

The structure of an N-acetyl- β -D-glucosaminidase from *Streptococcus gordonii*.

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Streptococcus gordonii is a primary coloniser of the oral cavity and contributes to the maintenance of a healthy oral microflora. However, should it gain access to the bloodstream it can also colonise damaged heart valve tissue resulting in infective endocarditis which in spite of antibiotic therapy is still 40% fatal. Survival and growth of the bacterium on the endocardium is believed to be facilitated by the production of numerous glycosidases which may degrade the glycan moiety of mammalian glycoproteins. A screen for such activity led to the cloning of an N-acetyl- β -D-glucosaminidase (*gcnA*), from this organism.

Se-methionine *gcnA* was crystallized and the structure solved by the MAD method. The 627 aa protein crystallizes as a dimer and has a canonical TIM-barrel fold. Two crystal forms of the enzyme have been refined. Only one of these has the putative catalytic residues orientated towards what is postulated to be the active site pocket, suggesting that dynamic substrate capture might be a feature of catalysis. The catalytic mechanism of this family 20 glycosidase, whereby the substrate rather than the enzyme provides the cleavage-inducing nucleophile, has been confirmed by co-crystallizing the protein with a putative transition state analogue. A mercury-soaked crystal reveals how the enzyme is poisoned by this and other heavy atoms.