggen K, Menschaert G, Vandepoele K, **Martens L**, Vandesompele J and Mestdagh P (2015) ‘An update on LNCipedia: a database for annotated lncRNA sequences and structures’, *Nucleic Acids Research*, **43**, D174-D180 (IF: 8.808).
143. Oveland E, Muth T, Rapp E, **Martens L**, Berven FS, and Barsnes H (2015) "Viewing the Proteome: How to Visualize Proteomics Data?", *Proteomics*, **15**, 1341-1355 (IF: 3.973).
144. Glibert P, Meert P, Van Steendam K, Van Nieuwerburgh F, De Coninck D, **Martens L**, Dhaenens M and Deforce D (2015) "Phospho-iTRAQ: Assessing Isobaric Labels for the Large-Scale Study Of Phosphopeptide Stoichiometry", *Journal of Proteome Research*, **14**, 839-849 (IF: 5.001).
145. Masuzzo P and **Martens L** (2015) “An open data ecosystem for cell migration research”, *Trends in Cell Biology*, **25**, 55-58 (IF: 12.314).
146. Vermeire T, Vermaere S, Schepens B, Saelens B, Van Gucht S, **Martens L** and Vandermarliere E (2015) 'Scop3D: three-dimensional visualization of sequence conservation', *Proteomics*, **15**, 1448-1452 (IF: 3.973).
147. Arora R, Di Michele M, Stes E, Vandermarliere E, **Martens L**, Gevaert K, Van Heerde E, Linders J, Brehmer D, Jacoby E and Bonnet P (2015) 'Structural Investigation of B-Raf Paradox Breaker and Inducer Inhibitors', *Journal of Medicinal Chemistry*, **58**, 1818-1831 (IF: 5.480).
148. Muth T, Behne A, Heyer R, Kohrs F, Benndorf D, Hoffmann M, Lehtevä M, Reichl U, **Martens L** and Rapp E (2015) "The MetaProteomeAnalyzer: A Powerful Open-Source Software Suite for Metaproteomics Data Analysis and Interpretation" *Journal of Proteome Research*, **14**, 1557-1565 (IF: 5.001).
149. Gonnelli G, Stock M, Verwaeren J, Maddelein D, De Baets B, **Martens L** and Degroeve S (2015) "A decoy-free approach to the identification of peptides", *Journal of Proteome Research*, **14**, 1792-1798 (IF: 5.001).
150. Vandermarliere E, Maddelein D, Hulstaert N, Stes E, Di Michele M, Gevaert K, Jacoby E, Brehmer D and **Martens L** (2015) “PepShell: visualization of conformational proteomics data”, *Journal of Proteome Research*, **14**, 1987-1990 (IF: 5.001).
151. Muth T, Kolmeder CA, Salojärvi J, Keskitalo S, Varjosalo M, Verdam FJ, Rensen SS, Reichl U, de Vos WM, Rapp E and **Martens L** (2015) "Navigating through metaproteomics data – a logbook of database searching", *Proteomics*, **15,** 3439-3453 (IF: 3.973).
152. **Martens L**, Kohlbacher O and Weintraub ST (2015) "Managing Expectations when Publishing Tools and Methods for Computational Proteomics", *Journal of Proteome Research*, **14**, 2002-2004 (IF: 5.001).
153. Vervliet T, Lemmens I, Vandermarliere E, Decrock E, Ivanova H, Monaco G,

Sorrentino V, Nadif Kasri N, Missiaen L, **Martens L**, De Smedt H, Leybaert L, Parys JB, Tavernier J and Bultynck G (2015) "Ryanodine receptors are targeted by anti-apoptotic Bcl-XL involving its BH4 domain and Lys87 from its BH3 domain", *Scientific Reports*, **5**, 9641 (IF: 5.078).

154. Bittremieux W, Willems H, Kelchtermans P, **Martens L**, Laukens K and Valkenborg D (2015) "iMonDB: Mass spectrometry quality control through instrument monitoring", *Journal of Proteome Research*, **14**, 2360-2366 (IF: 5.001).
155. Goeminne L, Argentini A, **Martens L** and Clement L (2015) "Summarization vs. Peptide-Based Models in Label-free Quantitative Proteomics: Performance, Pitfalls and Data Analysis Guidelines", *Journal of Proteome Research*, **14**, 2457-2465 (IF: 5.001).
156. Maddelein D, Colaert N, Buchanan I, Hulstaert N, Gevaert K and **Martens L** (2015) "The iceLogo web server and SOAP service for determining protein consensus sequences", *Nucleic Acids Research*, **43**, W543-W546 (IF: 8.808).
157. Degroeve S, Maddelein D and **Martens L** (2015) "MS2PIP prediction server: compute and visualize MS2 peak intensity predictions for CID and HCD fragmentation", *Nucleic Acids Research*, **43**, W326-W330 (IF: 8.808).
158. Nasso S, Goetze S and **Martens L** (2015) "Ariadne's thread: a robust software solution leading to automated absolute and relative quantification of SRM data", *Journal of Proteome Research*, **14**, 3779-3792 (IF: 5.001).
159. Glibert P, Meert P, Van Steendam K, **Martens L**, Deforce D and Dhaenens M (2015) "Phospho-iTRAQ data article: Assessing isobaric labels for the large-scale study of phosphopeptide stoichiometry.", *Data Brief.* **4**, 60-65.
160. Kolmeder CA, Ritari J, Verdam FJ, Muth T, Keskitalo S, Varjosalo M, Fuentes S, Greve JW, Buurman WA, Reichl U, Rapp E, **Martens L**, Palva A, Salonen A, Rensen SS and de Vos WM (2015) "Colonic metaproteomic signatures of active bacteria and the host in obesity", *Proteomics*, **15**, 3544-3552 (IF: 3.973).
161. Di Michele M, Stes E, Vandermarliere E, Arora R, Astorga-Wells J, Vandenbussche J, van Heerde E, Zubarev R, Bonnet P, Linders JT, Jacoby E, Brehmer D, **Martens L** and Gevaert K (2015) "Limited Proteolysis Combined with Stable Isotope Labeling Reveals Conformational Changes in Protein (Pseudo)kinases upon Binding Small Molecules." *Journal of Proteome Research*, **14**, 4179-4193 (IF: 5.001).
162. Masuzzo P, Van Troys M, Ampe C and **Martens L** (2015) "Taking aim at moving targets in computational cell migration", *Trends in Cell Biology*, **26**, 88-110 (IF: 12.314).
163. Kelchtermans P, C Silva AS, Argentini A, Staes A, Vandenbussche J, Laukens K, Valkenborg D and **Martens L** (2015) “Open-Source, Platform-Independent Library and Online Scripting Environment for Accessing Thermo Scientific RAW Files”, *Journal of Proteome Research*, **14**, 4940-4943 (IF: 5.001).
164. Olexiouk V, Crappé J, Verbruggen S, Verheggen K, **Martens L** and Menschaert G (2016) "sORFs.org: A repository of small ORFs identified by ribosome profiling", *Nucleic Acids Research*, **44**, D324-D329 (IF: 8.808).
165. Verheggen K, Maddelein D, Hulstaert N, **Martens L**, Barsnes H, Vaudel M (2016) "Pladipus enables universal distributed computing in proteomics bioinformatics", *Journal of Proteome Research*, **15**, 707-712 (IF: 5.001).
166. Meysman, Pieter, Kevin Titeca, Sven Eyckerman, Jan Tavernier, Bart Goethals, **Lennart Martens**, Dirk Valkenborg, and Kris Laukens. 2017. “Protein Complex Analysis : from Raw Protein Lists to Protein Interaction Networks.” Mass Spectrometry Reviews 36 (5): 600–614. (IF: 8.053).
167. Vaudel M, Verheggen K, Csordas A, Ræder H, Berven FS, **Martens L**, Vizcaíno JA, Barsnes H (2016) "Exploring the potential of public proteomics data", *Proteomics*, **16**, 214-225 (IF: 3.973).
168. **Martens L** (2016) "Public proteomics data: how the field has evolved from sceptical

inquiry to the promise of in silico proteomics.", *EuPA Open Proteomics*, **11**, 42-44.

169. Titeca K, Meysman P, Gevaert K, Tavernier J, Laukens K, **Martens L** and Eyckerman S (2016) 'SFINX: straightforward filtering index for affinity purification-mass spectrometry data analysis', *Journal of Proteome Research*, **15**, 332-338 (IF: 5.001).
170. Vandermarliere E, Stes E, Gevaert K and **Martens L** (2016) 'Resolution of protein structure by mass spectrometry', *Mass Spectrometry Reviews*, **35**, 653-665 (IF: 8.053).
171. Blackburn JM and **Martens L** (2016) ‘The challenge of metaproteomic analysis in human samples’, *Expert Review in Proteomics*, **13**, 135-138 (IF: 3.685).
172. Bittremieux W, Meysman P, **Martens L**, Valkenborg D and Laukens K (2016) ‘Unsupervised quality assessment of mass spectrometry proteomics experiments by multivariate quality control metrics’, *Journal of Proteome Research*, **15**, 1300-1307 (IF: 5.001).
173. Maes E, Kelchtermans P, Bittremieux W, De Grave K, Degroeve S, Hooyberghs J, Mertens I, Baggerman G, Ramon J, Laukens K, **Martens L** and Valkenborg D (2016) "Designing biomedical proteomics experiments: state-of-the-art and future perspectives", *Expert Review of Proteomics*, **13**, 495-511 (IF: 3.685).
174. Yılmaz Ş, Victor B, Hulstaert N, Vandermarliere E, Barsnes H, Degroeve S, Gupta S, Sticker A, Gabriël S, Dorny P, Palmblad M and **Martens L** (2016) "A pipeline for differential proteomics in unsequenced species", *Journal of Proteome Research*, **15**, 1963-1970 (IF: 5.001).
175. Vandemoortele G, Staes A, Gonnelli G, Samyn N, De Sutter D, Vandermarliere E, Timmerman E, Gevaert K, **Martens L** and Eyckerman S (2016) "An extra dimension in protein tagging by quantifying universal proteotypic peptides using targeted proteomics", *Scientific Reports*, **6**, 27220 (IF: 5.578).
176. Muth T, Renard BY and **Martens L** (2016) "Metaproteomic data analysis at a glance: advances in computational microbial community proteomics", *Expert Review in Proteomics*, **13**, 757-769 (IF: 3.465).
177. Deutsch E, Overall C, Van Eyk J, Baker M, Paik YK, Weintraub S, Lane L, **Martens L**, Vandenbrouck Y, Kusebauch U, Hancock W, Hermjakob H, Aebersold R, Moritz R, Omenn G (2016) "Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1", *Journal of Proteome Research*, **15**, 3961-3970 (IF: 4.173).
178. Bittremieux, Wout, Dirk Valkenborg, **Lennart Martens**, and Kris Laukens. 2017. “Computational Quality Control Tools for Mass Spectrometry Proteomics.” Proteomics 17 (3-4). (IF: 4.079)
179. Buthelezi SG, Dirrb HW, Chakauyaa E, Chikwambaa R, **Martens L**, Tsekoa TL, Stoycheva SH, Vandermarliere E (2016) "The lyssavirus glycoprotein: a key to cross-immunity", *Virology*, **498**, 250-256 (IF: 3.068).
180. Peters JS, Calder B, Gonnelli G, Degroeve S, Rajaonarifara E, Mulder N, Soares NC, **Martens L** and Blackburn JM (2016) "Identification of Quantitative Proteomic Differences between Mycobacterium tuberculosis Lineages with Altered Virulence", *Front Microbiol.*, 2016, **7**, 813 (IF: 4.165).
181. Vu LD, Stes E, Van Bel M, Nelissen H, Maddelein D, Inzé D, Coppens F, **Martens L**, Gevaert K and De Smet I (2016) "Up-to-Date Workflow for Plant (Phospho)proteomics Identifies Differential Drought-Responsive Phosphorylation Events in Maize Leaves.", *J Proteome Res.*, **15**, 4304-4317 (IF: 4.173).
182. Tanca A, Palomba A, Fraumene C, Pagnozzi D, Manghina V, Deligios M, Muth T, Rapp E, **Martens L**, Addis MF and Uzzau S (2016) "The impact of sequence database choice on metaproteomic results in gut microbiota studies", *Microbiome*, **4**, 51 (IF: 9.000).
183. Yılmaz Ş, Drepper F, Hulstaert N, Černič M, Gevaert K, Economou A, Warscheid B, **Martens L** and Vandermarliere E (2016) "Xilmass: A New Approach toward the Identification of Cross-Linked Peptides", *Analytical Chemistry*, **88**, 9949-9957 (5.886).
184. Lievens S, Van der Heyden J, Masschaele D, De Ceuninck L, Petta I, Gupta S, De

Puysseleyr V, Vauthier V, Lemmens I, De Clercq DJ, Defever D, Vanderroost N, De Smet AS, Eyckerman S, Van Calenbergh S, **Martens L**, De Bosscher K, Libert C, Hill DE, Vidal M and Tavernier J (2016) "Proteome-scale Binary Interactomics in Human Cells", *Mol Cell Proteomics*, **15**, 3624-3639 (IF: 5.912).

185. Argentini A, Goeminne LJ, Verheggen K, Hulstaert N, Staes A, Clement L and **Martens L** (2016) “moFF: a robust and automated approach to extract peptide ion intensities”, *Nature Methods*, **13**, 964-966 (IF: 25.328).
186. Gupta S, De Puysseleyr V, Van der Heyden J, Maddelein D, Lemmens I, Lievens S, Degroeve S, Tavernier J and **Martens L** (2017) "MAPPI-DAT: data management and analysis for protein-protein interaction data from the high-throughput MAPPIT cell microarray platform", *Bioinformatics*, **33**, 1424-1425 (IF: 5.766).
187. **Martens L** and Vizcaíno JA (2017) “A Golden Age for Working with Public Proteomics Data”, *Trends in Biochemical Sciences*, **42**, 333-341 (IF: 12.810).
188. Titeca K, Meysman P, Laukens K, **Martens L**, Tavernier J and Eyckerman S (2017) "sfinx: an R package for the elimination of false positives from affinity purification - mass spectrometry datasets", *Bioinformatics*, **33**, 1902-1904 (IF: 5.766).
189. Masuzzo P, Huyck L, Simiczyjew A, Ampe C, **Martens L** and Van Troys M (2017) "An end-to-end software solution for the analysis of high-throughput single-cell migration data.", *Nature Scientific Reports*, **7**, 42383 (IF: 5.228).
190. Willems P, Ndah E, Jonckheere V, Stael S, Sticker A, **Martens L**, Van Breusegem F, Gevaert K and Van Damme P (2017) "N-terminal proteomics assisted profiling of the unexplored translation initiation landscape in Arabidopsis thaliana." *Mol Cell Proteomics*, **16**, 1064-1080 (IF: 5.912).
191. Vizcaíno JA, Walzer M, Jiménez RC, Bittremieux W, Bouyssié D, Carapito C, Corrales F, Ferro M, Heck AJR, Horvatovich P, Hubalek M, Lane L, Laukens K, Levander F, Lisacek F, Novak P, Palmblad M, Piovesan D, Pühler A, Schwämmle V, Valkenborg D, van Rijswijk M, Vondrasek J, Eisenacher M, **Martens L**, Kohlbacher O (2017) "A community proposal to integrate proteomics activities in ELIXIR." *F1000Res.*, ELIXIR-875 (IF: N/A).
192. Gupta S, Verheggen K, Tavernier J and **Martens L** (2017) "An emp protein association study on the public human proteome reveals biological connections between co-occurring protein pairs.", *J Proteome Res*, *in press* (IF: 4.268).
193. Mesuere B, Van der Jeugt F, Willems T, Naessens T, Devreese B, **Martens L** and Dawyndt P (2017) "High-throughput metaproteomics data analysis with Unipept: A tutorial." *Journal of Proteomics*, **171**, 11-22 (IF: 3.914).
194. Verheggen K, Volders PJ, Mestdagh P, Menschaert G, Van Damme P, Gevaert K, **Martens L** and Vandesompele J (2017) "Noncoding after All: Biases in Proteomics Data Do Not Explain Observed Absence of lncRNA Translation Products.", *J Proteome Res.*, **16**, 2508-2515 (IF: 4.268).
195. Verheggen K, Ræder H, Berven FS, **Martens L**, Barsnes H, Vaudel M (2017) "Anatomy and evolution of database search engines - a central component of mass spectrometry based proteomic workflows", *Mass Spectrometry Reviews*, *in press* (IF: 9.373).
196. Sticker A, **Martens L**, Clement L (2017) "Mass spectrometrists should search for all peptides, but assess only the ones they care about.", *Nature Methods*, **14**, 643-644 (IF: 25.062).
197. Bittremieux, Wout, David L Tabb, Francis Impens, An Staes, Evy Timmerman, **Lennart Martens**, and Kris Laukens. 2017. “Quality Control in Mass Spectrometry-based Proteomics.” Mass Spectrometry Reviews 37 (5): 697–711. (IF: 9.373).
198. Chambers MC, Jagtap PD, Johnson JE, McGowan T, Kumar P, Onsongo G, Guerrero CR, Barsnes H, Vaudel M, **Martens L**, Grüning B, Cooke IR, Heydarian M, Reddy KL and Griffin TJ (2017) "An Accessible Proteogenomics Informatics Resource for Cancer Researchers", *Cancer Research*, **77**, e43-e46 (IF: 9.122).

199. De Wilde B, Beckers A, Lindner S, Kristina A, De Preter K, Depuydt P, Mestdagh P, Sante T, Lefever S, Hertwig F, Peng Z, Shi LM, Lee S, Vandermarliere E, **Martens L**, Menten B, Schramm A, Fischer M, Schulte J, Vandesompele J, Speleman F (2017) "The mutational landscape of MYCN, Lin28b and ALKF1174L driven murine neuroblastoma mimics human disease", *Oncotarget*, **9**, 8334-8349 (IF: 5.168).
200. Tardaguila, Manuel, Lorena de la Fuente, Cristina Marti, Cécile Pereira, Francisco Jose Pardo-Palacios, Hector del Risco, Marc Ferrell, Maravillas Mellado, Marissa Macchietto, Kenneth Verheggen, Mariola Edelmann, Iakes Ezkurdia, Jesus Vazquez, Michael Tress, Ali Mortazavi, Lennart Martens, Susana Rodriguez-Navarro, Victoria Moreno-Manzano, and Ana Conesa. 2018. “SQANTI : Extensive Characterization of Long-read Transcript Sequences for Quality Control in Full-length Transcriptome Identification and Quantification.” Genome Research 28 (3): 396–411. (IF: 11;922).
201. Muth T, Kohrs F, Heyer R, Benndorf D, Rapp E, Reichl U, **Martens L** and Renard BY (2018) "MPA Portable: A Stand-Alone Software Package for Analyzing Metaproteome Samples on the Go", Analytical Chemistry, 90, 685-689 (IF: 6.320).
202. Gupta S, Turan D, Tavernier J and **Martens L** (2018) "The online Tabloid Proteome: an annotated database of protein associations", *Nucleic Acids Res.*, **46**, D581-D585 (IF: 10.164).
203. Yilmaz-Rumpf, Sule, Genet Abay Shiferaw, Josep Rayo, Anastassios Economou, **Lennart Martens**, and Elien Vandermarliere. 2018. “Cross-linked Peptide Identification: a Computational Forest of Algorithms.” Mass Spectrometry Reviews 37 (6): 738–749. Impact factor: 9.068
204. Gouma S, Vermeire T, Van Gucht S, Martens L, Hutse V, Cremer J, Rota PA, Leroux-Roels G, Koopmans M, Binnendijk RV and Vandermarliere E. (2018) "Differences in antigenic sites and other functional regions between genotype A and G mumps virus surface proteins", Nature Scientific Reports, 8, 13337 (IF: 4.122).
205. C Silva AS, Palmer A, Kovalev V, Tarasov A, Alexandrov T, **Martens L** and Degroeve S. (2018) "Data-Driven Rescoring of Metabolite Annotations Significantly Improves Sensitivity.", *Anal Chem.*, **90**, 11636-11642 (IF: 6.042).
206. Sergeant, Gwendolien, **Lennart Martens**, Marleen Van Troys, and Paola Masuzzo. 2019. “DoRes within CellMissy : Dose-Response Analysis on Cell Migration and Related Data.” BIOINFORMATICS 35 (4): 696–697. (IF: 5.481).
207. Schuster M, Moeller M, Bornemann L, Bessen C, Sobczak C, Schmitz S, Witjes L, Kruithoff K, Kohn C, Just O, Kündgen A, Pundt N, Pelzer B, Ampe C, Van Troys M, Nusch A, Haas R, Germing U, **Martens L**, Jöckel KH and Gunzer M (2018) "Surveillance of Myelodysplastic Syndrome via Migration Analyses of Blood Neutrophils: A Potential Prognostic Tool", *J Immunol.*, **201**, 3546-3557 (IF: 4.539).
208. Volders, Pieter-Jan, Jasper Anckaert, Kenneth Verheggen, Justine Nuytens, **Lennart Martens**, Pieter Mestdagh, and Jo Vandesompele. 2019. “LNCipedia 5 : Towards a Reference Set of Human Long Non-coding RNAs.” Nucleic Acids Research 47 (D1): D135–D139 (IF: 11.561).
209. Gurdeep Singh, Robbert, Alessandro Tanca, Antonio Palomba, Felix Van der Jeugt, Pieter Verschaffelt, Sergio Uzzau, **Lennart Martens**, Peter Dawyndt, and Bart Mesuere. 2019. “Unipept 4.0 : Functional Analysis of Metaproteome Data.” Journal of Proteome Research 18 (2): 606–615. (IF: 3.950).
210. Buthelezi SG, Dirr HW, Chakauya E, Chikwamba R, **Martens L**, Tsekoa TL, Vandermarliere E and Stoychev SH (2018) "The study of degradation mechanisms of glyco-engineered plant produced anti-rabies monoclonal antibodies E559 and 62-71-3", *PLoS One*, **13**, e0209373 (IF: 3.955).
211. Kreft L, Turan D, Hulstaert N, Botzki A, **Martens L** and Vandermarliere E (2018) "Scop3D: online visualization of mutation rates on protein structure", *J Proteome Res.*, 8: 765-769. (IF: 3.950).
212. Nye, Leanne C, Jonathan P Williams, Nyasha C Munjoma, Marine PM Letertre,

Muireann Coen, Robbin Bouwmeester, **Lennart Martens**, Jonathan R Swann, Jeremy K Nicholson, Robert S Plumb, Michael McCullagh, Lee A Gethings, Steven Lai, James I Langridge, Johannes PC Vissers, and Ian D Wilson. 2019. "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." Journal of Chromatography A, 1602: 386–396. (IF: 4.049)

213. Argentini, Andrea, An Staes, Björn Andreas Grüning, Subina Mehta, Caleb Easterly, Timothy Griffin, Pratik Jagtap, Francis Impens, and **Lennart Martens**. 2019. "An Update on the moFF Algorithm for Label-free Quantitative Proteomics." Journal of Proteome Research 18 (2): 728–731. (IF: 3.950).
214. Mesuere, Bart, Felix Van der Jeugt, Toon Willems, Tom Naessens, Bart Devreese, **Lennart Martens**, and Peter Dawyndt. 2018. "High-throughput Metaproteomics Data Analysis with Unipept : a Tutorial." Journal of Proteomics 171: 11–22. (IF: 3.537)
215. Bouwmeester, Robbin, **Lennart Martens**, and Sven Degroeve. 2019. "Comprehensive and Empirical Evaluation of Machine Learning Algorithms for Small Molecule LC Retention Time Prediction." Analytical Chemistry, 91: 6394–3703. (IF: 6.785)
216. Schiebenhoefer, Henning, Tim Van Den Bossche, Stephan Fuchs, Bernhard Y Renard, Thilo Muth, and **Lennart Martens**. 2019. "Challenges and Promise at the Interface of Metaproteomics and Genomics : an Overview of Recent Progress in Metaproteogenomic Data Analysis." Expert Review of Proteomics 16 (5): 375–390. (IF: 3.614)
217. Gabriels, Ralf, **Lennart Martens**, and Sven Degroeve. 2019. "Updated MS2PIP Web Server Delivers Fast and Accurate MS2 Peak Intensity Prediction for Multiple Fragmentation Methods, Instruments and Labeling Techniques." Nucleic Acids Research 47 (W1): W295–W299. (IF: 11.501)
218. Hristina Ivanova, Larry E. Wagner II, Akihiko Tanimura, Elien Vandermarliere, Tomas Luyten, Kirsten Welkenhuyzen, Kamil J. Alzayady, Liwei Wang, Kozo Hamada, Katsuhiko Mikoshiba, Humbert De Smedt, **Lennart Martens**, David I. Yule, Jan B. Parys & Geert Bultynck. 2019. "Bcl-2 and IP3 compete for the ligand-binding domain of IP3Rs modulating Ca2+ signaling output." Cellular and Molecular Life Sciences 76, 3843-3859. (IF: 6.596)
219. Verheggen, Kenneth, Helge Raeder, Frode S Berven, **Lennart Martens**, Harald Barsnes, and Marc Vaudel. 2020. "Anatomy and Evolution of Database Search Engines : A Central Component of Mass Spectrometry Based Proteomic Workflows." Mass Spectrometry Reviews, 39: 292-306. (IF: 10.946)
220. Ferreira Diamantino Coelho e Silva, Ana Sílvia, Robbin Bouwmeester, **Lennart Martens**, and Sven Degroeve. 2020. "Accurate Peptide Fragmentation Predictions Allow Data Driven Approaches to Replace and Improve upon Proteomics Search Engine Scoring Functions." Bioinformatics, 35: 5243-5248. (IF: 6.937)
221. Hulstaert N, Shofstahl J, Sachsenberg T, Walzer M, Barsnes H, **Martens L**, Perez-Riverol Y. 2020. "ThermoRawFileParser: Modular, Scalable, and Cross-Platform RAW File Conversion." Journal of Proteome Research 19: 537-542. (IF: 4.466)
222. Van Puyvelde, Bart, Sander Willems, Ralf Gabriels, Simon Daled, Laura De Clerck, Sofie Vande Casteele, An Staes, Francis Impens, Dieter Deforce, **Lennart Martens**, Sven Degroeve, and Maarten Dhaenens. 2020. "Removing the Hidden Data Dependency of DIA with Predicted Spectral Libraries." Proteomics, 20: e1900306. (IF: 3.984)
223. Goeminne LJE, Sticker A, **Martens L**, Gevaert K and Clement L. 2020. "MSqRob Takes the Missing Hurdle: Uniting Intensity- and Count-Based Proteomics." Analytical Chemistry, 92: 6278-6287. (IF: 6.350)
224. Maia TM, Staes A, Plasman K, Pauwels J, Boucher K, Argentini A, **Martens L**, Montoye T, Gevaert K and Impens F. 2020. "Simple Peptide Quantification Approach

for MS-Based Proteomics Quality Control." ACS Omega. 5: 6754-6762. (IF: 2.584)

225. Bouwmeester R, Gabriels R, Van Den Bossche T, **Martens L** and Degroeve S. 2020. "The Age of Data-Driven Proteomics: How Machine Learning Enables Novel Workflows." Proteomics, 20: e1900351 (IF: 3.984)
226. Bouwmeester R, **Martens L** and Degroeve S. 2020. "Generalized Calibration Across Liquid Chromatography Setups for Generic Prediction of Small-Molecule Retention Times." Analytical Chemistry, 92: 6571-6578. (IF: 6.350)
227. Sticker A, Goeminne L, **Martens L** and Clement L. 2020. "Robust summarization and inference in proteome-wide label-free quantification." Mol Cell Proteomics, mcp.RA119.001624. (IF: 5.911)
228. Shiferaw GA, Vandermarliere E, Hulstaert N, Gabriels R, **Martens L** and Volders PJ. 2020. "COSS: A Fast and User-Friendly Tool for Spectral Library Searching." J Proteome Res., 19: 2786-2793. (IF: 4.466)
229. Gonzalez-Beltran AN, Masuzzo P, Ampe C, Bakker GJ, Besson S, Eibl RH, Friedl P, Gunzer M, Kittisopikul M, Dévédec SEL, Leo S, Moore J, Paran Y, Prilusky J, Rocca-Serra P, Roudot P, Schuster M, Sergeant G, Strömblad S, Swedlow JR, van Erp M, Van Troys M, Zaritsky A, Sansone SA and **Martens L**. 2020. "Community standards for open cell migration data." Gigascience, 9: giaa041. (IF: 6.524)
230. Smith S, Zhu S, Joos L, Roberts I, Nikonorova N, Vu LD, Stes E, Cho H, Larrieu A, Xuan W, Goodall B, van de Cotte B, Waite JM, Rigal A, R Harborough SR, Persiau G, Vanneste S, Kirschner GK, Vandermarliere E, **Martens L**, Stahl Y, Audenaert D, Friml J, Felix G, Simon R, Bennett M, Bishopp A, De Jaeger G, Ljung K, Kepinski S, Robert S, Nemhauser J, Hwang I, Gevaert K, Beeckman T and De Smet I. 2020. "The CEP5 peptide promotes abiotic stress tolerance, as revealed by quantitative proteomics, and attenuates the AUX/IAA equilibrium in Arabidopsis." Mol Cell Proteomics mcp.RA119.001826. (IF: 5.911)
231. Van Den Bossche T, Verschaffelt P, Schallert K, Barsnes H, Dawyndt P, Benndorf D, Renard BY, Mesuere B, **Martens L** and Muth T. 2020. "Connecting MetaProteomeAnalyzer and PeptideShaker to Unipept for seamless end-to-end metaproteomics data analysis." J Proteome Res. 19: 3562-3566. (IF: 4.466)
232. Verschaffelt P, Van Thienen P, Van Den Bossche T, Van der Jeugt F, De Tender C, **Martens L**, Dawyndt P and Mesuere B. 2020. "Unipept CLI 2.0: adding support for visualisations and functional annotations." *Bioinformatics*, 36: 4220-4221. (IF: 6.937)
233. Ramasamy P, Turan D, Tichshenko N, Hulstaert N, Vandermarliere E, Vranken WF and **Martens L**. 2020. "Scop3P: a comprehensive resource of human phosphosites within their full context." *J Proteome Res*., 19: 3478-3486. (IF: 4.466)
234. Mehta S, Easterly CW, Sajulga R, Millikin RJ, Argentini A, Eguinoa I, **Martens L**, Shortreed MR, Smith LM, McGowan T, Kumar P, Johnson JE, Griffin TJ, Jagtap PD. 2020. "Precursor Intensity-Based Label-Free Quantification Software Tools for Proteomic and Multi-Omic Analysis within the Galaxy Platform." Proteomes, 8: 15. (IF: 0.55)
235. Verschaffelt P, Collier J, Botzki A, **Martens L**, Dawyndt P, Mesuere B. 2021. "Unipept Visualizations: An Interactive Visualization Library For Biological Data." Bioinformatics, btab590. (IF: 6.931)
236. Van Puyvelde B, Van Uytfanghe K, Tytgat O, Van Oudenhove L, Gabriels R, Bouwmeester R, Daled S, Van Den Bossche T, Ramasamy P, Verhelst S, De Clerck L, Corveleyn L, Willems S, Debunne N, Wynendaele E, De Spiegeleer B, Judak P, Roels K, De Wilde L, Van Eenoo P, Reyns T, Cherlet M, Dumont E, Debyser G, t'Kindt R, Sandra K, Gupta S, Drouin N, Harms A, Hankemeier T, Jones DJL, Gupta P, Lane D, Lane CS, El Ouadi S, Vincendet JB, Morrice N, Oehrle S, Tanna N, Silvester S, Hannam S, Sigloch FC, Bhangu-Uhlmann A, Claereboudt J, Anderson NL, Razavi M, Degroeve S, Cuypers L, Stove C, Lagrou K, Martens GA, Deforce D, **Martens L**, Vissers JPC, Dhaenens M. 2021. "Cov-MS: A Community-Based Template Assay for

Mass-Spectrometry-Based Protein Detection in SARS-CoV-2 Patients." JACS Au., 1: 750-765. (IF: NyA)

237. Salz R, Bouwmeester R, Gabriels R, Degroeve S, **Martens L**, Volders PJ, 't Hoen PAC. 2021. "Personalized Proteome: Comparing Proteogenomics and Open Variant Search Approaches for Single Amino Acid Variant Detection." J Proteome Res., 20: 3353-3364. (IF: 5.370)
238. Gong S, Gaccioli F, Dopierala J, Sovio U, Cook E, Volders PJ, **Martens L**, Kirk PDW, Richardson S, Smith GCS, Charnock-Jones DS. 2021. "The RNA landscape of the human placenta in health and disease." Nature Communications, 12: 2639. (IF: 17.694)
239. Verbruggen S, Gessulat S, Gabriels R, Matsaroki A, Van de Voorde H, Kuster B, Degroeve S, **Martens L**, Van Criekinge W, Wilhelm M, Menschaert G. 2021. "Spectral Prediction Features as a Solution for the Search Space Size Problem in Proteogenomics." Mol Cell Proteomics., 20: 100076. (IF: 7.381)
240. Bandeira N, Deutsch EW, Kohlbacher O, **Martens L**, Vizcaíno JA. 2021. "Data Management of Sensitive Human Proteomics Data: Current Practices, Recommendations, and Perspectives for the Future." Mol Cell Proteomics., 20: 100071. (IF: 7.381)
241. Verschaffelt P, Van Den Bossche T, Gabriel W, Burdukiewicz M, Soggiu A, **Martens L**, Renard BY, Schiebenhoefer H, Mesuere B. 2021. "MegaGO: A Fast Yet Powerful Approach to Assess Functional Gene Ontology Similarity across Meta-Omics Data Sets." J Proteome Res., 20: 2083-2088. (IF: 5.370)
242. Verschaffelt P, Van Den Bossche T, **Martens L**, Dawyndt P, Mesuere B. 2021. "Unipept Desktop: A Faster, More Powerful Metaproteomics Results Analysis Tool." J Proteome Res., 20: 2005-2009. (IF: 5.370)
243. Bouwmeester R, Gabriels R, Hulstaert N, **Martens L**, Degroeve S. 2021. "DeepLC can predict retention times for peptides that carry as-yet unseen modifications." Nature Methods, 18: 1363-1369. (IF: 47.990)
244. Boone M, Ramasamy P, Zuallaert J, Bouwmeester R, Van Moer B, Maddelein D, Turan D, Hulstaert N, Eeckhaut H, Vandermarliere E, **Martens L**, Degroeve S, De Neve W, Vranken W, Callewaert N. 2021. "Massively parallel interrogation of protein fragment secretability using SECRiFY reveals features influencing secretory system transit." Nature Communications, 12: 6414. (IF: 17.694)
245. PDBe-KB consortium. 2022. "PDBe-KB: collaboratively defining the biological context of structural data." Nucleic Acids Res., 50: D534-D542. (IF: 19.160)
246. Van Den Bossche T, Kunath BJ, Schallert K, Schäpe SS, Abraham PE, Armengaud J, Arntzen MØ, Bassignani A, Benndorf D, Fuchs S, Giannone RJ, Griffin TJ, Hagen LH, Halder R, Henry C, Hettich RL, Heyer R, Jagtap P, Jehmlich N, Jensen M, Juste C, Kleiner M, Langella O, Lehmann T, Leith E, May P, Mesuere B, Miotello G, Peters SL, Pible O, Queiros PT, Reichl U, Renard BY, Schiebenhoefer H, Sczyrba A, Tanca A, Trappe K, Trezzi JP, Uzzau S, Verschaffelt P, von Bergen M, Wilmes P, Wolf M, **Martens L**, Muth T. 2021. "Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows." Nature Communications, 12: 7305. (IF: 17.694)
247. Delhaye L, De Bruycker E, Volders PJ, Fijalkowska D, De Sutter D, Degroeve S, **Martens L**, Mestdagh P, Eyckerman S. 2022. "Orthogonal proteomics methods to unravel the HOTAIR interactome." Nature Scientific Reports, 212:1513. (IF: 4.996)
248. Schallert K, Verschaffelt P, Mesuere B, Benndorf D, **Martens L**, Van Den Bossche T. 2022. "Pout2Prot: An Efficient Tool to Create Protein (Sub)groups from Percolator Output Files." J Proteome Res., 21: 1175-1180. (IF: 5.370)
249. Van Puyvelde B, Daled S, Willems S, Gabriels R, Gonzalez de Peredo A, Chaoui K, Mouton-Barbosa E, Bouyssié D, Boonen K, Hughes CJ, Gethings LA, Perez-Riverol Y, Bloomfield N, Tate S, Schiltz O, **Martens L**, Deforce D, Dhaenens M. 2022. "A

comprehensive LFQ benchmark dataset on modern day acquisition strategies in proteomics." Nature Scientific Data. 9: 126. (IF: 8.501)

250. Shiferaw GA, Gabriels R, Bouwmeester R, Van Den Bossche T, Vandermarliere E, **Martens L**, Volders PJ. 2022. "Sensitive and Specific Spectral Library Searching with CompOmics Spectral Library Searching Tool and Percolator." J Proteome Res., 21: 1365-1370. (IF: 5.370)
251. Ramasamy P, Vandermarliere E, Vranken WF, **Martens L**. 2022. "Panoramic Perspective on Human Phosphosites." J Proteome Res., 21: 1894-1915. (IF: 5.370)
252. Declercq A, Bouwmeester R, Hirschler A, Carapito C, Degroeve S, **Martens L**, Gabriels R. 2022. "MS2Rescore: Data-Driven Rescoring Dramatically Boosts Immunopeptide Identification Rates." Mol Cell Proteomics, 21: 100266. (IF: 7.381)
253. Mayer RL, Verbeke R, Asselman C, Aernout I, Gul A, Eggermont D, Boucher K, Thery F, Maia TM, Demol H, Gabriels R, **Martens L**, Bécavin C, De Smedt SC, Vandekerckhove B, Lentacker I, Impens F. 2022. "Immunopeptidomics-based design of mRNA vaccine formulations against Listeria monocytogenes." Nature Communications, 13: 6075. (IF: 17.694)
254. Provez L, Van Puyvelde B, Corveleyn L, Demeulemeester N, Verhelst S, Lintermans B, Daled S, Roels J, Clement L, **Martens L**, Deforce D, Van Vlierberghe P, Dhaenens M. 2022. "An interactive mass spectrometry atlas of histone posttranslational modifications in T-cell acute leukemia." Nature Scientific Data, 9: 626. (IF: 8.501)
255. van Cruchten RTP, van As D, Glennon JC, van Engelen BGM, 't Hoen PAC; OPTIMISTIC consortium; ReCognitION consortium. 2022. "Clinical improvement of DM1 patients reflected by reversal of disease-induced gene expression in blood." BMC Medicine, 20: 395. (IF: 8.775)
256. Van Puyvelde B, Van Uytfanghe K, Van Oudenhove L, Gabriels R, Van Royen T, Matthys A, Razavi M, Yip R, Pearson T, Drouin N, Claereboudt J, Foley D, Wardle R, Wyndham K, Hankemeier T, Jones D, Saelens X, Martens G, Stove CP, Deforce D, **Martens L**, Vissers JPC, Anderson NL, Dhaenens M. 2022. “Cov^{2}MS: An Automated and Quantitative Matrix-Independent Assay for Mass Spectrometric Measurement of SARS-CoV-2 Nucleocapsid Protein.” Anal Chem. 94:17379-17387. (IF: 7.4)
257. Verschaffelt P, Tanca A, Abbondio M, Van Den Bossche T, Moortele TV, Dawyndt P, **Martens L**, Mesuere B. 2023. “Unipept Desktop 2.0: Construction of Targeted Reference Protein Databases for Metaproteogenomics Analyses.” J Proteome Res. 22: 2620-2628. (IF: 4.4)
258. Sakarika M, Kerckhof FM, Van Peteghem L, Pereira A, Van Den Bossche T, Bouwmeester R, Gabriels R, Van Haver D, Ulčar B, **Martens L**, Impens F, Boon N, Ganigué R, Rabaey K. 2023. “The nutritional composition and cell size of microbial biomass for food applications are defined by the growth conditions.” Microb Cell Fact. 2023 22: 254. (IF: 6.4)
259. Holstein T, Kistner F, **Martens L**, Muth T. 2023. „PepGM: a probabilistic graphical model for taxonomic inference of viral proteome samples with associated confidence scores.” Bioinformatics. 39: btad289. (IF: 5.8)
260. Declercq A, Bouwmeester R, Chiva C, Sabidó E, Hirschler A, Carapito C, **Martens L**, Degroeve S, Gabriels R. 2023. Updated MS^{2}PIP web server supports cutting-edge proteomics applications. Nucleic Acids Res. 51: W338-W342. (IF: 14.9)
261. Gabriels R, Declercq A, Bouwmeester R, Degroeve S, **Martens L.** (2023) “psm_utils: A High-Level Python API for Parsing and Handling Peptide-Spectrum Matches and Proteomics Search Results.” J Proteome Res. 22: 557-560. (IF: 4.4)
262. Neely BA, Dorfer V, **Martens L**, Bludau I, Bouwmeester R, Degroeve S, Deutsch EW, Gessulat S, Käll L, Palczynski P, Payne SH, Rehfeldt TG, Schmidt T, Schwämmle V, Uszkoreit J, Vizcaíno JA, Wilhelm M, Palmblad M. 2023. “Toward na Integrated Machine Learning Model of a Proteomics Experiment.” J Proteome Res. 22: 681-696. (IF: 4.4)

263. Teschner D, Gomez-Zepeda D, Declercq A, Łącki MK, Avci S, Bob K, Distler U, Michna T, **Martens L**, Tenzer S, Hildebrandt A. 2023 “Ionmob: a Python package for prediction of peptide collisional cross-section values”. Bioinformatics. 39: btad486. (IF: 5.8)
264. Debrie E, Malfait M, Gabriels R, Declerq A, Sticker A, **Martens L**, Clement L. (2023). “Quality Control for the Target Decoy Approach for Peptide Identification.” J Proteome Res. 22: 350-358. (IF: 4.4)
265. Demeulemeester N, Gébelin M, Caldi Gomes L, Lingor P, Carapito C, **Martens L**,Clement L. 2023. “msqrob2PTM: differential abundance and differential usage analysis of MS-based proteomics data at the post-translational modification and peptidoform level.” Mol Cell Proteomics. 26:100708. (IF: 7.0)
266. Claeys T, Menu M, Bouwmeester R, Gevaert K, **Martens L.** (2023). “Machine Learning on Large-Scale Proteomics Data Identifies Tissue and Cell-Type Specific Proteins.” J Proteome Res. 22: 1181-1192. (IF: 4.4)
267. Claeys T, Van Den Bossche T, Perez-Riverol Y, Gevaert K, Vizcaíno JA, **Martens L**. 2023 “lesSDRF is more: maximizing the value of proteomics data through streamlined metadata annotation.” Nat Commun. 14: 6743. (IF: 16.6)
268. Koutrouli M, Nastou K, Piera Líndez P, Bouwmeester R, Rasmussen S, **Martens L**, Jensen LJ. 2024 “FAVA: high-quality functional association networks inferred from scRNA-seq and proteomics data.” Bioinformatics. 40:btae010. (IF: 5.8)

BOOKS

- ‘Computational Methods for Mass Spectrometry Proteomics’, 2007, *Wiley-VCH, Weinheim*
  Ingvar Eidhammer, Kristian Flikka, **Lennart Martens**, Svein-Ole Mikalsen.
  ISBN: 9780470512975
- ‘Computational Methods for Fragment Spectrum Interpretation’, 2009, *VDM Verlag*
  Jonathan Rameseder and **Lennart Martens**
  ISBN: 9783639228588
- ‘Computational and Statistical Methods for Protein Quantification by Mass Spectrometry’, 2012, *Wiley-VCH, Weinheim*
  Ingvar Eidhammer, Harald Barsnes, Geir Egil Eide, **Lennart Martens**
  ISBN: 9781119964001

EDITORIAL BOARD MEMBERSHIPS

- Member of the Editorial Advisory Board for **Molecular BioSystems** *(Royal Society of Chemistry Publishing)* (IF: 4.236), since 2008.
- Bioinformatics Section Editor for **Amino Acids** (*Springer*) (IF: 4.132), 2008-2013.
- Editor for **Biochimica et Biophysica Acta – Proteins and Proteomics** (*Elsevier*) (IF: 3.635), since 2009.
- Editor for **IEEE - Journal of Biomedical and Health Informatics** (*IEEE*) (IF: 1.978), (2014-2017).
- Associate Editor for Molecular & Cellular Proteomics (ASBMB), since 2018.
- Editorial Board Member for **PROTEOMICS** (*Wiley*), since 2011.
- Associate Editor for **PLoS ONE** (*PLoS*), since 2012.
- Academic Editor for **PeerJ** (*PeerJ*), since 2012.
- Editorial Board Member for **Molecular & Cellular Proteomics** (*ASBMB/Elsevier*), since 2019.
- Guest Editor for **Proteomics** (*Wiley*), for the *Proteomics Data Management Special Issue* (2009-2010).
- Guest Editor for **Proteomics** (*Wiley*), for the *Quality Control in Proteomics Special Issue* (2010-2011).

BOOK CHAPTERS

1. Adamski M, Blackwell T, Menon R, **Martens L**, Hermjakob H, Taylor C, Omenn GS and States DJ., ‘Data management in the HUPO PPP’. In: Omenn GS (Ed.) *Exploring the Human Plasma Proteome*, 2006, *Wiley-VCH, Weinheim.*
2. **Martens L**, Nesvizhskii AI, Hermjakob H, Adamski M, Omenn GS, Vandekerckhove J and Gevaert K, ‘The inclusion of raw data in proteomics data repositories’. In: Omenn GS (Ed.) *Exploring the Human Plasma Proteome*, 2006, *Wiley-VCH, Weinheim.*
3. **Martens L**, Jones P and Côté R, ‘Using the Proteomics Identications Database (PRIDE)’. In: Yates JR IIIrd (Ed.) *Current Protocols in Bioinformatics*, 2008, *John Wiley and Sons, Inc.*
4. **Martens L**, Montecchi Palazzi L and Hermjakob H, ‘Data Standards and Controlled Vocabularies for Proteomics’, *Methods in Molecular Biology: Functional Proteomics Vol. 484*, 2008, *Humana Press.*
5. **Martens L** and Apweiler R. ‘Algorithms and Databases’, *Methods in Molecular Biology: Proteomics Vol. 564*, 2009, *Humana Press.*
6. Vizcaíno JA, Reisinger F, Côté R and **Martens L**, ‘PRIDE: Data submission and analysis’, *Current Protocols in Protein Science*, 2009, *John Wiley & Sons, Inc.*
7. Jones P and **Martens L**, ‘Using the PRIDE proteomics identifications database for knowledge discovery and data analysis’, *Methods in Molecular Biology: Proteome*

Bioinformatics, 2010, *Humana Press.*

8. Vizcaíno JA, Reisinger F, Côté R and **Martens L**, 'PRIDE and "Database on Demand" as valuable tools for computational proteomics', *Methods in Molecular Biology: Data Mining in Proteomics*, 2011, *Humana Press.*
9. **Martens L**, 'Proteomics databases and repositories', *Methods in Molecular Biology: Bioinformatics for Comparative Proteomics*, 2011, *Humana Press*
10. Barsnes H, Vizcaíno JA, Reisinger F, Eidhammer I and **Martens L**, 'Submitting Proteomics Data to PRIDE Using PRIDE Converter'. *Methods in Molecular Biology: Bioinformatics for Comparative Proteomics*, 2011, *Humana Press.*
11. Vizcaíno JA, Reisinger F, Côté R and **Martens L**, 'PRIDE: Data submission and analysis'. In: Speicher DW (Ed.) *Current Protocols in Protein Science*, 2009, *John Wiley & Sons, Inc.*
12. **Martens L**, 'Data management in mass spectrometry-based proteomics', *Methods in Molecular Biology: Serum/Plasma Proteomics*, 2011, *Humana Press*.
13. Foster JM and **Martens L**, 'Bioinformatics challenges in the proteomic analysis of human plasma', *Methods in Molecular Biology: Serum/Plasma Proteomics*, 2011, *Humana Press*.
14. Helsens K, **Martens L**, Vandekerckhove J and Gevaert K, 'Mass spectrometry-driven proteomics: an introduction', *Methods in Molecular Biology: Gel-Free Proteomics*, 2011, *Humana Press*.
15. **Martens L**, 'Bioinformatics challenges in mass spectrometry-driven proteomics', *Methods in Molecular Biology: Gel-Free Proteomics*, 2011, *Humana Press*.
16. Colaert N, Vandekerckhove J, **Martens L** and Gevaert K, 'A case study on the comparison of different software tools for automated quantification of peptides', *Methods in Molecular Biology: Gel-Free Proteomics*, 2011, *Humana Press*.
17. Vaudel M, Burkhart JM, Zahedi RP, **Martens L**, Sickmann A, 'iTRAQ Data Interpretation', *Methods in Molecular Biology*, 2012, *Humana Press*.

SCIENTIFIC MEETINGS AND WORKSHOPS ORGANIZED

I have organised over 40 workshops, meetings, and conferences worldwide, including for the European Molecular Biology Laboratory (EMBL), Association of Biomolecular Resource Facilities (ABRF), Research on Computational Molecular Biology Conferences (RECOMB), International Society for Computational Biology (ISCB), European Conference on Computational Biology (ECCB), Human Proteome Organisation (HUPO), Lorentz Workshops, and the Novo Nordisk Foundation. I have also served as lead organiser for five consecutive Dagstuhl Seminars on Computational Proteomics.

PARTICIPATION IN MEETINGS AS INVITED SPEAKER

Scientific Meetings

1. Genomics Momentum 2004, Rotterdam, The Netherlands, August 2004, "Novel strategies to global and quantitative proteomics"
2. Human Brain Proteome Project 3rd Workshop, Rauischholzhausen, Germany, December 2004, "The PRIDE database"
3. Seminars of the Research Group on Theoretical Computer Science, Limburgs Universitair Centrum, Diepenbeek, Belgium, December 2004, "PRIDE and the PSI-GPS standards: keystones for the proteomics community"
4. Seminar at the Proteomic Unit at the University of Bergen (PROBE), Bergen, Norway, March 2005, "May you live in interesting times: proteomics anno 2005"
5. HUPO 2005 4th Annual World Congress, Munich, Germany, August 2005, "Lessons to be learned from HUPO BPP and PPP Pilot Studies"

6. Interaction Proteome Annual Meeting, Munich, Germany, September 2005, "The strong and silent types: bioinformatics tools for the COFRADIC gel-free proteomics technology"
7. Third International Symposium of the Austrian Proteomics Platform, Seefeld, Austria, January 2006, "Proteomics Data Handling and Analysis: Building the Stack and Enjoying the View"
8. Human Brain Proteome Project 5th Workshop, Dublin, Ireland, February 2006, "Report from the Jamboree: a gathering of youth"
9. Johns Hopkins University, Baltimore (MD), USA, May 2006, "Basic anatomy of a proteomics lab: building the backbone, nervous system and communication organs"
10. Seminar on bioinformatic challenges and solutions for proteomics research, Bergen, Norway, October 2006, "Proteomics, PRIDE and PSI: ample work for our generation"
11. ProDaC kick-off meeting, Long Beach (CA), USA, October 2006, "Standards for proteomics data representation"
12. Standardization Issues in Proteomics, Long Beach (CA), USA, October 2006, "Staying in orbit: why a repository needs standards"
13. HUPO Plasma Proteome Project workshop, Long Beach (CA), USA, October 2006, "Informatics challenges and insights for the HUPO PPP"
14. HUPO 2006 5th World Congress, Long Beach (CA), USA, October-November 2006, "Panning the data: looking for gold within and across proteomics experiments"
15. NPC Progress Meeting, Utrecht, The Netherlands, February 2007, "Don't let the sleeping patterns lie: The quest for latent information across proteomics experiments"
16. MGPI Breast Cancer and Proteomics workshop, Clare College, Cambridge, UK, July 2007, "The PRIDE proteomics repository; more than a data storage system!"
17. "Sociomics": A Multidisciplinary Workshop on the Transformation of Knowledge Production in the Biosciences, and its Consequences (CESAGen), Hinxton, Cambridge, UK, July 2007, "Transformation of Knowledge Production & the Biological Discovery Sciences: a Dry Lab Perspective"
18. Joint BSPR & EBI 2007 Conference: 'Integrative Proteomics: From Molecules To Systems', Hinxton, Cambridge, UK, July 2007, "Integrative proteomics: a pipe dream?"
19. Third Norwegian Proteomics conference, Ås, Norway, September 2007, "Pattern detection in large-scale proteomics experiments: beyond a divining rod"
20. Seminar on bioinformatics for proteomics, Rudolf Virchow Center, Würzburg, Germany, September 2007, "Three proteomics data challenges: quantity, quality and dissemination"
21. HUPO 2007 6th World Congress, Seoul, Seoul,South Korea, October 2007, "Answers from proteomics data, even if your question is complex or you speak a different language"
22. National Institute of Standards and Technology (NIST), Gaithersburg (MD), USA, November 2007, "PRIDE: a versatile proteomics data repository, based on community standards"
23. Bellairs Research Institute, McGill University, Barbados, January 2008, "The PRIDE database"
24. Niigata University, Niigata, Japan, January 2008, "Two proteomics bioinformatics bottlenecks: quality assessment and data dissemination"
25. Ghent University, Ghent, Belgium, February 2008, "Proteomics data storage and analysis: putting the cat next to the milk"
26. 3rd International Proteomics Conference of the Royal Flemish Chemical Society, Antwerp, Belgium, December 2008, "Proteomics by the numbers: bioinformatics analyses and tools that support the transition to targeted approaches"
27. Bellairs Research Institute, McGill University, Barbados, January 2009, "Data dissemination strategy for the HUPO Test Samples"
28. Korean HUPO 2009 Conference: Proteomics: From Discovery to Functions, Seoul, South Korea, March 2009, "Proteomics by the Numbers: Rethinking Proteomics Informatics"
29. Proteomic Forum 2009: The Proteomic Forum Berlin 2009, Berlin, Germany, March 2009, "Sandwiching the Lab Between Computers: Bioinformatics to both Guide and

Process Experiments”

30. Advances in Molecular Mechanisms of Disease: High Throughput Platforms and Advances in Imaging, Oslo, Norway, June 2009, “Proteomic studies in human diseases”
31. XXIVth International Symposium on Cerebral Blood Flow, Metabolism and Function, Chicago, IL, USA, June-July 2009, “What to do with all that data?!”
32. Ruhr-Universität Bochum, Bochum, Germany, July 2009, “Proteome bioinformatics: engineering bridges”
33. DAPSOC 5th Annual Symposium, Odense, Denmark, December 2009, “The case for Computational Proteomics: An analysis of what is, and of what could be.”
34. Centre de Recherche Public (CRP) Santé, Luxembourg, GD Luxembourg, March 2010, “An analysis of the public human proteome: footprints, biases, and recommendations.”
35. 4D Biology Workshop, European Commission, Brussels, Belgium, March 2010, “Construction of a public human proteome and corresponding lessons learned”
36. Analytica Conference 2010, Munich, Germany, March 2010, “Scale issues in protein quantification: why we must make our life difficult.”
37. Advances in Clinical Proteomics, Luxembourg, GD Luxembourg, September 2010, "Bioinformatics challenges in proteomics"
38. KFBS Data Biological Evaluation Workshop, Incheon, South Korea, January 2011, "A posteriori analysis of large-scale proteomics data to ascertain quality"
39. Ninth Asia Pacific Bioinformatics Conference (APBC2011), Incheon, South Korea, January 2011, “From proteomics informatics to computational proteomics: finding optimal and sensible targets for targeted proteomics”
40. Korean Basic Science Institute, Ochang, South Korea, January 2011, “Bioinformatics for the brain proteome”
41. University of Southern Denmark, Odense, Denmark, February 2011, “Understanding MS proteomics data first, then predicting it”
42. Fourth Congress of the Spanish Proteomics Society, Segovia, Spain, February 2011, “Quality control of proteomics data: performing local as well as global analyses”
43. ABRF 2011: Technologies to Enable Personalized Medicine, San Antonio, TX, USA, February 2011, “A Study on the Identification of Electron Transfer Dissociation (ETD) Mass Spectra”
44. Proteomic Forum 2011, Berlin, Germany, April 2011, “Bioinformatics to squeeze the lemon: getting the most from your hard-earned proteomics data”
45. Proteomics Workshop 2011, ISAS, Dortmund, Germany, September 2011, “Proteomics informatics: start to finish”
46. WOUD Symposium in Bioinformatics: Tools in Research, UGent, Gent, Belgium, September 2011, “Proteomics and cross-omics integration”
47. ProteoMMX 2.0, Chester, UK, March 2012, “Blue pills, red pills or purple pills: the importance of choosing the right algorithm(s) for quantitative data processing”
48. Max Planck Institute for the Dynamics of Complex Technical Systems, Magdeburg, Germany, May 2012, “Crystal balls and mass spectrometers: doing the experiment only if you can predict what will come out”
49. 60th ASMS Conference on Mass Spectrometry and Allied Topics, Vancouver, BC, Canada, May 2012, “The Future of Proteomics Repositories”
50. 5th FinnProt Symposium, Porvoo, Finland, June 2012, ‘It's raining data! Software to handle the flood and surf the waves.’
51. Bioinformatics 2012 Conference, Stockholm, Sweden, June 2012, ‘Snakes and ladders: where do proteomics assays fail and how can we fix them?’
52. BIOSS Seminars, Freiburg, Germany, July 2012, ‘Making the most of your experiments: powerful processing of proteomics data for optimal performance’
53. EuPA/BSPR Proteomics Meeting, Glasgow, Scotland, July 2012, ‘Trawling through proteomics data: analyzing and learning from the catch’
54. 10th Austrian Proteomic Research Symposium, Graz, Austria, September 2012, ‘Taking

a bioinformatics hike off the beaten track: metaproteomics and proteomics of non-model organisms'

55. Habana Bioinformatics, La Habana, Cuba, December 2012, 'Tapping into collective knowledge - mining the public proteome'
56. CeProMa/VITO Research Day, Antwerp, Belgium, December 2012, 'Three goals for proteomics: aim better, shoot straighter, find new targets'
57. Luxembourg Proteomics Center, Centre de Recherche Public de la Santé (CRP-Santé), GD Luxembourg, January 2013, 'The need for detailed understanding and accurate prediction in targeted proteomics'
58. Lecture Series in Molecular Life Sciences, Institute of Molecular Life Sciences, University of Zurich, March 2013, 'Tools for targeted proteomics: a path to efficient assay design'
59. DELSA Workshop 4, Bethesda, MD, USA, May 2013, "Endless Rebirth of Proteomics Data"
60. ASMS 2013, Minneapolis, MN, USA, June 2013, "Looking into protein quantification: a many-faceted jewel with some pretty sharp edges"
61. AuPA Bioinformatics Workshop, Salzburg, Austria, July 2013, "Going through your trash: building a future on yesterday's news"
62. Karolinska Institutet and Science for Life Laboratory, Stockholm, Sweden, September 2013, "Closing the proteomics data ecosystem: reactivating experimental sediments"
63. Oslo University, Oslo, Norway, October 2013, "Danse not so macabre: re-animating dead proteomics data"
64. CLASS Seminars, University College Dublin, Dublin, Ireland, January 2014, "Enough experiments already: the enormous utility of post-consumer proteomics data"
65. ProteoMMX 3.0, Chester, UK, March 2014, "Supporting reproducible proteomics: some small steps in targeted and not so targeted methods"
66. MCB 2014 / ERIBA Inaugural Congress, Groningen, The Netherlands, August 2014, "Tomb raider: the fruitful exploration of proteomics data graveyards"
67. ISCB European Student Council Symposium, Strasbourg, France, September 2014, "Saprotrophics: a new natural habitat for bioinformaticians?"
68. ECCB Workshop on Proteome and Metabolome Informatics, Strasbourg, France, September 2014, "Tsunami or alluvial plain? A primer on dealing with public data."
69. Joint VIB and Belgian EMBL Alumni Day, Ghent, Belgium, October 2014, "Life after (??) VIB and EMBL"
70. ThermoFisher Proteome Discoverer Annual User Meeting, Bremen, Germany, December 2014, "Fooled no more, or at least differently: ditching the decoys"
71. NPC Progress Meeting 2015, Utrecht, The Netherlands, January 2015, "The Cathedral and the Bazaar: crowd-sourcing proteomes"
72. Metadata Standards and Data Formats for imaging data, Heidelberg, Germany, February 2015, "Cell migration metadata annotation and storage"
73. EuPA Initiatives Meeting, Berlin, Germany, March 2015, "Facilitating crowdsourcing and crowdfunding of novel proteomics informatics tools"
74. Proteomic Forum 2015, Berlin, Germany, March 2015, "Speaking to spectra: what we can learn without using search engines"
75. Symposium at University of Vienna, Vienna, Austria, April 2015, "Weird tools: data analysis on the fringe of proteomics"
76. EuPA 2015 Meeting, Milan, Italy, June 2015, "small microbes, big problems metaproteomics tools and challenges"
77. BSPR 2015 Conference, Reading, UK, July 2015, "Into the Land of Confusion: a Travel Guide to the Metaproteome"
78. Dagstuhl Conference on Mass Spectrometry Informatics, Dagstuhl, Germany, August 2015, "Democratization of proteomics data"
79. SMODIA 2015, Valencia, Spain, September 2015, "Dig deep and dig greedily: what we awaken in omics data analyses"

80. Swedish Bioinformatics Conference 2015, Stockholm, Sweden, September 2015, "Our heaven is their hell: when data is easy, but results are not"
81. HUPO WOrld Congress 2015, Vancouver, Canada, October 2015, "Metaproteomics data analysis: charting war and peace in a microbiome"
82. Nature Conference on Life Science in the Age of Big Data, Beijing, China, October 2015, "from a small seed to a flowering forest: the benefits of a dynamic ecosystem for proteomics data"
83. Symposium at Jena Univeristy, Jena, Germany, December 2015, "Over the hedge: proteomics algorithms that could serve metabolomics"
84. Metaproteomics Symposium at Max Planck Institute, Magdeburg, Germany, Februari 2016, "a new trade requires new tools: meeting the bioinformatics challenge of the metaproteome"
85. VIB Conference on Applied Bioinformatics, Leuven, Belgium, March 2016, "Hunting for mythical beasts - an exploration of the hidden (or hard to get) proteome"
86. FOSTER Symposium, Kaunas, Lithuania, March 2016, "Benefits of open science"
87. Analytica 2016, Munich, Germany, May 2016, "Standards as the gateway to assured analytical quality in the field of proteomics"
88. Biological Colloquium, Kaiserslautern, Germany, May 2016, "Yesterday's data will deliver tomorrow's news: (orthogonal) re-use of public proteomics data to obtain new insights on our genome"
89. EMBL-EBI Symposia, Cambridge, UK, June 2016, "Proteomics as a small case study for the next golden age of biology"
90. EuPA 2016 Conference, Istanbul, Turkey, June 2016, "Where East meets West: the right bioinformatics tools for the most challenging proteomics analyses"
91. FASEB meeting on Calpains, Big Sky MT, USA, July 2016, "PeptideShaker and friends: analysis and interpretation of MS proteomic data"
92. University of Southern Denmark, Odene, Denmark, August 2016, "Why we cannot afford black boxes in science: the importance of open source software in omics analyses"
93. Danish Bioinformatics Conference, Odense, Denmark, August 2016, "Teaching our proteomics tools new tricks: innovative algorithms from old data"
94. Austrian Proteomics Society 2016 Conference, Vienna, Austria, September 2016, "Listening for protein gossip in proteomics data: who does it with who?"
95. HUPO 2016 World Congress, Taipei, Taiwan, September 2014, "More power and more depth: new tools for proteomics data processing"
96. Muenster Conference on Biomolecule Analysis, Max Planck Institute, Muenster, Germany, October 2016, "Novel algorithms for proteomics data: seeing more of what our mass specs have already seen"
97. VLIR Symposium on Scientific Integrity, Ghent, Belgium, December 2016, "When staying whole is much more important than being the sum of parts"
98. EuBIC Mid-winter Proteomics Symposium 2017, Semmering, Austria, January 2017, "Open data: why are we not doing more?"
99. ILVO Event on Scientific Integrity, Ghent, Belgium, January 2017, "Snakes, ladders and slippery slopes: do our academic career paths lead to research integrity?"
100. Biomina Research Symposia, Antwerpen, Belgium, February 2017, "The tabloid proteome - from public data to sneaky liaisons"
101. ELIXIR Proteomics workshop, Tuebingen, Germany, March 2017, "Proteomics Informatics at ELIXIR Belgium"
102. Proteomic Forum 2017, Potsdam, Germany, April 2017, "The other side of integration: proteomics as a vital tool in other omics"
103. Italian Proteomics Association Meeting 2017, Lecce, Italy, June 2017, "Micromanagement of the metaproteome: taking control of your data"
104. Research Symposium, Groningen University, Groningen, Netherlands, July 2017, “A digital zoom for proteomics: reliable identification and delineation of subset proteomes”

105. HUPO 2017 World Congress, Dublin, Ireland, September 2017, “False discovery rates in proteomics: a tale of two extremes”
106. Dagstuhl Seminar on Computational Proteomics, Dagstuhl, Germany, October 2017, Lead organizer.
107. Doctoral School of Public Health of Paris (Paris Descartes, Paris Diderot and University Pierre and Marie Curie), St. Malo, France, October 2017, “Snakes, ladders and slippery slopes: do our academic career paths lead to research integrity?”
108. OpenAIRE Open Science Event, Esch-sur-Alzette, GD Luxembourg, October 2017, “Do you speak Open Science? Here’s why you should!”
109. ASCB-EMBO Meeting 2017, Philadelphia, USA, December 2017, “An open data exchange ecosystem for cell migration data”
110. EuBIC meeting 2018, Ghent, Belgium, January 2018, “The Researcher-Developer: a primer on why you don't belong (yet) and what you can (possibly) expect in the future”
111. DSM seminar, Delft, The Netherlands, January 2018, “Dealing with the flood: namespaces and annotations for data, and possibly even their integration.”
112. Webinar for the Young Proteomics Investigators of the European Proteomics Association, March 2018, “A peek behind the curtain: what happens to your manuscript, and to your grant after you've submitted it”, YouTube link: https://www.youtube.com/watch?v=O39faEL7d1o&t=3156s
113. EMBL-EBI seminar, Cambridge, UK, July 2018, “The online Tabloid Proteome: a novel means of extracting protein associations from public human proteomics data”
114. HUPO-Human Immuno-Proteome Project (HIPP) conference, Madrid, September, 2018, “A new search engine for the neo-proteome”
115. Meet the Expert seminar, Lund University, Lund, Sweden, July 2018, “Computational Omics”
116. EMBL From Functional Genomics to Systems Biology, Heidelberg, Germany, November, 2018, “The tool of revelation: ionbot uncovers an exciting new view on the proteome”
117. Turku University LifeSpan Seminar, Turku, Finland, March 2019, “A proteomics-powered deep dive into the transcriptome”
118. Meet the Expert Seminar, Turku University, Turku, Finland, March 2019, “It's a kind of magic: how better algorithms can instantly upgrade data”
119. Young Proteomics Investigators Club Seminar, Potsdam, Germany, March 2019, “An inclusive future for proteomics: adding PTMs to the routine recipe”
120. Proteomic Forum 2019, Potsdam, Germany, March 2019, “A time of enlightenment: straightforward identification of protein modifications”
121. ELIXIR Proteomics Workshop on Proteomics Data Privacy, Amsterdam, The Netherlands, April 2019, “Prototyping Beacons for Proteomics”
122. Genome Biology Day, CNRS, Gif-sur-Yvette, France, May 2019, “A new frontier for discovery: uncovering protein post-translational modifications at the proteome scale”
123. Seminar KULeuven Animal Physiology and Neurobiology Department, Leuven, Belgium, May 2019, “Decrypting proteomics data: finding all PTMs in your spectra”
124. Alan Turing Institute and British Library, London, UK, June 2019, “Peptide idopenentification and the inexorable rise of database size”
125. ISCB Clinical Statistics Workshop, KULeuven, Belgium, July 2019, “Approaches to MS-based metrics for protein quantification”
126. ELIXIR Belgium All Hands Meeting, Brussels, Belgium, September 2019, “Form, function, and intervention: the central role or proteins in life sciences and health”
127. NETTAB/BBCC 2019 Joint Meeting, Salerno, Italy, November 2019, “To boldly go: uncovering protein post-translational modifications at the proteome scale”
129. EMBL course, Heidelberg, Germany, February 2020, “Proteomics / transcriptomics data integration”
130. Jim Waters Society Lecture, Waters Corp., Wilmslow, UK. January 2020. “A machine learning-based window to shed new light on mass spectrometry data.”

131. London Proteomics Discussion Group Webinar, July 2020, “Proteomics: The Role of Machine Leaning.” https://www.youtube.com/watch?v=KgqZYT0NjLA
132. Keystone Symposium on Proteomics in Cell Biology and Disease, online, September 2020, “Machine Learning Powered Next-Generation Proteomics.”
133. BELSACT Annual Symposium, November 2020, online, “The many joys of sharing, and some pitfalls too”
134. Life Sciences Switzerland Prestige Seminar, April 2021, online, "The dawn of new discovery: a proteome-wide view on protein modifications"
135. NordBioMedNet Seminar, August 2021, online, “Data sharing and data reprocessing in the life sciences”
136. de.NBI Summerschool, September 2021, online, “Back to the Future: Finding the Future of Proteomics in Yesterday's Data”Copenhagen Bioscience Conference, Copenhagen, Denmark, October 2021, “A Learning Revolution n Computational Proteomics”
137. Cancer Research Institute Ghent Industry Event, October 2021, Ghent, Belgium, “The novel ionbot proteomics search engine as a game-changer in cancer research”
138. MSCoreSys Summer School, October 2021, Bad Dürkheim, Germany, “The secret life of proteins: unbiased proteome-wide modification discovery”
139. Dagstuhl Seminar in Biological Data Visualisation, October 2021, Dagstuhl, Germany,”Proteomics Data - the Next Generation”
140. VLIR Scientific Integrity Event, November 2021, Leuven, Belgium, “Data sharing for integrity, or integrity in data sharing?”
141. French National Proteomics Society, February 2022, Strasbourg, France and online, “la recherche dans le residu: what can we learn from the leftovers?”
142. Seminars in Immunology, University Hospital Strasbourg, February 2022, Strasbourg, France, “La piqûre du futur: next-gen vaccine design for neo- and xenoepitopes”
143. Lorentz Workshop in Bioinformatics, March 2022, Leiden, The Netherlands, “the future of machine learning in proteomics”
144. European Bioinformatics Community, March 2022, online, “Feathering the dinosaurs: machine learning unveils the proteome-wide modification landscape”
145. European Proteomics Association/Proteomic Forum 2022, April 2022, Leipzig, Germany, “The advent of epi-proteomics: our first steps into an exciting new world!”
146. Interfaculty Institute for Biomedical Infirmatics (IBMI), Tübingen University, April 2022, Tübingen, Germany, “The Shock of the New - Machine Learning reveals the true complexity of the proteome”
147. Dagstuhl Seminar on Metabolomics, May 2022, Dagstuhl, Germany, “The advent of epi-proteomics: where the metabolome touches the proteome.”
148. Next-Generation Protein Analysis and Detection Conference, April 2022, Gent, Belgium, “Next-Generation Protein Analysis and Detection”
149. KULeuven Open Science Day, May 2022, Leuven, Belgium, “The open science of the everyday, and why it is our future.”
150. Asian Oncology Society 2022 Conference, June 2022, Seoul, Korea, “Machine learning powered next-generation proteomics”
151. ISMB 2022, July 2022, Madison, WI, USA, “Machine learning provides a new perspective on protein modification”
152. Canadian National Proteomics Network Annual Meeting, May 2022, Montréal, Canada, “A new wavelength to view proteins: revealing proteome-wide modifications.”
153. Novo Nordisk Foundation’s Copenhagen Bioscience Snapshot, September 2022, Copenhagen, Denmark, “The Proteome, version 2.0: time to take PTMs (even more) seriously”
154. Eurographics Workshop on Visual Computing for Biology and Medicine, September 2022, Vienna, Austria, “Proteomics’ modern era – new tools enable us to see in new ways (and require new visualisations!)”
155. EPIC-XS Webinar series, September 2022, online, “Unbiased exploration of the

proteome-wide modification landscape."

156. Human Proteome Organisation Early Career Researcher Day, September 2022, online, "Various notes on starting your own lab."
157. VPAP Singapore, October 2022, online, "Metaproteomics meets machine learning: a crucial combo."
158. SFSM/FPS, Institut Pasteur, Paris, France, March 2023, "Proteome-wide PTM discovery: our tools have evolved, now we need to too!"
159. ORPHEUS Conference 2023, KULeuven, Leuven, Belgium, April 2023, "Open Science = open for business - why you should make it your business!"
160. 16-ième Journées du Club Jeune de la FPS, Université de Strasbourg, Strasbourg, France, April 2023, "Greater depth on more solid ground: CompOmics tools for your data analysis"
161. Annual PhD retreat of the University of Vienna, April 2023, Vienna, Austria, "Interesting reactions at the interface of life sciences data and AI."
162. Workshop on Immune Polymorphism and Evolution, Université de Strasbourg, Strasbourg, France, April 2023, "Where the rubber meets the road: probing (neo-) epitopes with MS and AI."
163. 54th Annual DGMS Conference, Dortmund, Germany, May 2023, "The future has arrived, now try to enjoy it - AI meets MS."
164. Advanced Proteomics Summer School, Brixen, Italy, August 2023, "Next Generation Protein Identification"
165. European Single Cell Proteomics Conference, Vienna, Austria, August 2023, "It takes a village to analyse a single cell: where a lot is made of very little"
166. KULeuven Seminars on Advances in Protein Chemistry, Leuven, Belgium, September 2023, "The fashionable proteome: how AI reveals the protein wardrobe"
167. KG Jebsen Academy, Oslo, Norway, October 2023, "Making the mark - impactful science for an impactful proposal"
168. ECPM Journée d'IA en Chimique, Strasbourg, France, November 2023, "Advances in AI and mass spectrometry make for very exciting times in proteomics."
169. Microbiology Seminar, Strasbourg, France, December 2023, "Machine learning in metaproteomics: why, how, and what it (can) deliver(s)."
170. IPHC Seminars, Strasbourg, France, January 2024, "Open science: opportunity knocks at your door"
171. Data Coffee Seminar, Strasbourg, France, January 2024, "Opening a window into a whole new world"

Professional Meetings

(IS) Jackaroo II: The Securex Proof of Concept, Brussels, Belgium, January 2001,
"Jackaroo II: architecture and design"

(IS) Sun Developer Connection, Affligem, Belgium, October 2001,
"EJB 2.0, Will We Have Beans For Breakfast?"

(IS) Microsoft .Net launch, Brussels, Belgium, November 2001,
"The .Net framework and the Java language"

(IS) Microsoft Developer Days, Brussels, Belgium, December 2001,
Closing Keynote: "Ultimate Freedom with Visual Studio.NET"

(IS) STDC Best Practices Event, Rotterdam, The Netherlands, January 2002,
"The future of J2EE: EJB 2.0 and beyond"

(IS) Studiecentrum voor Automatische Informatieverwerking (SAI), Antwerp, Belgium, January 2002,
"J2EE vs. .Net"

(IS) IT Works: The J2EE framework, Brussels, Belgium, February 2002,
“Introduction”,
“JDBC & JTS/JTA”,
“EJB: The J2EE Component Model” and
“Current J2EE application server market & Microsoft .Net”

(IS) IT Works: The J2EE framework, Brussels, Belgium, June 2002,
“Introduction”,
“JDBC & JTS/JTA”,
“EJB: The J2EE Component Model” and
“Current J2EE application server market & Microsoft .Net”

AWARDS AND PRIZES

Scientific awards

- HUPO 2004 Young Scientist Award
- Recipient of the 2014 ‘Prometheus’ award of Ghent University for Excellence in Research
- Recipient of the 2015 ‘Juan Pablo Albar’ Proteomics Pioneer Award of the European Proteomics Association (EuPA)
- Recipient of a 2024 Prix Gutenberg, of the Cercle Gutenberg, Alsace, France.

Professional awards

- Sydney-Tristar 2001 Company Achievement Award

ELECTED MEMBERSHIP AND ROLES OF RESPONSIBILITY IN SCIENTIFIC ORGANISATIONS

- Member of the Scientific Directorate of the Leibniz Association’s Center for Informatics (since 2023)
- Elected as Full Member to the Sigma Xi Scientific Honor Society, USA (since 2022)
- Elected President of the European Proteomics Association (EuPA) (since 2020)
- Elected as Fellow of the Royal Society of Chemistry (FRSC), UK (since 2017)
- Chair of the Gamma Committee (combining the Faculties of Medicine and Health Sciences, Veterinary Sciences, and Pharmaceutical Sciences) in the UGent Research Council (since 2022)
- Member of the UGent Research Council (since 2018)
- Member of the Human Proteome Organisation (HUPO) Council (since 2016)
- Member of the Board of the Belgian Proteomics Association (since 2012)
- Elected member of the Young Academy of the Royal Flemish Academy for Sciences and Arts (2013-2018).
- Elected Vice-President of the European Proteomics Association (EuPA) (2017-2020)
- Member of the Human Proteome Organisation (HUPO) Executive Committee (2017-2019)
- Member of the Board of the Royal Flemish Society for Chemistry Proteomics Section (since 2009)
- Vice-Chair of the VIB Group Leader Committee (2015-2017)
- Chair of the Proteome Informatics Research Group (iPRG) of the association of Biomolecular Resource Facilities (ABRF) (2010-2011)
- Secretary of the Human Proteome Organisation (HUPO) Proteomics Standards Initiative (PSI) Mass Spectrometry working group (2006-2010).