

X-ray Crystallography Services Specializing in Protein Structure Biology for
Drug Discovery and the Biochemical Industry



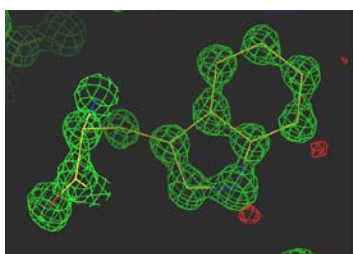
C-Platform

High-resolution X-ray crystallographic platform service for protein structural analysis

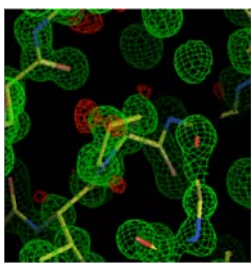
High-resolution data can provide more accurate structural information

In order to know structural details of a protein binding to a ligand, it is extremely important to study the electron density map (EDM) of the protein molecule and the ligand directly from experimental data. Higher resolution X-ray diffraction data is best.

Example of an electron density map of a high-resolution structure (**0.89 Å**)

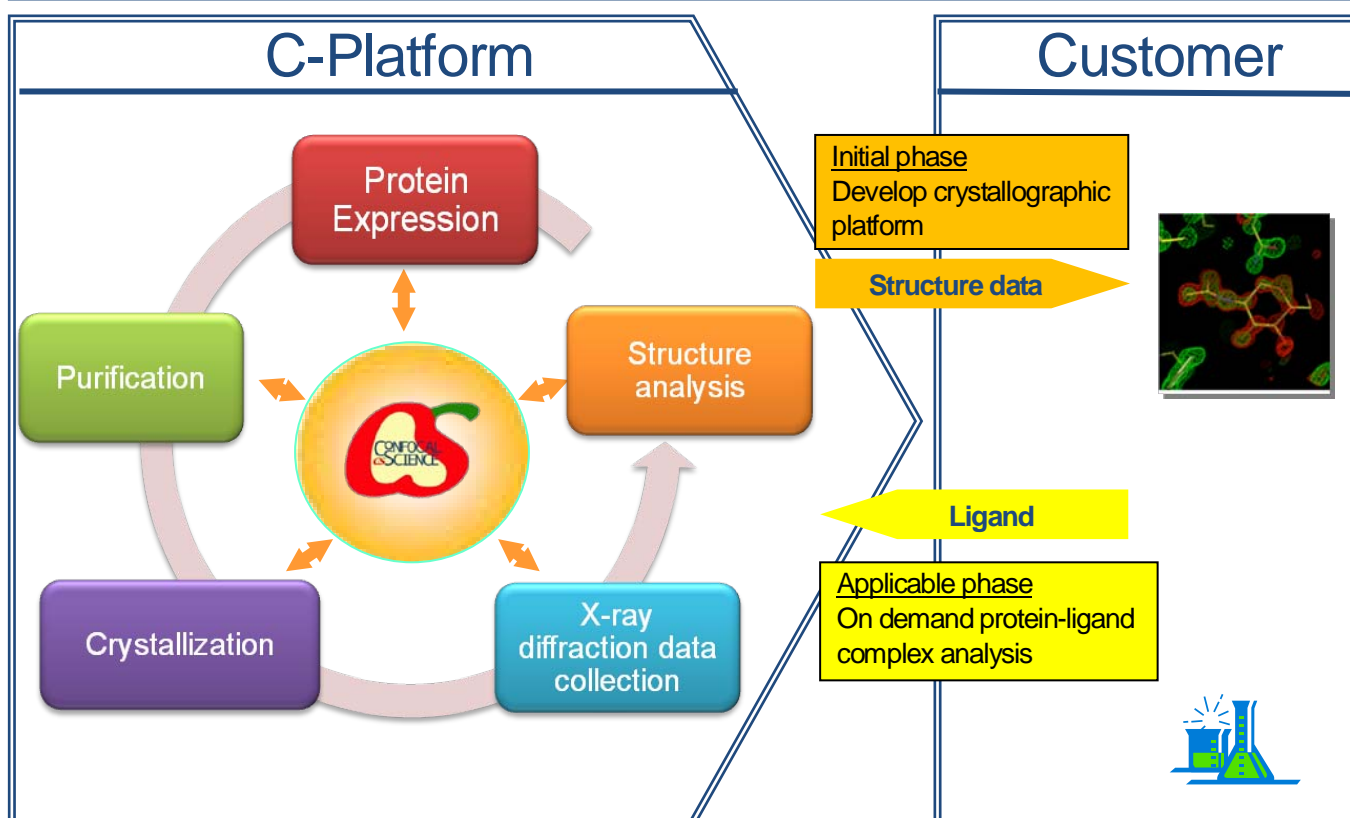


The electron density corresponding to core and bonding electrons, including those of hydrogen atoms (shown in red), can be observed.



The position and orientation of ligands (shown in red) at binding sites can be determined in detail.

(Spring-8 BL12 / JAXA's technical development)



C-Platform Services

After the initial high-throughput protein crystallographic analysis, higher resolution data is generally needed to obtain a finer electron density map, since it is far-reaching and more informative. We can provide high-resolution X-ray crystallography with our expert staff scientists. Our extensive experience allows us to provide a full range of the services our customers need, from protein expression to structure analysis, for high-resolution crystallography.

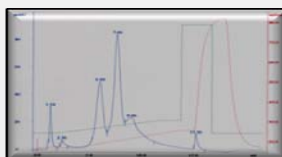
1. Protein expression

Protein with biological functions at crystallization quality is expressed in *E.coli* or baculovirus-infected insect cells.



2. Crystallization-grade protein purification

Highly purified protein samples are a key to successful crystallization. Purification of protein samples is our specialty.



3. Optimization of crystallization conditions

We optimize crystallization conditions by our original method based on copious experience. We search for the final crystallization solution which is compatible with a cryoprotectant.

NaCl (mM)	Protein A		Protein B			Protein C	
	pH4.5	pH7.0	pH5.5	pH7.0	pH9.0	pH7.0	pH9.0
0	x	x	x	x	x	x	x
100	x	x	0	x	x	x	x
200	x	x	0	0/0	0	0/P	0
300	x	0	0	0/0	0	0/P	0/P
400	0	0	0/0	0	0	0/P	0/P
500	0	0	-	0	0	0/P	0/P
600	0	0	-	0	0	0/P	0/P
700	0	0	-	0	0	0/P	0/P

7. Space crystallization

Since 2009, Confocal Science has been a service provider of commercial protein crystallization experiment opportunities on the International Space Station conducted by Japan Aerospace Exploration Agency. If you are interested in the high resolution of structure, space crystallization may be the answer to your needs.



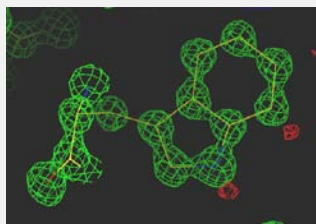
©NASA

5. X-ray diffraction data collection

The success rate of X-ray diffraction data collection using our cryoprotection skills is high.

6. Structural analysis

We have extensive experience in structural analysis using high-resolution X-ray diffraction data (e.g. beyond 0.8 Å).



4. Co-crystallization



Co-crystallization, in which we have acquired a lot of skill, is necessary for protein-ligand complexes. Customers can submit ligand compounds anytime after developing a crystallographic platform for the target protein.

Alliance for C-Platform Service

Confocal Science : Organizer of the alliance

Maruwa Foods and Biosciences, Experts in X-ray protein crystallography

Wako Pure Chemical Industries, Experts in protein expression



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