

Pablo Mínguez Paniagua

Post-doctoral fellow

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Personal details

Born 4th March 1976, Alcalá de Henares (Madrid), Spain; Spanish citizenship.

Academic education

31st October 2008 **PhD. in Biology (Molecular Biology, Bioinformatics).** *Summa cum laude.*
Universidad Autónoma de Madrid (Madrid, Spain).

2002 – 2003 **MSc. in Bioinformatics.** *Distinction.*
University of East Anglia (Norwich, UK).

2000 – 2001 **Postgraduate Certificate in Education** (subject Biology and Geology).
Universidad Complutense (Madrid, Spain).

1994 – 2000 **BSc. in Biological Sciences** (Microbiology and environmental biology).
Universidad de Alcalá (Alcalá de Henares, Madrid, Spain).

Merits and distinctions

2011 **Marie Curie Postdoctoral Fellowship award.** Call FP7-PEOPLE-2010-IEF.

2009 **Postdoctoral Fellowship award.** Fellowship Programme for Specialization in International Organizations, granted by the Spanish Ministry of Science and Innovation (MICINN).

2004 **Predocctoral Fellowship award.** Genome Canada PhD Fellowship.

2003 **Scholarship Award.** MSc dissertation Fellowship based on the masters' qualifications (John Innes Centre Norwich, UK). **Grade Distinction** in the MSc Bioinformatics.

Research experience

Sept 2009 – present **Post-doctoral researcher.** Bork group, Structural and Computational Biology Unit, EMBL Heidelberg, Germany.

Oct 2008 – Sept 2009 **Bridging postdoc.** Bioinformatics and Genomics Department, CIPF, Valencia, Spain.

Sept 2004 – Oct 2008 **PhD. Student.** Bioinformatics and Genomics Department, CNIO, Madrid/CIPF, Valencia, Spain.
PhD dissertation: *Functional profiling of genome-scale experiments. New approaches leading to a systemic analysis.*

Jan – Sept 2004 **Research Associate, Bioinformatician.** Nottingham Arabidopsis Stock Centre (NASC), University of Nottingham, Nottingham, UK.

Jun – Sept 2003 **Research Scholarship.** Computational and Systems Biology Department and Disease and Stress Biology Department. John Innes Centre, Norwich, UK.

Relevant publications (from a total of 23 publications) for updates and complete list, search for "Pablo Mínguez" in Pubmed

Mínguez P, Letunic I, Parca L, Bork P. (2012) PTMcode: a database of known and predicted functional associations between post-translational modifications in proteins. *Nucl. Acids Res.*; 41:D306-D311

Mínguez P, Parca L, Diella F, Mende DR, Kumar R, Helmer-Citterich M, Gavin AC, van Noort V, Bork P. (2012) Deciphering a global network of functionally associated post-translational modifications. *Molecular Systems Biology*; 8:599.

Mínguez P, Dopazo J. (2011) Assessing the biological significance of gene expression signatures and co-expression modules by studying their network properties. *PLoS One*; 6(3): e17474.

Al-Shahrour F, **Mínguez P**, Marques-Bonet T, Gazave E, Navarro A and Dopazo J. (2010) Selection upon genome architecture: conservation of functional neighborhoods with changing genes. *PLoS Computational Biology*; 6(10):e1000953.

Mínguez P, Dopazo J. (2010) Functional genomics and networks: new approaches in the extraction of complex gene modules. *Expert Rev Proteomics*; 7(1):55-63.

Mínguez P, Gotz S, Montaner D, Al-Shahrour F, Dopazo J. (2009) SNOW, a web-based tool for the statistical

analysis of protein-protein interaction networks. *Nucl. Acids Res.*; 37:W109-114.

Minguez P, Dopazo J. (2009) Protein Interactions for Functional Genomics. In: Li X-L, Ng S-K, eds. *Biological Data Mining in Protein Interaction Networks*. Hershey, USA: Idea Group Inc (IGI).

Horcajadas JA, **Minguez P**, Dopazo J, et al. (2008) Controlled ovarian stimulation induces a functional genomic delay of the endometrium with potential clinical implications. *J. Clin. Endocrinol. Metab.*; 93:4500-10.

Minguez P, Al-Shahrour F, Montaner D, Dopazo J. (2007) Functional profiling of microarray experiments using text-mining derived bioentities. *Bioinformatics*; 23:3098-9.

Minguez P, Al-Shahrour F, Dopazo J. (2006) A function-centric approach to the biological interpretation of microarray time-series. *Genome Inform.*; 17:57-66.

Al-Shahrour F, **Minguez P**, Tarraga J, et al. (2006) BABELOMICS: a systems biology perspective in the functional annotation of genome-scale experiments. *Nucleic Acids Res.*; 34:W472-6.

Teaching experience

4th - 6th July 2011 - DiGtoP-Bioinformatics Course on Protein Interactions and Networks. EMBL, Heidelberg, Germany.

21st - 25th March 2011 - VII International Course of Massive Data Analysis. Centro de Investigación Príncipe Felipe, Valencia, Spain.

30th September 2010 – Cytoscape Course. EMBL, Heidelberg, Germany.

21st - 23rd April 2009 - Microarray Data Analysis Course. University of Murcia, Murcia, Spain.

09th - 13th March 2009 - V International Course on Microarray Data Analysis. Centro de Investigación Príncipe Felipe, Valencia, Spain.

10th - 14th March 2008 - IV International Course on Microarray Data Analysis. Centro de Investigación Príncipe Felipe, Valencia, Spain.

12th - 16th March 2007 - III International Course on Microarray Data Analysis. Centro de Investigación Príncipe Felipe, Valencia, Spain.

5 Relevant communications and posters

XI Jornadas de Bioinformatica. Jan 23-25, 2012. Barcelona, Spain.

Oral Presentation: A global network of crosstalking post-translational modifications. **Minguez P**, Parca L, Diella F, Mende DR, Kumar R, Helmer-Citterich M, Gavin AC, van Noort V, Bork P.

ISMB/ECCB 2011. July 17-19, 2011. Vienna, Austria.

Poster: Assessment of the regulatory mechanisms of different protein post-translational modifications by studying their role within a realistic in silico model of the cell. **Minguez P** & Bork P.

VIII Jornadas de Bioinformatica. Feb 13-15, 2008. Valencia, Spain.

Oral Presentation: *SNOW: Studying Networks in the Omic World*. **Minguez P**, Götz S, Montaner D, Al-Shahrour F, Dopazo J.

Genome Informatics Workshop, GIW 2006. Dec 18-20, 2006. Yokohama, Japan.

Oral Presentation: *A Function-Centric Approach to the Biological Interpretation of Microarray Time-Series*. **Minguez P**, Al-Shahrour F and Dopazo J.

Genetics Society meeting, Arabidopsis 2004. Jun 2004. Warwick University, Warwick (UK).

Oral Presentation: *AtEnsembl, the Arabidopsis Ensembl Genome Browser*.

Bioinformatics software & databases developed

- **PTMcode** (<http://ptmcode.embl.de>): Database of known and predicted functional associations between protein posttranslational modifications
- **Snow** (<http://babelomics.org>): Extracts the hidden networks that are acting in the background of high-throughput experiments results and compares the network structure versus random generated networks.
- **Tissues Mining Tool** (<http://babelomics.org>): Finds tissues in which two sets of genes display different distributions.
- **MarmiteScan & Marmite** (<http://babelomics.org>): Use chemical and disease-related information to detect related blocks of genes in a gene list with associated values.
- **AtEnsembl** (<http://atensembl.arabidopsis.info>): The Arabidopsis thaliana Genome browser.

Other details

H-index and citations	<ul style="list-style-type: none">• H-index=16, >2500 citations (4th March 2014).
Ad hoc Reviewer	<ul style="list-style-type: none">• PloS Computational Biology, PloS One, Bioinformatics, BMC Genomics, BMC Bioinformatics, BMC Medical Genomics and BBA - Proteins and Proteomics.
Computing skills	<ul style="list-style-type: none">• Perl, Python, R(S), Basic knowledge in Java & C.• Relational databases: MySQL, Postgres, SQL and design.• GNU/Linux. Database APIs, Ensembl APIs, BioPerl, CGI scripts.
Language skills	<ul style="list-style-type: none">• Spanish. First language• English. Fluent