

A Dynamic Single-Molecule Approach to Directly Visualize the Molecular Mechanisms of DNA repair

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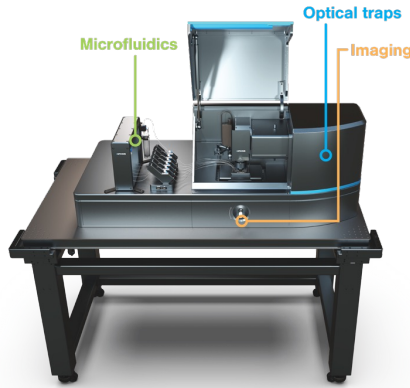
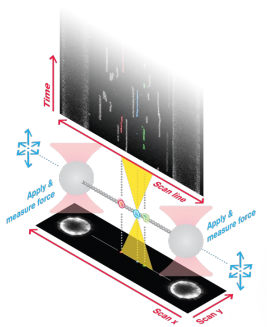
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C-Trap® Correlative Optical Tweezers & Fluorescence Microscopy

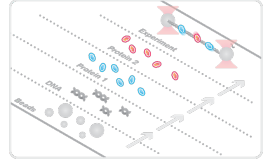
The C-Trap® is the world's first instrument that combines optical tweezers, fluorescence microscopy, and an advanced microfluidic system in a truly integrated and correlated way.

Its capability of live, simultaneous, and correlative manipulation and visualization of biomolecules allows the study of biological processes at the single-molecule level from multiple angles, providing a wide perspective on biomolecular interactions quickly and effectively.

Perform confocal scanning fluorescence to assess biomolecule dynamics in real time



Exploit the easy-to-use, high-throughput and highly stable laminar flow microfluidics to assemble biomolecular complexes bottom-up



Manipulate beads, biomolecules and condensates by light, and measure forces, fusion times and material properties



Contact us

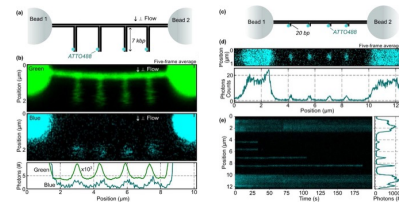
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OT-curtains to study double stranded breaks with the C-trap

OT-curtains enable direct study of protein interactions at free DNA ends while maintaining the standard optical tweezers dumbbell assay.

A custom DNA construct with a tethered backbone and free-ended branches supports flexible architectures, force-free probing of short branches, and 2D imaging of longer branches under mild flow.



Study DNA ends, force-free DNA strands and flexible architectures on the C-trap using OT-curtains

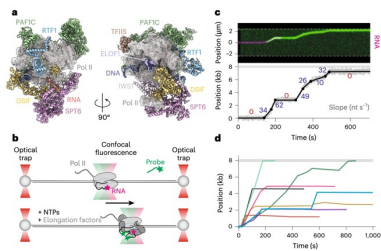
De Bragança et al. (2025) Preprint BioRxiv | Centro Nacional de Biotecnología CSIC Madrid, Prof. Fernando Moreno-Herrero

Directly visualize mammalian transcription elongation by RNA polymerase II

The C-Trap allows real-time visualization of mammalian transcription elongation, enabling detailed mechanistic insights that other methods cannot easily reveal.

The elongation complex operates like multiple gears with distinct kinetic states driven by its associated elongation factors and phosphorylation status.

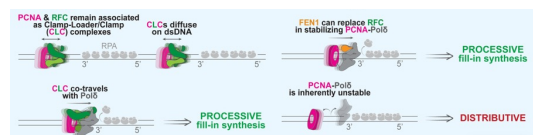
These factors act ordered and cooperatively to modulate elongation speed and pausing, revealing a complex kinetic regulation that enables cells to adapt to a changing environment.



Study the kinetic properties of mammalian transcription elongation in a fully reconstituted system.

Wang et al. (2025) Nature Structural & Molecular Biology | The Rockefeller University, Prof. Shixin Liu

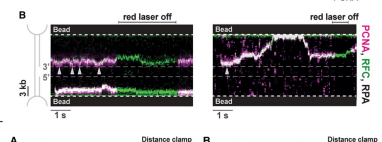
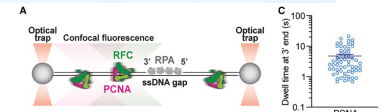
A non-catalytic role for RFC in PCNA-mediated processive DNA synthesis



C-Trap imaging reveals RFC remains bound to PCNA after loading, forming a stable Clamp-Loader/Clamp (CLC) complex that slides on dsDNA.

Visualizing the Long-Lived CLC Complex

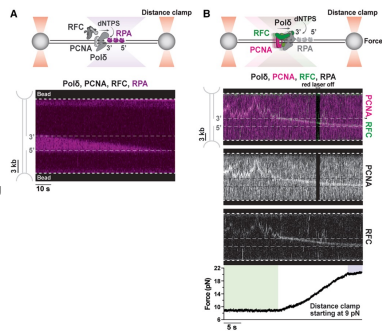
Contrary to the 40-year-old textbook paradigm stating that the clamp loader RFC dissociates immediately after loading PCNA, kymograph data reveals that RFC and PCNA frequently remain tightly coupled, forming a stable, long-lived Clamp-Loader/Clamp (CLC) complex that freely diffuses along double-stranded DNA.



RFC Escorts Polymerase δ During Synthesis

To determine the functional purpose of the CLC complex, the single-molecule assay was expanded to include Polymerase δ and dNTPs to observe active, long-gap DNA synthesis.

Three-color kymographs reveal that instead of being left behind at the starting site, RFC actively co-travels with both PCNA and Polδ as a unified, moving machine. This continuous association acts as a crucial mechanical scaffold, drastically boosting replication processivity.



the clamp loader RFC remains bound to PCNA after loading to form a stable complex with Polymerase δ, acting as a vital structural anchor that prevents premature clamp dissociation and ensures processive DNA synthesis.

Chua et al. (2026) Cell | The Rockefeller University, Prof. Shixin Liu

The LUMICKS store

DNA with single-stranded gap

17,853 bp

ATTO 647N

Custom DNA sequences

Sequence of interest

Handle 1, Handle 2

Custom RNA sequences

ssRNA/DNA

digoxigenin

Nucleosome tethering kit

Nucleosomal array

Handle 1, Handle 2

DNA reference kit

ATTO 647N (6275 bp)

LacI - ATTO 565

LacO (x12)

ATTO 647N (32425 bp)

6298 bp, 7292 bp, 31260 bp, 6298 bp

Download our new application note on nuclear extracts

Accelerating DNA-protein interaction experiments with nuclear extracts in the C-Trap

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