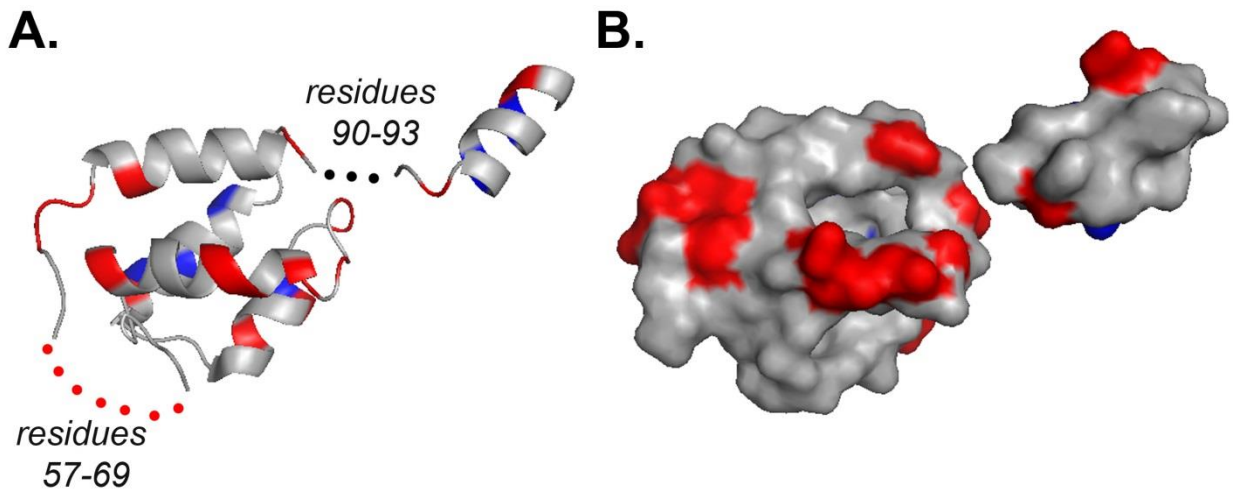
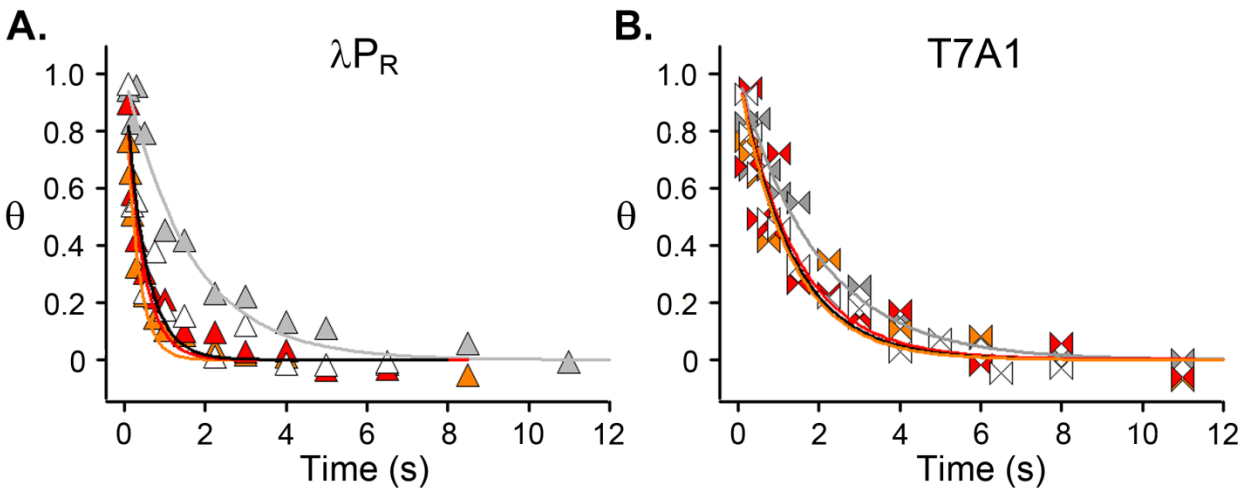
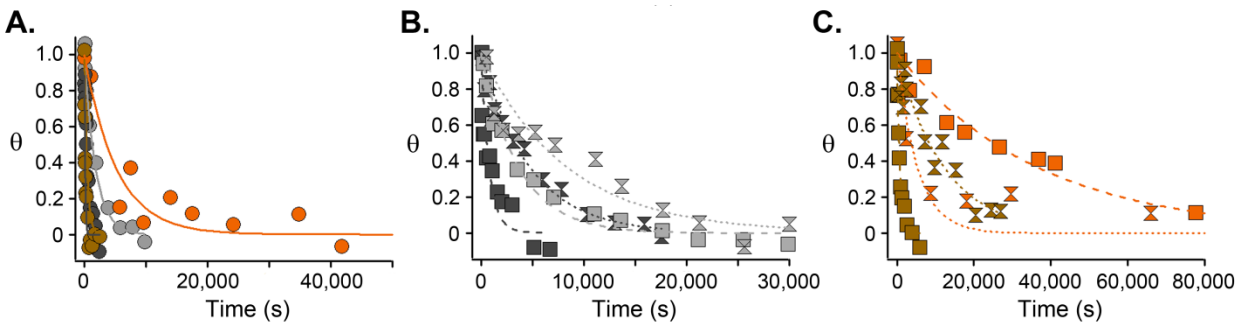
SUPPLEMENTAL INFORMATION



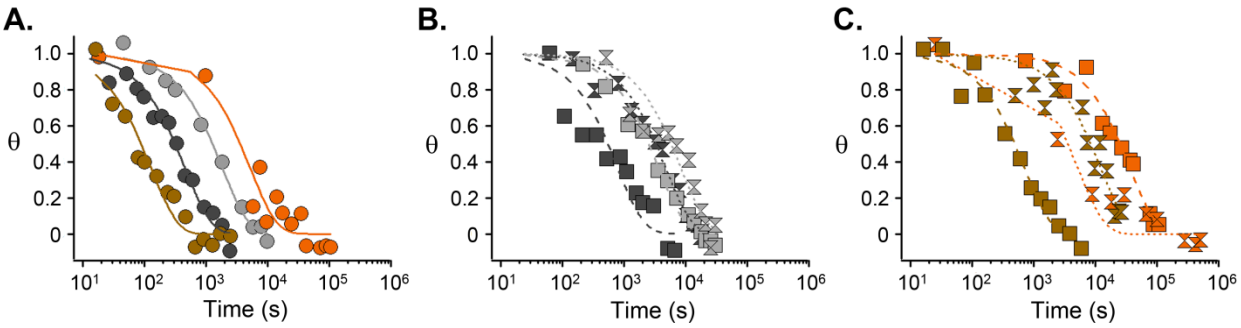
Supplemental Figure 1. Structure and charge distribution of $\sigma_{1.1}$ (residues 1-98) and residues 99-106 of $\sigma_{1.2}$, viewed from the top of β', in an *E. coli* holoenzyme structure (PDB 4LK1). $\sigma_{1.1}$ has 23 negatively-charged (11D, 12E) and 6 positively charged (2R, 2K, 1H, N terminus) residues. The N-terminal 3-helix bundle (residues 1-55) has 10 negatively-charged (5D, 5E) and 3 positively-charged (1R, 2K) residues. Negatively charged residues (E and D) are shown in red; positively charged residues (R, H, K) in blue; others in gray. **A.** Ribbon diagram. Regions for which electron density is not observed are labeled and represented by dots connecting the nearest observed residues. Residues 57-69, which include six negatively (57E, 57E, 61D, 63D, 64D, and 69E) and no positively charged residues, are represented by red dots; residues 90-93, which include one positively (93R) and one negatively charged residue (90E), are represented by gray dots. **B.** van der Waals surface representation.



Supplemental Figure 2. Nitrocellulose filter binding data for dissociation at 37 ^{o}C of OCs formed in transcription buffer (120 mM KCl) and then subjected to a rapid upshift to 1.1 M KCl. Data were fit to **Equation 1** using the nonlinear fitting program Igor Pro version 5.03. Fits to the data are shown as solid lines and kinetic constants are listed in **Table 1** and shown in **Figure 5**. Raw data are from single, representative assays, normalized to an initial θ of 1.0 and a final θ of 0 using information from fitting unnormalized kinetic data. Color coding: WT: white symbols, black fit, Δ98: red symbols and fit, ΔJAW: light gray symbols and fit, and ΔSI3: orange symbols and fit. **A.** Dissociation of OCs with the λP_R promoter. **B.** Dissociation of OCs with the T7A1 promoter.



Supplemental Figure 3. Nitrocellulose filter binding data for dissociation of OCs in transcription buffer at 37 ^{o}C with double and single RNAP deletion variants at the λP_R and T7A1 promoters. Data were fit to **Equation 1** using the nonlinear fitting program Igor Pro version 5.03. Fits to the data are shown as solid lines with the same color as the corresponding data points. Kinetic constants are listed in **Tables 1** and **2**, and lifetimes are shown in **Figures 5** and **6**. Raw data show an individual assay, normalized to an initial θ of 1.0 and a final θ of 0 using information from fitting unnormalized kinetic data. The following data are shown in each panel: **A.** λP_R-ΔSI3 (orange circles, solid fit); λP_R-ΔJAW (light gray circles, solid fit); T7A1-ΔJAW (dark gray circles, solid fit); and T7A1-ΔSI3 (brown circles, solid fit). **B.** λP_R-Δ98/ΔJAW (light gray hourglasses, dotted fit); T7A1-Δ98/ΔJAW (dark gray hourglasses, dotted fit); λP_R-Δ55/ΔJAW (light gray squares, dashed fit); and T7A1-Δ55/ΔJAW (dark gray squares, dashed fit). **C.** λP_R-Δ55/ΔSI3 (orange squares, dashed fit); T7A1-Δ98/ΔSI3 (brown hourglasses, dotted fit); λP_R-Δ98/ΔSI3 (orange hourglasses, dotted fit); T7A1-Δ55/ΔSI3 (brown squares, dashed fit).



Supplemental Figure 4. Data from **Supplemental Figure 3** are shown on a logarithmic time scale. Legend is the same as in **Supplemental Figure 3**.