Investigating a Major Glycan from N-Glycosylated Proteins

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We are investigating the conformation of the glycan portion of human IgG-Fc and its constituents by running molecular dynamics simulations and analyzing the glycosidic torsion angles. The idea for this project was inspired by the hypothesis that Rheumatoid Arthritis is caused by the removal of the terminal residues of human IgG-Fc. The 12mer glycan of IgG-Fc that we are studying is a prominent sequence found in many proteins. Presently we are analyzing the differences in the torsion angles of the 12mer glycan portion with that of its disaccharide and trisaccharide constituents. We are creating ramachandran-type plots from which we can compare the phi, psi, and omega torsion angles. We want to understand how adjacent carbohydrate groups effect the individual torsion angles in order to relate the behavior back to understanding why the truncation of IgG-Fc may be responsible for causing Rheumatoid Arthritis.

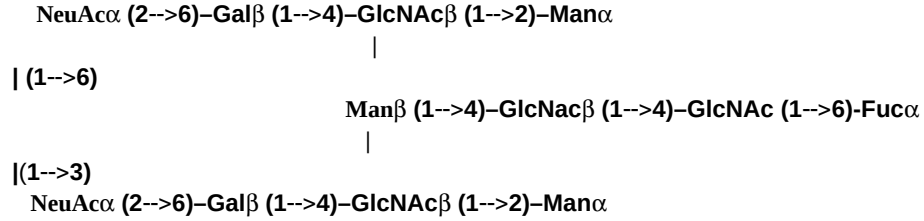

Figure 1: The glcan portion of human IgG-Fc, a 12mer that is embedded in a majoirty of N-glycosyl proteins. Man: Mannose, Fuc: Fucose, GlcNAc: N-acetylglucosamine, Gal: Galactose, NeuAc: N-acetylneuraminic acid (sialic acid)