

Cryo-electron microscopy structure of OBP chaperonin**Научный руководитель – Sokolova Olga****Wang Xi***Student (master)*Lomonosov Moscow State University, Биологический факультет, Кафедра биоинженерии,
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Chaperonin is a kind of structural protein which provide isolated environment to help protein folding and avoid inappropriate aggregations. Studied chaperonins are composed of 2 identical rings stacked back-to-back. Each ring contains several subunits that consist of three domains: equatorial, intermediate, and apical. The equatorial domain contains the nucleotide binding site, the apical forms the entrance to the folding chamber and the intermediate domain serves as a hinge between them providing flexibility (Skjærven *et al.*, 2015).

The working cycle of GroEL/GroES starts from binding of ATP and substrate protein to one ring of the GroEL. ATP and substrate binding facilitate GroES binding resulting in an encapsulation of the substrate (Chen *et al.*, 2013). ATP hydrolysis enables ATP binding in the opposite *trans* ring which triggers the discharge of ligands from the *cis* ring, a new cycle of GroEL mediated folding is initiated (Zang *et al.*, 2016). Besides, there is a new discovery that ring separation occurs after completion of ATP hydrolysis in the *cis* ring and is triggered by binding of a protein to the *trans* ring.

OBP chaperonin is encoded by the genome of *Pseudomonas fluorescens* bacteriophage OBP. Using cryo-EM method and data processing software RELION-3.0, we determined the structure of OBP chaperonin at 4.6 Å resolution. OBP chaperonin is purified as a single heptameric ring with identical subunits which is unlike the usual double-ring architecture of chaperonin (Semenyuk *et al.*, 2016). Owing to equatorial is a solid α -helical domain which is responsible for providing intra- and inter- ring contacts, it possesses C7 symmetry. However, asymmetry is found in the apical domain. This domain requires sufficient flexibility to serve as an entrance for the formation of the chamber, and three subunit pairs and one unpaired subunit are observed. In this case, the resolution varies depending on the flexibility of the different domains. The resolution in equatorial domain is the best while the apical domain has the lowest resolution owing to the most flexible structure. The resolution of intermediate domain is in between.

References

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Illustrations

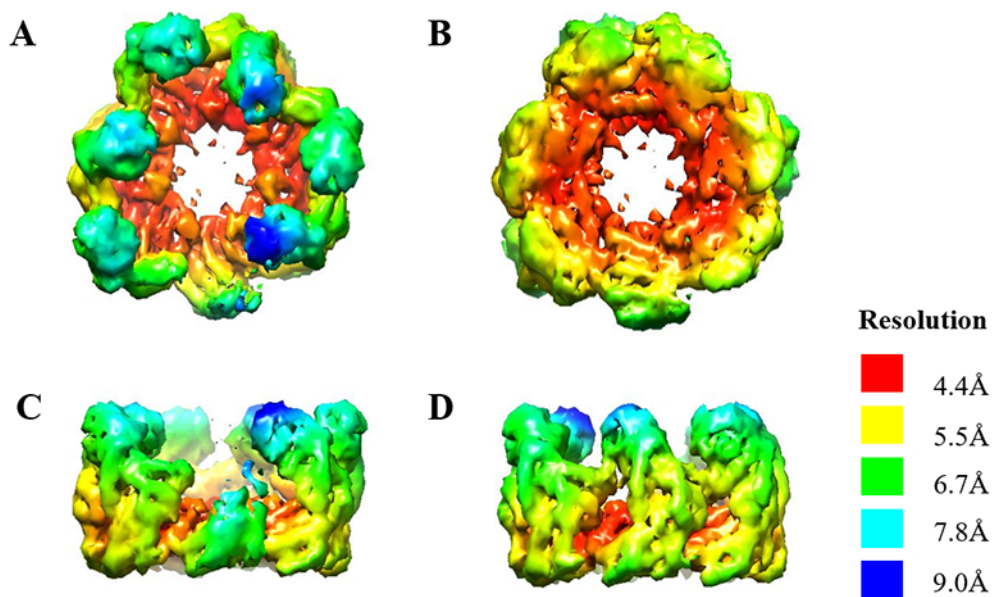


Рис. 1. Views of Native State OBP Chaperonin Reconstruction at 4.7 Å Resolution