

## SUPPLEMENTAL RESULTS

*Fig. S1 Hydrophobic profile of glycosylated regions of NA.* *In vitro* studies have determined that GT1 most efficiently reglycosylates glycopeptides containing a characteristic hydrophobic region C-terminal to the site of glycosylation (1). This method has been recently applied to the model glycoprotein *influenza* hemagglutinin in cellular studies of GT1 (2). Here, the hydrophobicity of the regions C-terminal to the glycans of NA (positions 42, 52, 63, 66, 87, 147, and 202) were analyzed, with the glycosidic linkage occurring at position 1 on the plots. For comparison, the hydrophobicity of an ideal glycopeptide substrate of GT1 was included. Overlapping glycosylation sites are denoted as stars in the plots. Kyte-Doolittle values were used for determining hydrophobicity with a window size of 3 starting with glycan 42 (3). The C-terminal glycans of NA, at positions 87, 147, and 202, are predicted to be the most efficient acceptors of GT1 activity due to their hydrophobic profile, whereas, the glycans at positions 42, 52, 63, and 66 are predicted to be poor substrates of GT1 due to the inherent hydrophilicity of these regions.

## SUPPLEMENTAL REFERENCES

1. Taylor, S.C., Thibault, P., Tessier, D.C., Bergeron, J.J. and Thomas, D.Y. (2003) *EMBO Rep.*, **4**, 405-41.
2. Pearse, B.R., Gabriel, L., Wang, N. and Hebert, D.N. (2008) *J. Cell Biol.*, **181**, 309-320.
3. Kyte, J. and Doolittle, R.F. (1982) *J. Mol. Biol.*, **157**, 105-132.

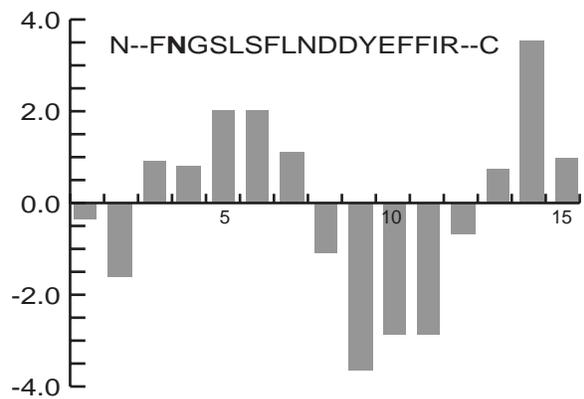
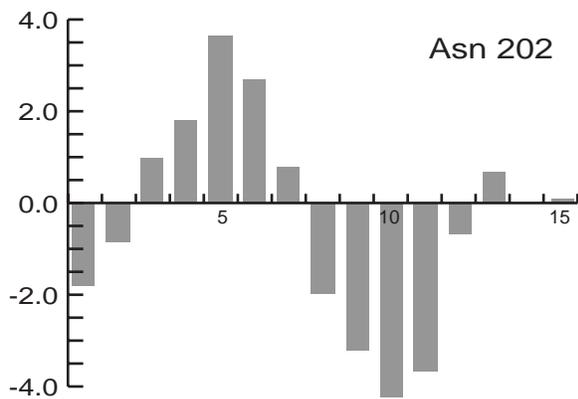
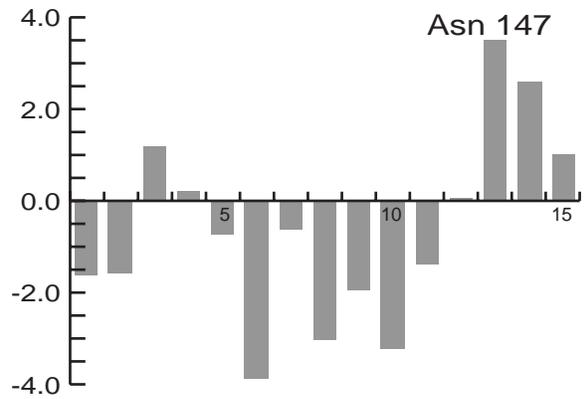
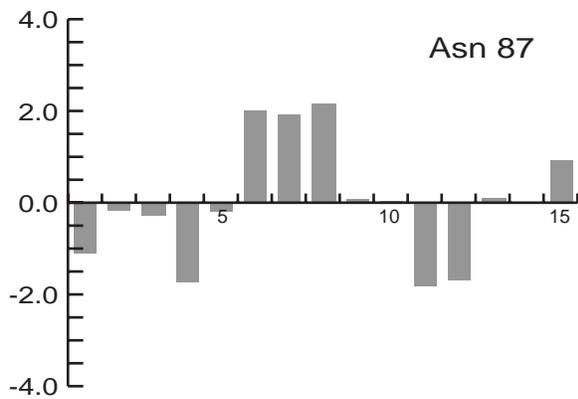
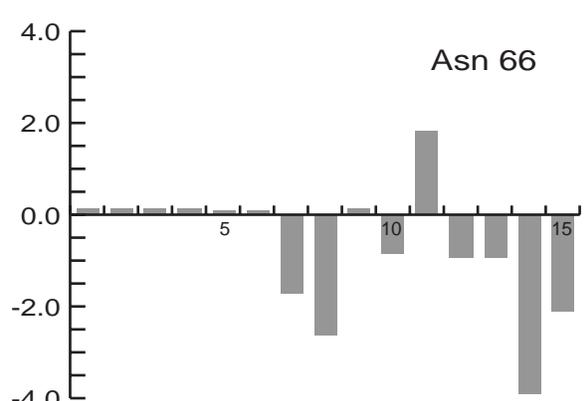
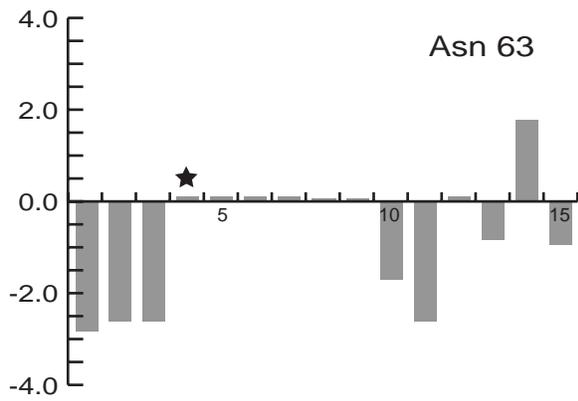
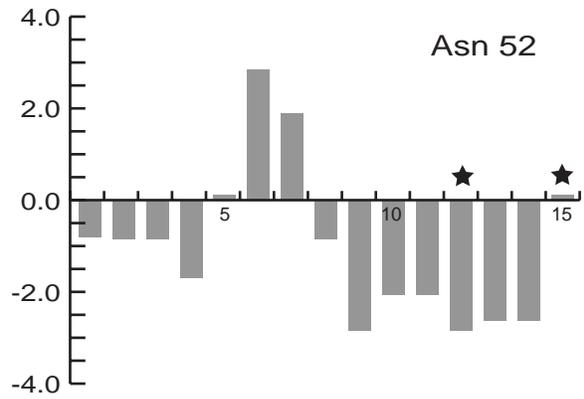
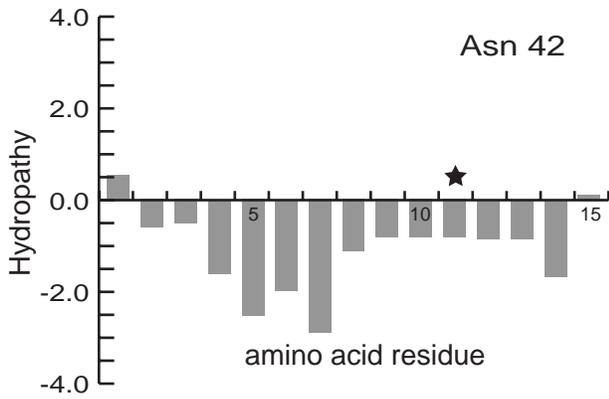


Fig. S1  
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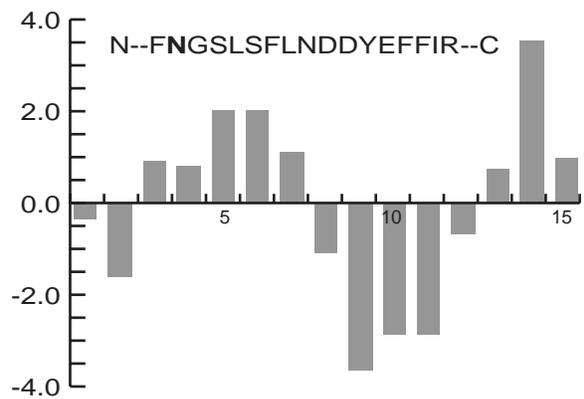
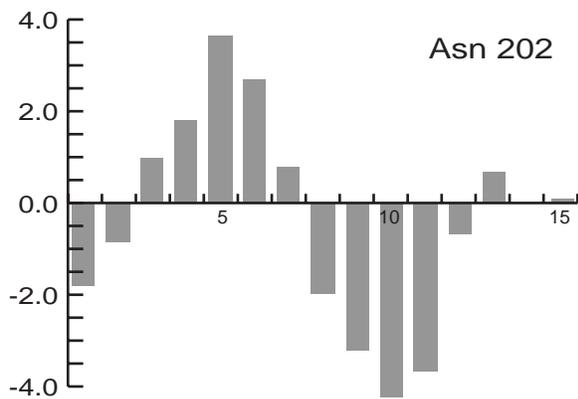
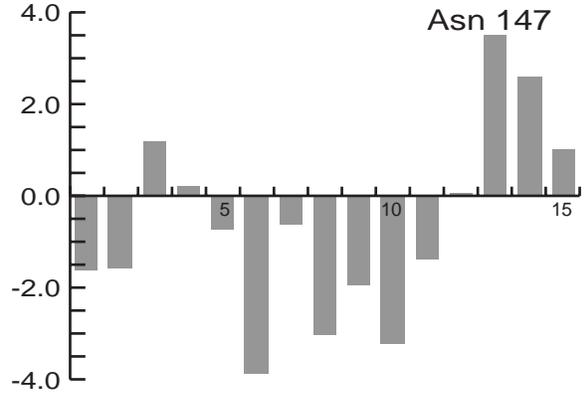
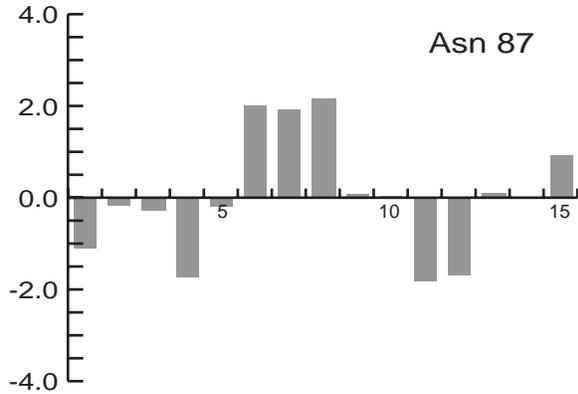
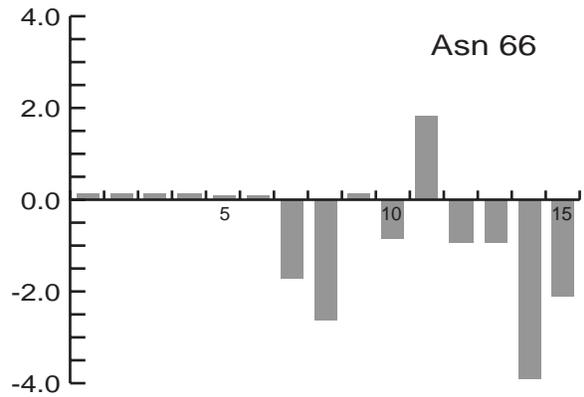
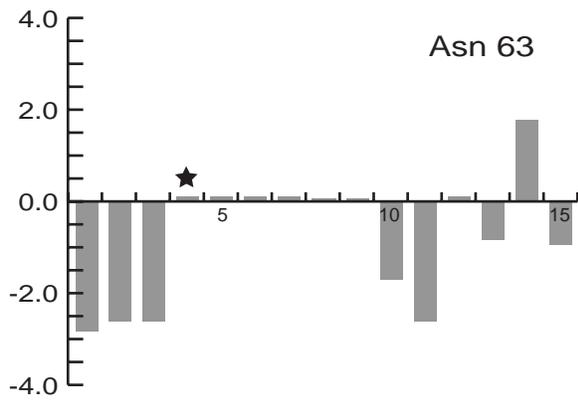
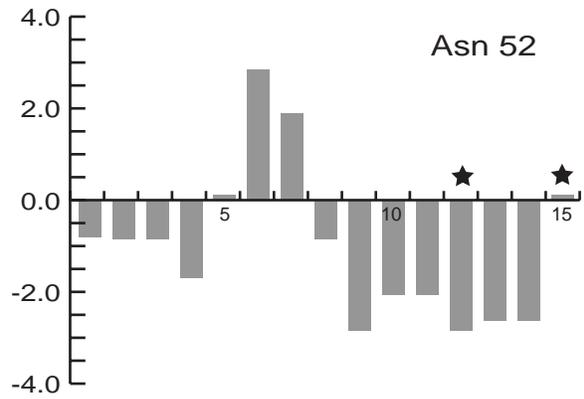
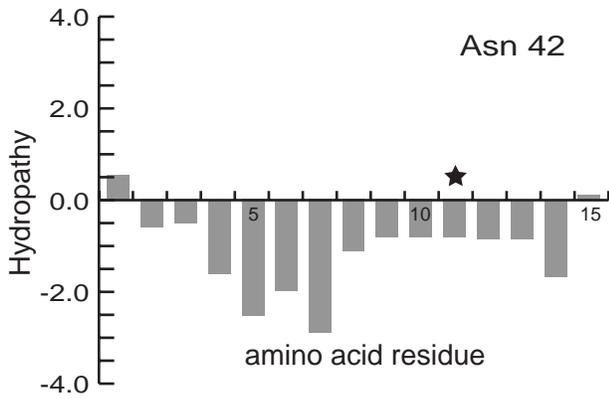


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