

Chemistry Department

## Macromolecular Crystallography

**xtal**  
Crystallography Group @ REQUIMTE  
<http://xtal.dq.fct.unl.pt/>

**requimte**  
rede de química e tecnologia

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- Benedita Pinheiro, *post-doc*
- Márcia Correia, *post-doc*
- Catarina Coelho, *post-doc*
- Aldino Viegas, *post-doc*
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**Maria João Romão**

Full Professor  
Group leader

Since 2012, Full Professor

1998-2012, Associate Professor,  
FCT-UNL

2001, Habilitation, FCT-UNL

1989, PhD in Chemistry, IST

## Objectives

**A** - Molybdenum enzymes – Molybdopterin-containing enzymes (Mo active site, associated to other electron transfer redox centers (Fe/S, hemes and flavins)).  
Novel enzymes; reaction mechanisms; co-factor assembly and enzyme maturation.

**B** - The Cellulosome: a cellulose degradation machinery – Enzymatic and molecular recognition components of the Cellulosome assembly.

**C** - Interaction of CO releasing molecules (CORM) with plasma proteins.

**D** - New tools and methodologies for protein crystallization and optimization.

## Methodology

- Crystallographic methods using data collected at the ESRF, SLS, SOLEIL & DIAMOND SR sources.

- SAXS data are being used as complementary information on complexes, protein-protein interactions and multiple enzyme conformations (ESRF & DESY).

- Structural data complemented by NMR data, in particular for defining a structural basis for substrate binding to CBMs (collab. NMR@REQUIMTE).

- Cryo-EM studies on mini-cellulosomes (collab. Madrid University).

- Carbohydrate microarrays for ligand discovery; protein-protein microarrays.

## Expected Results

**A**- Novel crystal structures – first mammalian aldehyde oxidase crystal structures; Substrate and inhibitor-bound forms. Structures of complexes with broad impact for drug companies (e.g. Pfizer).  
Structure-derived enzymatic mechanisms; Moco-binding and maturation mechanisms.

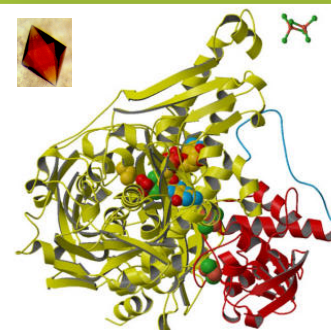
**B**- Novel enzymes and carbohydrate binding modes. Definition of molecular determinants for the function of the cellulosome machinery.

**C**- Mechanisms of drug binding to plasma proteins (model proteins; hemoglobin; transferrin; albumin) and in drug design strategies (collab. ITQB/Alfama (C.Romão).

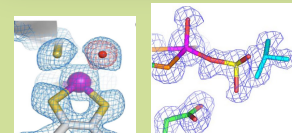
**D** - The effect of ionic liquids in protein crystallization with model proteins as well as real cases; the use of nanoparticles as crystallization inducers (collab. ITQB (L.Rebello) and REQUIMTE (R. Franco)).

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MINISTÉRIO DA EDUCAÇÃO E CIÊNCIA

Main collaborations:: ITQB; FMV-UTL; IST; ITN  
Univ. Potsdam; Magrio Negri Institute Milan



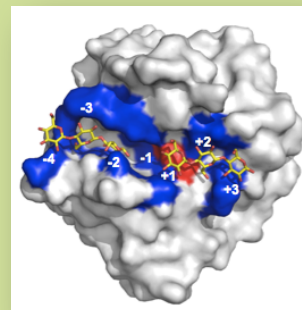
Molybdoenzymes



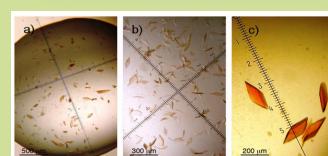
Mechanistic-relevant forms



CORMs Reactivity toward Proteins



Cellulosomal Proteins & Enzymes



Crystallization with IL