Fábio M. Marques Madeira

PhD student in Bioinformatics

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iaii.com	Education
2013 – 2016	College of Life Sciences – University of Dundee PhD in Bioinformatics (expected)
2008 – 2010	Faculdade de Ciências e Tecnologia – Universidade Nova de Lisboa Master in Molecular Genetics and Biomedicine (17/20, Honours 1 st) Merit award from Santander-UNL relative to the 1 st academic year
2004 – 2008	Faculdade de Ciências e Tecnologia – Universidade Nova de Lisboa Eurobachelor in Biochemistry (14/20, Honours 2:1) Ranked 2 nd in class
	Experience & Funding
2012 – 2013	Mapping the 14-3-3-binding 2R-ohnologue protein families of the human kinome , supervised by Prof. Carol MacKintosh (Division of Cell and Developmental Biology, CLS-UoD), 1 st Laboratory Rotation ^A
2011 – 2012	CREMA: Constrained Refining of Multiple Alignments to identify correlations between mutations, supervised by Prof. Ludwig Krippahl (CENTRIA-DI, FCT-UNL) ^B
2011 – 2011	Glycosylation and Lewis X motif in neuronal tissue, supervised by Dr. Júlia Costa
2009 – 2010	Production of a stable form of a human phenylalanine hydroxylase: towards the 3D structure determination , supervised by Prof. Maria João Romão (Crystallography, REQUIMTE/CQFB, FCT-UNL) and Prof. Ana Paula Leandro (Metabolism and Genetics, FF-UL) ^B
	Publications
2012	Fábio Madeira and Ludwig Krippahl. 2012. PYCOEVOL: A Python workflow to study protein-protein coevolution . Proceedings of the International conference on Bioinformatics Models, Methods and Algorithms - BIOINFORMATICS 2012, pp.143-9.
2011	Marco Correia, Fábio Madeira, Pedro Barahona and Ludwig Krippahl. 2011. Improving Multiple Sequence Alignments with Constraint Programming and Local Search. Proceedings of the Workshop on Constraint Based Methods for Bioinformatics - WCB11, pp.37-44.
2010	Fábio Madeira. 2010. Estudos Estruturais e Funcionais da Fenilalanina Hidroxilase Humana . Master Thesis in Molecular Genetics and Biomedicine (portuguese).
	Posters

2012

Michele Tinti, Catherine Johnson, Fábio Marques Madeira, Margaret Malcolm and Carol MacKintosh. Evolution of 14-3-3-binding sites and 2R-Ohnologue families. PTMs in 2012 Cell Signaling, Copenhagen, Denmark, December 2-5th

Paulo Roque Lino, Fábio Madeira, Isabel Tavares de Almeida, and Paula Leandro. 2010. Alternative Answers to Everlasting Problems: Protein Engineering Towards 2010 New Approaches for Phenylketonuria Treatment. 2010 SPDM Annual Symposium, Albufeira, Portugal, November 4-5th

Catarina Coelho, Fábio Madeira, Paulo Roque Lino, Isabel Tavares de Almeida, Paula Leandro and Maria João Romão. 2010. Crystallization of a Stable Form of Human Phenylalanine Hydroxylase: Towards the 3D Structure Determination. UK-Portuguese Teams Meeting. Protein-protein interaction and Protein folding. FCT-UNL, March 29-31st

^A PhD Studentship from the Wellcome Trust PhD Programme in Molecular and Cellular Biology (UK)

^B Research Studentship from Fundação para a Ciência e Tecnologia (PT)

Communications & Teaching

- Tutorial on Pycoevol. Practical session of the course in Applied Bioinformatics,
 Masters in Structural and Functional Biochemistry, Department of Chemistry, FCT-UNL,
 4th May
- Computational Analysis of Protein Coevolution and Interaction. Knowledge
 Discovery and Bioinformatics group, INESC-ID, 9th March
- PYCOEVOL: A Python workflow to study protein-protein coevolution. International conference on Bioinformatics Models, Methods and Algorithms BIOINFORMATICS 2012, Vilamoura, Algarve, Portugal, 1-4th February
- Improving Multiple Sequence Alignments with Constraint Programming and Local Search. Workshop on Constraint Based Methods for Bioinformatics WCB11, Perugia, Italy, 12th September
- Human Phenylalanine Hydroxylase Structure: Towards 3D Structure

 Determination. Met&Gen Ph.D. Students Workshop. Inborn Errors of Metabolism:
 Understanding the Molecular Mechanisms. FF-UL, 26-27th November

Training

- The PhD Journey Conference, Aberdeen, Scotland, November 6-7th
- **Tutorial on Zotero** (Bibliographic Management) with Maria do Rosário at the Library, 2011 FCT-UNL. November 30th
- BPB'11- Bioinformatics using Python for Biologists at the Gulbenkian Training Programme in Bioinformatics with Allegra Via and Fabrizio Ferrè (Sapienza Università di Roma), IGC, May 2-6th
- **Tutorial on EndNote Web** (Web of Knowledge) with Maria do Rosário at the Library, FCT-UNL, April 21st
- Advanced Course in Protein Crystallography at the Crystallography Lab., REQUIMTE/CQFB, FCT-UNL, February 1-5th
- Trainee on Structural and Computational studies of Metalloproteins at the Crystallography Lab., under supervision of Prof. Maria João Romão (Crystallography, REQUIMTE/CQFB, FCT-UNL), from September to December, 8 hours per week.

Skills

Structural Biology (X-ray crystallography), Bioinformatics (Data-mining, Protein docking, Sequence analysis), Molecular Evolution (Protein coevolution, Phylogenetics), Molecular Biology and Protein Expression & Purification (Protein expression systems, Gel electrophoresis, Blotting, HPLC, Enzymatic assays), Cellular Biology (Western Blot, Tissue Culture, Fluorescence Microscopy), Computer Programming (Python, R, Octave, Pascal), Operating Systems (Linux-unix, Windows, Mac OS), Database Management (MySQL, Microsoft Access), Web Development (HTML, Web2py, Wordpress, Joomla), Molecular & Scientific Illustration (Photoshop, Molecular Maya, UCSF Chimera, PyMOL), Utilities (Eclipse IDE, Microsoft Office, LaTeX, Git, EndNote), English (CEF Level C1, EILTS 7.5)