Tat System of *Escherichia coli*: Zn^{2+}-bound Structures of tatD, ycfH and yjjV

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The *Escherichia coli* Tat system mediates Sec-independent export of protein precursors bearing twin arginine signal peptides. Genes known to be involved in this process include *tatA, tatB,* and *tatC* that form an operon with a fourth gene, *tatD*. The *tatD* gene product has two homologues in *E. coli* coded by the unlinked *ycfH* and *yjjV* genes. The actual role of these enzymes and their substrates are not yet known, however, it was suggested that they might posses Zn^{2+}-dependent amidohydrolase activity. Significant number of amidohydrolases share TIM-barrel fold. The diversity of the catalytic mechanisms and substrate specificities is achieved through sequence and structural variation within the loop area. As a part of large-scale genomic effort to establish structure-function relationships within the amidohydrolase family, we determined high-resolution X-ray structures of tatD, ycfH and yjjV. Despite relatively low sequence identity of 24-29%, all three structures share similar overall fold, however, the number of Zn^{2+} ions in the active sites and their coordination differ significantly in three enzymes. Despite proposed deoxyribonuclease activity for tatD, none of the structures demonstrates nucleotide binding when co-crystallized with short DNA fragment. The potential functional roles of these enzymes will be discussed in the light of the structural and scarce biochemical data.

[1] Wexler M., Sargent F., Jack R.L., Stanley, R.L., Bogsch E.G., Robinson K., Berks B.C., Palmer T., *J. Biol. Chem.*, 2000, **275**, 16717.

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