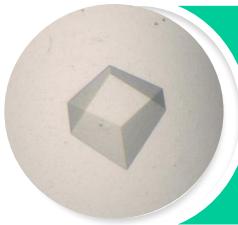


Communicating between multiple synchrotrons and home labs

Peter Murphy
Marquez Team
EMBL Grenoble



The Marquez Team, EMBL Grenoble Outstation

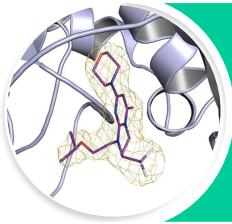


Services

Data Management



Automated Crystallography



Research

CRIMS CRystallization Data Management

HTXLab

CRIMS®
Data Management System

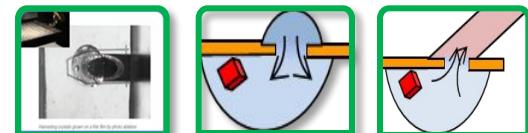
Installed in 10
labs in Europe!

The HTX lab

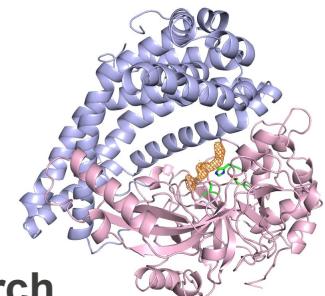
Automated, remote-controlled crystallization



CrystalDirect™ Crystal Mounting & Processing



Protein-to-structure pipelines



Research
13 Publications

CRIMS

The CRystallization Information Management System

- Web Application for crystallization laboratories
- Design and evaluation of experiments
- Integration of laboratory robots
- Automated data flow
- Operator interfaces

- EMBL Collaboration



Grenoble Hamburg Heidelberg
791 282 100

- License to 7 non-EMBL laboratories
- Weizmann : 158
- CNRS GIF : 18
- CNRS IBBMC : 29
- CNRS CBS : 30

....

More than 1500
users !

CRIMS[®]
CRystallization Information Management System
Developed by EMBL

Imaging (vis/uv)

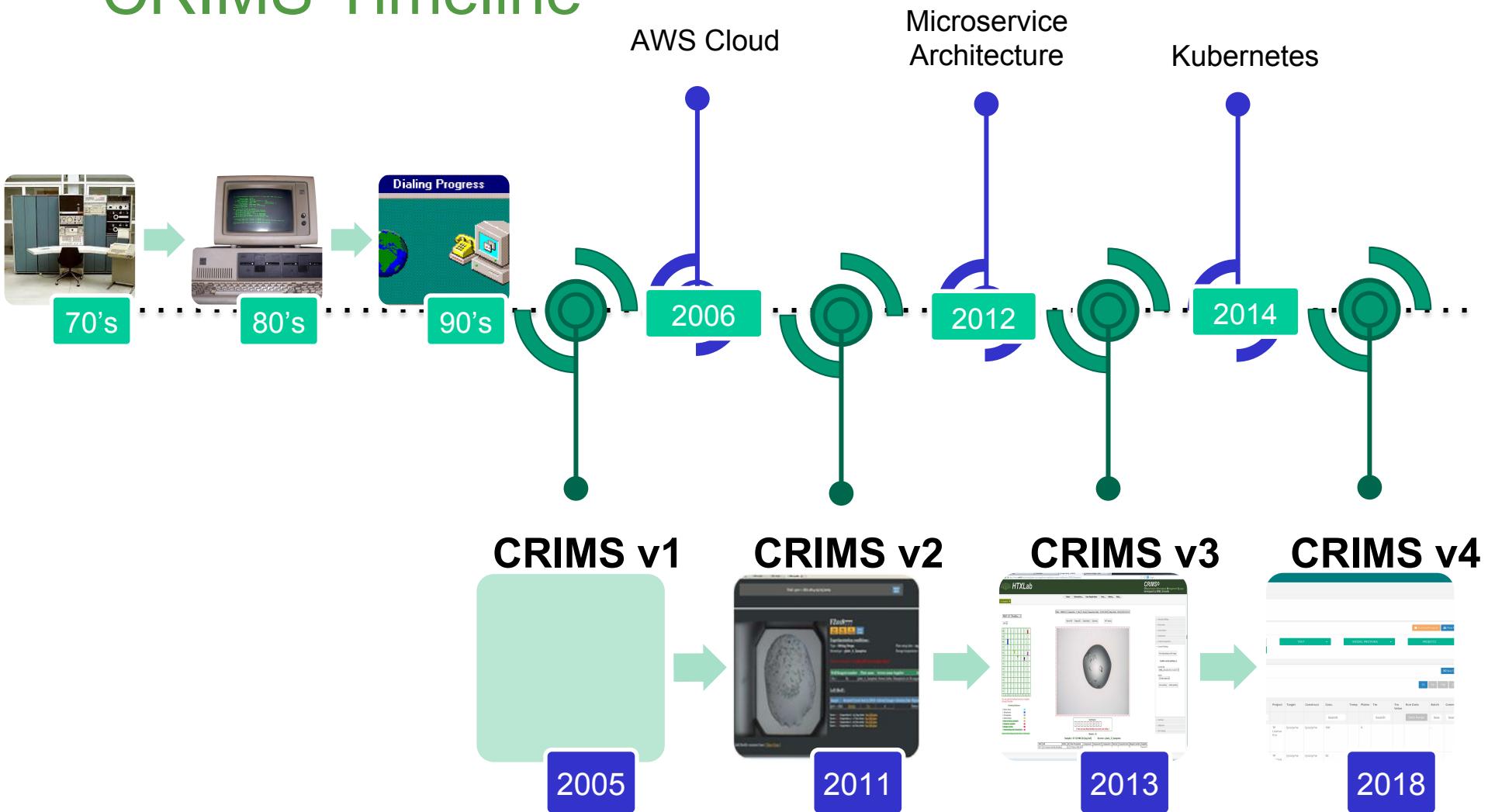


Automated crystal optimization

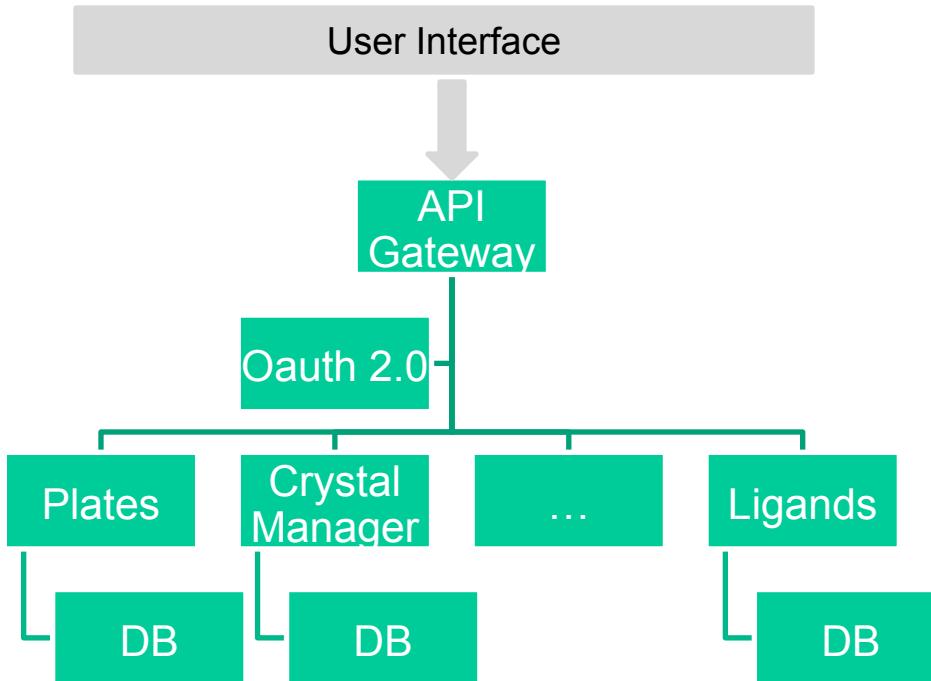
EMBL



CRIMS Timeline



CRIMS v4



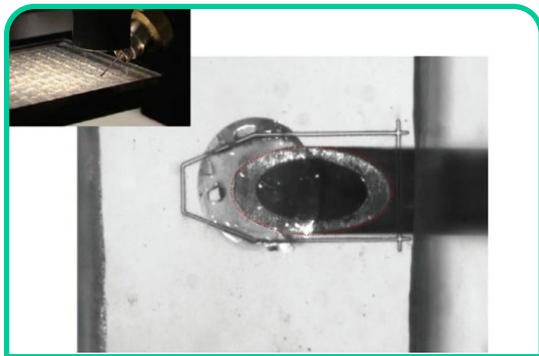
- Smaller application
- Easier to understand
- Modular (single responsibility rule)
- Choose the best tools for the job

Crystal Manager



Integrating crystallization and data collection

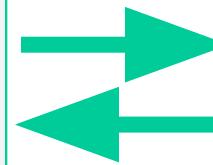
New Technologies
Automated Crystal Harvesting CrystalDirect



Zander et al., 2016

Data Management
CRystallization Information Management System (CRIMS[®])

Two screenshots of the CRIMS software interface. The top screenshot shows a 3D model of a crystal and a data entry form for a plate. The bottom screenshot shows another view of the crystal and a different data entry form.



ESRF
Grenoble



PETRAIII
Hamburg

CRIMS
Developed by EMBL
Crystallization Information Management System

First CRIMS-ISPyB API Implementation 2011

Manual Crystal Mounting

The screenshot shows the ISPyB software interface for manual crystal mounting. It includes:

- A main window displaying a crystal image and a "Send to ISPyB" button.
- A zoomed-in view of the crystal labeled "FZ018777".
- An "Add/Modify comment lines" button.
- A "Create a shipment for ISPyB" dialog box containing:
 - "Mounted Crystals not already sent to synchrotron":

Select	Sample	Barcode	Row	Column	Shelf	Datamatrix	Position in basket	Cryo conditions
<input type="checkbox"/>	PYL5	FZ018150	D	09	1	545454	4	35nhuh
<input type="checkbox"/>	PYL5	FZ018150	D	09	1	AA001GD2345	1	20 % Glycerol in 10% steps
<input type="checkbox"/>	PYL5	FZ018150	D	09	1	AA002GD1234	1	20% glycerol in 10% steps
<input type="checkbox"/>	PYL5	FZ018150	D	09	1	65454546+4	4	I;kl
<input type="checkbox"/>	PYL5	FZ018150	D	10	1	46262	1	pI[pl
<input type="checkbox"/>	PYL5	FZ018171	A	09	1	09890	i	10 gly
	Pyrl + Delta HAB1 + ABA	FZ018939	C	08	3	76798-09	1	15 glyc
 - "Mounted Crystals already sent to synchrotron":

Select	Sample	Barcode	Row	Column	Shelf	Datamatrix	Position in basket	Cryo conditions
<input type="checkbox"/>	CMNVI	FZ017448	D	01	2	f7382823	2	no cryo
<input type="checkbox"/>	CMNVI	FZ017448	D	01	2	f7898332	1	glycerol 20%
<input type="checkbox"/>	CMNVI	FZ017448	D	02	2	e4203232-	3	no cryo
<input type="checkbox"/>	MLHproteoPep	FZ015568	D	03	2	738273273827	1	Glyce 30%
<input type="checkbox"/>	MLHproteoPep	FZ015670	C	06	2	21818919	2	no cryo
<input type="checkbox"/>	pyrl + ABA	FZ018777	B	11	1	HA00AP3183	1	Cryo test freeze
<input type="checkbox"/>	pyrl + ABA	FZ018777	C	01	1	HA00AP9482	2	no cryo
 - "Select all" and "Unselect all" buttons.
 - "Send Selected as Shipment" and "Delete selected" buttons.



Gael Seroul (EMBL)
Ludovic Launer (ESRF-UK)



CRIMS-ISPyB API V2

2014

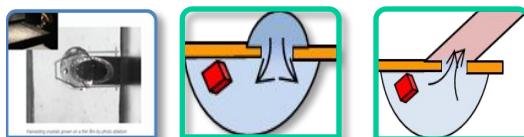
The HTX Lab

From Pure samples to Crystals



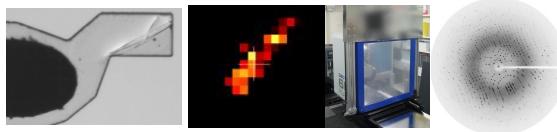
CrystalDirect

Crystal Mounting & Processing



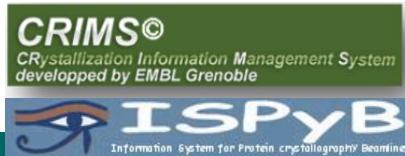
MASSIF

Automated Data Collection



Software

CRIMS & ISPyB



Alejandro de Maria (ESRF)
Solange Delageneire (ESRF)

EMBL

New Requirements

- Richer Information
 - More experimental parameters (Spacegroup, Redundancy...)
 - Workflows
 - Beamlines



Connect

- .. Select Facility
- .. User/Password
- .. Set ISPyB naming

Pucks

- .. Select Pucks
- .. Set acronyms

Parameters

- .. Set parameters

Shipments

- ☐ Users can log in with assigned proposal mx

1 Shipment Information 2 Pucks 3 Preview

→ Sign In ⏺ Cancel

Authenticate Or Create using the Following

Facility: ESRF INEXT

Proposal *: mx HTX

Password: ⏺ Cancel

Continue No Password

Shipments

- ☐ reusing home lab data to send pucks (no manual entry)

The screenshot shows the 'Shipments' module in the CRIMS system. The top navigation bar includes a search bar and a 'Shipments' icon. Below the header, the breadcrumb navigation shows 'Dashboard / Shipments / New'. The main content area is titled 'Shipments' and displays the '2 Pucks' step of a three-step process. The steps are indicated by tabs at the top: '1 Shipment Information' (disabled), '2 Pucks' (selected, highlighted in green), and '3 Preview'. On the right, there are buttons for 'Cancel', 'Previous', and 'Next'. The central part of the screen is divided into two sections: 'Available Pucks' on the left and 'Pucks to be Shipped' on the right. The 'Available Pucks' section contains a search bar and a list of pucks with their acronyms and position counts:

Puck Acronym	Positions
AA277A	1 positions >
AA276A	5 positions >
AA029A	2 positions >
AA035A	1 positions >
AA317A	1 positions >
AA000A	1 positions >

The 'Pucks to be Shipped' section is currently empty. A note above the puck list says: 'Add your Pucks to this Shipment. Drag the Pucks that you wish to ship to the container on the right.' Below this, there are three status indicators with corresponding icons: a green square for 'All Crystals in the Puck have a Valid Acronym', a red square for 'One or more Crystals in the puck do not have a Valid Acronym (Puck cannot be shipped)', and a grey square for 'The Puck is already involved in a Shipment (Puck cannot be shipped)'.

Shipments

- easy control of data collection parameters for hundreds of pins

Screenshot of the Shipments application interface showing the 'Advanced Options' section. The 'Advanced Options' section is highlighted with a green bar at the top. Four arrows point from the text below to specific controls in this section: 'Force Space Group', 'Workflow', 'Required Multiplicity', and 'Xtals per Pin'. Below this section is a table listing shipment details for three samples.

Choose a Beamlne:
Massif

Edit Naming Convention

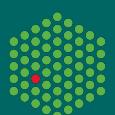
Puck AA032A

Advanced Options

Position	Sample	ISPyB Name	Xtals in Pin	Acronym	Spacegroup	Workflow	Multiplicity	Beamsize	Info
1	PgWT	_CD020145_C02-2 Comments	1		- Force the Spacegroup -	- Choose a Workflow -	4	50	i
1	PgWT	_CD020145_C02-2_2 Comments	1		- Force the Spacegroup -	- Choose a Workflow -	4	50	i
10	PgWT	PgDPP1__CD020145_C11-3 Comments	1	PgDPP1	- Force the Spacegroup -	- Choose a Workflow -	4	50	i

Crystal Manager Interface

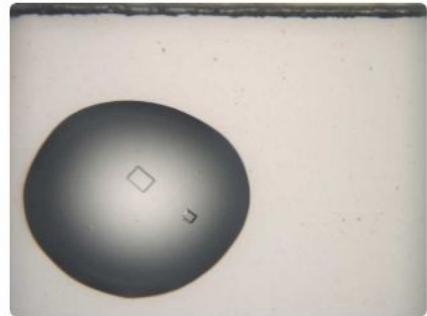
EMBL



Multi-crystal data collection

20170918_Pdomain — CD020585 — A04-3

♀ ID30A-1 ♂ 2017-10-04 08:39:00



Drop [View Drop](#)

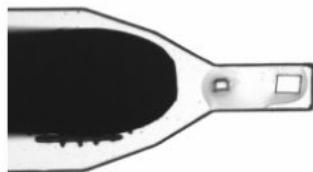


Plate CD020585

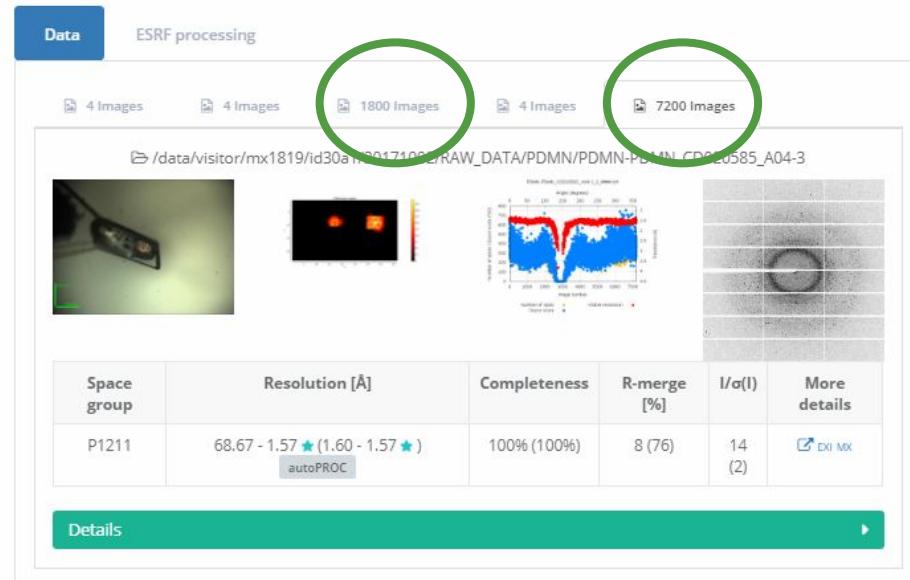
Drop A04-3

CD020585 -- A04-3

Component	Conc.	pH	Type

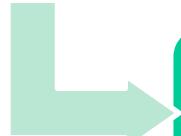
[View Harvesting Images](#)

Puck AA267A
Position 10
Status Recycled on 2017-11-24 13:10:06
Date 2017-09-29 14:05:00
Shipment DMSO validation PDMN



Integrated Pipelines for Ligand Screening

High Throughput Crystallization



Automated Crystal Soaking & Harvesting



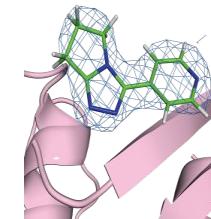
Automated Data Collection
(MASSIF, ESRF)

- Large amount of crystals sent to synchrotrons
- Crystal pedigree important for data processing
- Customized data collection and data processing



Automated Data Processing & Ranking

PIPEDREAM
✓ autoPROC
✓ Buster
✓ Rhofit



CRIMS

Developed by EMBL

Crystallization Information Management System

GΦL

Global Phasing Limited

*Gérard Bricogne
Andrew Sharff
Clemens Vonrhein
Leigh Carter
Rasmus Fogh*

Automated Data Flow

Dealing with hundreds to thousands of datasets!

CRIMS[©]
CRystallization Information Management System
developed by EMBL Grenoble



Home lab



PIPEDREAM

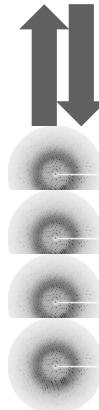
API



API



Synchotron



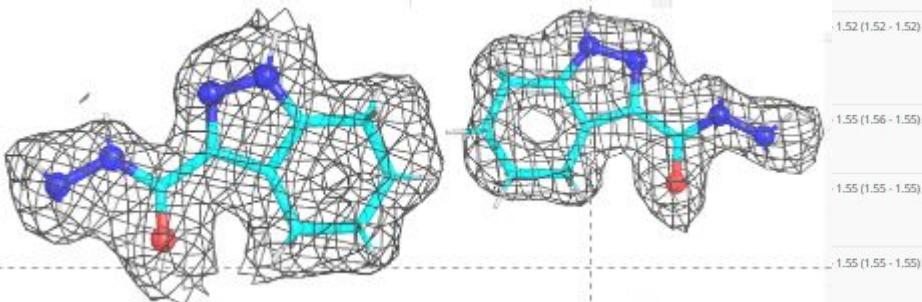
Pipedream Server

- ✓ Automated data transfer
- ✓ Pipedream initiated automatically
- ✓ Multiple space groups & ref datasets

Ranking, interpretation & validation

e ⁻ density	Traffic light :	Action :	Status :	Ligand code :	Resolution :	Res. limits :	R merge :	MR score :	Buster R :	Buster Rfree :	Bus
				msc2266930-1, msc2266930a-1	1.44 ★	44.12 - 1.44 (1.44 - 1.44) Å	0.024 (0.290)	54.7	0.202	0.2168	
				msc2267361-1, msc2267361a-1	1.46 ★	44.27 - 1.46 (1.46 - 1.46) Å	0.022 (0.257)	58.5	0.2032	0.2137	0.2228
				msc2267611-1, msc2267611a-1	1.48 ★	64.25 - 1.48 (1.49 - 1.48) Å	0.027 (0.278)	55.5	0.2111	0.2292	0.213
				msc2267282-1, msc2267282a-1	1.5 ★	49.48 - 1.50 (1.50 - 1.50) Å	0.019 (0.288)	51.3	0.2123	0.2291	
				msc1122779-2, msc1122779a-2	1.5 ★	64.49 - 1.50 (1.50 - 1.50) Å	0.021 (0.238)	63.1	0.2057	0.2243	
				msc2221541-1, msc2221541a-1	1.52 ★	49.58 - 1.52 (1.52 - 1.52) Å	0.035 (0.432)	57.6	0.2002	0.2216	
								60.8	0.1944	0.2114	
								56.1	0.2128	0.2391	
								52	0.2251	0.2433	
								67.6	0.1955	0.2155	
				msc2266930-1, msc2266930a-1	1.56 ★	49.76 - 1.56 (1.57 - 1.56) Å	0.034 (0.310)	58.6		0.2262	
				msc2255331-1, msc2255331a-1	1.56 ★	44.13 - 1.56 (1.56 - 1.56) Å	0.034 (0.310)	46.4		0.2509	
				msc2255303-1, msc2255303a-1	1.57 ★	64.26 - 1.57 (1.58 - 1.57) Å	0.034 (0.310)			0.2283	
				msc2267794-1, msc2267794a-1	1.58 ★	63.99 - 1.58 (1.58 - 1.58) Å	0.053 (0.421)	41.1		0.229	
				msc2266932-1, msc2266932a-1	1.58 ★	49.52 - 1.58 (1.59 - 1.58) Å	0.053 (0.421)	54.6		0.2542	
				msc2267227-1, msc2267227a-1	1.59 ★	49.58 - 1.59 (1.60 - 1.59) Å	0.023 (0.284)	Michal	Raphael	0.2212	

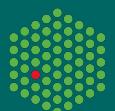
quick filtering and ranking of the potential hits



Michal

Raphael

EMBL



2017 - Present

The screenshot shows the CRIMS software interface. On the left, there's a sidebar with navigation options like Dashboard, Samples, Projects, Plates, User Manager, and Data Processing. The main area has tabs for Samples, Targets, and Projects. Under Samples, there's a table with columns for Sample ID, Project, Target, Concentration, Date, Time, Plates, Titre, Titre Value, Batch, Comments, and Constructs. Under Targets, there's a grid of targets labeled A through G, each with a color-coded legend. Below that is a table for Thaumatin_production with columns for Component, Concentration, pH, and Type. A large circular image on the right shows a crystal structure.

3,489 samples
&
6,001 Plates

This screenshot shows two overlapping windows. The top window is titled 'CS-1 Lysozyme 50 mg/ml' and shows a crystal image with harvesting paths overlaid. The bottom window is titled 'A1-1 Thaumatin_peter 18.4 mg/ml' and shows a similar crystal image with a harvesting tool icon. Both windows have tables for Harvesting, Manual Harvesting, and a Notes section.

13,744 pins

The screenshot shows the CRIMS software interface under the 'Shipments' tab. It includes a 'Sign In' form with fields for Username and Password, and options to 'Authenticate' or 'Create using the Following'. Below it is a table for a shipment titled 'Lysozyme_blue -- CD011909 -- ARI 2 -- Lyso(CD011909_ARI2.Green)' with columns for Drop, Date, Comp, and Status. Another table below it is for 'Lysozyme_blue -- CD011909 -- ARI 2 -- Lyso(CD011909_ARI2.red)'.

372 Shipments
&
10,130 Processed

Standard API

- Smaller labs are producing more and more crystals
 - More interest in the API's ispyb api
 - A need to standardise
- Meeting with ESRF, Diamond, Oulu In June
- We agreed that the RESTful API on github
<https://github.com/ispyb/ispyb-js-api>, should be the standard for all future developments.
- Wish to propose this to the rest of the ISPyB Developers Team

Future developments

- Connecting to more instances of ISPyB
- Transferring crystal coordinates to MXCuBE for fast crystal centring
- Automation of in situ data collection
- Implementing crystal groups and priorities
- Provide URL to Crystallisation experiment while at synchrotron

Acknowledgement



HTX Team

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- Guillaume Hoffmann
- Damien Clavel
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- Vincent Mariaule
- Florine Dupeux (IBS)

ESRF

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- Stephanie Malbet-Monaco
- Alejandro De Maria Antolinos
- Solange Delageniere

ISPyB Developers Team

Global Phasing Ltd.

- **Gérard Bricogne**
- Clemens Vonrhein
- Andrew Sharff
- Leigh Carter
- Rasmus Fogh

Synchrotron Crystallography Team

- **Andrew McCarthy**
- Matthew Bowler

EMBL Hamburg

- Ivars Karpics

DLS

- Neil Smith



Global Phasing Limited



Thank you for your attention

Peter Murphy
Marquez Team
EMBL Grenoble

