

# High Pressure Freezing

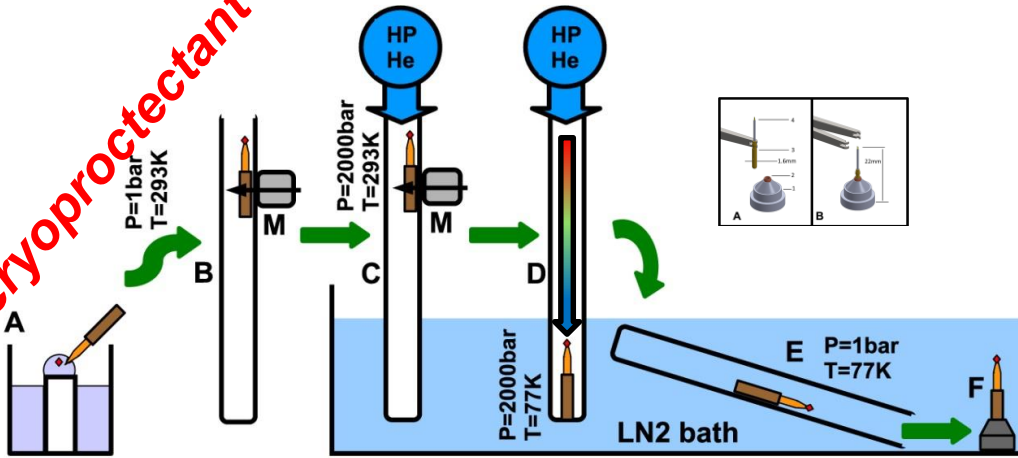
Philippe Carpentier,

**MX BAG Meeting, Monday February 8<sup>th</sup> 2016**

- 1- High pressure freezing of crystals without cryo-protectant.
- 2- Recent developments of oxygen and noble gas cryo-cells.
- 3- Perspectives for “very” high pressure freezing and room temperature pressure cell.

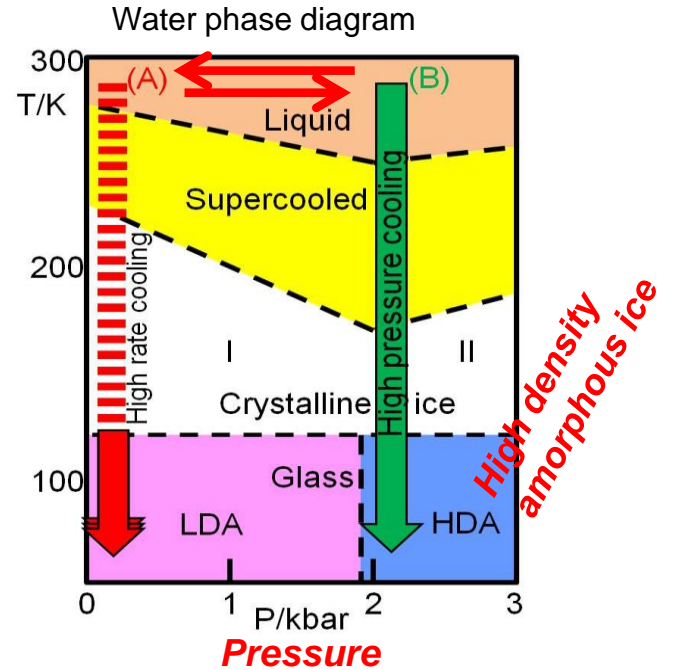
# HIGH PRESSURE FREEZING SYSTEM AND METHOD (P. VAN DER LINDEN)

**No cryoprotectant**

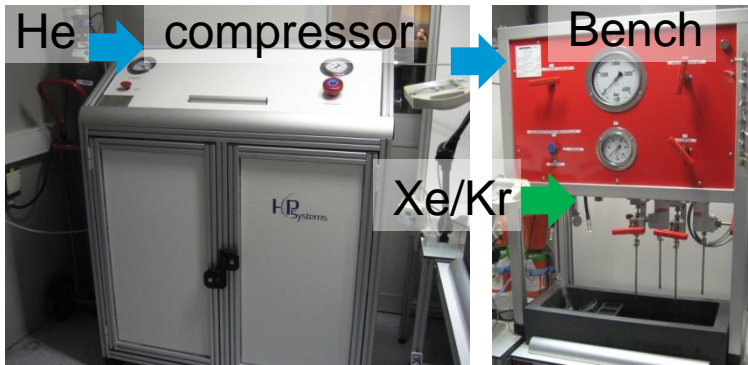
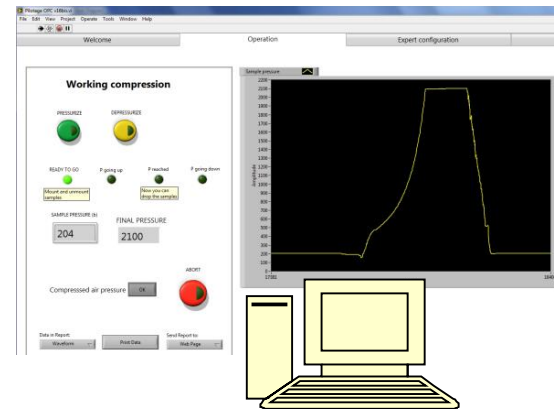


## HP-cooling process:

- (A) Crystal fishing ((293K, 1bar),
- (B) Loading in drop tubes, (293K, 200bar)
- (C) Pressurization (293K, 2000 bar),
- (D) Cooling under HP (77K, 2000bar),
- (E and F) Pins/bases assembly in LN2 @ 77K, 1bar



## Control software (automated)



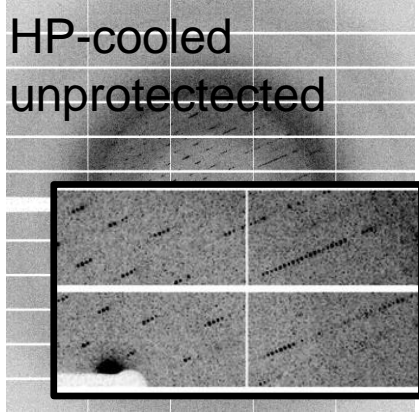
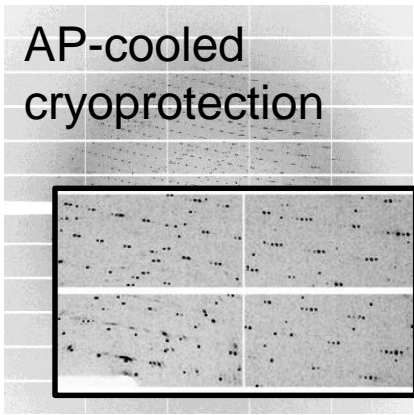
**User mode since June 2014**

# HIGH PRESSURE COOLING, APPLICATIONS

## (1) Cryoprotection-free, improvement of crystal quality

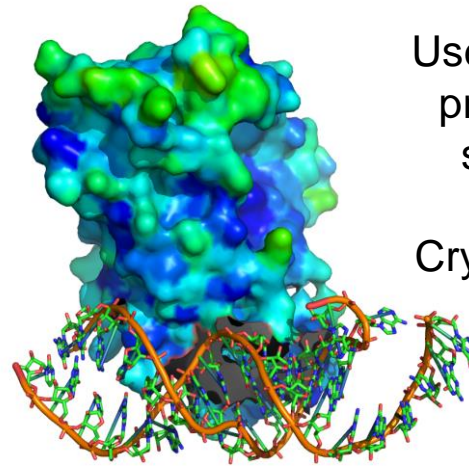
AP-cooled  
cryoprotection

HP-cooled  
unprotected



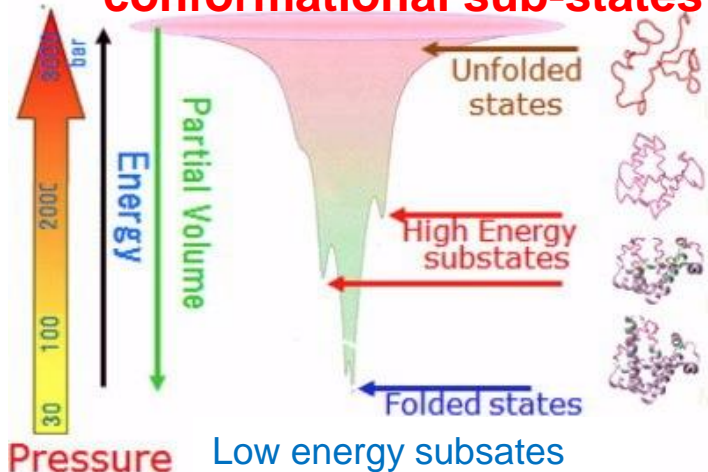
- space group  $P2_1?$
- Resolution  $\sim 3\text{\AA}$
- Mosaic/broken, twin

- space group  $P2_12_12_1$ ,
- Resolution  $\sim 2.5\text{\AA}$
- Lower mosaicity

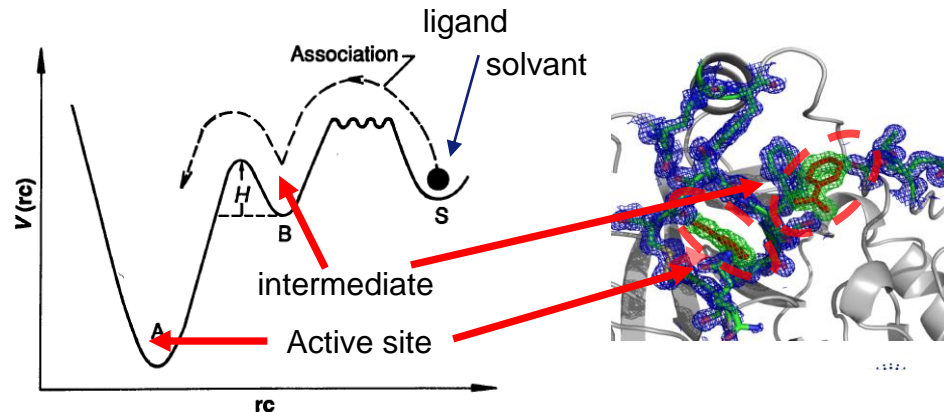


User challenging project  
protein-RNA complex  
structure solved by  
High Pressure  
Crystallography @  $2.5\text{\AA}$

## (2) Exploration of conformational sub-states

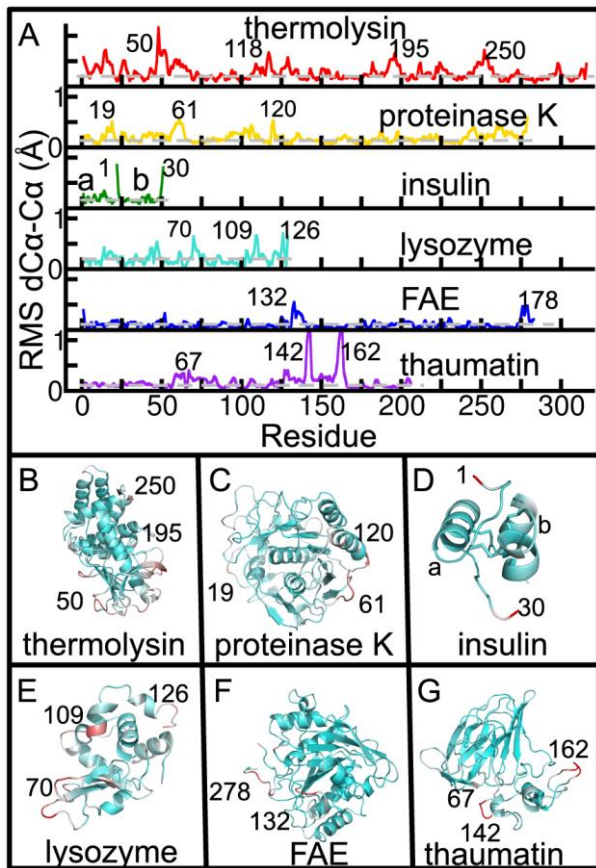


## (3) Studies of reaction, ligand binding intermediates



# ASSESSMENT OF THE SYSTEM WITH TEST CRYSTALS

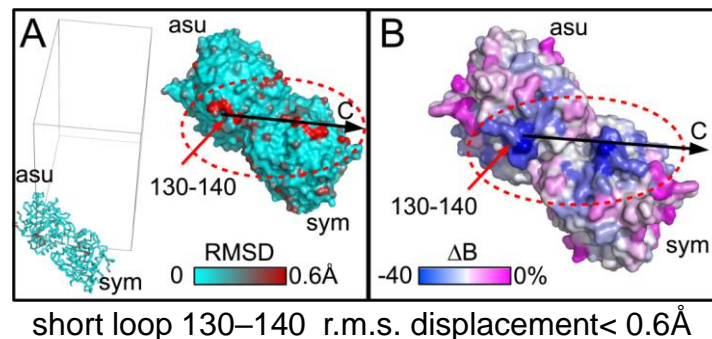
Gallery of HP-cooled protein crystals.  
 Ca backbone & 3d displacements representation



## Phase transition in FAE

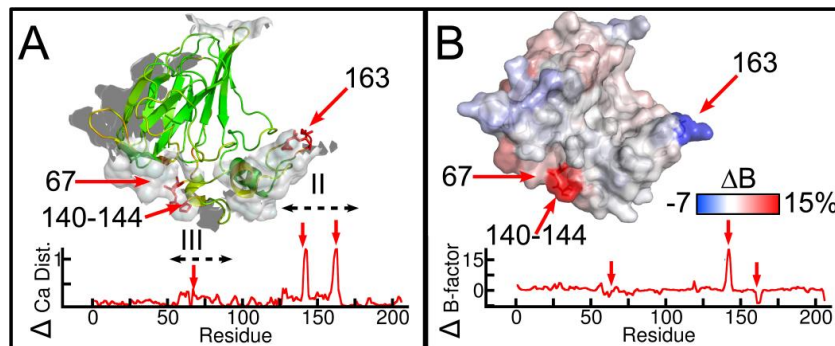
Flash freezing 1bar  
 Space group  $P2_12_12_1$   
 Bfact ( $\text{\AA}^2$ ): 14.2

2000bar  
 $P4_12_12$   
 19.6



Improvement of crystalline quality (few cases)

## flexible domains in thaumatin

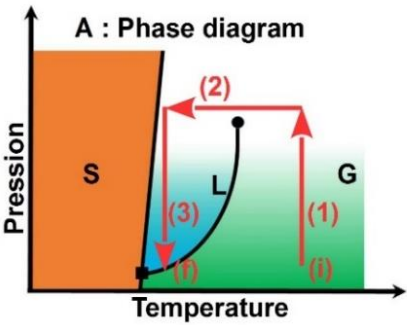


Pro141 buried in crystal contacts, Lys163 exposed to the solvent

Exploration of conformation sub-states (some case)

- Structural changes few and localized (surface)
- Structures HP-freezing isomorphous with AP -
- Method applicable to all projects
- Avoid search of cryoprotection conditions

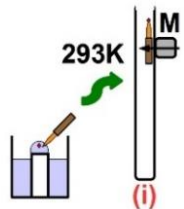
# FREEZE BIO-XTALS IN PRESSURIZED O<sub>2</sub> AND KR GASES



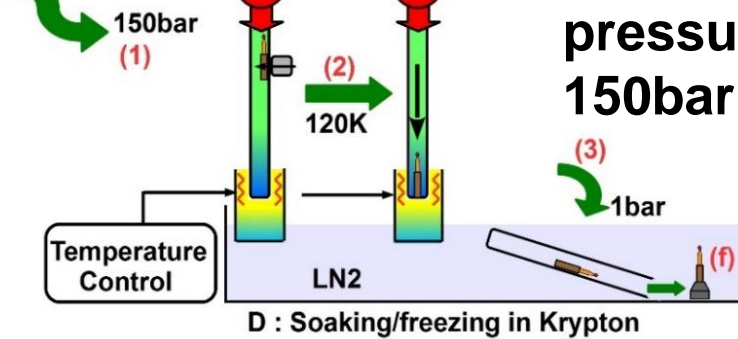
Cryogenic O<sub>2</sub>  
pressure cell  
50 bar



B : Sample loading



Cryogenic Kr  
pressure cell  
150bar



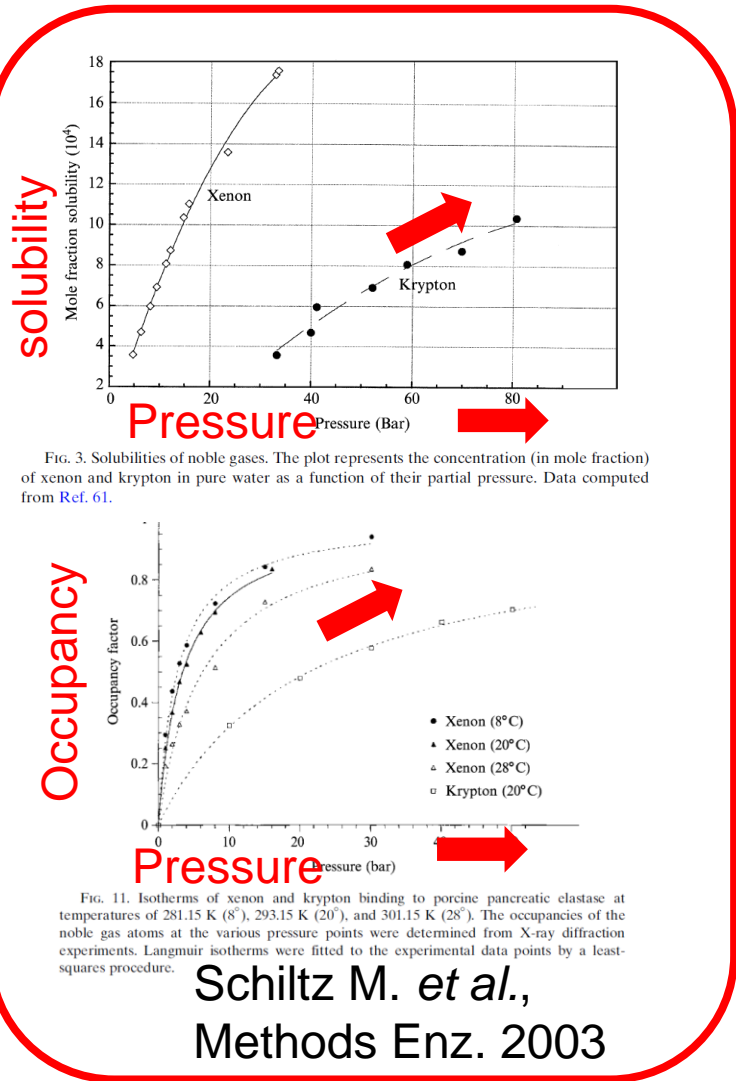
## (I) cryogenic oxygen pressure cell (P. van der Linden and A. Royant)

- System dedicated to proteins requiring O<sub>2</sub> as a cofactor or substrate  
Myoglobin, Hemoglobin, Cytochrome P450, oxidase, photosensitizers ....
- Reveal Oxygen sites of affinity in oxygen sensitive proteins

## (II) cryogenic noble gas pressure cell (P. van der Linden)

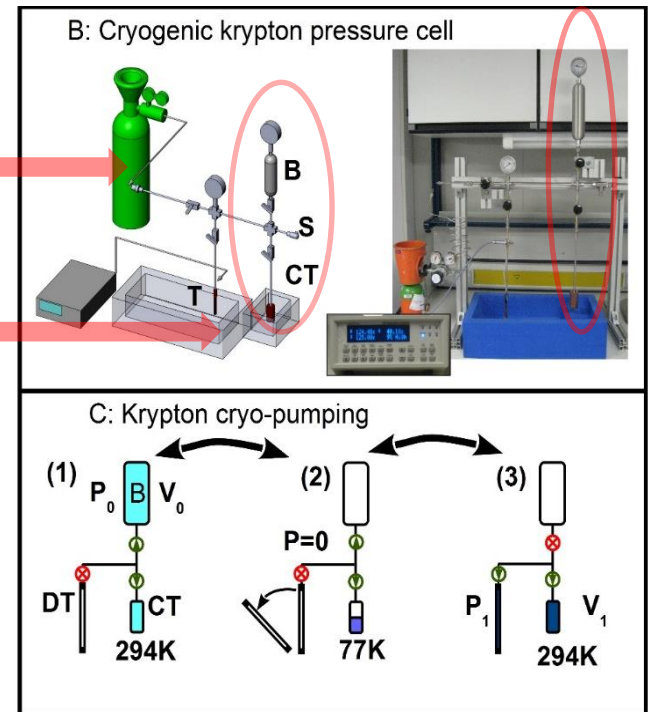
- Search of pores, channels and cavities in proteins
- Production of efficient derivative of crystals for phasing

# HIGHER PRESSURES BY CRYO-PUMPING



Cylinder 30bar

Sample 150bar

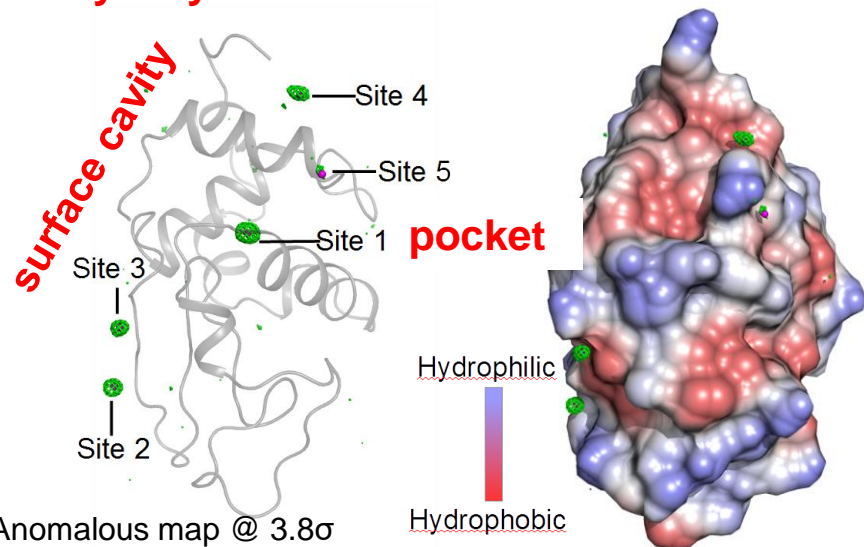


## Possible gases of biological interest

Gas	T point T(K)	$K_{\text{henry}}$ (mM/bar)
O <sub>2</sub>	54.4	1.3
CO	68.2	0.9
Ar	83.8	1.4
CH <sub>4</sub>	90.5	1.3
C <sub>2</sub> H <sub>4</sub>	103.2	4.9
NO	109.5	9.3
Kr	115.8	2.5

# ASSESSMENT OF THE CRYOGENIC KR-CELL USING TEST CRYSTALS

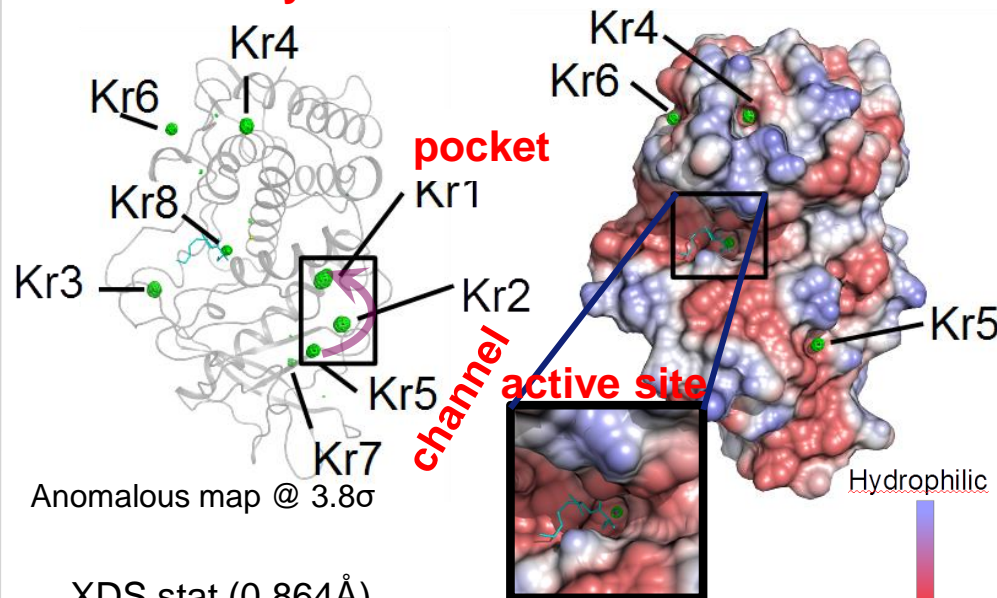
## Lysozyme 100bar of Kr



XDS stat (0.864Å)

RESOL	REFLECT	COMPL	R-FACT	I/SIGMA	CAno	SigAno	Nano
3.59	36495	99.9%	3.5%	79.29	82*	2.258	1079
1.20	154904	99.4%	53.9%	4.65	0	0.766	5388
total	964801	99.9%	5.9%	24.66	21*	1.066	32827

## Thermolysin 100bar of Kr



XDS stat (0.864Å)

RESOL	REFLECT	COMPL	R-FACT	I/SIGMA	Cano	SigAno	Nano
5.06	45271	99.8%	4.4%	56.24	82*	2.514	1029
1.70	182315	98.1%	64.5%	5.82	21*	0.920	5144
total	1189266	99.7%	10.9%	24.26	32*	1.158	31878

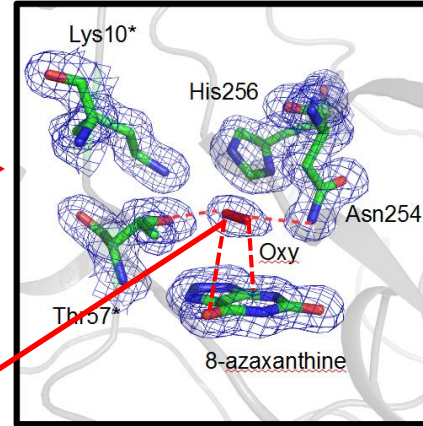
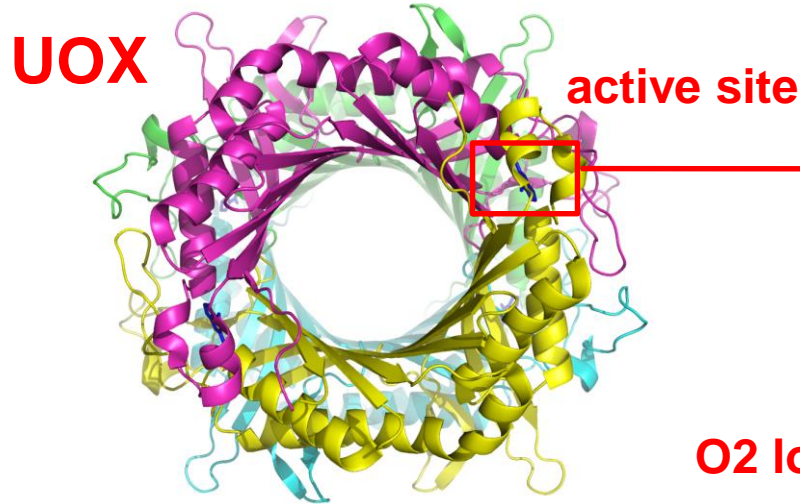
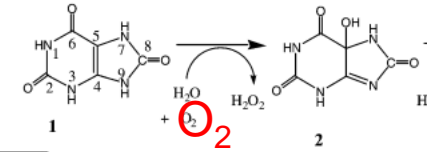
	thermolysin ID23-1	lysozyme ID29
Space group	P6 <sub>1</sub> 22	P4 <sub>3</sub> 2 <sub>1</sub> 2
Resol (Å)	1.70	1.20
λ (Å)	0.864/0.866	0.864/0.866
U cell (Å°)	93.0 93.0 129.1 90 90 120	79.0 79.0 37.1 90 90 90
R/Rfree(%)	15.9/18.0	12.9/15.3
Nb sites	8 Kr	5 Kr
Occ	1.00, 0.55, 0.34, 0.20, 0.28, 0.24, 0.22, 0.23	0.33, 0.25, 0.25, 0.20, 0.25
Lit, PDB	1QTK: 1 Kr, 1C10 : 2 Xe	3LS7: 1 Xe



- Phasing, kr anomalous signal @ k-edge
- Revealing pores and channels
- Labelling active sites
- Probing hydrophobicity (surface cavities)

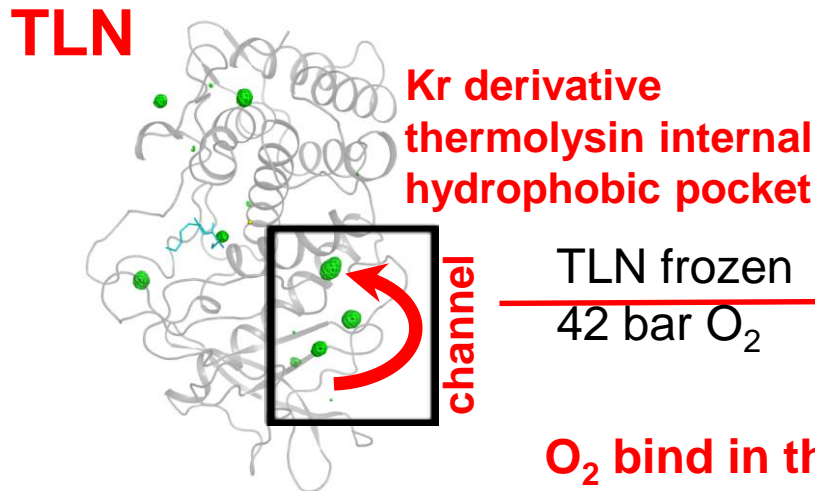
# ASSESSMENT OF THE CRYOGENIC O<sub>2</sub>-CELL USING TEST CRYSTALS

N. Colloc'h et al. Biophys. J. 2008  
 UOX catalyzes oxidation of uric acid to 5-hydroxyisourate

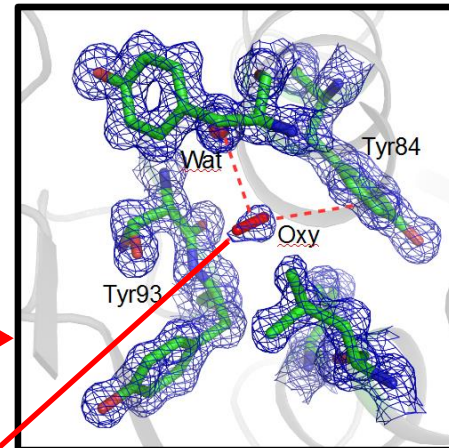


O<sub>2</sub> , 42bar  
 Omit map @ 1σ  
 Resol. 1.4 Å

**O<sub>2</sub> location, elements of UOX, mechanism**



TLN frozen  
 42 bar O<sub>2</sub>

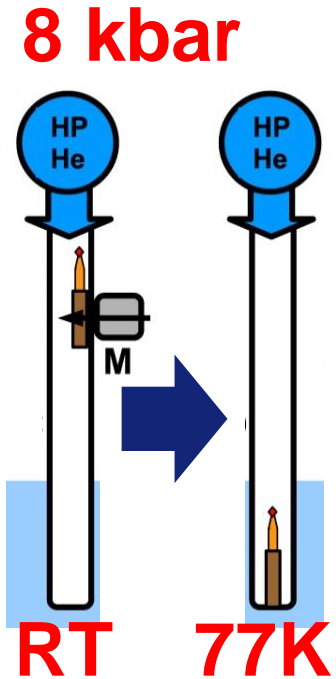
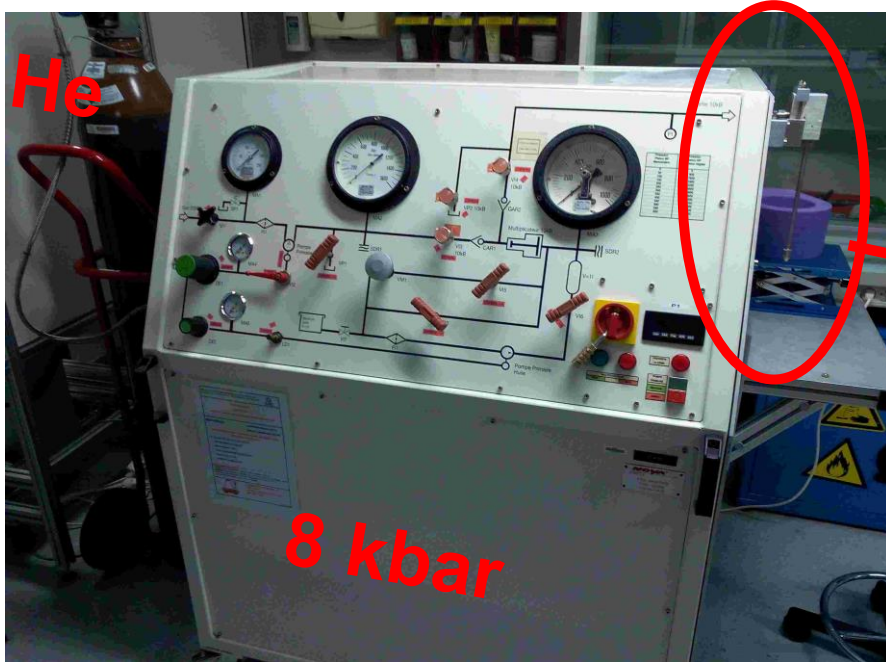


O<sub>2</sub> , 42bar  
 Omit map @ 1σ  
 Resol. 1.2 Å

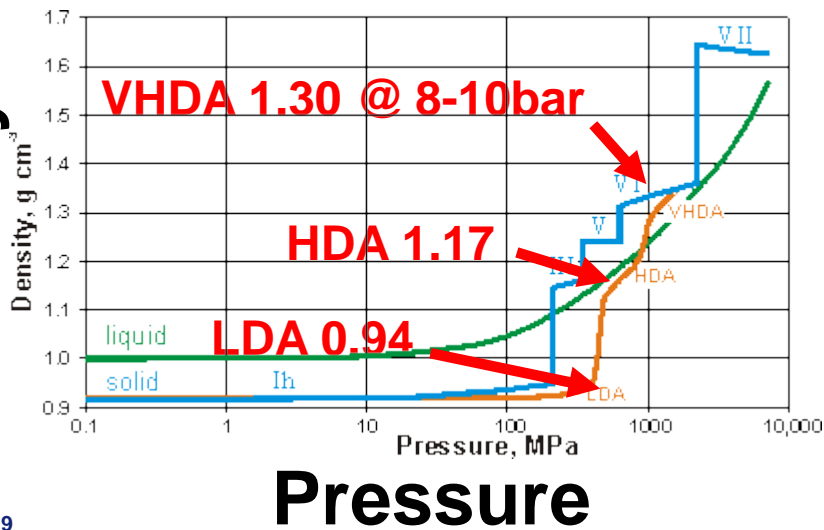
**O<sub>2</sub> bind in the TLN internal hydrophobic pocket  
 (small molecules as phenol, isopropanol, acetone, function?)**



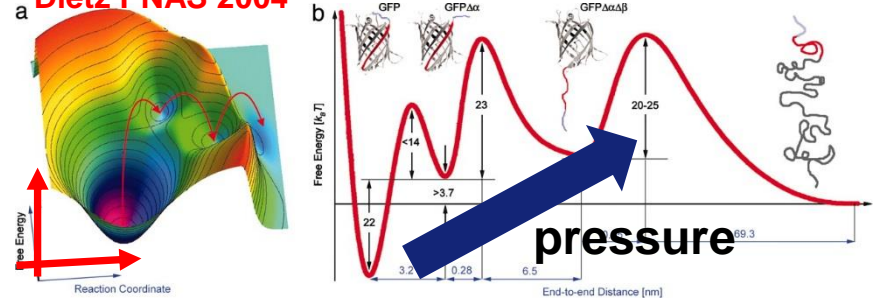
# “VERY” HIGH PRESSURE FREEZING



density



a Dietz PNAS 2004

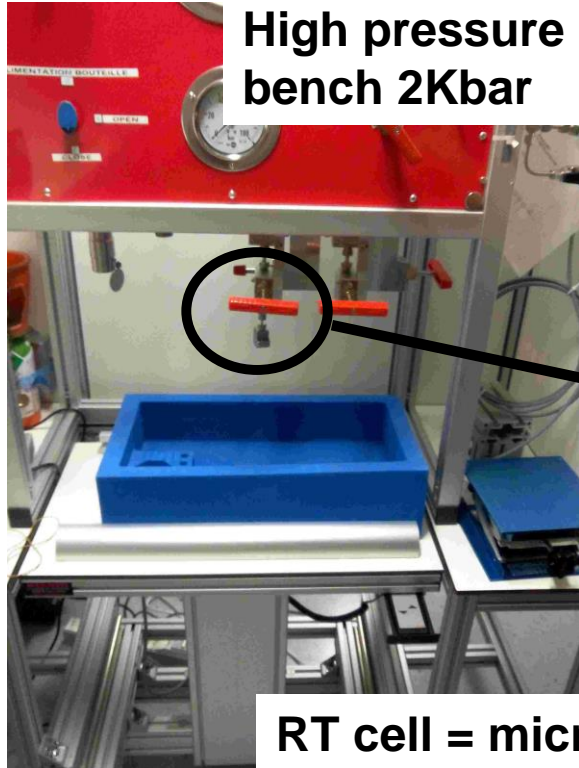


“Very” pressure cooling @ 8 kbar:

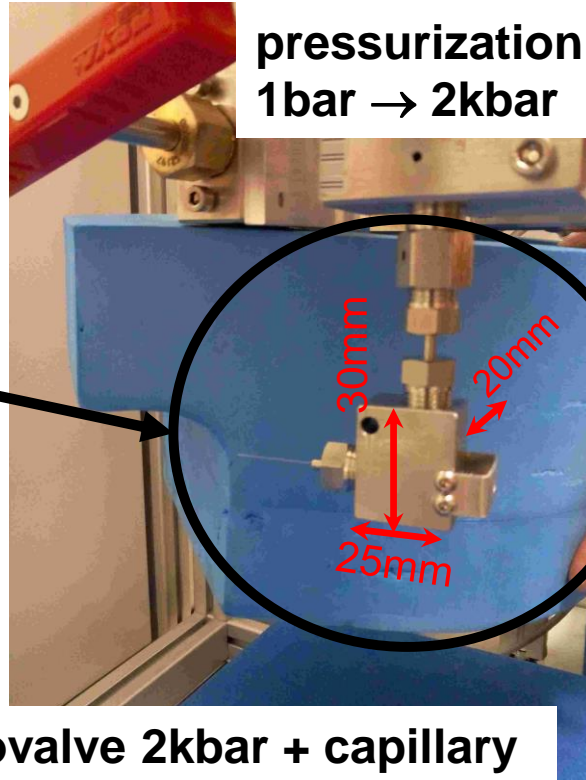
- Protein frozen in VHDA ice matrix ?
- Larger exploration of energy landscapes
- Protein unfolding ?

# RT PRESSURE CELL FOR MX EXPERIMENTS

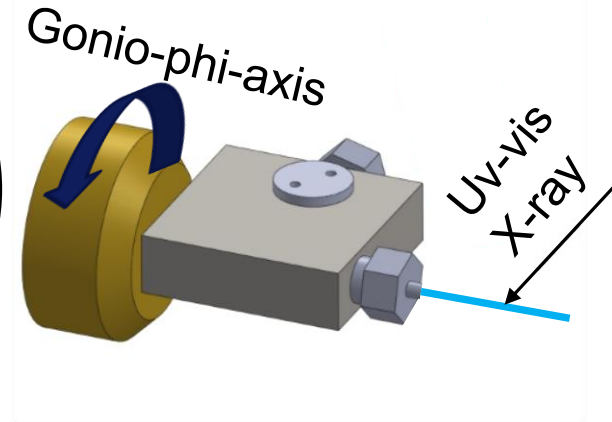
High pressure bench 2Kbar



pressurization  
1bar → 2kbar



RT cell = microvalve 2kbar + capillary



**RT pressure cell :**

- **Biological solutions/crystals**
- **High pressure (Cte ~ 2kbar), Room temperature**
- **X-ray diffraction**
- **UV/vis spectroscopy**

- **HP-Freezing in the laboratory of ID23 in User mode**
- **Freezing session for a mx experiment (2 weeks before mail @ Local contact or @ D. Flot)**

## Acknowledgements

- **HP-Freezing:** van der Linden P., Dobias F., Vitoux H., Kapp U., Jacobs J., Mueller-Dieckmann C., Leonard G.
- **Oxygen/krypton cryo-cell:** Mueller-Dieckmann C., Leonard G., Giraud T., Dobias F., Royant A., van der Linden P.
- **PhD Thesis:** Lafumat B.
- **All the SB-Group**



***And thanks to the audience for its attention !***