

## **Sample Alignment (CALSA) Part**



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## 1. How to set Part conditions

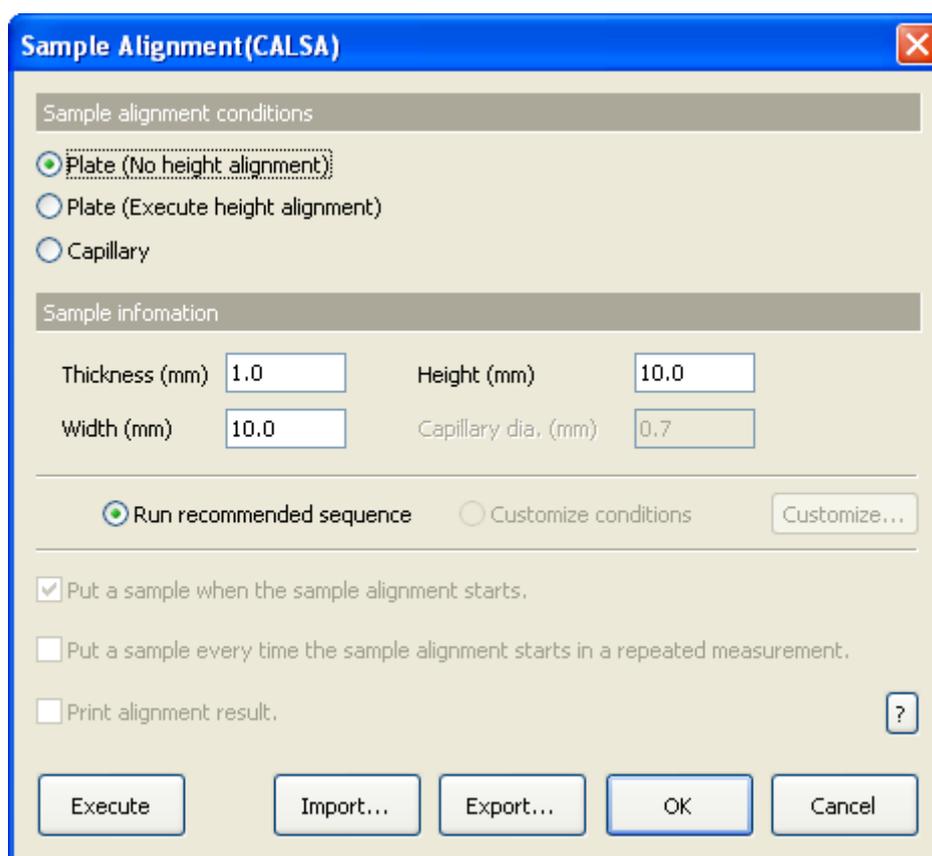
In this chapter, how to set the **Sample Alignment (CALSA)** Part conditions is described.



**CAUTION:** CALSA, the ultra-high resolution spiral analyzer, will be required for proper execution of this Part.

### 1.1 Setting conditions

Set the basic conditions in the **Sample Alignment (CALSA)** dialog box.



**Fig. 1.1.1 Sample Alignment (CALSA) dialog box**

**Plate (No height alignment)** Sets the omega zero offset to the predetermined optimal value for the current optics, and drives the Z axis to the reference position (factory default). No additional alignment will be performed.



**Tip:** The current optics attribute and predetermined optimal position of each axis can be confirmed in the **Optics Management** dialog box. For more information, refer to Chapter 17 of the *SmartLab Guidance Reference Manual (ME13365A)*.

**Plate (Execute height alignment)**

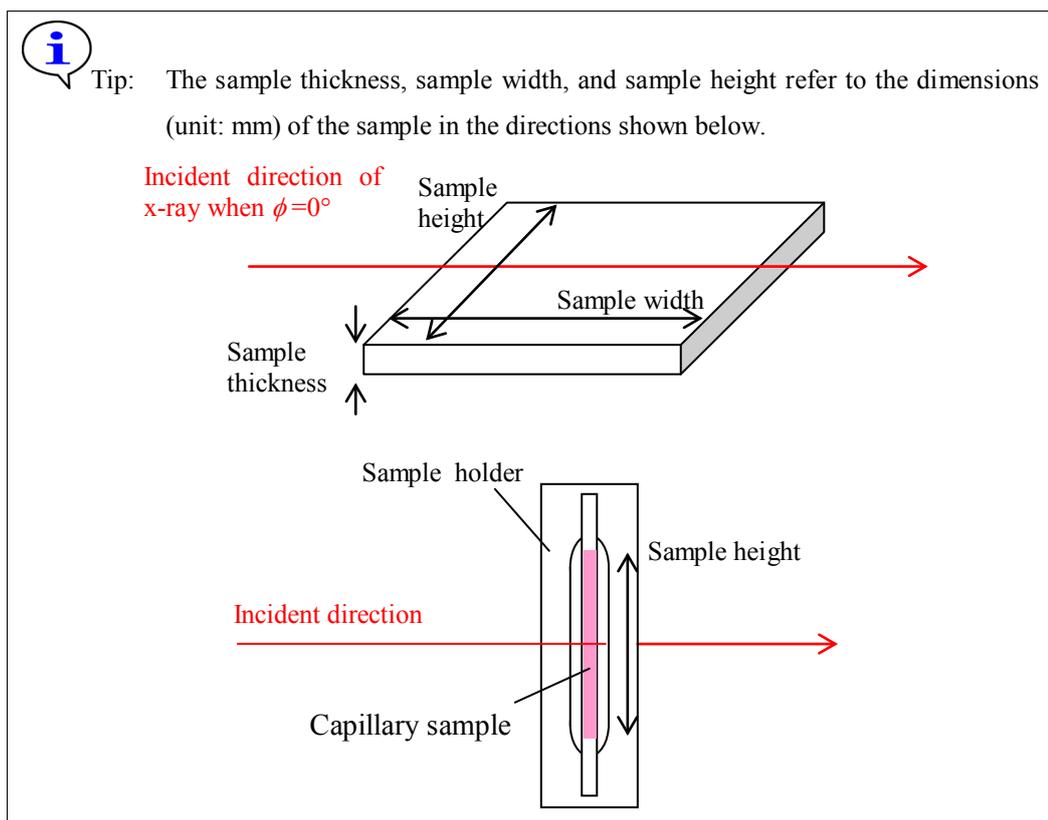
Performs the height alignment by the Z scan and Omega scan.

**Capillary**

Performs the height alignment by the Z scan.

## 1. How to set Part conditions

<b>Thickness (mm)</b>	Enter the sample thickness in mm. For a thin film sample, enter the overall thickness of the sample, including the thickness of the substrate.
<b>Width (mm)</b>	Enter the sample width.
<b>Height (mm)</b>	Enter the sample height.
<b>Capillary dia. (mm)</b>	If <b>Capillary</b> is selected, enter the diameter of the capillary to be used.



**Run recommended sequence** Performs the in-plane sample alignment using the recommended sequence.



**CAUTION:** This version does not allow the user to set scan conditions and slit conditions of the sample alignment.



**Tip:** It takes about 10 minutes for the plate sample alignment (Execute height alignment) and about 5 minutes for the capillary sample alignment to complete.

**Put a sample when the sample alignment starts.**

If the sample is mounted (or changed) before the sample alignment starts, check the **Put a sample when the sample alignment** box. If the sample alignment is performed using the currently-mounted sample, uncheck the **Put a sample when the sample alignment** box.

## Put a sample every time the sample alignment starts in a repeated measurement.

If the sample is changed every time the sample alignment starts in a repeated measurement using the loop Parts or XY mapping Parts, check the **Put a sample every time the sample alignment starts in a repeated measurement** box. If the sample is mounted during the first cycle only, uncheck the **Put a sample every time the sample alignment starts in a repeated measurement** box.

## Print alignment result

Only when **Capillary** is selected as the sample alignment condition, and if the Print alignment result box is checked, the alignment result will be printed out with the format shown below after alignment.

SmartLab Guidance(TM) administrator(Service Engineer)

Sample Alignment Results(Sample Alignment(CALSA))

Goniometer:SmartLab(In-plane)	Optics Attribute:Ultra high resolution parallel beam PB-Ge(220)x2/CALSA
Base attachment configuration:Chi phi Z cradle	Optics Alignment Name:@Ultra high resolution parallel beam PB-Ge(220)x2/CALSA
Base att. config:Standard	
CBO selection slit:CBO unit	
Incident optical device:Standard incident optical	
Incident parallel slit:Incident parallel slit	
Incident slit box:Standard incident slit box	
Length limiting slit:Length limiting slit	
Receiving slit # 1:Standard receiving slit box #	
Filter:None	
Standard receiving unit # 1:Standard receiving u	
Standard receiving optical unit:Standard receivi	
Receiving slit # 2:Standard receiving slit box #	
Attenuator:Standard Attenuator	
Diffraction beam monochromator:None	
Monochromator slit:None	
Detector # 1:D/teX Ultra	

Axis	Position	Offset
2-Theta		0.7932 deg
2-ThetaChi		0 deg
Omega		0.4954 deg
Theta_d		0 deg
Ts	-5.70488 mm	
Zs	-1.48719 mm	
Z	0.0000 mm	
Omega_a	0 pulse	
Zc	-1.384281 mm	

Z

Date : Jun-01-2010 13:34:55  
 X-Ray : 45 kV , 200 mA (CuKa)  
 Peak Position : 0.0708 mm

1/1

Jun-01-2010 14:03:19



Tip: If **Plate (No height alignment)** is selected and the **Print alignment result** box is checked, only the predetermined optimal axis positions for the current optics are printed out.

**Execute**

Executes the sample alignment under the conditions specified in the **Sample Alignment (CALSA)** dialog box.



**CAUTION:** Clicking the **Cancel** button after executing the sample alignment does not cancel the specified conditions.



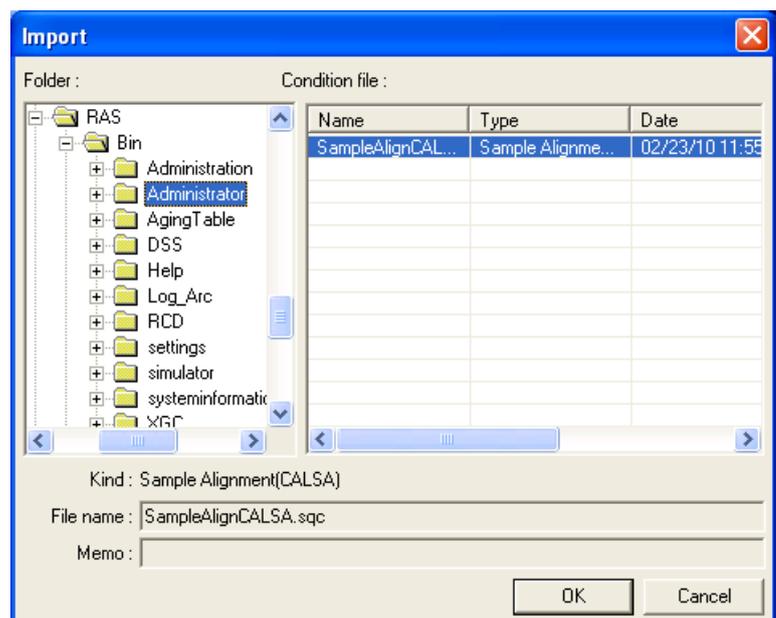
**Tip:** The sample alignment is executed with the **Sample Alignment (CALSA)** dialog box open. While the sample alignment is running, the Part conditions cannot be changed. They can be changed again after the alignment has been completed.

The setting of  (Show confirmation messages) on the flow bar becomes invalid.

**Import**

Loads the saved Part conditions.

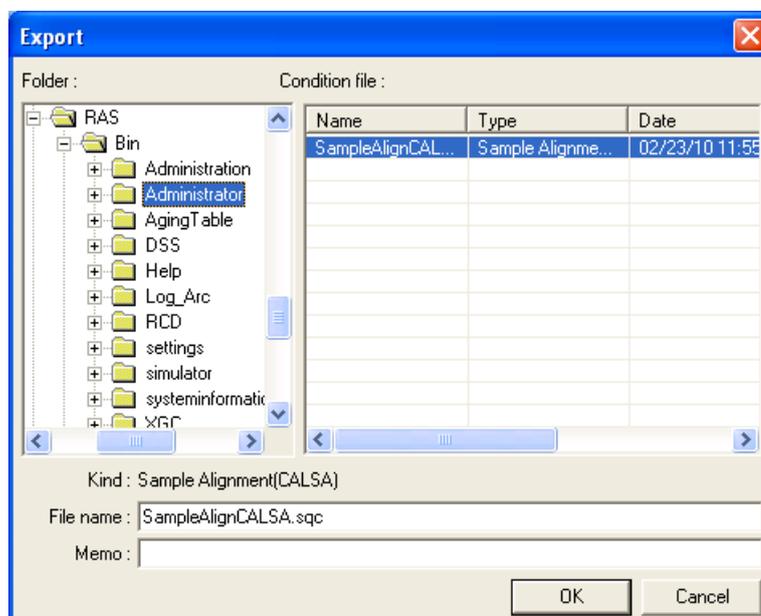
Clicking the **Import** button opens the **Import** dialog box. Select the folder including the file you want to import from the **Folder** tree view. In the **Condition file** list, select the condition file you want to import and click the **OK** button to load the Part conditions.



**Export**

Saves the specified Part conditions in a file.

Clicking the **Export** button opens the **Export** dialog box. From the **Folder** tree view, select a destination folder to save the conditions file then enter a file name in the **File name** box. Enter comments in the **Memo** box, if needed. After entering them, click the **OK** button.

**OK**

Sets the conditions and closes the dialog box.



**CAUTION:** When selecting another Package measurement or switching the task to the **Manual Control** task, etc. the specified conditions will be cancelled. To save the specified conditions in a file, click the **Export** button and save the conditions.

**Cancel**

Does not set the conditions and closes the dialog box.

**?**

Opens the online help of this Part.



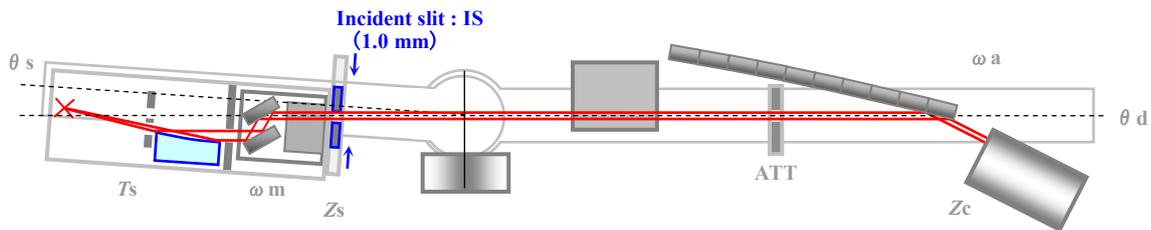
## 2. Sample alignment sequence

The sample alignment is performed automatically. However, the sample, and parts such as a Capillary spin attachment must be installed (or removed) manually as instructed by messages displayed on the screen.

Described below is the general sample alignment sequence.

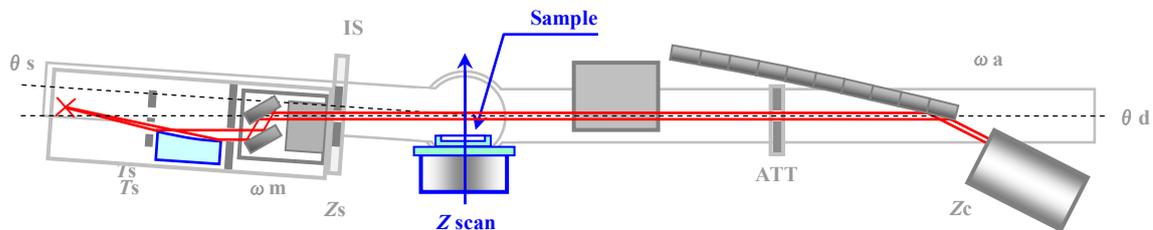
### 2.1 Plate (Execute height alignment)

- (1) Drive the omega axis and the 2-theta axis to the predetermined position for the current optics.  
Set the IS width to 0.1 mm.



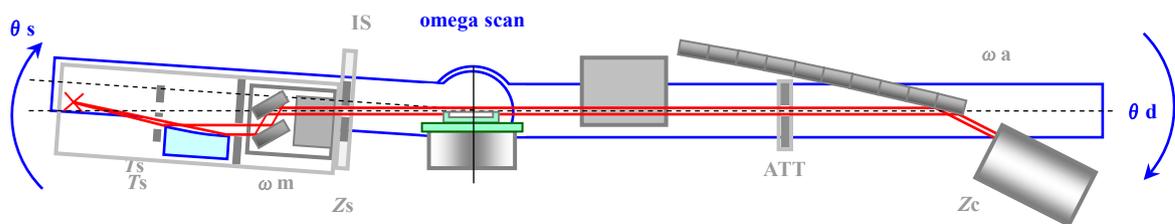
**Fig. 2.1.1 Setting of the initial positions of the goniometer axes**

- (2) Put the sample spacer, wafer sample plate, sample (Plate), and incident length-limiting slit to the attachment as instructed by the message.
- (3) Scan the Z axis, then drive the Z axis to the position at which the incident x-ray beam is blocked and reduced to 50% intensity by the sample.



**Fig. 2.1.2 Alignment based on Z scan**

- (4) Scan the omega axis, then drive the omega axis to the profile peak position.



**Fig. 2.1.3 Alignment based on omega scan**

- (5) Repeat steps (3) and (4).

