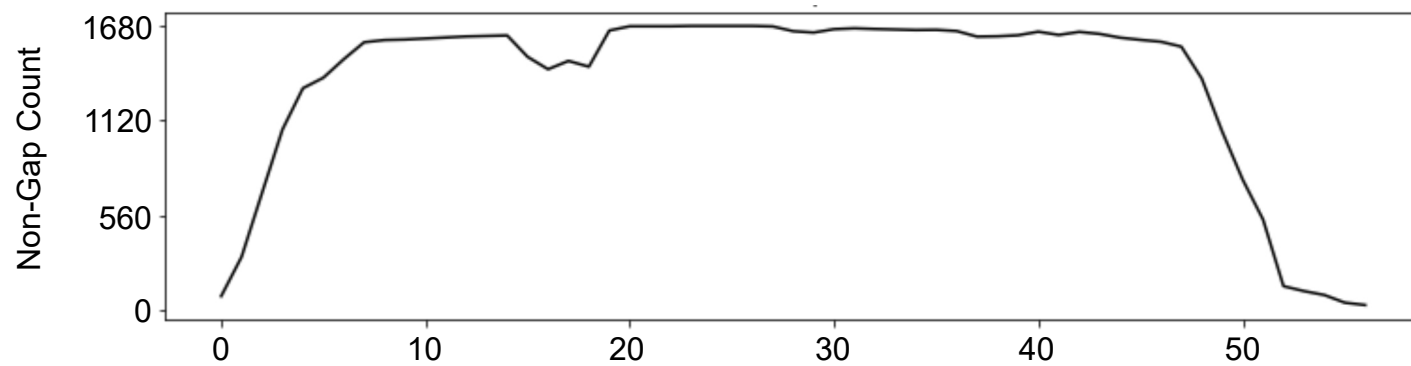


**A**

Per-Residue Count of Non-Gap Amino Acids in the MSA

**B**

Predicted Aligned Error

