

Protein Structure and Function Research at Essex

Proteins are the mainstay of cellular activity, performing a staggering variety of functions, from efficient chemical catalysis or the transport and storage of molecules like oxygen, to forming mechanical scaffolds, transmitting signals, acting as chemical switches, etc. These diverse functions stem from the wide ranging structural variation and complexity that proteins exhibit. Structural irregularities in proteins can lead to malfunction or gain of abnormal function, defects that can result in cellular damage or disease.

We seek to understand these processes and the structure-function relationship in soluble and membrane proteins and their complexes, particularly with importance in human health, the environment and biotechnology.

About the team

We are a community of internationally renowned researchers based in the School of Biological Sciences at the University of Essex. Our common focus is understanding the ways in which enzymes and other proteins work and how this is linked to their three-dimensional structures. We have a track record of successful collaborative work with business and industry, ranging from pharmaceutical companies to bioremediation. We are responsive to the priorities of industrial partners.

About Essex

Our team is based at the University of Essex which is one of the leading research-intensive universities in the UK. The School of Biological Sciences is the largest science department in the University with over 50 teaching and academic staff. Academics have expertise in the areas of biophysics, structural biology, biochemistry, bio-organic chemistry, genomics, cell/molecular biology environmental microbiology, plant productivity and photosynthesis. This broad-based structure provides for a strong multidisciplinary environment involving collaboration between chemists, biochemists and biologists, providing additional scope to develop technology and innovative approaches to problems.

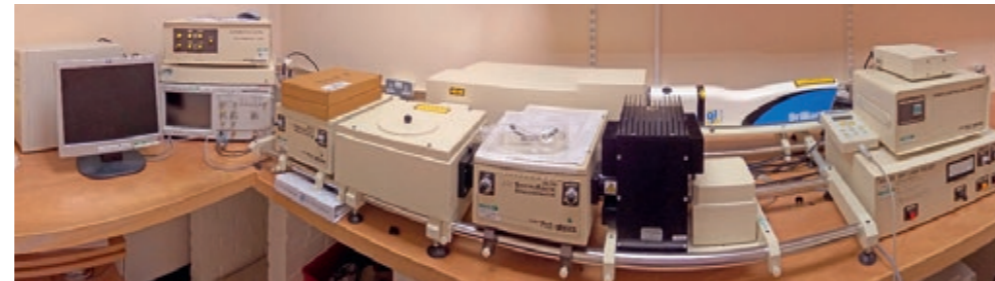
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Protein
Research at Essex

Technology and expertise available for partners

We welcome collaborative work with industry and SMEs where our expertise and infrastructure map on to the challenges and interests of your business. Some of the approaches we can offer are:

Large-scale protein expression, purification of soluble and membrane proteins

We have extensive experience in using bacterial and mammalian expression systems to produce large quantities of recombinant proteins for downstream analysis/testing. We maintain a library of expression plasmids and purification protocols to ensure efficient protein production and validation. We utilise a range of expression hosts and bioreactors/fermenters.

Spectroscopic characterization of proteins

We apply a wide range of biochemical methods to characterize protein function including electron paramagnetic resonance, enzyme assays, membrane transport assays and HPLC. We can determine the catalytic and binding properties of proteins on rapid time scales using stopped-flow and laser-flash photolysis facilities.

Understanding protein-ligand, protein-DNA and protein-protein interactions

We apply a range of techniques to identify and characterize the interactions between proteins and between proteins and ligands. Our expertise and equipment includes isothermal titration calorimetry, surface plasmon resonance, EPR, fluorescence spectroscopy, computational docking and structure determination of protein-ligand complexes.

Determining three dimensional protein structures

We use a range of structural biology methods (X-ray crystallography, X-ray scattering, circular dichroism, X-ray radiolytic footprinting) to gain information about protein structure. This is linked to the analysis mutations to probe function or those occurring in genetic diseases. The structural information gained is invaluable in identifying drug binding sites or optimizing enzymes for biotechnology. Our *Protein crystallisation facility* is equipped with an ARI Gryphon Robotic Protein Crystallography System that allows the highly automated screening of around one thousand crystallisation conditions in a reliable and reproducible way using as little as 100 nL protein sample per drop.

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Computational simulations

Three-dimensional crystal structures provide snapshots of proteins in static states, while dynamics and functional interactions are probed by other experimental methods, including spectroscopy (e.g. EPR, NMR) and computational simulations (molecular dynamics and QM/MM). Our team are experienced in applying these methods to understand protein dynamics, drug binding and catalysis, both in-crystallo and in-solution states.

Ways of working with us

We offer many ways for you to access our expertise, including consultancy, collaborative and commissioned research and Knowledge Transfer Partnerships. We have a very successful record in securing external funding for our research from research councils and charities and host several jointly-based PhD student projects with industry including via the iCASE scheme.

We can offer training in protein production and characterisation including data analysis.

These are some examples of the current and recently completed projects and programmes which are collaborative with and sponsored by industry:

- Modelling G protein-coupled receptor (GPCR) activation
- Development and application of QM/MM calculations for fragment-based drug design
- Novel modifications of Haemoglobin-Based Blood Substitutes for clinical use

