

## **Willy BIENVENUT**

Beatson Institute for Cancer Research  
Mass spectrometry & Proteomics Core Facility Manager  
Switchback road,  
Bearsden  
G61 1BD Glasgow  
UK

Tel: (44) (0)141 330 3953 or 8636  
Fax.: (44) (0)141 942 6521  
Email: W.Bienvenut@beatson.gla.ac.uk

Born the 10<sup>th</sup> August 1969 at Saintes (Charente Maritime, France), single, French.

### **SKILLS:**

- Protein identification based on PMF, LC-MS/MS on various instruments and other advanced MS techniques (Precursor Ion Scan, neutral loss, MRM, MS<sup>3</sup>...),
- Protein and peptides separation using IEF electrophoresis, SDS-PAGE, electroblotting,
- Multidimensional LC separations techniques for advanced analyses of complex mixtures (RP, SAX, SCX, affinity columns, size exclusion...)
- Post-translational protein modification characterisation (phosphorylation ,acetylation, methylation...),
- High throughput protein identification using the molecular scanner, robotized or manual approach,
- Active collaboration for experimental annotation of the UNIPROT-KB (Swiss-Prot) with the SWISS-PROT group in Geneva ,

### **WORK EXPERIENCE:**

#### **2006:**

Mass spectrometry & Proteomics Core Facility Manager **at the “Beatson Institute for Cancer Research”, Glasgow.**

- Protein identification based mainly on ESI-MS/MS (Q-Star Excel from PE-Sciex, on site instrument) and MALDI MS/MS (4700 Proteomics Analyser from ABI at the Welcome facility, Glasgow university),
- Characterisation of the phospho-proteins (Q-Trap P4000 from PE-Sciex, on site instrument,
- Complex sample and pull down characterisation,
- Differential protein quantification using SILAC approach in MS,
- Gel based protein separation facility including DIGE technology for differential protein quantitation,
- Consultation and expert advice to researchers on all aspects of proteomics and mass spectrometry analysis and validation of data

#### **2002-2005:**

**Mass Spectrometry specialist at the “Protein Analysis Facility”, Lausanne University, under the Direction of Dr Manfredo Quadroni.**

- Protein identification facility using ESI-MS/MS (Q-Trap & Q-Star from PE-Sciex) and proteomic analyser 4700 (ABI),
- Protein chemistry for higher identification specificity,
- Development of advanced analytical techniques for highly complex samples: long LC gradient separation, precursor ion scan, GPF
- PTM characterisation (N-term acetylation, methylation, phosphorylation...).

## **TEACHING EXPERIENCE:**

**2004:**

**Proteomics Using Bioinformatics Tools,**

Under the direction of [Laurent Falquet](#) and the [SIB](#)

**2003-2004:**

**Proteomics Courses in Mass Spectrometry**

Part of the organizers of a joint course between the [Biomedical Proteomics Research Group](#) and the [Protein Analysis Facility](#) in mass spectrometry applied to protein identification.

**1998-2004:**

**Swiss institute of bioinformatics,**

Under the direction of [Prof. Amos Bairoch](#) and [Marie-Claude Blatter-Guerin](#).

- Lectures concerning protein identification methods, protein chemistry and the molecular scanner (mostly and MS related lecture)

**2002:**

**Pre-congress proteomics workshop** during the SPS 2002 congress of applied proteomics. 3-5 of December, Lausanne (CH): Mass spectrometry: turning data into results.

## **Languages:**

- French: mother language,
- English: current,
- Italian: very basic knowledge,

## **Computing:**

- Specialised software: MASCOT, ProFound, ProteinProspector (Protein identification softwares), on-lines proteomics and sequences analysis tools, MS data treatment, imaging software...
- Good knowledge of bioinformatics tools for genomic and/or proteomic research,
- Involved in the development of few tools available on [ExpASy](#) servers.
- Utilisation of traditional office software,

## **EDUCATION:**

**1998-2002: PhD Student at the Geneva [University hospital](#) under the direction of the [Prof. D.F. Hochstrasser](#) et Prof J.-L. Veuthey in the R&D section of the central clinical chemistry laboratory.**

- Development of new parallel "Double Parallel Digestion" technique for proteins in the molecular scanner project,
- Advanced techniques in peptide mass fingerprints analysis for proteins identification by MALDI-TOF-MS,
- Chemical modification of the peptide (esterification, H/D exchange) to increase protein identification confidence (Technical formation in DJC. Pappin laboratory, ICRF, London, UK)

**1996-97: DEA (equivalent to Master level) in Material Science at l'INP-ENSC Toulouse, Paul Sabatier University of Toulouse and Mining school of Albi.**

- Material Science formation, developpement of an endoproteolytic polymeric membrane,

**1993-96: Chemist engineering degree at INP-ENSCT, (Toulouse, FRANCE).**

- General content: organic and general chemistry, spectroscopy, chemical engineering.
- Final year done at the University of Greenwich (London, UK).
- Specialisation in physiology, human nutrition, pharmacology and biology.

## **MISCELLANEOUS :**

- Driving licence for car and motorcycle.
- Compulsory military service: completed in May 1993 as sergeant.
- Hobbies: reading, riding, running, cooking, computing, snow boarding.

## **REFERENCES:**

[Prof Amos Bairoch](#), [Swiss Institute of Bioinformatics](#), [Swiss-Prot group](#), CMU  
Rue Michel Servet 1, CH-1211 Geneva 4, Switzerland  
Phone: (+41) (0)22 379 50 50, Fax: (+41) (0)22 379 58 58  
Email: [Amos.Bairoch@isb-sib.ch](mailto:Amos.Bairoch@isb-sib.ch)

[Dr Manfredo Quadroni](#), [Protein Analysis Facility](#), c/o Institute of Biochemistry F306,  
Chemin des Boveresses 155, CH-1066 Epalinges, Switzerland  
Phone: (41) (0)21 692 56 76, Fax.: (+41) (0)21 692 57 05,  
Email: [Manfredo.Quadroni@unil.ch](mailto:Manfredo.Quadroni@unil.ch)

[Dr Jean-Charles Sanchez](#), Département Biologie Structurale et Bioinformatique, CMU  
Rue Michel-Servet 1; CH-1211 Genève 4, Switzerland  
Phone: (+41) (0)22 379 54 86, Fax: 372 59 84  
Email: [jean-charles.sanchez@medcli.unige.ch](mailto:jean-charles.sanchez@medcli.unige.ch)

## **PUBLICATIONS :**

### - **Articles :**

Owen HR, Quadroni M, Bienvenut W, Buerki C, Hottiger MO. [Identification of novel and cell type enriched cofactors of the transcription activation domain of RelA \(p65 NF-kappaB\)](#). *J Proteome Res.* **2005**, **4(4)**:1381-90.

R.L. Martin, E. Raptakis, [W. Bienvenut](#); Characterization of Complex Protein Gel Bands by Offline LC-MALDI QIT TOF MS. [Proceedings of the 52nd ASMS Conference on Mass Spectrometry and Allied Topics](#), Nashville, Tennessee, May 23 - 27, **2004**.

D. Crettaz, L. Sensebe, D.H. Vu, P. Schneider, F. Depasse, [W.V. Bienvenut](#), M. Quadroni, J.D. Tissot JD. [Proteomics of methylene blue photo-treated plasma before and after removal of the dye by an absorbent filter](#). *Proteomics.* **2004**, **4(3)**:881-91.

F. Vuadens, C. Benay, D. Crettaz, D. Gallot, V. Sapin, P. Schneider, [W.V. Bienvenut](#), D. Lemery, M. Quadroni, B. Dastugue, J.D. Tissot; [Identification of biologic markers of the premature rupture of fetal membranes: proteomic approach](#). *Proteomics.* **2003**, **3(8)**:1521-5.

F. Vuadens, D. Crettaz, C. Scelatta, C. Servis, M. Quadroni, [W.V. Bienvenut](#), P. Schneider, P. Hohlfeld, L.A.Applegate, J.D. Tissot; [Plasticity of protein expression during culture of fetal skin cells](#). *Electrophoresis* **2003**, **24(7-8)**: 1281-91.

A. Gattiker, [W.V. Bienvenut](#), A. Bairoch, E. Gasteiger; [FindPept, a tool to identify unmatched masses in peptide mass fingerprinting protein identification](#). *Proteomics* **2002**, **2(10)**: 1435-44.

[W.V. Bienvenut](#), C. Déon, J-C Sanchez, D. F. Hochstrasser; [Enhanced protein recovery after electrotransfer using square wave alternating voltage](#). *Analytical Biochemistry* **2002**, **307**: 297-303.

[W.V. Bienvenut](#), C. Déon, C. Pasquarello, J. Campbell, J.C. Sanchez, M. Vestal, D.H. Hochstrasser; [MALDI MS-MS with high resolution and sensitivity for identification and characterization of proteins](#). *Proteomics* **2002**, **2**: 868-76.

M. Müller, R. Gras, R. D. Appel, [W. V. Bienvenut](#), D. F. Hochstrasser; [Visualization and Analysis of the Molecular Scanner Peptide Mass Spectra](#). *J. Am. Soc. Mass Spectrom.* **2002**, **13**, 221-31.

W. V. Bienvenut, C. Hoogland, A. Greco, M. Heller, E. Gasteiger, R. D. Appel, J.-J. Diaz, J.-C. Sanchez, D. F. Hochstrasser; [Hydrogen/Deuterium Exchange for Higher Specificity of Protein Identification by Peptide Mass Fingerprinting](#). *Rapid Commun. Mass Spectrom.* **2002**, *16*, 616-26.

A. Greco, W. Bienvenut, J.-C. Sanchez, K. Kindbeiter, D. Hochstrasser, J.-J. Madjar, J.-J. Diaz; [Identification of ribosome-associated viral and cellular basic proteins during the course of infection with herpes simplex virus type 1](#). *Proteomics* **2001**, *1*, 454-9.

D. Hochstrasser, J.C. Sanchez, P.A. Binz, W. Bienvenut, R.D. Appel. A clinical molecular scanner to study human proteome complexity. *Novartis Found Symp.* **2000**; **229**:33-8; discussion 38-40.

W. V. Bienvenut, J.-C. Sanchez, A. Karmime, V. Rouge, K. Rose, P.-A. Binz, D. F. Hochstrasser; [Toward a Clinical Molecular Scanner for Proteome Research: Parallel Protein Chemical Processing before and during Western-Blot](#). *Anal. Chem.* **1999**, *71*, 4981-8.

P.-A. Binz, M. Müller, D. Walther, W. V. Bienvenut, R. Gras, C. Hoogland, G. Bouchet, E. Gasteiger, R. Fabbretti, S. Gay, P. Palagi, M. R. Wilkins, V. Rouge, L. Tonella, S. Paesano, G. Rossellat, A. Karmime, A. Bairoch, J.-C. Sanchez, R. D. Appel, D. F. Hochstrasser; [A Molecular Scanner to Highly Automate Proteomic Research and to Display Proteome Images](#). *Anal. Chem.* **1999**, *71*, 4800-7.

R. Gras, M. Müller, E. Gasteiger, S. Gay, P.-A. Binz, W. V. Bienvenut, C. Hoogland, J.-C. Sanchez, A. Bairoch, R. D. Appel, D. F. Hochstrasser; [Improving Protein Identification from Peptide Mass Fingerprinting through a Parameterized Multi-level Scoring Algorithm and an Optimized Peak Detection](#). *Electrophoresis* **1999**; *20*, 3535-50.

#### - Patents

W.V. Bienvenut, J.-C. Sanchez, D. F. Hochstrasser; Kit for electroblotting polypeptides separated on an electrophoresis gel. PCT patent application No. [99 01775.8](#), UK patent application No. 99 07790.1.

W.V. Bienvenut, D. F. Hochstrasser; [Method of identifying polypeptides](#). US patent application No. [09/107,991](#), European patent application: [CA2244947](#).

#### - Books

W.V. Bienvenut, Acceleration and Improvement of Protein Identification by Mass Spectrometry. *Springer* Dordrecht, **2005**.

C. Déon, W. V. Bienvenut, M. Mueller, R. Gras, R. D. Appel, J.-C. Sanchez, D. F. Hochstrasser; The Molecular Scanner: an automated high-throughput protein identification approach. *Protein Analysis: A Laboratory Manual*. Ed. R. Simpson, *Cold Spring Harbor*, **2001**, pp93-145.

W.V. Bienvenut, M. Müller, P.M. Palagi, E. Gasteiger, m. Heller, E. Jung, M. Giron, R. Gras, S. Gay, P.-A. Binz, G. J. Hughes, J.-C. Sanchez, R.D. Appel, D.F. Hochstrasser; Mass spectrometry and genomic analysis; *Proteomics and mass spectrometry: Some aspects and recent developments*. J.N. Houbly Ed.; *Kluwer Academic Publishers*, **2001**, pp93-145.

#### - Awards

**French Society of Mass Spectrometry Price 2002** for the thesis called: "Accélération et amélioration de l'identification des protéines par spectrométrie de masse".

**Riottton price 2000 from the medicine university of Geneva** for the article called: "Toward a Clinical Molecular Scanner for Proteome Research: Parallel Protein Chemical Processing before and during Western Blot."