STRUCBIOCAT
INSTRUCT-FI

Research and Teaching Infrastructure for Structural Biocatalysis

Biocenter Oulu, Biocenter Finland and Faculty of Biochemistry and Molecular Medicine

What we can offer

Services and expertise in

- Bioinformatics
- Protein purification
- Molecular enzymology
- Protein biophysical characterization
- Protein binding studies
- Mass spectrometry
- Protein crystallization, structure determination and structure analysis
- Biocomputing using In silico modelling and simulation

Equipment infrastructure for

- Independent use
- Research collaboration

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Please contact any of the above researchers for initial project discussions and pricing guidelines.

www.oulu.fi/biocenter/strucbiocat
www.oulu.fi/biocenter/instruct-fi
www.oulu.fi/biocenter/core-facilities

BioStructX
INSTRUCT

INTEGRATING
 BIOLOGY
Introduction

The Biocenter Oulu core facilities for protein analysis, molecular enzymology, biocomputing and protein crystallography form together the center of expertise for structural biocatalysis - Strucbiocat. The Strucbiocat infrastructure is located at the Faculty of Biochemistry and Molecular Medicine, University of Oulu. It offers a wide range of state-of-the-art instruments and techniques for the benefit of local researchers and biotechnology companies as well as other Finnish and international operators. It is a setup for versatile protein characterization ranging from protein bioinformatics and purification to structure determination, analysis and modelling.

Protein Sample Characterization

- IC50 measurement
- Michaelis-Menten enzyme kinetics
- ITC measurement
- CD spectrum

Multimode plate reader (Tecan Infinite M1000)
- absorbance, fluorescence, luminescence and AlphaScreen affinity measurements

Spectrophotometer (Jasco V-660)
- enzyme kinetics

Circular dichroism (CD) spectrometer
- protein secondary structure determination

Isothermal titration calorimetry (ITC)
- studying protein-ligand interactions

Surface plasmon resonance (Biacore, Bionavis)
- studying protein-ligand interactions

Static light scattering (SLS)
- determination of absolute molecular weights of proteins

Dynamic light scattering (DLS) plate reader
- screening optimal buffer conditions for proteins

Mass spectrometry (Q-tof, MALDI ToF/ToF)
- e.g. identification and characterization of proteins

Pipetting robots (Mosquito, Tecan)
- crystallization screening

Crystallization plate hotels (Formulatrix)
- imaging of crystallization set-ups

xtalPiMS software
- viewing crystallization results (also off campus) and data tracking from crystals to PDB

Microfocus X-ray generator (Microstar X8 Proteum)
- crystal testing and data collection

Protein Structural Analysis

- protein structure determination
- support for structure determination and analysis

Ligand screening studies
- verifying ligand binding with crystallographic methods

In silico modelling and simulations
- e.g. Molecular dynamics, quantum mechanics/molecular mechanics, pKa predictions, and protein modelling