

**Marc R. Wilkins**

Professor of Systems Biology, University of New South Wales, Sydney, Australia

In 1994, Marc developed the concept of the proteome and coined the term. He wrote a number of seminal publications in the field and in 1997 co-wrote and co-edited the first book on proteomics (>4000 copies sold). These contributed to the establishment of the proteome and of proteome research. Proteomics is the most widely adopted of the new -omics, is now included in biochemistry textbooks and the undergraduate curriculum.

Marc has published 82 peer-reviewed research papers, review papers and book chapters and has edited 2 books. Research published in journals has been cited 2,640 times (ISI Web of Knowledge Feb 2006); books and book chapters have been cited > 250 times (Google Scholar Dec 2006). Marc's research has tackled many of the key issues in proteomics. A particular strength has been the capacity to combine analytical techniques with complex bioinformatics to open new avenues for biological investigation. Pioneering contributions were in the area of high-throughput protein identification, the automation of protein identification analyses, and the establishment of bioinformatic protein identification tools and data analysis pipelines. The development of mass spectrometry-based approaches for the discovery of post-translational modifications is also of note. Marc has also been a Chief Investigator or collaborator on many industrial and academic proteomic projects. These have sought to discover biomarkers and functionally significant proteins in renal cell carcinoma, gingivitis, tuberculosis, heart failure, exacerbation in cystic fibrosis, antibiotic resistance in *B. subtilis*, microbial toxin diversity and mad cow disease. A number of these proteins remain the subject of ongoing research. Interactome research is a new area of focus.

In 1999, Marc co-founded the biotechnology company Proteome Systems. This company is Australia's largest proteomics company, employs > 50 staff and is listed on the Australian Stock Exchange (code: PXL). Inside the company, Marc was a chief investigator on proteomics projects with industry partners (e.g. Dow AgroSciences, Cystic Fibrosis Therapeutics Inc.). He also led Proteome Systems bioinformatics R & D team; output which was commercialised into BioinformatIQ and Glycosuite products. These have been sold into laboratories in Australia, Japan, Malaysia and the United States. Glycosuite is now distributed internationally by Agilent.

**Education and Training:**

1990 B. Sc. Hons (class I) Macquarie University, Sydney, Australia  
 1996 Ph.D. Macquarie University, Sydney, Australia

**Positions and Employment**

1995 Postdoctoral Fellow, Faculty of Medicine, University of Geneva, Switzerland  
 1997 Senior Postdoctoral Fellow, Australian Proteome Analysis Facility, Sydney, Australia  
 1999 Vice President of Bioinformatics, Proteome Systems Limited, Sydney, Australia  
 2004 Head of Proteomics, Proteome Systems Limited, Sydney, Australia  
 2005 Professor of Systems Biology, University of New South Wales, Sydney, Australia

**Other Experience:****Journal Editorships**

1998 -2000 member of Editorial Board for the Journal Electrophoresis (Wiley-VCH)  
 2004- Senior Editor for the Journal Proteomics (Wiley-VCH)  
 2006- Member of Editorial Board Practical Proteomics (Wiley-VCH)  
 2007- Member of Editorial Board of Bioinformatics and Biology Insights (Libertas Academica)

## Advisory Board Membership

2003-2005 Member of the Australian Government's Expert Task Force for Bioinformatics.  
2004- Advisory Board, ARC Bioinformatics Centre of Excellence.  
2006- Scientific Advisory Board, NHMRC Australian Proteome Computational Facility.  
2007- Reference Advisory Group, Biomolecular Mass Spectrometry Facility, UNSW.

## Service to Professional Organisations

1999-2000 Secretary, Sydney Protein Group  
2005 Program Committee, Discovery, Science and Biotechnology Conference  
2006 Organising Committee, Bioinformatics Australia National Congress  
2007 Organising Committee, ComBio National Congress  
2007 Program Committee, Bioinformatics Australia  
2007 Co-Chair, Sydney HUPO 2010 bid

## Service in Industry

1999 Co-founder of Proteome Systems, an ASX-listed proteomics company  
2007 Consultant to Meat and Livestock Association

## Honors

1990 Bill Cantwell Memorial Prize, best Biology Honours graduate, Macquarie University

## **Selected peer-reviewed publications**

(selection from a total of 82 publications)

### **Recent Books and Book Chapters (2003-2007)**

1. Wilkins MR, Appel RD, Williams KL, Hochstrasser DF (Eds.) (2007) Proteome Research: concepts, technology and application. Springer, Berlin (book).
2. Wilkins MR (2007) Biomarker identification: the role of experimental design, statistics and data sharing. In: Clinical Proteomics: from Diagnosis to Therapy. Editors Van Eyk and Dunn. Wiley-VCH, in press.
3. Wilkins MR and Appel RD (2007) Ten years of the proteome. In: Proteome Research: concepts, technology and application. Editors: Wilkins, Appel, Hochstrasser. Springer, Berlin, in press.
4. Packer N, Gooley AA and Wilkins MR (2007) One gene, many proteins. In: Proteome Research: concepts, technology and application. Editors: Wilkins, Appel, Hochstrasser. Springer, Berlin, in press.
5. Hernandez P, Binz P.-A. and Wilkins MR (2007) Protein Identification in Proteomics. In: Proteome Research: concepts, technology and application. Editors: Wilkins, Appel, Hochstrasser. Springer, Berlin, in press.
6. Pang CNI and Wilkins MR (2006) Online resources for the molecular contextualisation of disease. In: Clinical Bioinformatics. Editor Ron Trent. Humana Press, in press 20<sup>th</sup> Sept 2006.
7. Wilkins MR, Arthur JW, Junius FK, Harrison MJ, Traini MD, Bizannes P, Doggett PE, McDonald W. (2006) Information management for proteomics. In: Microbial Proteome Databases. Editor Peter R. Jungblut, Ph.D. (Springer). In press 13<sup>th</sup> Dec 2006.
8. Wilkins MR, Hunt SM (2006) Bioinformatics and experimental design for biomarker discovery. In: Proteomics of Human Body Fluids: Principles, Methods, and Applications. Ed. Dr. Visith Thongboonkerd. Humana Press. pp 147-174.
9. Gasteiger E, Hoogland C, Gattiker A, Duvaud S, Wilkins MR, Appel RD, Bairoch A. (2005) Protein Identification and Analysis Tools in the ExPASy Server. In : *2-D Protein Gel Electrophoresis Protocols*, Humana Press. 2<sup>nd</sup> Edition. pp 571-607.

10. Cooper CA, Joshi HJ, Harrison MJ, Wilkins MR, Packer NP (2003) Querying GlycosuiteDB. *in Handbook of Proteomic Methods*. Conn PM (ed.) pp 233-240. Humana Press.

### Recent Journal Articles (2003 – 2007)

11. Taylor CF, Paton NW, Lilley KS, Binz PA, Julian RK, Jones AR, Zhu W, Apweiler R, Aebersold R, Deutsch EW, Macht M, Mann M, Neubert TA, Patterson SD, Seymour SL, Tsugita A, Wilkins MR, Xenarios I, Hermjakob H. (2007) The Minimum Information About a Proteomics Experiment (MIAPE). *Nature Biotechnology*, 25(8): 887-893. [IF = 22.7]
12. Hsu W-T, Pang CNI, Sheetal J, Wilkins MR (2007) Protein-protein interactions and disease: use of *S. cerevisiae* as a model system. *BBA Proteins and Proteomics*, 1774(7): 838-47. [IF = 3.3]
13. Pang CNI, Hayen A, Wilkins MR (2007) Surface accessibility and protein interactivity of post-translational modifications. *Journal of Proteome Research*, in press 22<sup>nd</sup> Feb 2007. [IF = 6.91]
14. Ho E, Hayen A, Wilkins MR (2006) Characterisation of organellar proteomes: subcellular proteomic fractionation and analysis. *Proteomics*, 6: 5746-5757. [IF = 6.08]
15. Wilkins MR, Appel RD, Van Eyk JE, Chung MCM, Görg A, Hecker MA, Huber LA, Langen H, Link AJ, Paik YK, Patterson SD, Pennington SR, Rabilloud T, Simpson RJ, Dunn MJ. (2006) Guidelines for the next 10 years of proteomics. *Proteomics* 6: 4-8. [IF = 6.08]
16. Wilkins MR (2006) How proteomics can assist in the detection and avoidance of adverse drug reactions. *Transfusion Medicine and Hemotherapy* 33: 97-105.(invited review).
17. Hunt SMN, Thomas MR, Sebastian LT, Pedersen SK, Harcourt RL, Sloane AJ, Wilkins MR (2005) Optimal replication and the importance of experimental design for gel-based quantitative proteomics. *Journal of Proteome Research* 4: 809-819. [NOTE : article featured in *Journal of Proteome Research* editorial, volume 4: 663]. [IF = 6.91]
18. Arthur, JW and Wilkins, MR. (2004) Using proteomics to mine genome sequences. *Journal of Proteome Research* 3: 393-402. [IF = 6.91]
19. Pedersen SK, Harry JL, Sebastian L, Baker J, Traini MD, McCarthy JT, Manoharan A, Wilkins MR, Gooley AA, Righetti PG, Packer NH, Williams KL, Herbert BR. (2003) Unseen proteome: mining below the tip of the iceberg to find low abundance and membrane proteins. *Journal of Proteome Research* 2:303-11. [IF = 6.91]
20. Van Dyk DD, Misztal DR, Wilkins MR, Mackintosh JA, Poljak A, Varnai JC, Teber E, Walsh BJ, Gray PP. (2003) Identification of cellular changes associated with increased production of human growth hormone in a recombinant Chinese hamster ovary cell line. *Proteomics* 3:147-156. [IF = 6.08]
21. Breen EJ, Holstein WL, Hopwood FG, Smith PE, Thomas ML, Wilkins MR. (2003) Automated peak harvesting of MALDI-MS spectra for high throughput proteomics. *Spectroscopy* 17: 579-596.
22. Herbert BR, Pedersen S, Harry JL, Sebastian L, Grinyer J, Traini M, McCarthy J, Wilkins MR, Gooley AA, Righetti PG, Packer NH, Williams KL. (2003) Mastering proteome complexity using two-dimensional gel electrophoresis. *Pharmagenomics* Sept 2003: 22-36.
23. Cooper CA, Joshi HJ, Harrison MJ, Wilkins MR, Packer NH (2003) GlycosuiteDB: a curated relational database of glycoprotein glycan structures and their biological sources – 2003 update. *Nucleic Acids Research* 31: 511-513. [IF=7.52]

### Ten career-best publications

1. Pang CNI, Hayen A, Wilkins MR (2007) Surface accessibility and protein interactivity of post-translational modifications. *Journal of Proteome Research*, in press 22<sup>nd</sup> Feb 2007. [IF = 6.91]
2. Wilkins MR, Appel RD, Van Eyk JE, Chung MCM, Görg A, Hecker MA, Huber LA, Langen H, Link AJ, Paik YK, Patterson SD, Pennington SR, Rabilloud T, Simpson RJ, Dunn MJ. (2006) Guidelines for the next 10 years of proteomics. *Proteomics* 6: 4-8. [IF = 6.08; 25 citations; Proteomics journal most accessed manuscript in 2006]
3. Cooper CA, Joshi HJ, Harrison MJ, Wilkins MR, Packer NH (2003) GlycosuiteDB : a curated relational database of glycoprotein glycan structures and their biological sources. 2003 Update. *Nucleic Acids Research* 31: 511-513. *Publication describing the now commercialised glycan structure database*. [IF = 7.52]
4. \* Wilkins, MR, Gasteiger E, Sexton D, Gooley AA, Herbert BR, Molloy MP, Binz P-A, Ou K, Bairoch A, Williams KL, Hochstrasser DF (1999) Large-Scale Mass Spectrometric Discovery of Protein Post-Translational

- Modifications. *Journal of Molecular Biology*, 289: 645-657. *Highly cited approach for identifying post-translational modifications in proteomics projects*. [IF=5.54, 130+ citations]
5. Binz, P.-A., Muller, M., Walther, D., Bienvenut, W., Gtas, R., Hoogland, C., Bouchet, G., Gasteiger, E., Fabbretti, R., Gay, S., Palagi, P., Wilkins, M.R., Rouge, V., Tonella, L., Paesano, S., Rossellat, G., Karmime, A., Bairoch, A., Sanchez, J.-C., Appel, R.D. and Hochstrasser, D.F. (1999) A molecular scanner to automate proteomic research and to display proteome images. *Analytical Chemistry* 71: 4981-4988. *Major and widely cited publication arising from SWISS SNRF funding*. [IF=5.45, 82+ citations]
6. Wilkins, M.R., Gasteiger, E., Sanchez, J.-C., Bairoch, A., and Hochstrasser, D.F. (1998) The limitations of two-dimensional gel electrophoresis for proteome projects: the effects of protein copy number and hydrophobicity. *Electrophoresis* 19: 1501-1505. [86+ citations]
7. Wilkins M.R., Williams KL (1997) Cross-species protein identification using amino acid composition, peptide mass fingerprinting, isoelectric point and molecular mass: A theoretical evaluation. *J. Theor. Biol.* 186: 7-15 [64+ citations]
8. Wilkins, M.R., Williams, K.L., Appel, R.D., Hochstrasser D.F. (Eds.) (1997) *Proteome Research: new frontiers in functional genomics*. Springer Verlag. *The first book on proteomics, over 4000 copies sold*.
9. Wilkins, M.R., Pasquali, C., Appel, R.D., Ou, K., Golaz, O., Sanchez, J.-C., Yan, J.X., Gooley, A.A., Hughes, G., Humphery-Smith, I., Williams, K.L. and Hochstrasser, D.F. (1996) From Proteins to Proteomes: Large scale protein identification by two-dimensional electrophoresis and amino acid analysis. *Bio/Technology* 14: 61-65. *This article introduced the concept and the term "proteome" to the world and outlined novel protein identification techniques*. [journal renamed in 1997 to *Nature Biotechnology* IF=22.4, 260+ citations]
10. Wilkins, M.R., Sanchez, J.-C., Gooley, A.A., Appel, R.D., Humphery-Smith, I., Hochstrasser, D.F. and Williams, K.L. (1995) Progress with proteome projects: why all proteins expressed by a genome should be identified and how to do it. *Biotechnology and Genetic Engineering Reviews* 13: 19-50. *The first review to comprehensively outline the emerging field of proteomics*. [170+ citations]

## **Recent Research Support**

1. Systems Biology Initiative. NSW Science Leveraging Fund, 2007-2010. Principle Investigator.
2. NSW Cancer Proteomics Infrastructure Initiative, Cancer Institute NSW 2007-2012. Co-Investigator.
3. Interactome Analysis of *S. cerevisiae*. University of New South Wales Faculty Research Grant 2007. Principle Investigator.
4. Proteome-wide discovery of protein post-translational modifications, University of New South Wales Faculty Research Grants 2006. Principle Investigator.
5. Inter-individual variation of the proteome. University of New South Wales Faculty Research Grants 2006. Co-Investigator.
6. High resolution bioanalytical Fourier transform mass spectrometer combined with liquid Chromatograph. ARC LEIF Grant 2006. Co-investigator.
7. IsoselectriQ multicompartement electrolyser and isoelectric focusing device. NHMRC Equipment Grant 2005. Principle Investigator.
8. Bacterial Proteomics: From Cell Division to Novel Antibiotic Targets. ARC Linkage grant 2003-2006. Co-Investigator.