Supporting information

Complete sequence of the DNA fragment used in this work:

```
5′-
cggccagtgaattgtaatacgactcactatagggcgaattcgagctcggtacccggggatcctctagagtcgggagccgg
aacactatccgactggcaccggcaaggtcgctgttcaatacatgcacaggatgtatatatctgacacgtgcctggaacta
gggagtaatccccttggcggttaaaacgcgggggacagcgcgtacgtgcgtttaagcggtgctagagcttgctacaccaa
ttgagcggcctcggcaccgggattctccagggcggccgcgtatagggtccatcacataagggatgaactcggtggaagaa
tcatgctttccttggtcattaggatcccg
```

Figure S0. The dependence of the protein volume measured with AFM on the protein molecular weight. The dependence is linear and similar to the one obtained in [1]. Black circles denote the proteins volumes calculated for images taken in air. Each point for the same protein corresponds to the mean value for the protein volume calculated for a set of measurements (over 100) in various experiments. For example, the data for five experiments are shown for EcoRII dimer (90 kD). Red stars correspond to the measurements performed in aqueous solution (10 mM HEPES, pH 7.5, 5mM $CaCl_2$) for EcoRII-DNA complexes that was initially dried. Blue starts correspond to the same sample wich never was dried.

References

1. Ratcliff, G. C. & Erie, D. A. (2001). A novel single-molecule study to determine protein--protein association constants. *J Am Chem Soc* **123**, 5632-5.

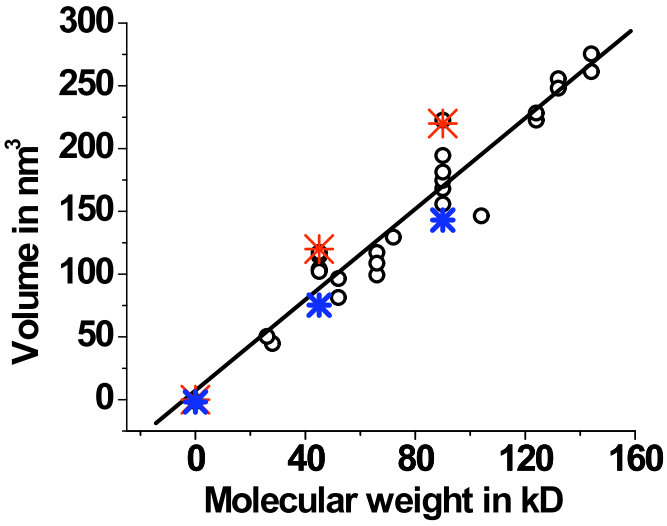


Figure S1(Movie-M3): (full core dissociation) shows rather stable NS with one step unfolding process followed by dissociation of the whole histone core. (A) Consecutive AFM images of nucleosomes taken during continuous scanning in the buffer. Scan size is 200 nm. (B) Dependence of the arm length on the frame number. Each frame takes about 170 second to scan.

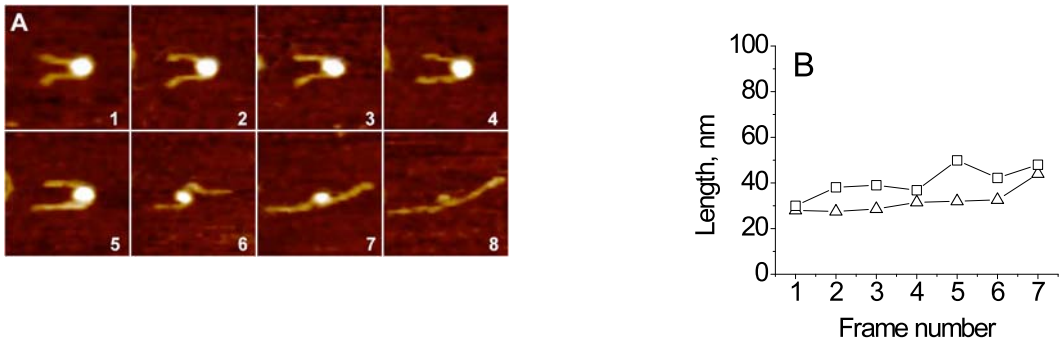


Figure S2 (Movie-M4): wrapping/unwrapping process demonstrates a very long living NS unfolding in two step process with dissociation of the full histone core at the last stage. (A) Consecutive AFM images of nucleosomes taken during continuous scanning in the buffer. Scan size is 200 nm. (B) Dependence of the arm length on the frame number.

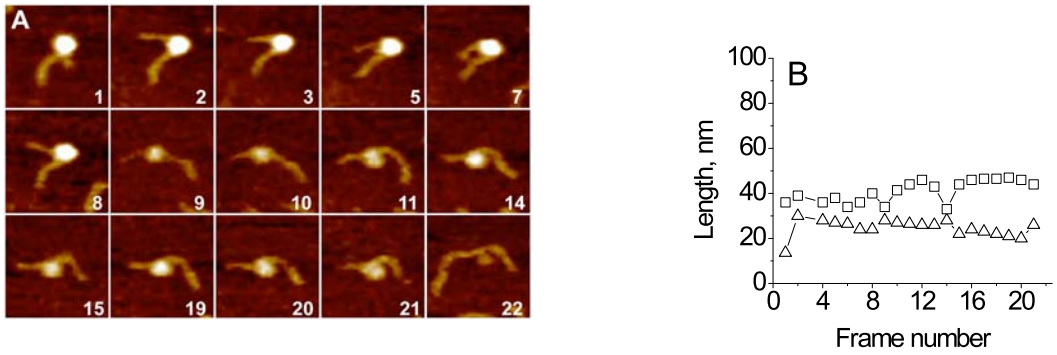
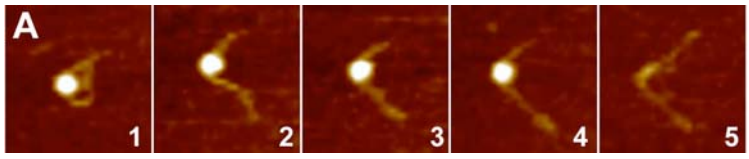
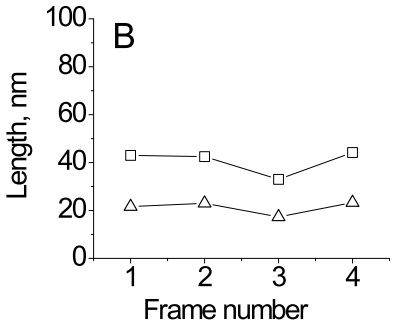


Figure S3 (movie-M5): one step full dissociation. (A) Time-lapse AFM experiment with 5 consecutive frames. Nucleosome particle sitting on the recognition site with about 1.5 turns of DNA wrapped around the core. Scale is 100 nm. (B) The dependence of the arm length on the frame number. (C) The number of DNA turns around the core calculated with arm length (black triangles) and the angle between DNA arms (red circles) and nucleosome volume (blue filled squares, right Y-axis).





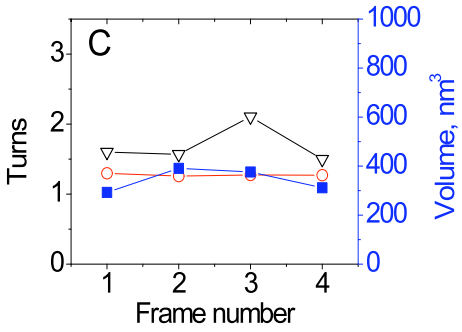
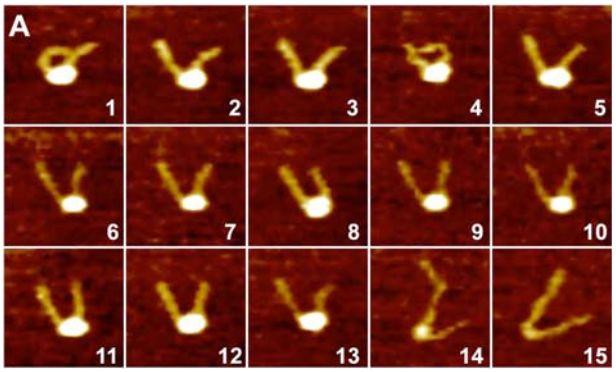
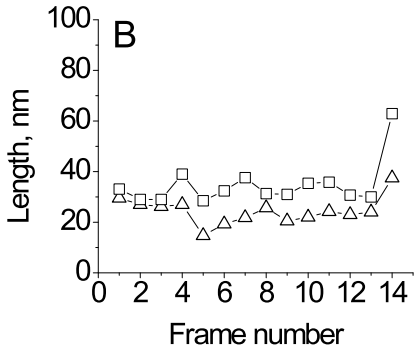


Figure S4 (movie-M6): wrapping/unwrapping. (A) Time-lapse AFM experiment with 15 consecutive frames. Scale is 100 nm. (B) The dependence of the arm length on the frame number. (C) The number of DNA turns around the core calculated with arm length (black triangles) and the angle between DNA arms (red circles) and nucleosome volume (blue filled squares, right Y-axis).





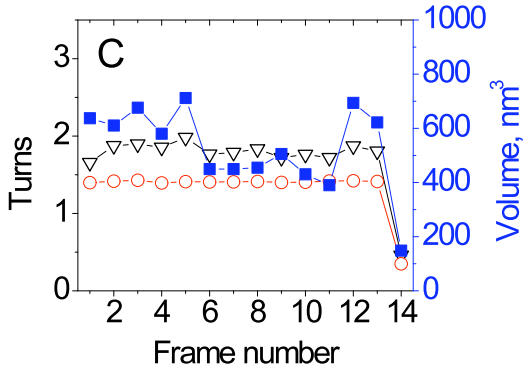


Figure S5: AFM images in aqueous solution. Bright frame in the top left corner of plate (A) shows the area over which a multiple continuous scanning was performed. Plate (B) shows the same area revisited after the continuous scanning over a smaller area (a dark area in the top left) was completed.