

SAXS study of iron-binding Dps protein from *E.coli*Alexander Timchenko¹, Olga Ozoline², Sergey Antipov³, Masaji Shinjo⁴, Hiroshi Kihara^{5-7*}¹ Institute of Protein Research, Pushchino, Russia, 142290;² Institute of Cell Biophysics RAS, Pushchino, Russia, 142290;³ Department of Biophysics and Biotechnology, Voronezh State University, Russia, 394006;⁴ Department of Physics, Kansai Medical University, Hirakata, Osaka 573-1010, Japan⁵ SR Center, Ritsumeikan University, 1-1-1 Noji-Higashi, Kusatsu 525-8577, Japan⁶ Nagoya University SR Research Center, Furo-cho, Chikusa-ku, Nagoya 464-8601, Japan⁷ Himeji-Hinomoto College, 890 Koro, Kodera-cho, Himeji 679-2151, Japan

1 Introduction

The design of new materials using biological macromolecules is one of the priority sphere of the modern biotechnology. Nowadays the main interest is towards the biopolymers that could create self-assembled structure, and ferritin proteins are outstanding representatives of such biopolymers. These proteins are involved in iron storage and in protection against reactive oxygen species. The most diverse activities has bacterial ferritin Dps. Its functional unit consists of 12 identical subunits, forming a large hollow protein roughly spherical in shape. The hollow center is a crucial part of the protein since it provides a cavity for the accumulation of several hundred of iron ions, stored in the form of Fe₂O₃. This feature enables usage of Dps as a building block with calibrated ferromagnetic property for creation of compact nanodevices with highly ordered distribution of nanodots. Here we present SAXS pattern and solution structure of DPS protein from *E.coli*.

2 Experimental

Recombinant DPS ($M_w = 18.7$ kDa for monomer) was studied in SAXS experiments. The buffer 50 mM Tris-HCl pH 8.0, 25mM NaCl, 5% glycerol was used. The protein concentration was 1.16 mg/ml. Synchrotron X-ray measurements were done on a small-angle camera BL-6A (Photon Factory, Tsukuba) using PILATUS 100K detector. The range of scattering vectors $Q = 0.01 - 0.25 \text{ \AA}^{-1}$.

3 Results

SAXS pattern of DPS is presented in Fig.1. The initial part of scattering curve plotted in the Guinier coordinates is good linear character (not shown) pointed out the homogeneous state of DPS. For better accuracy we evaluated radius of gyration (R_g) and molecular mass (M_w) of protein from the distance distribution function $P(r)$ calculated by GNOM program [1] in the range of $Q = 0.02 - 0.25 \text{ \AA}^{-1}$. It was found that $R_g = (37.6 \pm 0.2)$ The evaluated molecular mass was $M_w = (230 \pm 10.0)$ kDa indicating that oligomeric structure of DPS is dodecamer.

We recovered the solution structure of DPS using DAMMIF program [2]. Its structure is shown in the insert of Fig.1 where the oligomeric structure of DPS is explicitly seen. The scattering pattern for this structure fits the experimental one with good accuracy (see Fig.1).

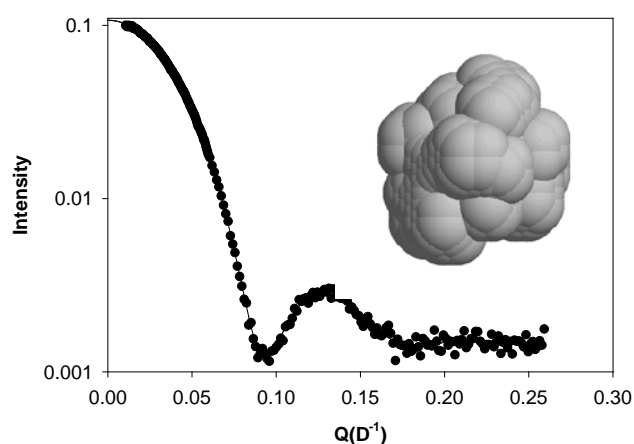


Fig. 1: The dependence $\log I$ versus Q for DPS (filled circles). Line is calculated scattering curve for the structure recovered by DAMMIF shown in the insert.

References

- [1] Svergun D., *J.Appl.Cryst.*, **25**, 495, 1992.
 [2] Franke D., Svergun D.I., *J.Appl.Cryst.*, **42**, 342, 2009.

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