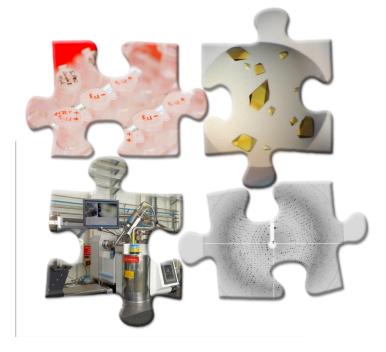
Integrated Pipelines for Ligand Screening





Jose A. Marquez

Head of the Crystallization Facility EMBL-Grenoble



Integrated Pipelines for Ligand Screening

 Crystallization and data collection occur at highly automated facilities ...



...but these operations are separated by manual steps

- ✓ Crystal mounting
 - Manpower & training
 - Loss of diffraction power
 - Time

- ✓ Data collection
 - Synchrotrons are sparsely distributed
 - Access to beam time every 1-3 months

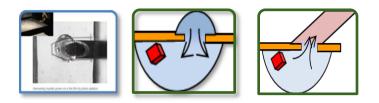


Integrated Pipelines for Ligand Screening

Integrated protein to X-ray data collection pipelines



CrystalDirect Crystal Mounting & Processing



MASSIF Automated Data Collection





Integrated Pipelines for Ligand Screening Four Key Components

The HTX Lab

From Pure samples to Crystals



The HTX lab has supported 791 Scientists since 2003



200 Regular Users Over 600 registered scientists



1.900 samples processed per year



IF



990.000 Crystallisation Experiments per year



Access to European Researchers Through





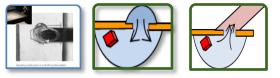
Integrated Pipelines; Four Key Components

The HTX Lab

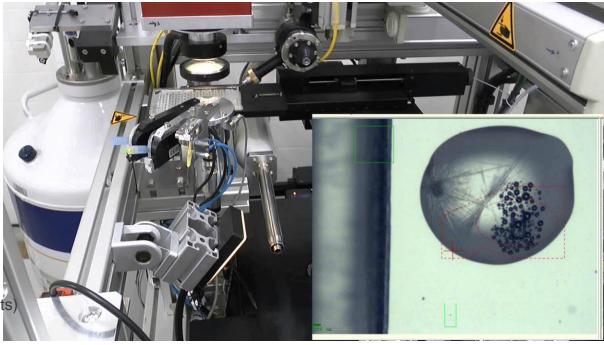
From Pure samples to Crystals



CrystalDirect Crystal Mounting & Processing



- Automated Crystal Harvesting
- Direct Cryocooling (no cryo protectants)
- Reduced mechanical stress
- Reduced background
- Multicrystal mounting
- Crystal Surgery

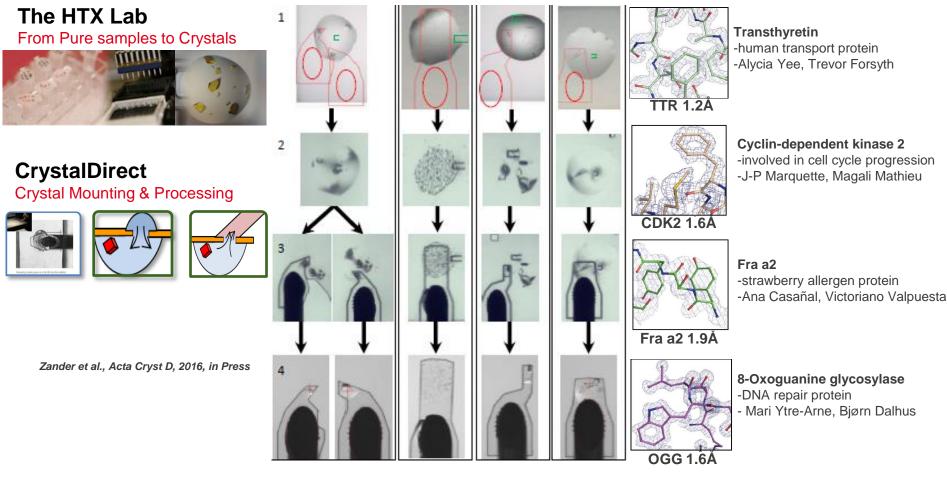


Zander et al., Acta Cryst D, 2016, in Press



Integrated Pipelines; Four Key Components

Available to all users of the THX lab



Over 5000 crystals processed !



CrystalDirect Crystal Soaking Through Controlled Diffusion

Zander et al., Acta Cryst D, 2016, in Press

Phasing agents Ligands K33 E81 E81 3.0 27 F82 K33 80 F80 K33 30 E81 2.1 E81 3.2 F82



Integrated Ligand Screening Four Key Components

Matthew Bowler Staff Scientist

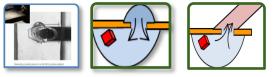


The HTX Lab

From Pure samples to Crystals



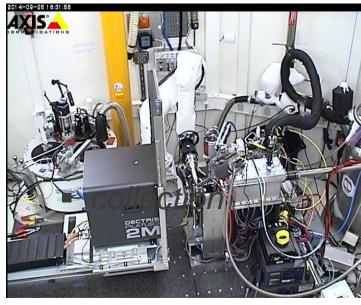
CrystalDirect Crystal Mounting & Processing



MASSIF Automated Data Collection



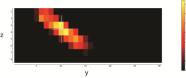
ESRF MASSIF 1



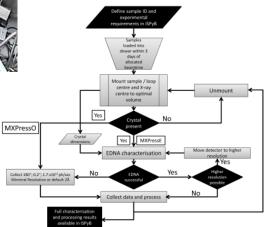
Hands-off data collection

150 Samples per session





Automated workflows





Integrated Pipelines for Ligand Screening Four Key Components

The HTX Lab

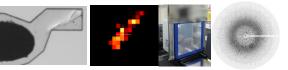
From Pure samples to Crystals



CrystalDirect Crystal Mounting & Processing



MASSIF Automated Data Collection



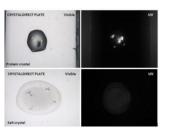
Software CRIMS & ISPyB

CRIMS© CRystallization Information Management System developped by EMBL Grenoble



The Crystallization Information Management System





CRIMS© CRystallization Information Management System developped by EMBL Grenoble

- Sample evaluation
- Screening
- Optimization
- Crystal Mounting
- From pure sample to mounted crystals
- Operating at EMBL, HD, HH & GR
- Licensed to 10 other laboratories

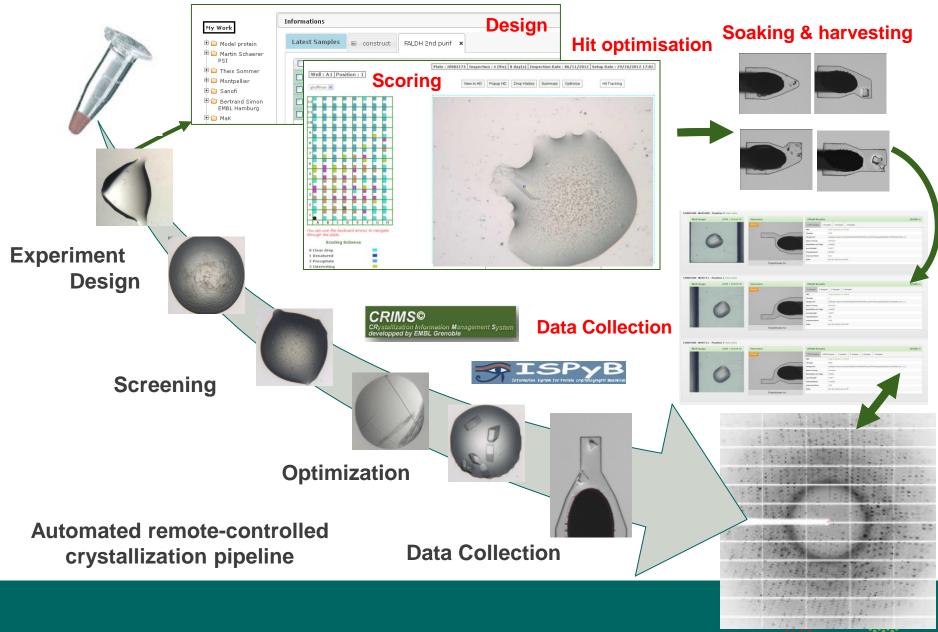
ISPyB Beamline Data management system



- Data Collection
- Data Processing
- Reporting



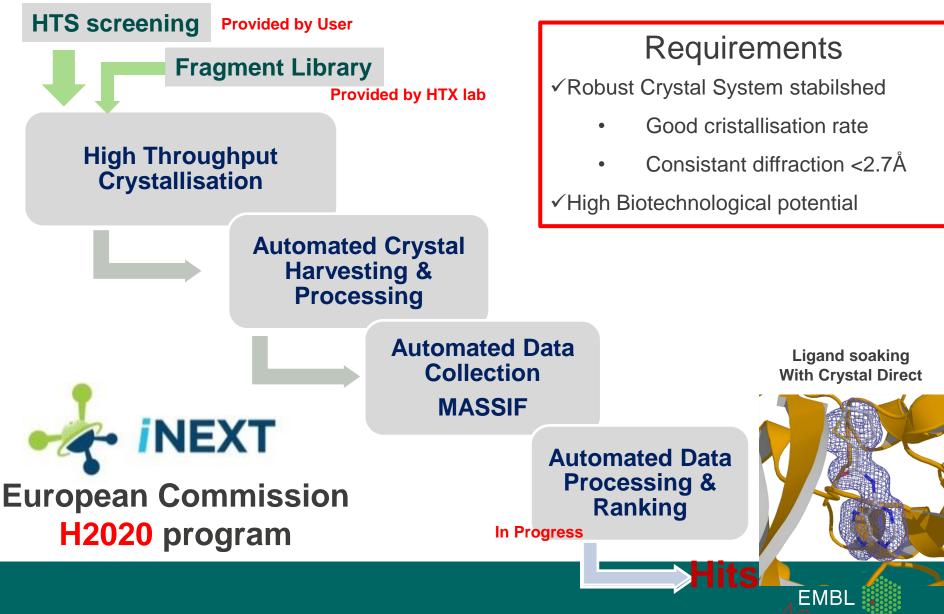
Remote Crystallography Pipeline



YEARS | 1974-2014







Thank you!

• The HTX Lab

- Irina Cornaciu
- Peter Murphy
- Guillaume Hoffmann
- Vincent Mariaule
- Sonia Rodriguez Puente
- Gael Seroul*
- Aine Barry
- Zuzanna Kaczmarska

Diffraction instrumentation team

- Florent Cipriani
- Jérémy Sinoir
- Christophe Landret*
- Gergely Papp
- Franck Felisaz
- Marcos Lopez Marrero
- Clement Sorez
- Christopher Rossi
- Robert Janocha
- * Former lab members



Synchrotron crystallography team

- Andrew Mc Carthy
- Matthew Bowler
- Alejandro De Maria Antolinos
- Max Nanao
- Adam Round

ESRF

- Gordon Leonard
- Christoph Mueller-Dieckmann
- Didier Nurizzo
- Olof Svensson
- Ulrich Zander
- Stephanie Malbet-Monaco



