Crystal Structure of the NAD Kinase from Listera Monocytogenes <u>Gilles Labesse</u><sup>a</sup>, Guillaume Poncet-Montange<sup>a</sup>, Liliane Assairi<sup>b</sup>, Emmanuel Margeat<sup>a</sup>, Stefan Arold<sup>a</sup>, Anne-Marie Gilles<sup>b</sup>, <sup>a</sup>Centre de Biochimie Structurale, Montpellier, France. <sup>b</sup>Institut Pasteur, Paris, France. E-mail: labesse@cbs.cnrs.fr

The NAD kinase is involved in the essential step for the biosynthesis of NADP the dinucleotidic cofactor for numerous enzymes. The NAD kinases was previously proposed to share the ATP-binding site of phosphofructokinases despite important sequence divergence [1]. The first crystal structure of a NAD kinases was recently solved [2]. We present, here, the structure of one of the two NAD kinases from *Listeria monocytogenes*, a food-borne human pathogen. The crystal structure, refined at 2.4 A resolution, reveals the conserved tetrameric structure of NAD kinases in agreeement with its oligomeric state in solution. Co-crystallization as well as complementary biophysical characterizations (SAXS, ...) in presence of the ligands are currently undertaken in order to analyse putative conformation changes. Meanwhile, the structure allows virtual screening in order to identify potential inhibitors.

[1] Labesse G., Douguet D., Assairi L, Gilles A.M., *TiBS*, 2002, 273-5. [2] Garavaglia S., Raffaelli N., Finaurini L., Magni G., Rizzi M., *J. Biol. Chem.*, 2004, 40980-6.

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