Figure 1: A) Initial purifications of WaaL (left) and RodA (right). α-Strep western was used to confirm presence of tagged target and SDS-page gel shows copurified bands. **B)** Mass spectrometry analysis hits corresponding to specific bands of the WaaL elution. **C)** Representative micrograph from a preliminary Glacios screening of the purified endogenous WaaL complex, with representative 2D-classes.

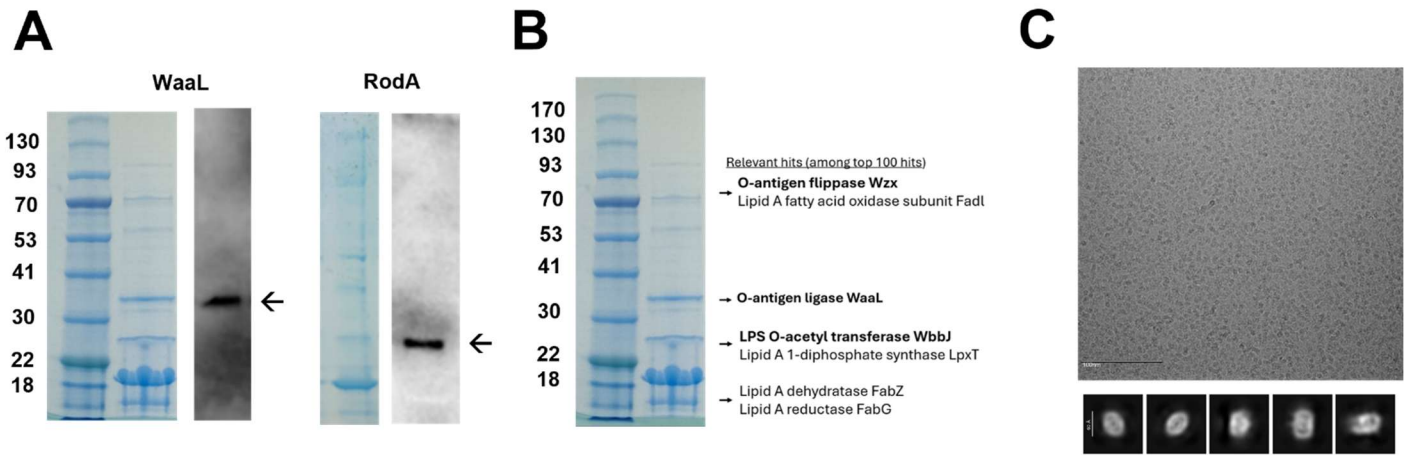

Figure 2: A) Endogenous 3xFlag tag purifications of AftA, AftB, and AftC revealed novel binding partners which were identified with mass spectrometry. **B)** Screening gel filtration traces of the purified AftB and AftC complexes show the samples are stable and homogenous following purification. **C)** AlphaFold3 predictions of AftA, AftB, and AftC in complex and their respective binding partners. Although predictive, the ipTM score of each reflects a confident model, indicating these proteins are likely forming specific interactions. Interestingly, the proteins are predicted to bind at the entrance to the active sites, possibly implying a mode of regulation