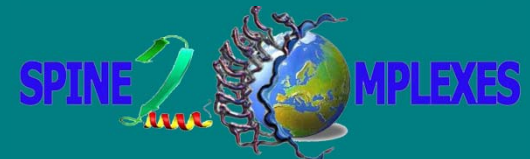


# GETTING BETTER DATA DIFFRACTION

## On line crystal dehydration

**Silvia Russi**

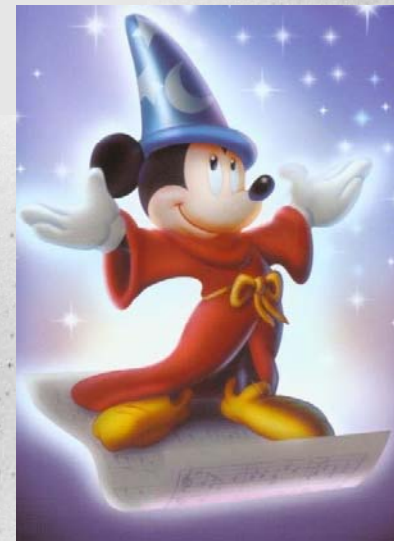
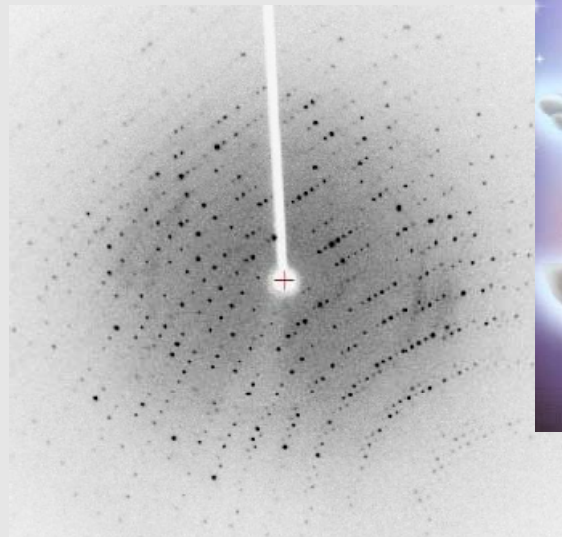
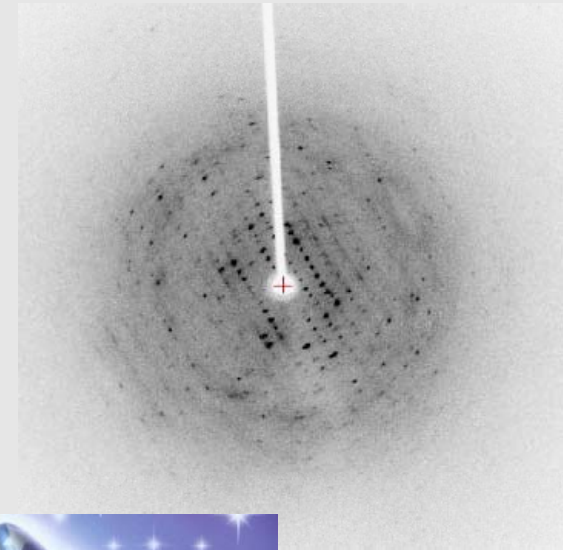
MX School “Getting the most from the ESRF MX Beamlines”  
February 2010



# Introduction

## *How to improve crystal diffraction ?*

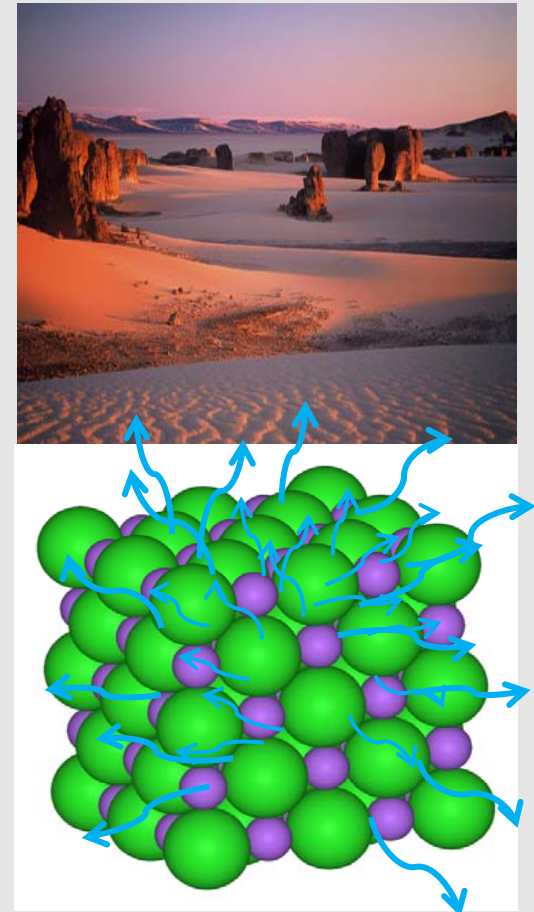
- ❖ Soaking with different compounds
- ❖ Cross-linking
- ❖ Crystal annealing
- ❖ Dehydration



# Introduction

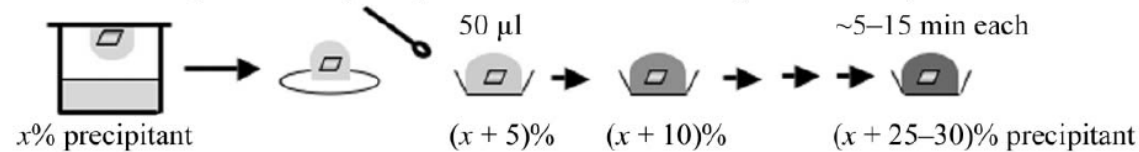
## *Crystal dehydration*

- ❖ Improves protein/solvent ratio
- ❖ Induces different packing (unit cell, space group)
- ❖ Improves the internal order of the lattice (mosaicity, diffraction power)
- ❖ Changes the behavior towards cryo-solutions

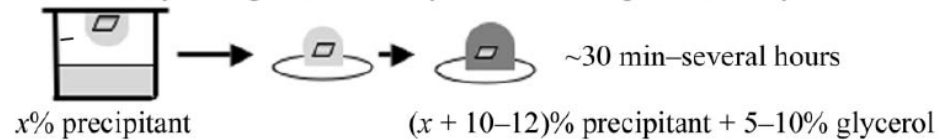


# How to dehydrate protein crystals ?

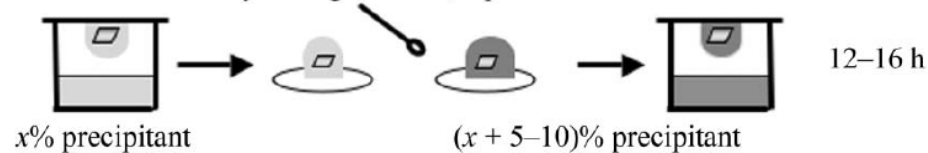
**Method 1:** Serial transfer to increasing concentration of precipitant; dehydrate either over reservoir or exposed to air (example increments and soaking times shown)



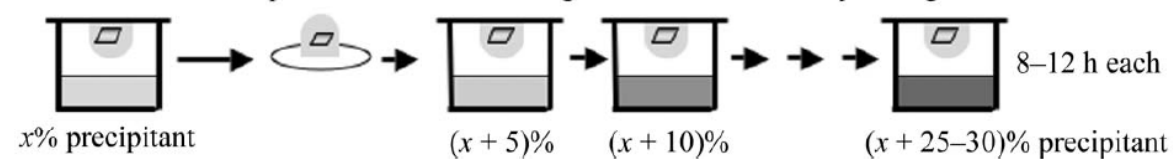
**Method 2:** Add dehydrating solution to crystallization drop and air dehydration



**Method 3:** Transfer to dehydrating solution, equilibrate over reservoir



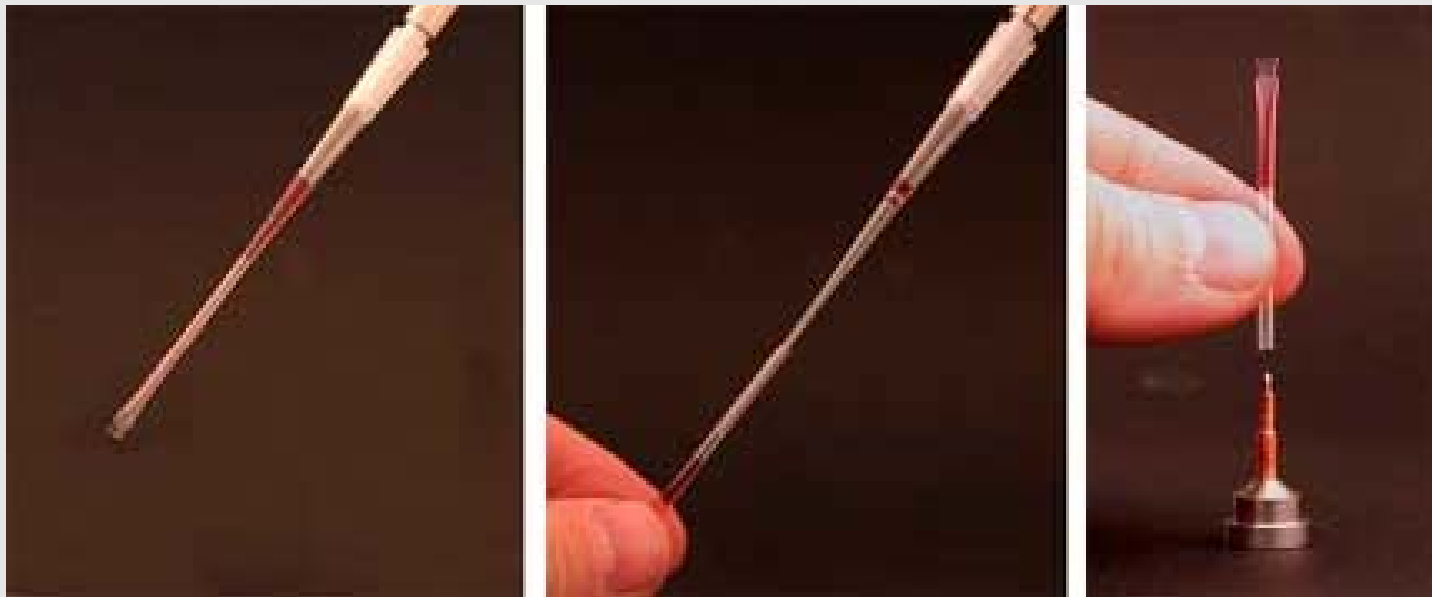
**Method 4:** Transfer cover slip to reservoirs containing serial increase of dehydrating solution



*Heras B., Acta Cryst. D61 (2005) 1173-1180*

## *How to dehydrate protein crystals ?*

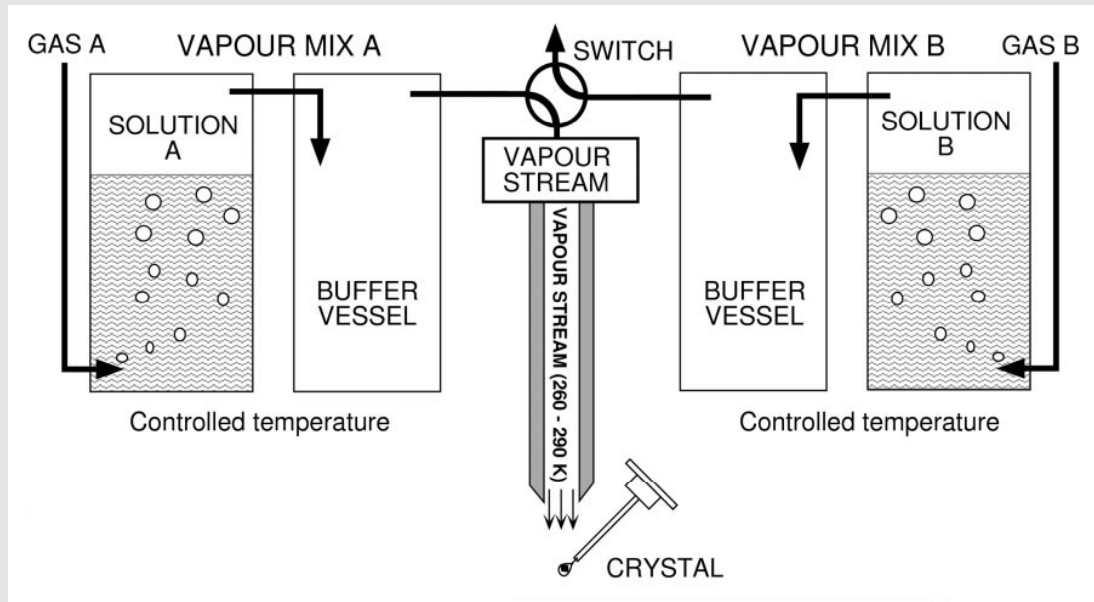
### The MiTeGen MicroRT system



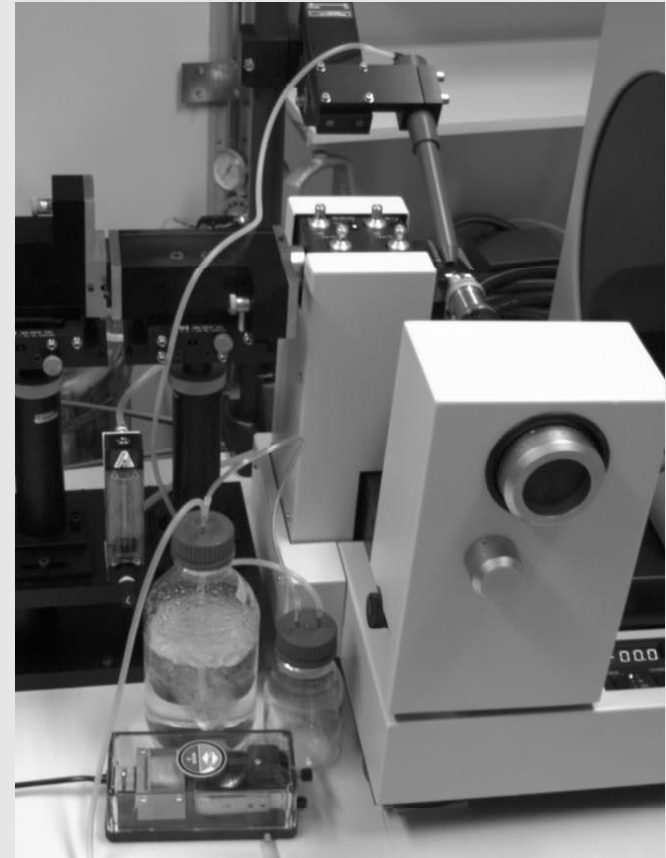
The crystal is equilibrated against a saturated salt solution of known RH during 1-2 hours.

# How to dehydrate protein crystals ?

## Dehydration using a vapor stream



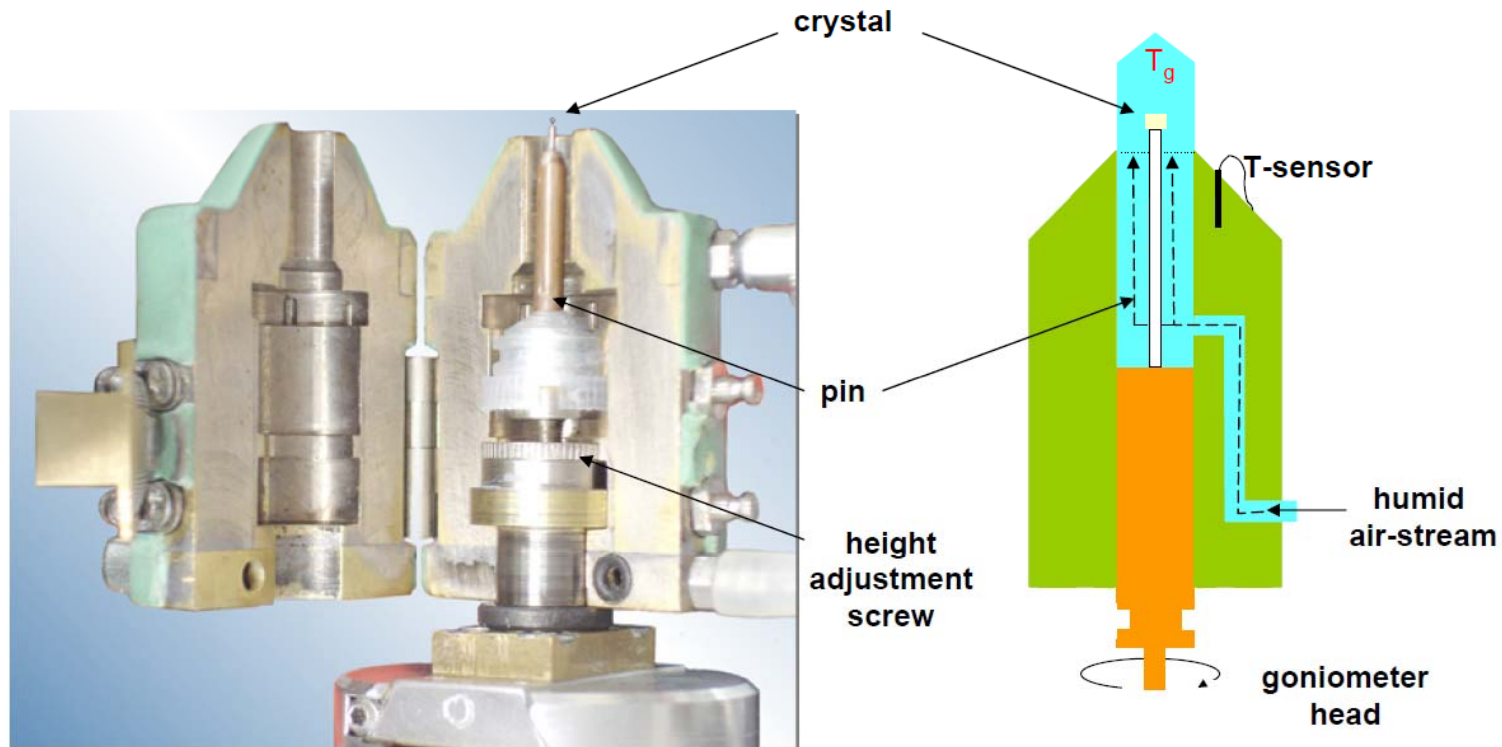
*Sjögren T., Appl. Cryst. 35 (2002), 113-116*





# *How to dehydrate protein crystals ?*

## Free Mounting System



 **proteros**  
biostructures

## *How to dehydrate protein crystals ?*

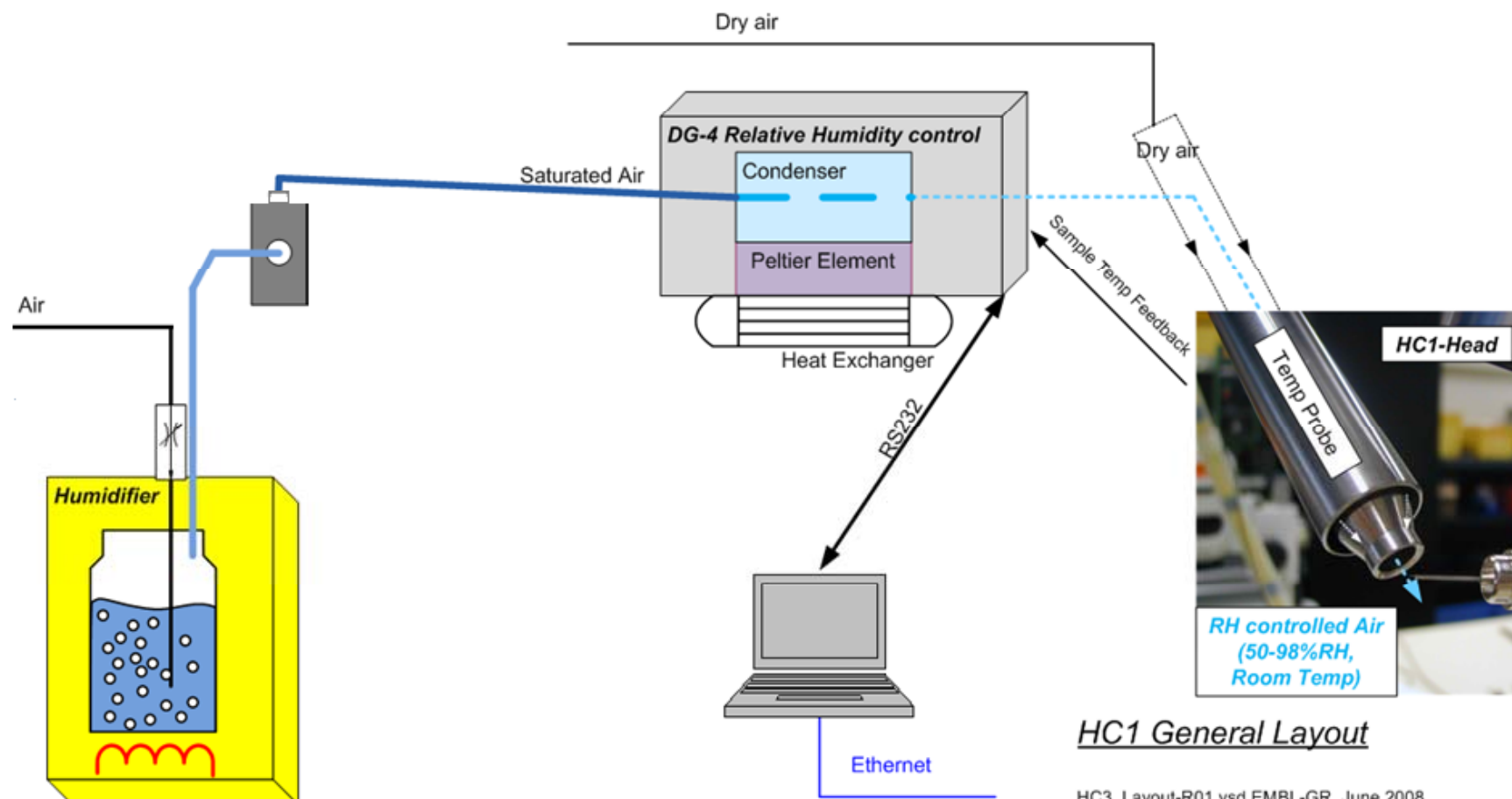
### **The humidity control device (HC1b)**

by the EMBL Diffraction Instrumentation Team

- ❖ Designed to be user friendly and completely adapted to MX beamlines
- ❖ Based on simpler but robust technology
- ❖ With similar, or better, performance to the FMS
- ❖ Available to all users of the ESRF



## The humidity control device (HC1b)



HC1 General Layout

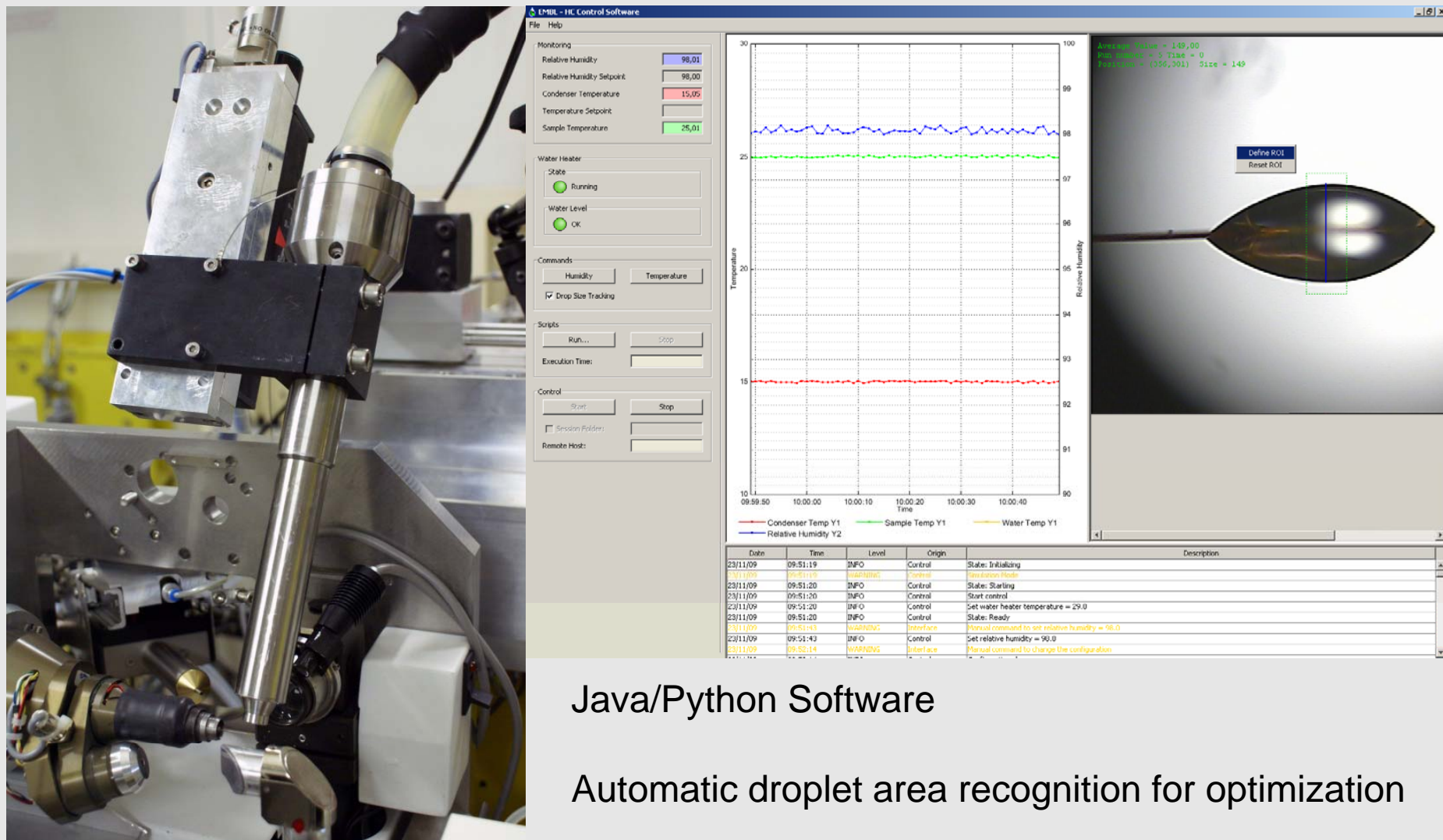
HC3\_Layout-R01.vsd EMBL-GR, June 2008



The device on site  
(BM14, ID14-1 or ID14-2)







Java/Python Software

Automatic droplet area recognition for optimization

## *Samples*

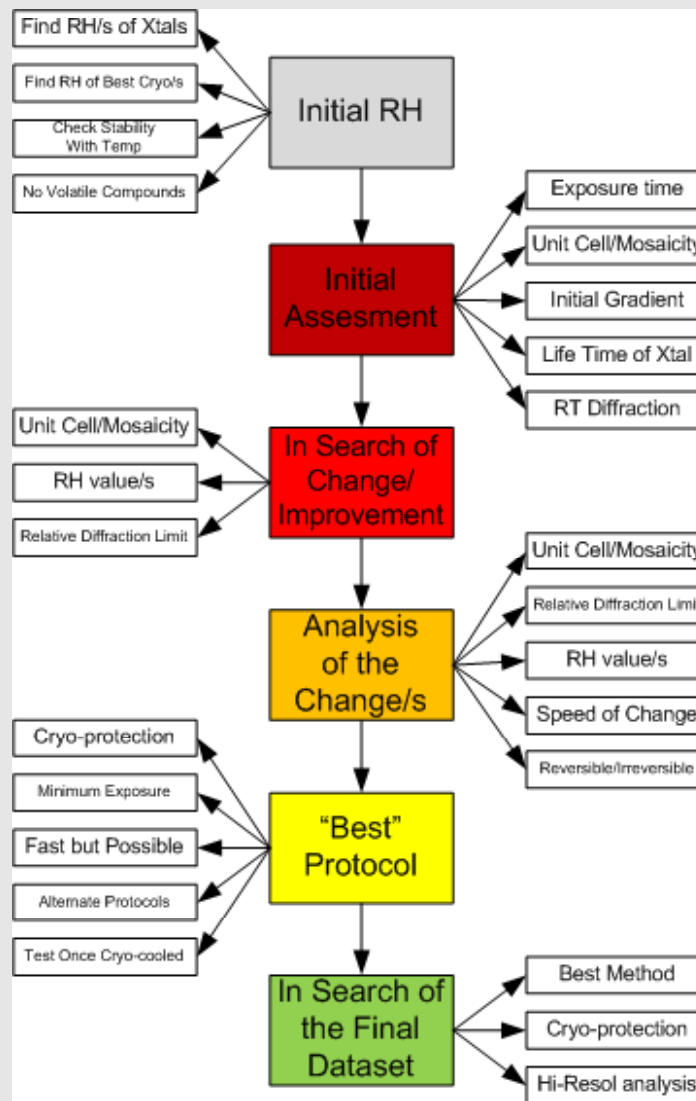
- ❖ The experiments are, for the moment, carried out at RT
- ❖ Crystals need to be stable between 20 and 25 °C
- ❖ Crystals need to be brought in their plates to the synchrotron or crystallized on site
- ❖ The crystallization condition can't include high amounts of volatile compounds

## *Samples*

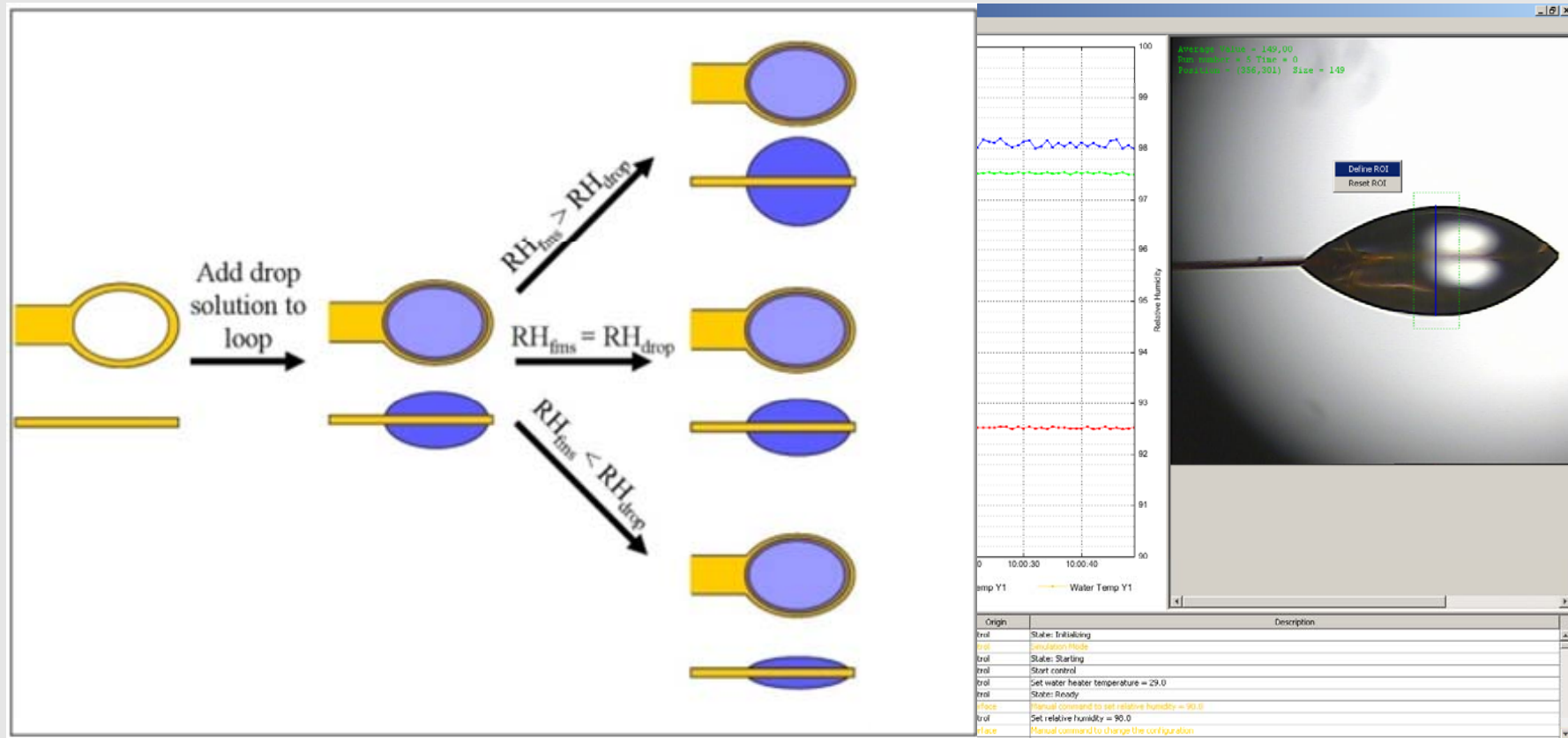
- ❖ Crystals need to have enough scattering power to be able to index the image/s
- ❖ Exposure time and flux need to be minimized to prevent radiation damage
- ❖ These experiments are time and crystal consuming so that a good stock of crystals is necessary

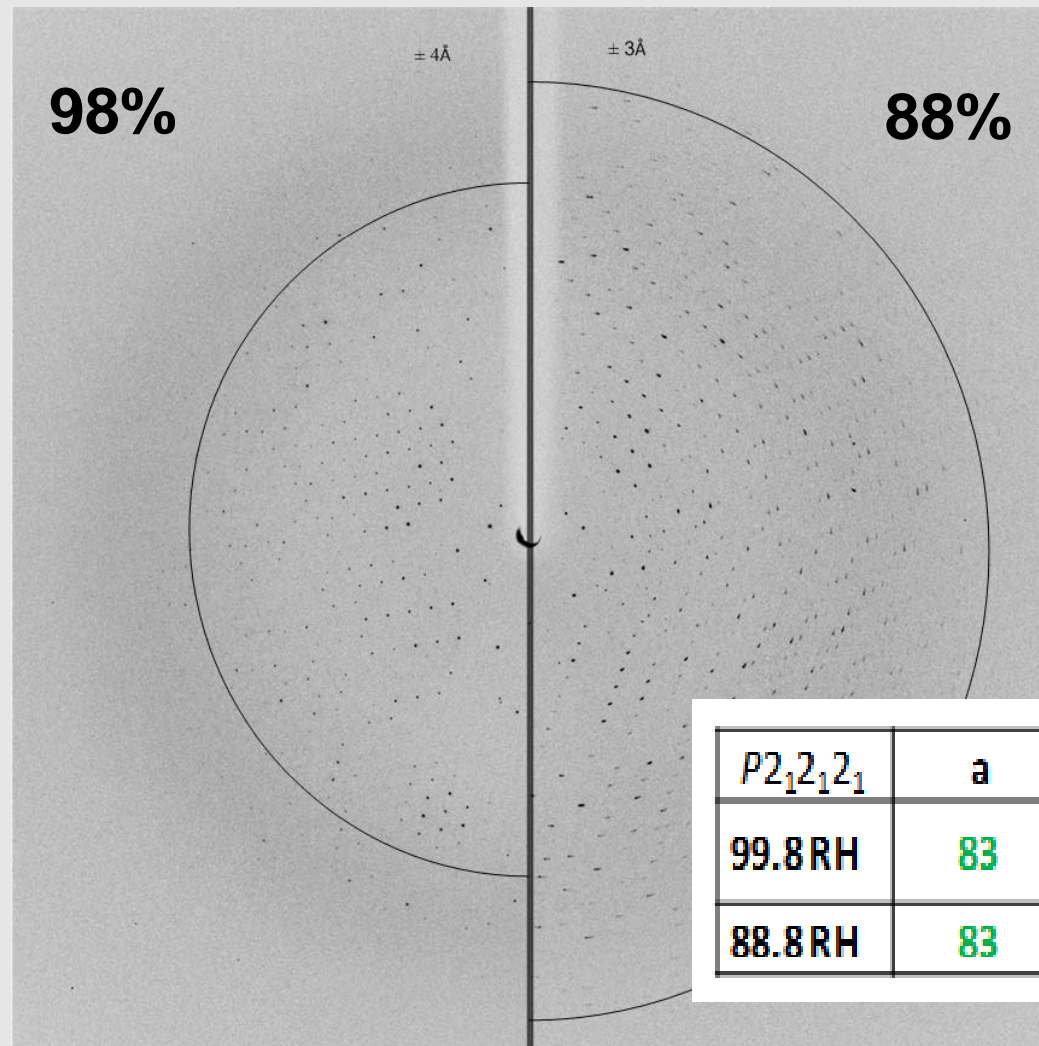


## The dehydration experiment workflow



## Determining the initial RH value



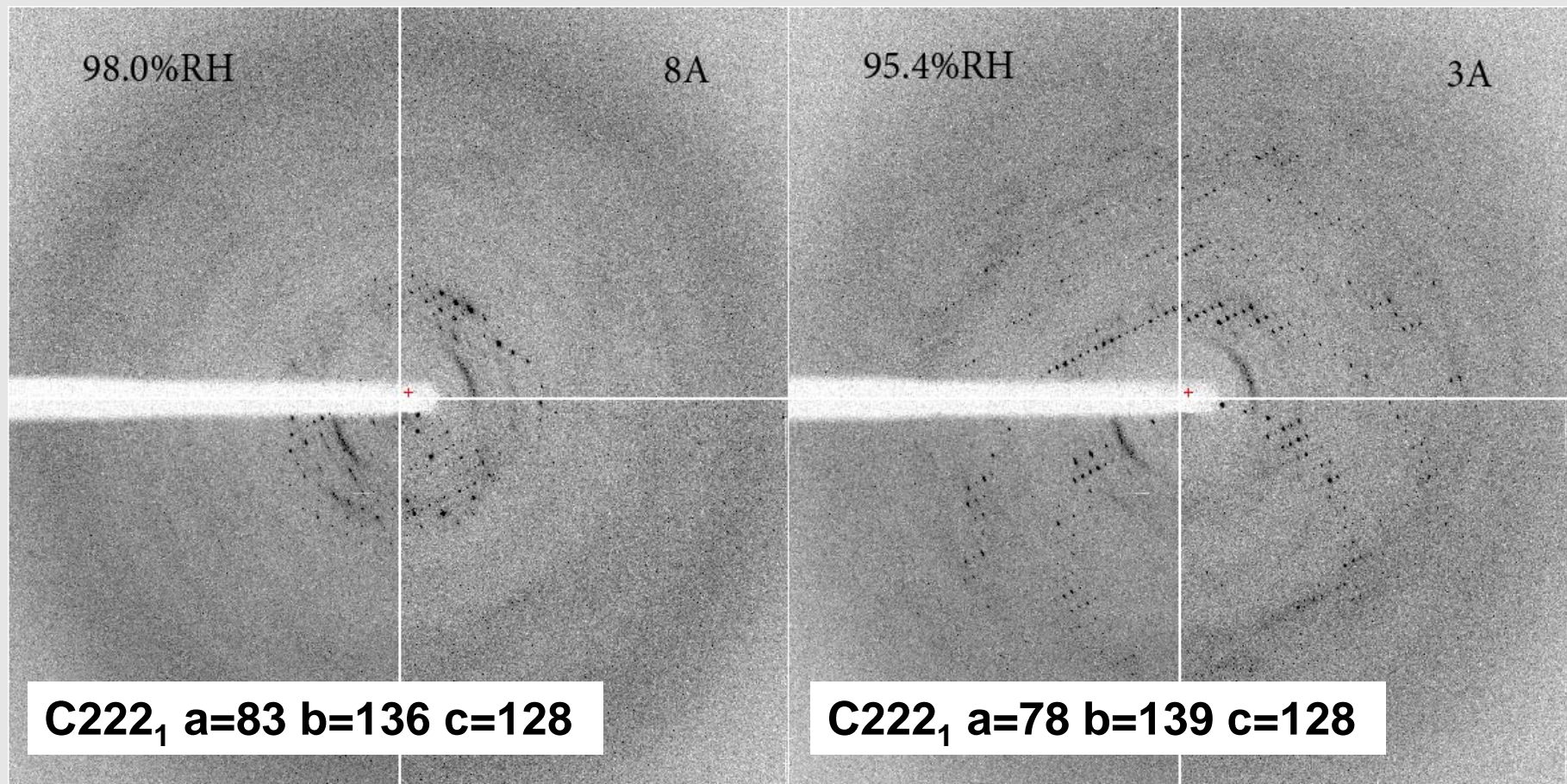


“Real life” cases ....

DNA polymerase III

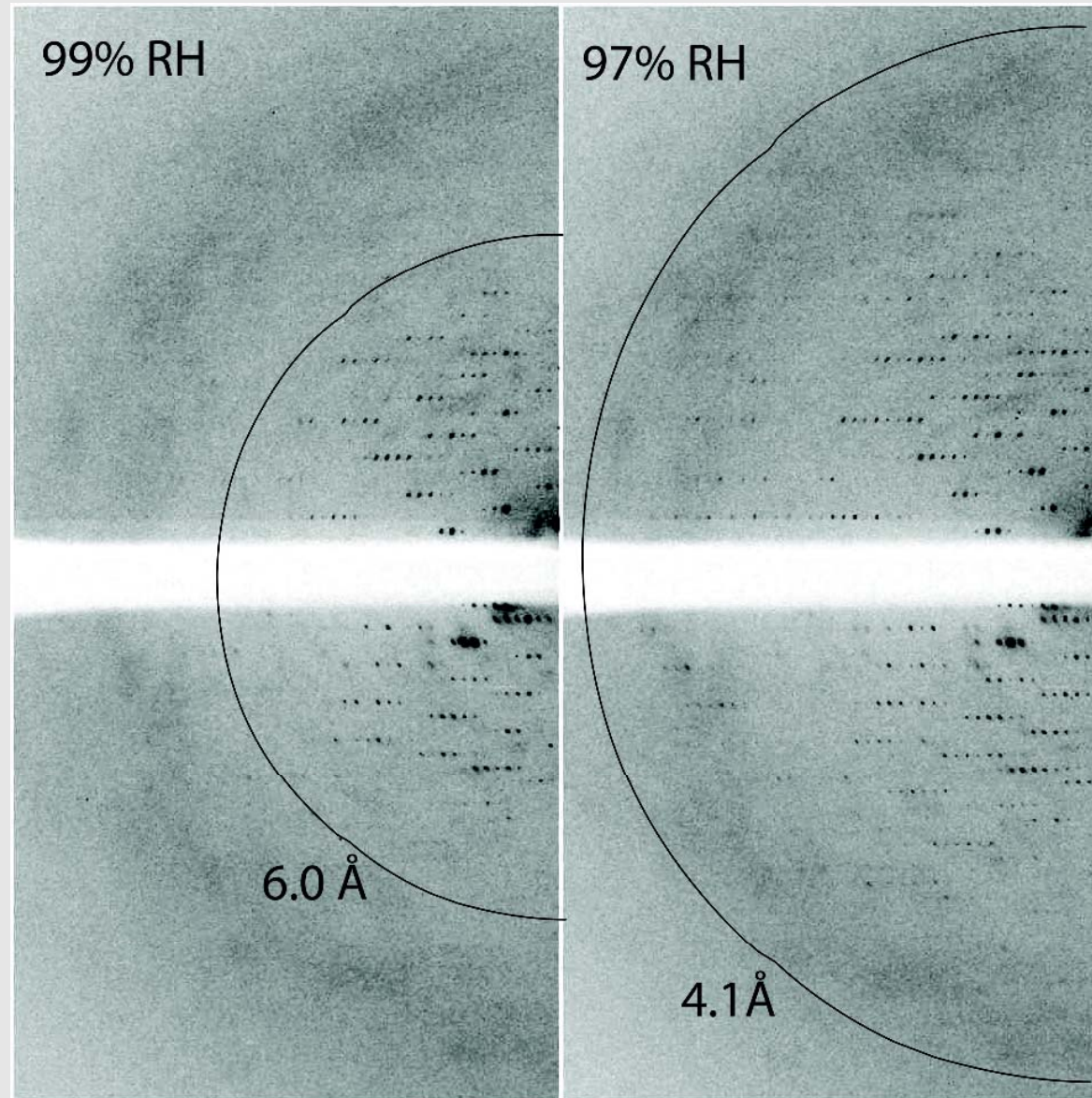
$P2_12_12_1$	a	b	c	Mos.	Res
99.8RH	83	99	144		
88.8RH	83	94	131	↓	↑





## Chromatin-modification complex





## Photosystem I

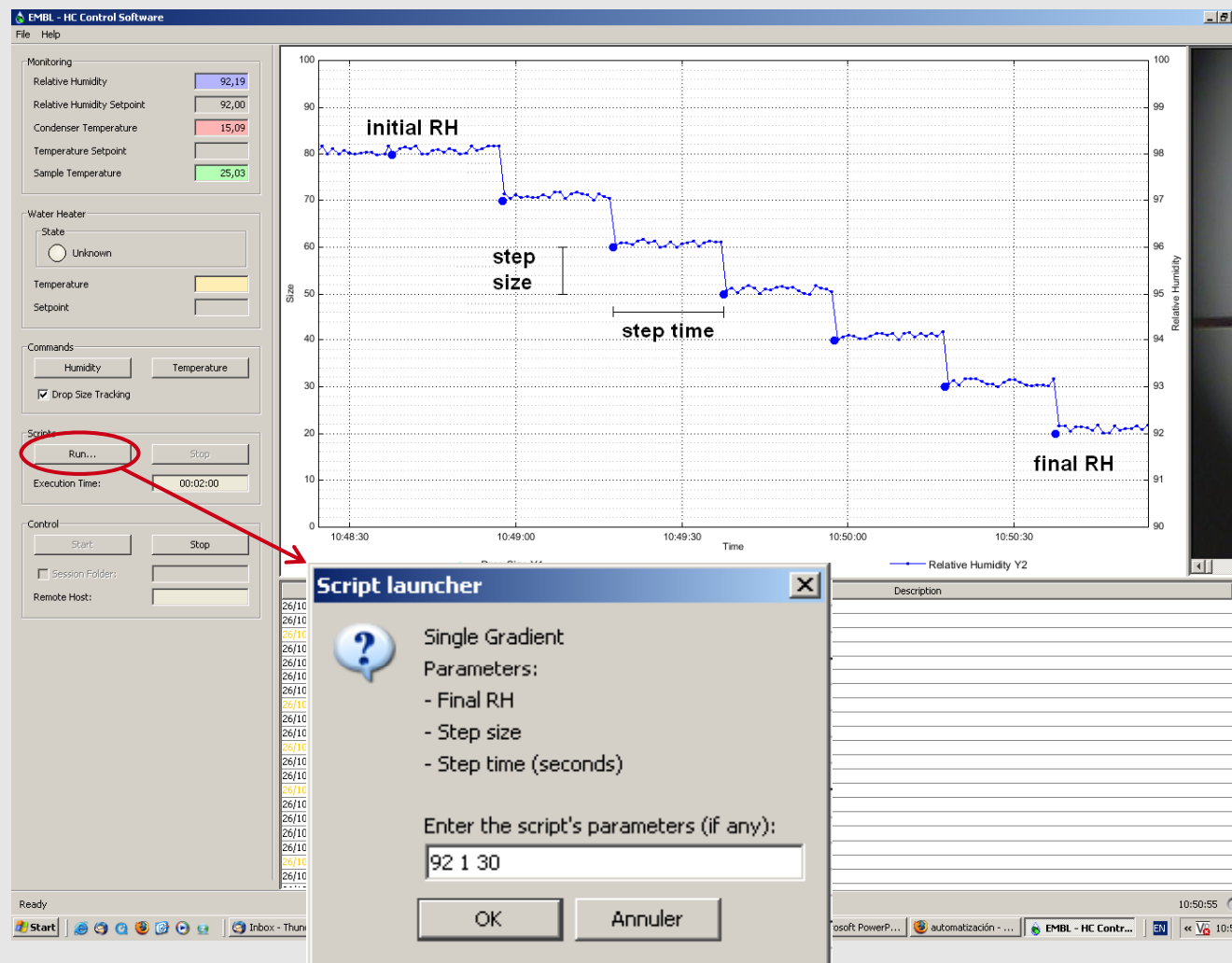
Multiprotein complex  
~ 500 kDa

# What's next ?





# HC1b Automation



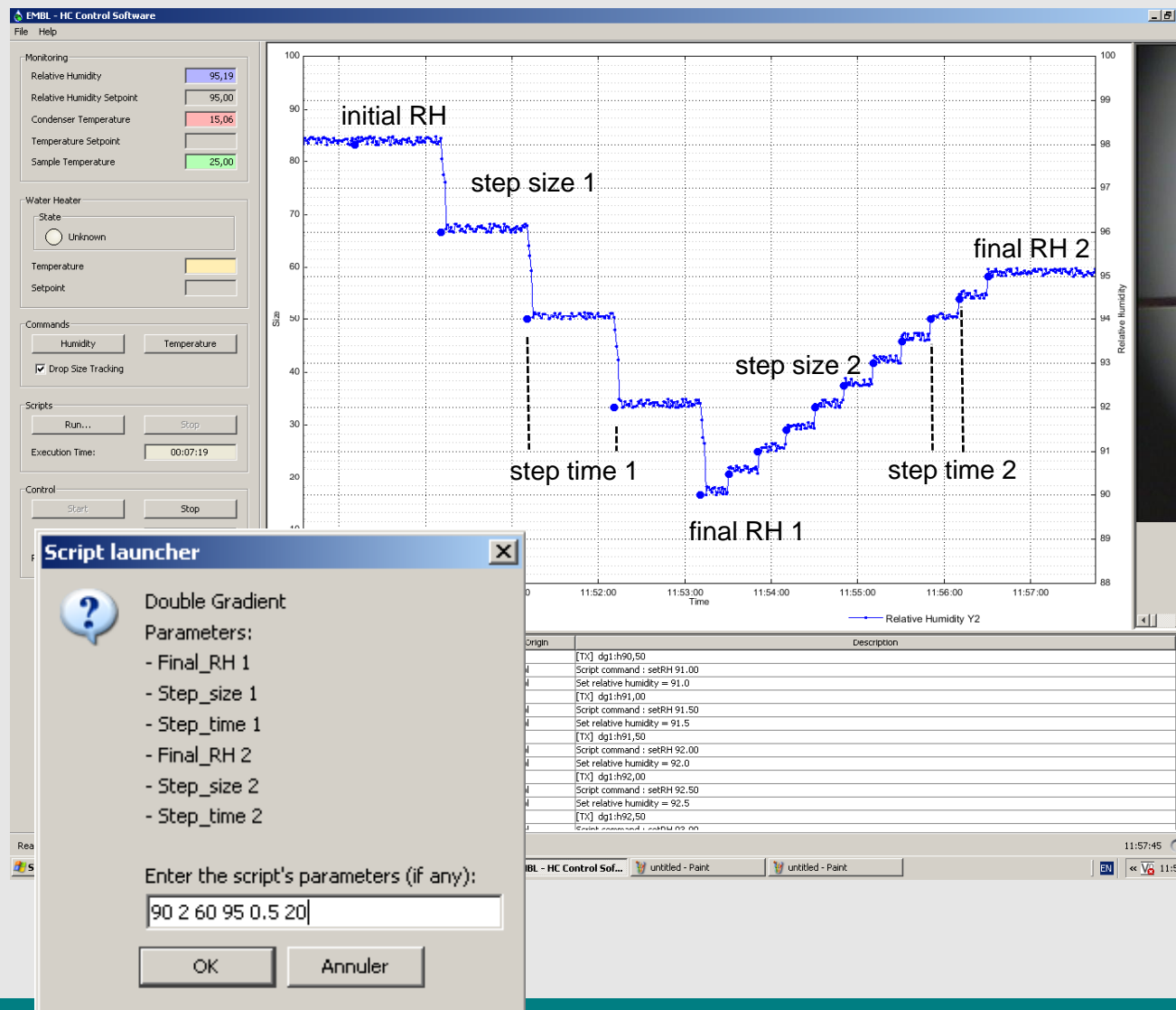
Prebuilt scripts

Flexible single gradient

Variables:

- final RH value
- step size
- step time

# HC1b Automation



Prebuilt scripts

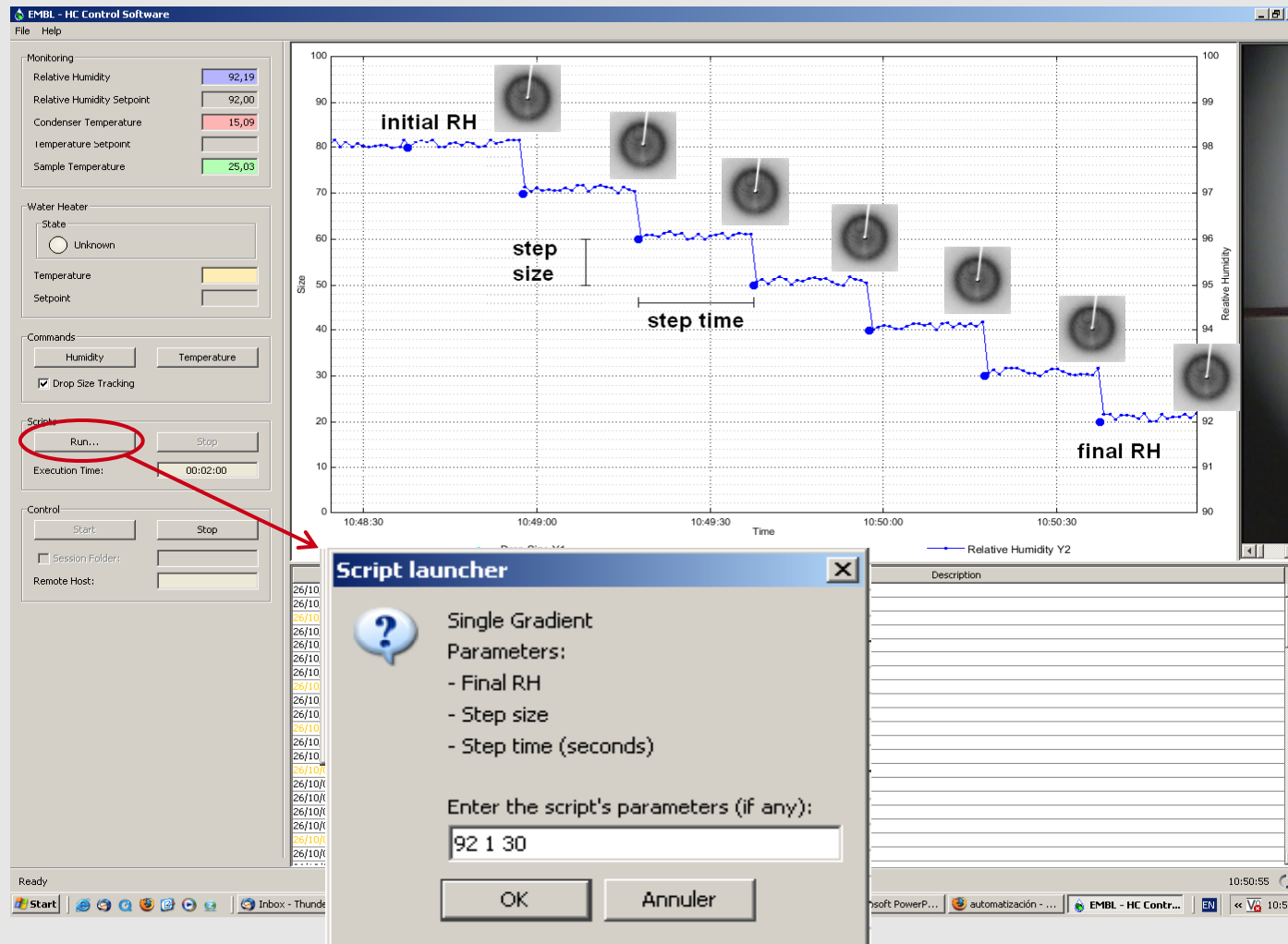
Flexible double gradient

Variables:

- final RH 1
- step size 1
- step time 1

- final RH 2
- step size 2
- step time 2

# HC1b Automation



# HC1b Survey

## HC1b HUMIDITY CONTROL DEVICE SURVEY



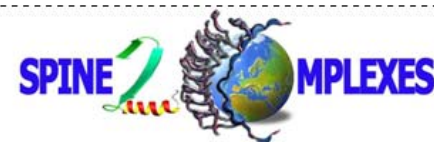
BEAMLINE:  USER ID:  DATE:

E-MAIL ADDRESS:  INSTITUTE:

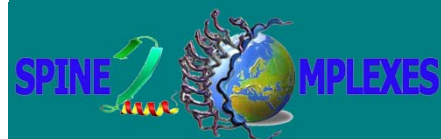
USUAL CRYSTAL PARAMETERS AT CRYO TEMPERATURE

SAMPLE NAME/ACRONYM		MOLECULAR WEIGHT (kDa)	
PROTEIN TYPE	<input type="checkbox"/> SOLUBLE	<input type="checkbox"/> MEMBRANE-BOUND	
SAMPLE TYPE:	<input type="checkbox"/> DNA/RNA	<input type="checkbox"/> PROTEIN	<input type="checkbox"/> PROTEIN-DNA/RNA <input type="checkbox"/> PROTEIN-PROTEIN
CRYSTALLISATION CONDITIONS			
USUAL CRYO PROTECTANTS			

The HC1b Partners



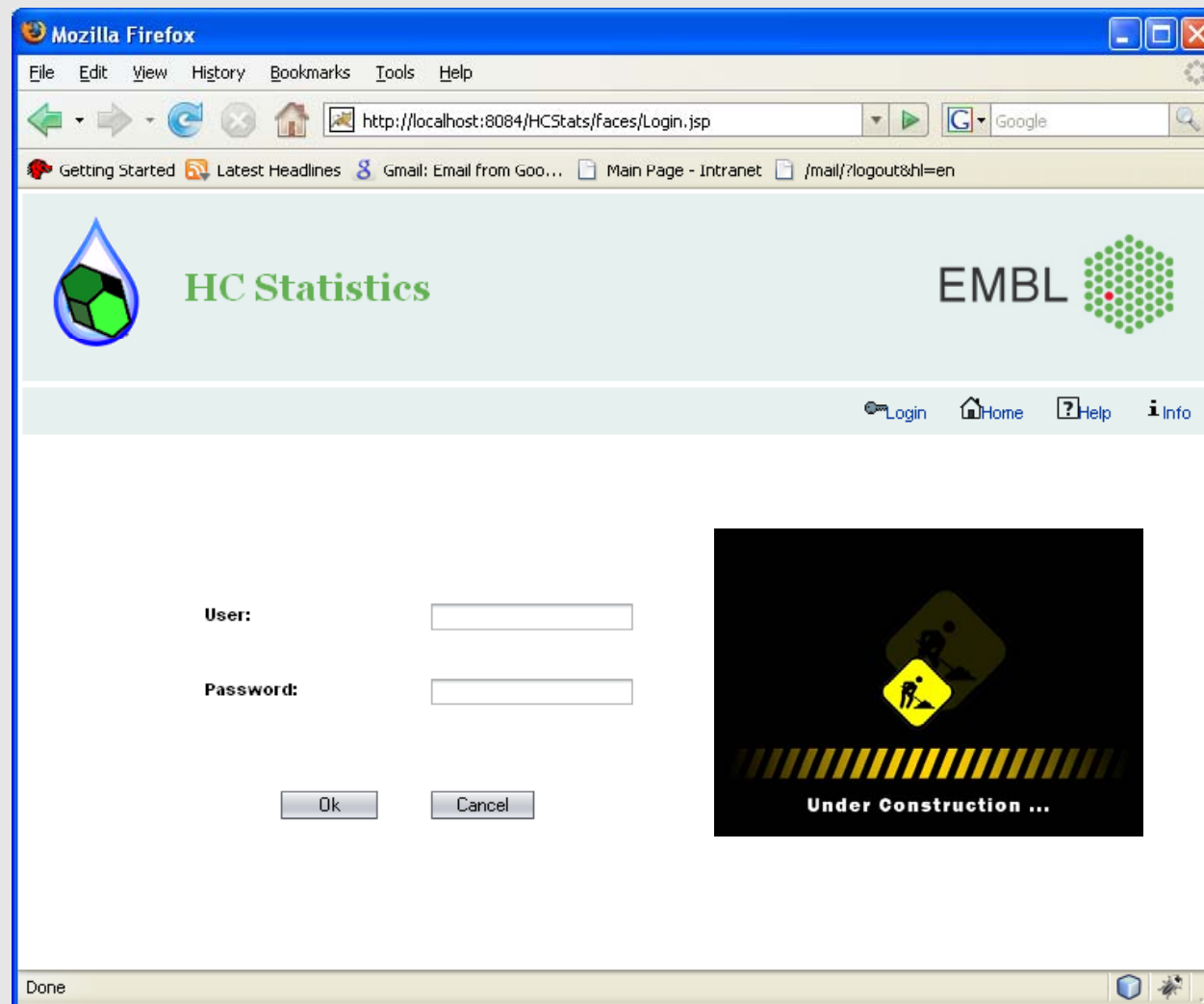
EMBL  
Grenoble



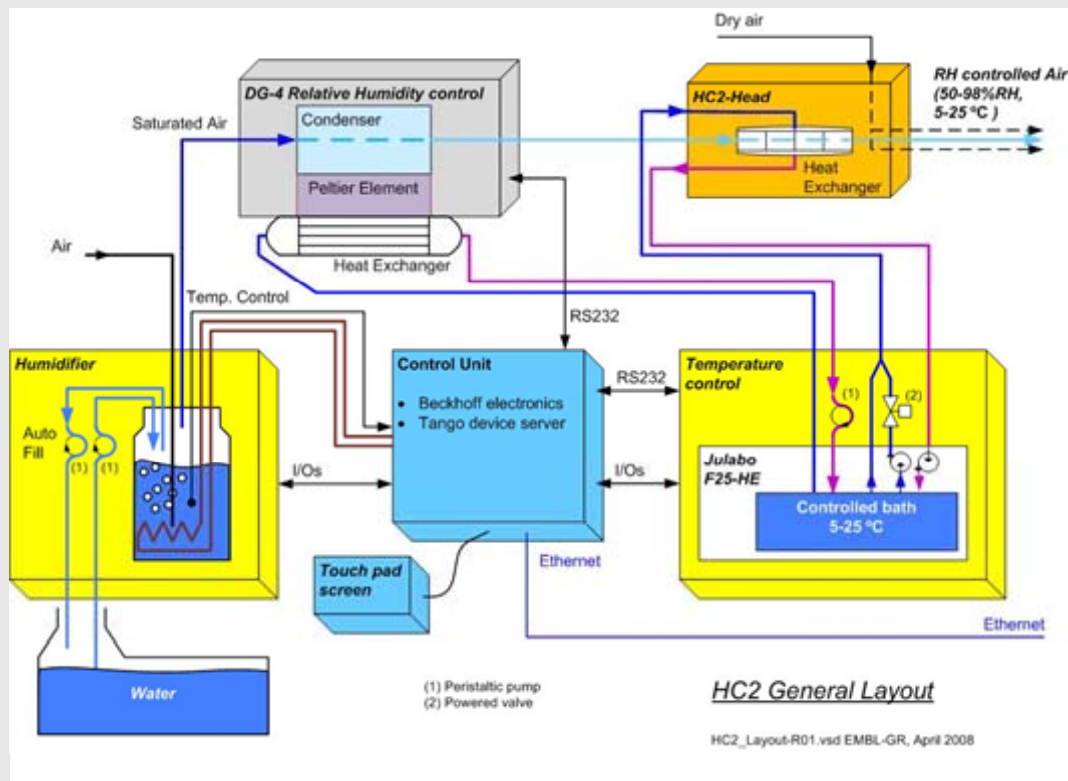
Getting better diffraction – On line crystal dehydration



# HC1b web server



# Next generation HC



Sample T control between 4°C and room temperature





# Aknowledgements



## Diffraction Instrumentation Team

Florent Cipriani, Franck Felisaz  
Alexandre Gobbo, Julien Huet  
Raphael Moya, Christophe Landret



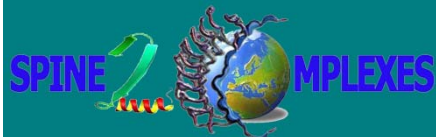
Matthew Bowler



Thomas Sorensen  
Juan Sánchez-Weatherby



Marjolein Thunnissen  
Thomas Ursby  
Wimal Ubhayasekera



Getting better diffraction – On line crystal dehydration

