

## Narcis Fernandez-Fuentes

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### Bio sketch

Dr Narcis Fernandez-Fuentes is a Reader in Bioinformatics and Genomics at the Institute of Biological, Environmental and Rural Sciences at Aberystwyth University, United Kingdom. He received his B.Sc. degree in Biology from the University of Girona in 1997. Then, moved to Barcelona where he received his B.Sc. degree in Biochemistry from the University Autonomus of Barcelona in 1999. On 2004 he received a Ph.D. in Computational Biology by the same university under the supervision of Prof Baldo Oliva. From 2004 to 2007 he was a Research Associate at the Albert Einstein College of Medicine in New York, USA, under the supervision of Prof Andras Fiser. On 2007 he moved to Leeds, United Kingdom as Lecturer in Computational Biology to start his independent career funded by RCUK Academic Fellowship scheme. From 2012, he is Reader in Bioinformatics at Aberystwyth University, United Kingdom. Dr Fernandez-Fuentes has been recipient of a EMBO and FEBS short-term fellowships, a Marie-Curie training fellowship, an RCUK academic fellowship, a TecnioSpring Incoming Fellowship, and travel bursaries from the Royal Society (United Kingdom), the Boehringer Ingelheim travel fond, and the Worldwide University Network (WUN, United Kingdom). Dr Fernandez-Fuentes' research has been funded by the Wellcome Trust (UK), BBSRC (UK), Era-NET and ClimateKIC (EU), Biomedical Health Research Center (UK) and HPC Wales/Fujitsu UK.

**Current members:** 2 PhDs, 2 PDRA; 2 RA

### Research Experience

<b>Reader in Bioinformatics</b> Aberystwyth University, Aberystwyth U.K.	2012-
<b>TecnioSpring Incoming Fellow</b> University Pompeu Fabra, Barcelona, Spain	2014-2016
<b>Lecturer - RCUK Academic Fellow</b> University of Leeds, Leeds, U.K.	2007-2011
<b>Research Associate</b> Albert Einstein College of Medicine. New York, U.S.A. <b>Mentor:</b> Prof Andras Fiser.	2004-2007
<b>Ph.D. student and research fellow</b> Universitat Autònoma de Barcelona, Barcelona, Spain. <b>Mentor:</b> Prof Baldomero Oliva	1999-2004

**Visiting Fellow** Oct 2003-Mar 2004  
Albert Einstein College of Medicine. NY, U.S.A.  
**Mentor:** Prof Andras Fiser

**EMBO and FEBS fellow** Oct 2002-Mar 2003  
Imperial College, London, U.K.  
**Mentor:** Prof Michael JE. Sternberg

**Marie Curie Fellow** Sep 2001-Feb 2002  
EMBL-EBI, Hinxton UK.  
**Mentor:** Prof Liisa Holm

### Education

2000-2004	<b>PhD Computational Biology</b>
2000-2002	<b>M.Sc., Biotechnology</b>
1997-1999	<b>B.Sc. Biochemistry</b>
1992-1997	<b>B.Sc. Biology</b>

### Personal Awards and Fellowships

2014-2016	<b>TecnioSpring Incoming Fellow</b>
2007-2011	<b>RCUK Academic Fellow</b>
2003	<b>Boehringer Ingelheim Fellowship</b>
2003	<b>FEBS short term Fellowship</b>
2002	<b>EMBO short term Fellowship</b>
2001-2002	<b>Marie Curie Fellowship (EMBL-EBI)</b>
1999-2003	<b>FI-FIAP Pre-doctoral Fellowship</b>

### Professional Activities

Since 2014 **Pool Expert, NSF, USA.**  
Since 2012 **Expert AgreeSkills Fellowships, France**  
Since 2011 **Expert Evaluator, AGAUR, Spain**  
Since 2009 **Pool Expert BBSRC, United Kingdom**  
Since 2009 **Academic Editor, PLOS One.**  
Since 2007 **Evaluator, SECYT, Argentina**  
Since 2007 **Expert evaluator EU: FP7, H2020**

### Funding ID

**£135,353** Oct 2015- Sep 2018 **BBSRC**. "Bioinformatics and Biomathematics training grant" **PI**  
**£46,250** April 2015- Apr 2016 **BBSRC BB/N004469/1**. "Using computational novel methods to characterise the genetics of tan spot resistance in wheat" **Co-I**  
**£422,285** Jan 2015- Dec 2017 **BBSRC BB/M009459/1**. "Can cyclin dependent kinase activity be manipulated to control chromosome pairing and recombination in plants" **Co-I**  
**€1.83M** Mar 2015- Apr 2018 **ERA-IB-14-071**. "OXYPOL: Optimized laccase systems for high-value bio-plastics production from biomass" **Co-I and WP leader**  
**£1.38M** Apr 2012- Mar 2017 **BBSRC BBS/E/W/10962A01D**. "Bioinformatics and genomics and phenomics platform development" **Co-I**

## Patents

**UK Patent GB1311111.7** “*Binding partners and inhibitors*” **Narcis Fernandez-Fuentes**, Tomo Tanaka and Terence H Rabbitts.

## Selected Publications

Peer-reviewed: 51  
Reviews: 3  
Book Chapters: 3  
Citations: 1193 h-index: 19 i10-index: 26

<http://scholar.google.com/citations?user=NQLTzpoAAAAJ>

Javier Garcia-Garcia, Victoria Valls-Comamala, Emre Guney, David Andreu, Francisco J Muñoz, **Narcis Fernandez-Fuentes**, Baldomero Oliva, “iFraG: a protein-protein interface prediction server based on sequence fragments” *Journal of Molecular Biology*, *IN PRESS*

Roni HG Wright, **Narcis Fernandez-Fuentes**, Baldo Oliva, Miguel Beato “Insight into the machinery that oils chromatin dynamics”. *Nucleus*, 28:1-8 (2016)

Hanen Bouraoui, Marie-Laure Desrousseaux, Eleni Ioannou, Pablo Alvira, Mohamed Manaï, Caroline Rémond, Claire Dumon, **Narcis Fernandez-Fuentes**, Michael J O’Donohue “The GH51  $\alpha$ -L-arabinofuranosidase from *Paenibacillus* sp. TSH1 is multifunctional, hydrolyzing main-chain and side-chain glycosidic bonds in heteroxylans”. *Biotechnol Biofuels*, 8:9:140 (2016)

Altan Kara, Martin Vickers, Martin Swain, Davie Withworth, **Narcis Fernandez-Fuentes** “MetaPred2CS: a sequence-based meta-predictor for protein-protein interactions of prokaryotic two-component system proteins” *Bioinformatics*, 32(21):3339-3341 (2016)

Daniel Poglayen, Manuel Alejandro Marín-López, Jaume Bonet, Oriol Fornes, Javier Garcia-Garcia, Joan Planas-Iglesias, Joan Segura, Baldo Oliva, **Narcis Fernandez-Fuentes** “InteractoMIX: a suite of computational tools to exploit Interactomes” *Biological and Clinical Research* *Biochemical Society Transactions*, 44:3 (2016)

Jaume Bonet, Javier Garcia-Garcia, Joan Planas-Iglesias, **Narcis Fernandez-Fuentes**, Baldo Oliva “Archer: Predicting protein function using local structural features. A helpful tool for protein redesign” *Protein Science*, 24:221 (2015).

Altan Kara, Martin Vickers, Martin Swain, Davie Withworth, **Narcis Fernandez-Fuentes** “Genome-wide prediction of prokaryotic two-component system networks using a sequence-based meta-predictor” *BMC-Bioinformatics*, 16:297 (2015).

Manuel-Alejandro Marin-Lopez, Joan Planas-Iglesias, Jaume Bonet, Daniel Poglayen, Javier Garcia-Garcia, **Narcis Fernandez-Fuentes**, Baldo Oliva “Understanding protein recognition using structural Features” *Protein Science*, 24:245 (2015).

Joan Segura, Manuel-Alejandro Marin-Lopez, Pamela F Jones, Baldo Oliva, **Narcis Fernandez-Fuentes**, “VORFFIP-Driven Dock: V-D2OCK, a Fast and Accurate Protein Docking Strategy” *PLoS One*, 10(3):30118107 (2015).

Baldo Oliva and **Narcis Fernandez-Fuentes**, “Knowledge-based modeling of peptides at protein interfaces: PiPreD” *Bioinformatics*, btu838 [Epub ahead of print] (2015).

Jaume Bonet, Andras Fiser, Baldo Oliva, **Narcis Fernandez-Fuentes**, “Smotifs as structural local descriptors of supersecondary elements: classification, completeness and applications” *Bio-Algorithms and Med-Systems*, 10(4):195-212 (2014).

Jaume Bonet, Joan Segura, Joan Planas-Iglesias, Baldo Oliva, **Narcis Fernandez-Fuentes**, “Fra’r’Us: knowledge-based sampling of protein backbones for *de novo* structure-based protein design” *Bioinformatics*, 30(13):1935-6 (2014).

A. Cruz-Migoni, **Narcis Fernandez-Fuentes\*** and Terence H Rabbitts “*Peptides: minimal drug surrogates to interrogate and interfere with protein function*” *Medicinal Chemistry Communications*, *MedChemComm* 4:1218-21 (2013) (\*) Corresponding author

**Narcis Fernandez-Fuentes** and Andras Fiser “*A modular perspective of protein structures: application to fragment based loop modelling*” *Methods Mol Biol*. 932:141-58 (2013)

**Narcis Fernandez-Fuentes** “*Inhibiting RAS interactions using peptides; computational design and experimental validation*” *FEBS Journal* 279(Suppl. 1):455 (2012)

Joan Segura, Pamela F Jones and **Narcis Fernandez-Fuentes** “*A holistic in silico approach to predict functional sites in protein structures*” *Bioinformatics* 28(14):1845-50 (2012)

Kamron Khan, [6 authors], **Narcis Fernandez-Fuentes**, [12 authors] and Manir Ali “*Next generation sequencing identifies mutations in Atonal homolog 7 (ATOH7) in families with global eye developmental defects*” *Hum Mol Genet* 21(4):776-83 (2012)

Joan Segura, Baldo Oliva and **Narcis Fernandez-Fuentes** “*CAPS-DB: A structural classification of helix-capping motifs*” *Nucleic Acids Res*. D479-85 (2012)

Joan Segura, Pamela F Jones and **Narcis Fernandez-Fuentes** “*Improving the prediction of protein binding sites by combining heterogeneous data and using Voronoi Diagrams*” *BMC Bioinformatics* 23;12:352 (2011)

Joan Segura, **Narcis Fernandez-Fuentes** “*PCRPI-DB: a Database of computationally annotated hot spot in protein interfaces*” *Nucleic Acid Research* 39:D755-60 (2011)

**Narcis Fernandez-Fuentes**, Joseph Dybas, Andras Fiser “*Structural characteristics of protein folds*” PLOS Computational Biology 22:6 (2010)

Salam A. Assi, Tomoyuki Tanaka, Terence H. Rabbits and **Narcis Fernandez-Fuentes** “*PCRPI: Presaging Critical Residues in Protein Interfaces: a new computational tool to chart hot spot in protein interfaces*” Nucleic Acids Research. Nucleic Acids Research 38:e86 (2010)

**Narcis Fernandez-Fuentes**, Brajesh K. Rai, Carlos J. Madrid-Aliste, J. Eduardo Fajardo and András Fiser “*Comparative protein structure modeling by combining of multiple templates and optimizing sequence-to-structure alignments*” Bioinformatics. 23:2558-65 (2007)

**Narcis Fernandez-Fuentes**, Carlos J. Madrid-Aliste, Brajesh K. Rai, J. Eduardo Fajardo and András Fiser “*M4T: a comparative protein structure modeling server*” Nucleic Acids Research. 35:173-6 (2007)

Marcela Torres, **Narcis Fernandez-Fuentes**, Andras Fiser and Arturo Casadevall “*The immunoglobulin heavy chain constant region affects kinetic and thermodynamic parameters of antibody variable region interactions with antigen*” Journal of Biological Chemistry 282:13917-13927 (2007)

**Narcis Fernandez-Fuentes\***, Hui Xiao\*, Pascal Verdier-Pinar\*, Berta Burd, Ruth Angeletti, Andras Fiser, Susan Band Horwitz and George Orr “*Insights into the mechanism of microtubule stabilization by Taxol*” PNAS. 27:10166-10173 (2006). (\*) Jointly first authorship.

**Narcis Fernandez-Fuentes** and Andras Fiser “*Saturating representation of conformational fragments in structure databanks*” BMC Structural Biology. 6:15 (2006)

**Narcis Fernandez-Fuentes**, Jun Zhai and Andras Fiser “*ArchPred: a template based loop structure prediction server*” Nucleic Acids Research. 34:W173-6 (2006).

**Narcis Fernandez-Fuentes** and Andras Fiser “*A supersecondary structure library and search algorithm for modeling loops in protein structures*” Nucleic Acids Research. 34:7:2085-2097 (2006).

Jordi Espadaler, **Narcis Fernandez-Fuentes**, Antoni Hermoso, Enrique Querol, F.X. Aviles, Michael J.E. Sternberg and Baldomero Oliva “*ArchDB: Automated protein loop classification as a tool for Structural Genomic*” Nucleic Acids Research. 32:1:D185-D188 (2004).

Sabine Dietmann, **Narcis Fernandez-Fuentes** and Liisa Holm. “*Automated detection of remote homology*” Current Opinion in Structural Biology 12:3:362-367 (2002).

## Meetings and Invited Talks

**June 2016.** Academy of Medical Sciences – Immunology, Cancer Biology and Beyond. London, United Kingdom. “**Needles, haystacks and RAS**”

**Dec 2015.** Societat Catalana de Biologia – III Conference in Bioinformatics and Computational Biology. Barcelona, Spain. “**De novo design of peptides to modulate protein–protein interactions**”

**Dec 2015.** Biochemical Society – New Developments in Protein Structure Modeling for Biological and Clinical Research. London, United Kingdom. “**Knowledge-based modelling of orthosteric peptides to modulate protein–protein interactions – a route to discover novel therapeutic agents**”

**May 2015.** 11<sup>th</sup> Carbohydrate Bioengineering Meeting. Espoo, Finland. “**Development of novel enzymatic tools for the production of xylose-based products within a lignocellulosic biorefinery concept**”

**February 2014.** ACC10. TECNIOSpring presentation day. Barcelona, Spain. “**ComPepts: Computational Design of peptides disruptors of protein complexes**”

**April 2013.** SAHMRI/EMBL. Biomedical Informatics Day. Adelaide, Australia. “**Interactomes, inhibition of protein interactions and drug discovery**”

**March 2013.** Weatherall Institute of Molecular Medicine. WIMM seminar program. Oxford. UK. “**A computational strategy to design orthosteric peptides to modulate protein-protein interaction: validation on HRAS**”

**September 2012.** IUBMB-FEBS conference. From Single Molecules to System Biology. Seville. Spain. “**Inhibiting RAS interactions using peptides; computational design and experimental validation**”

**March 2012.** Fujitsu-HPC Wales. Genomics and Bioinformatics. Gwynnog, Wales. UK. “**Finding needles in the PDB databank haystack**”

**March 2011.** Peptide Arrays Conference. Charles Darwin House, London. Oxford. UK. “**A knowledge-based computational method for the design of peptide modulators of protein interactions**”

**November 2010.** National Grid Service Innovation Forum. STFC Rutherford Appleton Laboratory. Oxford. UK. “**Early stages in drug discovery and the NGS**”

**January 2010.** Protein interfaces mini-symposium. University of Cambridge. UK. “**Towards a novel, knowledge-based, approach to model peptide on protein interfaces**”

**December 2009.** All Hands UK e-Science Meeting. University of Oxford. UK. “**Using NGS grid infrastructure to run a massive in silico drug screening**”

Poster communications: 6  
Invited talks: 14  
Courses and Conferences: 8

**April 2009.** National Grid Service Roadshow. University of Bath. UK. ***“Deploying a large in silico screening on NGS grid infrastructure”***

**December 2005.** XIII Workshop Recent Advances in Molecular Biology. Madrid. Spain ***“Saturating representation of conformational fragments in current databanks”***

**September 2002.** XXV Meeting of the Spanish Society of Biochemistry and Molecular Biology. Spain. ***“Protein Loop Classification Update: Functional Implication”***