

**P002** Computational and biochemical analysis of the metal-binding properties of EfeO, a component of the EfeUOB iron-transport system of *E. coli*

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EfeUOB of *Escherichia coli* is a tripartite, low pH, Fe<sup>2+</sup> transporter. This system resembles the iron transporter (Ftr1p-Fet3p) of yeast in that EfeU is homologous to Ftr1p, an integral-membrane iron-permease. However, the EfeUOB system lacks any apparent equivalent of the Fet3p component - a multicopper oxidase with three cupredoxin-like domains which is required for oxidation of Fe<sup>2+</sup> during translocation by Ftr1p. The *E. coli* EfeO and EfeB proteins are required for EfeUOB function, but their biochemical roles remain unclear. We have embarked upon a bioinformatic and biochemical study of EfeO to determine its role in EfeUOB-mediated iron transport.

Our results suggest the presence of an N-terminal cupredoxin-like domain and a C-terminal Peptidase M75 domain. We have generated a comparative model for the cupredoxin (Cpx) domain and used the programme GRID to predict metal-binding sites. The results indicate that the Cpx domain contains both a divalent-metal ion (Cu<sup>2+</sup>, Mg<sup>2+</sup>, Zn<sup>2+</sup>) and a Fe<sup>2+/3+</sup> binding site. This suggests an even closer similarity between the bacterial and yeast iron transporters than was previously apparent.