

Structural Investigation on Proteasome α 7 ring in solution

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The 20S proteasome is known as a degrading factory for an unnecessary protein and then plays a very important role in protein-metabolic and immune systems. This huge complex protein has a hollow cylindrical shape consisting of four rings, α , β , β , α -rings. Both α and β rings are heptamers with α 1- α 7 subunits and β 1- β 7 ones, respectively. It has been reported that α 7 subunits in the solution also make a (homo) heptamer ring similar to a true (hetero) α -ring and then two rings make one dimer[1], which we call "double ring". But the detailed structure of this double ring is not clarified. Therefore, we performed SANS experiment of proteasome α 7 ring solution in order to solve the packing structure in detail.

The SANS experiment was carried out with SANS-U spectrometer of ISSP of University of Tokyo installed at JRR-3 of JAEA. The sample was proteasome α 7 solution with the concentration of 5mg/ml. The observed SANS intensity was corrected for background, cell, buffer scattering, and transmission factor.

Figure 1(a) shows structural parameters of packing structure of double ring: L is a radius of a ring and D is a distance between two rings. Figure 1(b) shows the observed SANS profile and some simulated SANS curves of which L is 42 Å and D is varied from 35 to 45 Å. As you can see from Fig. 2, the best compromised values are D of 35 Å in L of 42 Å: With the other value of L , the SANS curves show the larger deviation in all D values. With this structure model, analysis of a subunit exchange kinetics are now in progress.

Reference

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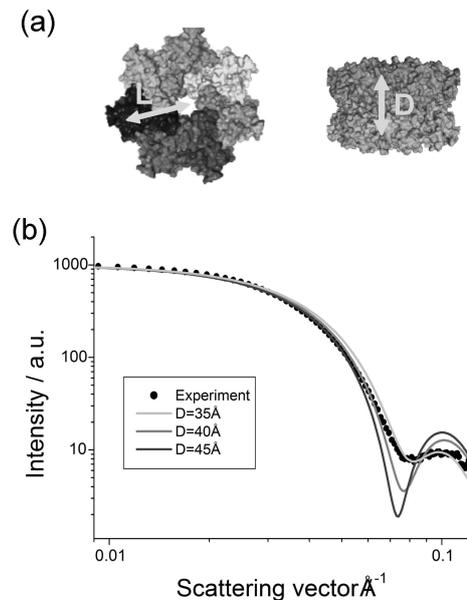


Fig. 1. Figure 1. (a) Structure parameters of a double ring. (b) Experimental and simulated SANS profiles of proteasome α ring.