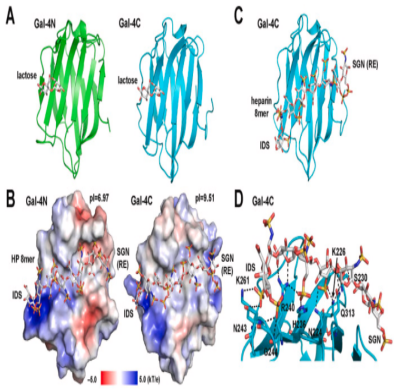
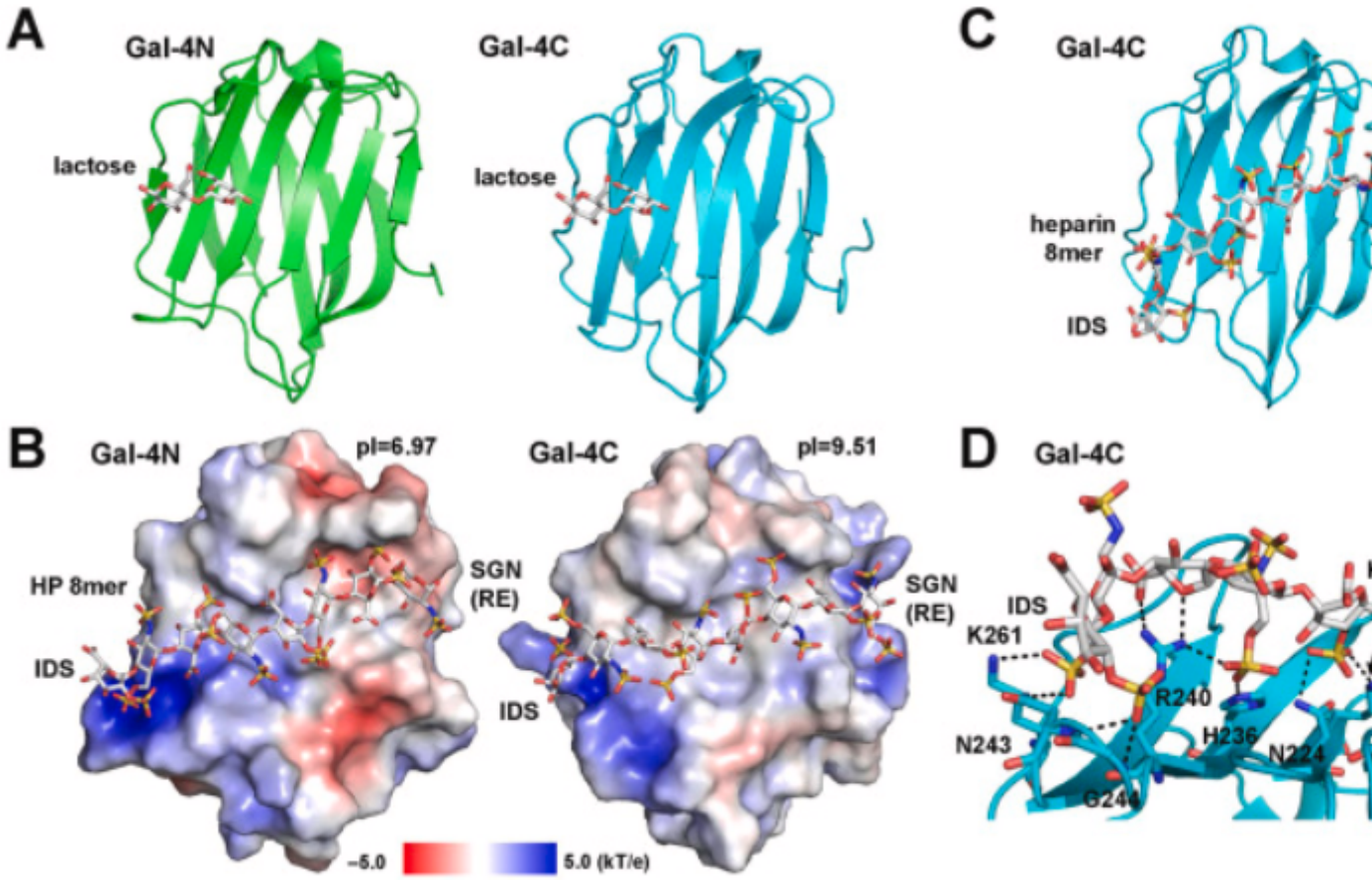



# A glycosaminoglycan microarray identifies galectin-4 binding to sulfated glycosaminoglycans

## Description

Using GAG microarrays, the authors profiled the binding specificity of 49 human lectins, including SIGLECs, C-type lectins, and galectins. GAGs containing 6-O-sulfation, particularly heparin, chondroitin sulfate C, and chondroitin sulfate E, bound broadly to SIGLECs and C-type lectins, whereas weakly sulfated GAGs showed limited interactions. Most galectins did not bind GAGs, but galectin-4 displayed strong affinity for 6-O-sulfated GAGs, especially heparin (Kd = 4.70 Ã? 10â•»â•¸ M). Experimental and simulation data indicated cooperative involvement of both carbohydrate-recognition domains. Galectin-4 also bound heparin-positive mast cells, revealing a noncanonical sulfated-GAG recognition mechanism.




Molocular Dynamics -assisted modeling of the Gal-4â??HP interaction. (A) Crystal structures of N- and C-terminal CRDs (Gal-4N and Gal-4C) binding lactose. (B) Electrostatic surfaces of CRDs (the left and right panels are for Gal-4N and Gal-4C, respectively) generated by the Adaptive Poisson-Boltzmann Solver (APBS) [31] used via PyMOL ver. 2.5 (Schrodinger, LLC). A HP octasaccharide (IDS[Î±1-4]SGN[Î±1-4]IDS[Î±1-4]SGN[Î±1-4]IDS[Î±1-4]SGN[Î±1-4]IDS[Î±1-4]SGN[Î±1]-OH derived from PDB entry 1HPN) was fitted into the groove that includes the lactose binding site, and used as the starting structure of the MD simulation. SGN: *N*, *O6*-disulfo-glucosamine. IDS: *O2*-sulfoglucronic acid. R: reducing end. (C) The representative structure of the MD simulation for the HP bound to Gal-4C. (D) Intermolecular hydrogen bonds observed in the representative structure of the Gal-4C-HP complex (black dashed lines; donor-acceptor distance <3.5â?¯Ã ).

## Category

1. News