

SUPPLEMENTAL DATA

Bacterial N-glycosylation efficiency is dependent on the structural context of target sequons

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Content:

Figure S1. Size exclusion chromatographs of PEB3 variants.

Figure S2. Full-length western blot images.

Table S1. *In silico* analysis of secondary structures of N-glycosylation sequons.

Table S2. Strains and plasmids used in this study.

Supplemental Figure 1

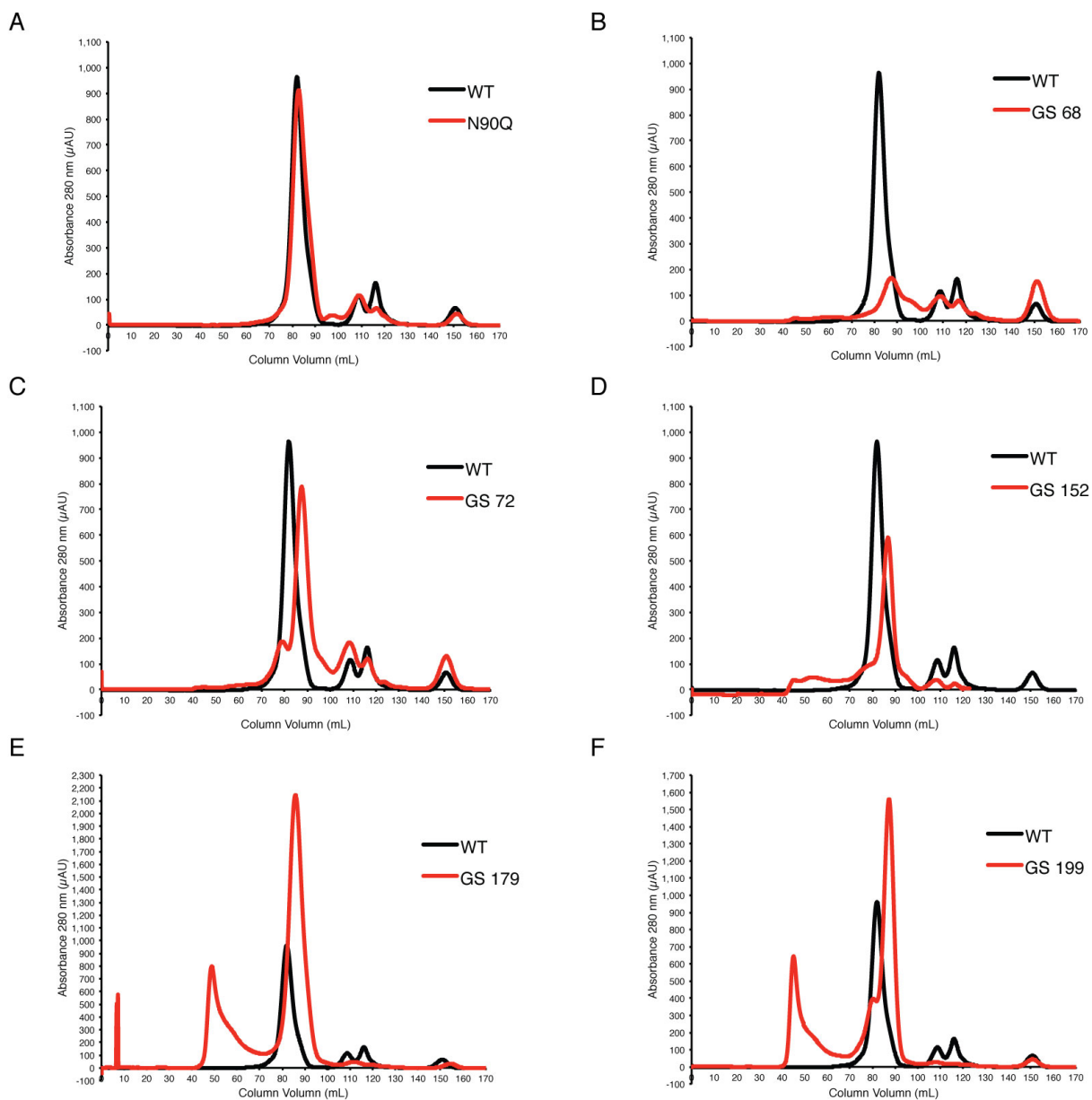


Figure S1. Size exclusion chromatographs of PEB3 variants, monitored by Absorbance at 280nm. Each chromatograph is an overlay with PEB3 wild type (black line) and PEB3 variant (red line).

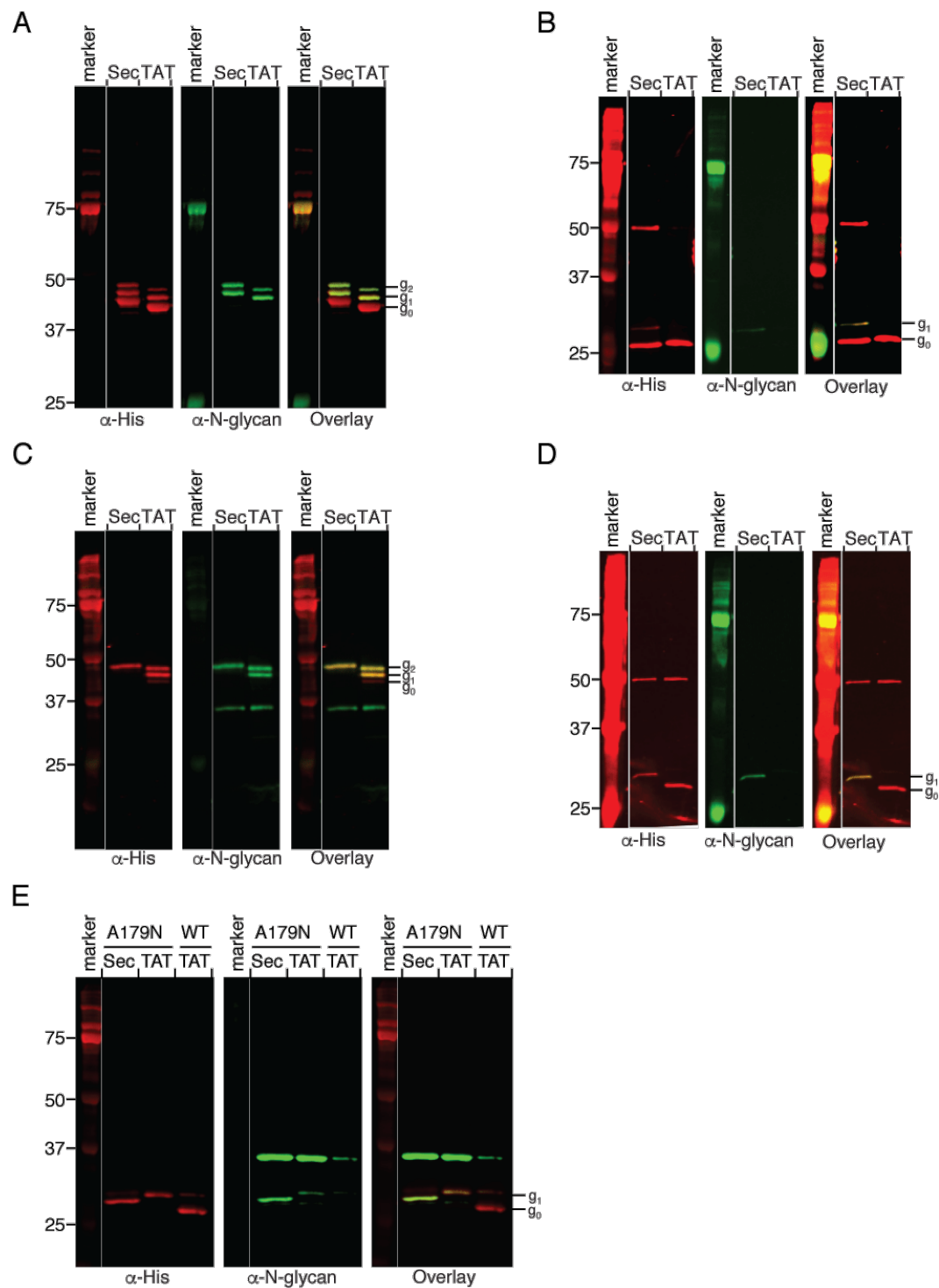


Figure S2. Full-length western blots images of Figures 4A, 4C, 5A, 5C and 6. Periplasmic Sec or TAT translocated AcrA (A) and PEB3 (B) purified from glycocompetent *E. coli*. Periplasmic Sec or TAT translocated AcrA (C) and PEB3 (D) purified from *C. jejuni*. (E) Periplasmic Sec or TAT translocated PEB3 A179N and TAT translocated PEB3 WT purified from *C. jejuni*. Immunoblots were probed with anti-His and anti-N-glycan antibody.