

X-ray crystallography facility

Dr. Thomas Monecke and Prof. Dr. Dierk Niessing

Institute of Pharmaceutical Biotechnology
Room 2.028, James-Franck-Ring N27, 89081 Ulm

universität
ulm



Contact



Dr. Thomas Monecke

Office: 2.069

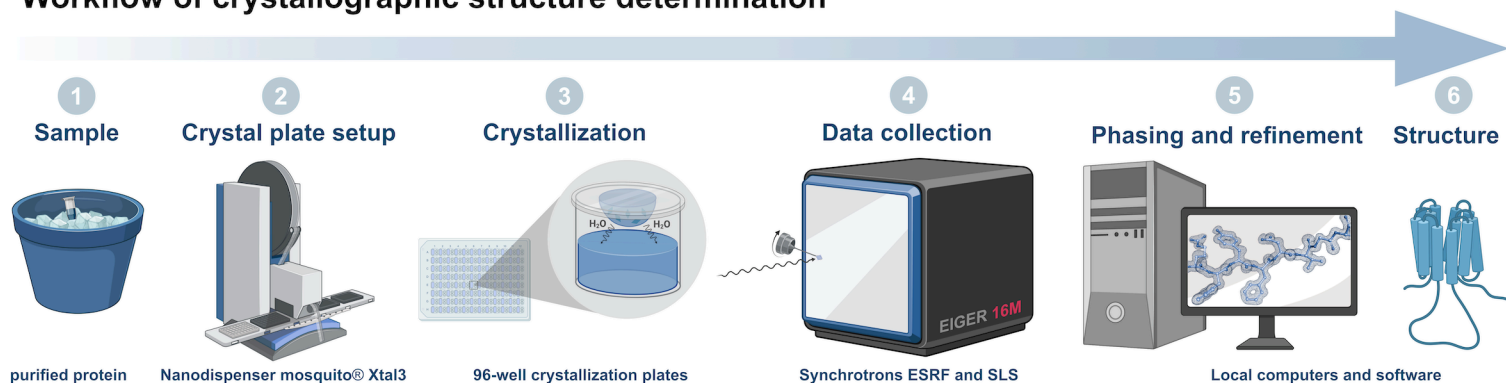
Email: thomas.monecke@uni-ulm.de

Tel.: (0731-50) 23163

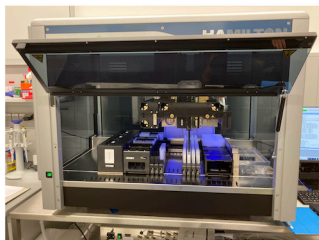
General considerations for the crystallization of proteins

- purified protein (purity >95%)
- monodisperse sample without aggregates or co-purified DNA/RNA contaminants
- typical concentration range: 2-20 mg/mL
- volume for complete initial screening: 320 μ L (200 nL/drop)
- salt concentration as low as possible
- add reducing agent if necessary (e.g. 2 mM DTT or β -Mercaptoethanol)
- low buffer concentration (typically 20 mM)
- no phosphate buffers
- usage regulations at www.uni-ulm.de/nawi/institute-of-pharmaceutical-biotechnology

Workflow of crystallographic structure determination



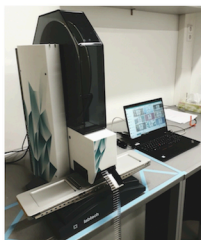
Equipment of the X-ray crystallography facility



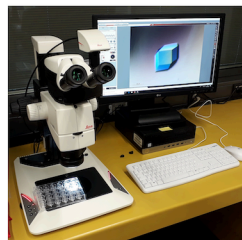
Liquid handling station
Hamilton Microlab STAR



Crystallization screens
Commercially available crystallization screens comprising 800 different conditions



Nano-crystallization robot
TTP labtech Mosquito Xtal3



Stereo Microscopes
Leica M165C (MC170 HD cam) and Olympus SZX16

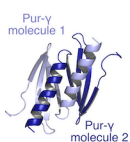


Plate incubator
Rumed

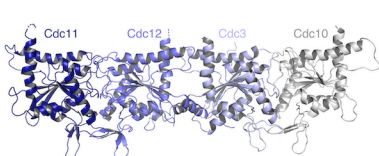


Crystal storage dewar
Worthington HC35

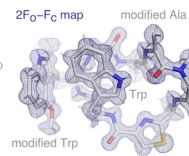
Selected structures of the crystallography facility and the Niessing lab



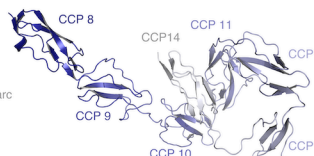
1.05 Å X-ray structure of the human Pur-y repeat III dimer



3.33 Å X-ray structure of the yeast quaternary septin complex Cdc11-Cdc12-Cdc3-Cdc10



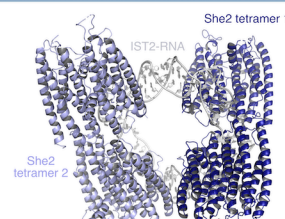
1.1 Å 3D electron diffraction structure of the modified cyclic octapeptide Arginyl D from *Myxobacteria*



2.13 Å X-ray structure of the human Complement Factor H CCP domains 8-15



2.03 Å X-ray structure of the mouse Pumilio 2 homology domain



3.41 Å X-ray structure of yeast She2 bound to the IST2-RNA localization element