

# Structural characterization of the *Lactobacillus plantarum* FlmC protein involved in biofilm formation

Gianluca D'Abrosca<sup>1</sup>, Antonella Paladino<sup>1,2</sup>, Emilio Cuoco<sup>1</sup>, Rosangela Marasco<sup>1</sup>, Severina Pacifico<sup>1</sup>, Simona Piccolella<sup>1</sup>, Valeria Vastano<sup>1</sup>, Margherita Sacco<sup>1</sup>, Carla Isernia<sup>1</sup>, Lidia Muscariello<sup>1\*</sup> and Gaetano Malgieri<sup>1\*</sup>

<sup>1</sup>Department of Environmental, Biological and Pharmaceutical Science and Technologies, University of Campania – Luigi Vanvitelli, Via Vivaldi, 43 - 81100 Caserta (Italy)

<sup>2</sup>Institute of Chemistry of Molecular Recognition, CNR, via M. Bianco, 9 20131, Milan (Italy).

\*correspondence: Lidia Muscariello ([lidia.muscariello@unicampania.it](mailto:lidia.muscariello@unicampania.it)) and Gaetano Malgieri ([gaetano.malgieri@unicampania.it](mailto:gaetano.malgieri@unicampania.it)).

Supplementary Informations

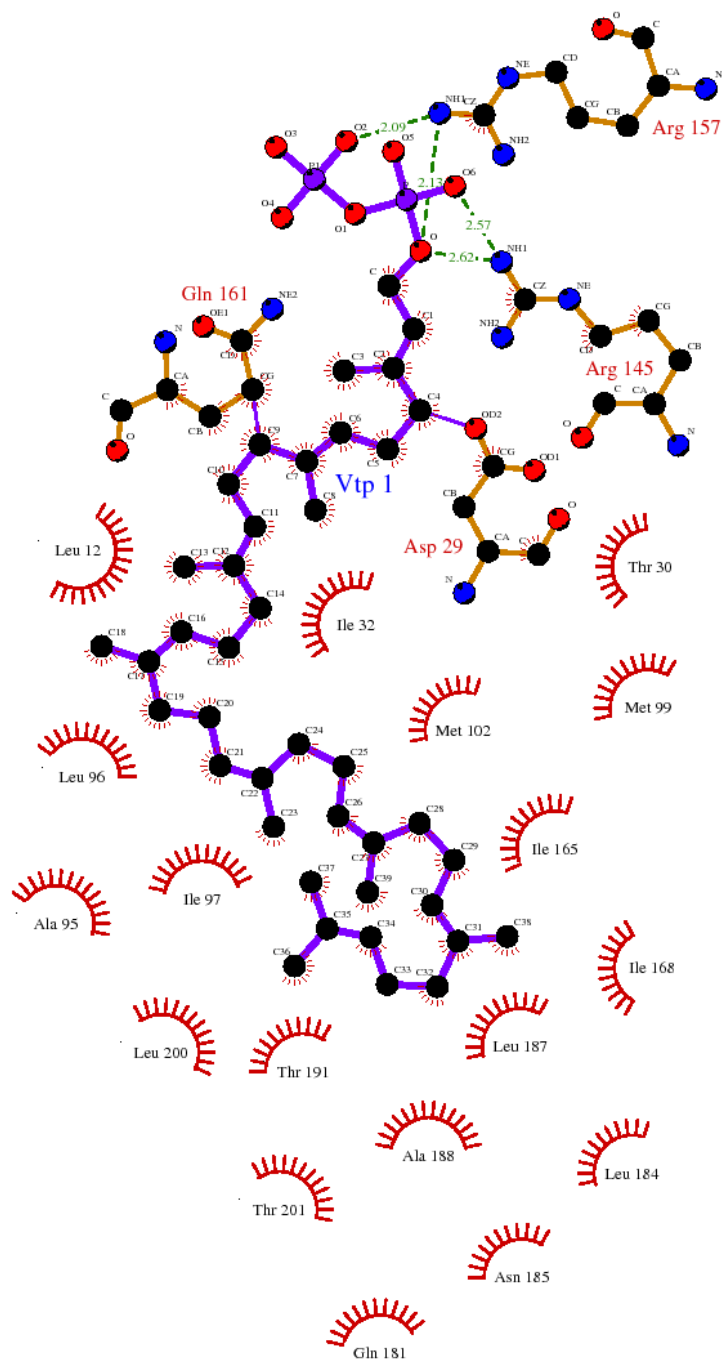


Figure S.I. 1. Binding site interactions analysis predicted by Galaxy on the first docking pose, built using PDB 4DE9 as template for protein-ligand complex.

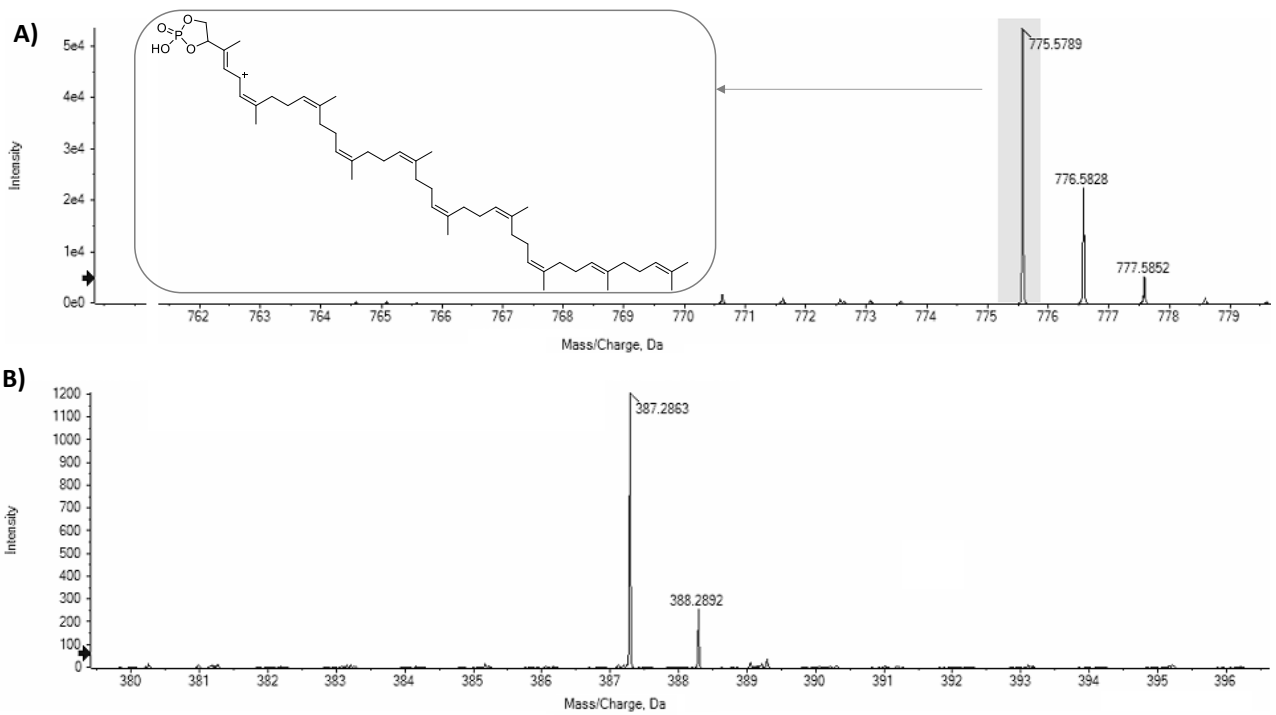


Figure S.I.2 A) TOF-MS acquired in positive ion mode and structure proposed for the ion at  $m/z$  775.5789; B) Doubly charged ion at  $m/z$  387.2863 recorded in negative ion mode acquisition.

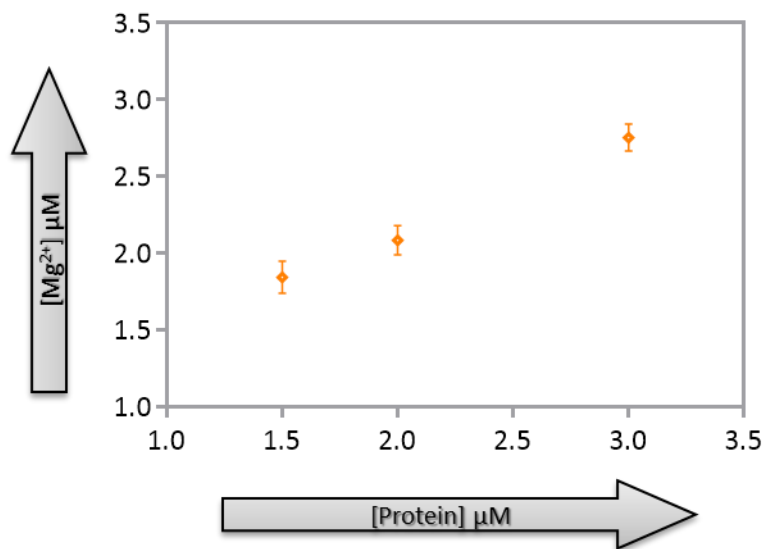


Figure S.I. 3: ICP-MS analysis. Magnesium presence as a function of protein concentration.

