

P018 Proteome analysis of the anammox bacterium
Kuenenia stuttgartiensis
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In this study the proteome of the *Kuenenia stuttgartiensis* was investigated. This bacterium is of special interest for global nitrogen cycling and for application in wastewater treatment because it catalyses the anammox reaction. The genomic sequence of *K. stuttgartiensis* was recently assembled. Analysis of the genome revealed many ORF's with the heme binding motif CXXCH, most notably the 8 heme containing HAO. This enzyme constituted 10% of the total protein and is located in a unique organelle, the anammoxosome. Other annotated genes potentially involved in N conversion and electron transport are nitrate and nitrite reductase, various cytochrome c, the BC1 complex, and the NUO complex.

Proteins from *K. stuttgartiensis* were separated by two-dimensional gel electrophoresis. As many as 200 protein spots were detected on gels within a pH range of 4-7. Using MALDI-TOF MS and peptide mass fingerprinting about 50% of the analyzed protein spots were positively identified. Among these proteins were: HAO, nitrate and nitrite reductase, two subunits of the NUO complex, and soluble subunits of the ATP synthase. Further studies will use pre-fractionation of cell extract into soluble and membrane proteins and isolation of intact anammoxosome organelles to identify the role and location of the proteins.