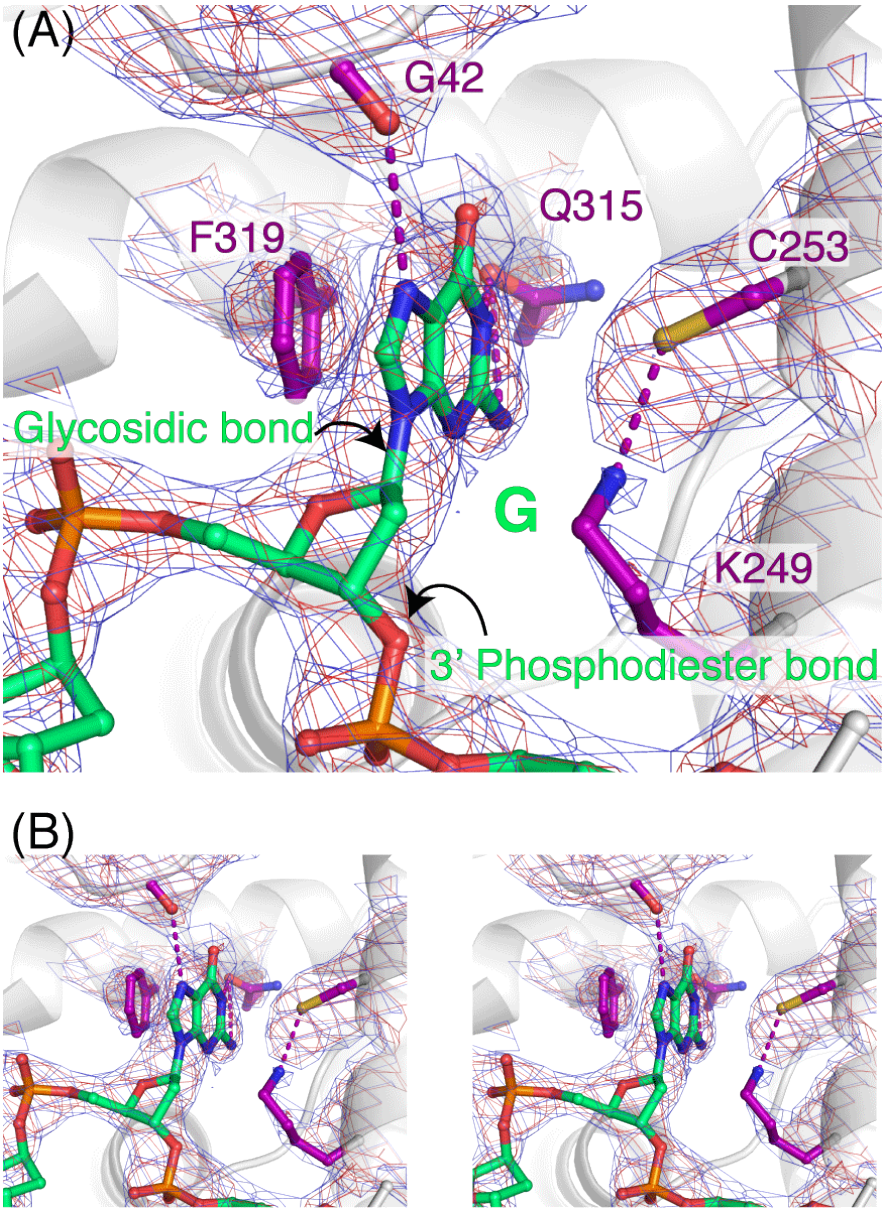

Supplemental Fig. 2. The dDXL G-complex active site electron density. *A*, The final model was used to calculate a σA-weighted (1) simulated annealing omit electron density map contoured at 1σ (blue mesh) or 1.5σ (red mesh) around selected active site side chains (purple sticks). Dashed lines highlight recognition between the target guanine (green sticks) and the active site side chains (purple). Strong density for the glycosidic and 3'-phosphodiester bonds of guanine confirms little to no catalysis has taken place, while the weak electron density for the Lys249 side chain reflects its relative conformational disorder. In *B*, this map is contoured at 1σ and the active site shown as a stereo view.

1. Read, R. J. (1986) *Acta Crystallogr. Sect. A* **42**, 104