



Structural Biology Research Center

 Inter-University Research Institute Corporation
High Energy Accelerator Research Organization, KEK

 Institute of Materials Structure Science, IMSS

 Photon Factory, PF

BL-1A
Native SAD



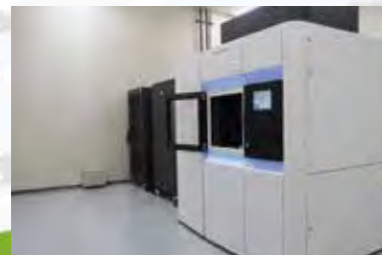
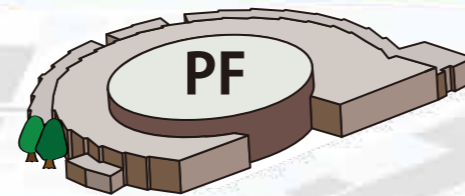
BL-17A
Native SAD/In-situ



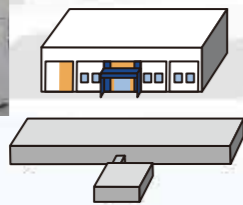
AR-NW12A
Spectroscopy



BL-5A
High resolution



Cryo-EM

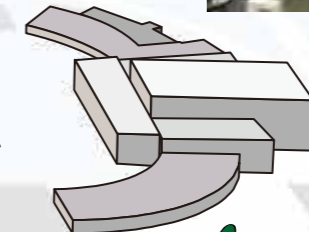


BL-10C
Standard SAXS



BL-15A2
High flux SAXS

PF-AR



AR-NE3A
Fully automated
data collection



Biochemistry Lab



Crystallization facility



Crystallization facility



96-well SBS format
Crystallization plate

- Automatic observation on Schedule
- Two temperature (20 °C & 4 °C)
- Drop size 0.1-0.2 μ L (14- 23 μ L protein/plate)
- Mail-in service available



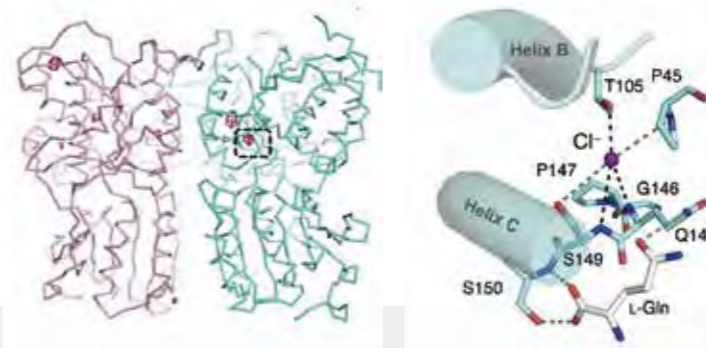
PX beamlines



Native-SAD (BL- 1 A)

No heavy atom derivatives needed for phasing
Identify light atoms (Ca, Cl, P, S, etc.) by anomalous signal

Identifying biological important light atoms in protein molecule



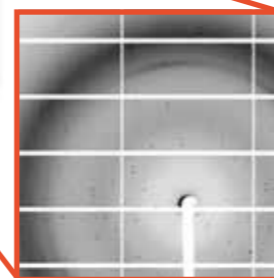
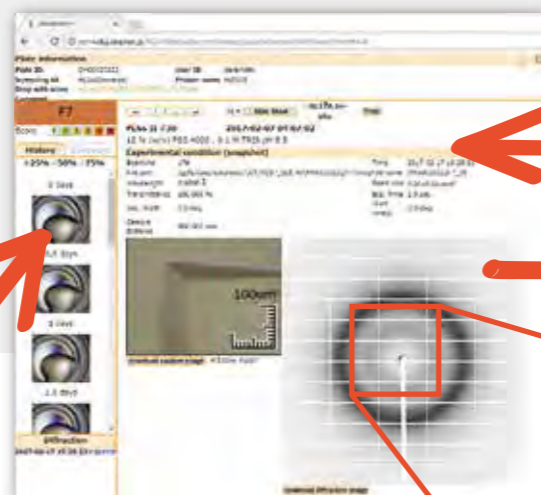
Atsumi *et al.* (2023) eLife.84291



Native SAD phasing from laser-processed crystal

Juniar *et al.* (2021) Acta Cryst. F 77

If you find crystals



In situ screening (BL-17A)



Mail-in service, Expert data collection support,
Pixel array detectors in all BLs,
Automatic data processing

Full automation (NE3A)



Experiment result	
Sample	Result
1	OK
2	OK
3	OK
4	OK
5	OK
6	OK
7	OK
8	OK
9	OK
10	OK
11	OK
12	OK
13	OK
14	OK
15	OK
16	OK
17	OK
18	OK
19	OK
20	OK

You can monitor crystal growth from anywhere in the world via the internet.

SAXS beamlines

BL-15A2

BL-10C

SEC-MALS/RI

SAXS and UV-Vis. spectroscopy in line with Size-Exclusion Chromatography (SEC-SAXS/UV-Vis.)

Multi-angle light scattering and differential refractive index in line with SEC (SEC-MALS/dRI)

Cryo-EM

Titan Krios G4 (300kV)

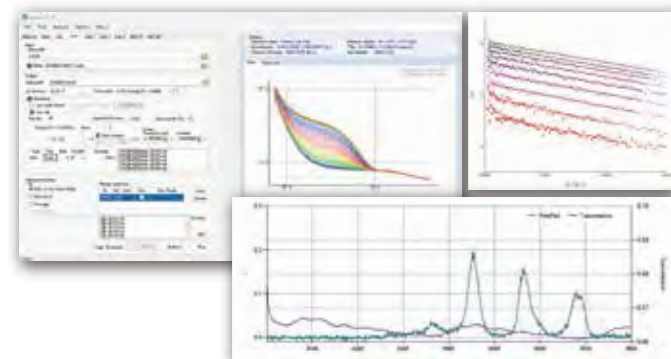
Talos Arctica (200kV)

Biochemistry Lab.

A light harvesting complex of *Prasiola crista* determined at 3.13Å resolution.



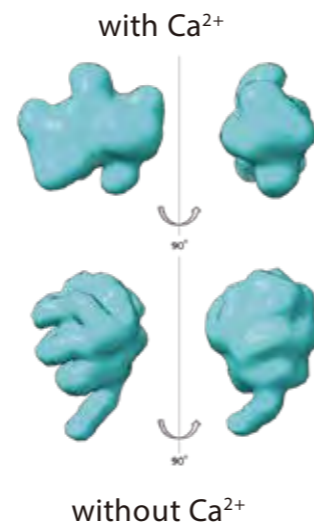
Light-harvesting complex, LHC



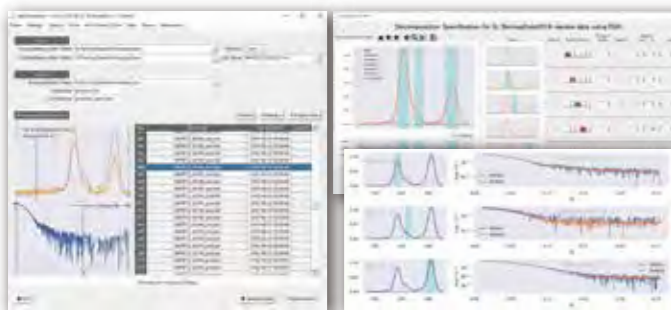
SAXS data basic analysis
Shimizu *et al.* (2016) AIP Conf. Proc.

Ab initio modeling

Solution structure estimation of the N-terminal domain of lipid kinase DGK α .



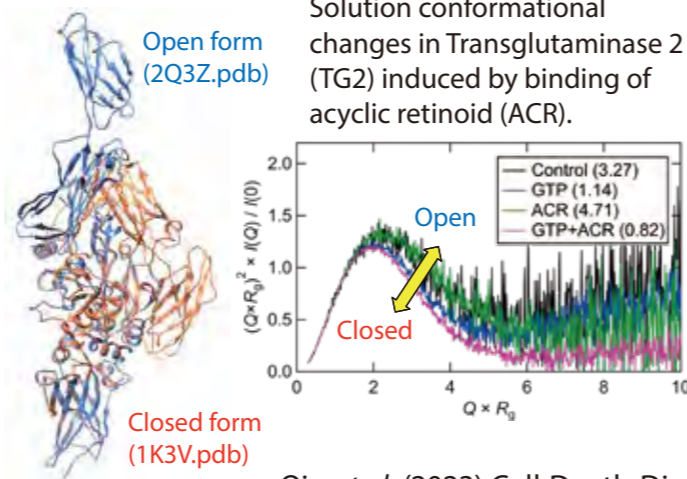
Takahashi *et al.* (2022) Protein Sci.



Automatic SEC-SAXS/UV-Vis. analysis
Yonezawa *et al.* (2023) BPPB.

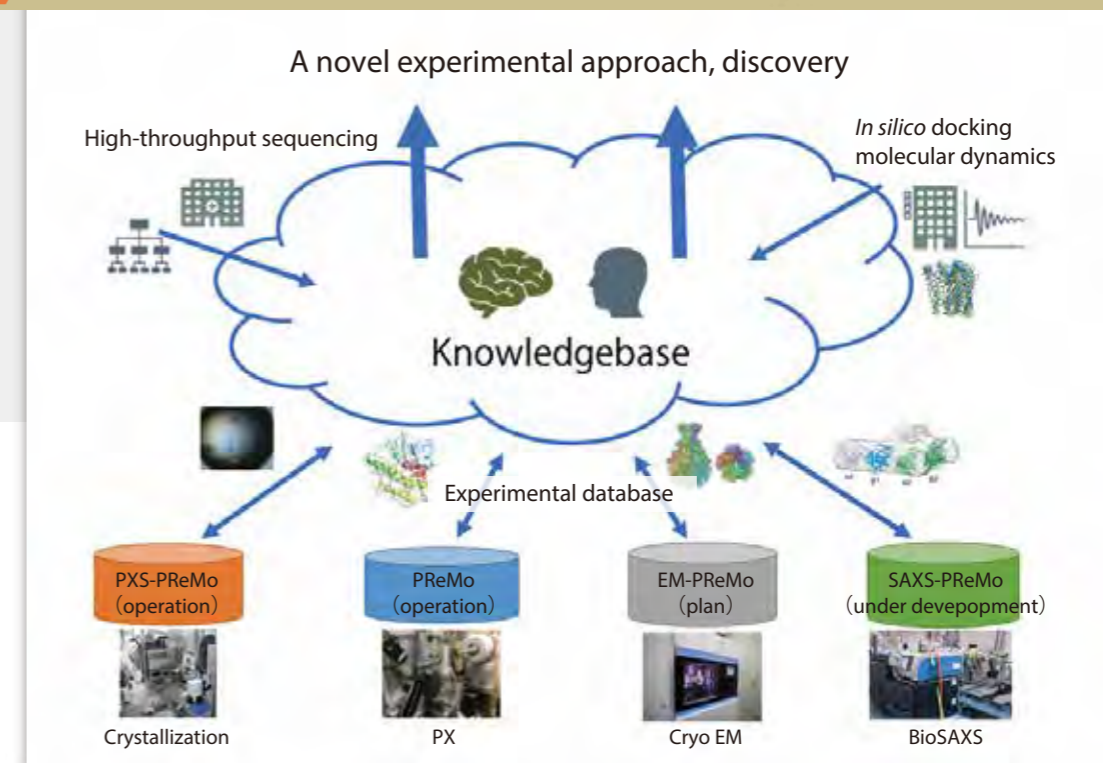
Integrative approach

Solution conformational changes in Transglutaminase 2 (TG2) induced by binding of acyclic retinoid (ACR).



Qin *et al.* (2023) Cell Death Dis.

PReMo-database future plan

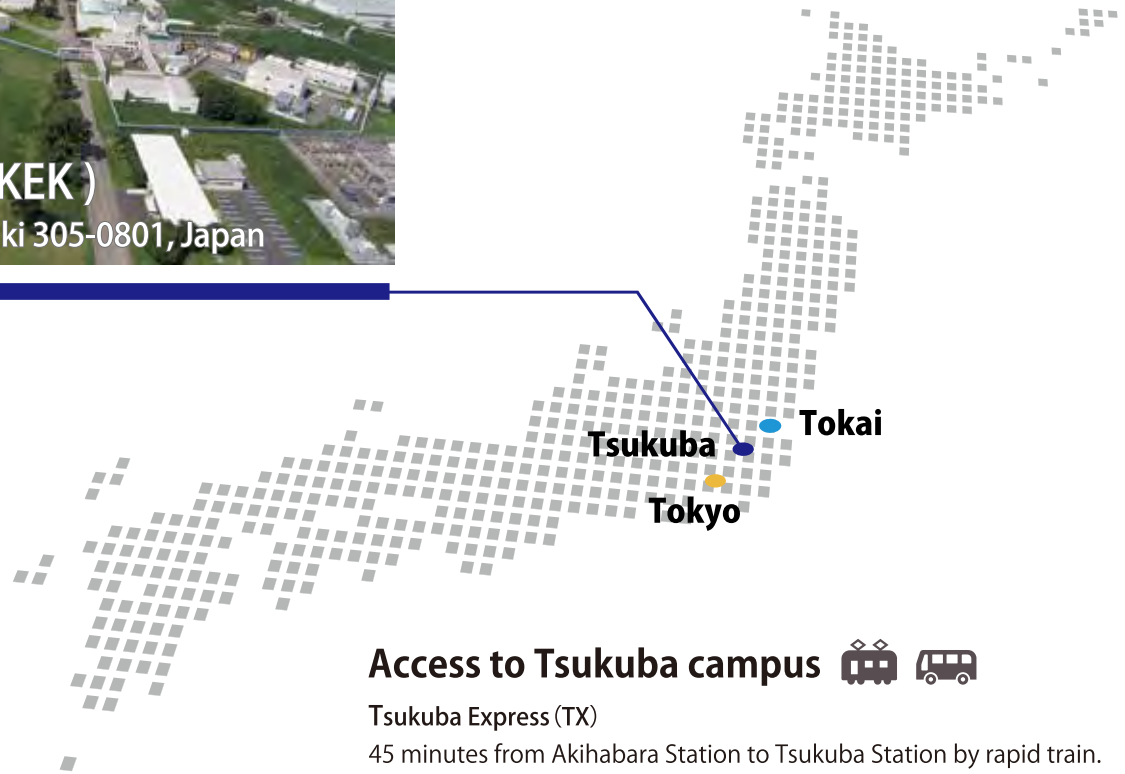


We try to integrate all databases to support biology!!



Tsukuba campus (KEK)

1-1 Oho, Tsukuba-shi, Ibaraki 305-0801, Japan

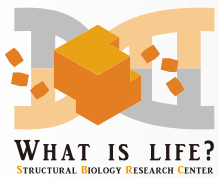


Tokai
Tsukuba
Tokyo



Access to Tsukuba campus

Tsukuba Express (TX)

45 minutes from Akihabara Station to Tsukuba Station by rapid train.
After getting off at Tsukuba Station, about 20 minutes by bus or taxi
from the Tsukuba Center bus terminal.



SBRC

 **KEK** High Energy Accelerator Research Organization
 **IMSS** Institute of Materials Structure Science

<https://www2.kek.jp/imss/eng/sbrc/>

