

## NEIL F.W. SAUNDERS RESUMÉ (PAGE 1 OF 2)

### CURRENT POSITION

#### Research Officer

School of Molecular and Microbial Sciences  
The University of Queensland

#### Current research interests

- Computational prediction of protein-protein interactions; particularly protein kinases and substrates
- Microbial genomics: comparative analysis, annotation, gene discovery, structural prediction
- Application of bioinformatics to problems in genetic regulation, physiology and protein structure
- Use of high-performance Linux clusters in computational biology
- Open source software tools for mining, integration, analysis and presentation of biological data
- Web 2.0 technology for science communication

### PREVIOUS POSITIONS

#### Research Fellow

School of Biotechnology and Biomolecular Sciences  
The University of New South Wales

2005 - 2006

#### Australian Postdoctoral Fellow

School of Biotechnology and Biomolecular Sciences  
The University of New South Wales

2002 - 2005

#### Research summary

- Played key role in the integration and analysis of high-throughput proteomics data
- Used bioinformatics skills to approach new research topics (archaeal pathogens, serpin evolution)
- Furthered development of computational tools and infrastructure in the school
- First author on paper in *Genome Research* describing genomic analysis of cold-adapted archaea

#### Vice Chancellor's Research Fellow

School of Biotechnology and Biomolecular Sciences  
The University of New South Wales

2000 - 2002

#### Research summary

- First genomic analysis of factors contributing to cold adaptation in archaea
- First draft genome sequences of cold-adapted archaea
- Established computational infrastructure and tools for microbial genomics research

#### Marie Curie Research Fellow

Department of Molecular Cell Physiology,  
Vrije Universiteit,  
Amsterdam, The Netherlands

1998 - 2000

#### Research summary

- First elucidation of a role in denitrifying enzyme maturation for the NosX/NirX protein family
- First determination that nitric oxide is a signal for transcriptional activation during denitrification
- Discovery of new transcriptional regulation mechanisms in denitrifying bacteria

### RELEVANT SKILLS AND EXPERIENCE

- High level of computer literacy. Advanced knowledge of computational biology in a Linux environment. Programming skills in Perl/Bioperl, PHP, MySQL, HTML, website design. Knowledge of Linux system administration including servers and building/maintenance of Linux clusters. High level of familiarity with current software, databases and WWW resources in all areas of computational biology. Familiarity with software in other environments (Windows, Macintosh, Unix).
- Wide range of laboratory experience in microbiology, molecular biology and protein chemistry, including the areas of DNA cloning, DNA sequencing, PCR, mutagenesis, gene expression systems, RNA purification and transcript analysis, protein purification and analysis, spectroscopy.

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<b>GRANTS, FELLOWSHIPS AND SCHOLARSHIPS</b>		
<b>Year</b>	<b>Award</b>	<b>Project</b>
2006 - 2008	ARC Discovery DP0662883 \$ 259 000	R. Cavicchioli (CI), M. Guilhaus (CI), N.F.W. Saunders. The molecular basis of cold adaptation: an integrated genomic and proteomic study of cold-adapted Antarctic archaea
2002 - 2005	ARC Discovery DP0208130 \$ 446 145	R. Cavicchioli, P. Curmi, B. Mabbutt, K.R. Sowers, N.F.W. Saunders. The biology of cold-adapted extremophiles: an integrated genomic-protein analysis approach
2002 - 2005	APD Fellowship	As part of DP0208130
2000 - 2002	UNSW Vice Chancellor's Research Fellowship	Genome sequencing of the psychrophilic archaeon <i>Methanogenium frigidum</i>
1998 - 2000	EU Marie Curie Research Fellowship	Hierarchical control of denitrification
1993 - 1996	Wellcome Trust Postgraduate Fellowship	Structure and function of cytochrome <i>cd<sub>1</sub></i> nitrite reductase

<b>EDUCATIONAL QUALIFICATIONS</b>	
<b>Postgraduate</b> Department of Biochemistry The University of Oxford 1993 - 1997	<b>D. Phil. (1997)</b> Thesis title: "Cloning, sequence analysis and studies on the expression of the <i>nirS</i> gene, encoding cytochrome <i>cd<sub>1</sub></i> , from <i>Thiosphaera pantotropha</i> "
<b>Graduate</b> The University of Edinburgh 1989 - 1993	<b>BSc. (Hons.) Biological Sciences (Biochemistry)</b> <b>First Class (1993)</b>

<b>REFEREES</b>		
Prof. Bostjan Kobe School of Molecular and Microbial Sciences, University of Queensland, Brisbane 4072  Ph: +61 7 3365 2132  email: b.kobe@uq.edu.au	Dr. Thomas Huber, School of Molecular and Microbial Sciences, University of Queensland, Brisbane 4072  Ph: +61 7 3346 9073  email: t.huber@uq.edu.au	Prof. Paul Curmi School of Physics, University of New South Wales, Sydney 2052  Ph: +61 2 9385 4552 Fx: +61 2 9385 4484 email: p.curmi@unsw.edu.au

## PUBLICATIONS (2 PAGES)

### JOURNAL ARTICLES

1. Frith, M.C., **Saunders, N.F.W.**, Kobe, B. and Bailey, T.L. (2008). Discovering Sequence Motifs with Arbitrary Insertions and Deletions. *PLoS Computational Biology*, 4:e1000071.
2. Lonic, A., Barry E.F., Quach, C., Kobe, B., **Saunders, N.** and Guthridge, M.A. (2008). FGFR2 phosphorylation on Serine 779 couples to 14-3-3 and regulates cell survival and proliferation. *Mol. Cell. Biol.*, online doi:10.1128/MCB.01837-07.
3. Thakur, A.S., Robin, G., Guncar, G., **Saunders, N.F.W.**, Newman, J., Martin, J.L. and Kobe, B. (2007). Improved Success of Protein Crystallization Sparse Matrix Screening with Heterogeneous Nucleating Agents. *PLoS ONE* 2:e1091.
4. **Saunders, N.F.W.**, Ng, C., Raftery, M., Guilhaus, M., Goodchild, A. and Cavicchioli, R. (2006). Proteomic and Computational Analysis of Secreted Proteins with Type I Signal Peptides from the Antarctic Archaeon *Methanococcoides burtonii*. *J. Prot. Res.* 5: 2457 -2464.
5. Goodchild, A., Raftery, M., **Saunders, N.F.W.**, Guilhaus, M. and Cavicchioli, R. (2005). Cold adaptation of the Antarctic archaeon, *Methanococcoides burtonii* assessed by proteomics using ICAT. *J. Prot. Res.* 4: 473-480.
6. **Saunders, N.F.W.**, Goodchild, A., Raftery, M., Guilhaus, M., Curmi, P.M.G and Cavicchioli, R. (2005). Predicted roles for hypothetical proteins in the low-temperature expressed proteome of the Antarctic archaeon *Methanococcoides burtonii*. *J. Prot. Res.* 4: 464-472.
7. Goodchild, A., Raftery, M., **Saunders, N.F.W.**, Guilhaus, M. and Cavicchioli, R. (2004). The biology of the cold-adapted Archaeon, *Methanococcoides burtonii*, determined by proteomics using liquid chromatography tandem mass spectrometry. *J. Prot. Res.* 3: 1164-1176.
8. Roberts, T.H., Hejgaard, J. **Saunders, N.F.W.**, Cavicchioli, R. and Curmi, P.M.G. (2004). Serpins in unicellular Eukarya, Archaea, and Bacteria: sequence analysis and evolution. *J. Mol. Evol.* 59: 437-447.
9. Goodchild, A., Saunders, N.F.W., Ertan, H., Raftery, M., Guilhaus, M., Curmi, P.M.G. and Cavicchioli, R. (2004). A Proteomic Determination of Cold Adaptation in the Antarctic Archaeon, *Methanococcoides burtonii*. *Mol. Microbiol.* 53: 309-321.
10. **Saunders, N.F.W.**, Curmi, P.M.G. and Cavicchioli, R. (2004). An online database for the detection of novel archaeal sequences in human ESTs. *Bioinformatics* 20: 2361-2362.
11. Cavicchioli, R., Curmi, P.M.G., **Saunders, N.F.W.** and Thomas, T. (2003). Pathogenic archaea: do they exist? *Bioessays* 25: 1119-1128.
12. **Saunders, N.F.W.**, Thomas, T., Curmi, P.M.G., Mattick, J.S., Kuczek, E., Slade, R., Davis, J., Franzmann, P., Boone, D., Rusterholtz, K., Feldman, R., Gates, C., Bench, S., Sowers, K., Kadner, K., Aerts, A., Dehal, P., Detter, C., Glavina, T., Lucas, S., Richardson, P., Larimer, F., Hauser, L., Land, M. and Cavicchioli, R. (2003). Mechanisms of thermal adaptation revealed from the genomes of the Antarctic Archaea, *Methanogenium frigidum* and *Methanococcoides burtonii*. *Genome Res.* 13: 1580-1588.
13. **Saunders, N.F.W.**, Hornberg, J.J., Reijnders, W.N.M., Westerhoff, H.V., de Vries, S. and van Spanning, R.J.M. (2000). The NosX and NirX Proteins of *Paracoccus denitrificans* are functional homologues: Their Role in Maturation of Nitrous Oxide Reductase. *J. Bacteriol.* 182: 5211-5217.
14. **Saunders, N.F.W.**, Ferguson, S.J. and Baker, S.C. (2000). Transcriptional analysis of the *nirS* gene, coding for *cd1* nitrite reductase, of *Paracoccus pantotrophus* LMD 92.63. *Microbiology* 146: 509-516.
15. **Saunders, N.**, van Spanning, R.J.M., Houben, E., Koefoed, S., de Weert, S., Reijnders, W.N.M., Westerhoff, H.V. and de Boer, A.P.N. (1999). Transcription regulation of the *nir* gene cluster involves NNR and NirI, a novel type of membrane protein. *Mol. Microbiol.* 34: 24-36.
16. Van Spanning, R.J.M., Houben, E., Reijnders, W.N.M., Spiro, S., Westerhoff, H.V. and **Saunders, N.** (1999). Nitric Oxide is a signal for NNR-mediated transcription activation in *Paracoccus denitrificans*. *J. Bacteriol.* 181: 4129-4132.
17. Baker, S.C., **Saunders, N.F.W.**, Willis, A.C., Ferguson, S.J., Hajdu, J. and Fülöp, V. (1997). Cytochrome *cd1* structure: unusual haem environments in a nitrite reductase and analysis of factors contributing to beta-propeller folds. *J. Mol. Biol.* 269: 440-455.
18. Hu, W., Van Driessche, G., Devreese, B., Goodhew, C.F., McGinnity, D.F., **Saunders, N.**, Fülöp, V., Pettigrew, G.W. and Van Beeumen, J.J. (1997). Structural characterization of *Paracoccus denitrificans* cytochrome *c* peroxidase and assignment of the low and high potential heme sites. *Biochemistry* 36: 7958-7966.
19. Williams, P.A., Fülöp, V., Garman, E.F., **Saunders, N.F.W.**, Ferguson, S.J. and Hajdu, J. (1997). Haem-ligand switching during catalysis in crystals of a nitrogen cycle enzyme. *Nature* 389: 406-412.

20. Page, M.D., **Saunders, N.F.W.** and Ferguson, S.J. (1997). Disruption of the *Pseudomonas aeruginosa* *dipZ* gene, encoding a putative protein-disulfide reductase, leads to partial pleiotropic deficiency in *c*-type cytochrome biogenesis. ***Microbiology*** 143: 3111-3122.
21. Goodhew, C.F., Pettigrew, G.W., Devreese, B., Beeumen, J.V., van Spanning, R.J.M., Baker, S.C., **Saunders, N.F.W.**, Ferguson, S.J. and Thompson, I.P. (1996). The cytochromes *c* -550 of *Paracoccus denitrificans* and *Thiosphaera pantotropha* : a need for re-evaluation of the history of *Paracoccus* cultures. ***FEMS Microbiol. Letts.*** 137: 95-101.

## BOOK CHAPTERS

1. **Saunders, N.F.W.**, Brinkworth, R.I., Kemp, B.E. and Kobe, B. (2008). Substrates of Cyclic Nucleotide-Dependent Protein Kinases. In: Handbook of Cell Signalling (Bradshaw, R.A., Dennis, E., eds.). Academic Press San Diego, in press.
2. Cavicchioli, R., **Saunders, N.** and Thomas, T. (2001). Cold shock response in microorganisms. In: Extremophiles: Basic Concepts, (Gerday, C. and Glansdorff, N., eds.). UNESCO Encyclopedia of Life Support Systems ([www.eolss.net](http://www.eolss.net)).

## CONFERENCE PRESENTATIONS AND POSTERS

1. **Saunders, N.F.W.**, Brinkworth, R.I., Huber, T. and Kobe, B. (2007). Predikin and PredikinDB: tools to predict protein kinase peptide specificity. Bioinformatics Australia 2007, Brisbane, Australia, 23-24 October 2007.
2. **Saunders, N.F.W.**, Brinkworth, R.I., Huber, T. and Kobe, B. (2007). Predikin and PredikinDB: computational tools for the prediction of protein kinase substrate specificity. ComBio 2007, Sydney, Australia, 22-26 September 2007.
3. **Saunders, N.F.W.**, Brinkworth, R.I., Huber, T. and Kobe, B. (2006). Prediction of protein kinase substrates using sequence-structure information. ComBio 2006, Brisbane, Australia, 24 - 28 September 2006.
4. **Saunders, N.F.W.**, Curmi, P.M.G., Thomas, T. and Cavicchioli, R. (2003). Pathogenic archaea: do they exist? Intelligent Systems in Molecular Biology, Brisbane, Australia, 29 June - 3 July 2003.
5. **Saunders, N.F.W.** (2003). BioPerl in 2003: a users perspective. Bioinformatics Open Source Conference 2003, Brisbane, Australia, 27 - 28 June 2003.
6. **Saunders, N.F.W.** (2003). Microbial genomes. 7th Australasian Gene Mapping Workshop, The University of New South Wales, 10 - 12 July 2002.
7. Neilan, B.A. and **Saunders, N.F.W.** (2001). Junk DNA in microbial genomes: microcystin synthetase and other large clusters encoding secondary metabolites. 2nd Annual Symposium on functional genomics, gene expression and proteomics, University of Otago, New Zealand. 28 - 29 November 2001.
8. Cavicchioli, R., Thomas T., **Saunders, N.**, Curmi, P., Kuczek, E., Slade, R., Davis, J. and Mattick, J. (2000). Towards the genome of the psychrophilic archaeon *Methanogenium frigidum*. 8th International Conference on Small Genomes. 24 - 28 September 2000, Lake Arrowhead, CA.
9. Baker, S.C., **Saunders, N.**, Fulop, V., Hajdu, J. and Ferguson, S.J. (1995). The structure of *cd*<sub>1</sub> nitrite reductase and analysis of the *nirS* gene of the denitrifying bacterium *Thiosphaera pantotropha*. Beijerinck Centennial Conference on Microbial Physiology and Gene Regulation: Emerging Principles and Applications. 10 - 14 December 1995, The Hague, The Netherlands.