



ID de Contribution: 30

Type: Non spécifié

## Probing a label-free local bend in DNA by single molecule tethered particle motion

Being capable of characterizing DNA local bending is essential for the thorough understanding of many biological processes that involve a local bending of the double helix axis, either intrinsic to the sequence or induced by the binding of proteins.

Developing a method to evaluate DNA bend angles that does not perturb the conformation of the DNA itself or the DNA-protein complex is a challenging task. Here, we propose a joint theory-experiment high-throughput approach to rigorously measure such bend angles using the Tethered Particle Motion (TPM) technique. By carefully modeling the TPM geometry, we propose a simple formula based on a kinked Worm-Like Chain model to extract the bend angle from TPM measurements.

Using constructs made of 575 base-pair DNAs with in-phase assemblies of one to seven 6A-tracts, we find that the sequence CAAAAACGG induces a bend angle of  $19^\circ \pm 4^\circ$  [1]. Our method is successfully compared to more theoretically complex or experimentally invasive ones such as cyclization, NMR, FRET or AFM. We further apply our procedure to TPM measurements from the literature and demonstrate that the angles of bends induced by proteins, such as Integration Host Factor (IHF) can be reliably evaluated as well.

[1] **Annaël Brunet**(1,2), Sébastien Chevalier(1), Nicolas Destainville(2), Manoel Manghi(2), Philippe Rousseau(3), Maya Salhi(3), Laurence Salomé(1) and Catherine Tardin(1), *Probing a label-free local bend in DNA by single molecule tethered particle motion*, **Nucleic Acids Res.**, doi:10.1093/nar/gkv201 (2015)

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