

STRUCBIOCAT INSTRUCT-FI

Research and Teaching
Infrastructure for
Structural Biocatalysis

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



UNIVERSITY of OULU
OULUN YLIOPISTO



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



Contact information

Kristian Koski, PhD (protein purification and bioinformatics)
kristian.koski@oulu.fi Tel. +358 294 481174

Hongmin Tu, PhD (protein biophysical analysis)
hongmin.tu@oulu.fi Tel. +358 294 485821

Lari Lehtiö, PhD (ligand binding studies)
lari.lehtio@oulu.fi Tel. +358 294 481169

Tiila Kiema, PhD (crystallization and structure determination)
tiila.kiema@oulu.fi Tel. +358 294 481179

Ulrich Bergmann, PhD (mass spectrometry)
ulrich.bergmann@oulu.fi Tel. +358 294 481209

Andre Juffer, PhD (biocomputing)
andre.juffer@oulu.fi Tel. +358 294 481161

Rik Wierenga, Prof. (structure analysis and enzymology)
rik.wierenga@oulu.fi Tel. +358 294 481199

Faculty of Biochemistry and Molecular Medicine
Biocenter Oulu, Aapistie 7A, 90220 Oulu, Finland

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

www.oulu.fi/biocenter/strucbiocat

www.oulu.fi/biocenter/instruct-nac

www.oulu.fi/biocenter/core-facilities

BioStructx



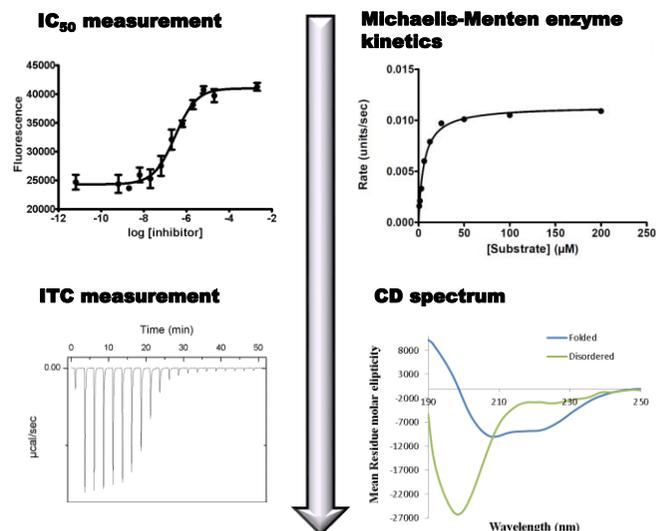
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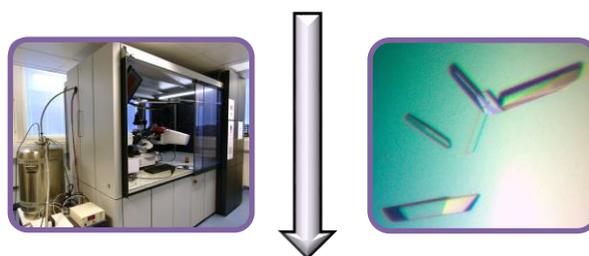
Introduction

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.

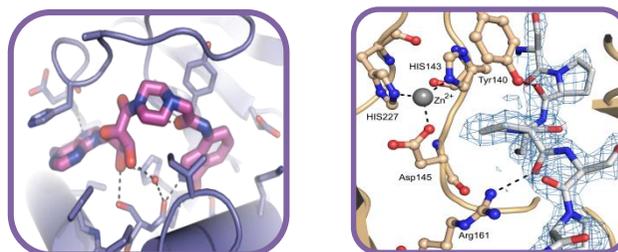
Protein Sample Characterization



Protein Crystallography



Protein Structural Analysis



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 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

