

Mechanism of Facilitated Diffusion during DNA Search in Crowded Environments - Supporting Information

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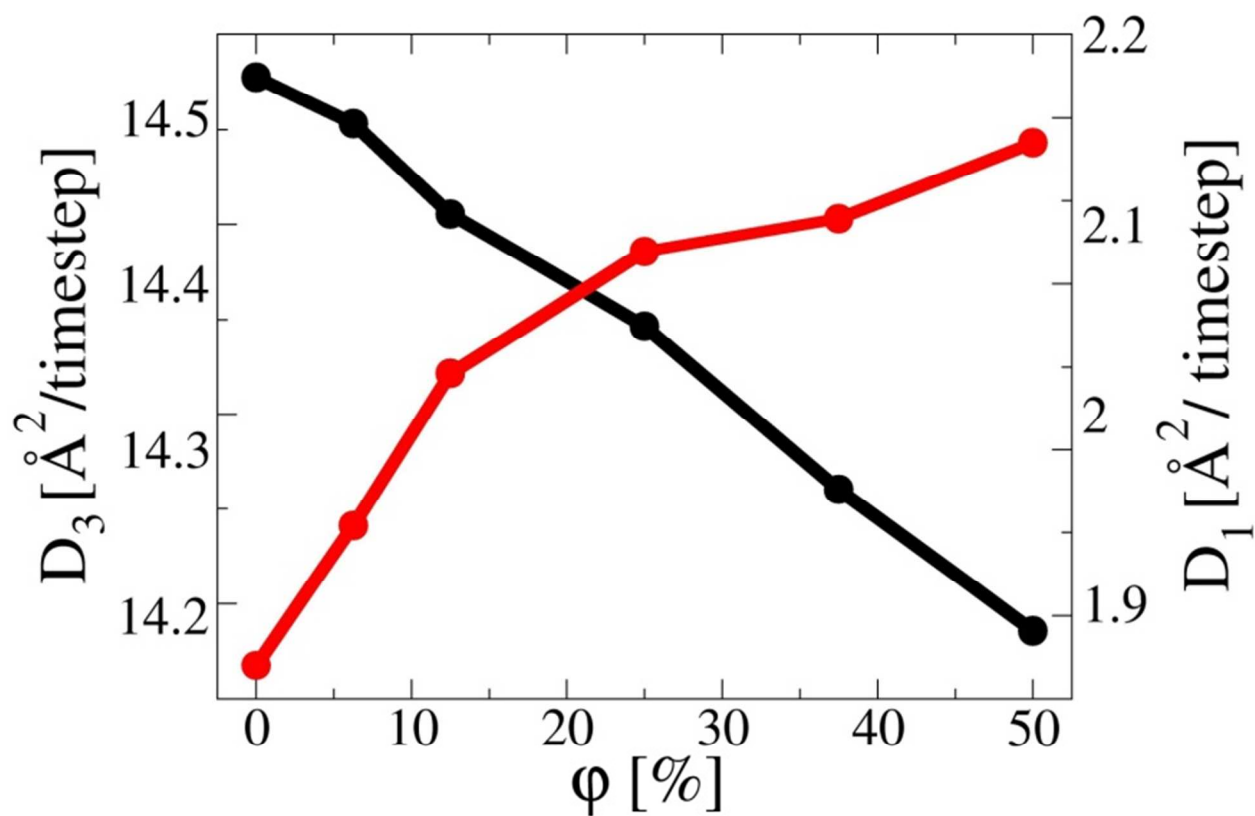


Figure S1. The values of the 1D and 3D diffusion coefficient (D_1 in red and D_3 in black) as a function of the fractional volume of the crowding molecules. These values were taken from Figures 2B and 2D.

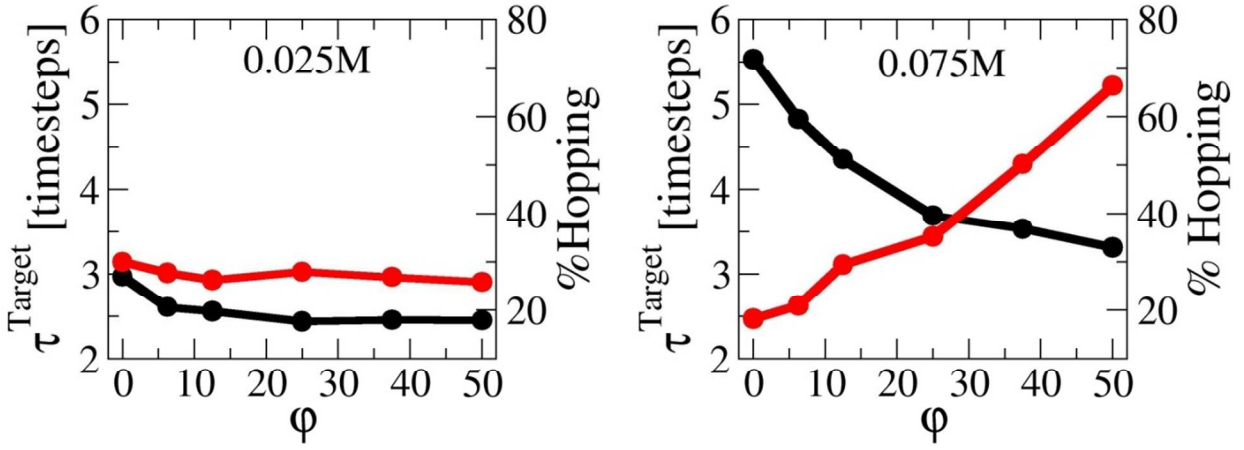


Figure S2. τ^{Target} (black) and hopping (red) at different fractional volume. The values correspond to plot 2A and 3A.

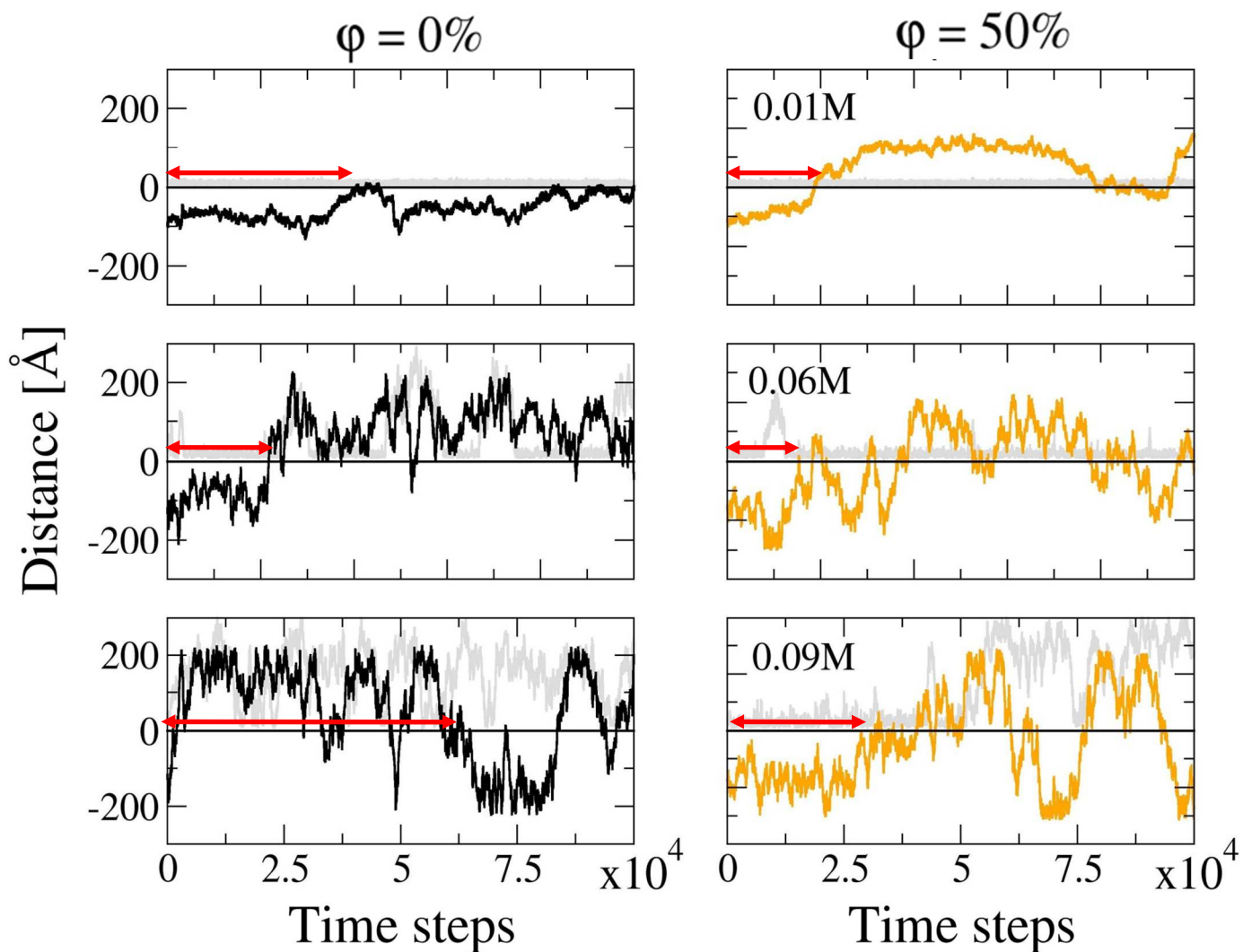


Figure S3. Raw trajectories data of the displacement of the protein during 10^5 time steps along the DNA axis under salt concentrations of 0.01M (upper panels), 0.06M (middle panels) and 0.09M (lower panels) at $\phi=0\%$ (left panels, black lines) and $\phi=50\%$ (right panels, orange lines). At each trajectory, Protein displacement from DNA axis is shown as grey lines. At each trajectory red arrow represents the value of τ^{Target} . Corresponding to Fig. 3A in the main text, τ^{Target} decreases with increasing fractional volume, ϕ , for all three salt concentrations.

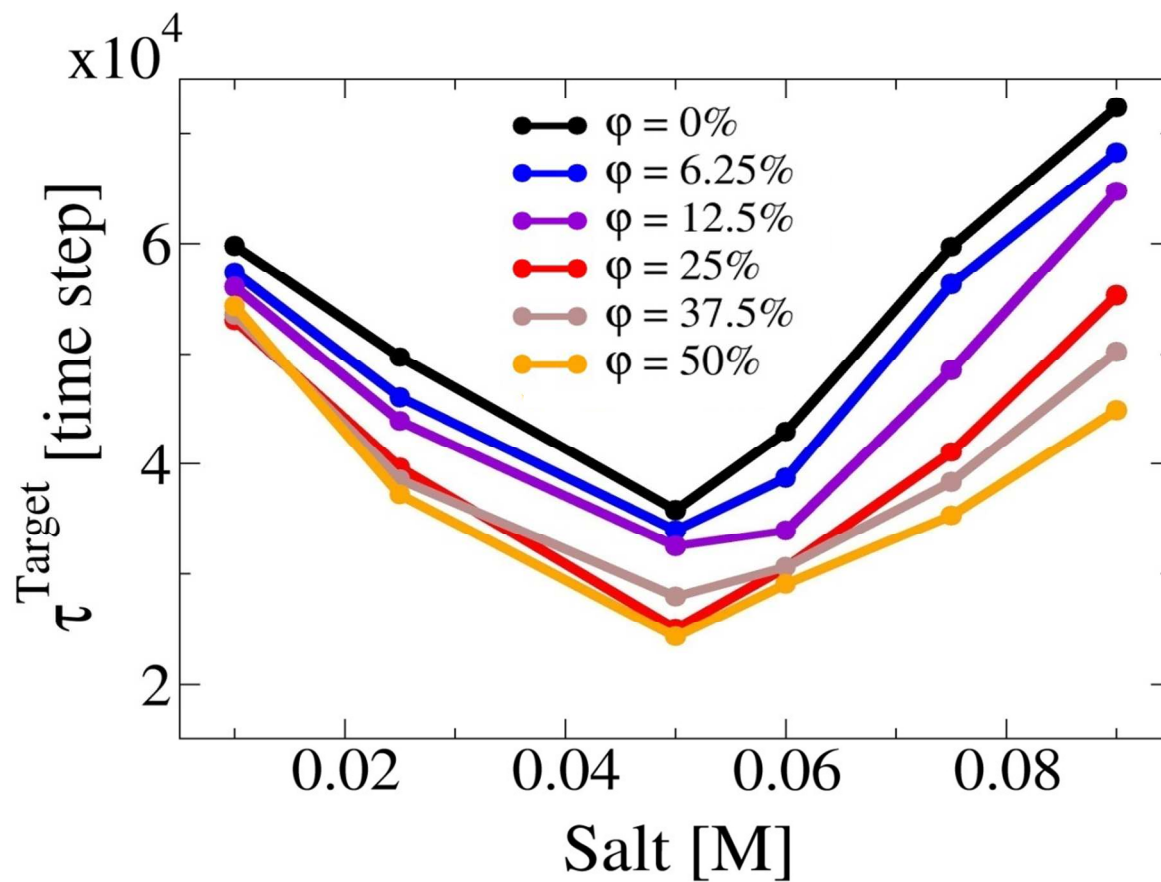


Figure S4. The effect of molecular crowding (modeled as ϕ , the fractional volume) on τ^{Target} , when placing the protein far from the DNA, at different salt concentrations. Although this results in higher values of τ^{Target} , the overall shape resembles that of Fig. 3A in main text, with τ^{Target} decreasing with increasing fractional volume, ϕ , for all salt concentrations.

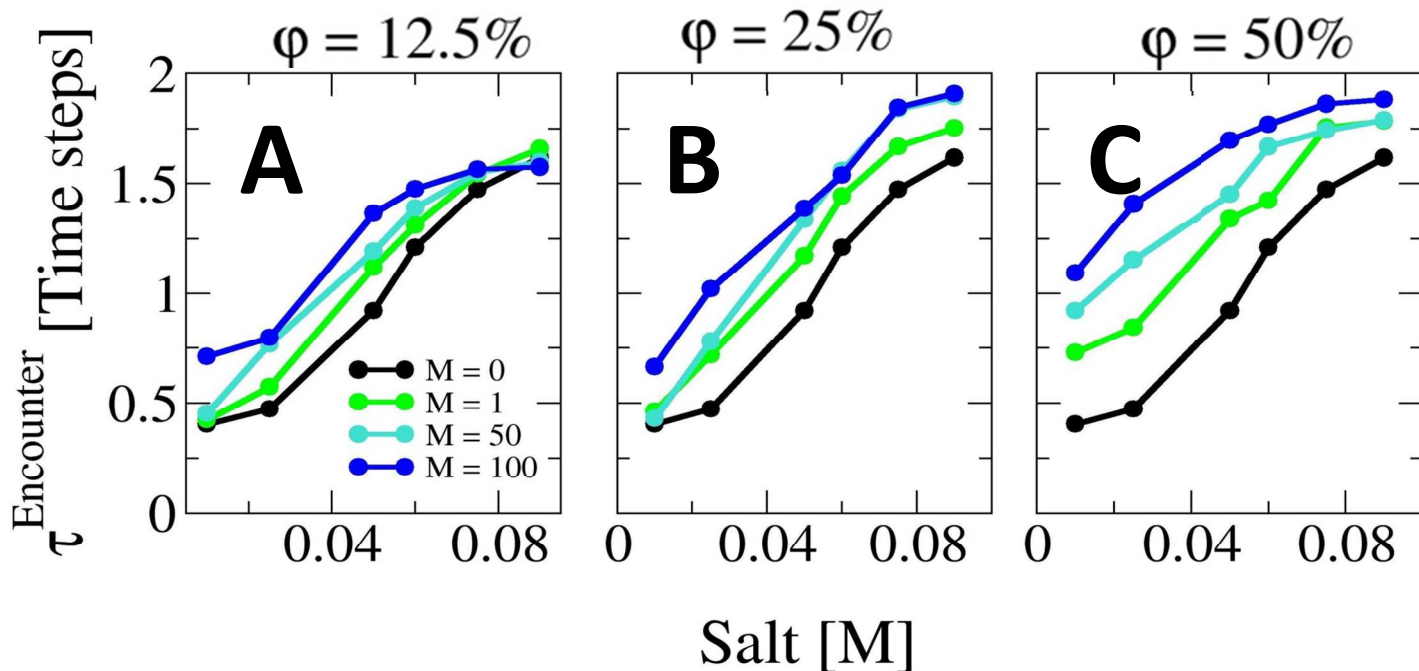


Figure S5. The effect of molecular crowding mass on $\tau_{\text{Encounter}}$ when placing the protein far from the DNA at fractional volumes of $\phi=12.5\%$ (left panel), $\phi=25\%$ (middle panel) and $\phi=50\%$ (right panel), as a function of salt concentrations. Corresponding to Fig. 4A in main text, the slow movement of crowders induces the effect of confinement, resulting in the increase of $\tau_{\text{Encounter}}$ with increasing fractional volume, ϕ , for all salt concentrations.

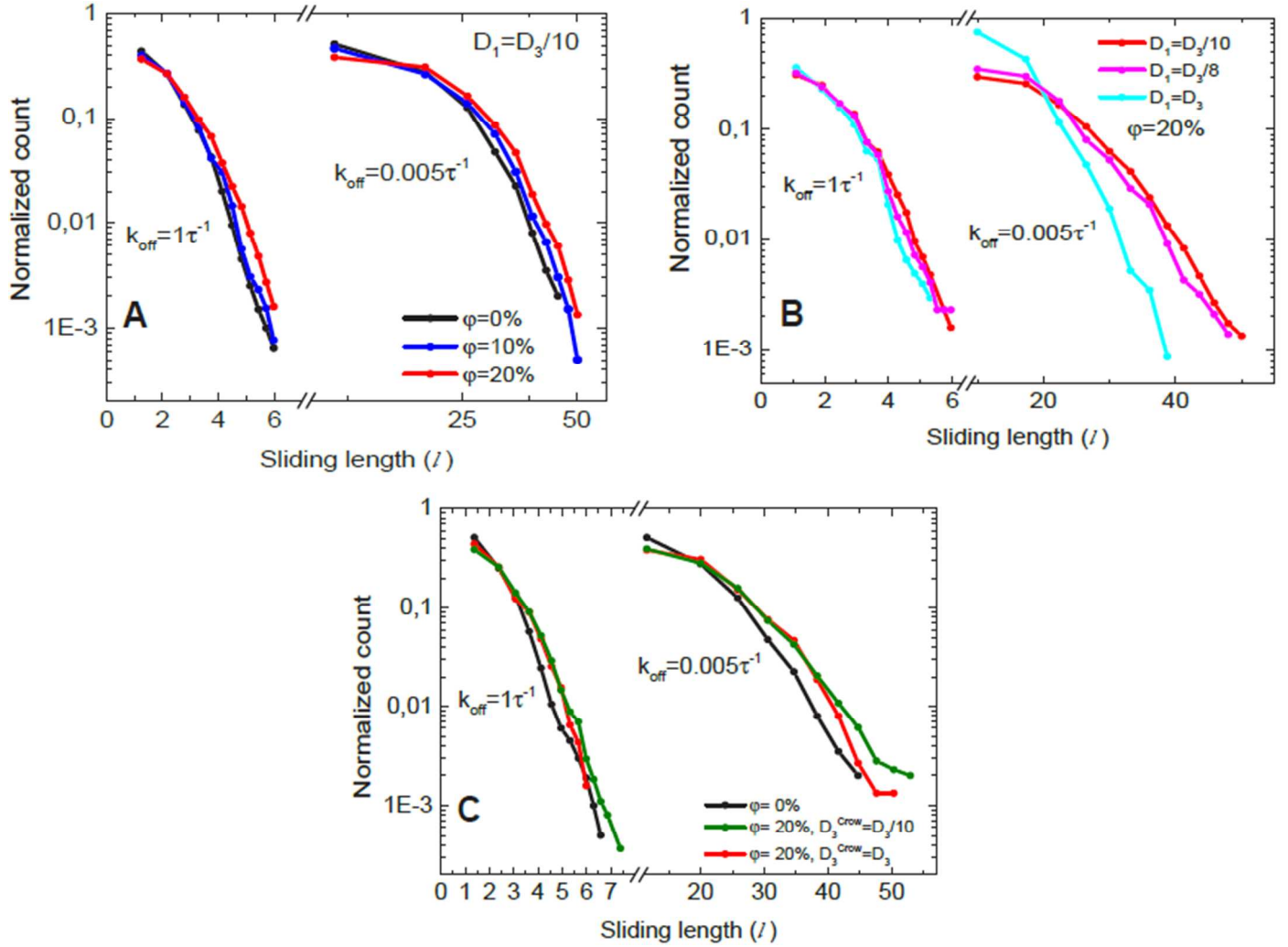


Figure S6. Sliding length distributions of the DBP along the DNA for various values of k_{off} , D_1 and ϕ . A) As molecular crowding increases, DBP-DNA binding is enhanced and the sliding length distributions shift towards larger values. B) As the 1D diffusion constant increases, the distributions get narrow around a smaller value of sliding length, because scanning of lattice sites become faster. C) In addition to the enhancement of DBP-DNA binding by crowding, heavy crowdors increase the effect. Sliding length distributions shift towards higher values. We note that despite the enhancement in DBP-DNA binding, the strong effects that heavy crowdors have on 3D diffusion make that the average finding time drastically increases (Fig. 5B main text). All data shown here correspond to $\phi = 20\%$.