

Neutron Crystallography Study of Host-Pathogen Recognition Enhanced by Hydrogen/Deuterium Exchange on Carbohydrates

Description

Neutron macromolecular crystallography (NMX) is a unique method for locating hydrogen atoms. Its effectiveness is greatly improved by using deuterium-labeled molecules. Human glycans are the targets of virulence factors from pathogens, such as soluble lectins from the opportunistic bacterium *Pseudomonas aeruginosa*. Deuterated galactose was produced by hydrogen isotope exchange and co-crystallized with a fully deuterated bacterial receptor, LecA, a lectin involved in *P. aeruginosa* tissue adhesion and biofilm formation. The structure of the complex determined through neutron diffraction shows the positions of all hydrogen atoms as deuterium, emphasizing the role of a charged histidine in the binding site, the bridging water molecule, and the impact of the coordinating calcium ion on nearby hydrogen bonds. LecA is a target for pathoblockers, and these structural details can aid in the design of glycomimetics to combat multidrug-resistant infections.

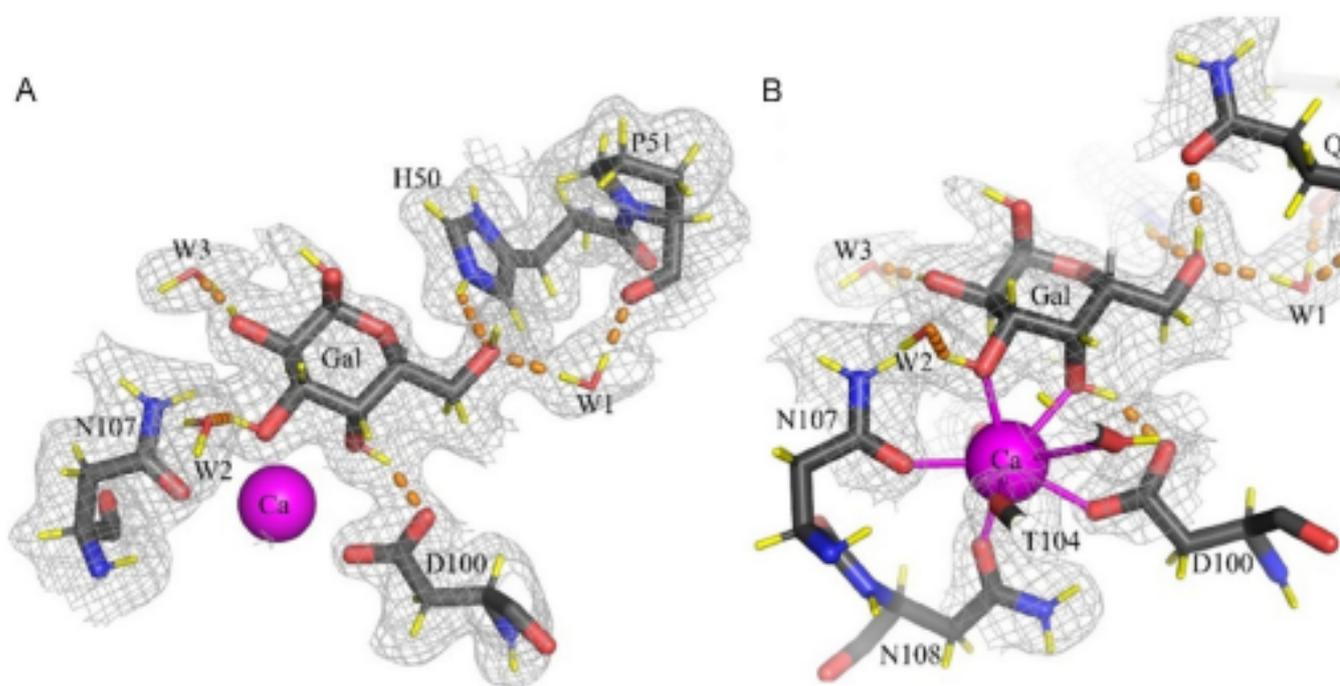


Figure. The galactose-binding site in the neutron structure of the D-LecA/Gal-d10 complex (chain H). The hydrogen bonds are shown as orange dashed lines. The $2mF_o - DF_c$ neutron density map (gray mesh) is contoured at 0.8σ . (A) Upper view of the binding site with Q53 omitted for clarity. (B) Alternative view including Q53 and displaying the coordination of the calcium ion.

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