

## Supporting Information

# Free Energy Landscape and Dynamics of Supercoiled DNA by High-Speed Atomic Force Microscopy

Tine Brouns,<sup>a</sup> Herlinde De Keersmaecker,<sup>a</sup> Sebastian F. Konrad,<sup>b</sup> Noriyuki Kodera,<sup>c</sup> Toshio Ando,<sup>c</sup> Jan Lipfert,<sup>b,\*</sup> Steven De Feyter,<sup>a,\*</sup> and Willem Vanderlinden<sup>a,b,\*</sup>

<sup>a</sup> *KU Leuven, Division of Molecular Imaging and Photonics, Celestijnenlaan 200F, 3001 Leuven, Belgium.*

<sup>b</sup> *Department of Physics, Nanosystems Initiative Munich, and Center for NanoScience, LMU Munich, Amalienstrasse 54, 80799 Munich, Germany.*

<sup>c</sup> *Nano-Life Science Institute (WPI-NanoLSI), Kanazawa University, Kakuma-machi, Kanazawa, 920-1192, Japan.*

**Supplementary Movie:** Supplementary Movie 1

**File:** Supplementary\_Movie\_1.avi

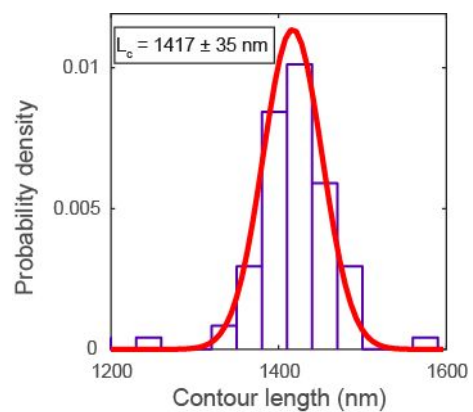
**Title:** Dynamics of positively supercoiled pBR322 on mica

**Description:** High-speed AFM image sequence of positively supercoiled pBR322 at the interface of muscovite mica and an aqueous buffer supplemented with 5 mM MgCl<sub>2</sub>.

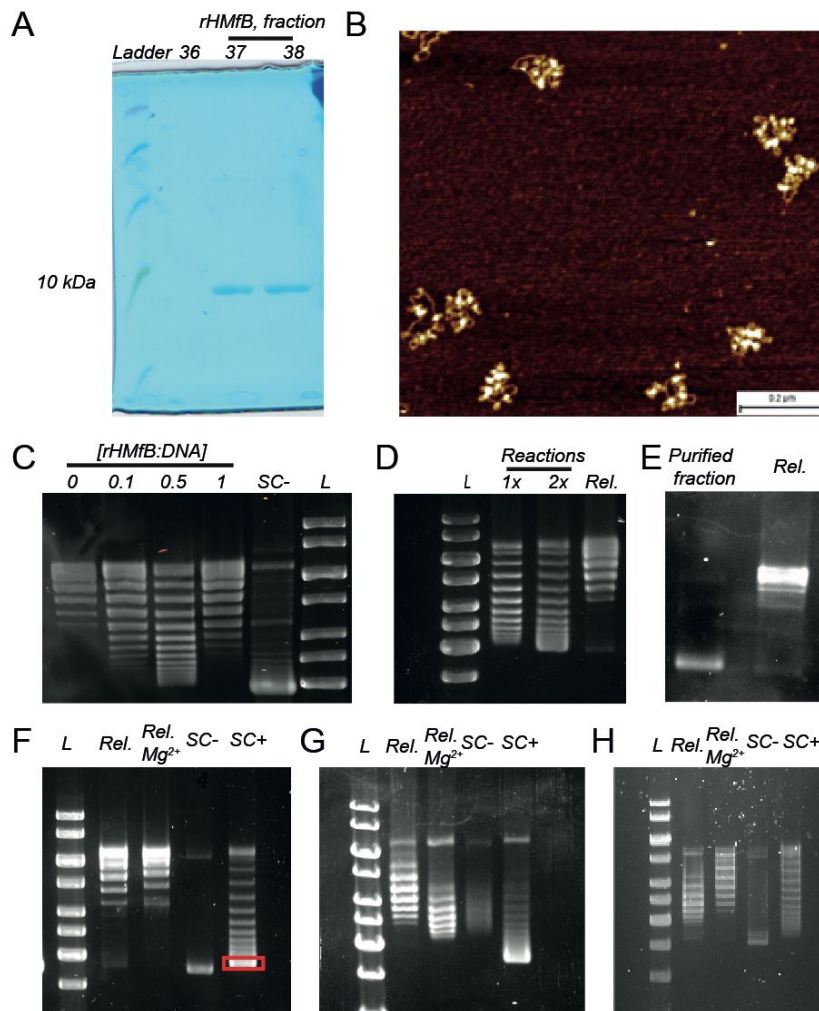
**Movie parameters:** Image size: 500 nm. Image acquisition speed: 0.6 s. (10 × real-time)

	<b>2D</b>	<b>3D</b>	<b>3D-2D PROJECTED</b>
<b>PLL-MICA</b>	$A = 11 \text{ nm}$ $\chi_{\text{Red}}^2 = 0.77$	$A = 22 \text{ nm}$ $\chi_{\text{Red}}^2 = 2.17$	$A = 40 \text{ nm}$ $\chi_{\text{Red}}^2 = 1.24$
<b>BARE MICA</b>	$A = 48 \text{ nm}$ $\chi_{\text{Red}}^2 = 0.84$	$A = 105 \text{ nm}$ $\chi_{\text{Red}}^2 = 3.6$	$A = 135 \text{ nm}$ $\chi_{\text{Red}}^2 = 1.06$

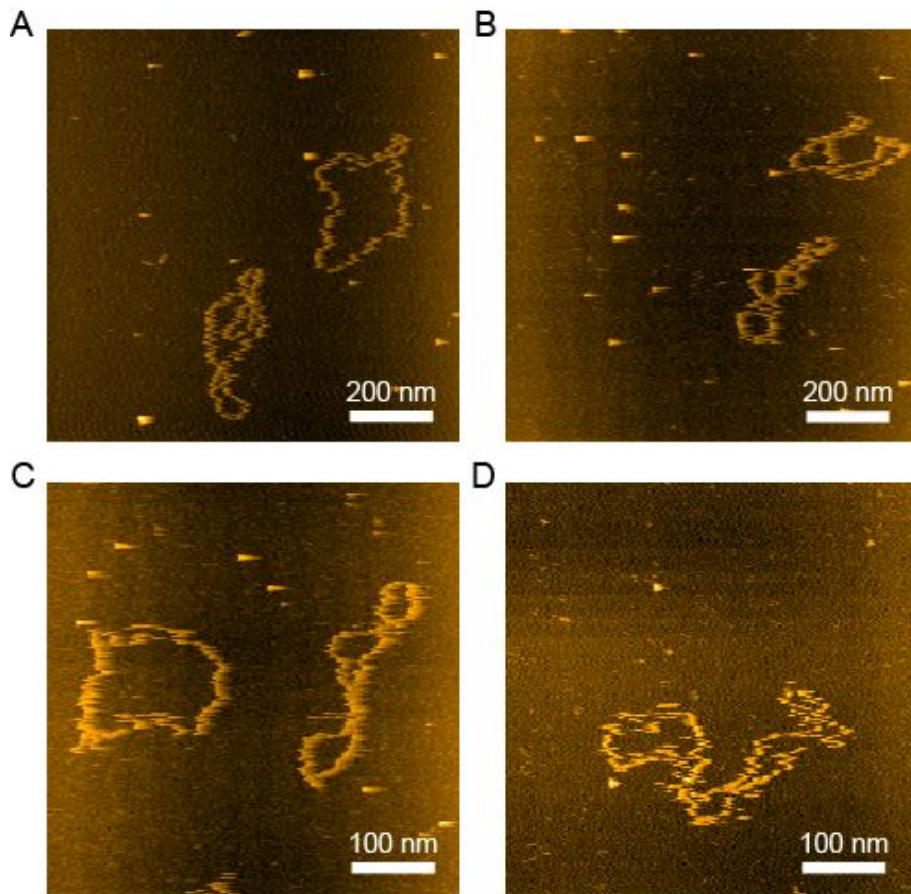
**Supporting Table S1.** Best fit parameters for end-end distance distributions of linear pBR322 adsorbed onto PLL-mica and bare mica, for different adsorption models: 2D equilibration (“2D”), kinetic trapping with conservation of the 3D end-end distance (“3D”), or kinetic trapping according to a 2D projection of the 3D end-end distance (“3D-2D projected”). For each adsorption model,  $10^5$  chains were simulated for a range of bending persistence lengths  $A$  and compared to the experimental distributions. The fitted persistence lengths  $A$  that yielded the lowest reduced chi-square value  $\chi_{\text{Red}}^2$  are listed for each model and for both deposition surfaces.



**Supporting Figure S1.** Contour length distribution as determined by automated tracing of linear pBR322 molecules adsorbed onto bare mica, and single Gaussian fit.



**Supporting Figure S2.** Generation and characterization of positively supercoiled pBR322. **A.** SDS PAGE of purified rHMfB showing the purity of two different fractions of purified rHMfB. **B.** AFM topograph of rHMfB incubated with relaxed pBR322. **C.** Gel electrophoresis data of pBR322 relaxed in the presence of different concentrations of rHMfB, and negatively supercoiled pBR322 (SC-) and ladder (L). **D.** Gel electrophoresis data of the effect of a single versus dual round of topoisomerization in the presence of rHMfB, as well as the in the absence of rHMfB (“Rel.”). **E.** Gel electrophoresis photograph of gel-purified highly positively supercoiled pBR322, and relaxed pBR322. **F.** Comparison of pBR322 relaxed with topoisomerase Ib in assay buffer (50 mM Tris.HCl (pH 7.9), 1 mM EDTA, 1 mM DTT, 20 % (v/v) glycerol, 50 mM NaCl) or in AFM deposition buffer (“Rel. Mg<sup>2+</sup>”), negatively supercoiled pBR322, and positively supercoiled pBR322. The red box indicates the position of the gel excised for purification and AFM analysis. Note that a different gel was used for this purpose. **G.** Gel electrophoresis photograph of pBR322 plasmids in 1xTAE buffer supplemented with chloroquine. Lanes contain samples identical to those in (F). **H.** Gel electrophoresis photograph of pBR322 plasmids in 1xTAE buffer supplemented with CaCl<sub>2</sub> (5 mM). Lanes contain samples identical to those in (F).



**Supporting Figure S3.** *In situ* AFM topographs of negatively supercoiled pBR322 deposited on bare mica and imaged in aqueous buffer comprising 5 mM MgCl<sub>2</sub>.