

## Supplementary Material

### **Supplementary Fig. 1. DNA fragments accelerate dissociation of fluorescent-labeled-Fis in a direct visualization experiment.**

Left panel: Sequential images of DNA tether during exchange of pre-bound GFP-Fis with 20 ng/μl herring sperm DNA (HS-DNA) fragments. Initial binding to a phage λ chromosomal DNA (49152 bp, Promega) was done with 200 nM Fis in 100 mM KCl buffer, pH 7.6. Middle and bottom panels are images 180 s and 690 s, respectively, post addition of 5 ng/μl HS-DNA.

Right panel: Plot of control data (blue squares), exchange of GFP-Fis with 5 ng/μl HS-DNA fragments (green diamonds) and 50 ng/μl HS-DNA fragments (red circles). Dissociation rates are  $0.0033 \pm 0.00081$  ( $s^{-1}$ ) for 5 ng/μl HS-DNA and  $0.0062 \pm 0.0018$  ( $s^{-1}$ ) for 50 ng/μl HS-DNA, from N=4 trials for each case.

### **Supplementary Fig. 2. Comparison of HS-DNA-facilitated dissociation of Fis from DNA at 100 mM and 200 mM KCl concentration**

Off-rate of Fis from DNA as a function of HS-DNA concentration at fixed salt concentration of 100 mM KCl (black squares) and 200 mM KCl (gray triangles). The off-rates are uniformly faster at the higher salt concentration, with a higher initial exchange rate (initial slope) and a higher saturation value of off-rate, reflecting the weakening of electrostatic interactions between Fis and DNA with increased salt concentration.

## Mean reaction time for the facilitated dissociation model

We consider the reaction  $0 \leftrightarrow 1 \leftrightarrow 2 \rightarrow 3$  with rates  $k_{ij}$  for transitions from  $i \rightarrow j$ . The objective is to compute the mean time for the transition from 0 to 3 to occur, given that the final reaction from 2 to 3 is irreversible. Following the general approach of Ref. <sup>45</sup>, we compute the mean first passage time to state 3 by enumerating all possible sequences of states leading from 0 to 3, appropriately averaging their mean transit times based on the reaction rates, using the branching probability at each step from state  $i$  to state  $j$ ,  $p_{ij} = k_{ij}/(\sum_l k_{il})$ :

$$\begin{aligned} \langle \tau_{03} \rangle &= \frac{1}{k_{01}} + \sum_{n=1}^{\infty} p_{01}^n \left( \frac{1 + p_{12}}{k_{10} + k_{12}} + \frac{1}{k_{01}} \right) + \frac{p_{12}}{k_{10} + k_{12}} + \frac{p_{23}}{k_{21} + k_{23}} \\ &\quad + \sum_{n=1}^{\infty} p_{21}^n \left[ \frac{1 + p_{23}}{k_{21} + k_{23}} + \frac{p_{12}}{k_{10} + k_{12}} + \sum_{m=1}^{\infty} p_{10}^m \left( \frac{1 + p_{12}}{k_{10} + k_{12}} + \frac{1}{k_{01}} \right) \right] \\ &= \frac{k_{01}(k_{12} + k_{21} + k_{23}) + k_{10}(k_{21} + k_{23}) + k_{21}k_{23}}{k_{01}k_{12}k_{23}} \end{aligned}$$

For this paper we make the symmetry assumption  $k_{21} = k_{23}$ , (which does not affect the fit function in the main text but only the interpretation of the fit parameters) plus we include the bulk DNA concentration  $c$  in the rate  $k_{12}$ , by replacing  $k_{12} \rightarrow k_{12}c$  in the above equation (see Fig. 7). The result is Eq. 1 of the main text. We note that addition of a “direct” dissociation transition from state 0 to 3 is possible with only a slight complication of the results, but is not needed for this paper.