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## Structural and functional characterisation of a lytic transglycosylase and two $\omega$ -transaminases

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STELLINGEN

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**Structural and functional characterisation of a lytic transglycosylase and two  $\omega$ -transaminases**

door

Eswar Reddy Reddem

Groningen, 22 Dec 2015

1. Even though PLP dependent enzymes are among the best studied enzyme classes, their classification is confusing.
2. The reaction specificity of a PLP dependent enzyme is mainly dependent on the perpendicular position of the scissile  $\sigma$ -bond and the presence of a catalytic acid/base residue near the C4' atom of PLP, but one shouldn't forget the role of the residue interacting with the N1 atom of the PLP ring (Chapter 1).
3. It is amazing how truncation of 30 instead of 28 at the C-terminus of MltF changed the resolution of diffracting crystals from 4.0 Å to 1.85 Å (Chapter 2).
4. Despite its sequence and structural similarity with the substrate binding proteins (SBPs) of the ABC transporter family, the function of the N-terminal domain of MltF is unclear even after solving structures with bound SBP ligands (Chapter 3).
5. The movement of an arginine side chain near the active site in the D-alanine bound structure of the  $\omega$ -transaminase from an *Arthrobacter* species is a strong indication that an arginine switch mechanism exists in Fold type IV transaminases (Chapter 4).
6. A complete proposal for the catalytic mechanism of an enzyme can only be reached with the availability of structural information on the enzyme.
7. Failed projects can't give you a publication, but they give you considerable experience for dealing with new projects.
8. When you don't come across any problems - you can be sure that you are travelling a wrong path (Swami Vivekananda). This is particularly true for a PhD student.
9. In science one tries to tell people, in such a way as to be understood by everyone, something that no one ever knew before. But in the case of poetry, it's the exact opposite (Paul Dirac).