Mirror Alignment Part

Contents

1.   How to execute the Part

In this chapter, how to execute the **Mirror Alignment** Part conditions is described.

> **i** Tip: The user does not have to set conditions for the **Mirror Alignment** Part because
> all the scan conditions and slit conditions are determined automatically.

1.1   Executing the Part

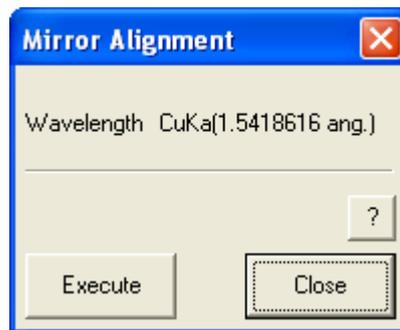Execute the mirror alignment from the **Mirror Alignment** dialog box.

Fig. 1.1.1   Mirror Alignment dialog box

Wavelength	Displays the wavelength of the incident x-rays obtained using the current optics.
Execute	Executes the mirror alignment.

☞   2.   Mirror alignment sequence

> **i** Tip: The mirror alignment is executed with the **Mirror Alignment** dialog box open.
> While the alignment is running, the buttons in the dialog box are disabled. They
> are enabled again after the alignment has been completed.
>
> The setting of ☷ (Show confirmation messages) on the flow bar becomes
> invalid.

Close	Closes the dialog box.
?	Opens the online help of this Part.

Parabolic multilayer mirror

A "parabolic multilayer mirror" is an artificial lattice of alternating film layers of heavy elements and light elements.

By altering the shape of the mirror and the thickness of the deposited layers, it is possible to convert divergent x-rays into parallel (less divergent) x-rays through the diffraction process.

Parallel beam measurements have applications in powder diffraction, general asymmetric diffraction measurements, and in conjunction with high resolution crystal optics.

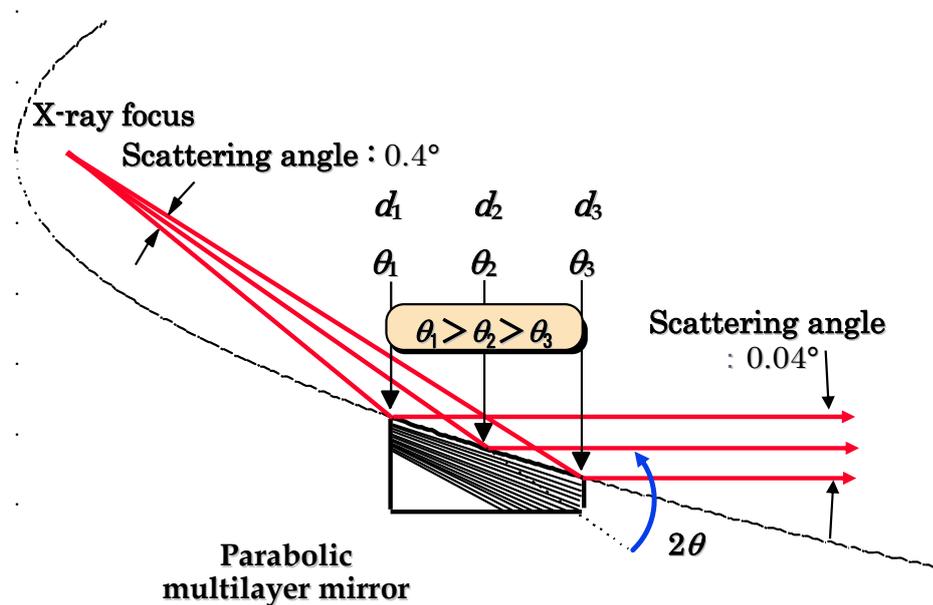The multilayer mirror is included as part of the Rigaku CBO unit to produce a parallel beam.

X-ray focus
Scattering angle : 0.4°

d_1 d_2 d_3
θ_1 θ_2 θ_3

$\theta_1 > \theta_2 > \theta_3$

Scattering angle : 0.04°

Parabolic multilayer mirror

2θ

Fig.   Parabolic multilayer mirror

2. Mirror alignment sequence

The mirror alignment is performed automatically. <u>However, the Kβ filter for Cu, Soller slit, etc. must be installed (or removed) manually as instructed by messages displayed on the screen.</u>

Described below is the mirror alignment sequence.

(1) Drive each axis of the goniometer to the initial position (theta_s = 1.0°, theta_d = 0.0°). Adjust each slit width as shown in Fig. 2.1.
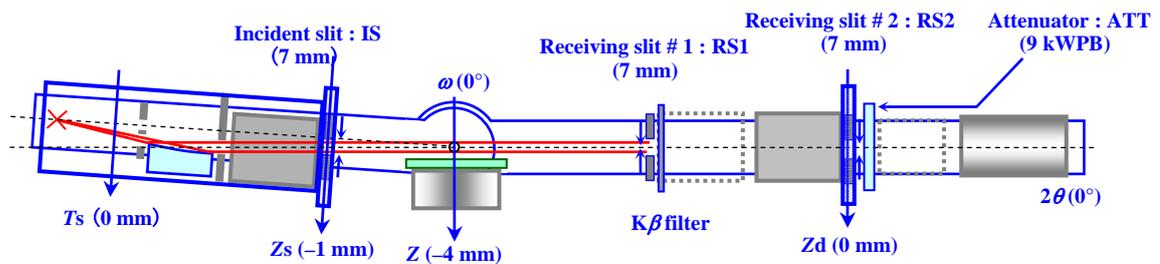

Fig. 2.1   Setting of the initial positions of the goniometer axes
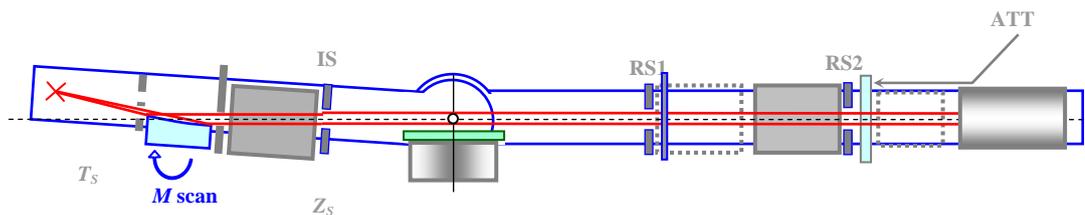
(2) Scan the *M* axis.

Fig. 2.2   Mirror alignment

(3) Drive the *M* axis to the position at which the x-ray intensity is the highest (the profile peak position).

(4) Perform the fine *M* scan around the peak position determined in step (3).

(5) Drive the *M* axis to the peak position, and set the position to the origin of the *M* axis (0 pulse).