

# New Technique of Manipulating a Protein Crystal

Kazufumi Takano, Tomoya Kitatani, Shigeru Sugiyama, Hiroyoshi Matsumura,  
Hiroaki Adachi, Satoshi Murakami, Tsuyoshi Inoue, and Yusuke Mori

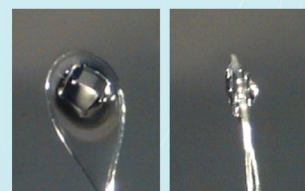
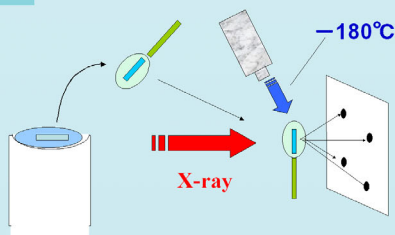
Osaka University, SOSHO Inc., JST-CREST



## Loop-based mount method



Protein crystals consist of 30~80% solvent.  
⇒ Very fragile



**Hold a protein crystal in nylon loop with cryoprotectant solution without direct contacting**

### Advantage

• **Avoid the contact damage between loop and a crystal**



### Problems

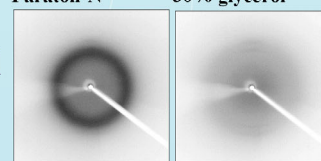
• **Require users to skill in the step of mounting of a crystal**

• **The excess solution in the loop**

- Increasing background scattering
- Reducing diffraction signal-to-
- Decreasing the cooling rate

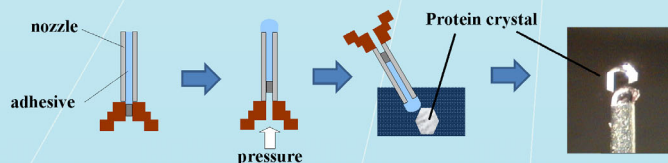
Paraton-N

30% glycerol



→ *Degrade the quality of XRD data*

## Crystal Catcher™



**Directly capture of a protein crystal by adhesive material**

### Advantages

• **Easy capturing of a crystal**

• **Reducing the excess solution around a crystal**

### CT-100

Protein crystals in **salt conditions**

lysozyme



AcrB  
(membrane protein)



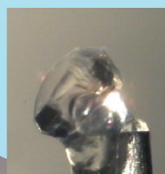
### CT-200

Protein and organic crystals in **organic solvents** and **high viscosity solutions**

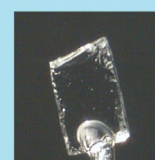
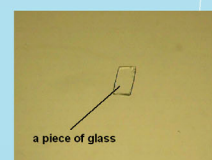
trypsin



glucose isomerase



<Under 100% ethanol>



→ **Our tool can capture and hold a small molecular crystal under high concentrated organic solvent**

### XRD images



- Single crystal without causing significant
- Reducing background scattering
- Reducing cryoprotectant

[References]

Kitatani *et al.* (2008) *Appl. Phys. Express* 1, 037002.  
Kitatani *et al.* submitted.