**Roles of the telomerase reverse transcriptase N-terminal domain in the assembly and activity of *Tetrahymena* telomerase holoenzyme**

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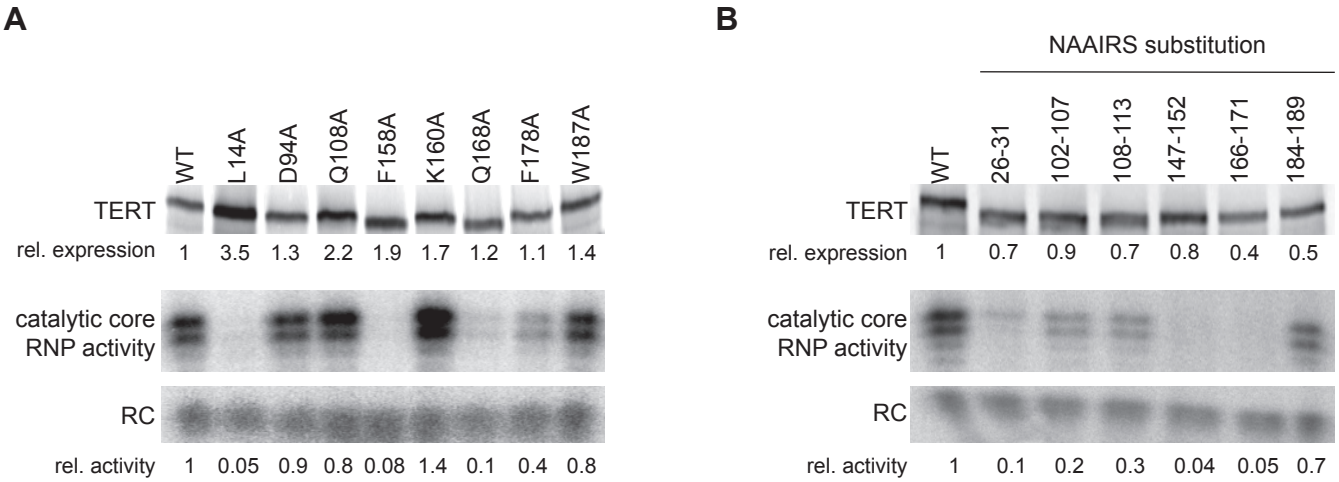
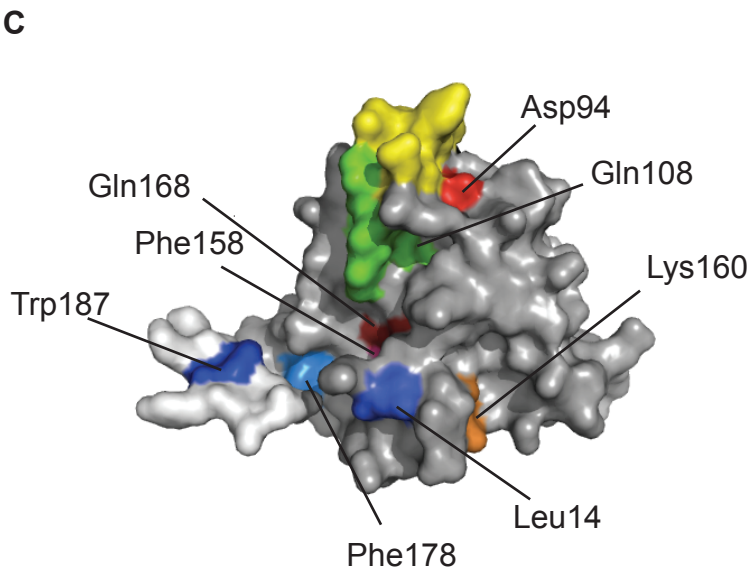
## SUPPLEMENTAL FIGURE LEGENDS

**SUPPLEMENTAL FIGURE S1.** Catalytic core RNP activity phenotypes of sequence substitutions in the TERT TEN domain. *A* and *B*, Activity assays of p65-TER-TERT catalytic core RNPs with the indicated TEN domain sequence substitutions. Quantification of relative activity was done by normalizing activity to the product precipitation recovery control (RC) then normalizing to relative TERT expression before normalizing to wild-type TERT catalytic activity. Note that the TERTs used in these panels have slightly different N-terminal tag sequences and thus slightly different mobilities by SDS-PAGE. *C,* Depiction of TEN domain locations of sequence substitution using the structure of Jacobs et al. (24). Green coloring indicates amino acids 108-113 and yellow coloring indicates the contiguous residues that compose the extended beta-hairpin surface. Lightened density at the lower left indicates amino acids 184-189, which are functionally dispensable (see main text Fig. 3A and Supplemental Fig. 2). Other amino acid side chains substituted in this study are colored and labeled individually.

**SUPPLEMENTAL FIGURE S2**. Investigation of the TEN domain C-terminal boundary by *trans* complementation. A, Assays were performed as described in the main text using TERT $core_{216}$ with the indicated TEN domain protein. The TEN domain proteins differed in their C-terminal endpoint. B, Assays were performed in the absence of dTTP, using only dGTP, for quantification of relative catalytic activity. Quantification of relative activity was done by normalizing activity to the product precipitation recovery control (RC) and then normalizing to the highest product intensity.

Supplemental Figure S1



Supplemental Figure S2