
Supplementary information

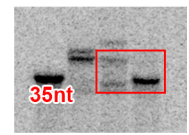
**Structural basis of Rho-dependent
transcription termination**

In the format provided by the
authors and unedited

Figure 1b



Figure 3a



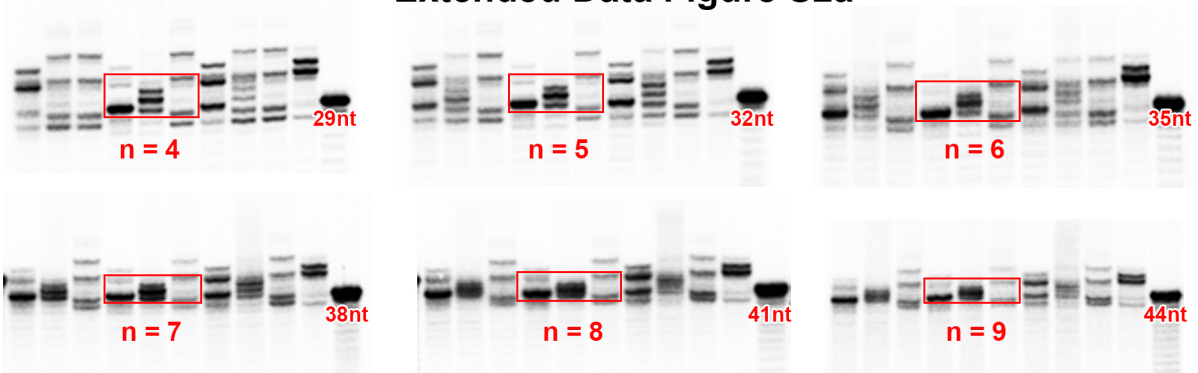
Extended Data Figure S1a



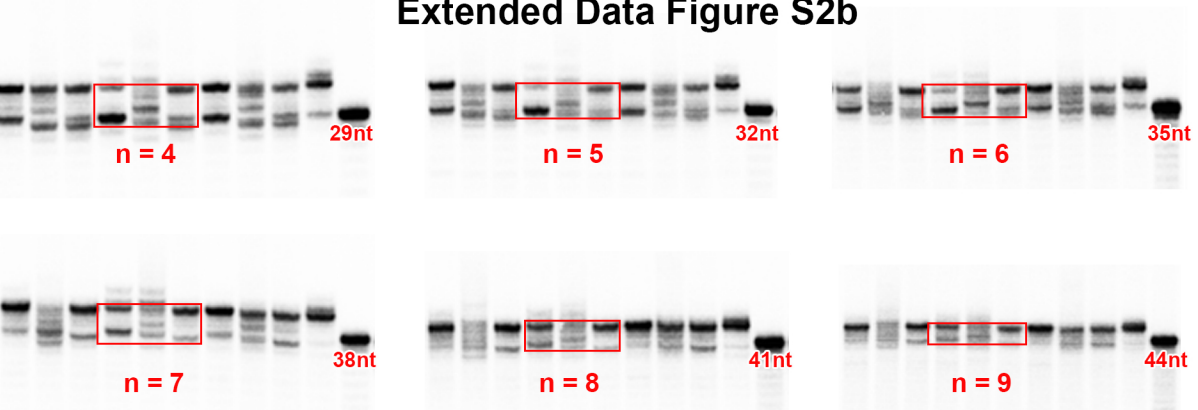
Extended Data Figure S1b



Extended Data Figure S2a



Extended Data Figure S2b



Supplementary Table 1. Cryo-EM structures: λ tR1-Rho-NusG-TEC (n = 6), dC75-Rho-NusG-TEC (n = 6), and Rho-NusG-TEC (n = 6, 7, and 8)

complex	n (codons)	facility	particles	resolution	EMDB code ^a	PDB code ^b
λ tR1-Rho-NusG-TEC	6	NCCAT	69,316	4.3 Å	EMD-27930 EMD-27928 EMD-27929 EMD-27931	8E6X 8E6W
dC75-Rho-NusG-TEC	6	NCCAT	194,518	4.1 Å	EMD-27932 EMD-27933 EMD-27864	8E6Z 8E70
Rho-NusG-TEC	6	Rutgers	15,936	6.5 Å	EMD-27865 EMD-27897 EMD-27913	8E3F 8E3H
Rho-NusG-TEC	7	Rutgers	31,098	4.2 Å	EMD-27914 EMD-27915 EMD-27916	8E5K 8E5L
Rho-NusG-TEC	8	SLAC	270,373	4.4 Å	EMD-27917 EMD-27918	8E5O 8E5P

^aThe first, second, and third EMDB codes for each complex are for (i) density map, processed by focused refinement, for TEC, NusG, and spacer RNA, (ii) density map, processed by focused refinement, for Rho, PBS-ligand RNA (where present), SBS-ligand RNA, and Mg-ADP-BeF₃, and (iii) lower-resolution density map of full complex, without focused refinement to improve resolution of components.

^bThe first and second PDB codes for each complex are for (i) atomic coordinates for TEC, NusG, SBS-ligand RNA, and spacer RNA and (ii) atomic coordinates for Rho, PBS-ligand RNA (where present), and Mg-ADP-BeF₃.