Supplemental material

Winsor et al., https://doi.org/10.1083/jcb.201805039

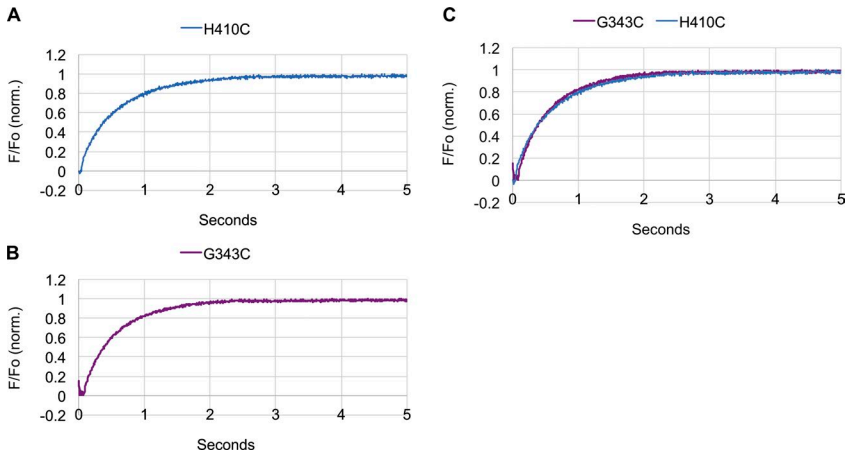

Figure S1. **Comparison of H410C and G343C cyt-*D*ATL PIFE kinetics. (A and B)** Stopped-flow PIFE of WT cyt-*D*ATL labeled with Cy3 on H410C (A) or G343C (B) after addition of excess GTP. **(C)** H410C and G343C PIFE traces overlaid for comparison. For each, cyt-*D*ATL was 2 µM, and GTP was 1 mM (final concentrations). Traces were normalized (minimum value = 0; maximum value = 1). All traces are the average of three to five individual traces and representative of two independent protein preparations.

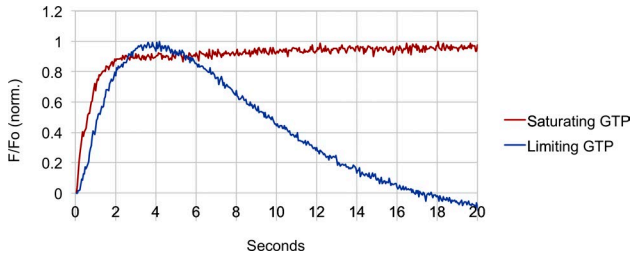

Figure S2. **Comparison of WT cyt-DATL PIFE kinetics under single- (limiting GTP) and multiple (saturating GTP)-turnover conditions.** The multiple-turnover condition had 2 µM cyt-*D*ATL and 1 mM GTP, whereas the single-turnover condition had 15 µM cyt-*D*ATL and 7.5 µM GTP. Traces were normalized for ease of comparison (initial value = 0; maximum value = 1).

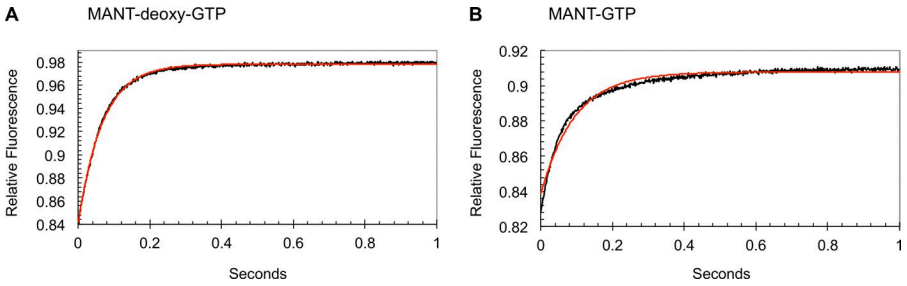

Figure S3. **Atlastin binds mant-dGTP and mant-GTP with similar kinetics. (A and B)** Binding of 10 µM mant-dGTP (A) or 10 µM mant-GTP (B) to 100 nM cyt-*D*ATL (black lines) shows similar kinetics. A fit of each to a single exponential decay equation (red lines) shows a lesser fit for mant-GTP (B) that was likely due to the presence of a mixture of 2′- and 3′-OH–labeled nucleotides, whereas mant-dGTP (A) binding fit well.