Structural insights into nickel trafficking along the urease maturation pathway

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Urease catalyzes the hydrolysis of urea into ammonia, which is essential to the survival of *Helicobacter pylori* in human stomach. Maturation of urease requires the insertion of two nickel ions in its active site. However, nickel ions, a competitive ion at the top of the Irving-Williams series, are toxic and tightly regulated because they can inactivate enzymes that requires less competitive ions (e.g. magnesium) to function. Correct metalation of urease is ensured by specific protein-protein interactions among the four urease accessory proteins, namely UreD, UreE, UreF and UreG. Our group has previously determined the crystal structure of UreFD [1], GDP-bound UreGFD [2] complexes and nickel-/GMPPNP bound UreG dimer [3]. Recently, we determined the crystal structure of a UreEG complex. Combining structural and biochemical studies, we have elucidated how nickel ions move from one urease assessor protein to another and eventually to urease without releasing the “free” toxic metal to the cytoplasm.

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[3] M.H. Yuen, Y.H. Fong, Y.S. Nim, P.H. Lau, K.B. Wong. *Proc. Natl. Acad. Sci. USA*, **2017**, *114*, E10890