

The Titan Krios microscope at the ESRF and Lysine decarboxylases from bacteria: similar structures and different functions

C.Mueller-Dieckmann¹ & E. Kandiah²

Affiliation: ¹ESRF, 71, Ave. des Martyrs, 38000 Grenoble, France, muellerd@esrf.fr

²IBS, 71, Ave. des Martyrs, 38000 Grenoble, France, isai.kandiah@ibs.fr

The delivery of state-of-the-art high end Titan Krios cryo electron microscope (cryoEM) at the ESRF will allow ESRF's international users community to get free access to this device and to a cryoEM platform comprising several other machines located at the EPN campus. Access will be given at the beginning based on rolling access proposals and granted purely on scientific merit. Users support will be provided by scientists from the three partner institutes ESRF, EMBL and the IBS.

The inducible lysine decarboxylase LdcI is an enterobacterial acid stress response enzyme whereas LdcC is its close paralogue thought to play mainly a metabolic role. A unique macromolecular cage formed by two decamers of the *E. coli* LdcI and five hexamers of the AAA+ ATPase RavA was shown to counteract acid stress under starvation [1]. The pseudo-atomic resolution cryo-EM structures of the *E. coli* LdcI and LdcC, at pH optimal for their enzymatic activity [2] uncover differences between LdcI and LdcC explaining why only the acid stress response enzyme is capable of binding RavA. We identify interdomain movements associated with the pH-dependent enzyme activation and with RavA binding. Phylogenetic analysis reveals that certain enterobacteria exert evolutionary pressure on the lysine decarboxylase towards the cage-like assembly with RavA, implying that this complex may have an important function under particular stress conditions. In the same line, we also determined the cryo-EM structure of Lysine decarboxylase (LdcA) from *Pseudomonas aeruginosa* to 4.2Å resolution. LdcA forms a distinct group in Proteobacteria but lacks structural and functional characterization when compared to its *E.coli* counterparts such as lysine, arginine and ornithine decarboxylases. Together with phylogenetic and functional studies, the cryo-EM structure of LdcA presents several unique features.

References

- [1] - Malet H et al, Assembly principles of a unique cage formed by hexameric and decameric *E. coli* proteins. *Elife*. 2014 Aug 5;3:e03653. PMID:25097238
- [2] - Kandiah E et al, Structural insights into the *Escherichia coli* lysine decarboxylases and molecular determinants of interaction with the AAA+ ATPase RavA. *Sci Rep*. 2016 Apr 15;6:24601. PMID: 27080013