

生物化學所蛋白質 X-光結晶學設施使用規範

一、使用前須知

1. 初次使用者，請先至中研院線上預約系統申請帳號（連結顯示於下），並利用預約系統申請本設施的服務。
(<https://reservation.iis.sinica.edu.tw/servlet/SignInHandler>)
2. 本設施所有服務項目、收費標準及相關注意事項請見本規範第 3 頁。
3. 用戶如需洽詢初步的諮詢或細節討論，可根據預約系統上每個服務項目指定聯絡人之聯絡資訊進行洽詢。本設施 3 位人員聯絡資訊如下：
黃開發 博士: (Tel) 02-27855696 ext. 3090; (Email) huangkf@gate.sinica.edu.tw
施惠玲 小姐: (Tel) 02-27855696 ext. 3140; (Email) mbce00326@gate.sinica.edu.tw
柯子平 博士: (Tel) 02-27855696 ext. 3090; (Email) kotping@gate.sinica.edu.tw

二、蛋白質晶體篩選送件須知

1. 送件前，請先查詢與樣品相同或性質相近之蛋白質的養晶條件，以利於養晶篩選條件的選擇。
2. 於線上預約系統勾選擬欲使用的養晶篩選條件，並填寫樣品相關資料。本設施所有養晶篩選條件資料可由下面連結取得。
(<https://www.ibc.sinica.edu.tw/facilities/protein>List of screening suite-20230410.pdf>)
3. 送出案件申請後，本設施人員將於一個工作天內與您確認上機及進行 pre-crystallization test (PCT) 的時間。原則上，用戶送出案件申請的先後將決定其預約日期的優先順位。
4. 進行 PCT 測試時，用戶請於預約之時間攜帶約 10 μl 蛋白質樣品（濃度約 10 mg/ml）至生化所 3 樓 314 室，由本設施人員帶領進行測試。
5. 為避免晶體篩選設備針頭塞住，用戶樣品需事先離心過，樣品緩衝液應避免含高鹽類或 detergents，如因用戶樣品的雜質或沉澱物導致晶體篩選設備針頭塞住，用戶需負擔購買新針頭的費用。
6. 用戶如已預約晶體篩選時間，但未如期將樣品送至本設施，除有特殊理由，仍要負擔當日基本維運費用 NT\$1000。

7. 進行晶體篩選時，當樣品有突發狀況往往需要緊急詢問用戶的意見，因此用戶應盡量能夠在場，否則篩選過程一旦樣品出現預期外的狀況，所有後果將由用戶自行負責。

三、X-光數據收集、晶體結構解析、電腦分子模擬及整合性服務送件須知

1. 在案件受理的優先順位上，當同時有生化所（案件編號為 CA○○○○○）及非生化所用戶（案件編號為 DI○○○○○）送件時，優先處理生化所用戶委託的案件。當同為生化所用戶或同為非生化所用戶案件時，將以案件送出時間先後作為優先順位，亦即案件編號小者優先。
2. 針對晶體結構解析、電腦分子模擬及整合性服務，原則上採取合作的模式。當發表論文時，本設施人員對於 IP 有貢獻者將共享 authorship。

四、生化所 3 樓 314 室使用須知

1. 用戶未經許可勿擅自將 314 室之物品攜出，如欲借用請告知管理者（黃開發博士或施惠玲小姐）並填寫借用登記簿。
2. 禁止攜入毒化物、放射性、感染性、生物檢體或腐蝕性物質，液態氮及有機溶劑請在指定地方操作。
3. 本設施禁止飲食，禁止戴手套開門、開抽屜、操作顯微鏡及其它儀器，也禁止在本設施電腦上網、看影片、安裝軟體或進行任何非實驗相關事情。
4. 用戶如違反上述規定，第一次違規將告知所屬 PI 並停用本設施服務 2 周，第二次違規則停用本設施服務 2 個月，第三次違規則喪失本設施服務使用資格。

五、致謝

1. 用戶使用本設施各項服務於發表論文時請務必予以致謝，範例如下：

We acknowledge the services provided by the Protein X-ray Crystallography Facility at the Institute of Biological Chemistry, Academia Sinica, Taiwan

Summary of service items and fee about the IBC Protein X-ray Crystallography service

Service items and fees (NTD/per unit)

	Only for IBC users
A. Robotic crystallization screening with 96-well plate⁽¹⁾	
A.1 Sitting-drop plate with 1 drop/per well (TW brand)	A.1 (550/plate)
A.2 Sitting-drop plate with 1 drop/per well (Greiner)	A.2 (1050/plate)
A.3 Sitting-drop plate with 3 drops/per well (Intelli-plate)	A.3 (850/plate)
A.4 Additive screening with sitting-drop plate (TW brand)	A.4 (550/plate)
A.5 Additive screening with sitting-drop plate (Intelli-plate)	A.5 (850/plate)
A.6 Screening with user-prepared plate	A.6 (500/plate)
A.7 Screening with user-prepared conditions ⁽²⁾	A.7 (640/plate)
A.8 Screening with user-prepared plate and conditions	A.8 (340/plate)
B. Manual crystallization screening with 96-well plate^{(1),(3)}	
B.1 Sitting-drop plate with 2 drops/per well (Intelli-plate)	B.1 (570/plate)
B.2 Sitting-drop plate with 1 drop/per well (TW brand)	B.2 (340/plate)
C. Incubators for crystallization plates	
Incubators for crystallization plates ⁽⁴⁾	(20/plate/month)
D. Crystal inspection with UV-imaging system	
Crystal inspection with UV-imaging system ⁽⁵⁾	Free of charge
E. Crystal refinement, soaking and co-crystallization⁽⁶⁾	
E.1 24-well hanging-drop plate (TW brand)	E.1 (200/plate)
E.2 24-well hanging-drop plate without sealant (int'l brand)	E.2 (250/plate)
E.3 24-well hanging-drop plate with sealant (int'l brand)	E.3 (350/plate)
E.4 96-well sitting-drop plate (TW brand)	E.4 (150/plate)
E.5 24-well sitting-drop plate (int'l brand)	E.5 (250/plate)
E.6 48-well sitting-drop plate (int'l brand)	E.6 (350/plate)
E.7 96-well sitting-drop plate (int'l brand)	E.7 (350/plate)
F. Stock solutions for crystallization condition optimization	
Stock solutions of various polymers, organics, salts and buffers (2-22 ml/per unit)	(200/per unit)
G. Customized crystallization strategy	Consultation
H. Design of expression construct for increasing crystallization probability	Consultation
I. X-ray data collection	
I.1 Crystal shipping to synchrotron radiation center	I.1 (200/puck) ⁽⁷⁾
I.2 X-ray diffraction test with synchrotron light source ⁽⁸⁾	I.2 (400/condition)
I.3 X-ray data collection with synchrotron light source ⁽⁹⁾	I.3 (1500/condition)
J. Structure determination, model building, refinement and validation	
J.1 Crystal structure determination ⁽¹⁰⁾	Collaboration. User should pay the manpower cost at 400/per hour .
J.2 Model building, refinement and validation for X-ray crystallographic data ⁽¹⁰⁾	Collaboration. User should pay the manpower cost at 400/per hour .
J.3 Model building for cryo-EM data ⁽¹¹⁾	Collaboration. User should pay the manpower cost at 400/per hour .
K. Integrated service (from purified protein to validated crystal structure)	Collaboration ⁽¹²⁾
L. Homology modeling, molecular docking and simulation	Collaboration. User should pay the manpower cost at 400/per hour .

⁽¹⁾A pre-crystallization test (PCT) of protein concentration is included. Free for 3-month storage of the plates in our incubators.

⁽²⁾The facility provides the sitting-drop Intelli-plate.

⁽³⁾The facility provides all the consumables and reagents, but users should set up the crystallization plates themselves.

⁽⁴⁾User gets 3-month free storage if the plates are set up via the core service.

⁽⁵⁾Only the UV-compatible plates are allowed.

⁽⁶⁾The facility provides cover slides, tape and other relevant tools, **but not** crystallization solutions.

⁽⁷⁾Each puck can be loaded with up to 16 crystals.

⁽⁸⁾User should pay the fee of crystal shipping.

⁽⁹⁾User should upload the preliminary diffraction data for full data set collection and pay the fee of crystal shipping. All publications resulting from the use of TPP synchrotron beamtime should acknowledge TPP.

⁽¹⁰⁾User should upload the crystal picture, X-ray diffraction image and data-collection statistics and the facility has the right to decide whether a case will proceed.

⁽¹¹⁾The facility has the right to decide whether a case will proceed.

⁽¹²⁾User must provide manpower and pay the usage fee for the fee-based service items.