Folding-analogs of ATPase *RavA* of *Lokiarchaeota*

Tabulina A.M.1, Venger A.M.1, Venger O.O.2, Pasternak S.L3.

1 Department of microbiology, virology and immunology, Odessa National Medical University, Valychovski Lane, 2, Odesa-65000, Ukraine.

E-mail: *email.of.* *corresponding\_author@server.com*

2 Plant Breeding and Genetics Institute – National Center of Seed and Cultivar Investigation, Ovidiopol’ska doroga Str., 3, Odesa-65036, Ukraine.

3 Odessa National University of I. I. Mechnikov, Dvoryan’ska Str., 2,Odesa-65082, Ukraine.

*ATPase RavA* is important membrane enzyme in prokaryotes. Genetic relationship of microorganisms can be associated with polymorphism of this enzyme.The aim of current scientific work was the modulation of the three-dimensional structure and search of folding-analogs of ATPase *RavA* of *Lokiarchaeota*. Models were built based on the target-template alignment using ProMod3. Coordinates which are conserved between the target and the template are copied from the template to the model. Insertions and deletions are remodeled using a fragment library. The geometry of the resulting model is regularized by a force field. In case loop modelling with ProMod3 fails, an alternative model is built with PROMOD-II [1]. As result, three-dimensional structure of CaCA was calculated by folding-analogs (fig. 1). Three of them are statistically correct: Magnesium chelatase, DNA replication licensing factor MCM7 and Minichromosome maintenance protein MCM.

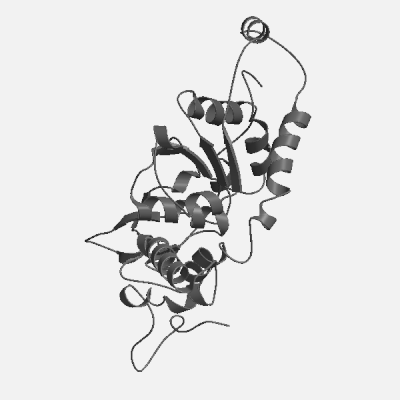


Fig. 1. Structure of ATPase RavA of *Lokiarchaeota*

*1 Guex N., Peitsch M. C.* SWISS-MODEL and the Swiss-PdbViewer: an environment for comparative protein modeling // Electrophoresis.-1997.-**18**, N 15.-P. 2714-2723.