

Crystal Spec Sheet

Page number (/)

This file name should be "proposal number"_sample.pdf.

ex: 2016B0000_sample.pdf

Please copy and add this page, if you have more than three types of samples.

Sample type ID				
Objective & purpose ※1				
Experimental time required				
Target	Name of protein etc.			
	Molecular weight			
	Preparation method ※2			
	Safety ※3			
Crystal	Size			
	Reproducibility			
	Time to Growth			
Preliminary study	Lattice constant			
	Space Group			
	#Mol / asymm. unit			
	Max resolution			
	X-ray source			
	Condition of cryocool			
Meas. condition	#Types (WT/mutants)			
	#Heavy atoms			
	#Crystals to be checked			
	#Data sets			
	Frames x exp. time			
	Beamline devices			

※1: Select from following, **A**: For molecular replacement and mutant study, drug binding etc,
B: For isomorphous replacement phasing (incl. anomalous diffraction) cf. MIR, SAD, **C**:
 Crystal check only, **D**: Other, Please describe its detail. Ex. High resolution data collection.

※2: **A**: E. coli expression, **B**: Baculovirus-insect cell expression, **C**: Human cell expression
 cf. HEK293, **D**: Other [Please describe its detail.]

※3: Ex. Protein toxin, Poisonous heavy atom (Hg etc), Contamination of baculovirus.

Crystal Spec Sheet [Example]

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Sample type ID		HMP-TETR	HDN-ORTH	MDN-Unk
Objective & purpose ※1		A (Ligand-cmplx)	B (SIR-AS)	C
Experimental time required		5 hr	3 hr	6 hr
Target	Name of protein etc.	Human Matrix protease	Human DNase	Mouse DNase
	Molecular weight	25k	33k	33k
	Preparation method ※2	A: BL21(DE3)	B: Sf9	C: HEK 293
	Safety ※3	Safe	Hg deriv, Contam. baculovirus	Safe
Crystal	Size	100 um cubic	200 x 100 x 10 um	100 x 100 x 20 um
	Reproducibility	Well	Unknown	Well
	Time to Growth	3 d ~ 1 w	> 6 m	< 2 w
Preliminary study	Lattice constant	105,105,45	50, 55, 82	Not determined
	Space Group	<i>P</i> ₄ ₃ <i>2</i> ₁ <i>2</i>	<i>P</i> ₂ ₁ <i>2</i> ₁ <i>2</i> ₁	-
	#Mol / asymm. unit	Monomer	2 Monomers	-
	Max resolution	1.8 Å	3.5 Å	-
	X-ray source	SPring-8 BL38B1	Rigaku FR, Raxis	-
	Condition of cryocool	Determined	Determined	Not determined
Meas. condition	#Types (WT/mutants)	3 (Ligand 3)	1 (WT only)	1 (WT only)
	#Heavy atoms.	0	1 (Hg)	0
	#Crystals to be checked	25	10	50
	#Data sets	6	4	2
	Frames x exp. time	180 x 4 sec@BM	180 x 4 sec@BM	180 x 10 sec@BM
	Beamline devices	Cryostream	Cryo or HAG	Cryo or HAG

Very rough estimates of experimental time:

Crystal Check: 5 min @ID & BM

Data Set: 5 min = 1,800 fr. x 0.1 deg x 0.1 s. exp @ID,

0.5 hr = 180 fr. x 5 s. exp @BM

Diffraction scan: 5 min @ ID

(incl. sample mount/unmount, centering etc.)