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How urease accessory proteins coupled GTP hydrolysis/binding to nickel delivery to urease?

Urease is a nickel-containing metalloenzyme that catalyzes the hydrolysis of urea into ammonia and carbon dioxide. This enzymatic reaction, which produces the acid-neutralizing ammonia, is essential for the survival of *Helicobacter pylori* in human stomach. In *Helicobacter pylori*, nickel ions delivery for urease maturation is assisted by four urease accessory proteins, UreE, UreF, UreG and UreH. Specific protein-protein interactions among these urease accessory proteins are essential for the control of binding/release of nickel along the metal delivery pathway. We have previously determined the crystal structures of UreF/UreH and GDP-bound-UreG/UreF/UreH complexes. Upon binding of UreH, the C-terminal residues of UreF are induced to form an extra helix and a loop structure stabilized by Arg-250. These conformational changes facilitate the recruitment of UreG to the UreG/UreF/UreH complex, which is essential to urease maturation. Recently, we have determined the crystal structure of the nickel/GTP-bound UreG dimer, which reveals how GTP hydrolysis induces conformational changes that induce dissociation of UreG from the UreG/UreF/UreH complex and the release of nickel to the urease.

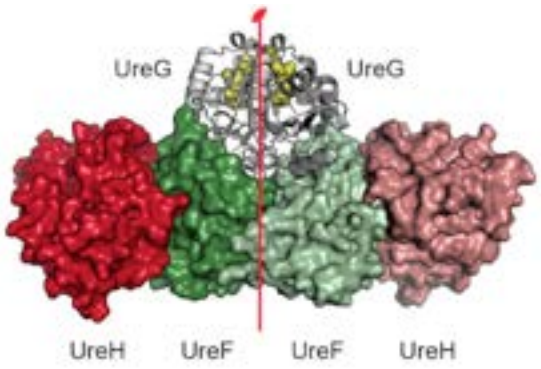

Figure : Crystal structure of UreG/UreF/UreH complex.

Biography

Kam Bo Wong obtained his BSc and MPhil from the Chinese University of Hong Kong. He then pursued his PhD degree in the laboratory of Prof. Alan Fersht at the University of Cambridge. After Postdoctoral training in the University of Washington and University of Cambridge, he joined the Chinese University of Hong Kong in 1999, where he is now a Professor at the School of Life Sciences. His research interests are on the structure-function studies of proteins. His research group uses multi-disciplinary techniques, including protein engineering, biophysical characterization, computational methodologies, and structure determination by NMR and X-ray crystallography, to study how proteins function on the atomic and molecular levels.

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