INSTITUT DE BIOTECNOLOGIA I DE BIOMEDICINA

ANNUAL REPORT

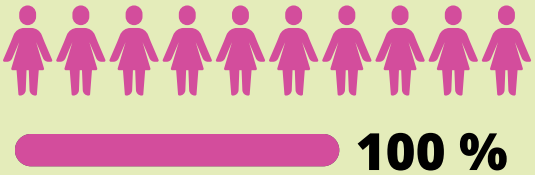
2020

INDEX

FIGURES

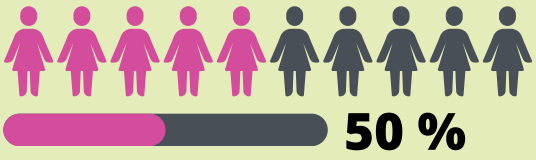
Staff 128 people

13 ADMINISTRATIVE & TECHNICAL STAFF



115 RESEARCHERS

10 %
INTERNATIONAL



3 RESEARCH PROGRAMMES
17 RESEARCH GROUPS

Projects and publications

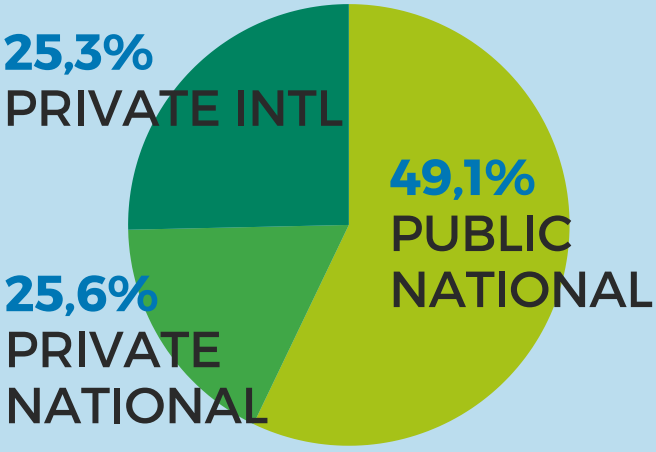
86 PUBLICATIONS

80% Q1 **49%** D1

36 PROJECTS

4 INTERNATIONAL

Funding 1,2M€



FIGURES

Academic merits

6 THESIS

2 ICREA

3 ICREA ACADEMIA

2 PRIZES

Premi SCB Trajectòria Professional Leandre Cervera 2020 a F.X. Avilés

Premi Bruker "Manuel Rico" a S. Ventura

Tech transfer & outreach

5 PATENTS

15 INDUSTRY CONTRACTS

+ 900 SOCIAL MEDIA FOLLOWERS

+ 20 EVENTS & VISITS

ABOUT IBB

The Institut de Biotecnologia i de Biomedicina (IBB) was created in 1970 as a research institute of the Universitat Autònoma de Barcelona (UAB). Although the institute was originally devoted to promoting fundamental biological research, we have been focusing in the Biotechnology and Biomedicine fields for the last 20 years.

We conduct top-level multidisciplinary scientific research with the mission to improve the health and quality of life of the population through the production and dissemination of scientific knowledge.

Among the almost 120 researchers currently working at the IBB, there are lecturers and professors from the UAB, ICREA professors and senior researchers, postdoctoral fellows, and PhD and Master students.

Relevant institutional facts

- **AGREEMENT WITH THE UAB LIBRARY SERVICE.** INCORPORATION OF SCIENTIFIC PRODUCTION INTO THE DDD DIGITAL REPOSITORY, CREATION OF A SINGLE PAGE FOR THE IBB AND IMPLEMENTATION OF AN INTERNAL MATERIAL COLLECTION PROCEDURE

- **AN R&D&I PROJECT PROMOTER JOINS THE IBB ADMINISTRATIVE TEAM.**THIS IS A NEW PERMANENT POSITION CREATED WITHIN THE INSTITUTE TO FOSTER RESERCH

- **EDUCATIONAL COOPERATION AGREEMENTS FOR ACADEMIC TRAINNING FOCUSED MAINLY ON THE FIELD OF COMMUNICATION**: SIGNED WITH UAB (FACULTY OF COMMUNICATION), UNIVERSITAT DE BARCELONA AND UNIVERSITY OF VALENCIA

- **RECONFIGURATION AND UPDATING OF THE WEBSITE** TO PROMOTE TECHNOLOGY TRANSFER, DISSEMINATION AND TALENT RECRUITMENT

RESEARCH SUPPORT STAFF

SCIENTIFIC DIRECTOR

Nerea Roher

MANAGER

Eva Vila

RESEARCH TECHNICIANS

Almudena Merino
Francesca Mestres
Àngels Torres
Francisca Palma

ADMINISTRATIVE SUPPORT

Natividad Infante
Manuela Romero
Rosa Calzada
Lourdes Benítez
Laura Bueno
Eli Carrascosa

R&D&I PROMOTION

Montserrat Solé

RESEARCH PROGRAMES

Applied proteomics and protein engineering

Computational Biology

Theoretical Molecular Biology

Nanobiotechnology

Molecular Biology

Protein Engineering and Proteomics

Protein Folding and Conformational Diseases

Protein Structure

Biomedical Applications of Nuclear Magnetic Resonance

Genomics in evolution and disease

Genome Integrity and Instability

Comparative Molecular Physiology

Comparative and Functional Genomics

Bioinformatics of Genomics Diversity

Response mechanisms to stress and disease

Molecular Immunology

Cellular Immunology

Bacterial Molecular Genetics

Evolutive Immunology

Yeast Molecular Biology

APPLIED PROTEOMICS AND PROTEIN ENGINEERING PROGRAM

APPLIED PROTEOMICS AND PROTEIN ENGINEERING PROGRAM

COMPUTATIONAL BIOLOGY

TThe main objective of our research group, led by **Xavier Daura**, is the development of new strategies to combat infections by multidrug-resistant (MDR) bacteria, in particular of the gram-negative (GN) group.

The discovery of new targets and modes of action (MoA), less propitious to the evolution of resistance, has therefore become a pressing need. In parallel, the development of effective vaccines is expected to offer a solution for high-risk population groups. Our team combines a range of computational and experimental techniques for the identification of vaccine-antigen and antimicrobial-target candidates with new modes of action in gram-negative bacteria. Much of this research is done in collaboration with the group of Bacterial Molecular Genetics of IBB, led by Dr. Isidre Gibert. On the antimicrobial side we aim to exploit conserved virulence factors as novel drug targets, reducing the pathogenic capacity of the bacteria as well as the selection pressure for drug-resistant phenotypes and preventing the devastating effect of the treatment with antibiotics on the patient's microbiota.

We are engaged in the following types of activities:

- Development of bioinformatic methods for the identification of novel antimicrobialdrug targets, antigens and their epitopes in pathogenic bacteria.
- Experimental validation and characterisation of identified antigens and antimicrobial-drug targets (in collaboration).
- Biomolecular modelling and simulation for the design of synthetic vaccines.
- Target-based virtual screening for antimicrobial-drug discovery.
- Experimental validation of hit antimicrobial compounds (in collaboration).

APPLIED PROTEOMICS AND PROTEIN ENGINEERING PROGRAM

THEORETICAL MOLECULAR BIOLOGY

Our group, led by **Josep M. Lluch**, works in the field of Theoretical Molecular Biology. We use mainly Quantum Mechanics/Molecular Mechanics and Molecular Dynamics methods to carry out Biomolecular Simulations in silico for the study of enzyme activity: substrate binding, enzyme-substrate interactions, enzyme catalysis...

The main purpose of our work is the understanding of these phenomena at a detailed molecular-level, and then the design/modification of the proteins/enzymes under study (using inhibitors, alosteric effects, mutations, radiation, electric fields or a combination of them) with the aim to control/modify their activity and/or function in a predefined direction, always with important biomedical and biotechnological applications. Progress in this direction can be relevant for the understanding and control, for instance, of inflammatory processes, in biocatalysis and in photopharmacology.

We also develop other methods to solve the challenges raised by the biological systems we study. Our purpose is to open new venues of experimental research starting from our theoretical results. We hope that we can contribute to the rational design of new methods and drugs to act on human illnesses but also to design new enzymes as engineered biomolecular catalysts for the preparation of relevant organic molecules with better, faster, cheaper and with more selective synthetic processes than the ones currently available.

APPLIED PROTEOMICS AND PROTEIN ENGINEERING PROGRAM

NANOBIOTECHNOLOGY

The Nanobiotechnology Unit, led by **A. Villaverde**, is committed to develop biomaterials, mostly based on recombinant proteins, for application in different therapeutic situations, as either drug carriers or therapeutic materials themselves. The team is member of the CIBER in the subject area of Bioengineering, Biomaterials and Nanomedicine. The team holds the Protein Production Platform which is offering services to both public and private sectors in protein production, technical advice and formation.

JL Corchero deals with the production, in mammalian cells as expression system, of recombinant human proteins for their use as therapeutics in the treatment of rare diseases (Fabry disease and Sanfilippo syndrome). and is involved in the development of new drug delivery systems. Neus Ferrer, in collaboration with IRTA, is developing protein-based nanomaterials as substitutes of antibiotics in animal medicine. Esther Vázquez develops tumor targeted protein nanoparticles as drug carriers, and smart nanoconjugates, for the treatment of colorectal cancer and triple negative breast cancer, in collaboration with Hospital Vall d'Hebron and Hospital de Sant Pau. Dr. A. Villaverde designs nanostructured protein-only antitumoral drugs for application in colorectal cancer, using intrinsically cytotoxic proteins and nanoarchitectonic peptide motives, in collaboration with E. Vázquez and Hospital de Sant Pau.

APPLIED PROTEOMICS AND PROTEIN ENGINEERING PROGRAM

MOLECULAR BIOLOGY

The Molecular Biology Group, led by **Enrique Querol**, uses *Mycoplasma genitalium* as a model of minimal cell and genome to study molecular mechanisms of pathogenicity and virulence. Also, we do reverse vaccinology and bioinformatics analysis of protein structure and function. Moonlighting proteins.

APPLIED PROTEOMICS AND PROTEIN ENGINEERING PROGRAM

PROTEIN ENGINEERING AND PROTEOMICS

Our group, led by **Francesc Xavier Avilés**, devotes our best efforts to the application of molecular/structural biology, protein engineering, proteomics biotechnology on proteases (in particular metallocarboxypeptidases) as well us on their inhibitors. In the last years, the group has also specialized in the development of biocompatible nanomaterials and the study of their biological properties and interactions.

Thus, we try to characterize and redesign proteins that naturally control such proteases in nature: i.e. in animals or invertebrates or in plants, or synthesize organopeptidic molecules, to unveil its properties and develop and use them, or derivatives, for potential biomedical or biotechnological uses. Metallo-carboxypeptidases pancreatic-like or regulatory (M14 family, as A1, A2, A3, B, O, D, Z ...) and their small protein inhibitors, as the ones from potato or the marine snail Nerita v., are among the best studied models by us. The experimental approaches used, directly on extracts or on purified molecules, are HPLC, Mass spectrometry, protein & cDNA sequencing & cloning, proteomics, NMR, Xray crystallography and computerbased approaches. We also work in the development of nanomaterials for specific delivery, encapsulation, or nanoconjugation of enzymes/inhibitors and small compounds for biomedical purposes as well as in the assays in cell cultures and in animal models to test their efficacy and safety.

We also intend to develop our own methodologies for affinity proteomics, protein modelling, rational design of ligands and drugs, protein/peptide engineering and in the development and characterization of nanomaterials with biomed/biotech purposes.

APPLIED PROTEOMICS AND PROTEIN ENGINEERING PROGRAM

PROTEIN FOLDING AND CONFORMATIONAL DISEASES

Our group, led by **Salvador Ventura**, uses a multidisciplinary approach to address fundamental aspects of protein folding, misfolding and aggregation. In addition to define the basic mechanistic principles underlying these processes, we aim to understand how their deregulation leads to the onset of human conformational diseases and to develop innovative therapeutics to target these pathologies. Moreover, this knowledge should allow us to design and produce novel and better protein-based biopharmaceuticals as well as the development of new self-assembled materials for nanotechnology applications.

The group is focused mainly on the study of Parkinson's disease (PD), the second most common neurodegenerative disorder. There is substantial evidence supporting the aggregation of the protein a-Synuclein (a-Syn) as a key event in pathogenesis of PD, We have recently identified and designed small compounds and peptides able to inhibit a-Syn aggregation and we aim to develop these molecules into lead compounds for the therapeutics of PD. We aim also to develop an orthogonal approach towards the development of a sensitive automated diagnostic assay based on the specific detection of early a-Syn aggregates in biofluids. The group works also in Transthyretin amyloidosis (ATTR) disease.

APPLIED PROTEOMICS AND PROTEIN ENGINEERING PROGRAM

PROTEIN STRUCTURE

Our group, led by **David Reverter**, uses protein crystallography with synchrotron radiation as a major procedure to decipher the molecular mechanisms that lay behind the atomic structure of proteins and protein complexes. In our lab we combine this powerful structural technique with a functional and biochemical characterization using either in vitro or in vivo methods. In the last decades protein-function characterization of proteins and protein complexes have shed light into the most relevant discoveries in biochemistry and molecular biology.

The group foccuses on:

- The structural and functional studies on post-translational modification of proteins by SUMO conjugation
- The structural and functional characterization of the Human USP25 (and USP28) deubiquitinase enzyme
- The structural and functional characterization of the SM56 complexes, a multimeric SUMO E3 ligase enzyme
- The structural mechanism for the temperature-dependent activation of the hyperthermophilic Pf2001 esterase

SUMO and ubiquitin are small protein modifiers that can be attached via an iso-peptidic bond to lysine residues of target proteins. This type of post-translational modification is very common and regulate almost all processes of cell life, including cell division, DNA repair or gene expression. Esterases and lipases are very important biocatalysts for industrial purposes, since they catalyze reactions of synthesis or hydrolysis of lipidic ester bonds.

APPLIED PROTEOMICS AND PROTEIN ENGINEERING PROGRAM

BIOMEDICAL APPLICATIONS OF NUCLEAR MAGNETIC RESONANCE

The aim of our group, led by **Carles Arús**, is to improve the diagnostic and prognostic evaluation of patients bearing abnormal brain masses. We use magnetic resonance spectroscopy (MRS), which can be performed concominantly to a conventional magnetic resonance imaging (MRI) study.

The information provided by MRS allows us to characterise the metabolic profile of these abnormal brain masses without the need to perform a biopsy.

Our group is distributed between the Department of Biochemistry and Molecular Biology of the Bioscience Faculty, where we perform the preclinical studies in animal models, and the IBB. What the IBB subgroup does is to analyse all clinical patient data from our collaborating hospitals. We also work in the improvement of current processing and analysis tools for analysing MRS data.

GENOMICS IN EVOLUTION AND DISEASE PROGRAM

GENOMICS IN EVOLUTION AND DISEASE PROGRAM

GENOME INTEGRITY AND INSTABILITY

Our research group, led by **Aurora Ruiz-Herrera** and **Ignasi Roig**, studies the mechanism(s) that are responsible for the origin and maintenance of mammalian genome integrity through a multidisciplinary approach, combining computational analysis and whole-genome comparisons with cutting-edge experimental technologies in both somatic and meiotic cells. Our studies may help to better diagnose human infertility and provide the basis for the detection and isolation of therapeutic targets in complex human disorders and its future treatments.

More specifically, the group is currently working in the following research lines:

- Investigate the conservation and functionality of the high-structural organization of mammalian genomes, both in the somatic and the germ line
- Analysis of the signaling pathway that controls the progression of meiotic recombination in mammalian meiocytes
- Identification of the role of the DNA damage response machinery in the DSB repair occurring during the meiotic prophase
- How the DNA damage response mechanism controls the oocyte pool in mammals
- Identification of non-annotated genes in the mammalian genome required to complete meiosis
- Identification of the genetic basis of reproductive isolation and barriers of gene flow in mammalian natural populations
- Development of a cell line repository of endangered mammalian species.
- Implementation of integrative bioinformatics and informatic tools for the analysis of the conservation and function of vertebrate genomes
- Analysis of the mechanisms implicated in the origin of chromosome instability associated to solid tumors, in particular to colon and bladder cancer

GENOMICS IN EVOLUTION AND DISEASE PROGRAM

COMPARATIVE MOLECULAR PHYSIOLOGY

Our research group, led by **Joan Cerdà**, is interested in studying he molecular basis of gamete (germ cell) formation and function towards the development of biotechnological inventions for animal production and conservation biology.

Present research lines include:

- Comparative studies on the evolution, structure and function of molecular water channels (aquaporins)
- Molecular physiology of aquaporins and ion channels in male and female gametes
- Development of new biotechnological methods based on aquaporins for cell preservation
- Molecular endocrinology of spermiogenesis.

Research Keywords: Spermatogenesis, oogenesis, endocrinology, aquaporin, physiology, evolution, cell preservation

GENOMICS IN EVOLUTION AND DISEASE PROGRAM

COMPARATIVE AND FUNCTIONAL GENOMICS

Our laboratory, led by **Mario Cáceres**, is focused in the study of genome evolution and the genetic changes associated with individual and species differences, applying the newest genomic techniques and the great wealth of genomic data available. In particular, a great degree of structural variation, including hundreds of copy number variants (insertions, duplications and deletions) and inversions have been discovered in multiple organisms. In addition, we now have the information of the variation of expression levels of thousands of genes in different tissues and individuals of many species. However, we still know very little about the functional consequences of these changes and the role that might have played during evolution. To address these questions, we use humans as a model and take a multidisciplinary approach that combines experimental and bioinformatic analysis, generating results of interest to diverse fields.

Our main research lines are:

- Functional and evolutionary analysis of polymorphic inversions in the human genome
- Genomic determinants of gene-expression changes in humans.

GENOMICS IN EVOLUTION AND DISEASE PROGRAM

BIOINFORMATICS OF GENOMICS DIVERSITY

The Bioinformatics of Genome Diversity group, led by **Antonio Barbadilla**, is aimed to explain the nature of genome variation and its relationship with phenotypic variation and fitness. A new dimension of genetic variation studies is provided by the complete genomes that are increasingly being deciphered (e.g. 1000 Genomes Project), as well as new high-throughput data coming from other omics layers, such as transcriptomic and epigenomic data from the ENCyclopedia Of Dna Elements (ENCODE/modENCODE) or the International Human Epigenome Consortium (IHEC). We follow an interdisciplinary approach, merging methods and knowhow from genomics, population genetics, data science, systems biology and bioinformatics, to address, both in Drosophila and humans, the following objectives:

- Mapping selection onto (a) embryo development in Drosophila and (b) human brain
- Define parameters that measure the adaptive potential of a genome
- PopFly and PopHuman, updating the reference population genomics browsers of Drosophila and humans

RESPONSE MECHANISMS TO STRESS AND DISEASE PROGRAM

RESPONSE MECHANISMS TO STRESS AND DISEASE PROGRAM

MOLECULAR IMMUNOLOGY

Our group, led by **Raul Castaño**, is interested in studying the recognition of CD1d by iNKT lymphocytes from a molecular and structural point of view in order to understand and manipulate the essential function of these lymphocytes in the regulation of the immune response, with especial focus in immune tumor surveillance.

CD1d presents glycolipids that are recognized by iNKT cells, inducing the production of cytokines and the activation of effector cells, depending on the structural characteristics of the antigen, thus determining the development of the immune response. Different glycolipids and molecular analogs recognized by iNKT cells, modify, modulate and regulate their function and the subsequent activation of the immune response and may be used as immunotherapeutic reagents with anti-tumor, adjuvant or immune-modulator capabilities with application to cancer, microbial infections or autoimmune diseases. We are currently performing preclinical animal studies analyzing several synthetic analogs that induce potent anti-tumor immune responses able to control metastases establishment and tumor growth in different tumor models in order to dissect their mechanism of action and asses their therapeutic possibilities.

RESPONSE MECHANISMS TO STRESS AND DISEASE PROGRAM

CELLULAR IMMUNOLOGY

The group, led by **Dolores Jaraquemada**, is mainly foccused on the study of leukocyte cell-surface molecules, their signal transduction pathways, and their role in regulating immune responses in normal and pathological conditions.

Dolores Jaraquemada aims at the identification of the protein autoantigens in Type 1 Diabetes.

Carme Roura-Mir is working on the lipid autoantigens in human type I Diabetes.

Iñaki Ruiz aims at the (1) study of the specificity and contribution on the HLA peptide repertoires of different proteasomes and its role in tolerance and disease, (2) analysis of the role of the autoimmune regulator (AIRE) in antigen expression, processing and presentation, and (3) study of standard and post-translational modificated HLA ligands in tolerance and disease.

Mercè Martí is running two parallel lines of research: (1) Characterization of infiltrating T lymphocytes in samples of breast cancer (BREASTILs), in collaboration with the VHIO, and (2) Design of biosensors in the field of biomedicine (EXOSENS) with the collaboration of Dra. María Isabel Pividori.

RESPONSE MECHANISMS TO STRESS AND DISEASE PROGRAM

BACTERIAL MOLECULAR GENETICS

The group, led by **Isidre Gibert**, foccuses on the field of bacterial pathogenesis and antimicrobial resistance (PatoBAnt). Our research have been focused on the study of virulence and resistance determinants in different human pathogens. We try to unveil the genomic and molecular bases, from a genetic and functional point of view, of processes involved in pathogenesis, virulence and drug resistance.

Currently we have four research lines:

- Molecular and genomic bases of bacterial pathogenesis and antimicrobial agent resistance
- Quorum sensing signal-response systems in Stenotrophomonas maltophilia
- Study of the mechanisms of resistance to colistin in Gram-negative bacteria
- Validation of novel hit compounds as potential antibacterial drugs against Gram-negative pathogens

In collaboration with groups at IBB and other outside groups, we apply a multidisciplinary approach, ranging from classical microbiology and bacterial molecular genetics to genomics, proteomics, and bioinformatics that should end with a selection of validated targets and drugs to suppress bacterial virulence and/or resistance phenotypes.

RESPONSE MECHANISMS TO STRESS AND DISEASE PROGRAM

EVOLUTIVE IMMUNOLOGY

The group, led by **Nerea Roher**, aims to understand host-pathogen interactions and how we can modulate the host immune system to have a good performance against pathogens. To do so, we use a combination of molecular, in vitro and in vivo methodologies.

We develop our research using zebrafish as a model organism due to its high versatility and the availability of mutants. We do both basic and translational research on fish immunology in three main areas:

- Development of vaccines for animal health. Our approach is based on protein nanoparticles made with relevant viral antigens that will induce a good and sustained immunization through the intestinal mucosa
- Evolution of pathogen recognition in vertebrates. We are interested on Pathogen Recognition Receptors (PRRs) and specifically on Toll-like Receptors (TLRs) and in the role and biology of macrophages after pathogen exposure
- Development of diagnostic tools: biosensors for fish skin mucus. We take advantage of the high production of mucus by the fish skin to use mucus to monitorize fish health

RESPONSE MECHANISMS TO STRESS AND DISEASE PROGRAM

YEAST MOLECULAR BIOLOGY

The group, led by **Joaquín Ariño**, is interested in several topics concerning the biochemistry, the molecular biology and the genomics of the yeast Saccharomyces cerevisiae, specifically those that are related to cell signaling trough processes of phospho-dephosphorylation of proteins. For this purpose, we investigate issues such as ion homeostasis, the response to various stresses or the cell cycle regulation and how these circumstances affect specific protein kinases and/or phosphatases (activity, localization, binding to other proteins, postraductional modifications,...).

The main objective is to obtain an overview on the yeast response to perturbations in its environment, so that we can both understand in deep the biology of this organism and to guide us towards new biotechnological applications or the identification of novel antifungal drugs targets.

We currently have 3 different research lines:

- Signalling salt and high pH stress response
- Interactions between nutritional and cation homeostatic mechanisms
- The Ppz protein phosphatase as potential drug target: understanding its regulation and structure

FEATURED OUTREACH

Nit Europea de la Recerca

28/11 **Conference "Desmuntant el LEGO: A la cerca d'una cura per les malalties neurodegeneratives"**
Salvador Ventura

16-29/11 **Interactive activities "Adapta't: la nostra història evolutiva llegida en el genoma"**
Sònia Casillas

24/11 **Talk "La importància de la ciència bàsica en el desenvolupament de noves teràpies" - Institut Can Peixauet**
Sergi Rodríguez

27/11 **Talk "Món Bacterià, Cèl·lula mínima (Mycoplasma genitalium) i Multiresistències" - Institut escola Antoni Ubach i Soler**
Marina Marcos

3/12 **Talk "Un mar de plàstics: la mida si que importa" - INS Miquel Bosch i Jover**
Irene Brandts i Mariana Teles,

Social media followers

341	383	199	20
↑32%	↑5%	↑437%	

10 subscribers, 6 new videos uploaded

Open-research implementation

Micromecenatge VAB

Implementation of the Industry Talks seminars

13/11 Johnson&Johnson

20/11

Creation of a promotional IBB flyer

- ✓ **Remodeling and updating of the webpage**
- ✓ **70 news published in the web**

FOLLOW US

www.ibb.uab.cat

VISIT US

Institut de Biotecnologia i de Biomedicina
Edifici MRB, Campus UAB
08193 Cerdanyola del Vallès
promocio.ibb@uab.cat