

The Structure of an Ester Synthesising Peptidase

Matthew Bennett^a, Bryan Anderson^a, Ross Holland^b, Gillian Norris^a,

^a*Institute of Molecular BioSciences, Massey University, New Zealand.*

^b*Fonterra Marketing and Innovation, Palmerston North, New Zealand.* E-mail: M.D.Bennett@massey.ac.nz

X-prolyl dipeptidyl peptidase (PepX) is a dipeptidase that appears to be ubiquitous in dairy lactic acid bacteria. PepX is best characterised for its highly specific peptidase activity, namely the ability to remove dipeptides from the N-terminus of larger peptides, where proline is residue 2 in the peptide sequence. PepX however is also able to synthesise esters via a transferase mechanism.

The structure of PepX from *Streptococcus thermophilus* has been solved by molecular replacement methods to 1.9Å resolution using PepX from *Lactococcus lactis* [1] as a model. The refined structure has an R factor of 18.2% and R_{free} of 23%.

Characterisation of the ester synthetic activity showed that PepX was capable of producing ethyl butanoate, only if the synthetic triacylglyceride tributyrin was the donor molecule. The basis for this specificity is discussed in terms of the structure of the enzyme, and the topology of the active site. A model for the catalytic activity that is in agreement with the observed kinetic data is presented.

[1] Rigolet P., Mechin I., Delage M.M., Chich J.F., *Structure*, 2002, **10**, 1383.

Keywords: peptidase, transferase, enzyme kinetics