Structural characterization of a metal transporter from *Bacillus subtilis*

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A precise balance of copper is necessary for survival and growth, serving as an essential cofactor for nearly all living organisms. Currently, knowledge of how Gram-positive bacteria import and export copper and maintain homeostasis is largely unknown. To obtain a better understanding of how these processes work, we are focusing on the *ycn*KJI operon responsible for regulating copper levels in the Gram-positive bacterium *Bacillus subtilis*. This operon encodes three Cu-related proteins: a copper-dependent transcriptional repressor (YcnK), a putative copper importer (YcnJ), and a copper-binding protein of unknown function (YcnI). To initiate investigations on the mechanism of copper import, here we focus on the of the extracellular domain of the YcnJ protein, $\mathrm{YcnJ}^{\mathrm{CopC}}$. We investigate the copper-binding capabilities and structure of $\mathrm{YcnJ}^{\mathrm{CopC}}$ using an array of biophysical methods. We determine the structure of the protein to 1.5 Å resolution. We also demonstrate that it can bind a single Cu(II) ion. These data add additional insight into the copper uptake mechanism and to elucidation of potential Cu transfer events between YcnI and YcnJ.

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