

## A structural investigation into an alpha-mannosidase found in *Bacteroides thetaiotaomicron*

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Glycoside hydrolase family 38 (GH38) enzymes contain a myriad of alpha-mannosidases ranging in substrate specificity. All of the enzymes within this family share a common catalytic retaining mechanism with a conserved catalytic residue of aspartic acid. Despite structural studies across the kingdoms - notably from *Drosophila melanogaster* to *Streptococcus pyrogenes* - these enzymes vary strongly in kinetic preferences and structure. Recently, we've expressed a predicted alpha-mannosidase originating from *Bacteroides thetaiotaomicron*. This enzyme is predicted to contain a metal-binding region within the structure and may contain similar stabilizing disulfide-bridges similar to those in the *Drosophila melanogaster* alpha-mannosidase. The recombinant enzyme has been structurally modelled within ITASSER<sup>1,2,3</sup> and current work focuses on crystallization of the enzyme for model validation.

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