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Current position Research Associate, University of Cambridge, Department of Oncology

Nationality UK/EU citizen

Employment	LGC Ltd, London	Senior Researcher, Life Sciences	2003-2005
	InforSense Ltd., London	Applications Specialist	2002-2003
	ProteoMetrics plc, New York	Biological Software Designer	2000-2002
	Imperial College London	Research Fellow, Biochemistry	1995-1999
	Applied Biosystems, USA	Genetic Applications Specialist	1993-1995
	UCSF	Postdoctoral Fellow, Dept. Surgery	1992-1993
	The Rockefeller University	Postdoctoral Associate	1989-1992

Education	B.A. (conv. MA) Biochemistry (2.i)	University of Oxford	1984
	D.Phil. in Molecular Biology	University of Oxford	1988
	M.Sc. Information Technology	University College London	2000

- Qualifications**
- Accomplished life sciences researcher with over 13 years experience in molecular cell biology, biochemistry and postgenomics methodologies. 18 peer reviewed papers (12 first author) in international journals. Founding research scientist of >£6 million academic laboratory.
 - Experienced bioinformatician and programmer (5 years). Skills in software design and programming in JAVA, PERL, HTML and VisualC++ as well as in data analysis. Database design, interrogation and setup in MySQL.
 - Technical presentations and research seminars in Powerpoint; manuscript and figures preparation, *et cetera*.
 - Training of students, technicians and project supervision. Laboratory and computer network management.
 - Able to work to stringent Quality Control procedures and A17025 accreditation.

Research

Bioinformatics: Creation of new tools, accessible via website, for collecting gene information, and creating assay sequences. Automation of genotyping assay procedures with knowledge management including population of databases and providing controlled access to statistical information on multiple subjects.

Genotyping: Validation for accuracy of rapid, mass spectral scanning of human disease genes to identify variants. Proceeding to operation as a service for inherited colorectal cancer. Sequenom MALDI-TOF Discovery utilizes mass fingerprinting across an entire exon after RNase digestion at each of four base positions. Generation of SOPs and staff training. Design and coding of bespoke software to automatically retrieve mutation data and to streamline analysis.

Novel software development for an interactome viewer in JAVA, from requirements gathering to production of a functional prototype with an intuitive user interface for biologists.

Molecular cell biology of Trypanosoma brucei (protozoan): Defining the roles of trypanosome intracellular compartments using novel Rab GTPases. Cloned *T. brucei* Rab genes, created recombinant proteins and purified antibodies for immunofluorescence and biochemical analysis. These were used to determine function, with transformed parasites overexpressing Rabs. Genomic environment of Rab genes. Cloning and characterisation of *C. fasciculata* trypanothione reductase gene by PCR, creating and screening a genomic library. Isolation of *T. brucei* telomere binding proteins.

Antibody engineering: Creation of recombinant immunoglobulin Fv (mini-antibodies) actively binding ligand by recombinant DNA methods and site directed mutagenesis.

Expertise

Project management: Formal training in and use of tools for planning and communicating a genotyping project designed for SNP discovery and used for mutation detection. Acquisition and management of resources, and control of the progress of the validation of novel software with complex mass spectrometry technology involving laboratory procedures and software. Complete supervision, including training, of one member of staff and collaboration with programmers. These skills in communication complement some experience in presentation of new software for statistical analysis of microarray and other complex data and mass spectrometry.

Computation: Object-Oriented planning, user intuitive GUI and webpage design, prototype software creation and testing. Programming in Perl using CGI.pm/Apache, Java, C++, SQL; specialised web browsers, cross platform development for MacOS9, MacOSX, Windows2000 and Linux/Unix; Metrowerks Code Warrior, Visual C++, Sun and Apple java tools. Excel, Word, Powerpoint, Flash, Dreamweaver, Adobe Photoshop, Illustrator. Intranet maintenance, web site construction, email account management. GCG (Wisconsin), BLAST, RNA/protein analysis, PAUP/Phylip (phylogeny), Sequence multiple alignment (Clustal, Smith Waterman), Primer3, RealSNP. Genotyper for PCR fragment analysis, Autoassembler for DNA sequence assembly (Applied Biosystems), Rasmol, Homology (molecular model builder, Silicon Graphics), RADARS (ProteoMetrics) for automatic proteomic mass spectral data archiving, analysis and retrieval, Kensington Discovery Edition (InforSense/Imperial College) for microarray data analysis. Sequenom Discovery for gene variant / SNP analysis.

Databases: Relational database design for non-redundant protein information using ERWin, Oracle. Creation of a database for mutation and Discovery data, and for customer sample tracking. Access-Oracle interfaces and web front ends for automatic population and controlled data access.

Assay development and biotechnology: Ligand binding (protein interactions), immunofluorescence, endocytosis, T-cell proliferation, nucleotide-binding and hydrolysis, Sequenom SNP discovery by termination across the SNP (massExtend), or by general cleavage of an RNA product covering the site

(massCleave). Automated sequencing and genotyping (Applied Biosystems), oligonucleotide synthesis, fluorescence spectroscopy.

Recombinant proteins & protein chemistry: Purification, characterisation, mass spectrometry, HPLC, FPLC, column chromatography, transformation of bacteria, yield optimisation, protein refolding.

Molecular biology: PCR, real-time PCR, HyBeacons, Southern, Northern blotting, gel shift assay, triple helix DNA, cloning, subcloning, manual sequencing (Maxam and Gilbert, Sanger), restriction mapping, site-directed mutagenesis.

Microscopy and immunochemistry: Confocal microscopy, digital microscopy, immunofluorescence with mammalian and trypanosome cells. Raising antibodies, purifying antisera by affinity chromatography against recombinant protein and peptides, ELISA, Ocherlony, Western blotting.

Cell culture and transformation: Yeast, bacteria, mammalian and trypanosomes.

Publications

1. **Field, H.**, Yarranton, G., Rees, A.R. (1987) *Production of mini-antibodies in E. coli*. In: *Modern Approaches to New Vaccines including Prevention of AIDS*. Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, USA September 9-13
2. **Field, H.**, Rees, A.R., Yarranton, G.T. (1988) *A functional recombinant immunoglobulin variable domain from polypeptides produced in Escherichia coli*. *Vaccines*88, Publ. Cold Spring Harbor Laboratory, Eds. Ginsberg, Lerner, Brown and Chanock, pp. 29-34
3. **Field, H.** (1988) *On recombinant immunoglobulin variable domains*. D.Phil. (Ph.D.) thesis, Oxford University, Oxford, UK
4. **Field, H.**, Yarranton, G.T., Rees, A.R. (1990) *Expression of immunoglobulin light and heavy chain variable regions in Escherichia coli and reconstitution of antigen-binding activity*. *Protein Engineering*, 3, 641-647
5. **Field, H.**, Yeung, H.L.H., Rees, A.R. (1990) *Production of a recombinant immunoglobulin variable fragment from polypeptides produced in Escherichia coli cytoplasm*. *Analytical Proceedings of the Royal Society of Chemistry (GB)*, 27, 2-5
6. **Field, H.** (1990) *Recombinant immunoglobulin variable domain production - feasibility, progress and directions*. *Chimica Oggi*, September, pp. 33-36
7. Kuriyan, J., Kong, X.-P., Krishna, T.S.R., Sweet, R.M., Murgolo, N.J., **Field, H.**, Henderson, G.B., Cerami, A. (1991) *X-ray structure of trypanothione reductase from Crithidia fasciculata at 2.4Å resolution*. *Proceedings of the National Academy of Science USA*, 88, 8764-8768
8. **Field, H.**, Cerami, A.C., Henderson, G.B. (1992) *Cloning, sequencing, and demonstration of polymorphism in trypanothione reductase from Crithidia fasciculata*. *Molecular and Biochemical Parasitology*, 50, 47-56
9. **Field, H.**, Garovoy, M.R. (1994) *Positive impact of DNA typing on solid organ transplantation*. *Transplantation Reviews*, 8, 151-173
10. Field, M.C., **Field, H.**, Boothroyd, J.C. (1995) *A homologue of the nuclear GTPase Ran/TC4 from Trypanosoma brucei*. *Molecular and Biochemical Parasitology*, 69, 131-134
11. Frankel, G., Philips, A.D., Novakova, M., **Field, H.**, Candy, D., Schauer, D.B., Douce, G., Dougan, G. (1996) *Intimin from enteropathogenic Escherichia coli restores murine virulence to a Citrobacter rodentium eaeA mutant: induction of an immunoglobulin A response to intimin and EspB*. *Infection and Immunity*, 64, 5315-5325
12. **Field, H.**, Field, M.C. (1996) *Trypanosoma brucei, Leptomonas seymouri: a methodology for the production of telomere binding proteins*. *Experimental Parasitology*, 83, 155-158
13. **Field, H.**, Blench, I., Croft, S., Field, M.C. (1996). *Protein isoprenylation in Trypanosoma brucei brucei*. *Biochemical Society Transactions*, 24, 433
14. **Field, H.**, Blench, I., Croft, S., Field, M.C. (1996). *Characterization of protein isoprenylation in Trypanosoma brucei*. *Molecular and Biochemical Parasitology*, 82, 67-80
15. **Field, H.**, Field, M.C. (1997) *Tandem duplication of rab genes followed by sequence divergence and acquisition of distinct functions in Trypanosoma brucei*. *Journal of Biological Chemistry*, 272, 10498-10505
16. **Field, H.**, Farjah, M., Pal, A., Gull, K., Field, M.C. (1998) *Complexity of trypanosomatid endocytosis pathways revealed by Rab4 and Rab5 isoforms in Trypanosoma brucei*. *Journal of Biological Chemistry*, 273, 32102-32110
17. **Field, H.**, Ali, B.R.S, Sherwin, T., Gull, K., Croft, S.L., Field, M.C. (1999) *TbRab2p, a marker for the endoplasmic reticulum of Trypanosoma brucei, localises to the ERGIC in mammalian cells*. *Journal of Cell Science*, 112, 147-156

18. Field, M.C., Ali, B.R.S., **Field, H.** (1999) *GTPases in protozoan parasites: tools for cell biology and chemotherapy*. Parasitology Today 15, 365-371
19. **Field, H.**, Sherwin, T., Smith, A., Gull, K., Field, M.C. (2000) *Cell-cycle and developmental regulation of TbRab31p localisation , a GTP-locked Rab protein from Trypanosoma brucei*. Molecular and Biochemical Parasitology, 106, 21-35
20. **Field, H.I.**, Fenyő, D., Beavis, R. (2001) *RADARS, a bioinformatics solution that automates proteome mass spectral analysis, optimises protein identification, and archives data in a relational database*. Proteomics 2, 36-47
21. Pal, A., Hall, B.S., Nesbeth, D.N., **Field H.I.**, Field M.C. (2001) *Differential endocytic functions of Trypanosoma brucei Rab5 isoforms reveal a glycosylphosphatidylinositol-specific endosomal pathway*. Journal of Biological Chemistry 277. 9529-9539
22. Guo, Y., Chattratichat, J., Köhler, M., **Field, H.I.** (2002) *Enterprise Discovery Planning: organizing knowledge production in discovery informatics*. Innovations in Pharmaceutical Technology, 36-37
23. **Field, H.**, Fenyő, D., Beavis, R, Rout, M.P., Chait, B.T. (Manuscript in preparation.) *Software for creating and displaying a customisable network of protein interactions*.
24. Cowen, S., **Field, H.** and Thomson, J. (Manuscript in preparation) *Converting Nomenclatures for Gene Mutation*. Human Mutation,
25. **Field, H.**, Buys, J., Cowen, S., Lucas, C., Thomson, J., Debenham, P. (Manuscript in preparation) *Rapid Mutation Detection in a Gene using Mass Spectrometry*.