

## CURRICULUM VITAE

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### Prof. Dr. Lennart MARTENS

Ghent University and VIB, Ghent, Belgium

*Last update: 14 April 2015*

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<b>NAME</b>	MARTENS
<b>FIRST NAME</b>	Lennart
<b>PLACE OF BIRTH</b>	Hasselt (Belgium)
<b>NATIONALITY</b>	Belgian
<b>MARITAL STATUS</b>	Married, with two children
<b>NAME OF SPOUSE</b>	KESTENS Leen
<b>PROFESSIONAL ADDRESS</b>	A. Baertsoenkaai 3 B-9000 Gent Belgium Tel.: +32 9 264 93 58 (Direct Line) Fax: +32 9 264 94 84 Skype: lennart_martens e-mail: <a href="mailto:lennart.martens@UGent.be">lennart.martens@UGent.be</a>
<b>ACADEMIC TITLES</b>	<ul style="list-style-type: none"><li>- <b>Candidature Biology</b> (<i>Bachelor degree</i>) July 1998, Limburgs Universitair Centrum (LUC – now Hasselt University), Belgium.</li><li>- <b>Licentiate Biotechnology</b> (<i>Master in Science degree</i>) July 2000, Ghent University, Belgium.</li><li>- <b>Doctorate (Ph.D.) in Sciences: Biotechnology</b> 15 June 2006, Ghent University, Belgium.</li></ul>
<b>TITLE OF MASTER'S THESIS</b>	"The development of novel algorithms for the identification of proteins via MALDI-PSD mass spectrometry"
<b>TITLE OF PH. D. THESIS</b>	"Novel bioinformatics tools assisting targeted peptide-centric proteomics and global proteomics data dissemination"
<b>PROFESSIONAL TITLES</b>	Sun Certified Programmer for the Java 2 Platform (score of 93%).
<b>PRESENT APPOINTMENTS</b>	Professor of Systems Biology in the Department of Biochemistry, Faculty of Medicine and Health Sciences, Ghent University, Ghent, Belgium (since October 2009). Group Leader, Computational Omics and Systems Biology Group, Department of Medical Protein Research, VIB, Ghent, Belgium (since October 2009). Visiting Scientist, European Bioinformatics Institute (EBI), European Molecular Biology Laboratory (EMBL) outstation, Hinxton, Cambridge, United Kingdom (since January 2014).

## PAST APPOINTMENTS

- February 2008 to October 2009: PRIDE Group Coordinator at the European Bioinformatics Institute (EBI), European Molecular Biology Laboratory (EMBL) outstation, Hinxton, Cambridge, United Kingdom.
- July 2006 to February 2008: Senior Software Developer 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 (F.W.O.-Vlaanderen).
- March 2002 to October 2002: Predoctoral researcher of the Flanders Interuniversity 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).

### *University courses*

- Lecturer for the course Biochemistry II, for the third bachelor Biomedical Sciences Ghent University, Belgium (since 2010).
- Lecturer for the course Informatics II: bio-informatics for the third bachelor Biomedical Sciences, Ghent University, Belgium (since 2010).
- One week Proteomics Course, University of Cape Town, National Bioinformatics Node, and Centre for Proteomics and Genomics Research, Cape Town, South Africa (June 2007).
- One week Proteomics and Data Analysis Course, University of Cape Town, National Bioinformatics Node, and Centre for Proteomics and Genomics Research, Cape Town, South Africa (March 2008).
- One week Proteomics Course in the Masters in Bioinformatics course series, Stellenbosch University, National Bioinformatics Node and Cape Biotech Trust, Stellenbosch, South Africa (March 2009).
- One week Proteomics Bioinformatics Course, University of Cape Town and Centre for Proteomics and Genomics Research, Cape Town, South Africa (September 2012).

### *EBI courses*

- Proteomics, an introduction to current techniques and methods and PSI: standards for proteomics, EBI Industry Collaboration Workshop, EBI, Cambridge, United Kingdom (November 2006).
- Proteomics: an introduction and Proteomics data repositories, EBI roadshow, Philips, Eindhoven, The Netherlands (March 2007)
- The central role of the peptide in present-day proteomics, Decoy databases: an overview, and Custom sequence databases for picking up (un-)expected peptides, EBI Industry Collaboration Workshop, EBI, Cambridge, United Kingdom (June 2007).

- Introduction on proteomics technologies, PRIDE/ENFIN workshop, EBI, Cambridge, United Kingdom (November 2007).
- Proteomics identification algorithms and databases and Proteomics: PRIDE, OLS, and PICR, EBI roadshow, VIB and Ghent University, Ghent, Belgium (February 2008).
- A general introduction to proteomics, Programmatic access of Proteomics Resources Course, EBI, Cambridge, United Kingdom (July 2008).
- A hands-on introduction to Ensembl, UniProt, BioMart, and other EBI resources, Bioinformatics Workshop for Lipidomics, Regensburg, Germany (September 2008).
- Proteomics at EBI, EBI primer for Predocs, EBI, Cambridge, United Kingdom (February 2009).
- The PRIDE Repository for Proteomics Data, Masters Open Day, EBI, Cambridge, United Kingdom (March 2009).
- Proteomics at the EBI, A walkthrough EBI Bioinformatics Resources, EBI, Cambridge, United Kingdom (May 2009).
- PRIDE, PICR and BioMart, Interactions & Pathways: towards a whole system perspective, EBI, Cambridge, United Kingdom (June 2009).

#### *Other academic courses*

- Mass Spectrometry Basics, MS Search engines, Identification Reliability, Sequence Databases, and Proteomics Data Formats for the annual Wellcome Trust Advanced Course on Proteomics Bioinformatics, EBI, Cambridge, United Kingdom (2007 - present).
- Proteomics Data Repositories, EuPA MS bioinformatics analysis for proteomics: a tutorial for tutors, CMU, Geneva, Switzerland (June 2007).
- Proteomics Bioinformatics, Proteomics Course 2008, Würzburg, Germany (September 2008).
- Mass Spectrometry Data Analysis, Proteomics Data Analysis Course 2008, Gulbenkian Institute, Oeiras, Portugal (September 2008).
- Sequence Databases and Online Resources and Data Standards and Public Data Dissemination, Real-life Proteome Bioinformatics for Laboratories, ABRF 2009 Satellite Workshop, Memphis, TN, USA (February 2009).
- The pivotal role of the sequence database in peptide and protein identification and Protein quantification: interpreting, comparing and combining quantification results from different software packages, 4th Mass Spectrometry in Biotechnology and Medicine Summer School, Center for Advanced Academic Studies, Dubrovnik, Croatia (July 2010).
- Validating peptide identifications using Peptizer, 4th European Summer School "Proteomic Basics - High-Throughput Data Analysis and Statistics", Bressanone, Italy (August 2010).
- Zen in the Art of Meeting Journal Requirements: Stressless Submission of MS Proteomics Data, Late Summer Practical Proteomics Seminar, Vienna, Austria (September 2010).
- PRIDE: the Proteomics Identifications Database, Workshop on Mastering Proteomic Data, Royal Flemish Society for Chemistry, Hasselt University, Diepenbeek, Belgium (September 2010).
- Proteomics Data Analysis course 2010 (PDA10), Gulbenkian Institute, Oeiras, Portugal (September 2010).
- KVCV Proteomics one-day Workshop on Proteome Informatics, Belgium, two times a year, since April 2011.
- Data Processing, Search Algorithms, Sequence Databases, FDR Calculation and Protein Inference, Proteomics Workshop, ISAS, Dortmund, Germany (September 2011).
- Peptizer and Identification Reliability, FinnProt Workshop on Protein Identification by MS/MS, Helsinki University, Helsinki, Finland (October 2011).

## PUBLICATIONS

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. 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).
5. 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).
6. **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).
7. 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).
8. 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).
9. **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).
10. **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).
11. 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).
12. **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).
13. 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).
14. 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).

15. 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).
16. 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.
17. **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).
18. 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).
19. 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).
20. **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).
21. 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).
22. 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).
23. 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).
24. 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).
25. 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).
26. **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).
27. Hanouille 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).
28. **Martens L**, Helsen 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).
  29. 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).
  30. **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).
  31. 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).
  32. **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).
  33. 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).
  34. Gevaert K, Van Damme P, Ghesquière B, Impens F, **Martens L**, Helsen K and Vandekerckhove J (2007) 'A la carte proteomics with an emphasis on gel-free techniques', *Proteomics*, **7**, 2698-2718 (IF: 5.479).
  35. **Martens L** and Hermjakob H (2007) 'Proteomics data validation: why all must provide data', *Molecular BioSystems*, **3**, 518-522 (IF: 4.121).
  36. 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 Supérieure, Lyon, France', *Proteomics*, **7**, 3034-3037 (IF: 5.479).
  37. 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).
  38. Flikka K, Meukens J, Helsen 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).
  39. **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).
  40. 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).
  41. 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).
  42. 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).
43. **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).
  44. 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).
  45. 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).
  46. 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).
  47. 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).
  48. **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).
  49. 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).
  50. 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).
  51. 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).
  52. 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).
  53. 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).
  54. Taylor CF and **Martens L** (2009) 'Progress by the Proteomics Standards Initiative', *European Pharmaceutical Review* **1/09**, 33-37 (IF: N/A).
  55. **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).
  56. 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).
  57. 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).
  58. 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).

59. 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).
60. 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).
61. 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).
62. 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).
63. 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).
64. 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).
65. 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).
66. 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).
67. 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).
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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 Identifications 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. Helsen 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, Burkhardt JM, Zahedi RP, **Martens L**, Sickmann A, 'iTRAQ Data Interpretation', *Methods in Molecular Biology*, 2012, Humana Press.

## SCIENTIFIC MEETINGS AND WORKSHOPS ORGANIZED

- 'Industry Workshop: Computational Identification of Peptides', 28-29 June 2007, EMBL-EBI, Hinxton, Cambridge, UK.
- 'Bioinformatics Workshop for Lipidomics', 15-17 September 2008, University Clinic Regensburg, Regensburg, Germany.
- 'Real-life Proteome Bioinformatics for Laboratories', ABRF 2009 Satellite Workshop, 7 February 2009, Memphis, TN, USA.
- Session on 'High-Throughput Data Analysis and Pathway Modeling', LipidomicNet High Throughput Technology Workshop, 16-17 March 2009, Kraków, Poland.
- ESF Quality Control in Proteomics Workshop, 25-27 November 2009, Cambridge, UK.
- First International ms\_lims Workshop, 25-27 January 2010, Dortmund, Germany.
- RECOMB 2010, 27-28 March 2010, San Diego, CA, USA, Program Committee Member Computational Proteomics.
- Proteomics Data Analysis workshop 2010 (PDA10), 13-17 September 2010, Gulbenkian Institute, Oeiras, Portugal.
- Flanders Proteomics International Congress IV: Proteomics and the World of Tomorrow, Antwerp, Belgium, 16-17 December 2010.
- RECOMB 2011, 11-13 March 2011, San Diego, CA, USA, Program Committee Member Computational Proteomics.
- ISMB/ECCB 2011, 15-19 July 2011, Vienna, Austria, Program Committee Member.
- 'Workshop on Quality Control in Proteomics', 15-16 September 2011, Ghent University, Ghent, Belgium.
- KVCV Proteomics hands-on Workshop on Proteome Informatics, UGent, Gent, Belgium (18 September 2011).
- Benelux Bioinformatics Conference 2011, 12-13 December 2011, Luxembourg, G.D. Luxembourg, Scientific Programme Committee Member.
- RECOMB 2012, 21-24 April 2012, Barcelona, Spain, Program Committee Member.
- ISMB 2012, 15-17 July 2012, Long Beach, CA, USA, Program Committee Member.
- ECCB 2012, 9-12 September 2012, Basel, Switzerland, Program Committee Member.
- Wellcome Trust Advanced Course in Proteomics Bioinformatics, Scientific Organizer and Lead Instructor
- Graph Databases in the Life Sciences Workshop, 12 November 2012, Ghent, Belgium, Organizer.
- 1<sup>st</sup> Belgian Proteomics Association Conference, 29-30 November 2012, Ghent, Belgium, Organizer.
- Data Management and Standardization in Cell Migration Research, 3-5 March 2014, Ghent, Belgium, Organizer.



## PARTICIPATION IN MEETINGS

as speaker	(S)
as invited speaker	(IS)
as session chair	(SC)
poster presentation	(P)
as participant	(*)

### *Scientific Meetings*

- (S) Swiss Proteomics Society 2002 Congress in Applied Proteomics, Lausanne, Switzerland, December 2002,  
"Fitting the data to the protocol: the quest for more resourceful databases in gel- free proteomics"
- (\*) Special FEBS 2003 meeting on signal transduction, Brussels, Belgium, July 2003
- (\*) Human Proteome Organization Plasma Proteome Project Jamboree, Ann Arbor (MI), USA, June 2004
- (IS) Genomics Momentum 2004, Rotterdam, The Netherlands, August 2004,  
"Novel strategies to global and quantitative proteomics"
- (P) HUPO 2004 3<sup>rd</sup> Annual World Congress, Beijing, China, October 2004,  
"The PRIDE database: giving researchers access to proteomics data and providing this data with a home"
- (IS) Human Brain Proteome Project 3<sup>rd</sup> Workshop, Rauschholzhausen, Germany, December 2004,  
"The PRIDE database", and  
"Some lessons learned from the Plasma Proteome Project"
- (IS) 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"
- (IS) Seminar at the Proteomic Unit at the University of Bergen (*PROBE*), Bergen, Norway, March 2005,  
"May you live in interesting times: proteomics anno 2005"
- (IS) VIB Permanent Training Project, Module 4: 'Expression Profiling', Katholieke Universiteit Leuven, Leuven, Belgium, March 2005,  
"Fundamentals of protein profiling and the 'old' techniques" and  
"High-throughput protein profiling"
- (P) NRPP Proteome Informatics Workshop, University of Michigan, Ann Arbor (MI), USA, June 2005,  
"The PRIDE database: a publicly available, open source proteomics data repository"
- (S) ISMB 2005, Detroit(MI), USA, June 2005,  
Academic demo: "The PRIDE database: plugging the hole that is leaking proteomics data"
- (IS) Human Brain Proteome Project 4<sup>th</sup> Workshop, Munich, Germany, August 2005,  
"Lessons to be learned from HUPO BPP and PPP Pilot Studies"
- (P) HUPO 2005 4<sup>th</sup> Annual World Congress, Munich, Germany, August-September 2005,  
"The PRIDE project: enabling you to deliver your data to the world"
- (IS) Interaction Proteome Annual Meeting, Munich, Germany, September 2005,  
"The strong and silent types: bioinformatics tools for the COFRADIC gel-free proteomics technology"
- (\*) Human Proteome Organization Brain Proteome Project Jamboree, Hinxton, Cambridge, UK, January 2006

- (IS) Third International Symposium of the Austrian Proteomics Platform, Seefeld, Austria, January 2006,  
"Proteomics Data Handling and Analysis: Building the Stack and Enjoying the View"
- (IS) Human Brain Proteome Project 5<sup>th</sup> Workshop, Dublin, Ireland, February 2006,  
"Report from the Jamboree: a gathering of youth"
- (IS) Johns Hopkins University, Baltimore (MD), USA, May 2006,  
"Basic anatomy of a proteomics lab: building the backbone, nervous system and communication organs"
- (S) 7<sup>th</sup> Siena Meeting from Genome to Proteome: Back to the Future, Siena, Italy, September 2006,  
"Promoting proteomics to a data producer: bioinformatics tools to manage, validate and disperse proteomics data in order to really make it work"
- (\*) HUPO Proteomics Standards Initiative (PSI) Fall Workshop, Washington DC, USA, September 2006
- (IS) Seminar on bioinformatic challenges and solutions for proteomics research, Bergen, Norway, October 2006.  
"Proteomics, PRIDE and PSI: ample work for our generation" and  
"A river runs through it: data-driven proteomics research"
- (IS) ProDaC kick-off meeting, Long Beach (CA), USA, October 2006  
"Standards for proteomics data representation"  
"Proteomics repository adaptation"  
"Data Flow Management"  
"Proteomics Data Exploitation"
- (IS) Standardization Issues in Proteomics, Long Beach (CA), USA, October 2006  
"Staying in orbit: why a repository needs standards"
- (IS) HUPO Plasma Proteome Project workshop, Long Beach (CA), USA, October 2006  
"Informatics challenges and insights for the HUPO PPP"
- (IS) HUPO 2006 5<sup>th</sup> World Congress, Long Beach (CA), USA, October-November 2006  
"Panning the data: looking for gold within and across proteomics experiments"
- (IS) NPC Progress Meeting – Master Classes, Utrecht, The Netherlands, February 2007  
"Don't let the sleeping patterns lie: The quest for latent information across proteomics experiments"
- (IS) Human Brain Proteome Project 7<sup>th</sup> Workshop, Hinxton, Cambridge, UK, March 2007,  
"Databases, data storage and PRIDE"
- (\*) HUPO Proteomics Standards Initiative (PSI) Spring Workshop, Lyon, France, April 2007
- (IS) 1<sup>st</sup> ProDaC workshop, Lyon, France, April 2007  
"Bringing it all together: Standards for proteomics data representation"  
"On common ground for fair comparison: Proteomics repository adaptation"
- (\*) ProDaC/HUPO Proteomics Standards Initiative (PSI) Workshop, Hinxton, Cambridge, UK, June 2007
- (IS) MGPI Breast Cancer and Proteomics workshop, Clare College, Cambridge, UK, July 2007  
"The PRIDE proteomics repository; more than a data storage system!"
- (IS) "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"
- (IS) Joint BSPR & EBI 2007 Conference: 'Integrative Proteomics: From Molecules To Systems', Hinxton, Cambridge, UK, July 2007  
"Integrative proteomics: a pipe dream?"

- (IS) Third Norwegian Proteomics conference, Ås, Norway, September 2007  
"Pattern detection in large-scale proteomics experiments: beyond a divining rod"
- (IS) Seminar on bioinformatics for proteomics, Rudolf Virchow Center, Würzburg, Germany, September 2007  
"Three proteomics data challenges: quantity, quality and dissemination"
- (IS) 2<sup>nd</sup> ProDaC workshop, Seoul, South Korea, October 2007  
"Standards for proteomics data representation"  
"Proteomics repository adaptation"  
"Proteomics data exploitation"
- (IS) HUPO Plasma Proteome Project workshop, Seoul, South Korea, October 2007  
"Informatics and databases for the HUPO Plasma Proteome Project"
- (IS) HUPO Proteomics Standards Initiative workshop, Seoul, South Korea, October 2007  
"PSI mass spectrometry"
- (S) HUPO 2007 6<sup>th</sup> World Congress, Seoul, South Korea, October 2007  
"Answers from proteomics data, even if your question is complex or you speak a different language"
- (IS) National Institute of Standards and Technology (NIST), Gaithersburg (MD), USA, November 2007  
"PRIDE: a versatile proteomics data repository, based on community standards"
- (\*) Strategies for Improving Reliability in Protein/Peptide Identification Workshop, NCI/NIST, Gaithersburg (MD), USA, November 2007.
- (S) Bellairs Research Institute, McGill University, Barbados, January 2008.  
"The PRIDE database"
- (IS) Niigata University, Niigata, Japan, January 2008.  
"Two proteomics bioinformatics bottlenecks: quality assessment and data dissemination"
- (IS) Ghent University, Ghent, Belgium, February 2008.  
"Proteomics data storage and analysis: putting the cat next to the milk"
- (IS) 3<sup>rd</sup> ProDaC workshop, Toledo, Spain, April 2008  
"Standards for proteomics data representation"  
"Proteomics repository adaptation"  
"Proteomics data exploitation"
- (\*) HUPO Proteomics Standards Initiative (PSI) Spring Workshop, Toledo, Spain, April 2008
- (\*) Joint BSPR & EBI 2008 Conference: 'Proteomics: From technology to new biology', Hinxton, Cambridge, UK, July 2008
- (IS) 4<sup>th</sup> ProDaC workshop, Amsterdam, Netherlands, August 2008  
"Standards for proteomics data representation"  
"Proteomics repository adaptation"  
"Proteomics data exploitation"
- (IS) Bioinformatics Workshop for Lipidomics, University Hospital Regensburg, Regensburg, Germany, September 2008  
"EMBL-EBI resources and databases"
- (IS) 3<sup>rd</sup> 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"
- (IS) Bellairs Research Institute, McGill University, Barbados, January 2009.  
"Data dissemination strategy for the HUPO Test Samples"
- (P) ABRF 2009: Optimization and Application of Existing and Emerging Biotechnologies, Memphis, TN, USA, February 2009.  
"The PRIDE Database: a hub for proteomics data and associated tools"

- (S) US HUPO 2009: Integrative Proteomics for the Future, San Diego, CA, USA, February 2009.  
 "Proteomics by the Numbers: The Use of Computers to Aid Analysis, Understanding and Prediction in Mass Spectrometry Proteomics"
- (\*) 11<sup>th</sup> Workshop of the HUPO Brain Proteome Project, Kolympari, Greece, March 2009.
- (IS) 5<sup>th</sup> ProDaC workshop, Kolympari, Greece, March 2009.  
 "Standards for Proteomics Data Representation"  
 "Proteomics Repository Adaptation"  
 "Proteomics Data Exploitation"
- (SC) Korean Forum for Bioinformation Standardization 2009 Conference: Proteome Informatics and Standardization, Seoul, South Korea, March 2009.
- (IS) Korean HUPO 2009 Conference: Proteomics: From Discovery to Functions, Seoul, South Korea, March 2009.  
 "Proteomics by the Numbers: Rethinking Proteomics Informatics"
- (IS) Proteomic Forum 2009: The Proteomic Forum Berlin 2009, Berlin, Germany, March 2009.  
 "Sandwiching the Lab Between Computers: Bioinformatics to both Guide and Process Experiments"  
 "Doctor's Office: Proteins, Algorithms and Databases"
- (IS) MCP Guidelines Workshop 2.0, Pennsylvania, PA, USA, May 2009.
- (P) 57<sup>th</sup> ASMS Conference on Mass Spectrometry, Pennsylvania, PA, USA, May-June 2009.  
 "Significant improvements to the PSI mass spectrometer data file standard: mzML 1.1"
- (IS) Advances in Molecular Mechanisms of Disease: High Throughput Platforms and Advances in Imaging, Oslo, Norway, June 2009.  
 "Proteomic studies in human diseases"
- (IS) XXIV<sup>th</sup> International Symposium on Cerebral Blood Flow, Metabolism and Function, Chicago, IL, USA, June-July 2009.  
 "What to do with all that data?!"
- (IS) Ruhr-Universität Bochum, Bochum, Germany, July 2009  
 "Proteome bioinformatics: engineering bridges"
- (SC) ESF Quality Control in Proteomics workshop, Cambridge, UK, November 2009.
- (IS) DAPSOC 5<sup>th</sup> Annual Symposium, Odense, Denmark, December 2009.  
 "The case for Computational Proteomics: An analysis of what is, and of what could be."
- (SC) First Annual ms\_lims Workshop, Dortmund, Germany, January 2010.
- (IS) Centre de Recherche Public (CRP) Santé, Luxembourg, GD Luxembourg, March 2010  
 "An analysis of the public human proteome: footprints, biases, and recommendations."
- (IS) 4D Biology Workshop, European Commission, Brussels, Belgium, March 2010  
 "Construction of a public human proteome and corresponding lessons learned"
- (SC) ABRF 2010, Sacramento, CA, USA, March 2010.
- (SC) Analytica Conference 2010, Munich, Germany, March 2010.
- (IS) Analytica Conference 2010, Munich, Germany, March 2010  
 "Scale issues in protein quantification: why we must make our life difficult."
- (IS) Advances in Clinical Proteomics, Luxembourg, GD Luxembourg, September 2010  
 "Bioinformatics challenges in proteomics"
- (SC) Advances in Clinical Proteomics, Luxembourg, GD Luxembourg, September 2010.
- (IS) EMBL-EBI Pre-Doc Bioinformatics Workshop, Cambridge, United Kingdom, November 2010  
 "Large scale proteomics data analysis: greater strength in numbers!"

- (SC) Flanders Proteomics International Congress IV: Proteomics and the World of Tomorrow, Antwerp, Belgium, December 2010.
- (IS) KFBS Data Biological Evaluation Workshop, Incheon, South Korea, January 2011  
"A posteriori analysis of large-scale proteomics data to ascertain quality"
- (IS) 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"
- (IS) Korean Basic Science Institute, Ochang, South Korea, January 2011  
"Bioinformatics for the brain proteome"
- (IS) University of Southern Denmark, Odense, Denmark, February 2011  
"Understanding MS proteomics data first, then predicting it"
- (IS) Fourth Congress of the Spanish Proteomics Society, Segovia, Spain, February 2011  
"Quality control of proteomics data: performing local as well as global analyses"
- (IS) 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"
- (SC) ABRF 2011: Technologies to Enable Personalized Medicine, San Antonio, TX, USA, February 2011
- (IS) Proteomic Forum 2011, Berlin, Germany, April 2011  
"Bioinformatics to squeeze the lemon: getting the most from your hard-earned proteomics data"
- (IS) Proteomics Workshop 2011, ISAS, Dortmund, Germany, September 2011  
"Proteomics informatics: start to finish"
- (IS) WOULD Symposium in Bioinformatics: Tools in Research, UGent, Gent, Belgium, September 2011  
"Proteomics and cross-omics integration"
- (IS) 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"
- (IS) 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"
- (IS) 60th ASMS Conference on Mass Spectrometry and Allied Topics, Vancouver, BC, Canada, May 2012  
"The Future of Proteomics Repositories"
- (SC) 60th ASMS Conference on Mass Spectrometry and Allied Topics, Vancouver, BC, Canada, May 2012
- (SC) 206<sup>th</sup> Meeting of the Belgian Society of Biochemistry and Molecular Biology: 'Proteomics and interactomics in signaling networks', Ghent, Belgium, May 2012
- (IS) 5<sup>th</sup> FinnProt Symposium, Porvoo, Finland, June 2012  
'It's raining data! Software to handle the flood and surf the waves.'
- (IS) Bioinformatics 2012 Conference, Stockholm, Sweden, June 2012  
'Snakes and ladders: where do proteomics assays fail and how can we fix them?'
- (IS) BIOS Seminars, Freiburg, Germany, July 2012  
'Making the most of your experiments: powerful processing of proteomics data for optimal performance'
- (IS) EuPA/BSPR Proteomics Meeting, Glasgow, Scotland, July 2012  
'Trawling through proteomics data: analyzing and learning from the catch'
- (IS) 10<sup>th</sup> Austrian Proteomic Research Symposium, Graz, Austria, September 2012  
'Taking a bioinformatics hike off the beaten track: metaproteomics and proteomics of non-model organisms'

- (SC) Graph Databases in the Life Sciences, Ghent, Belgium, November 2012.
- (SC) 1<sup>st</sup> Belgian Proteomics Association Conference, Ghent, Belgium, November 2012.
- (IS) Habana Bioinformatics, La Habana, Cuba, December 2012  
‘The CompOmics toolsuite, helping you take a few steps in the right direction’, and  
‘Tapping into collective knowledge - mining the public proteome’
- (IS) CeProMa/VITO Research Day, Antwerp, Belgium, December 2012  
‘Three goals for proteomics: aim better, shoot straighter, find new targets’
- (IS) 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’
- (IS) 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’
- (IS) DELSA Workshop 4, Bethesda, MD, USA, May 2013  
“Endless Rebirth of Proteomics Data”
- (IS) Mascot User Meeting at ASMS, Minneapolis, MN, USA, June 2013  
“Looking into protein quantification: a many-faceted jewel with some pretty sharp edges”
- (IS) AuPA Bioinformatics Workshop, Salzburg, Austria, July 2013  
“Going through your trash: building a future on yesterday's news”
- (IS) Karolinska Institutet and Science for Life Laboratory, Stockholm, Sweden, September 2013  
“Closing the proteomics data ecosystem: reactivating experimental sediments”
- (IS) Oslo University, Oslo, Norway, October 2013  
“Danse not so macabre: re-animating dead proteomics data”
- (SC) Dagstuhl Seminar on Computational Mass Spectrometry, Dagstuhl, Germany, December 2013.
- (IS) CLASS Seminars, University College Dublin, Dublin, Ireland, January 2014.  
“Enough experiments already: the enormous utility of post-consumer proteomics data”
- (SC) Data management and standardization in cell migration research, Ghent, Belgium, March 2014.
- (IS) ProteoMMX 3.0, Chester, UK, March 2014  
“Supporting reproducible proteomics: some small steps in targeted and not so targeted methods”
- (IS) MCB 2014 / ERIBA Inaugural Congress, Groningen, The Netherlands, August 2014  
“Tomb raider: the fruitful exploration of proteomics data graveyards”
- (IS) ISCB European Student Council Symposium, Strasbourg, France, September 2014  
“Saprotrophics: a new natural habitat for bioinformaticians?”
- (IS) ECCB Workshop on Proteome and Metabolome Informatics, Strasbourg, France, September 2014  
“Tsunami or alluvial plain? A primer on dealing with public data.”
- (S) HUPO 2014 World Conference, Madrid, Spain, October 2014  
“Re-analysis of public data: does the future of proteomics lie in the past?”
- (SC) HUPO 2014 World Conference, Madrid, Spain, October 2014

### *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"

## GRANTS AND FELLOWSHIPS

- Research Assistant of the Fund for Scientific Research - Flanders (Belgium) (F.W.O. - Vlaanderen) 2002-2004
- Research Assistant of the Fund for Scientific Research - Flanders (Belgium) (F.W.O. - Vlaanderen) 2004-2006
- Marie Curie fellowship of the European Commission at the European Bioinformatics Institute (EBI), Hinxton, Cambridge, United Kingdom, September-December 2003.
- 'ProDaC' Coordination Action project in the 6<sup>th</sup> Framework Programme of the European Commission (2006-2009). Workpackage leader for WP1 (Standards Development), WP4 (Repository Adaptation) and WP6 (Proteomics Data Exploitation)
- 'Database on Demand' BBSRC Tools and Resources grant (2008).
- 'LipidomicNet' Collaborative Project (large-scale integrating project) in the 7<sup>th</sup> Framework Programme of the European Commission (2008-2012). Workpackage leader for WP7 – Bioinformatics.
- BBSRC 'Industrial CASE Ph. D. studentship', 2008-2011, United Kingdom.
- 'PRIDE – The Proteomics Identifications Database' Biomedical Resources Development Grant of the Wellcome Trust (2009-2014).
- 'Exploring the bioinformatics of quantitative proteomics: processing, evaluation, storage and dissemination of quantitative data', NPCII Ph.D. Student Research Project, The Netherlands (2009-2013).
- 'SLING' Infrastructure Project in the 7<sup>th</sup> Framework Programme of the European Commission (2009-2012). Workpackage leader for WP8 – Quantitative Proteomics.
- European Science Foundation Frontiers in Functional Genomics Exploratory Workshop Grant for a workshop on 'Quality Control in Proteomics' (2009).
- VIB Tech Watch *Disruptive Technologies* grant for Cloud Computing in Proteomics (2009).
- 'Bioinformatics: from Nucleotides to Networks (N2N)' Multidisciplinary Research Partnerships (MRP) project, Ghent University, Belgium (2009).
- 'ProteomeXchange' Coordination Action project in the 7<sup>th</sup> Framework Programme of the European Commission (2011-2014). Workpackage leader for WP3 – Data management system.
- 'PRIME-XS' Infrastructure Project in the 7<sup>th</sup> Framework Programme of the European Commission (2011-2015). Joint Research Activity Leader – Bio-informatics enabling high-throughput proteomics.
- IWT O&O Grant 'Evaluation of the kinase switch mechanism and the impact of active scaffold function for novel drug design' (2012 – 2014).
- InterUniversity Attraction Poles (IUAP) Grant 'Integration of cellular signaling pathways in health and disease' (2012-2017)
- FWO project 'Complementary use of ribosome profiling and positional proteomics for mapping the translation initiation and nascent protein modification landscape in human cell lines' (2013-2017).
- IWT SBO Grant 'InSPECTor: An Integrated Informatics Platform for Mass Spectrometry-based Protein Assays' (2013-2017).
- UGent CRA 'Integrated proteome-centric analysis of immune regulation' (2014-2019).



## **AWARDS AND PRIZES**

### *Scientific awards*

- HUPO 2004 Young Scientist Award
- Recipient of the 2015 'Prometheus' award of Ghent University for Excellence in Research

### *Professional awards*

- Sydney-Tristar 2001 Company Achievement Award

## **APPOINTMENTS IN SCIENTIFIC COMMITTEES AND ADVISORY BOARDS**

- Member of the Board of Directors of the Data-Enabled Life Sciences Alliance (DELSA) (since 2013).
- Member of the Board of the Belgian Proteomics Association (since 2012)
- Member of the Board of the Royal Flemish Society for Chemistry Proteomics Section (since 2009)
- Co-chair of the Human Proteome Organisation (HUPO) Disease Biomarker Initiative (DBI) informatics committee (since 2006)
- Chair of the Human Proteome Organisation (HUPO) Brain Proteome Project (BPP) bioinformatics committee (since 2005)
- 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).
- Member of the Human Proteome Organisation (HUPO) Test Samples committee (since 2008)
- Member of the HUPO Initiative for Model Organism Based Proteomics (iMOP) (since 2011).
- Member of the Human Proteome Project (HPP) KnowledgeBase resource pillar Committee (since 2012).

## **MEMBERSHIP OF SCIENTIFIC ORGANISATIONS**

- Founding member and content contributor of the 'Fixing Proteomics' educational campaign, <http://www.fixingproteomics.org>
- Elected member of the Proteome Informatics Research Group (iPRG) of the Association of Biomolecular Resource Facilities (ABRF) (2008 - 2011)
- Admitted as Member of the Royal Society of Chemistry (MRSC), UK (since 2012).
- Elected member of the Young Academy of the Royal Flemish Academy for Sciences and Arts (since 2013).

## **OTHER PROJECTS**

- Management and coordination of the Human Proteome Organisation (HUPO) Proteomics Standards Initiative (PSI) website (<http://www.psidev.info>).

## **SUPERVISION OF MASTER'S STUDENTS**

- 2004-2005: Jeroen Meukens (Universiteit Gent, Belgium)  
'Supporting present-day proteomics: from the standardization and intelligent interpretation of mass spectrometry data to the worldwide distribution of the resulting identifications in public data repositories'.  
Awarded with *greatest distinction*.
- 2005-2006: Kenny Helsens (Universiteit Gent, Belgium)  
'Development of flexible criteria for the efficient selection of mass-spectrometry derived identifications, obtained by a COFRADIC analysis, for manual validation'.  
Awarded with *greatest distinction*.
- 2006-2007: Sebastian Klie (Martin Luther University Halle-Wittenberg, Germany – EMBL-EBI, UK)  
'Ähnlichkeits-Analyse von Proteomik-Experimenten durch Information Retrieval Methoden'  
Awarded with *greatest distinction*.
- 2007-2008: Jonathan Rameseder (Upper Austria University of Applied Sciences, Hagenberg Campus, Austria – EMBL-EBI, UK)  
'Computational Interpretation of Tandem MS Spectra Including Fragment Ions With Post-Translational Modifications'.  
Awarded with *greatest distinction*.  
Recipient of the *Oesterreichische Computergesellschaft (OCG) Förderpreis FH 2009*.
- 2010-2011: Thilo Muth (Friedrich Schiller University Jena, Germany and Universiteit Gent, Belgium)  
'Cloud computing in proteomics for the in-depth analysis of high-quality unidentified spectra'  
Awarded with *greatest distinction*.

## **SUPERVISION OF PH.D. STUDENTS AT GHEENT UNIVERSITY**

- August 2006 - May 2010: Dr. Kenny Helsens  
'Improving the sensitivity and the specificity in peptide centric proteomics'.  
Ph.D. awarded on 31 May 2010 by Ghent University, Ghent, Belgium
- August 2007 – May 2011: Dr. Niklaas Colaert  
'Digging deeper in the data, novel approaches and analysis methods in quantitative peptide-centric proteomics'  
Ph.D. awarded on 13 May 2011 by Ghent University, Ghent, Belgium
- December 2008 – December 2012: Dr. Marc Vaudel  
'Detailed analysis of the blood platelet proteome through the use of innovative bioinformatics methods for protein identification, quantification and post-translational modification localization'  
Ph.D. awarded on 12 December 2012 by Ghent University, Ghent, Belgium
- January 2013 – September 2014: Pieter Kelchtermans  
'Computational methods for targeted proteomics research
- July 2011 - present: Giulia Gonnelli  
'Accurate identification of peptides through unbiased whole-genome searching of fragmentation mass spectra'
- November 2011 – present: Paola Masuzzo  
'A Bioinformatics approach to cell migration.'
- October 2012 – present: Şule Yılmaz  
'The development of novel bioinformatics tools and algorithms to support data processing and result interpretation in metaproteomics analyses'
- October 2012 – present: Kenneth Verheggen  
'Novel biology from public proteomics data'

- May 2013 – present: Elvis Ndah  
'Complementary use of ribosome profiling and positional proteomics for mapping the translation initiation and nascent protein modification landscape in human cell lines.'
- June 2013 – present: Nicolas Housset  
'Algorithms for the detection and identification of modified proteins in complex samples'
- September 2013 – present: Tessa Vermeire  
'Research on the cause of possible vaccine failure in recent mumps outbreak through variation analysis of the virus protein and epitope analysis'
- October 2013 – present: Surya Gupta  
'Building a memory and a brain for the human interactome'
- October 2014 – present: Adriaan Sticker  
'Detecting rare biomolecules by mining public omics data'
- November 2014 – present: Ana Sílvia Ferreira Diamantino Coelho e Silva  
'Predictive algorithms for much more efficient targeted proteomics'

#### **SUPERVISION OF PH.D. STUDENTS AT EMBL-EBI (WITH DR. ROLF APWEILER)**

- July 2006 – July 2009: Dr. Michael Mueller  
'Integrated analysis of proteomics data to assess and improve the scope of mass spectrometry based genome annotation'  
Ph.D. awarded in 2009 by Cambridge University, Cambridge, UK.
- August 2008 – July 2012: Dr. Joseph M. Foster  
'Transomics: Integrating core omics concepts'  
Ph.D. awarded in 2012 by Cambridge University, Cambridge, UK.

#### **SUPERVISION OF INTERNATIONAL STUDENTS**

##### *Master's students*

- Steffen Huber (Technische Universität München, Germany – Würzburg University, Germany), 2007-2008.
- Christian Peikert (Albert-Ludwigs-Universität Freiburg, Germany), 2012-2013.
- Clemens Thölken (Albert-Ludwigs-Universität Freiburg, Germany), 2013-2014.

##### *Ph.D. students*

- Dr. Harald Barsnes (Department of Informatics, University of Bergen, Norway), 2007-2010.  
'Development of Tools for Analyzing and Sharing Proteomics Data'  
Ph.D. awarded in 2010 by University of Bergen, Bergen, Norway
- Thilo Muth (Max Planck Institute for Dynamics of Complex Technical Systems, Magdeburg, Germany), since 2012.