

SUPPLEMENTARY FIGURE CAPTIONS

Supplementary Figure 1. Overview of the WT human MTERF1 structure (PDB:3MVA) solved to 2.2Å. The three nucleotides involved in the base flipping event are colored magenta and labeled.

Supplementary Figure 2. T3243 spontaneously flips-in during unrestrained MD simulations. (A) The crystal structure showing F243 and R162 as green sticks. In the final 40ps of this simulation, the interaction energy between F243 and T3243 was -1.2kcal/mol and between F243 and C3242 was -3.8 kcal/mol. (B) T3243 flips back into the pseudo duplex, forming a t-stacking interaction with F243 and a second t-stacking interaction with C3242.

Supplementary Figure 3. (A) An overlay of wild type (gray) and the R162A substitution (yellow and orange), demonstrating a t-stacking interaction between Phe243 and T3243 that is absent in the wild type structure and the formation of a hydrogen bond between O2 of T3243 and N4 of Arg195. (B) The Y288A substitution structure shows that Phe243 stacks with both C3242 and T3243 simultaneously in the heavy strand.

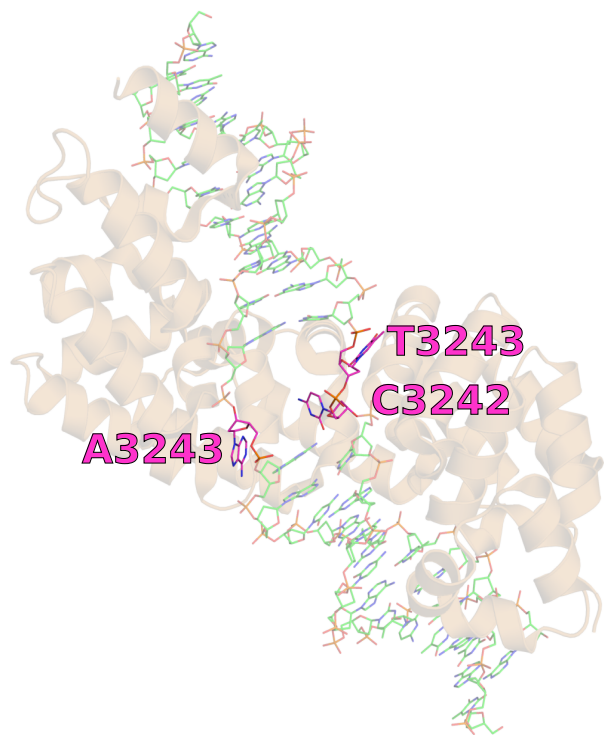
Supplementary Figure 4. Phe243 and Phe322 sequence conservation information analysis using sequence logos ^[1,2].

SUPPLEMENTARY TABLE CAPTION

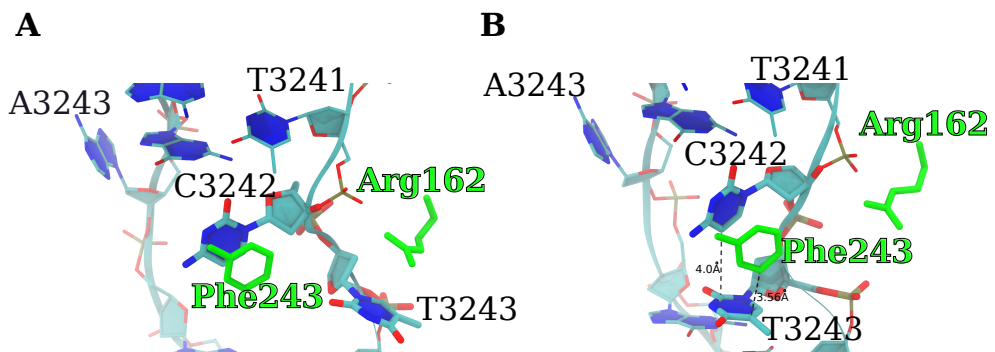
Supplementary Table 1. Summary of alterations to the flipped bases for the wild-type (WT) system and the four mutants. Legend: I, intrahelical; X, extrahelical; termination efficiency colored from maximal to minimal (red to white to blue).

REFERENCES

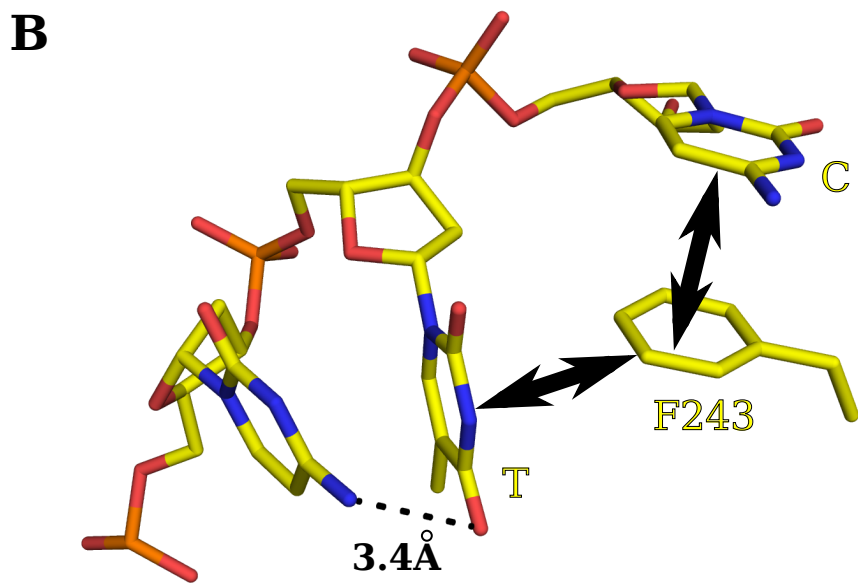
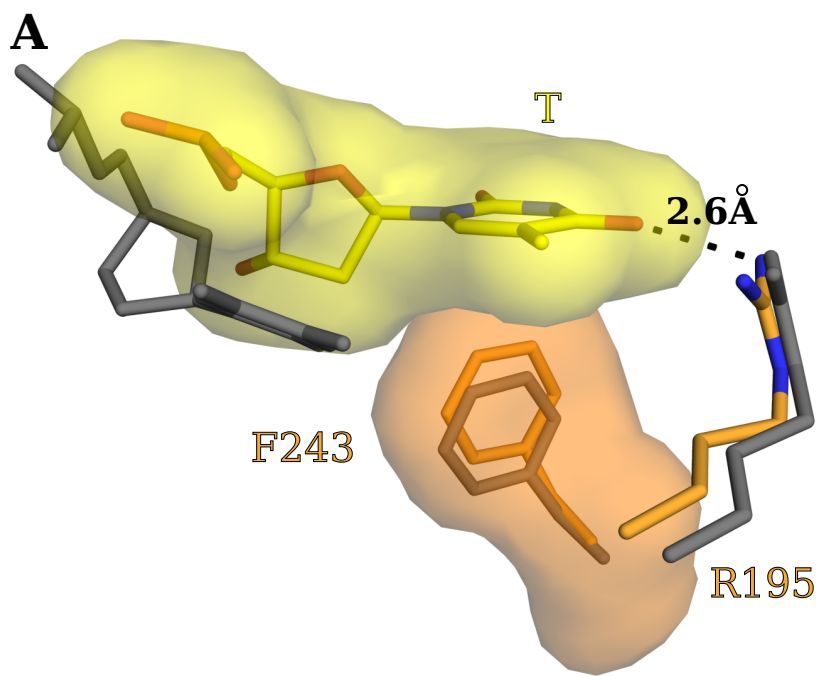
- [1] Schneider TD, Schneider TD, Stephens RM, Stephens RM. Sequence logos: a new way to display consensus sequences. *Nucleic Acids Res* 1990;18:6097–100.
- [2] Crooks GE, Crooks GE, Hon G, Hon G, Chandonia J-M, Chandonia J-M, et al. WebLogo: a sequence logo generator. *Genome Res* 2004;14:1188–90.



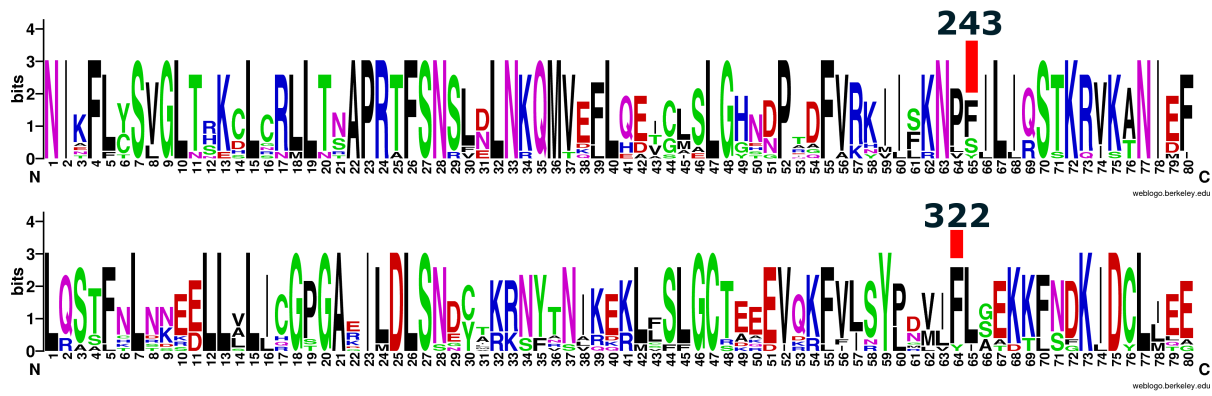
Supplementary Figure 1 Byrnes, et al.



Supplementary Figure 2 Byrnes, et al.



Supplementary Figure 3 Byrnes, et al.



Supplementary Figure 4 Byrnes, et al.