

Sample Alignment (PB/PSA) Part

Contents

1.	How to set Part conditions	1
1.1	Setting conditions	1
1.2	Customizing scan conditions and slit conditions	6
2.	Sample alignment sequence	11

1. How to set Part conditions

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

1.1 Setting conditions

Set the basic conditions in the **Sample Alignment (PB/PSA)** dialog box.

The scan conditions and slit conditions of the sample alignment are determined based on the basic conditions. The scan conditions and slit conditions can also be customized.

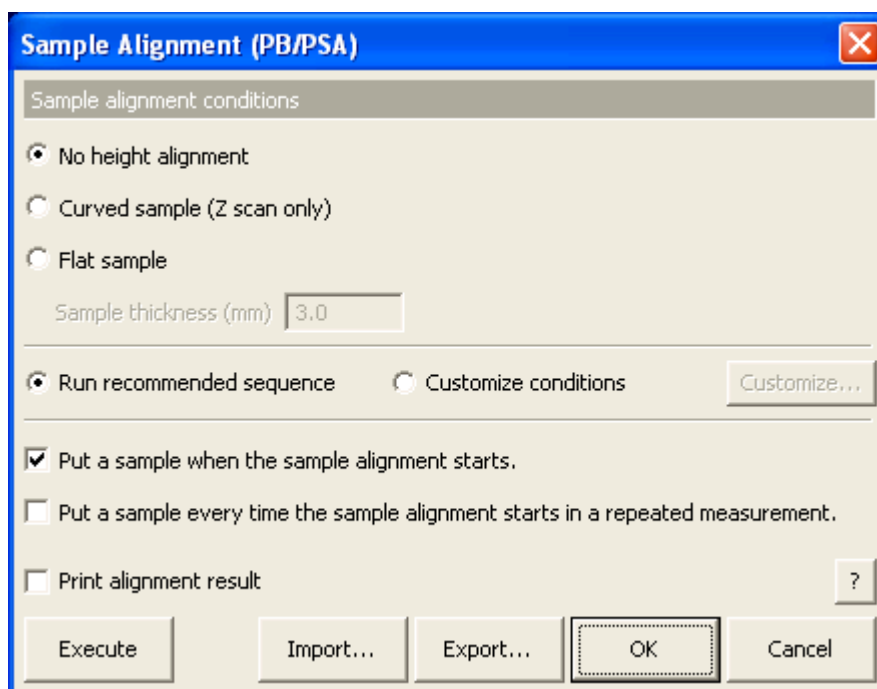


Fig. 1.1.1 Sample Alignment (PB/PSA) dialog box

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.



CAUTION: If the current optics attribute is “Bragg-Brentano focusing”, this Part cannot be executed.



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)*.

Curved sample (Z scan only) Performs the height alignment by the Z scan.

Flat sample	Performs the sample alignment according to the sequence described in Chapter 2.
Sample thickness (mm)	Enter the sample thickness when Curve sample (Z scan only) or Flat sample is selected.
Run recommended sequence	Performs the sample alignment using the recommended sequence.
Customize conditions	Performs the sample alignment under the conditions specified in the Customize dialog box.
Customize	When the Customize conditions radio button is selected, click the Customize button, then set the scan conditions and slit conditions.



[1.2 Customizing scan conditions and slit conditions](#)



Tip: It takes about 10 minutes for the sample alignment to complete.

Put a sample when the sample alignment starts.

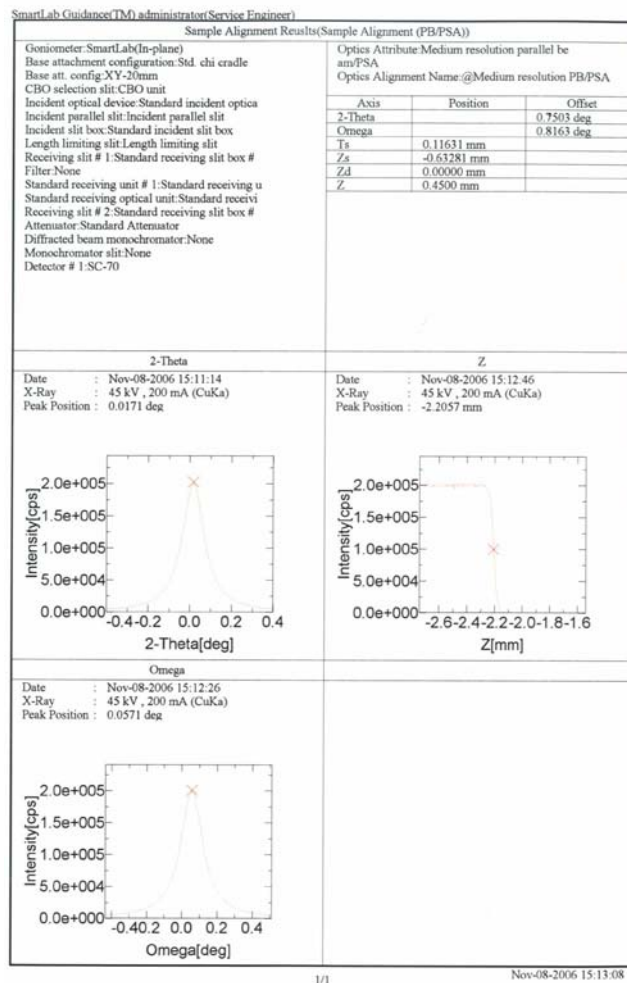
If the sample is mounted (or changed) before the sample alignment starts, check the **Put a sample when the sample alignment** box. If the sample alignment is performed using the currently-mounted sample, uncheck the **Put a sample when the sample alignment** box.

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

Check the **Print alignment result** box to print out the alignment results with the format shown below after alignment.



Tip: If **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 (PB/PSA)** dialog box.



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



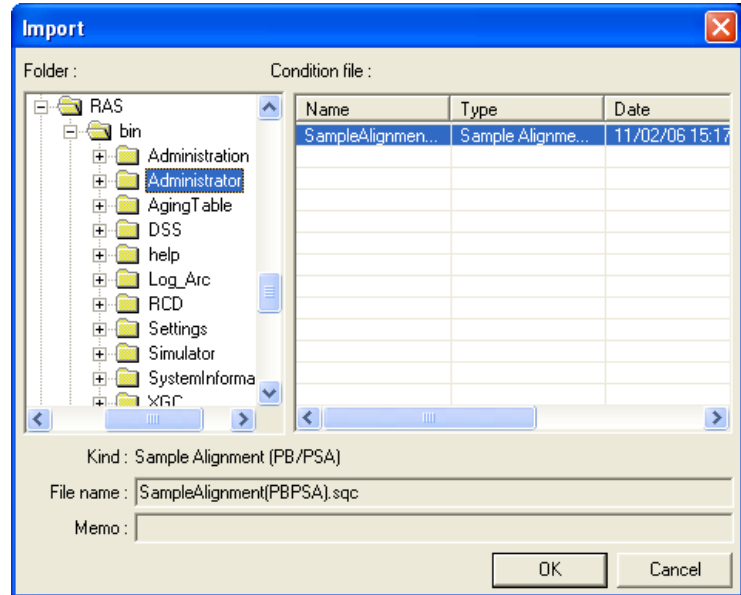
Tip: The sample alignment is executed with the **Sample Alignment (PB/PSA)** dialog box open. While the sample alignment is running, the Part conditions cannot be changed. They can be changed again after the alignment has been completed.

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

Import

Loads the saved Part conditions.

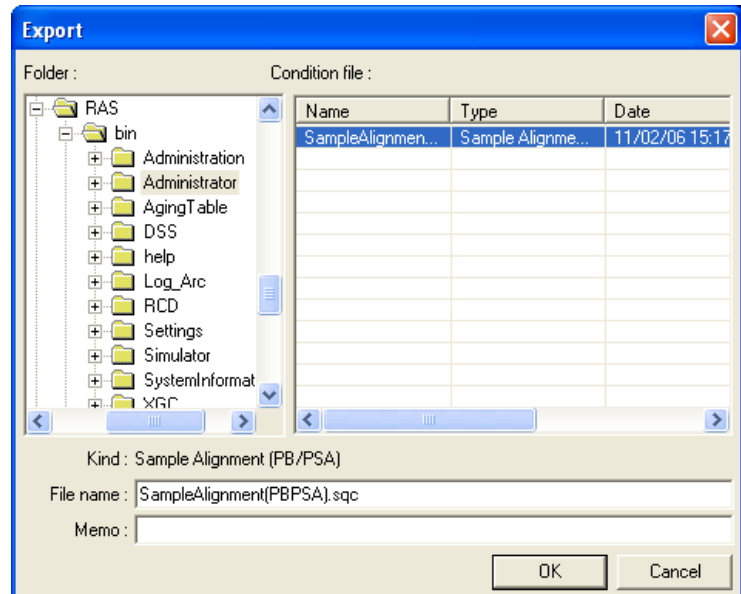
Clicking the **Import** button opens the **Import** dialog box. Select the folder including the file you want to import from the **Folder** tree view. In the **Condition file** list, select the condition file you want to import and click the **OK** button to load the Part conditions.



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.




Tip: Clicking the **Cancel** button also cancels the conditions specified in the **Customize** dialog box.

? Opens the online help of this Part.

1.2 Customizing scan conditions and slit conditions

If you want to customize the scan conditions and slit conditions of the sample alignment, set the conditions in the **Customize** dialog box.

 Tip: Refer to [2. Sample alignment sequence](#) to set the scan conditions and slit conditions.

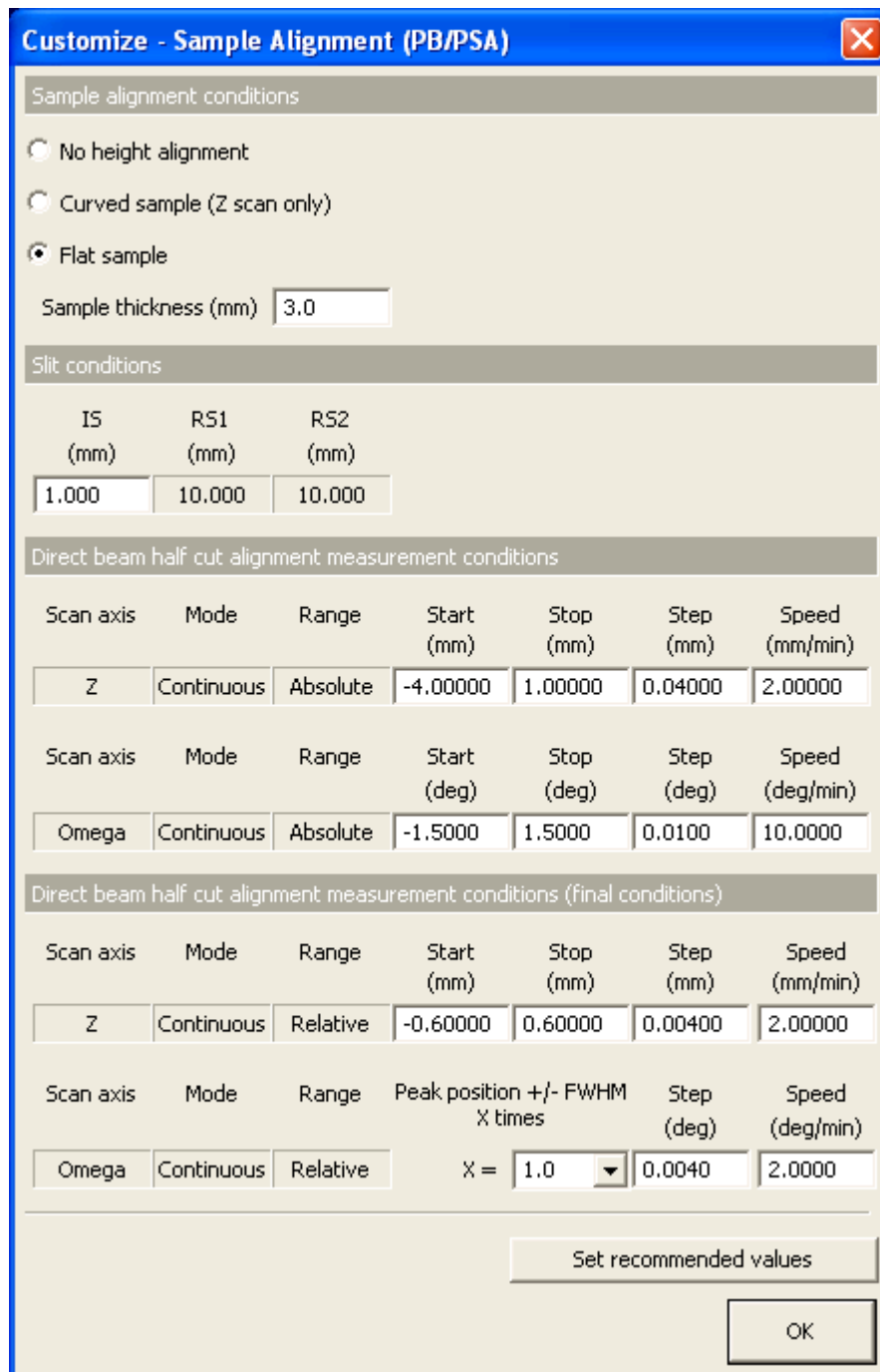


Fig. 1.2.1 Customize dialog box

Sample alignment conditions	
<input type="radio"/>	No height alignment
<input type="radio"/>	Curved sample (Z scan only)
<input checked="" type="radio"/>	Flat sample
Sample thickness (mm)	<input type="text" value="3.0"/>

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.



CAUTION: If the current optics attribute is “Bragg-Brentano focusing”, this Part cannot be executed.



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)*.

Curved sample (Z scan only) Performs the height alignment by the Z scan.

Flat sample

Performs the sample alignment according to the sequence described in Chapter 2.

Sample thickness (mm)

Enter the sample thickness when **Curve sample (Z scan only)** or **Flat sample** is selected.



Tip: When the **Close** button is clicked after setting conditions in the **Sample alignment conditions** section in the **Customize** dialog box, the conditions in the **Sample Alignment (PB/PSA)** dialog box will also be changed.

Slit conditions		
IS (mm)	R51 (mm)	R52 (mm)
<input type="text" value="1.000"/>	<input type="text" value="10.000"/>	<input type="text" value="10.000"/>

IS (mm)

Enter the incident slit width.



Tip: If data measurement will be made with a PSA of lower resolution (larger angular aperture) than that used for the sample alignment, it is not required to do sample alignment again.

resolution: PSA_0.114 deg > PSA_0.5 deg > PSA_1.0 deg



[2. Sample alignment sequence](#)

1. How to set Part conditions

Direct beam half cut alignment measurement conditions						
Scan axis	Mode	Range	Start (mm)	Stop (mm)	Step (mm)	Speed (mm/min)
Z	Continuous	Absolute	-4.0000	1.0000	0.0400	6.0000

Scan axis	Mode	Range	Start (deg)	Stop (deg)	Step (deg)	Speed (deg/min)
Omega	Continuous	Absolute	-1.5000	1.5000	0.0100	10.0000

Start (mm)

Enter the start position of the first and second Z scans. The value entered here will be used only when **Curved sample (Z scan only)** is selected.

Stop (mm)

Enter the stop position of the first and second Z scans. The value entered here will be used only when **Curved sample (Z scan only)** is selected.

Step (mm)

Enter the step width of the first and second Z scans. The value entered here will be used only when **Curved sample (Z scan only)** is selected.

Speed (mm/min)

Enter the scan speed of the first and second Z scans. The value entered here will be used only when **Curved sample (Z scan only)** is selected.

Start (deg)

Enter the start angle of the first omega scan.

Stop (deg)

Enter the stop angle of the first omega scan.

Step (deg)

Enter the step width of the first omega scan.

Speed (deg/min)

Enter the scan speed of the first omega scan.

Direct beam half cut alignment measurement conditions (final conditions)						
Scan axis	Mode	Range	Start (mm)	Stop (mm)	Step (mm)	Speed (mm/min)
Z	Continuous	Relative	-0.6000	0.6000	0.0040	2.0000
Scan axis	Mode	Range	Peak position +/- FWHM X times		Step (deg)	Speed (deg/min)
Omega	Continuous	Relative	X =	1.0	0.0040	2.0000

- Start (mm)** Enter the relative distance of the start position of the final Z scan from the direct-beam-half-cut position determined by the second Z scan.
- Stop (mm)** Enter the relative distance of the stop position of the final Z scan from the direct-beam-half-cut position determined by the second Z scan.
- Step (mm)** Enter the step width of the final Z scan.
- Speed (mm/min)** Enter the scan speed of the final Z scan.
- Peak position +/- FWHM X times**
Determine the start and stop angles of the final omega scan based on the peak position and FWHM obtained by the first omega scan. Select the **X** value from **0.5, 1.0, 1.5, 2.0, 3.0, or 5.0**.
- Step (deg)** Enter the step width of the final omega scan.
- Speed (deg/min)** Enter the scan speed of the final omega scan.



Set recommended values Sets the conditions in the **Direct beam half cut alignment measurement conditions** and **Direct beam half cut alignment measurement conditions (final conditions)** sections to the recommended values. The recommended values are shown in Table 1.2.1.

Table 1.2.1 Recommended values of direct beam half cut alignment measurement conditions and its final conditions

Direct beam half cut alignment measurement conditions	Scan axis	Range	Start	Stop	Step	Speed
	Z	Absolute	-4 mm	1 mm	0.04 mm	6 mm/min
	Omega	Absolute	-1.5 deg	1.5 deg	0.01 deg	10 deg/min
Direct beam half cut alignment measurement conditions (final conditions)	Scan axis	Range	Start	Stop	Step	Speed
	Z	Relative	-0.6 mm	0.6 mm	0.004 mm	2 mm/min
	Omega	Relative	Peak position +/- FWHM x 1		0.004 deg	2 deg/min

Close Closes the **Customize** dialog box.

2. Sample alignment sequence

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

Described below is the sample alignment sequence when **Flat sample** is selected in the **Sample alignment conditions** section.

- (1) Install the sample spacer, wafer sample plate, and sample as instructed by the messages displayed on the screen.
- (2) Drive the omega axis to the predetermined position for the current optics.
Adjust each slit width as shown in Fig. 2.1.

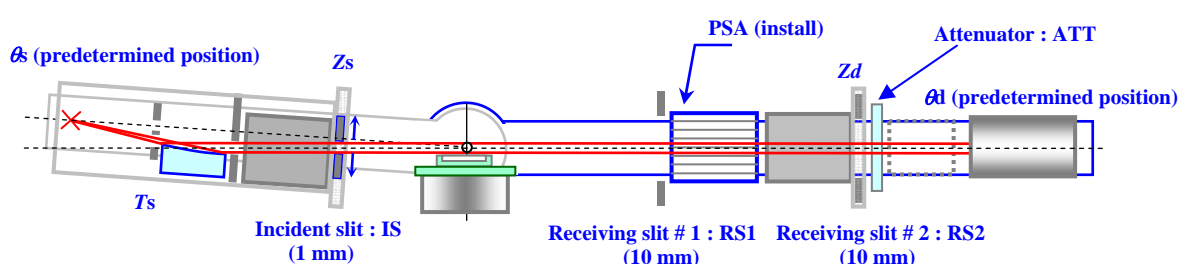


Fig. 2.1 Setting of the initial positions of the goniometer axes

- (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.

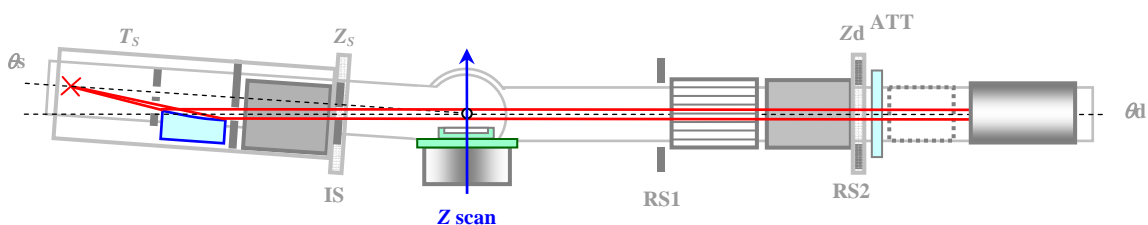


Fig. 2.2 Alignment based on Z scan

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

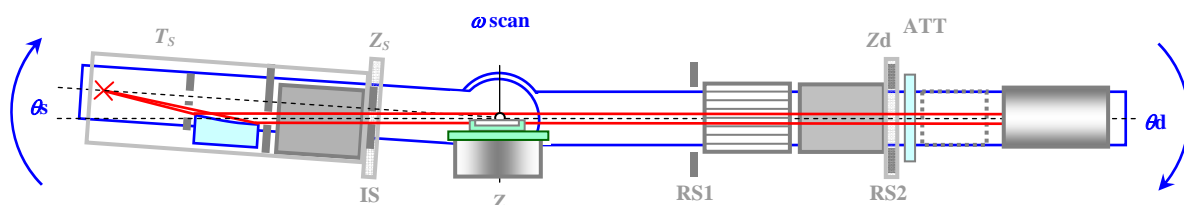


Fig. 2.3 Alignment based on omega scan

2. Sample alignment sequence

- (5) Repeat steps (3) and (4).
- (6) Scan the Z axis again, 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.

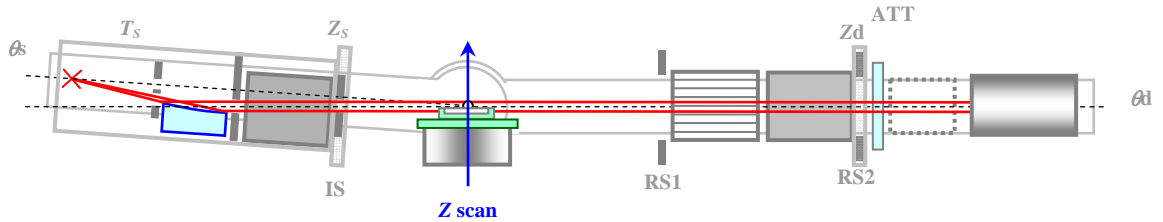


Fig. 2.4 Alignment based on Z scan

- (7) The position of the omega axis determined in step (5) is the position at which the sample surface is parallel to the incident x-ray beam. Set the omega zero offset value so that the position is 0° . The position of the Z axis determined in step (6) is the direct-beam-half-cut position of the sample.