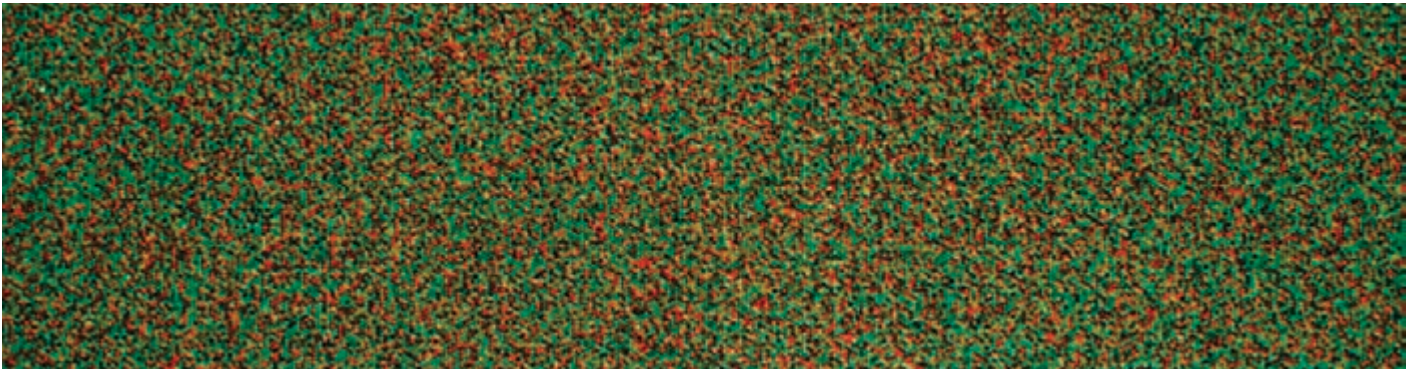


# EXPERT PARTNERS FOR YOUR RESEARCH

The CIC bioGUNE's Technology Platforms





## INTRODUCTION



**Prof José M Mato**  
General Director

CIC bioGUNE (Biosciences Cooperative Research Centre, [www.cicbiogune.es](http://www.cicbiogune.es)), a non-profit biomedical research organization founded at the initiative of the Basque Government, has invested over 35 million Euro into a modern animal facility and state-of-the-art infrastructure for research in Genomics, Proteomics, Metabolomics, Cell and Structural Biology.

Thus, advanced technology platforms have been set up for genotyping, gene silencing, mass spectrometry, cryo-electron microscopy, X-ray diffraction, NMR spectroscopy, and diverse computational analyses.

CIC bioGUNE offers access to its high-end equipment, specialised services and expert consultation to external users from academic institutions, technology centres and companies. To this end, CIC bioGUNE has created this catalog of core facilities where the main equipment and services are listed. Policies regarding services, access, fees and prioritization vary by facility. For more information, please contact the core facility directly through our web site.



<b>01</b>	<b>STRUCTURAL BIOLOGY</b>	
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CIC bioGUNE ENJOYS STATE-OF-THE-ART X-RAY CRYSTALLOGRAPHY FACILITIES FOR IN-HOUSE USERS AS WELL AS EXTERNAL USERS: AS A SERVICE OR COLLABORATIVE RESEARCH.

# 01\_01

## STRUCTURAL BIOLOGY

Macromolecular Crystallography Platform



CIC bioGUNE's Macromolecular Crystallography Platform offers competitive services in structure determination for in-house users as well as external users. Today there are more than twenty structural genomic (SG) groups around the world working in the high-throughput (HT) determination of protein structures. Much effort has been invested in the development of protocols for automatization of all the steps during protein structure determination process (cloning, expression, crystallization, data collection, processing and phasing). CIC bioGUNE enjoys state-of-the-art X-ray crystallography facilities that today can support HT crystallization experiments and conventional in-house data collection.

Our aim is to promote the use of the crystallization facility as a HT service, offering most of the commercial crystallization methods and customized solutions for the specific user's requirements. The image analysis platform allows users to check their crystallization experiments on-line. This feature might be appealing for external users since they will be able to track their own experiments remotely.

There are many scientists that may be interested in incorporating crystallographic studies in their own projects but do not have the infrastructure or the expertise to perform the experiment; the Macromolecular Crystallography Platform at CIC bioGUNE can offer them the infrastructure as a service, including training in proper use of the equipment and advice on the preparation of high quality crystallization samples.

Within collaborative research we can also offer: data collection, data processing, structure determination, validation and coordinates deposition in the PDB data bank.



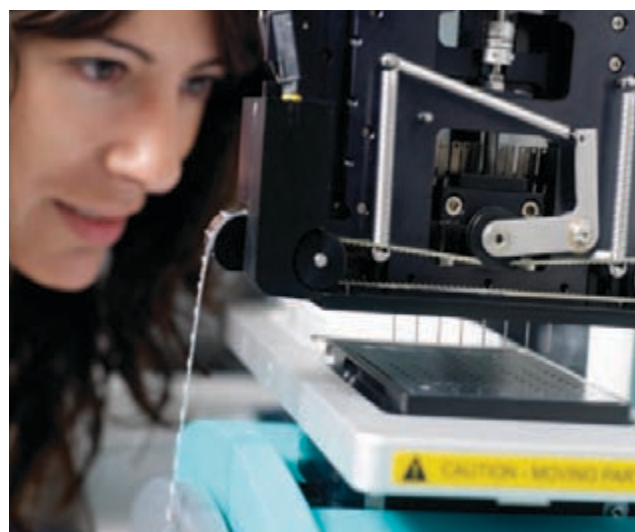
## Services

- 01** Advice on crystallization procedures and quality sample preparation.
- 02** High-throughput screening with more than 1000 commercial or customized crystallization solutions for specific user requirements.
- 03** Crystallization plates storage at 4°C, 10°C, 18°C, 27°C.
- 04** Crystallization plates storage and imaging at 21°C in a Bruker Crystal Farm.
- 05** Images will be accessible via web-interface.
- 06** Personal training in data collection using the X-ray home system.
- 07** Support and training in quikcryosoaking 1 technique for in-house derivatization.
- 08** Individual and group training in all the steps of the procedure; from data collection to structure determination.
- 09** Within collaborative research we offer data collection, data processing, structure determination, validation and coordinates deposition.



## Equipment

- 01** TECAN liquid handling.
- 02** MOSQUITO crystallization robot.
- 03** BRUKER Crystal Farm and image analysis platform.
- 04** Two crystallization rooms: at 4°C and 18°C.
- 05** Two temperature controlled incubators (Molecular Dimensions).
- 06** X8-PROTEUM system from BRUKER with two detectors, a CCD and Mar345 image plate.
- 07** Two Oxford Cryosystems 700.
- 08** Storage dewar for crystal samples.



CIC bioGUNE ENJOYS STATE-OF-THE-ART  
CRYO-ELECTRON MICROSCOPY FACILITIES  
FOR IN-HOUSE AND EXTERNAL USERS.

**01\_02**

STRUCTURAL BIOLOGY

Electron Microscopy Platform



The Electron Microscopy (EM) Platform at CIC bioGUNE provides high tech instrumentation and advanced image processing methods to research groups within the institute as well as to external researchers. The advantages of cryo-electron microscopy (Cryo-EM) over traditional EM techniques include the preservation of the sample in a near-native hydrated state without the distortions from stains or fixatives needed for traditional EM.

Cryo-EM is a very direct method of structure determination that complements the well-established techniques of X-ray crystallography and NMR spectroscopy. Fitting of individual structures into 3D cryo-EM maps of large assemblies allows the characterization of multi-component interactions, to distinguish different functional states. The method known as *single-particle analysis* allows structural elucidation of large biological macromolecules with sub-nanometer resolution and near-atomic resolution in the case of highly symmetric viruses. On the other hand, *cryo-electron tomography* is the only method that allows pleomorphic structures, such as cells, organelles, and many macromolecular assemblies to be imaged at nanometer resolution in a near-native frozen-hydrated state.

To achieve these goals EM platform provides two transmission electron microscopes, 120 kV and 200 kV machines with associated digital cameras, and the auxiliary equipment required for cryo-EM. This high-tech equipment allows us to make use of advanced methods of image processing and computation to elucidate the structure of large macromolecular assemblies.



## Services

- 01** Sample preparation for specific user requirements (negative staining, vitrification and drop casting for either life science or material science samples).
- 02** Transmission electron microscopy (TEM) analysis service. TEM is the primary characterization method for determining the size and shape of nanoparticles and some biological organelles. Our basic TEM service includes grid preparation and high resolution images of your samples. Size statistics and 2D studies are available as an option.
- 03** Immuno-electron microscopy.
- 04** Technical support and introductory training.
- 05** Cryo-transmission electron microscopy (Cryo-EM) service.
- 06** 3D structure determination by single-particle analysis or electron tomography techniques.

## Technical equipment

- 01** Jeol JEM-2200FS/CR transmission electron microscope, equipped with a 200kV field emission gun (FEG) and an OMEGA in-column energy filter. A digital camera Gatan Ultrascan 4000 SP (4008 x 4008 pixels) is used to acquire high and medium resolution digital micrographs, recorded under *low-dose cryo* conditions.
- 02** Jeol JEM-1230 transmission electron microscope, equipped with a 120kV thermionic gun. A digital camera CCD Gatan Orius SC1000 (4008 x 2672 pixels) is used for life sciences and materials science applications.
- 03** Vitrobot, automated vitrification robot (FEI).
- 04** 3 cryotransfer holders used for cryo electron microscopy.
- 05** 1 double tilt cryotransfer holder used for cryo electron microscopy.
- 06** 1 ultra-high tilt cryotransfer holder used for cryo-electron tomography.
- 07** Darkroom and Z/I PhotoScan scanner (ZEISS).
- 08** High vacuum coating system (MED 020 BALTEC) for carbon evaporation and glow discharge.
- 09** HP Graphics Workstation for EM data processing.



CIC bioGUNE HAS A STATE-OF-THE-ART,  
VERSATILE HIGH-FIELD NUCLEAR MAGNETIC  
RESONANCE FACILITY FOR THE FULL RANGE  
OF ADVANCED BIOMOLECULAR NMR STUDIES.

# 01\_03

## STRUCTURAL BIOLOGY

Nuclear Magnetic Resonance (NMR) Platform



CiC bioGUNE's NMR Platform is equipped to play a leading role among biomolecular NMR facilities in Europe, and aims to interact broadly with both academic and private partners.

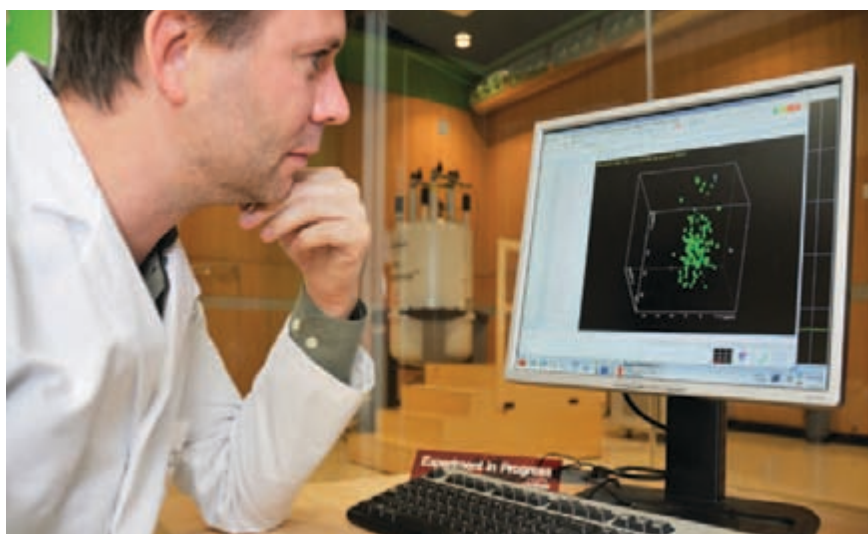
NMR spectroscopy is the most versatile analytical technique to study molecules with atomic resolution. For structure analysis, it ideally complements X-ray crystallography by probing the solution state, and covering also intrinsically disordered proteins. Yet, NMR can provide important information far beyond this main objective of structural biology. It also is the only technique to study, e.g., protonation states and molecular dynamics at atomic level.

NMR spectroscopy offers unique capabilities for metabolomics, functional proteomics, and drug discovery and development (DD&D). NMR screening for ligands exploits the extreme sensitivity in detecting even the weakest interaction between components simply added in solution. NMR can thereby reveal and distinguish binding sites, discriminate between site specific and unspecific binding, and resolve details of interaction to guide assembly of novel high-affinity ligands from weakly binding molecular fragments.

CiC bioGUNE's NMR Platform has most advanced hardware to carry out the full range of solution-state NMR studies: Our 800 MHz high-field spectrometer enables biomolecular analyses with maximal sensitivity and resolution, while the 600 MHz spectrometer has ample accessory to reach far beyond standard applications. The platform is supported by a specialized laboratory to produce proteins with the required isotope labeling.

CiC bioGUNE's scientists have long-standing international experience in the various fields of biomolecular NMR and protein biosynthesis. Their research covers NMR methods development, analysis of protein structure and dynamics, and interaction studies.

CiC bioGUNE's NMR Platform offers its expertise, assistance and resources for the full range of biomolecular solution-state NMR: from protein expression and isotope labeling, implementation of NMR experiments, spectra recording, spectral assignment, small-scale NMR screening, to analysis of molecular structures, dynamics and interactions. We also offer consultations, training and teaching, and set-up services for protein biosynthesis and NMR spectroscopy.



## Services

- 01 NMR consulting:** defining, developing and supervising NMR projects (also at customer facilities).
- 02 NMR programming:** designing, programming and implementing customized NMR experiments (also at customer facility).
- 03 NMR teaching and training** (also at customer facility).
- 04 NMR measurements** (standard and customised).
- 05 NMR interaction studies:** hit validation, small-scale screening (particularly by  $^{19}\text{F}$ -NMR), elucidation of binding sites and modes.
- 06 NMR structure elucidation:** for small molecules, amenable proteins, and amenable ligand-protein complexes (analysis of interactions for rational drug design).
- 07 NMR spectral assignment:** for amenable target proteins (e.g., for use in NMR screening and hit validation).
- 09 Specialized protein biosynthesis for NMR:** expression of proteins with various stable isotopes ( $^2\text{H}$ ,  $^{13}\text{C}$ ,  $^{15}\text{N}$ ).

## Equipment

### 01 800 MHz BRUKER AVANCE III spectrometer:

- equipped with TCI cryo-probe (with z-gradients) for detection of  $^1\text{H}$  or  $^{13}\text{C}$  with highest sensitivity.

### 02 600 MHz BRUKER AVANCE III spectrometer with a vast range of probe-heads for diverse, special applications:

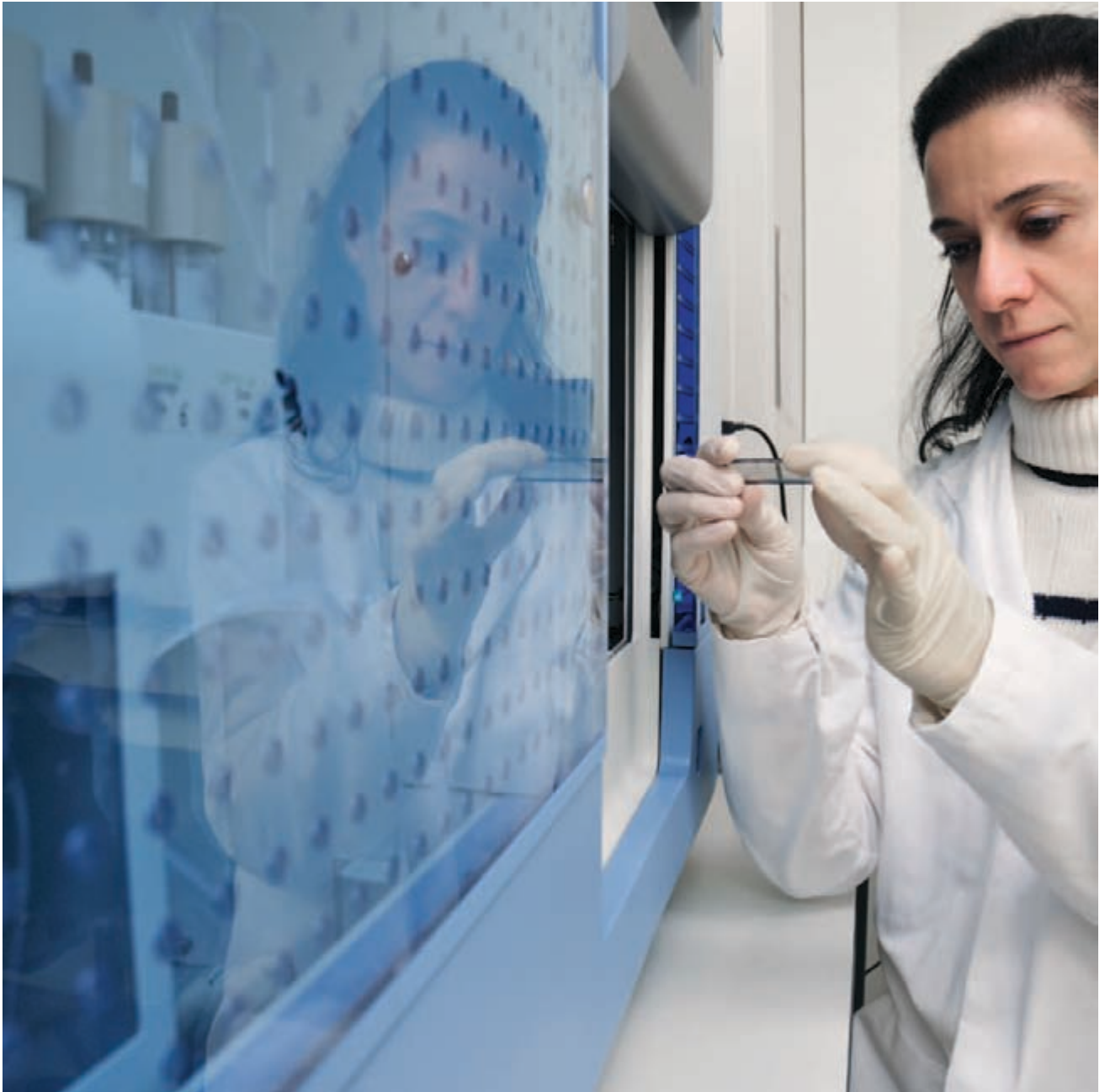
- QXI ( $^1\text{H}$ ,  $^2\text{H}$ ,  $^{13}\text{C}$ ,  $^{15}\text{N}$ ,  $^{31}\text{P}$ ) with x,y,z-gradients.
- TXI ( $^1\text{H}$ ,  $^2\text{H}$ ,  $^{13}\text{C}$ ,  $^{15}\text{N}$ ) with x,y,z-gradients.
- TXI ( $^1\text{H}$ ,  $^2\text{H}$ ,  $^{13}\text{C}$ ,  $^{15}\text{N}$ ) with x,y,z-gradients, tuned for high salt concentrations ( $> 1\text{ M}$ ).
- TBI ( $^1\text{H}$ ,  $^2\text{H}$ ,  $^{13}\text{C}$ , BB) with z-gradients and tunable BB coil ( $^{31}\text{P}$  -  $^{109}\text{Ag}$ ).
- SEF ( $^1\text{H}$ ,  $^2\text{H}$ ,  $^{19}\text{F}$ ) with z-gradients.
- QXI ( $^1\text{H}$ ,  $^2\text{H}$ ,  $^{13}\text{C}$ ,  $^{15}\text{N}$ ,  $^{19}\text{F}$ ) with z-gradients.
- HR-MAS TXI ( $^1\text{H}$ ,  $^2\text{H}$ ,  $^{13}\text{C}$ ,  $^{15}\text{N}$ ).



CIC bioGUNE EMPLOYS THE MOST RECENT  
TECHNOLOGIES FOR WHOLE GENOME  
ANALYSIS USING MICROARRAYS AND  
MASSIVE SEQUENCING.  
BOTH EXTERNAL SERVICES AND  
COLLABORATIONS ARE ON OFFER.

# 02

## GENOME ANALYSIS PLATFORM

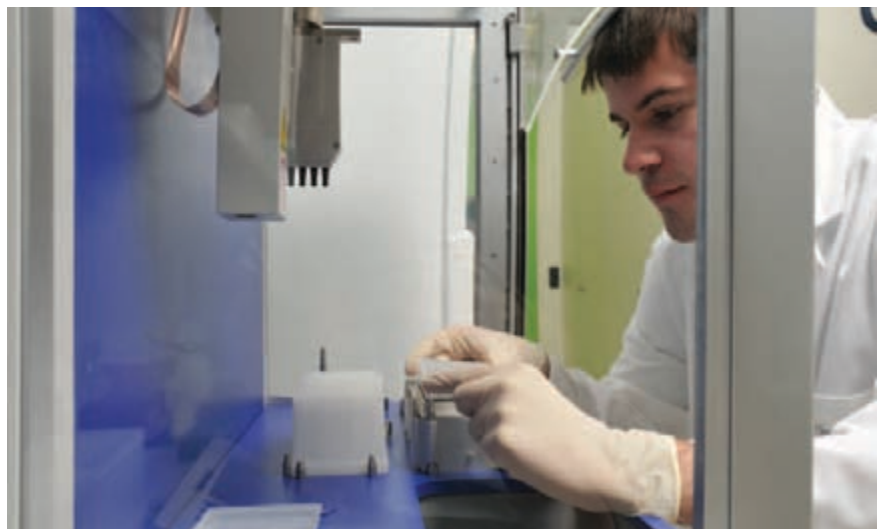


The main goal of the Genome Analysis Platform is the optimization of sample processing protocols for a set of sophisticated, state-of-the-art, **high-throughput genome analysis technologies**. The principal methodologies used deal with the characterization of variants at gDNA sequence level (mainly Single Nucleotide Polymorphisms – SNPs and Copy Number Variations – CNVs), the study of mRNA or smallRNA expression profiles and the identification of epigenetic modifications such as DNA methylation. All these techniques are applied in projects whose aim is the **understanding of complex biological systems**, such as the genomic regulatory effect of a drug-treatment in a particular tissue (Pharmacogenomics), the identification of genetic variants that confer susceptibility to certain diseases (association studies), or the genomic description of economically-optimal agriculture variants (plant and animal breeding).

Recently, the group has been also establishing appropriate work-flow procedures for some data analysis, as well as developing new bioinformatics tools.

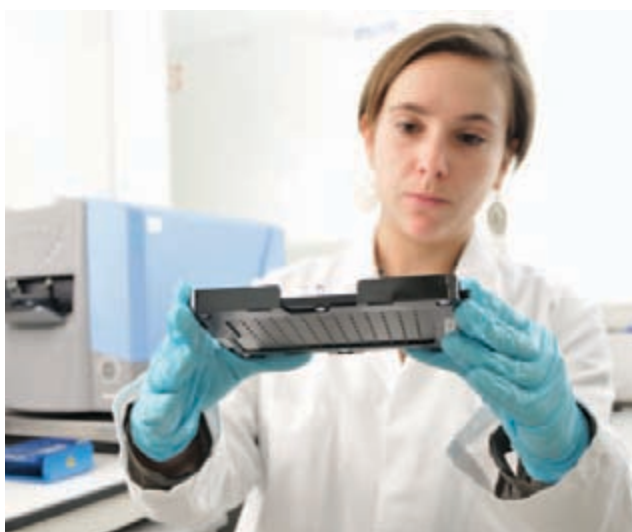
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## Services

- 01** High-throughput genotyping: standard panels (from 10,000 up to 5 million SNPs for different species) and customized panels (from 96 to 60,000 SNPs).
- 02** High-throughput gene expression characterization: whole genome transcriptome analysis of human and mouse tissues using standard Illumina chips.
- 03** Characterization of differential methylation as epigenetic modification: analysis of 27,000 CpG islands or 450,000 *loci* in the human genome.
- 04** Next-generation sequencing: *de novo* sequencing and re-sequencing of genomic DNA and RNA:
  - Genomic regions of interest
  - Complete genes
  - Complete chromosomes
  - Whole genomes
  - DNA methylation analysis at whole genome level
  - Expression analysis (complete transcriptome)
  - Identification and analysis of microRNA and smallRNA
  - DNA-protein interactions (ChIP-Seq).
- 05** Assistance in the design of the customized SNP panels (for genotyping projects).
- 06** Assistance in bioinformatics analysis.



## Equipment

- 01** BeadStation 500 GT/GX (Illumina, Inc.)
- 02** Genome Analyzer II (Illumina, Inc.)
- 03** HiScan-SQ (Illumina Inc.)

The Platform has all the equipment required to perform basic molecular biology experiments and quality controls, such as Experion (BioRad) and Bioanalyzer (Agilent Technologies) systems, EpiMotion (Eppendorf) liquid handling, centrifuges, electrophoresis apparatus, gel imaging systems, etc.

For details of offered services and quote requests, please go to: <http://genomics.cicbiogune.es/GAP/service/service.php>



THE PROTEOMICS PLATFORM IS CHIEFLY FOCUSED ON THE ANALYSIS OF PROTEINS BY MASS SPECTROMETRY. STATE-OF-THE ART TECHNOLOGIES ARE CURRENTLY USED TO SUPPORT RESEARCH IN PROTEOMICS. THE PROTEOMICS PLATFORM PROVIDES SERVICES TO THE IN-HOUSE GROUPS AND EXTERNAL USERS.

# 03

## PROTEOMICS PLATFORM



By analyzing the abundance of proteins under different physiological or experimental conditions it is possible to identify groups of proteins that are relevant for these specific conditions. Differential in-gel electrophoresis (DIGE) is nowadays the most powerful technique for gel-based differential proteomic analysis.

During the last decade genomes from many organisms, including human, have been sequenced. The availability of genomic sequences has boosted the proteomic research as the data obtained by analyzing proteins and peptides by mass spectrometry can be directly linked to the genomic information, using bioinformatics methods. Continuous optimization of sample preparation while employing the latest generation of tandem mass spectrometers, with their constantly improving high mass accuracy, high resolution and sensitivity, makes the protein identification process increasingly fast and accurate. The Proteomics Platform provides services to in-house groups and external users and offers joining forces for collaborative research projects.

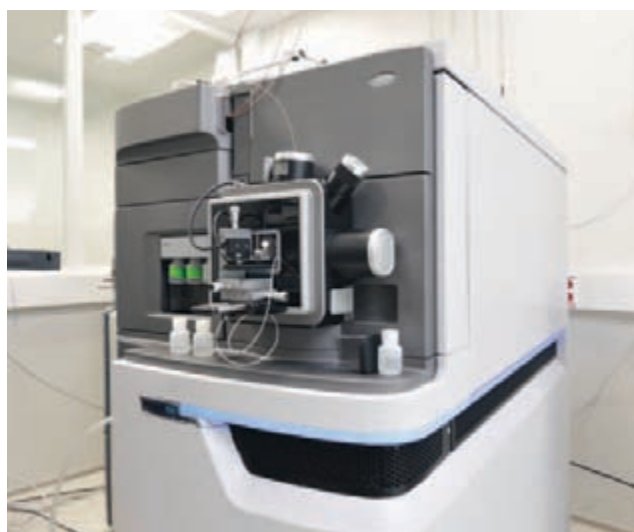
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## Services

- 01** Molecular mass determination by MALDI TOF.  
Peptide and/or protein mass can be measured in a straight forward fashion by linear mode type of analysis.
- 02** Protein identification by MALDI TOF/TOF.  
The proteins previously purified or resolved on a gel can be identified by peptide mass fingerprinting (PMF). The process includes: protein digestion by trypsin, peptide extraction when required, sample preparation, analysis by MALDI TOF, data processing and database search by Mascot search engine. The sample, when possible, can also be analyzed by peptide fragment fingerprinting using MALDI TOF/TOF.
- 03** Protein identification by nano scale liquid chromatography coupled on-line to tandem mass spectrometry.  
Complex protein mixtures can be analysed and identified in such systems.
- 04** Differential in-gel-electrophoresis (DIGE).  
Due to the special nature of DIGE experiments, please contact the head of the unit.

Useful information is shown in the web page like correct sample handling tips etc. On top of that we offer advice to choose the right sample preparation, handling procedures and analytical methodology of choice.



## Equipment

### MALDI:

- 01** Autoflex III TOF/TOF (Bruker): this mass spectrometer allows performing different types of analysis:  
  
Intact peptide/protein molecular mass analysis can be performed.  
  
Protein identification by peptide mass fingerprinting (MALDI-TOF) and/or peptide fragment fingerprinting MALDI TOF/TOF).
- 02** Agilent 1200 nano scale chromatography system for off-line MALDI TOF/TOF analysis.
- 03** Proteineer DP robotic station (Bruker) for automatic tryptic digestion of gel spots.

### Liquid chromatography coupled to tandem mass spectrometry systems:

- 04** Nano Acquity UPLC chromatography system coupled on-line to Synapt G2 (Waters).
- 05** Nano Acquity UPLC chromatography system coupled on-line to LTQ-Orbitrap XL (Thermo-Fisher).

These two high sensitivity, mass accuracy and resolution systems have the latest technical features for optimal identification of proteins from complex mixtures.

### Differential in-gel electrophoresis (DIGE):

- 06** Typhoon TRIO, spot picker and DeCyder.  
DIGE is nowadays the most robust approach for gel-based differential proteomic analysis.



CIC bioGUNE HAS ESTABLISHED A GROUP OF STATE-OF-THE-ART TECHNOLOGIES TO PROVIDE POWERFUL TOOLS TO APPROACH AND UNDERSTAND COMPLEX BIOLOGICAL PROCESSES. THE METABOLOMICS PLATFORM IS DEVOTED TO THE STUDY OF THE METABOLOMICS THAT IS THE MOST RECENT OF THE "OMICS" TECHNOLOGIES.

# 04

## METABOLOMICS PLATFORM



In this “Global Systems Biology” era, metabolomics constitutes one of the most powerful technologies to understand how a living organism interacts with its environment. Metabolomics can be defined as the quantitative and qualitative analysis of all metabolites (molecules with a molecular weight of less than 1,500 Da) in a given organism. This results in the construction of a metabolome or metabolic fingerprint, analogous to the genome or the proteome. It is the latest member of the “omics” family and has already proven its strength in the field of biomarker discovery and biochemical pathway elucidation.

Metabolomics has clear advantages in that metabolites are closely related to real biological end-points. Furthermore it takes into account the complete biological system, including e.g. interactions with other genomes like gut microflora. Because metabolomics makes use of biofluids (urine, serum, CSF) it is a minimal invasive technique. Metabolomics makes use of well established, robust analytical platforms, which results in very reproducible, fast and cost effective analysis.

The Metabolomics Platform focuses primarily on changes in the metabolome since these can be indicative for alterations in the physiological state of the organism. Altered metabolic profiles can be caused disease or exposure to drugs and toxins. In order to detect relevant metabolites, the platform uses high-resolution mass spectrometers coupled to ultra-performance liquid chromatography (UPLC).

CIC bioGUNE’s Metabolomics Platform is currently applying this technology to understand molecular mechanisms involved in infectious, neurological and metabolic disorders.

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## Services

The aim of this platform is to provide support to research groups interested in including a full systems analysis in their current research line. The platform offers:

- 01** Assistance in the experimental design including attainable and appropriate statistical sampling and logistic aspects in order to achieve satisfactory data.
- 02** Untargeted metabolomics: biomarker discovery by analysis of metabolites in biofluids, cells and tissues with UPLC-MS/MS.
- 03** Targeted metabolomics: analysis of xenobiotic metabolites and screening of identified biomarkers.
- 04** Multivariate Analysis of data.

## Equipment

Discovery of biomarker candidates is carried out with the SYNAPT G2 HDMS mass spectrometer (Waters®). The SYNAPT G2 combines ion mobility separation with high-resolution time-of-flight (ToF) mass analysis and tandem mass spectrometry. This instrument greatly facilitates identification metabolites. Once suitable biomarkers are found, they can be screened in high throughput mode with an orthogonal acceleration ToF instrument (LCT Premier XE, Waters®).

### 01 Waters LCT Premier XE coupled to acquity UPLC

High separation efficiency (UPLC)  
High mass accuracy (ToF)  
High full-scan sensitivity  
High throughput

### 02 Waters SYNAPT G2 HDMS coupled to acquity UPLC

High separation efficiency (UPLC)  
High mass accuracy (ToF)  
Tandem MS (up to MS<sup>3</sup>)  
Ion mobility separation based on molecular shape of the analytes  
High full-scan sensitivity



CIC bioGUNE OFFERS THE EXPERTISE OF  
THE GENE SILENCING PLATFORM TO EXPAND  
THE POTENTIAL OF RNAi TECHNOLOGY.

# 05

## GENE SILENCING PLATFORM



The Gene Silencing Platform (GSP) at CIC bioGUNE is a facility to develop and execute cell-based screening using RNAi. It has dedicated staff to manage platform resources and help in assay development and data analysis. The main goal of this platform is to make RNAi-mediated gene silencing as widely accessible as possible.

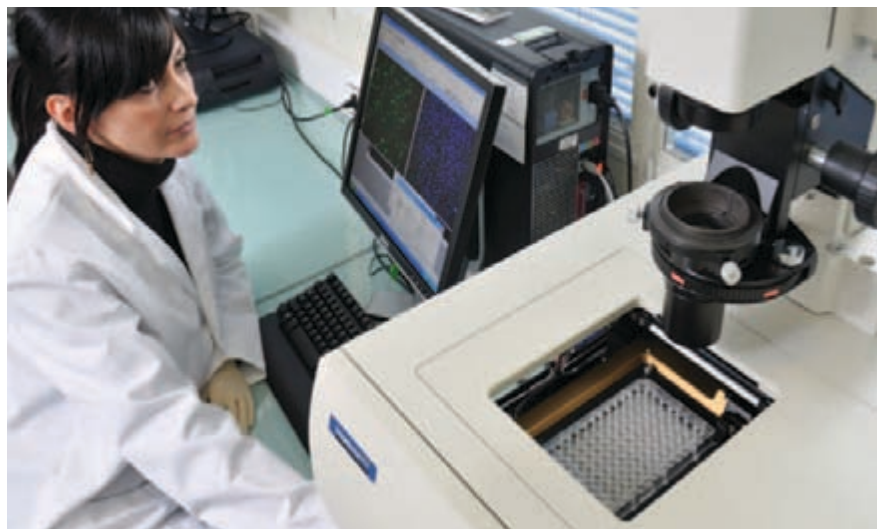
Within collaborative research, we can facilitate silencing of individual genes to elucidate their functions. Upon request, the GSP advises users on customer design of siRNAs to silence specific genes (mostly in cases of targets obtained from point mutations and/or chromosomal rearrangements).

An additional goal of the GSP is genome-wide or high-throughput, high-content screening to identify the genes implicated in particular biological processes. The GSP can also provide CIC bioGUNE investigators and their collaborators with sub-collections or sub-libraries targeting requested pathways or families of genes. We offer expertise in designing, developing, evaluating and implementing such screens. We can adapt our protocols (cellular models and biological assays) to meet user needs: human, mouse or *Drosophila* primary or tumor cells, for the analysis of stem cell differentiation, tumor invasion, cellular adhesion, angiogenesis, etc.

Because of the highly specific and efficient silencing of the target gene, RNAi emerges as a very promising technique for drug discovery, target validation in cell culture and also as a novel therapeutic strategy. The GSP at CIC bioGUNE can facilitate not only *in vitro* but also *in vivo* silencing and advise users on RNAi technology as a therapeutic approach.

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## Possibilities of collaborative researches

- 01 *In vitro* and *in vivo* silencing of individual genes.
- 02 Customer design of siRNAs.
- 03 Adapted cell-based screening using sub-libraries targeting requested pathways or families of genes.
- 04 Genome-wide screening using the *Drosophila* library.

## Equipment and Facilities

- 01 The Human retroviral shRNA<sup>mir</sup> library developed by Greg Hannon (CSHL), Stephen Elledge (Harvard) and colleagues. The library includes about 62.500 microRNA<sub>30</sub>-based hairpin constructs targeting the whole human genome.
- 02 Silencer®*Drosophila* RNAi library distributed by Ambion/ Applied Biosystem. This library is a collection of 13,071 dsRNAs targeting the best-annotated *Drosophila* genes.
- 03 Sciclone ALH 3000 (liquid handling system) + Twister II.
- 04 Cytomat 2C (CO<sub>2</sub> incubator with plate shuttling).
- 05 Detection systems:
  - Microplate reader (Synergy HT).
  - Automated wide-field microscope (ImageXpress) including MetaXpress Analysis Application Modules for cell scoring, translocation, cell cycle, etc.



THE ANIMAL UNIT IS EQUIPPED WITH STATE-OF-THE-ART FACILITIES AND A TEAM IN CONTINUOUS TRAINING TO DEVELOP PROJECTS IN ACCORDANCE WITH THE MOST STRINGENT ETHICAL AND LEGAL STANDARDS IN THE USE OF ANIMALS IN RESEARCH.



The CIC bioGUNE's Animal Unit (AU) is an AAALAC accredited facility. It includes a Specific Pathogen Free (SPF) area to house rodents from commercial sources and to produce and keep some strains of genetically engineered mice (GEM). The AU works on continually improving their services and develops new services through the collaboration with researchers from different areas of interest. Our main objective for the near future is focusing on the use of ultrasounds (echography) to detect and follow-up lesions in murine models of hepatic and prostate cancer. We are also developing preliminary echocardiography assays in order to assess the heart function in new strains of GEM.

The main functions of the AU are:

- Covering the CIC bioGUNE users' needs by providing them with the assessment and equipment necessary to carry out their research on laboratory animals.
- Providing the care and looking after the welfare of laboratory animals and carrying out periodic health monitoring.
- Ensuring observance of all legal and ethical standards concerning the use of animals in research and for other scientific purposes.

Accredited by



## Services

- 01 Ordering of animals (from vendor to the cage).
- 02 Animal export/importation to/from overseas institutions for research use (paperwork, shipment).
- 03 Consultations and technical support (experiment design, techniques, equipment).
- 04 Animal maintenance.
- 05 Breeding of genetically engineered mice.
- 06 Health monitoring.
- 07 Equipment provision.
- 08 Administration of substances.
- 09 Sample collection (blood, urine, faeces).
- 10 Necropsy procedures.
- 11 Tissues/organs extraction.
- 12 Biochemical analysis.
- 13 Hematological analysis.
- 14 Hepatic echography.

## Equipment

- 01 7 racks for individual ventilated cages (IVC).
- 02 15 racks for automatic watering cages.
- 03 2 portable machines for inhalatory anesthesia.
- 04 SPINLAB 100 for biochemical analysis.
- 05 ABACUS VET for hematological analysis.
- 06 Vevo-770 for small rodents' echography.





## CONTACTS

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PCT-A48177752-2006/PCT-01000-2006-2

