Table S1. CryoEM Data Collection and Processing Statistics, Related to Figure 1

	DNA-bound telomerase (EMD-7821)	DNA-free telomerase (EMD-7820)
Magnification	36,764×	36,764×
Voltage (kV)	300	300
Electron exposure ($e^{-}/Å^2$)	52	52
Defocus range (μm)	–1.7 to –4.1	–1.8 to –5.3
Pixel size (Å)	1.36	1.36
Symmetry imposed	C1	C1
Initial particle images (no.)	3,200,000	2,300,000
Final particle images (no.)	52,506	123,684
Map resolution (Å)	4.8	6.4
FSC threshold	0.143	0.143
Map resolution range (Å)	4.0 – 8.0	5.5 – 9.0

Table S2. Model Refinement and Validation Statistics, Related to Figure 1

	DNA-bound telomerase (PDB 6D6V)
CC_{mask}	0.8021
R.m.s. deviations	
Bond lengths (Å)	0.013
Bond angles (°)	1.691
Ramachandran plot	
Favored (%)	83.87
Allowed (%)	16.43
Disallowed (%)	0.70
Rotamer outliers (%)	0.82
MolProbity score	2.53
Clashscore	22.20
C_β deviations	0