

The European Bioinformatics Institute In a nutshell



EMBL-European Bioinformatics Institute
Wellcome Trust Genome Campus
Hinxton, Cambridge CB10 1SD
United Kingdom

Tel: +44 (0)1223 494 444
Fax: +44 (0)1223 494 468
E-mail: outreach@ebi.ac.uk
Web: www.ebi.ac.uk/information

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The hub of bioinformatics in Europe

The European Bioinformatics Institute (EBI) is an academic research institute based in the UK, and is part of the European Molecular Biology Laboratory (EMBL). EMBL-EBI was established in 1994 and grew out of EMBL's commitment to making biological data and information accessible to life scientists in all disciplines.

We serve the scientific community by providing freely available bioinformatics resources, promoting basic research, providing training to scientists at all levels and disseminating cutting-edge technologies to industry.

We manage several large, public databases containing biological data and information spanning genomics, proteomics, cheminformatics, transcriptomics, pathways and systems. We also create tools that allow researchers to analyse this information, and to upload and share their work.

We offer a top-quality research environment with countless opportunities for interdisciplinary collaboration. The research we do helps to inform the services we provide, and vice versa.

Because access to large data sets is a basic requirement for life science research, we provide our user training at the EBI and through training events all over the world. We also offer extensive training to our industry partners.

Why bioinformatics is important

We define 'bioinformatics' as the application of computer technology to the storage, management and analysis of biological data. This is essential for research in all areas, including health, agriculture, energy, the environment, and biotechnology.

The ultimate goal of bioinformatics is to identify biologically meaningful information in experimental data so that we can gain a better understanding of organisms on many different levels – from chemical reactions to entire systems.

High-throughput technologies such as next-generation sequencing produce incredible amounts of new information every day. In fact, the amount of data generated in these experiments doubles every five months or so, while processor power and storage double only every two years.

But storage is only one challenge. As new types of data emerge, they need to be integrated with the old. There is an increasingly pressing need to find innovative ways to collect, curate, store and retrieve biological data so that it can be analysed in meaningful ways.

Our mission

- To provide freely available data and bioinformatics services to all facets of the scientific community in ways that promote scientific progress
- To contribute to the advancement of biology through basic investigator-driven research in bioinformatics
- To provide advanced bioinformatics training to scientists at all levels, from PhD students to independent investigators
- To help disseminate cutting-edge technologies to industry
- To coordinate biological data provision across Europe

Strength through collaboration

Our major data resources are the products of international collaborations. We work with other data providers to ensure that our data repositories, and those of our collaborators, are comprehensive and up to date. For example:

- The European Nucleotide Archive (ENA) is produced by the International Nucleotide Sequence Database Collaboration. The other partners are GenBank in the US and the DNA Databank of Japan.
- The UniProt databases contain protein sequence and annotation data that is maintained cooperatively by three centres: EMBL-EBI, the Swiss Institute of Bioinformatics and the Protein Information Resource in the US.
- The PDBe, our macromolecular structure database, is the European arm of the worldwide Protein Data Bank (wwPDB). The other partners are the Research Collaboratory for Structural Bioinformatics and the Biological Magnetic Resonance Data Bank in the US and the Protein Data Bank of Japan (PDBj).
- Ensembl is a joint project between EMBL-EBI and the Wellcome Trust Sanger Institute to develop a software system which produces and maintains automatic annotation on selected eukaryotic genomes.
- IntAct, our protein interactions resource, is a contributing database to the International Molecular Exchange Consortium (IMEx). IMEx holds a non-redundant set of protein-protein interaction data from a broad taxonomic range of organisms. It is funded by the European Commission.



Setting standards

We actively participate in international efforts to develop data standards, which are essential for ensuring the accuracy of the scientific record.

For example, EMBL-EBI was a leading partner in developing the MIAME standard, which sets out the minimum information required to describe a microarray experiment in a published article. Another example is the Human Proteome Organisation's Proteomics Standards Initiative (PSI), which develops standards for data from experiments involving molecular interactions, mass spectrometry, protein separations, protein modifications and protein informatics.

A unique working environment

We share the Wellcome Trust Genome Campus with the Wellcome Trust Sanger Institute in rural Cambridgeshire, and are part of one of the world's largest concentrations of expertise in genomics, bioinformatics and computational biology.

The campus in Hinxton is set in 22 hectares of parkland on the banks of the river Cam. We have the advantage of being housed in modern buildings in a beautiful setting, whilst being only a few miles away from the academic centre of Cambridge.

The campus provides an inspiring environment for all staff. We are regularly visited by some of the greatest minds in biomedical research, and the workshops, seminars and conferences held on campus are open to all staff.

We have excellent computational facilities and a comprehensive library. The campus also enjoys a highly active social life, with events held on campus throughout the year and all manner of sports teams. We have a gym, a choice of places to eat, and free transport by shuttle bus to Cambridge, Saffron Walden and some of the surrounding villages.

For information about visiting the campus, please see the inside back cover.





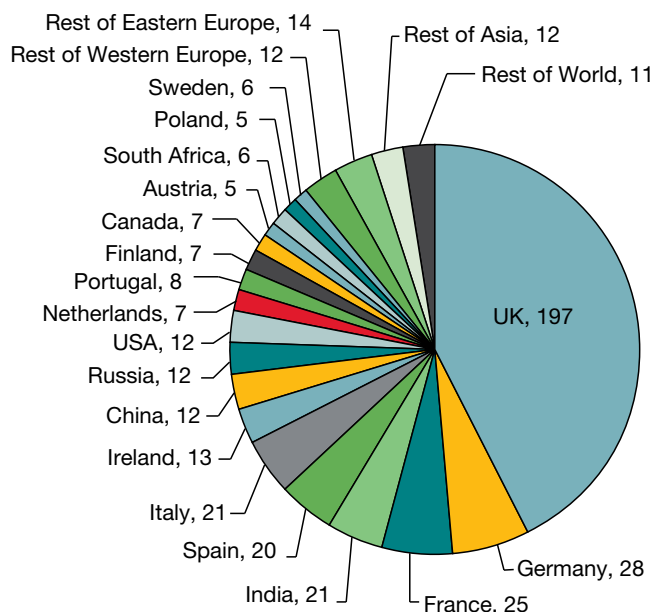
Who We Are

Professor Janet Thornton Director

Janet has been Director of EMBL-EBI since October 2001. Her research group focuses on understanding biological processes from a structural perspective using computational approaches. After a physics degree, she moved into biophysics at the National Institute for Medical Research, Mill Hill, London. Before moving to EMBL-EBI she held a joint appointment at University College London and the Bernal Chair in the Crystallography Department at Birkbeck College. She is a Fellow of the Royal Society, a Member of EMBO and a foreign associate of the US National Academy of Sciences.

Graham Cameron Associate Director

Graham has been Associate Director of EMBL-EBI since September 2001. He was responsible for EMBL-EBI's launch in 1993 and ran its information services until 1998, when he became EMBL-EBI's joint head (with Michael Ashburner). Previous to that he worked at EMBL-Heidelberg in the DNA Data Library, first in software and database design, then leading the project from 1986. His educational background is in psychology, and he has experience in data provision for many disciplines, including primate behaviour, health information, social behaviour and British economic behaviour.



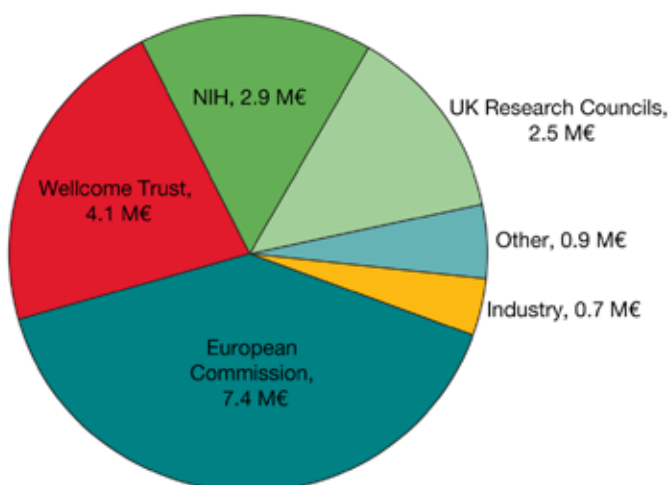
Our personnel, including long-term visiting scholars, hail from 37 different countries. This chart shows the nationalities of our 500 members of staff as of June 2010.

A part of the European Molecular Biology Laboratory

EMBL is a basic research institute funded by public research monies from 20 member states: Austria, Belgium, Croatia, Denmark, Finland, France, Germany, Greece, Iceland, Ireland, Israel, Italy, Luxembourg, the Netherlands, Norway, Portugal, Spain, Sweden, Switzerland and the United Kingdom, and associate member state Australia.

Research at EMBL covers the spectrum of molecular biology. Its main laboratory is in Heidelberg. In addition to EMBL-EBI in Hinxton, EMBL has outstations in Grenoble, France; Hamburg, Germany; and Monterotondo, Italy.

EMBL's mission is: to perform basic, investigator-driven research in molecular biology; to train scientists, students and visitors at all levels; to provide facilities and services for the scientific community; and to actively engage in technology transfer activities.



EMBL-EBI receives most of its funding from EMBL's 20 member states. In addition, we receive funding from outside sources, shown here for 2010.

How we're funded

As part of EMBL, the largest part of our funding comes from the governments of EMBL's member states. The global importance of our work is reflected in the fact that we also attract significant funds from external sources, including some beyond Europe. Some of our other major funders include the European Commission, Wellcome Trust, UK Research Councils, US National Institutes of Health and our industry partners.

The UK's Biotechnology and Biological Sciences Research Council (BBSRC) awarded a further €11.4m in August 2009 in support of EMBL-EBI's planned role as the central hub of ELIXIR. These funds have been used to develop a robust compute infrastructure that will allow the EBI to efficiently manage an ever-expanding and diversifying range of services.

Genomes

Ensembl: Browse and compare vertebrate (and selected invertebrate) genomes. Ensembl is produced through a collaboration between EMBL-EBI and the Wellcome Trust Sanger Institute.

Ensembl Genomes: Access to non-vertebrate genomes, including plants and prokaryotes.

EGA: The European Genome-phenome Archive contains information on individual human genotypes.

Nucleotide sequence

ENA: Find any DNA or RNA sequence in the public domain, including completed genomes and sequences associated with patents.

Functional Genomics

ArrayExpress Archive: Access annotated microarray experiments.

Gene Expression Atlas: Contains a subset of curated and re-annotated data from ArrayExpress, which can be used to search gene expression under different biological conditions.

Protein families, domains and motifs

InterPro: Perform integrated searches for protein families, motifs and domains. InterPro combines the strength of 11 member databases to yield a powerful resource for large-scale protein classification and annotation.

Protein activity

IntAct: Access information on protein-protein interactions. Build graphical views of interaction networks and annotate them with functional information.

PRIDE: A centralised public data repository for proteomics data, including information on post-translational modifications.

Key

Molecular components

Molecular behaviours

Services

We maintain the world's most comprehensive range of molecular databases, and are the European node for globally coordinated efforts to collect and disseminate biologically relevant data.

Many of our databases are household names to biologists and biochemists, such as the European Nucleotide Archive (ENA), Ensembl, ArrayExpress, UniProt, PDB, IntAct, Reactome, the Gene Expression Atlas, ChEMBL, ChEBI and CiteXplore. All of our databases uphold the same principles of service provision (see box).

We are the custodians (not the owners) of biological data submitted by the community and we provide unrestricted open access to these data. Our website (www.ebi.ac.uk), which receives more than 4 million requests a day, provides direct access to all our databases and tools.

The EBI search provides easy access to our data, allowing you to explore our many resources from a simple results summary. Our tools allow you to submit your own data, perform complex queries across multiple databases, analyse data and view the results in different ways. You can download data and software from <ftp://ftp.ebi.ac.uk>, and access a growing number of our resources programmatically using web services.

Supporting our users

To help you make the most of our resources, we offer help pages (www.ebi.ac.uk/help) and can be reached at support@ebi.ac.uk. We will get back to your request within two working days.

Principles of service provision

Accessibility – Our data and tools are freely available to the research community without restriction. The only exception is potentially identifiable human genetic information, for which access depends on research consent agreements.

Compatibility – We are a world leader in promoting the adoption of standards in bioinformatics.

Literature

CiteXplore: Search the scientific literature and automatically add links to biological data resources.

GO: The Gene Ontology project aims to produce an unambiguous, universal language to describe biological phenomena across all species.

Protein sequence

UniProt: The world's most comprehensive catalogue of information on proteins – to gain user-friendly access to richly annotated information on individual proteins, and to full proteome sets.

Macromolecular structure

PDB: Contains the Protein Data Bank's structures. View predicted quaternary structures, interactions with ligands and structure comparisons.

Chemical entities

ChEBI: Bridge the gap between the protein world and that of small molecules.

Chemogenomics

ChEMBL: Explore structure–activity relationships of drugs and drug-like molecules.

Pathways

Reactome: Navigate a map of human biological pathways, ranging from metabolic processes to hormonal signalling.

Systems

BioModels: Search and retrieve published mathematical models of biological interest. Models are annotated and linked to relevant data resources.

Other

Comprehensive data sets – We share data to ensure that our resources are comprehensive and up to date. We also work with publishers to ensure that, wherever practicable, biological data are placed in a public repository as part of the publication process and cross-referenced in the relevant publication.

Portability – Many of our data sets are made available for download from the EMBL-EBI website. In many cases the entire software system can be downloaded and installed locally.

Quality – Our databases are enhanced through annotation: information is added to the original data to provide context and help with interpretation. Much of our annotation is performed by highly qualified biologists, and the automated annotation that we do is subjected to rigorous quality control. In many cases we also call on expertise outside the EBI for specialist annotation.

Research

We provide a unique environment for bioinformatics research, and our broad palette of research interests complements our data resources. EMBL-EBI researchers have the expertise of hundreds of bioinformaticians close at hand – even in the lunch queue or on the volleyball pitch. Our research teams aim to understand biology by developing new approaches to interpreting biological data. Our services teams, who develop and maintain our resources, also perform research, often focusing on enhancing our existing services or creating new ones.

Genomics

Ewan Birney: Nucleotide data resources

Ewan's team is responsible for the nucleotide sequence resources at EMBL-EBI, which includes the ENA, Ensembl and Ensembl Genomes. The group's research focuses on developing sequence algorithms and using intra-species variation to study basic biology. Future projects involve developing algorithms to study segmental duplication and to expand intra-species variation studies to other basic biological phenotypes in other species.

Paul Flicek: Vertebrate genomics

Paul's team is a combined service and research group that brings together the tools and resources of the Ensembl genome analysis framework for comparative genomics, variation and functional genomics. The team also develops the large-scale bioinformatics infrastructure for human variation projects such as the 1000 Genomes Project and European Genome-phenome Archive (EGA) as a first step towards annotating all human variation. Their research involves exploring the evolution of transcriptional regulation and developing algorithms to study epigenomic data.

Nick Goldman: Evolutionary analysis of sequence data

Nick's group is developing improved mathematical and statistical methods for analysing DNA and amino acid sequences to study how these sequences evolve. The team uses information from evolutionary studies to increase the accuracy of other data analyses in bioinformatics, including the use of next-generation sequencing technology. By seeing which biological features add most to the accuracy of the models, they hope to find out which proposed evolutionary forces are responsible for the patterns of sequence variation within and among species.

Transcriptomics

Alvis Brazma: Functional genomics

Alvis's team is responsible for the development of the ArrayExpress Archive and Gene Expression Atlas resources for gene expression and related functional genomics data. The group's research focuses on analysis of gene expression, development of new algorithms and methods for integrative data analysis, and building a global map of gene expression. They also investigate the relationship between gene expression and disease.

Anton Enright: RNA genomics

Anton's group has a particular interest in small non-coding RNAs and develops computational tools, systems and algorithms to predict the function and interactions of small RNAs. The group collaborates extensively with experimental labs in order to build better data sets for helping us to understand these important regulatory molecules. They also have interests in the visualisation of large data sets, graph-clustering and analysis of biological networks.

John Marioni: Computational and evolutionary genomics

John's group develops computational and statistical methods to better understand how changes in genetic architecture (e.g. the relationship between sequence and gene expression) provide insights into the adaptive evolution of complex organisms and developmental processes. They also develop methods for storing, visualising and analysing genetic features at a single-cell level to improve our understanding of both key developmental processes and neural function in an evolutionary context.

Text mining

Dietrich Rebholz-Schuhmann: Automatic extraction of facts from the scientific literature

Dietrich's group focuses on building semantic resources, extracting facts from the literature and knowledge discovery. Their goal is to connect literature content automatically to biomedical databases and to evaluate new findings against existing knowledge. All solutions contribute to the standardisation and semantic enrichment of the scientific literature.

Proteomics

Janet Thornton: Proteins – structure, function and Evolution

Janet's research group aims to understand more about the three-dimensional structure and evolution of proteins. For example, they analyse how enzymes perform catalysis, how these molecules recognise their cognate ligands, and how proteins and organisms have evolved to create life, and the modelling of the insulin signalling pathway in ageing. Much of their research is collaborative, involving either experimentalists or other computational biologists.

Rolf Apweiler: Protein data resources

Rolf's team is responsible for the protein and proteomics-related activities at EMBL-EBI, which include the production of protein sequence and protein family databases (e.g. UniProt). The group's research activities involve finding new ways to improve protein identification from mass spectrometry data and improved data mining of large biological datasets.

Gerard Kleywegt: Protein Databank in Europe (PDBe)

Gerard's group handles the deposition and annotation of structural data in the PDBe and EMDB and maintains in-house expertise in all the major structure-determination techniques (i.e. X-ray crystallography, Nuclear Magnetic Resonance spectroscopy, Electron Microscopy).

Chemistry

Christoph Steinbeck: Cheminformatics and metabolism

Chris's group studies the small molecule metabolism in biological systems. Research includes reconstructing metabolic networks from genomic data and structure elucidation and identification of metabolites from metabolomics experiments. The group will also launch an Enzyme Portal, which will integrate all enzyme-related information resources at the EBI.

John Overington: Chemogenomics and drug discovery

John's group develops and manages ChEMBL: the EBI's database of bioactive, drug-like small molecules. The group is building a computational system to analyse functional and binding data for peptides and analysis of 'chemical probes'. Other projects include analysis of drug attrition, biotherapeutic drug discovery and open source competitive intelligence.

Pathways and systems

Nicolas Le Novère: Computational systems biology

Nicolas's group aims to gain a better understanding of signal transduction in neurons by building computational models. They plan to expand their research activities to incorporate whole neuron behaviour. The group hosts the BioModels database, a repository for annotated biological models. Nicholas has been instrumental in the development of Systems Biology Markup Language (SBML), which is designed to facilitate the exchange of biological models between different types of software, and in the development of 'minimum information' standards.

Nick Luscombe: Genome-scale analysis of regulatory systems

Nick's group uses computational techniques to understand how transcription is regulated and how this regulatory system is used to control biologically interesting phenomena. By integrating diverse information – from genome sequence to the results of functional genomics experiments – they can study the regulatory system of an entire organism. Their work focuses on higher eukaryotes and bacteria.

Paul Bertone: Differentiation and development

Paul's group investigates the cellular and molecular processes underlying mammalian stem cell differentiation and induced pluripotency. One strand of their research is to map the transition between the pluripotent state and early lineage commitment. The group will also work to further characterise the molecular properties of neural cancer stem cells and assess the role of genetic changes across individuals.

Julio Saez-Rodriguez: Systems biomedicine

Julio's group develops computational methods and tools to analyse signalling networks. They also develop mathematical models to better understand how signalling is altered in human disease and to predict effective therapeutic targets. Research aims to investigate questions such as: what are the origins of the profound differences in signal transduction between healthy and diseased cells? Can we use these differences to predict disease progression and to reveal targets for drug development?

Training

Training future bioinformaticians

Bioinformatics is a rapidly expanding discipline that touches on all areas of biology – pure and applied. We help bioscientists from all disciplines, regardless of whether they have any formal training in computational biology, to harness the power of bioinformatics.

EMBL International PhD programme

We have a lively graduate community that is part of EMBL's International PhD Programme. Many of EMBL-EBI's PhD students join the University of Cambridge; they participate fully in Cambridge graduate life and leave EMBL-EBI with a PhD from the University of Cambridge. We encourage potential candidates to visit www.embl.ac.uk/training/studentships/ for more information.

Postdoctoral fellows

We offer many opportunities for postdoctoral fellows. Most of our postdocs have external funding, but some fellowships may be offered as specified positions on our jobs page. If you are interested in doing your postdoc with us, the first step is to contact the group leader of your choice directly. See: www.embl.de/training/postdocs

The EMBL Interdisciplinary Postdoctoral Programme (EIPOD) encourages candidates whose research crosses scientific boundaries. EIPOD projects bring together scientific fields that are usually separate or transfer techniques to a novel context. See: www.embl.de/training/postdocs/eipod/

The EBI-Sanger Postdoctoral Programme (ESPOD) is for researchers who take both an experimental and computational approach to their work. ESPOD

postdocs are supported by easy access to scientific expertise, well-equipped facilities and an active seminar programme. See: www.embl.ac.uk/training/postdoc/ESPOD

Visitors and scholars programme

There are opportunities for researchers at all stages of their career to spend time at the EBI. See: www.embl.ac.uk/training/Visitors_Programme/

User training at EMBL-EBI

We hold training courses in our purpose-built IT training suite to help experimental biologists get to grips with their data using our wide range of data resources. These courses are very hands-on, and offer direct contact with expert trainers and high-quality training materials. See the full programme at: www.embl.ac.uk/training/hands-on

User training at your place

Our bioinformatics roadshow provides a mobile training programme covering Europe's most widely used biological data resources. Roadshows can be tailored to create bespoke courses suitable for the host institute. Learn more about how to host a roadshow at: www.embl.ac.uk/training/roadshow

User training online

Our eLearning portal is being designed to enable you to learn at your own pace and at a time that suits you. eLearning modules compliment our face-to-face training programmes. To learn how you can participate in the testing of our new eLearning platform, please contact: elarning@ebi.ac.uk



Supporting industry

A comprehensive programme for Europe's life science industries

Our industry programme enables industry to adapt quickly to – and maximise the benefit from – innovations in bioinformatics. We have been supporting the needs of industry for over 14 years.

We do this by:

- kick-starting research of importance to industry;
- providing expert training;
- developing bioinformatics standards;
- assisting with technical development; and
- providing regular networking opportunities.

EMBL-EBI's industry programme is driven by its partners and membership is by invitation. Annual member subscriptions fund the programme.

Support for SMEs

We also serve small-to-medium enterprises through our SME Support Forum: www.ebi.ac.uk/industry/SME

The Forum meets on an annual basis, offering discussion and networking opportunities. Members range from drug discovery and biotech start-ups to bioinformatics service providers, and have access to:

- expert tuition;
- opportunities for technical development through collaboration;
- consultancy.

Join us

To learn more about how your company can benefit from our Industry Programme, visit us online and download the programme brochure: www.ebi.ac.uk/Information/Brochures/

To discuss joining the programme, please contact Dominic Clark: clark@ebi.ac.uk

Joint pre-competitive initiatives

Our programme provides invaluable support for industry partners working on pre-competitive projects, which aim to translate research discoveries into advances in medicine, health and agriculture for the benefit of society.

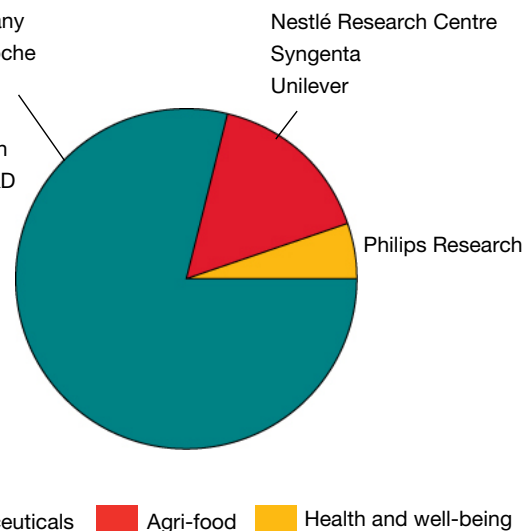
EMBL-EBI is a member of the Pistoia Alliance (www.pistoiaalliance.org), a not-for-profit organisation established by life science companies wishing to streamline non-competitive elements of the pharmaceutical drug discovery process.

The Innovative Medicines Initiative (IMI; <http://imi.europa.eu>) is a joint initiative to foster pre-competitive collaboration within the pharmaceutical industry and is co-sponsored by the European Commission and EFPIA (European Federation of Pharmaceutical Industries and Associations). EMBL-EBI is a partner on several IMI projects (see next page).

Our industry partners



- Astellas Pharma Inc
- AstraZeneca
- Bayer Pharma
- Boehringer Ingelheim
- Eli Lilly and Company
- F. Hoffmann-La Roche
- Galderma
- GlaxoSmithKline
- Johnson & Johnson
- Pharmaceutical R&D
- Merck Serono
- Novo Nordisk A/S
- Orion Pharma
- Pfizer Ltd
- Pfizer Research
- Sanofi-Aventis
- UCB Pharma



EMBL-EBI and the European Research Area

Europe has always been at the forefront of bioinformatics research, but as we move towards the European Union's goal of a single European Research Area, there is a greater need than ever for bioinformatics experts and experimental biologists throughout Europe to work together towards common goals that will expedite biological research. To this aim, EMBL-EBI coordinates the preparatory phase of the ELIXR project and several other EU-funded projects.

ELIXIR

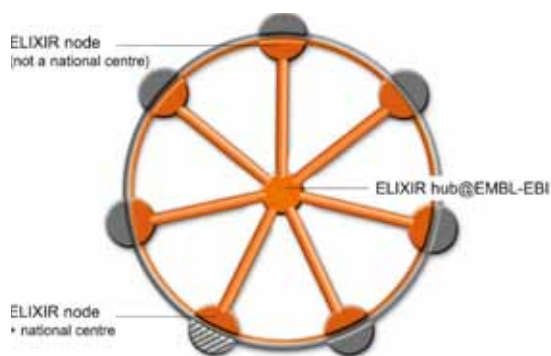
Research and innovation in the life sciences is helping us tackle some of the more serious challenges facing society, including healthcare for an ageing population, security of food supply, protection of the environment and economic competitiveness.

EMBL-EBI coordinates ELIXIR (www.elixir-europe.org), a research infrastructure that is defining how Europe will manage and integrate its growing volume and variety of biological data.

This large-scale initiative will provide the facilities necessary for life science researchers to share, analyse and protect our rapidly growing store of information about living systems.

ELIXIR brings together Europe's leading bioscience facilities to manage biological data in a sustainable way. This should enable all facets of the life science community – from health to agriculture – to extract optimum value from work that has already been done, and whose nature we can now only imagine.

EMBL-EBI is involved in data management in several other ESFRI projects (e.g. EU Openscreen, EMBRC, Instruct). Indeed, we are leading the BiomedBridges project, which will ensure transparent data access between all of the Biological and Medical Sciences Research Infrastructures in Europe.



ELIXIR will complement the capabilities of its participating organisations, including EMBL-EBI.



Other EU-funded projects

DDMoRe (www.ddmore.eu), the Drug Disease Model Resources consortium, will develop a new common definition language for data, models and workflows, along with an ontology based standard for storage and transfer of models and associated metadata. The project will also develop a publicly-available drug and disease model library.

EHR4CR (www.ehr4cr.eu) aims to design and demonstrate a scalable and cost-effective approach to interoperability between electronic health record systems and clinical research.

EMTRAIN (www.emtrain.eu) will establish a sustainable, pan-European platform for education and training covering the whole life-cycle of medicines research, from basic science through clinical development to pharmacovigilance.

ENFIN (www.enfin.org) brings together experimentalists and computational biologists to develop the next generation of informatics resources for systems biology.

eTOX (www.etoxproject.eu) is developing a drug safety database from the pharmaceutical industry legacy toxicology reports and public toxicology data. The project also aims to develop innovative in silico strategies and novel software tools to better predict the toxicological profiles of small molecules in early stages of the drug development pipeline.

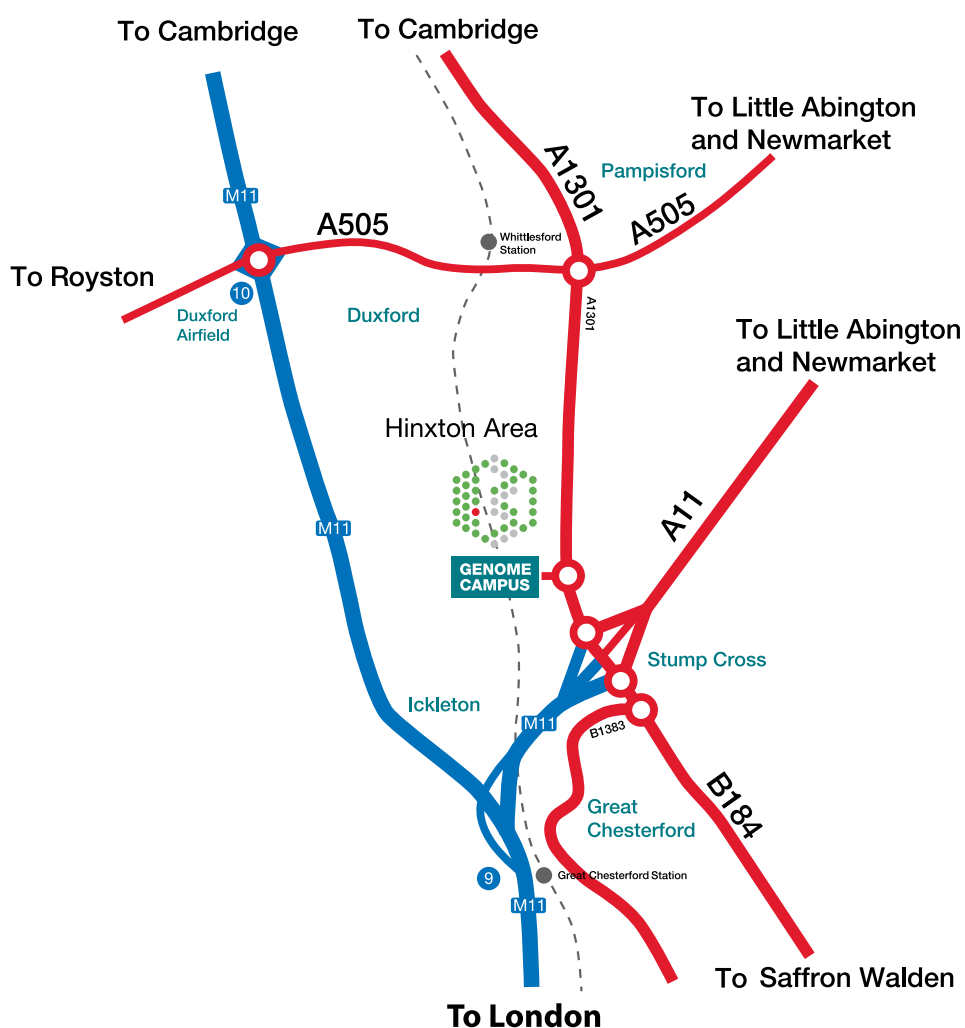
SLING (www.sling-fp7.org/training) aims to make sure that advances in European science are supported by the best possible biomolecular information, and that European scientists are optimally equipped to exploit it. To do this, the project makes available a comprehensive range of databases and services, enhancing them to keep pace with changing science, and providing user training.

How to find us

EMBL-EBI is situated on the Wellcome Trust Genome Campus in the village of Hinxton, which is 12 miles south of the city of Cambridge in the UK.

We are 14 miles from London Stansted airport and can be easily reached by car. For more details about getting to the EMBL-EBI, please visit www.ebi.ac.uk/Information/Travel.

Our address: EMBL-EBI, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire CB10 1SD



Driving directions

From the South:

leave the M11 at junction 9 and take the A1301 towards Cambridge. From the Stump Cross roundabout system take the first left (about 800m). At the next small roundabout follow the signpost for the Genome Campus.

From the North:

leave the M11 at junction 10, marked 'Saffron Walden'. Travel a mile or so in the direction of Saffron Walden to a roundabout and take the third exit (A1301 towards Saffron Walden). Pass two turnings to Hinxton, and take the next right, a small roundabout, with a sign post for Genome Campus.



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A part of the European Molecular Biology Laboratory