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Crystal structure of 23S rRNA-binding protein L13 from hyperthermophilic archaeon *Pyrococcus horikoshii*

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Introduction

Ribosome, the enormous complex of proteins and RNAs, plays a principal role in the biosynthesis of protein. Recently, studies of the entire structure of ribosome, and the complex structure of ribosomal protein and rRNA have been rapidly advanced. Much information about translational mechanism was obtained from these results. The ribosomal assembly runs through a series of intermediate particles with increasing S-values, (i.e. increasing compactness). Ribosomal protein L13 is one of early assembly proteins essential for the functionally important conformational state during the early assembly. Ribosomal protein L13 is one of primary 23S rRNA-binding proteins. Three-dimensional structure of L13 may give structural basis on the principles of protein-RNA recognition.

Table 1. Data collection and refinement statistics

Wavelength (Å)	1.0
Temperature	room temperature
Space group	$P2_12_12_1$
Cell parameters (Å)	a = 41.08
	b = 51.54
	c = 64.20
Resolution (Å)	22.7-1.6 (1.69-1.60)
Total reflections	124,718
Unique reflections	17,561
Completeness (%)	94.8 (77.2)
Redundancy	7.1 (6.6)
R_{meas} (%)	3.3 (14.8)
Averaged $I/\sigma(I)$	12.6 (5.0)
Resolution range (Å)	8.0-1.6
Number of reflections	17,382
Residues included	127
Number of non-hydrogen atoms	
protein	1,038
solvent	300
R-factor (%)	21.2
R_{free} –factor (%)	22.7
Average B factor (Å^2)	24.42
Rms deviations	
bond lengths (Å)	0.0044
bond angles (°)	1. 15
dihedral angles (°)	21.5

Values in parentheses are for the outermost resolution shell.

Results

Ribosomal protein L13 from hyperthermophilic archaeon *Pyrococcus horikoshii* (PhoL13) was crystallized at 20°C by the hanging-drop vapor diffusion technique. The crystal of native PhoL13 was mounted a glass capillary. X-ray diffraction data set for native PhoL13 was collected up to 1.6 Å resolution at room temperature using the ADSC CCD detector and synchrotron radiation with 1.0 Å wavelength. Data were processed with MOSFLM and scaled with SCALA. Crystal of *Pho*L13 belongs to the space group $P2_12_12_1$, with unit-cell parameters of a=41.08 Å, b=51.54 Å and c=64.20 Å. The cell parameters of native PhoL13 were slightly different from ones of Se-Met PhoL13.

The structure of *Pho*L13 was determined by MAD method using Se-Met MAD data set, which was collected up to 1.8 Å resolution using cryogenic technique previously. Because the native crystal was not isomorphous with the Se-Met L13 crystal, a native PhoL13 model (Fig. 1) was obtained by molecular replacement using program AMORE. The model was rebuild on the electron density map after positional and temperature factor refinements. These steps were repeated several cycles and water molecules were added. The data collection and refinement statistics are summarized in Table 1. The structure detail of PhoL13 will be published elsewhere.

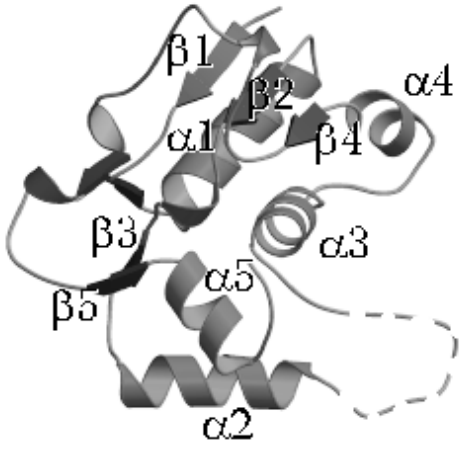

Figure 1. Ribbon diagram of *Pho*L13. The disordered region (residue 53-67) was connected with a dashed line.

References

[1] T. Nakashima et al., in preparation for publication.

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