

Genomics Core Unit



Orlando Domínguez

Unit Head

Orlando Domínguez was born in Asturias (Spain) in 1960. He obtained an MSc in 1984 and a PhD in 1993 in Biology from the *Universidad de Oviedo* for studies on gene structure and regulation of genetic diseases.

Orlando joined Prodesfarma pharmaceutical company in 1994 to work on a project under the supervision of R. Pujol-Borrell at the *Universidad Autónoma de Barcelona*. He focused his work on searching for novel inflammation and cancer genes as potential therapeutic targets.

In 1998 he joined L. Blanco's Lab at the *Centro de Biología Molecular "Severo Ochoa"*, CSIC-UAM in Madrid, where he contributed to the cloning and first descriptions of two novel mammalian DNA polymerases.

He then joined the CNIO in 2000 to lead the Genomics Core Unit where he has coordinated the implementation of a variety of services such as a complete microarray production facility and a transgenic mouse genotyping service.

Summary

The field of Genomics encompasses research into the structural basis of genetic variation associated with disease as well as the determination of the functional repertoire of interplaying gene activity in a living cell or tissue.

In the context of cancer research, genomics studies can reveal basic clues behind the causes and evolution of the disease, prognostic markers as well as valid therapeutic targets.

As a service provider, the Genomics Core Unit represents a toolbox for DNA and RNA analyses dedicated to an array of applications of diverse complexity, either at the single locus or at the more global genomic level. These resources help CNIO scientists to further decipher the molecular processes involved in cancer.

Main Objectives

- To provide specialised services in genomic technologies
- Implement services of interest to a broad range of CNIO Research Groups
- DNA microarray analysis, DNA sequencing, both standard and second-gen technologies, and epigenetic analysis





Technicians: Purificación Arribas, Martha L. Campo, Guadalupe Luengo, Jorge Monsech, David B. Rodríguez and Ángeles Rubio.

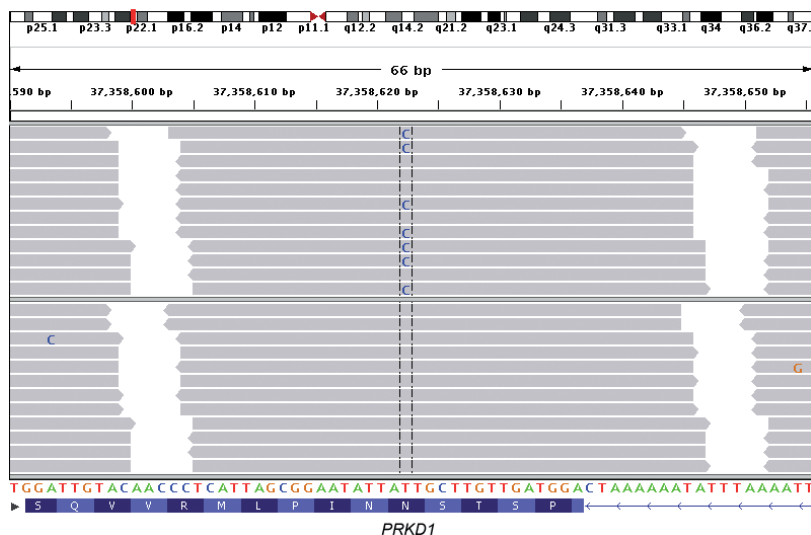
Highlights

In addition to standard services such as Sanger dideoxi sequencing and DNA microarray analysis, we have just recently implemented the massively parallel sequencing technology. With the capacity of sequencing complete genomes within days it provides a new level in data production and information content for a variety of applications. Most demanded services in this area have been ChIPseq and exome sequencing, although RNAseq and DNA methylation projects have also been performed.

ChIPseq, the sequencing of chromatin immunoprecipitates (ChIPs), locates protein interactions on chromosomal

DNA and studies chromatin remodelling under different circumstances. Standard procedures have been adapted to improve efficiencies in those frequent cases of limited sample availability.

For exome sequencing projects, target enrichment is also provided using Agilent SureSelect solution-based enrichment as a platform. Some technical fine-tuning and development resulted in consistently improved specificity and efficiency. The Unit's regular services include library prep, sequencing on an Illumina Genome Analyzer IIx instrument and primary data analysis, mapping the results to the corresponding reference genome.



Other equipment includes a Covaris S2 sample preparation instrument, a Beckman Coulter FX liquid handler, an Agilent high-resolution (2 µm) microarray scanner and an Applied Biosystems 3730xl DNA Analyzer.

Figure: Identification of cancer mutations by DNA sequencing. Exome fractions are extracted from tumours with capture probes and massively sequenced simultaneously. Grey horizontal bars represent overlapping reads mapped here to a gene on chromosome 14. Two samples from the same patient, tumour versus normal tissue, are being compared. The tumour sample shows a mutation ("C" highlighted here in blue) that changes the normal amino acid at the protein level. Further research will be needed to ascertain which detected mutations have significant impact on tumour development.

Publications

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