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$tRNA^{Ile}$ リシジン合成酵素 TilS の反応メカニズム
Structural basis of the initial binding of $tRNA^{Ile}$ lysidine synthetase TilS with ATP and L-lysine

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In the bacterial genetic-code system, the codon AUA is decoded as isoleucine by tRNAIle2 with the lysidine residue at the wobble position. Lysidine is derived from cytidine, using ATP and L-lysine, by tRNAIle lysidine synthetase (TilS), which is an N-type ATP pyrophosphatase. In this study, we determined the crystal structure of Aquifex aeolicus TilS, complexed with ATP, Mg2+, and L-lysine, at 2.5-Å resolution. The presence of the TilS-specific subdomain causes the active site to have two separate gateways, a large hole and a narrow tunnel on the opposite side. ATP is bound inside the hole, and L-lysine is bound at the entrance of the tunnel. The conserved Asp36 in the PP-motif coordinates Mg2+. In these initial binding modes, the ATP, Mg2+, and L-lysine are held far apart from each other, but they seem to be brought together for the reaction upon cytidine binding, with putative structural changes of the complex.

Reference, Kuratani M. *et al.* (2007) Structural basis of the initial binding of tRNA(Ile) lysidine synthetase TilS with ATP and L-lysine. *Structure*, 15:1642-1653.