Abstract

Molybdenum cofactor biosynthesis protein A (MoaA) is a protein belonging to the radical S-adenosylmethionine (radical SAM) enzymes superfamily, which are proteins characterized by 4Fe-4S clusters. These 4Fe-4S clusters initiate radical reactions that are essential in all kingdoms of life. In humans, MoaA is one of two enzymes responsible for the synthesis of Molybdenum cofactor, Moco. Moco is an organometallic cofactor essential to many organisms, which can not be consumed and must be synthesized. A genetic mutation in humans can lead to Moco deficiency, a metabolic disorder with many fatal neurological symptoms. The current characterization structure of the active site of MoaA has helped to understand steps of Moco biosynthesis, but finding a complete crystal structure of this protein that includes the capture of the carbon terminal tail will allow further understanding of the biosynthesis of Moco. Past research has indicated that the C-terminal tail containing diglycines (GGs) is crucial to synthetic function because when a glycine is replaced with any bulkier amino acid or carbon group, function is hindered. By isolating MoaA from *Escherichia coli*, performing purification, and conducting structural characterization, we aim to obtain a crystal structure of this protein. We expect that with new crystallization conditions, a successful capture of this carbon tail in its catalytically active position can lead to further understanding of how MoaA's biosynthetic pathway functions. This can provide us with results that allow us to understand how many other biosynthetic enzymes with unstable radical intermediates, including those in the radical SAM superfamily, also function.