acid/base glutamate hydrogen-bonds to the glycosidic oxygen; and the conserved asparagine hydrogen-bonds to the C2-hydroxyl near the cleavage site. A close approach of two key glutamate residues provides an elegant mechanism for the shift in the pKₐ of the acid/base for the glycosylation and deglycosylation half-reactions. The structure also identifies and defines the roles of five further residues which are well-conserved within the superfamily. The structure is entirely consistent with a large body of kinetic data observed for wild-type and mutated forms of superfamily members, and allows us to extend the known chemical mechanism with a detailed sequence of physical steps that we propose are involved in catalysis by the enzymes. This superfamily includes a large number of cellulases, so the insights will aid protein engineering efforts to improve cellulase activities for use in biomass conversion.

**References:**


Lectins form a group of structurally diverse proteins that bind to specific oligosaccharide sequences. They occur in almost all living organisms and despite having their roles well characterised in mammals are of largely unknown function in plants.

Two isolectins (TCAI and TCAII) have been isolated from seed extracts of the Nigerian walnut (Tetraparoidium conophorum). Both TCAI and TCAII are glycosylated and have the respective molecular weights of 70 and 30kDa. TCAI exists as a disulphide linked dimer and TCAII as a monomer. Both isolectins have specificities for oligosaccharides with terminal galactose residues consistent with this lectin family which includes Ricin and Ricinus communis agglutinin.

Orthorhombic crystals of TCAII were obtained (space group P2₁2₁2₁) with cell dimensions a=65.7 Å, b=86.3 Å, c=118.3 Å and two molecules in the asymmetric unit which diffracted beyond 2.4 Å. It was possible to locate the position of both molecules in the unit cell using molecular replacement with a search model consisting of the Ricin B-chain. The overall fold of TCAII is very similar to that of Ricin where the molecule can be divided into two globular domains which are formed from a series of disulphide linked gamma loops (there is little significant secondary structure). TCAII was crystallised in the presence of lactose and it is possible to identify electron density for at least galactose in both sugar binding sites. The structure is currently undergoing refinement.

**References:**