

**Behavior of silver(I) ion binding with peptides inspired from SilE protein**A. Bianchi<sup>1</sup>, K. M. Fromm<sup>1\*</sup><sup>1</sup>Department of Chemistry, University of Fribourg, Fribourg, Switzerland

Since many years, silver has been used in medicine for its antimicrobial properties.<sup>[1]</sup> However, as for antibiotics, bacteria can develop a certain resistance or tolerance to the antimicrobial action of silver.<sup>[2]</sup> For the *Salmonella Typhimurium*, this silver resistance is based on a silver efflux pump, composed of eight proteins which act together to export silver(I) ions, named Sil system.<sup>[2]</sup> While most of these proteins could be attributed in analogy to the copper efflux system Cus, the SilE protein is unique and proposed to act like a silver sponge.<sup>[2,3]</sup> SilE is composed by 143 amino acids (aa) and contains many histidine (His, H) and methionine (Met, M) residues, which are able to bind silver(I) ions.<sup>[4]</sup> The study of HXXM tetrapeptides has shown that the nature of the aa "X" influences the association binding constant  $\log(K_{\text{ass}})$ .<sup>[4]</sup>

Based on these observations and in order to gain a more basic understanding of silver ion binding in peptides and proteins, HXXM / MXXH / HXXH / MXXM tetrapeptides were synthesized and studied for their interactions with  $\text{Ag}^+$ . Differences and similarities in the coordination behavior between HXXH and MXXM, but also HXXM and MXXH were noticed. Some first trends will be presented in this work.

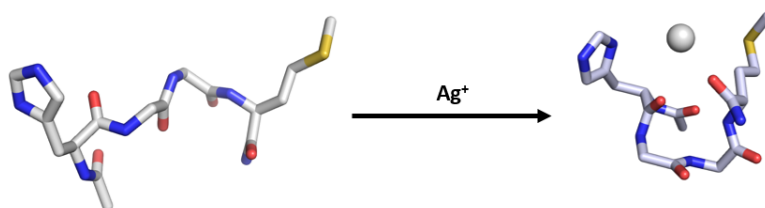


Fig. 1 : Folding of HXXM upon coordination with  $\text{Ag}^+$

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[3] Karishma R. Asiani, Huw Williams, Louise Bird, Matthew Jenner, Mark S. Searle, Jon L. Hobman, David J. Scott, Panos Soultanas, *Mol Microbiol.*, **2016**, 101, 731-742.

[4] Valentin Chabert, Maggy Hologne, Olivier Sénéque, Aurélien Crochet, Olivier Walker, Katharina M. Fromm, *Chem. Commun.*, **2017**, 53, 6105-6108.