m-Trap®

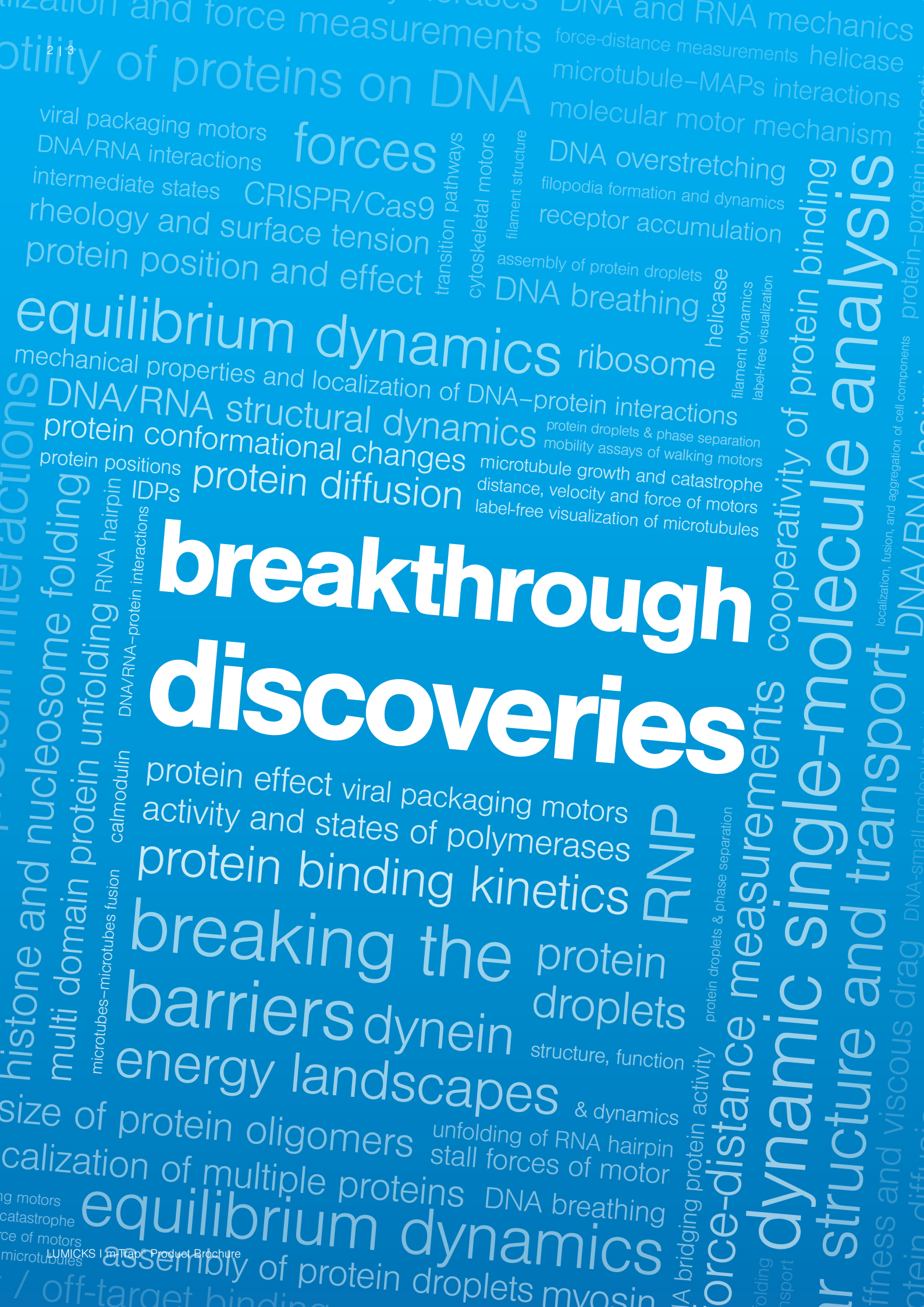
Entry-level Optical Tweezers

The m-Trap® is the first entry-level optical tweezers instrument specifically developed for high resolution single-molecule research. It combines ultra-high force resolution and stability, with incredible throughput, and ease of use – all at an unprecedented price level.

LUMICKS

2022 m-Trap brochure

Visit **www.lumicks.com**


breakthrough
discoveries
equilibrium dynamics
DNA/RNA structural dynamics
protein conformational changes
protein diffusion
protein positions
IDPs
RNA hairpin
DNA/RNA–protein interactions
calmodulin
microtubes–microtubes fusion
protein effect viral packaging motors
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protein droplets & phase separation
size of protein oligomers
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force-distance measurements
dynamic single-molecule analysis
cooperativity of protein binding
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multi domain protein unfolding
microtubule growth and catastrophe
distance, velocity and force of motors
label-free visualization of microtubules
protein droplets & phase separation
mobility assays of walking motors
mechanical properties and localization of DNA–protein interactions
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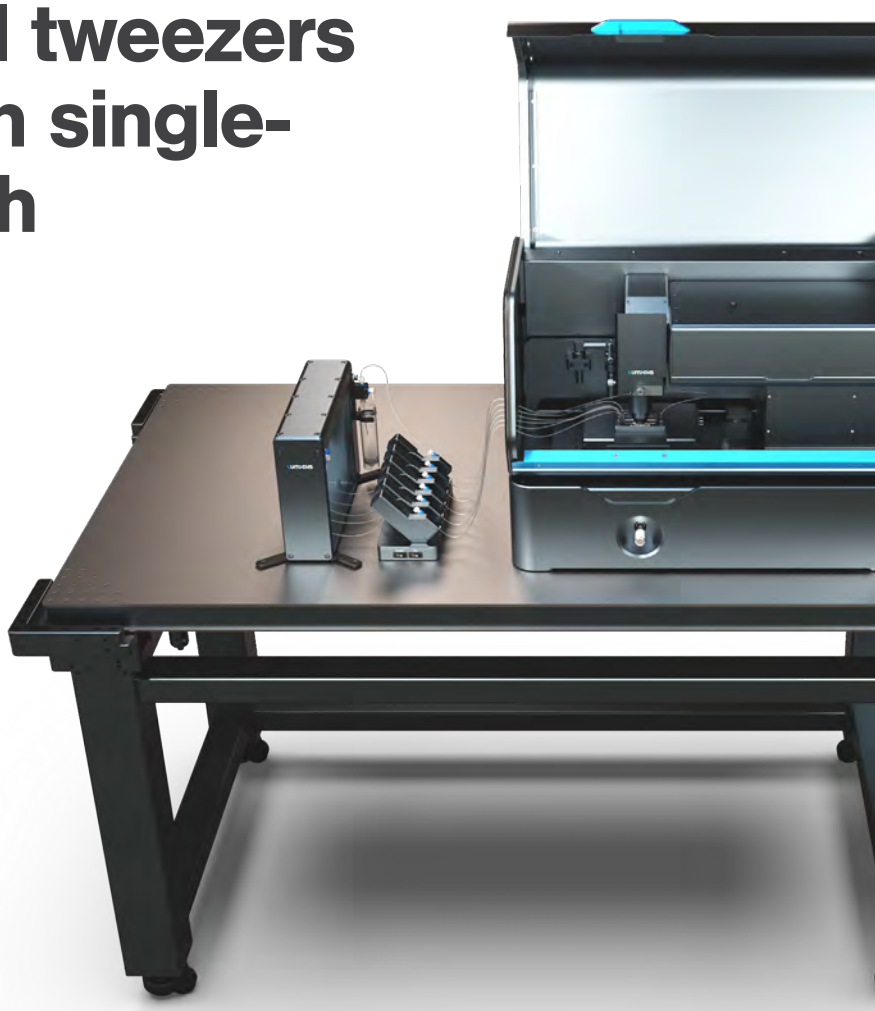
molecular motor mechanism
DNA overstretching
filopodia formation and dynamics
receptor accumulation
assembly of protein droplets
DNA breathing
viral packaging motors
DNA/RNA interactions
forces
intermediate states
CRISPR/Cas9
rheology and surface tension
protein position and effect
transition pathways
cytoskeletal motors
filament structure
utility of proteins on DNA
lization and force measurements

Entry-level optical tweezers for high resolution single-molecule research

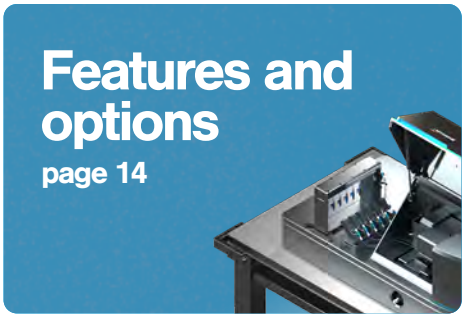
Understanding the molecular cause of disease is one of today's greatest scientific challenges. The key to developing future therapeutic interventions lies in an enhanced understanding of the biological processes at the root of disease development. We are always looking for ways to advance your research and bring new features that empower breakthrough discoveries.

We bring you the **m-Trap® Optical Tweezers**, a high-resolution system that lowers the price barrier of state-of-the-art single-molecule force spectroscopy without compromising key performance specifications. Now available with a complete array of workflow solutions to make your research faster, easier, and more repeatable – from concept to results.



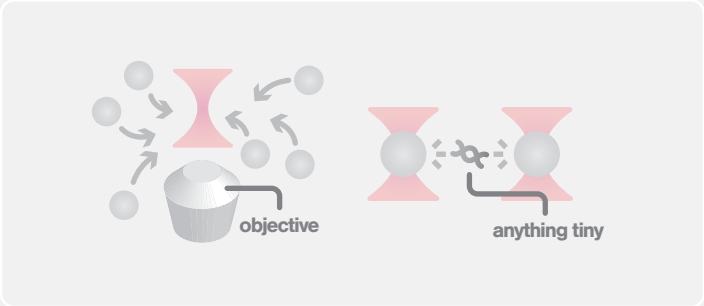
Lowering the price barrier and bringing ultra-high performance

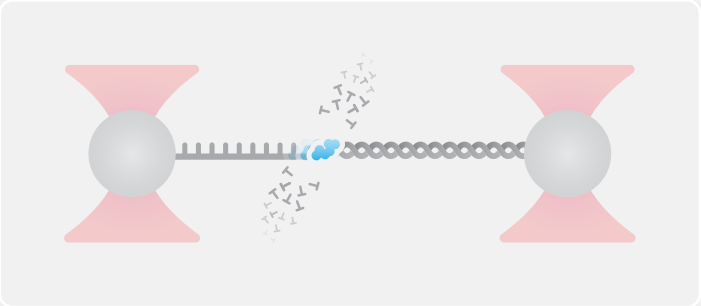
The m-Trap was developed to lower the price barrier of single-molecule force spectroscopy instrumentation without compromising on performance characteristics. We went back to the essence of force spectroscopy. Every single component and every process, have been considered and measured to measure the applications and enhance the user experience. The m-Trap is capable of manipulating and characterizing structural transitions and interactions of biomolecules at the ångström scale with ultra-high force resolution, stability, and throughput.



Revolutionazing biology with **optical tweezers, microfluidics, and imaging**

Revealing the full picture of the working principle behind the m-Trap, a Nobel Prize-winning technology, and what results it can deliver for your experiments through **3 simple steps.**





Step 1

Optical tweezers

Catch and manipulate your molecule of interest

The focused light generated by the optical tweezers is strong enough to trap any tiny object. You can trap your molecule of interest directly (e.g., protein droplets) or microscopic beads that can tether your molecule, e.g., a DNA between two beads. You can study the properties of your captured single molecules by manipulating them in different conditions. For example:

- Stretch and release your molecule to study conformational properties.
- Expose your molecules to interacting proteins (e.g., endonucleases or motor proteins) to measure their effects on your captured construct.
- Fuse your droplets to study their density and viscosity.

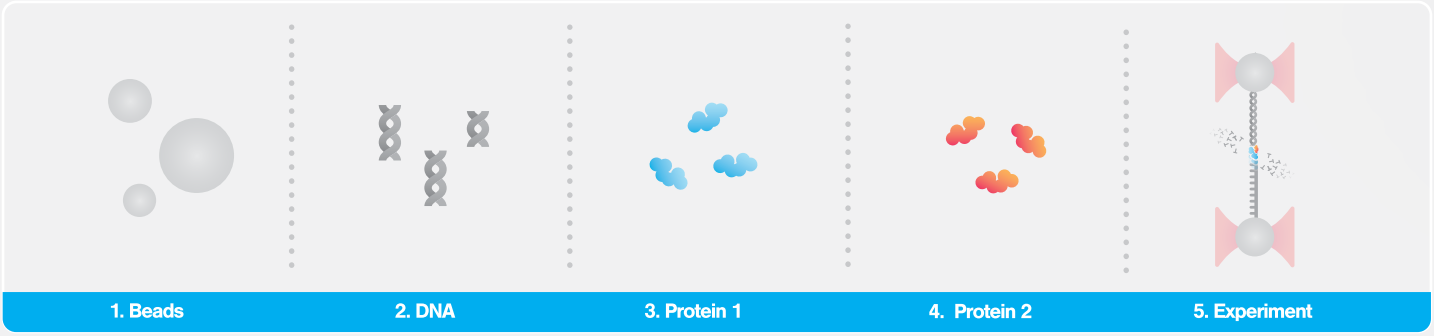
Step 2

Follow or unfold your proteins

Record your captured molecules in real time

The m-Trap optical tweezers offers you the ability to manipulate and probe your structure while you measure their associated processes.

For example, i) trap a protein between two beads ii) induce it's unfolding by pulling the beads away from each other, and iii) measure the force-distance curve to uncover the unfolding steps. Alternatively, trap a DNA between two beads and measure the steps and activity of a polymerase as it processes the DNA.=

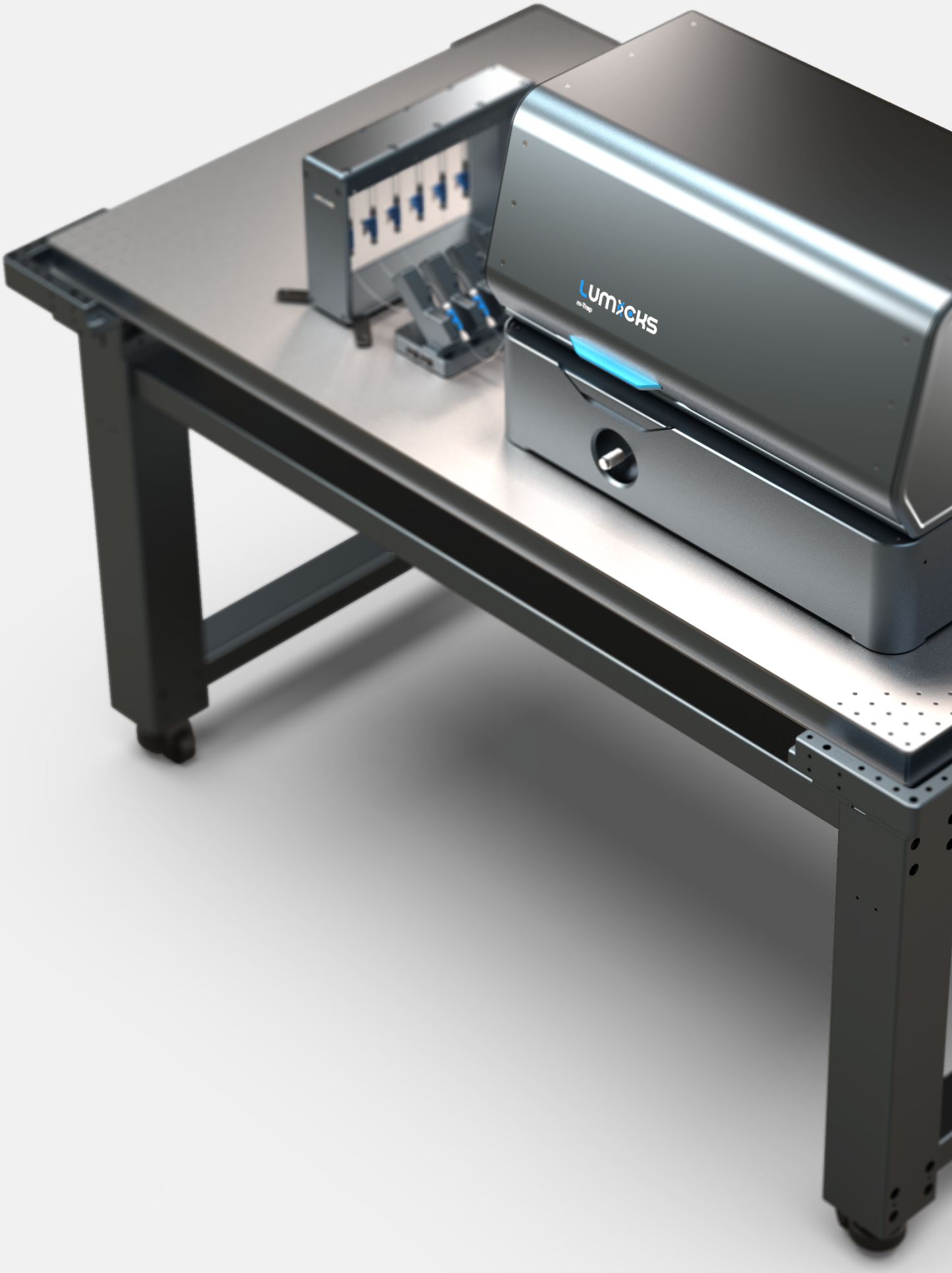


Step 3

Laminar flow microfluidics

Introduce, assemble, and position your reagents

The integrated microfluidics system separates your reagents into neighbouring laminar flow channels, which are separated without physical barriers. Since the optical traps can move between channels, they are perfect for introducing and assembling your reagents in separate channels and easily evaluating your construct under different conditions.


Lumicks

Applications

in dynamic single-molecule analysis

Today's scientific trends are racing toward smaller scales and experiments that provide both structural and mechanistic insights. Here, we showcase the applications that can help you get there.

Applications in dynamic single-molecule analysis

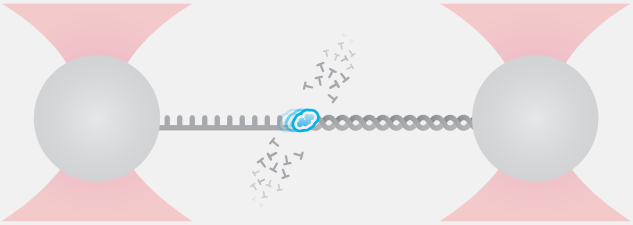
DNA-binding proteins

Uncover the structure, function, and dynamics of DNA-binding proteinsc acids involved in DNA repair, replication, transcription, editing, and nucleosome organization.

Follow DNA-binding proteins in real time

Overview of applications:

- Measure the effect and stepping of DNA-processing proteins in real time
- Investigate DNA-protein interactions and correlated mechanical events with protein function



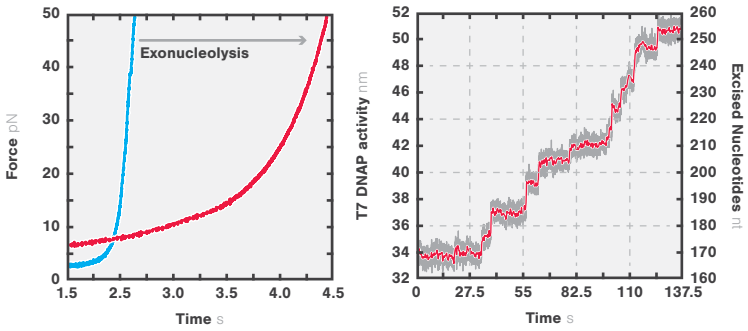
Check out the papers

[1] Newton et al. (2019) Nat Struct Mol Biol.
[2] Zhang et al. (2019) Science Advances

Base-pair resolution measurements that reveal the hidden properties of DNA-processing enzymes

The m-Trap offers you base-pair resolution readouts to assess the activity of enzymes as they process a DNA molecule. As unwinding double-stranded DNA to single-stranded DNA increases its length, you to track the activity of enzymes on the DNA. **Figure 1** shows the exonuclease activity of T7 DNA polymerase as it converts double-stranded DNA to single-stranded DNA.

In this experiment, optical tweezers maintained a DNA molecule tethered between two beads at a force that induced exonucleolytic activity of T7 DNA polymerase. The data shows that the enzyme exerted short activity bursts of 3 to 10 nucleotides interspersed by frequent pauses of varying duration.



1 Left: Force–distance curves of double-stranded DNA (blue) and single-stranded DNA (red). **Right:** Activity bursts of T7 DNA polymerase performing force-induced exonucleolysis on a double-stranded DNA.

"We believe that the **great force resolution** and **time stability** of the m-Trap will be precious assets for us to depict crucial information about the mechanics and work processes of biological and artificial molecular machines."

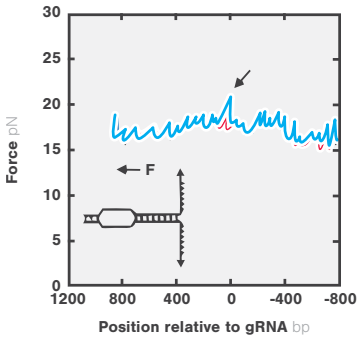
- Dr. Damien Sluysmans, m-Trap user, lab of Prof. Dr. Anne-Sophie Duwez University of Liège, Belgium.

Effects of interaction points on Cas9 binding and cleaving

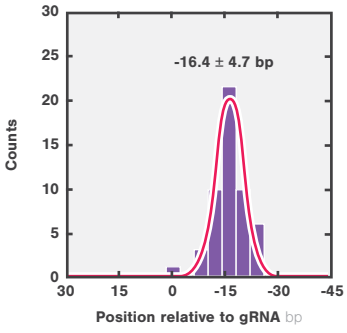
Here, to measure Cas9–DNA interactions, researchers constructed a Y-shaped DNA consisting of consisiting of two arms and a trunk containing the Cas9 target site. They subsequently tethered the two arms to a bead and a glass surface, respectivel [2].

Upon complex binding between a catalytically dead Cas9 (dCas9) and its target site, the researchers next moved the coverslip away from the trapped bead to unzip the DNA. Comparative force measurements between the dCas9-targeted molecule and baseline naked DNA served to establish both the location and strength of the DNA–protein interaction (**Figure 3** and **4**).

The results showed additional interactions flanking the protospacer adjacent motif (PAM). Disruption of one of these interactions through unzipping caused the ternary formation between the dCas9 complex and the DNA to collapse.



3 Representative tracing of unzipping. The diagonal arrow indicates the force peak. Below: a schematic representing the unzipping DNA construct with the force direction (F). Adapted from Zhang et al. (2019) *Science Advances.*



4 Histogram of DNA interactions relative to the gRNA. Negative values in the x-axis indicate sequence-positions downstream of the PAM. Adapted from Zhang et al. (2019) *Science Advances*

Applications in dynamic single-molecule analysis

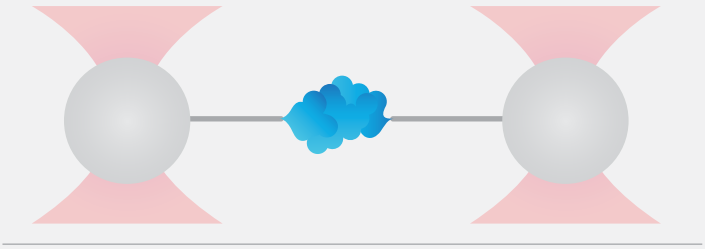
Protein folding

Use sensitive optical tweezers to study how proteins fold and undergo conformational changes that underlie their biological functions.

Reveal conformational changes of DNA, RNA, and proteins and their energy landscapes

Overview of applications:

- Measure short-lived and long-lived conformational changes of single proteins, DNA, or RNA molecules in real time and under different biological conditions.
- Identify rare conformational states of biomolecules to study their folding pathways.
- Stretch and relax the captured biomolecule to evaluate its unfolding and folding properties and map the associated energy landscapes.



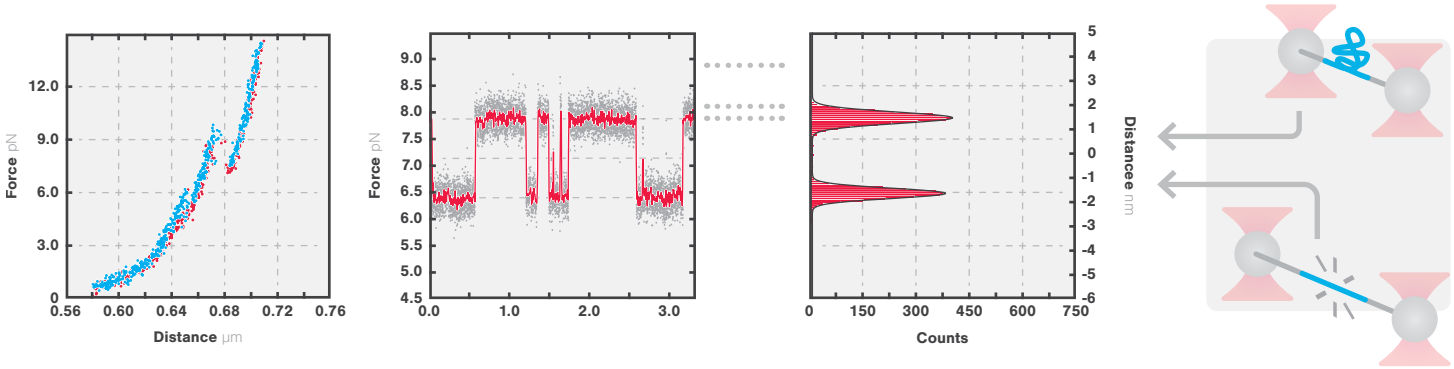
Data courtesies

[1] Prof. Dr. Carlos Bustamante at UC Berkeley (for figures 1 and 2)
[2] Prof. Dr. Hang Shi at Tsinghua University for the RNA-hairpin experiment

Tracking major and "hidden" conformational states of proteins

Characterize highly dynamic conformational states of enzymes to improve the selection of protein-specific drug candidates. In this study [1], we tethered the calcium-binding messenger protein calmodulin between two optically trapped beads to study the unfolding and folding properties. The resulting force–distance curve derived upon pulling and subsequent relaxation highlights a reversible two-step unfolding process, corresponding to two helix-loop-helix domains on the enzyme (**Figure 1**).

The protein transition states, observed when holding the optical traps at a constant distance, revealed stochastic fluctuations between two major states (open and closed). The assay also distinguished a third, brief intermediate state (**Figure 2**).



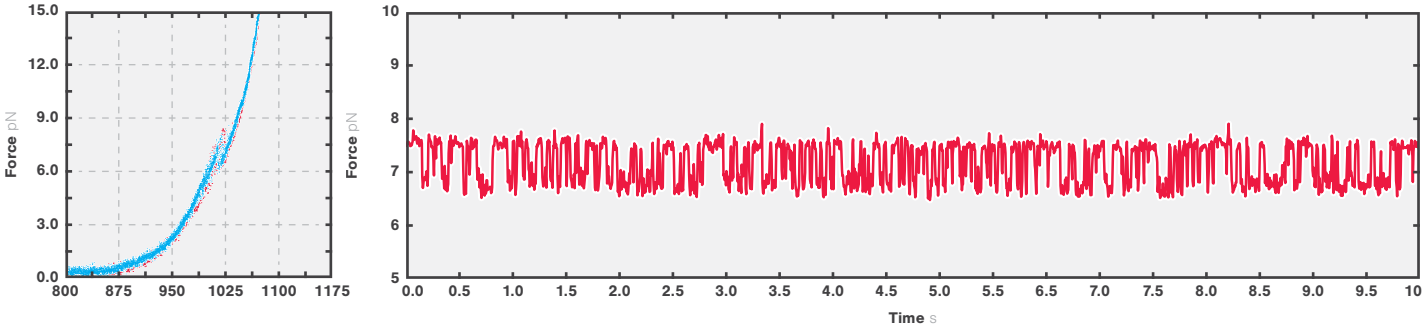
1 Force–distance curves of stretching (blue) and relaxing (red) cycle of a calmodulin protein reveal that the protein unfolds and refolds in two steps.

2 Left: A force trace of equilibrium measurements over 3 seconds displaying the structural fluctuations of a single calmodulin molecule. The gray data show a 50 kHz sampling rate, while the red line shows data decimated to 200 Hz. **Center:** A histogram representing the two major states upon holding the optically trapped beads at a constant distance. The third intermediate state is negligible due to its transitory profile. **Right:** A schematic representation of the two states observed in the histogram (center).

Investigate the unfolding and folding properties of RNA hairpins and uncover their different conformational states

Characterize the stability of DNA and RNA hairpins to understand their physiological properties and improve gene-silencing tools. You can tether an RNA hairpin between two beads using DNA/RNA hybrid handles [2]. In this example, we stretched and relaxed the RNA molecule at a constant pulling speed while determining the resulting mechanical and structural properties (**Figure 3, left**). An approximately 15 nm long unfolding rip appeared at about 8 pN. Relaxing the molecule initiated a protein-folding process that followed the unfolding trace – including the 15-nm rip at 8 pN – which demonstrates the reversibility of RNA hairpin unfolding and its structural stability.

Further evaluation of the RNA structural transitions over time, indicating the structural equilibrium, revealed two major states at tensions around 6.7 pN and 7.7 pN. The assay also exposed a third conformational state, occasionally appearing between the two main states (**Figure 3, right**).

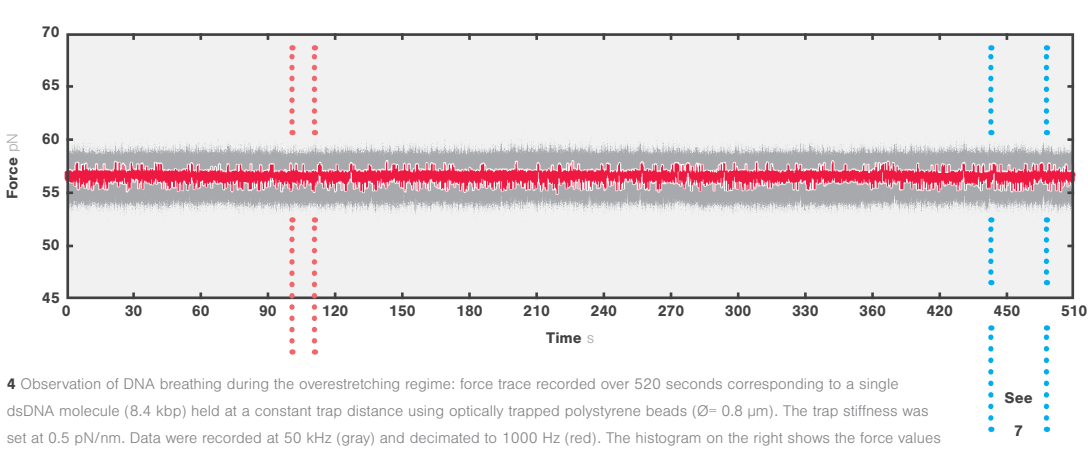


3 Left: Extension (red) and retraction (blue) of a tethered RNA molecule upon increasing pulling forces. **Right:** Ten-second time trace of a single RNA molecule held at an initial tension of 7.5 pN. Data were decimated to 200 Hz from the high resolution dataset collected at 50 kHz.

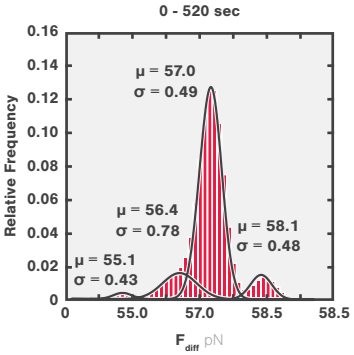
Investigate the conformational properties of RNA hairpin properties

The superior stability of the m-Trap minimizes force drift and improves the characterization of folding and unfolding transitions during long experiments. **Figure 4** shows the spontaneous conformational transitions of a double-stranded DNA molecule during a 10-minute stretching regime at approximately 56 pN . A closer look into a 10-second segment of the complete trace reveals the fast transitions between multiple states (**Figure 6**).

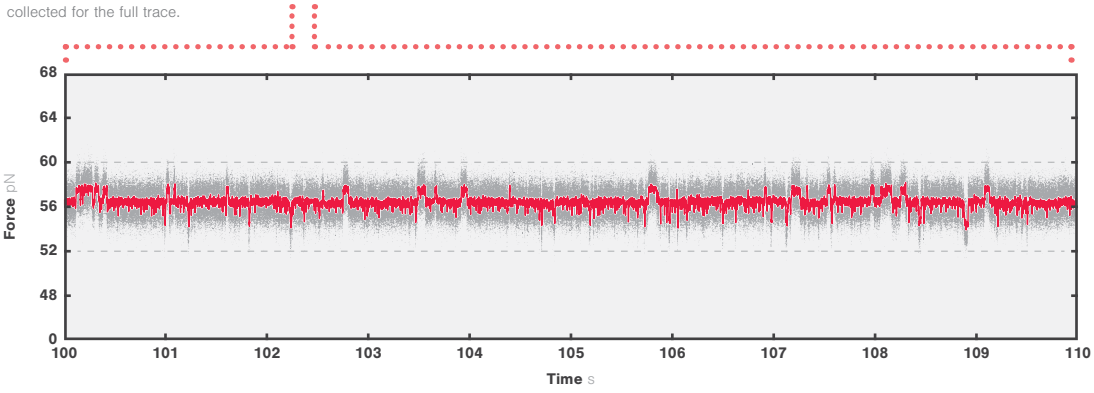
The histograms derived from both the complete trace and a selected section of the same trace (**Figures 5** and **7**) show near-identical distributions of force values. These reproducible measurements of transition kinetics underscore the stability of the system, which protects your assays from undesired external factors, such as force drift.



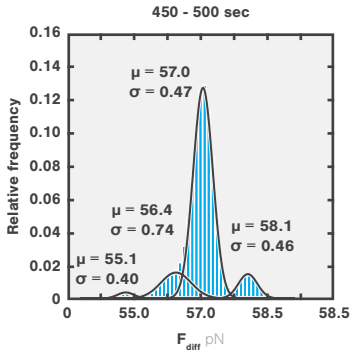
4 Observation of DNA breathing during the overestretching regime: force trace recorded over 520 seconds corresponding to a single dsDNA molecule (8.4 kbp) held at a constant trap distance using optically trapped polystyrene beads (Ø= 0.8 µm). The trap stiffness was set at 0.5 pN/nm. Data were recorded at 50 kHz (gray) and decimated to 1000 Hz (red). The histogram on the right shows the force values collected for the full trace.



6 Histogram of the force values collected for the full trace. The mean and sigma values are reported for each peak obtained from a Gaussian fit.



5 Fragment with a duration of 10 seconds of the trace shown within the blue inset in **Figure 4**.

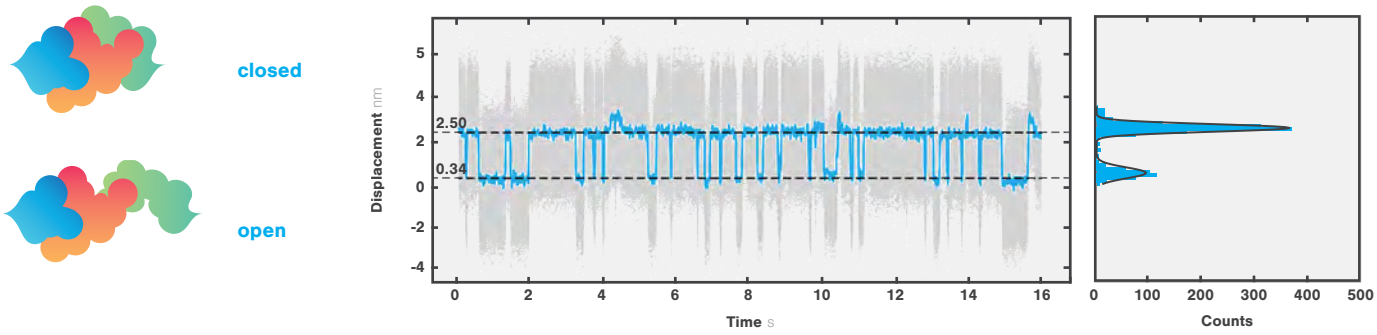


7 Histogram of the force values during a time fragment of 50 seconds.

Recording an enzyme with nanometer precision to reveal inhibitor-induced conformational properties

Characterize highly dynamic conformational states of enzymes to understand their fundamental dynamics and improve the selection of protein-specific drug candidates. By capturing an enzyme, such as phosphotransferase enzyme AdK between two beads, you can test its conformational properties based on the distance-changes between the trapped beads.

To evaluate the equilibrium dynamics associated with conformational states, we pulled an AdK protein at low forces (between 6 and 10 pN) in the presence of a substrate analog (AP5A). Exposing AdK with this small-molecule inhibitor induced conformational fluctuations with a bead-distance range of approximately 2 nm, corresponding to the open and closed states (**Figure 8**). Hence, with the m-Trap, you can extract data from highly dynamic processes with nanometer precision to reveal protein conformational properties in varying conditions.



8 Graph depicting the two-state displacement of the protein-tethering beads in the presence of 50 nM of AP5A upon pulling. The dashed lines represent the average bead displacement in the closed and opens states, respectively. The biochemistry protocols used here for tethering the protein to the DNA handles were developed in collaboration with the lab of Prof. Matthias Rief (TUM) and were based on Pelz et al. (2016) Nature Communications.

Publications and resources to inspire your future optical tweezer experiments

Some of the recent publications using the m-Trap technology

- Zhang et al. **The post-PAM interaction of RNA-guided spCas9 with DNA dictates its target binding and dissociation**. Science Advances 2019
- Zhang, et al. **Dynamics of Staphylococcus aureus Cas9 in DNA target Association and Dissociation**. EMBO Rep 2020
- Wasserman et al. **A Tour de Dorce on the Double Helix: Exploiting DNA Mechanics to study DNA-based molecular machines** Biochemistry 2019 (Review)
- Mandal et al. **Force Spectroscopy on Single Molecules of Life**. ACS Omega 2020 (Review)
- Alshareedah et al. **Methods for Characterizing the Material Properties of Biomolecular Condensates**. Methods in Enzymology 2020 (Review)
- Lehmann et al. **Optical Tweezers Approaches for Probing Multiscale Protein Mechanics and Assembly**. Front Mol. Bio. 2020 (Review)

User insights

Dr. Adrian Olivares

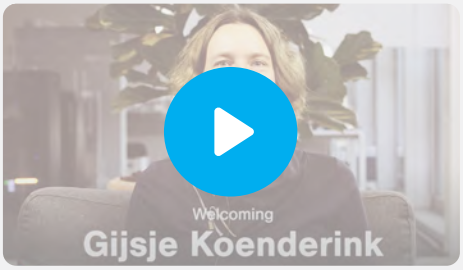
Assistant Professor at the Vanderbilt University, Nashville, TN, USA

"The m-Trap and Bluelake software have allowed my lab to get started immediately on experiments due to a user-friendly interface and technical support from LUMICKS. We are excited to use this technology to decipher how the nucleus senses and uses mechanical force."

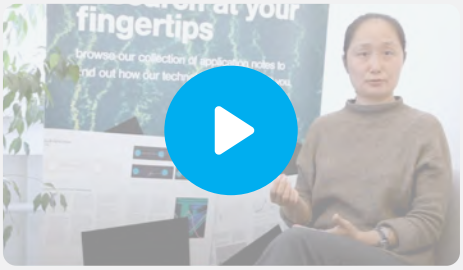
Watch how our technologies make a difference in research!

Visit **www.lumicks.com** to find exclusive interviews, webinars, and video testimonials from our customers and experts on dynamic single-molecule around the world, sharing their views and their research DSM analysis.

On-demand webinars
Educational webinars with key guest speakers, experimental webinars and more.



DSM symposium series
Key speakers discussing their work, the C-Trap and the benefits of the instrument in their work.



Video testimonials
Training sessions testimonials, production workflow introductions and more.

Features and options

With the ever-increasing pressure to produce breakthrough discoveries in the least amount of time, you need an instrument that brings unprecedented insights with high precision, accuracy, and reliability in the shortest amount of time.

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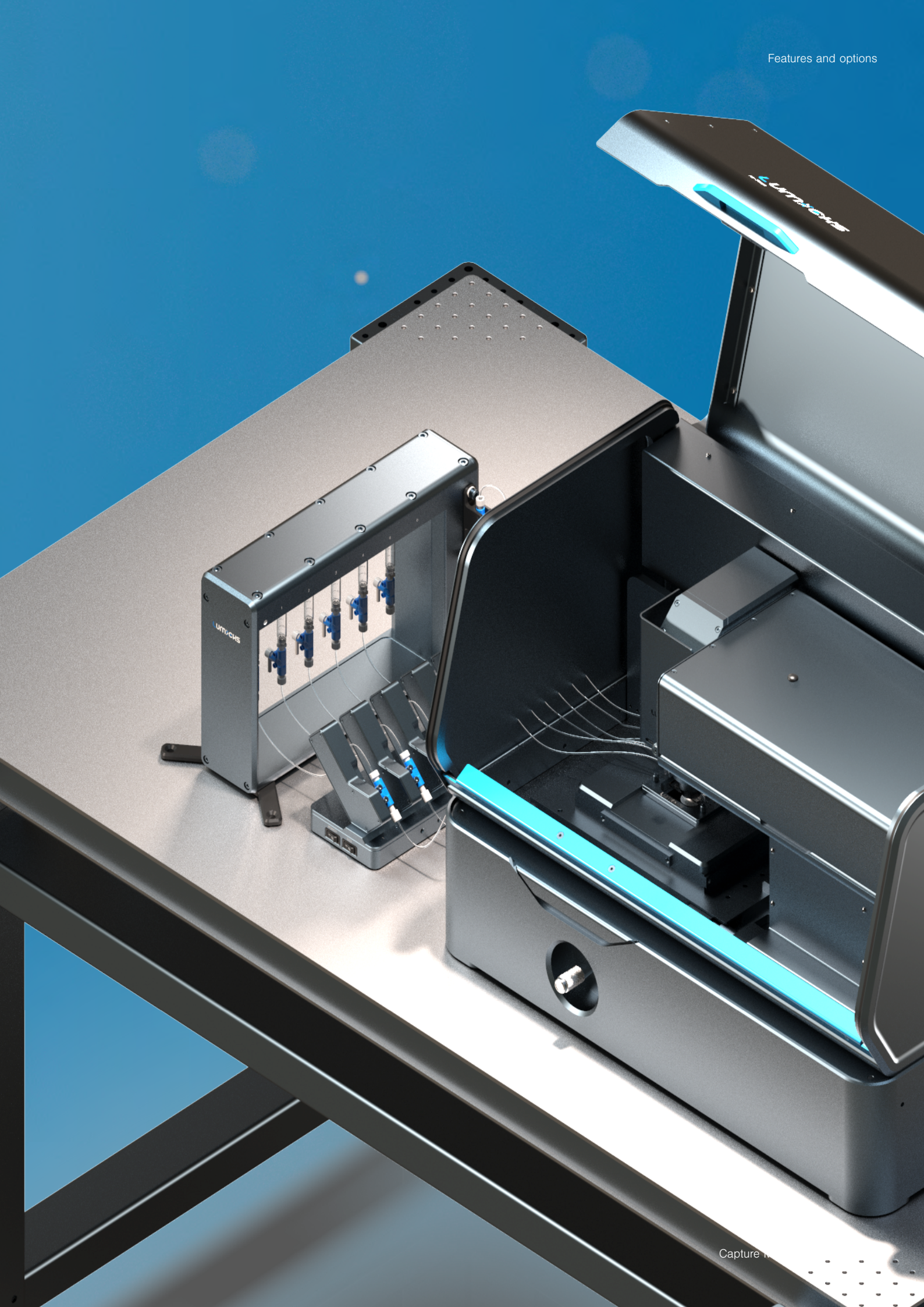
Manipulation

page 18
High throughput experimental workflow

page 20
Easy and intitive software package



Stable and precise sample manipulation

Measuring small, transient, and rare conformational changes with top-notch stability and resolution

Discrete trap fluctuations can arise from both extrinsic or intrinsic factors, such as mechanical vibrations, thermal effects, or laser power, and can cause trap distance drift. To avoid these experimental artifact, you need optimal trap stability and resolution to quench the trap distance drift and measure rare structural changes.

Revealing small steps or transient conformational states requires low force drift to enable long measurements and average out the Brownian noise. Additionally, a multi-state biological system requires extremely low drift to avoid confounding changes on the molecule that would skew the populations of the different recorded conformational states.

The LUMICKS solution

The m-Trap is purposefully built and optimized to provide extreme force stability and resolution. With a drift below 0.3 pN over minutes and a trap distance resolution below 3 Å (at 100 Hz), we achieve the highest combination of force and bandwidth resolution.

Controls and sensors

Temperature control

Perform your experiments under relevant conditions

The m-Trap temperature control option enables the user to measure molecular interactions at different temperatures and investigate temperature-dependent events. The temperature can be controlled with an absolute accuracy of 0.2°C and stability of 0.05°C, ranging from room temperature to 45 °C, without compromising the other specifications of the m-Trap.

Force detection

From sub-pNs to nN and beyond

The force on the sample is measured with sub-picoNewton resolution on one of the traps through an ultra-sensitive position sensing detector. Tension values ranging from a few tengths of pNs to the nN level and beyond can be applied and measured. This allows for monitoring extremely small steps on a broad regime, relevant for example in protein folding experiments.

Configurations

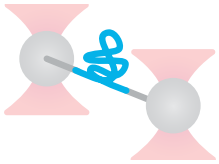
The m-Trap was developed to lower the price barrier of advanced single-molecule force spectroscopy instrumentation without compromising on performance characteristics. Every component was considered to optimize reliability and deliver the most complex force application. We designed an instrument that is easy to use, requires no alignment, and offers state-of-the-art experiments while serving research scientists of all disciplines and backgrounds. The m-Trap has been created after and developed to provide you with extremely stable measurements and reproducible results.

Dual trap for dumbell assays in solution

The m-Trap is equipped with two ultra-stable optical traps for manipulating single biomolecules. The extreme stability, with less than 0.3 pN over minutes, enables long acquisitions at a constant distance, revealing even the rarest states, otherwise hidden by Browninan motion or instrumental drift.

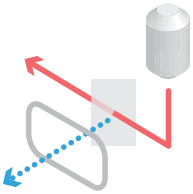
Dual trap

For your assays in solution



Custom optical layout allowing for 3rd party system integration

The m-Trap Flex option provides access to the optical path, allowing for the integration of custom hardware. Imaging and spectroscopy techniques can be added to the m-Trap offering full flexibility to combine locally developed optical hardware with the m-Trap's ultra-high force resolution and stability.



High-throughput experiment workflow

Load your sample and analyze your data set in less than 30 minutes.

1 Load your sample into the flow

with fast and simple pipetting

For solution assays, load your samples and conditions into the syringes of the 5-channel u-Flux™ Laminar Flow Microfluidics system. Pipetting each reagent takes seconds thanks to the twist-and-lock syringe adaptor, with which you can quickly and easily refill individual syringes.

Regulate the pressure and control each of the channels with a mouse click.

2 Assemble your assay without physical barriers

with our optimized workflows for solution assays

For surface assays, double-click on a bead to trap it. You can easily locate your samples using, for example, IRM or fluorescence microscopy. The high-resolution piezo-controlled nanostage, allows you to accurately move between positions (x and y) to place the trapped bead at the end of the microtubule and start your experiment.

3 Perform and automate your experiments

with our Bluelake software suite

Bluelake™ is an intuitive user-friendly software suite containing programs that simplify, automate, and enhance single-molecule experiments and real-time data gathering with a mouse click. For example, use Bluelake to:

- Assemble your samples and run your experiment in 80 seconds.
- Extract 18 sets of data in only 30 minutes.

Bluelake can automate your m-Trap experiments to relieve you from the screen while performing repeated experiments. Automating your assays also guarantees that you maintain identical procedures across replicates and experiments when needed.

Automate your experiments through Python scripting

4 Organize and analyze your data

with a dedicated software suite

Generate a structured experiment overview with a fast and smooth navigation through multiple days of measurements.

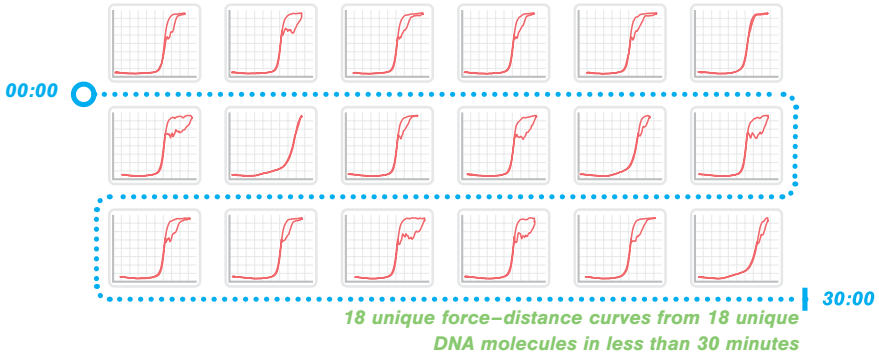
View, compare, and export your data stream during or after the experiment. The dedicated software automatically stores all your metadata so you never lose valuable information and always have the option to reproduce your experiments.

Analyzing and repeating experiments has never been easier, as our analysis software comes with tutorials and sample notebooks that can serve as a scaffold for your own analyses.

Use the open-source **Harbor** platform to upload, download, and review user scripts for free: **https://harbor.lumicks.com**


Microfluidics

in **solution**


00:00
30:00
18 unique force–distance curves from 18 unique
DNA molecules in less than 30 minutes

Easy and intuitive software package

Check how you can completely automate your experiments using our user-centered software workflow.

Bluelake™

Bluelake is our extensive software suite for C-Trap and m-Trap systems. It is a single package that features intuitive controls for assembling and manipulating your assay, as well as a fully correlated data overview to ensure you can easily view and study the results of your experiment.

Bluelake is ready for automation features thanks to the ability to script almost every part of the system.

Open source

A commitment to your data

Data integrity is crucial for research and scientific instruments. All the m-Trap data are stored in the standardized HDF5 open data format, which ensures that you can access them at any time.

It's essential that you have direct access to all raw data and data processing algorithms within the software (e.g., power spectrum fitting). This gives you full flexibility to understand, inspect, adapt, share, and publish the algorithms used for online and offline analysis.

The open format and inclusion of extensive experiment metadata directly increase the reproducibility and reliability of your experiments.

User insights

Prof. Dr. Ben Schuler

University of Zurich

"The user-friendly software combined with the high throughput experimental workflow and the dedicated training we received from LUMICKS, has fully equipped us to perform state-of-the-art single-molecule force spectroscopy experiments in no time."

Intuitive controls

Quick and easy sample interfacing

The software gives you total control over your experiments. Whether you are visually navigating through the laminar flow cell on the screen or selecting the area you wish to visualize in the the bright-field camera, our approach puts you in the front seat.

Fully correlated data

Everything in a single timeline

Bluelake was designed to control all aspects of your system from a single interface. The trap positions, force data, bright-field, images use the same software package, which truly correlates the experiments. All data streams are saved and sychronized using the same hardware clock.

Beyond the product

Faster, easier, and more reproducible with our new biochemistry services and script-sharing platform: Dynamic single-molecule research has never been so accessible to so many backgrounds.

page 24

Harbor: The meeting place for DSM scripts

page 25

Reagents, kits, and services store


Protein Handles
Kit
- 5 +
Add to cart
LUMICKS
m-Trap
LUMICKS

Harbor: the meeting place for dynamic sin-gle-molecule scripts and biochemistry samples

Welcome to an interactive community that collaborates in scripting and sample preparation, taking your single-molecule studies to the next level.

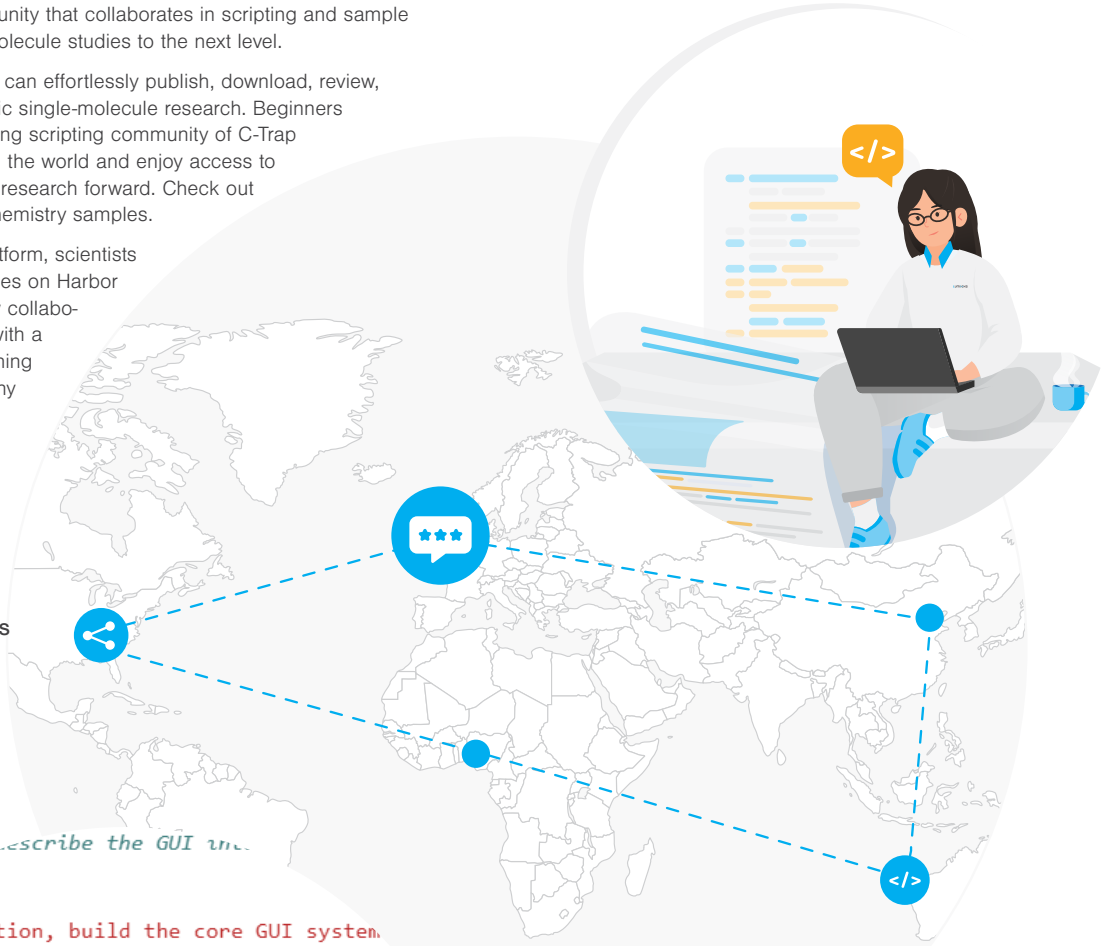
Harbor is a platform where users can effortlessly publish, download, review, and cite scripts related to dynamic single-molecule research. Beginners and experts can join the welcoming scripting community of C-Trap and m-Trap users from all around the world and enjoy access to data analysis methods that push research forward. Check out the new section for sharing biochemistry samples.

NEW Just like the script-sharing platform, scientists can now also share their molecules on Harbor for others to use. Begin your new collabo-ration today and equip your lab with a variety of proteins, plasmids, running reagents, DNA samples, and many more.

harbor

The meeting place for dynamic single-molecule scripts

- **Backed up by science**
- **All in one place**
- **Easy to cite**



```
escribe the GUI in
):

initialization, build the core GUI system
"change folder" button can then be used to c
"
def __init__(self, master):
    self.__version__ = "1.0.0"
    self.__versionDate__ = "9/26/20"
    self.__cite__ = "Watters, J.W. (2020) C-Trap .h5 V

    """
    Function that when called takes all of the force o
    and extracts the correct force and time/distance v
    Used a different function for FD curves to limit
    """
    def extract_force_relevant(h5file,timestampsForI
        amtToDS = float(entryDownSample.get())
        forceString = forceChannelPulldown.get()
        distanceVarString = whichDistanceValue.g
        downsampleOpt = checkValueDownsampleOp
        stringForceChannel = 'Force ' + forc

mple rate to determi
```

User insights: script by

John Watters

in Shixin Liu's Lab at the Rockefeller University

"Through Harbor I can help the community with ready-to-go scripts, while getting credit for the work I've done through extra citations."

Watters, J.W. (2020) C-Trap .h5 Visualization GUI. Retrieved from https://harbor.lumicks.com/

→ Join for free today **www.harbor.lumicks.com**

Reagents, kits, and services store

The reagents, kits, and services in the LUMICKS Store helps C-Trap and m-Trap users to generate data faster by optimizing the time spent on the system.

All items in our store have been selected to simplify the user experience and enhance the efficacy of our instruments through:

- **Ready-to-use products** that allow you to start your experiments quicker by eliminating the need to invest time, money, and personnel to set up experiment workflows.
- **Established, tested, and optimized protocols** that ensure your instrument is optimally used – no loss of time or materials for troubleshooting. The samples work right away with a high tethering efficiency.
- **Standard experiment kits** that facilitate the practical training of new users and necessary application testing.

User insights

Prof. Kasia Tych

University of Groningen

"The kit is very easy to use and worked right away. I saved a lot of time compared with setting up the whole biochemistry production workflow myself."

What's in store for you?

DNA/RNA–protein interaction kits

- Ready-made ssDNA and dsDNA samples, ideal for localizing fluorescent DNA-binding proteins or measuring local conformational changes of the DNA molecule.
- Custom constructs such as DNA and RNA hairpins, DNA with specific binding sites, or site-specific fluorescent markers for FRET measurements.

Protein folding and conformational changes

- Protein-tethering master kit, including DNA handles and oligonucleotides, labeling protocol, quality control test protein, beads, and all reagents needed for your single-molecule experiments.
- Custom protein service taking care of the full package: design, purification, and labeling of your protein of interest. Give us your protein wish list, we'll take care of the rest.

Running reagents and consumables

- Ultrapure filtered buffers of the highest quality.
- Ready-made solutions optimized for single-molecule tethering.
- Functionalized beads in multiple sizes, to cover all of your needs.

→ Start shopping today **www.store.lumicks.com**

Specifications of the m-Trap

m-Trap Optical Tweezers

Force resolution	< 0.1 pN @100 Hz (1 µm beads at ≥ 0.35 pN/nm trap stiffness)
Maximum escape force	>1000 pN using 4.5 µm polystyrene beads
Force stability	< 0.3 pN over 2 minutes (1 µm beads at ≥ 0.35 pN/nm trap stiffness)
Force acquisition rate	30 kHz
Bead displacement resolution using force signal	< 3 Å @100 Hz
Minimum incremental step size	2 nm
Bead displacement resolution using live brightfield bead tracking	< 3 nm @100 Hz
Field of movement	38 µm (x)
Number of independent traps	2

Temperature control

With the temperature control, the microfluidic chip can be kept at a set temperature between room temperature and **45 °C**, with an absolute accuracy of **0.2 °C**. Because of the closed-loop system, the temperature is highly stable, with fluctuations that are smaller than **0.02 °C**. Users are able to set the temperature with a resolution of **0.01 °C**. The temperature control system has specifically been designed to achieve optimal performance and perform sensitive single-molecule experiments guaranteeing the same force stability (<0.3 pN over 2 minutes) at any set temperature after temperature stabilization.

Microfluidics

Multichannel laminar-flow microfluidics system without physical barriers between the channels to introduce reagents in a controlled manner and in-situ assembly of a wide range of multi-step single-molecule assays.

Remote fluidics valve control to program the software's user-interface for high data-throughput applications.

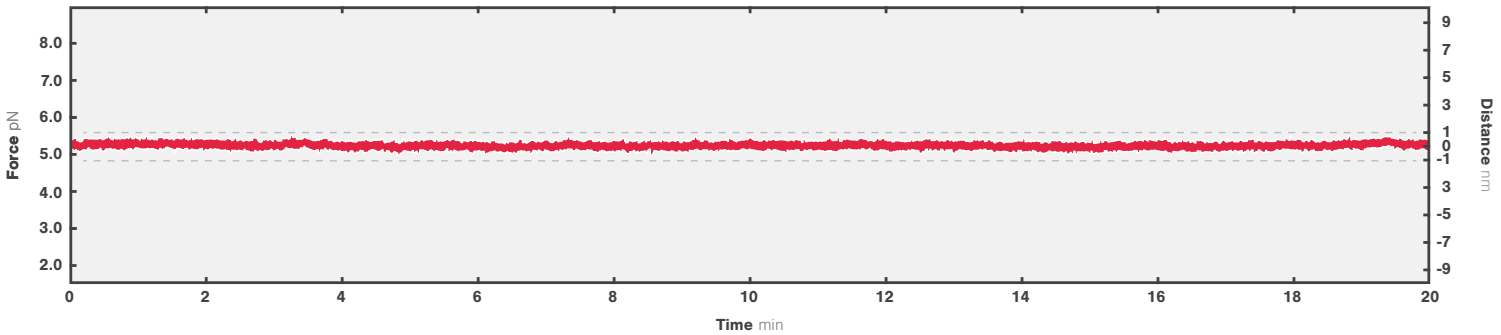
Software

Bluelake software suite with optimized workflow for high throughput single-molecule experiments. Trap microspheres, and tether, manipulate, and measure biomolecules within minutes.

Software support through LUMICKS' software team that works relentlessly to optimize and adapt the m-Trap software for novel applications. We work with our users to implement features that help them improve their research, as well as enhancing the system with every release.

General

On-site application and scripting training for expert support from our specialists dedicated to the customer's scientific application.



Force trace recorded over 20 minutes to a single dsDNA molecule (8.4 kbp) held at a constant distance using optically trapped polystyrene beads (Ø= 1.0 µm). Data are shown at 100 Hz.

A history of milestones

About **LUMICKS**

2021

- LUMICKS raised $93 million in series D funding.
- With 128 new hires – including 10 in key senior positions – we more than doubled in company size.
- Continued to empower researchers with more than 35 articles published in high-impact journals using LUMICKS' technology.
- Installed C-Trap and m-Trap instruments in renowned institutes, including at VIB, Westlake University, TU Munich, and the University of Pittsburgh.
- Launched new services and initiatives tackling the full DSM experimental workflow from experimental design to data analysis.

VIB

Westlake University

TU Munich

University of Pittsburgh

2020

- Launched the z-Movi® Cell Avidity Analyzer.
- New office in China.
- Launched the biochemistry services and scripting platform for the C-Trap®.

2019

- Validated the z-Movi for immuno-oncological cell therapies with strategic partnerships.
- Built new team for immuno-oncology product line.
- Key sales to Harvard University, Stanford University, Yale University, and more.
- Grew team to 100 full-time employees.
- New Office HQ.

Harvard University

Stanford University

Yale University

2018

- Key sales to National Institutes of Health, Delft University of Technology, Tsinghua University, Northeastern University, and more.
- Established US team in Boston and Bay Area.
- Partnership with AstraZeneca.
- Developed the z-Movi® Cell Avidity Analyzer prototype.

National Institutes of Health

Delft University of Technology

Tsinghua University

Northeastern University

2017

- Key sales to Imperial College London, University of Zurich, and more.
- Launched the m-Trap® High-Resolution Optical Tweezers.
- New office in the US.
- 38 full-time employees.

Imperial College London

University of Zurich

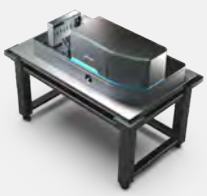
2016

- Introduced into the market Acoustic Force Spectroscopy (AFS(R)) for single-molecule manipulation.
- Key sales to: Rockefeller University, Göttingen University, Shanghai-Tech, and more.
- First Nature publication with data captured using the C-Trap®.
- 18 full-time employees.

Rockefeller University

Göttingen University

Shanghai-Tech



2015

- Launch of the C-Trap® Correlated Optical Tweezers – Fluorescence Microscopy.
- First sales to BIOCEV, Max Planck Institute of Molecular Cell Biology and Genetics.

2014

- LUMICKS founded.

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