

Biomolecular Interaction Analytics using MicroScale Thermophoresis

The Monolith NT.115

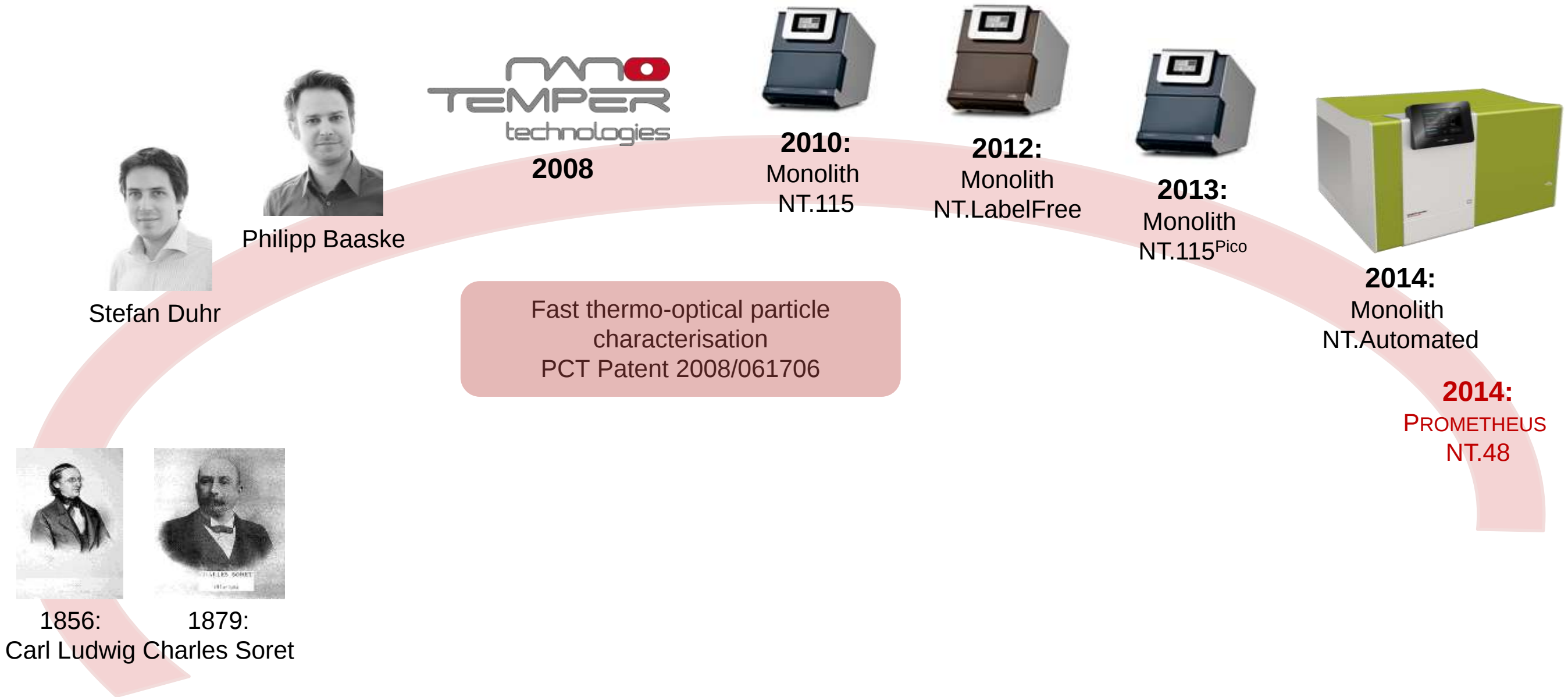
Dinorah Leyva, Ph.D.

NanoTemper Technologies Inc.

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www.nanotemper-technologies.com





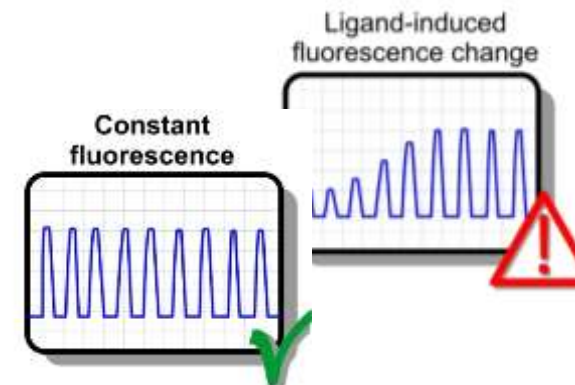
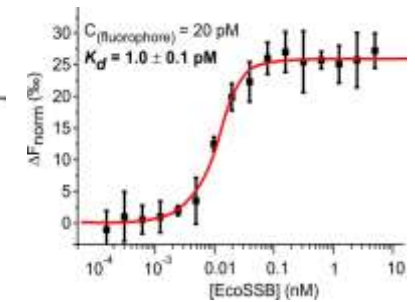
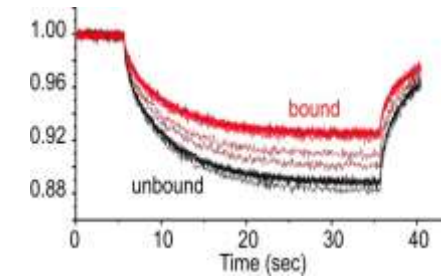
Seminar

- ▶ MicroScale Thermophoresis (MST) Basics
- ▶ Assay Setup
- ▶ Assay Optimization

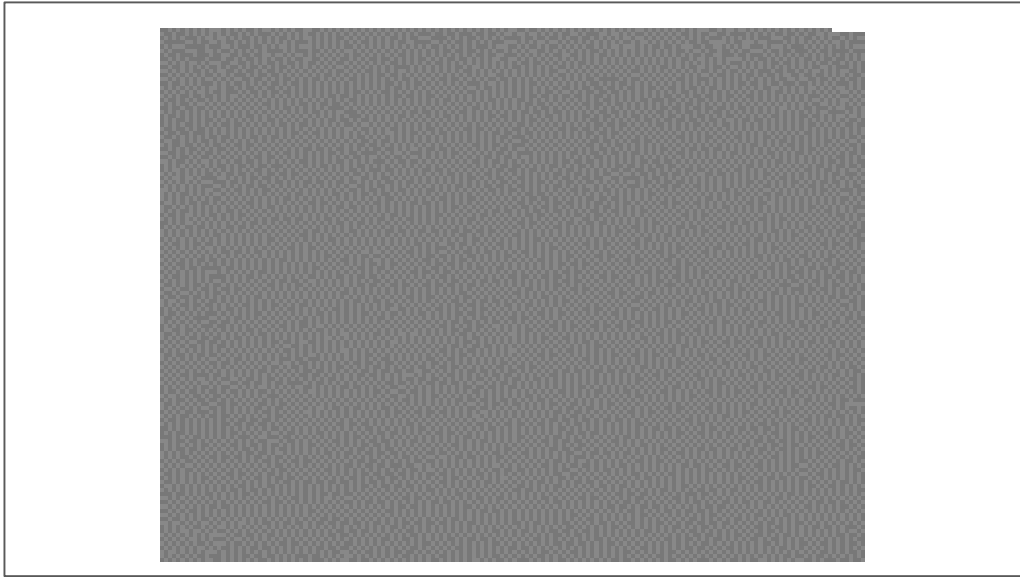


Experimental work

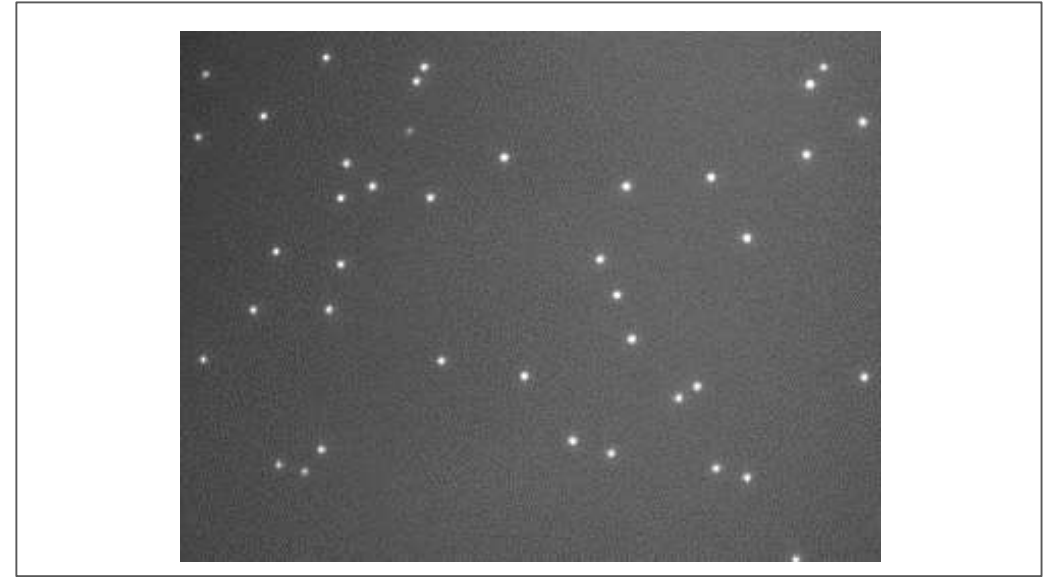
- ▶ Measurement of positive control
- ▶ Sample handling and assay setup
- ▶ NT.Control and NT.Analysis Software
- ▶ Run experiments with your own samples



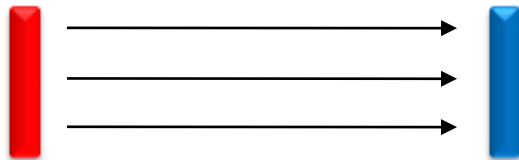
DNA



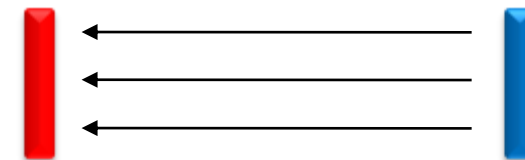
Microbeads



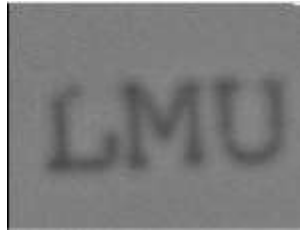
„Positive“ thermophoresis



„Negative“ thermophoresis



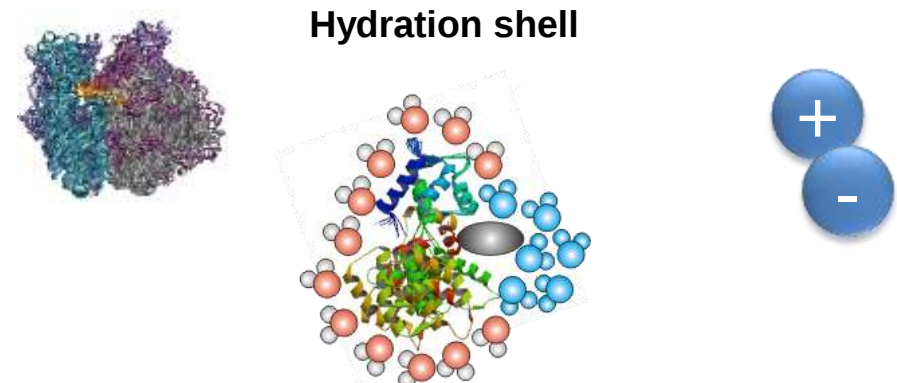
$$C_{\text{hot}} / C_{\text{cold}} = \exp(-S_T \Delta T)$$



Laser
„on“



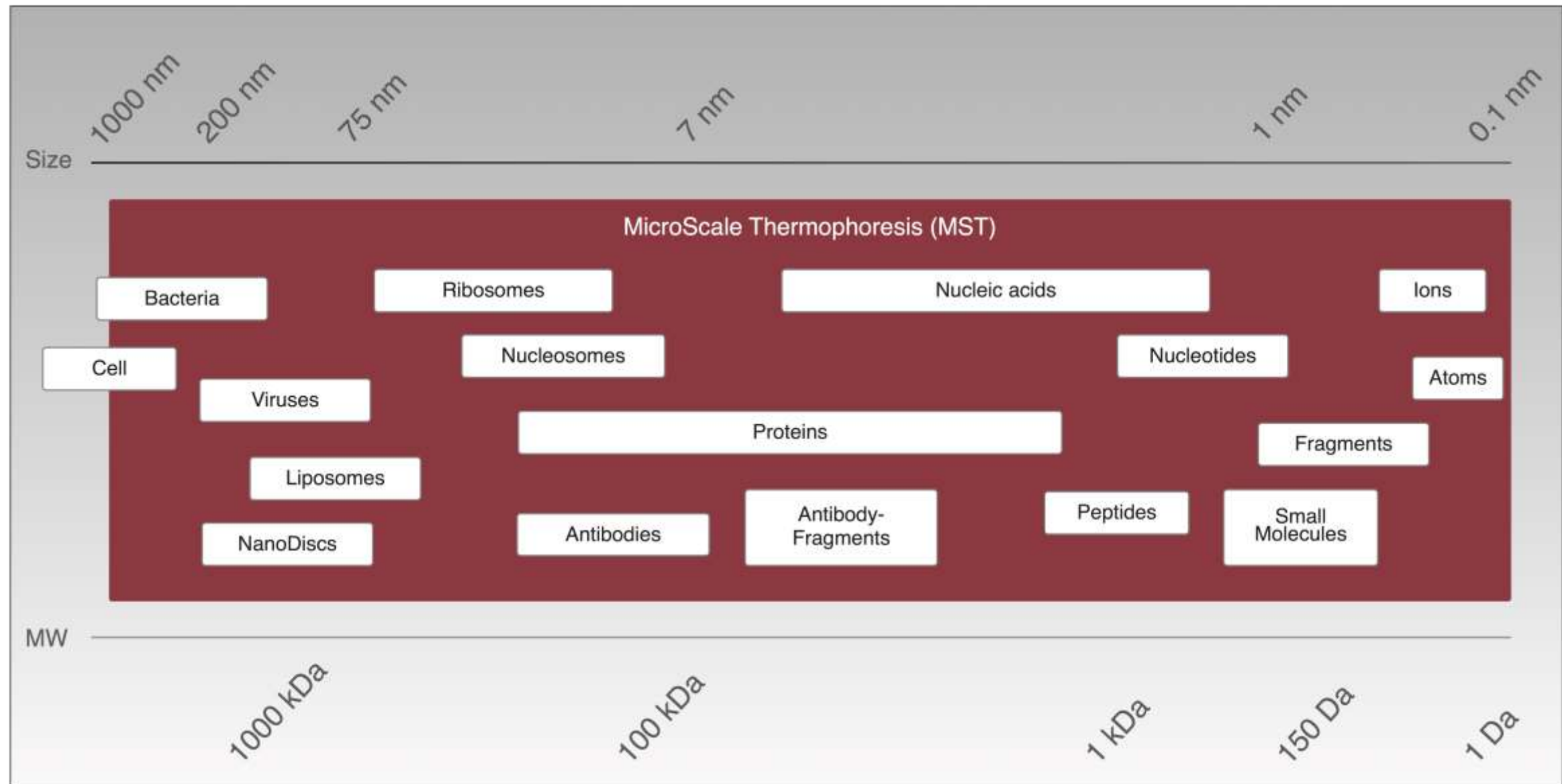
Laser
„off“

$$S_T = \underbrace{\frac{A}{kT}}_{\text{Size}} \left(\underbrace{-\Delta s_{\text{hyd}}(T)}_{\text{Hydration shell}} + \underbrace{\frac{\beta \sigma_{\text{eff}}^2}{4\epsilon\epsilon_0 T}}_{\text{Charge}^2} \times k_{DH} \right)$$


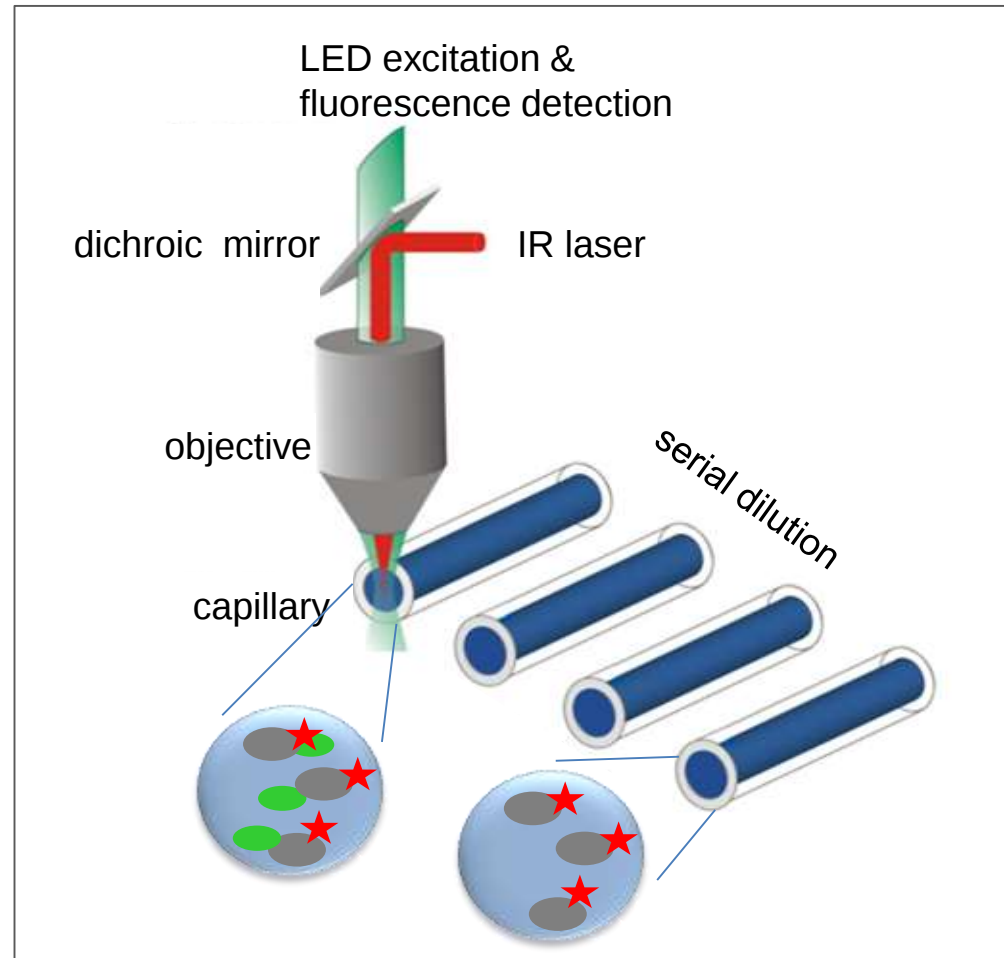
The diagram illustrates the components of the thermophoresis coefficient S_T . It shows a protein structure for 'Size', a hydration shell diagram for 'Hydration shell', and a charge diagram with '+' and '-' signs for 'Charge²'.

Duhr and Braun PNAS 103, 19678–19682 (2006)

Duhr and Braun PRL 96, 168301 (2006)

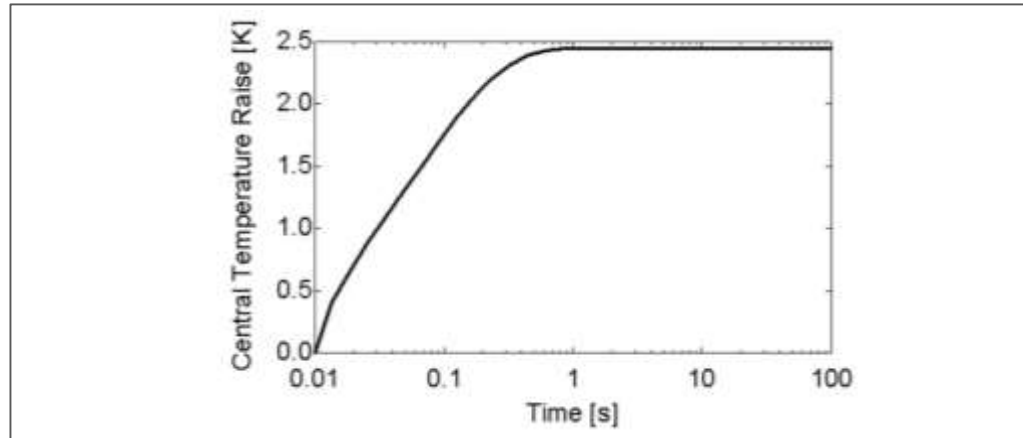


Basic setup of the instrument

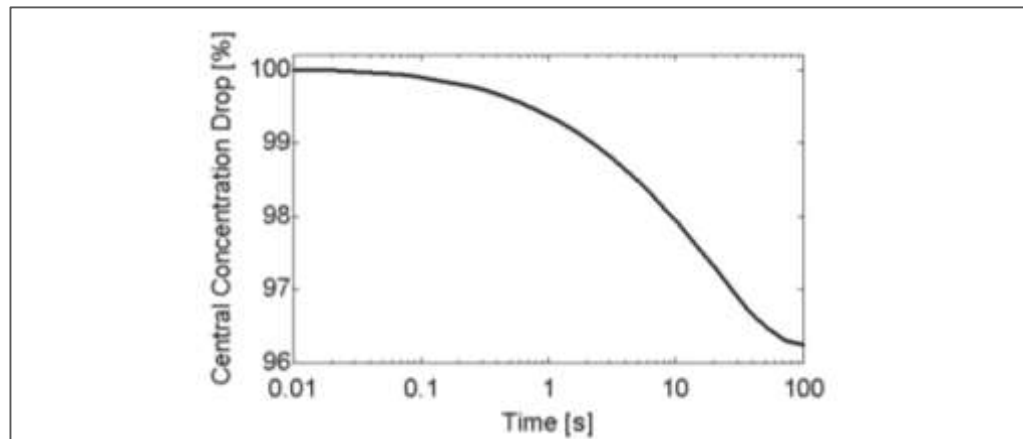


- ▶ **Immobilization-free** in buffer or complex bioliquids
- ▶ **4 μ l** of sample per titration point
- ▶ **nM concentrations** of fluorescent molecule
- ▶ **40 sec** measurement per titration point

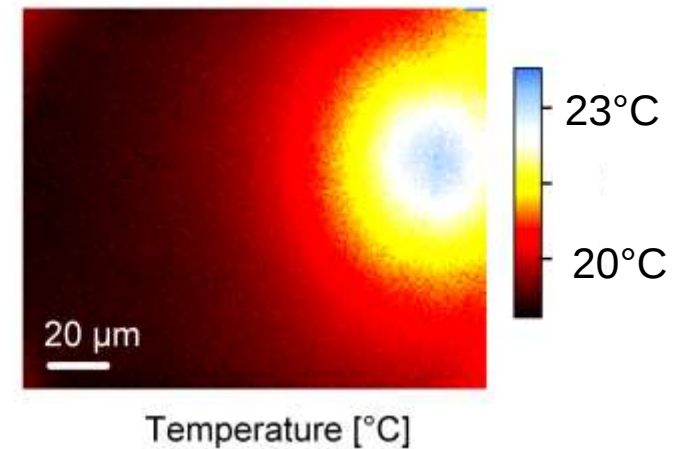
Sample heating < 1 sec



Thermophoresis ~ 30 sec

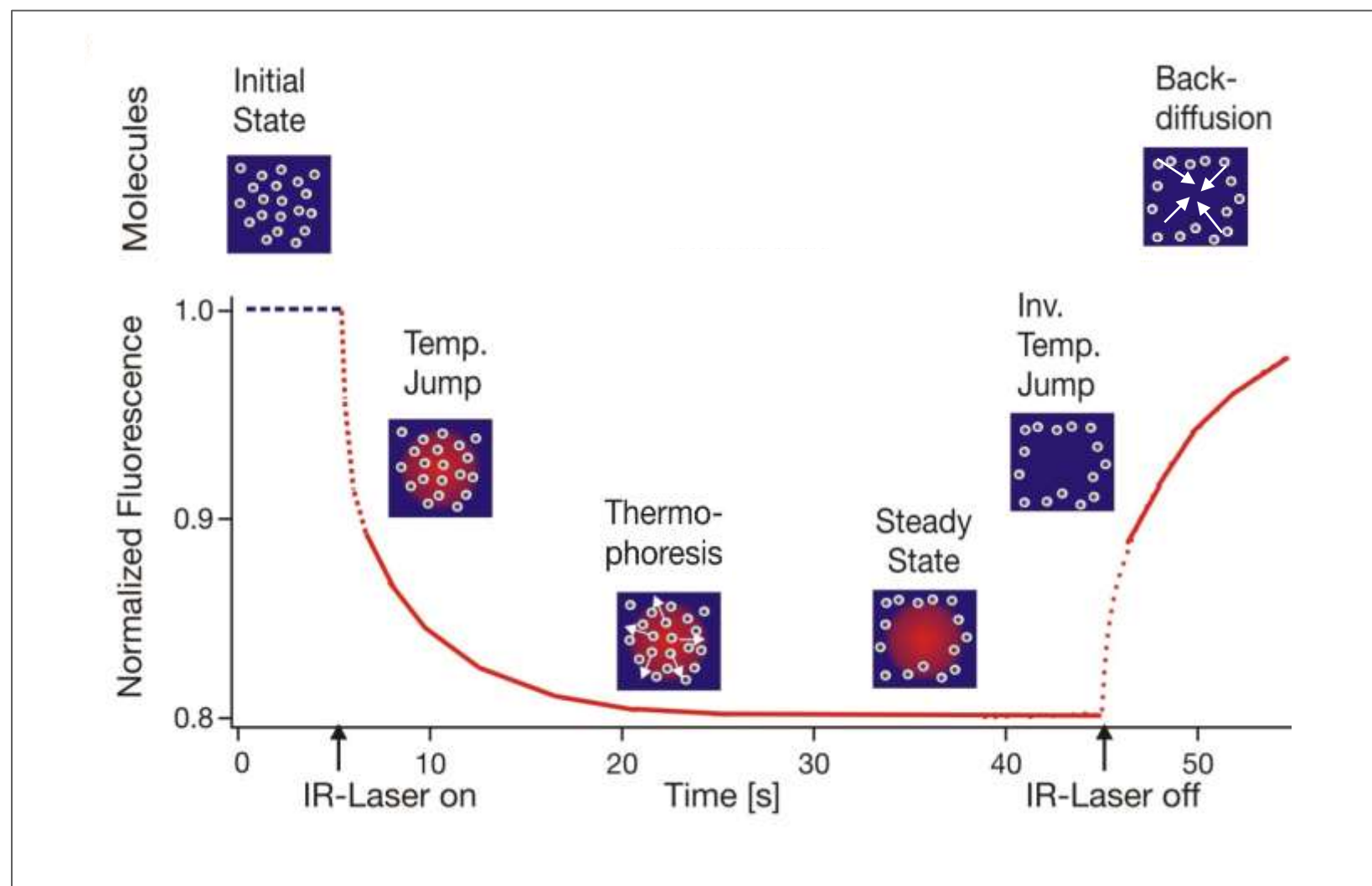
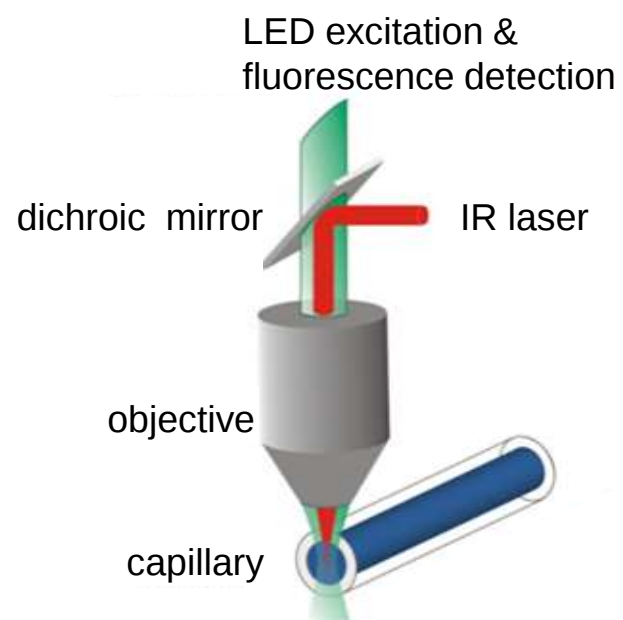


IR laser induced temperature field

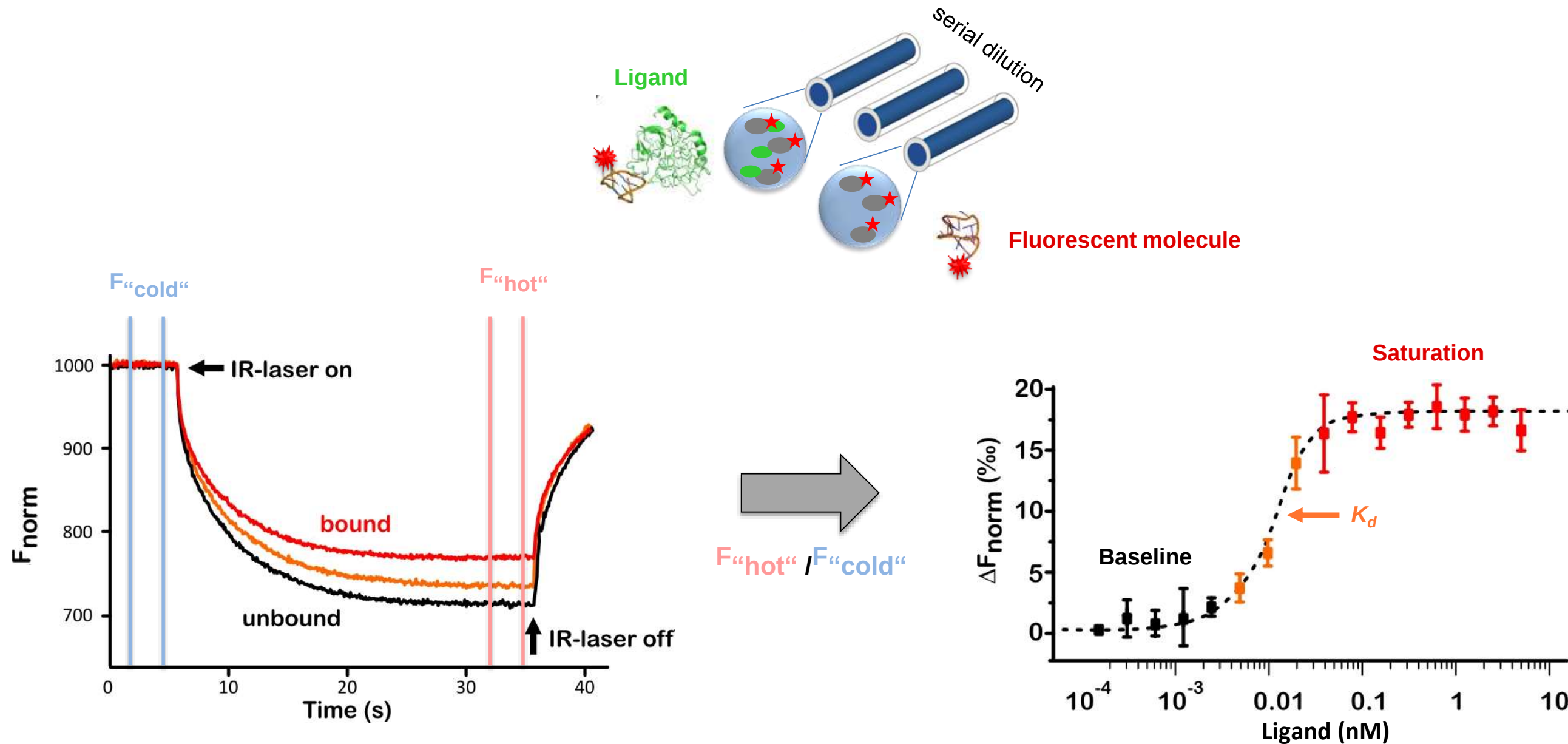


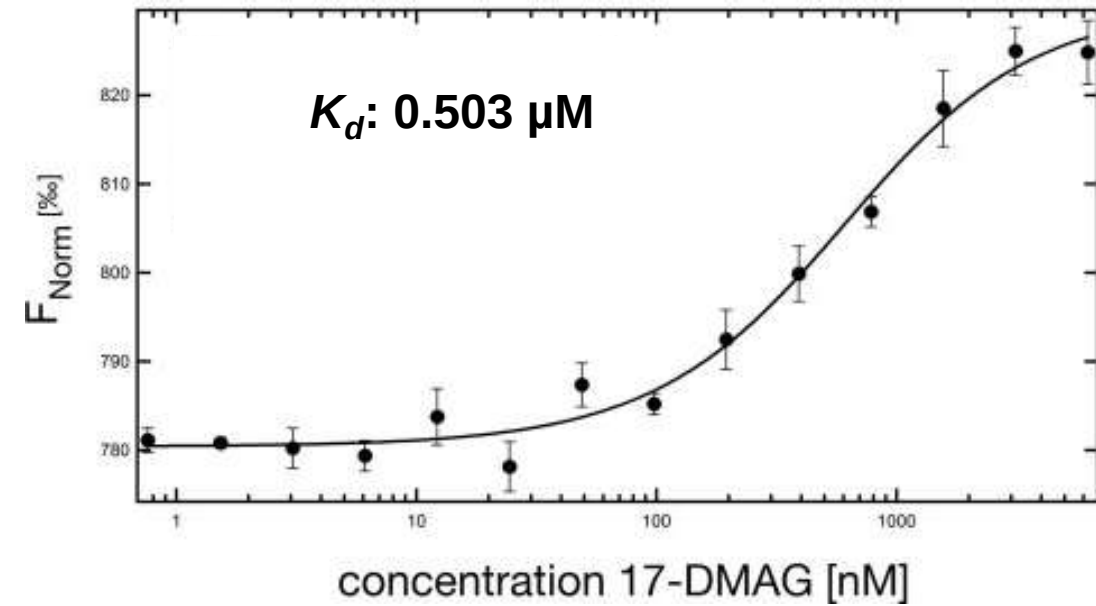
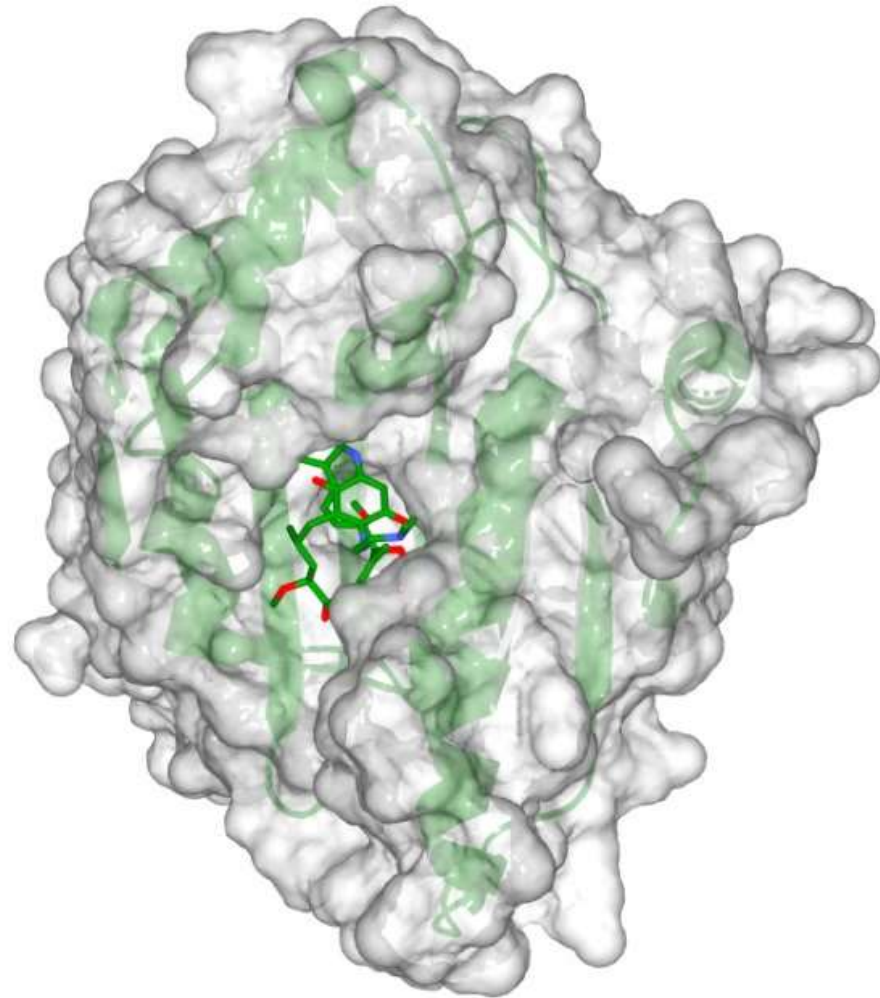
1K/10 μm corresponds to 1000K/cm

Jerabek-Willemsen et al, ADDT, 2011



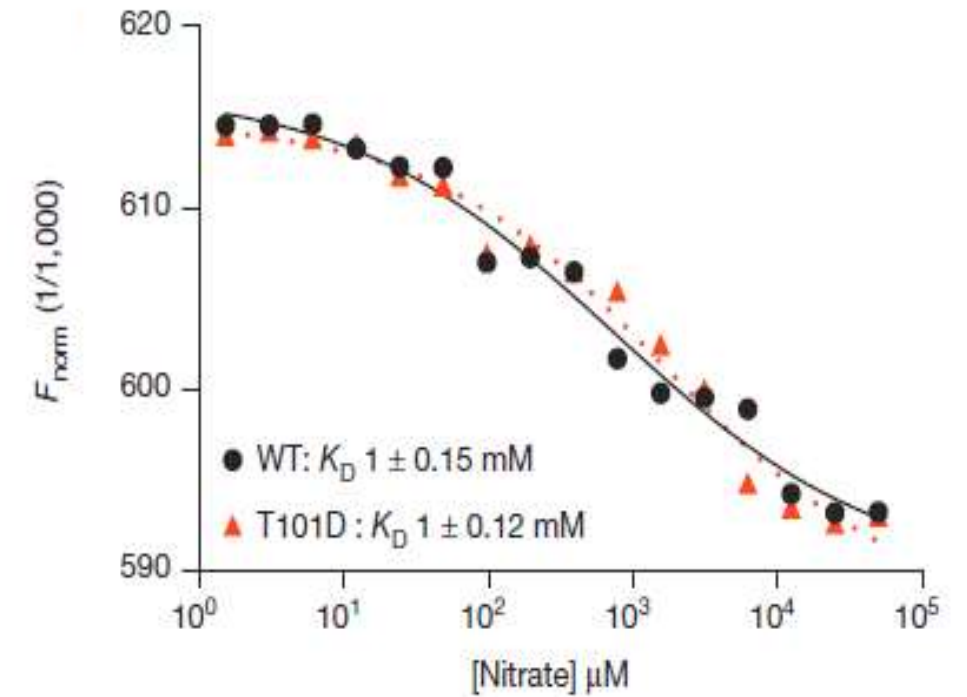
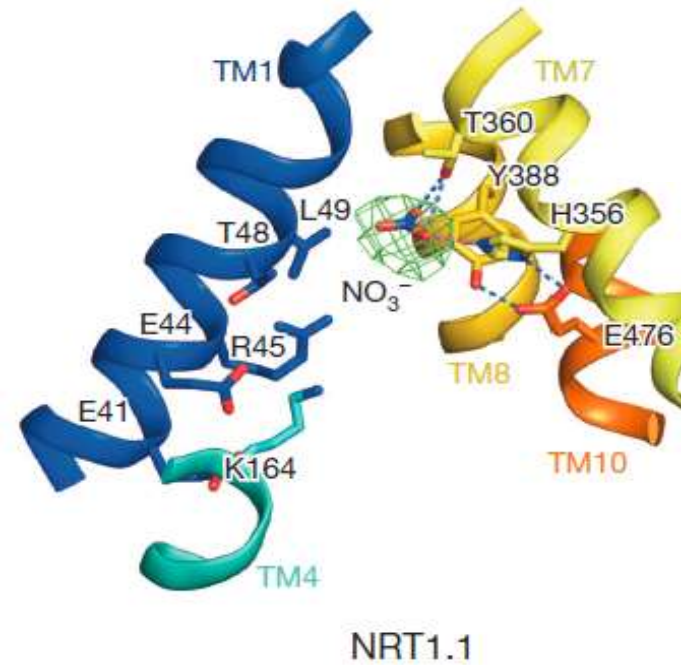
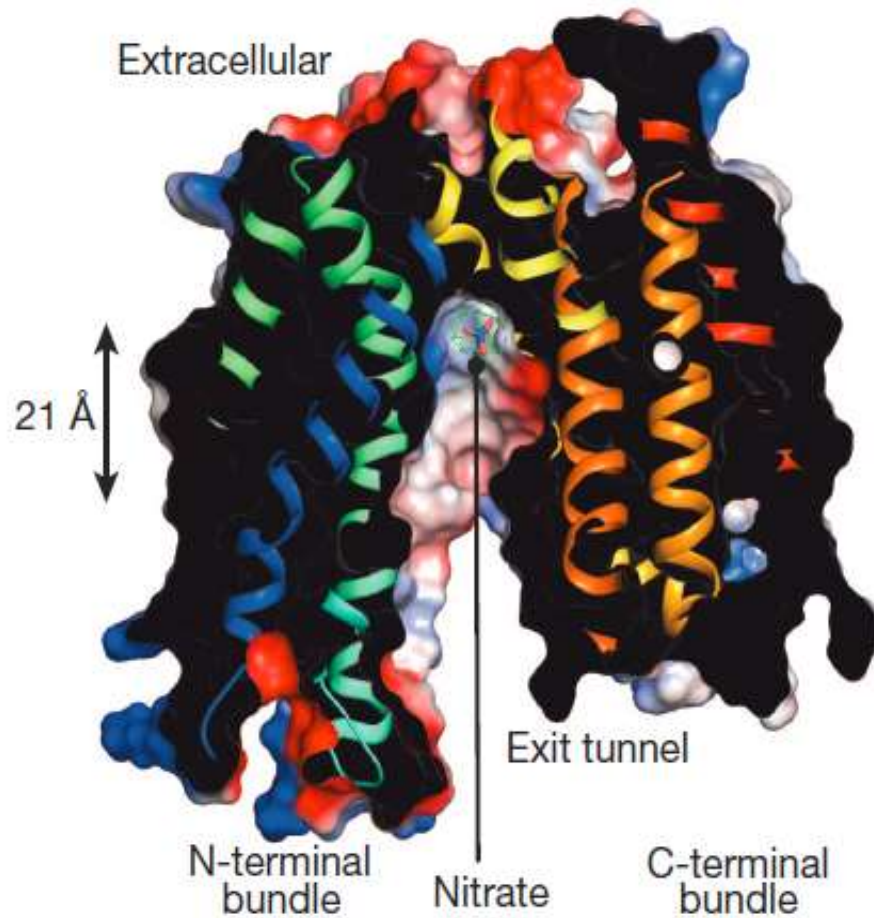
Jerabek-Willemsen et al, ADDT, 2011





Results were kindly provided by Stephen McLaughlin, MRC-LMB, Cambridge, UK

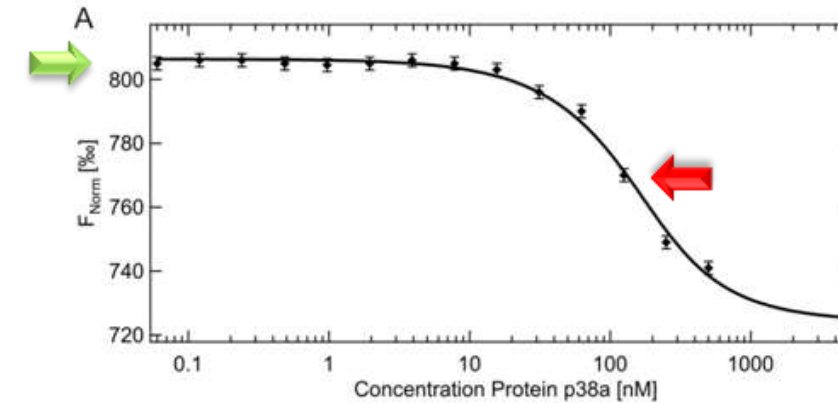
- Interactions that do not alter the MW of a protein, only the conformation (hydration shell)



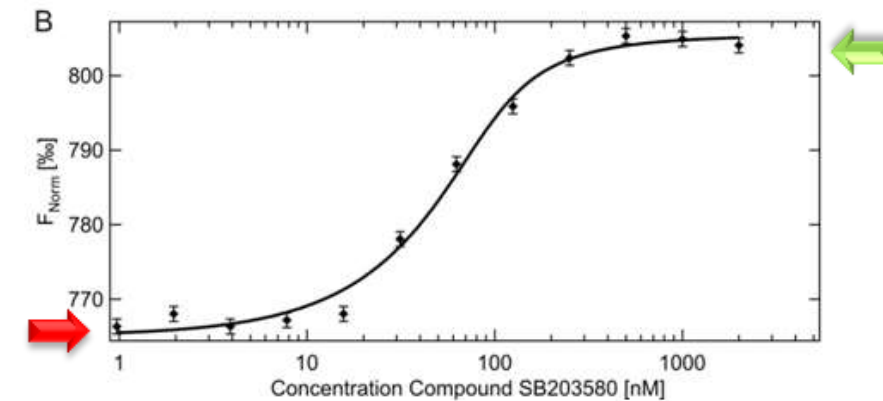
Parker & Newstead, Nature, 2014

► Unmatched sensitivity of MST: small nitrate molecule binding to a large 12 Transmembrane-Helices Transporter

Binding of p38 to Tracer

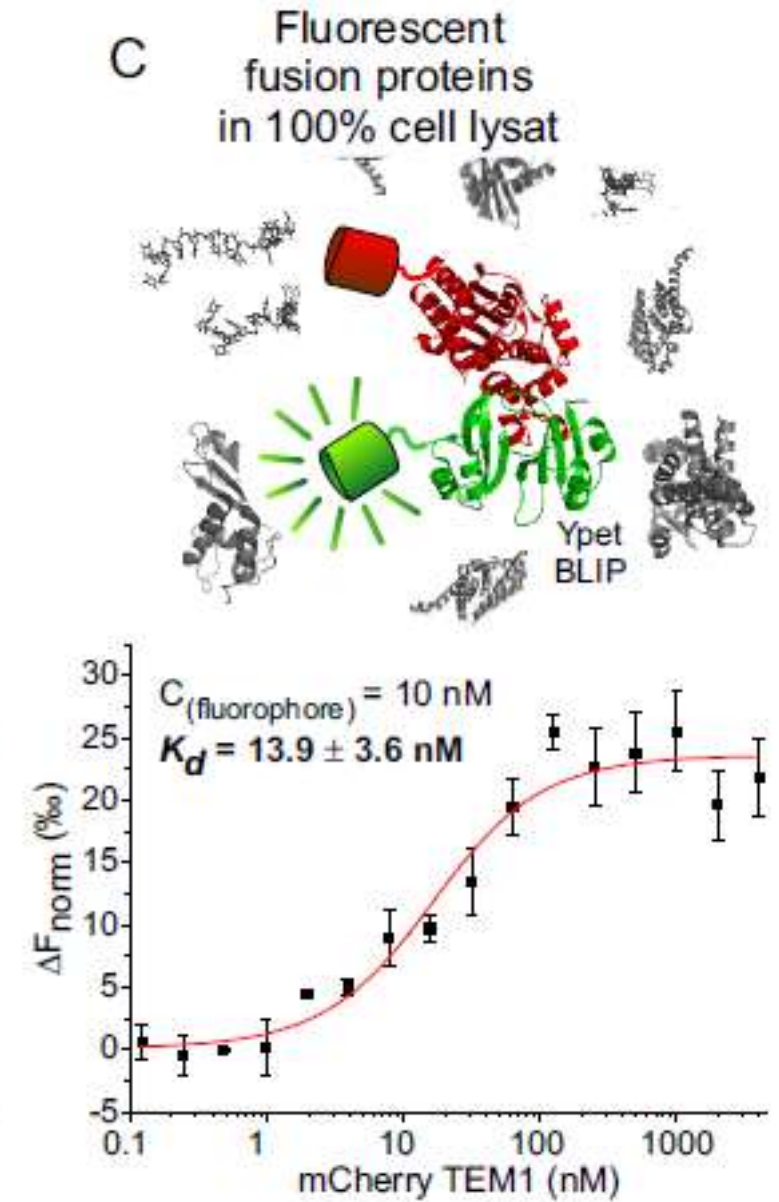
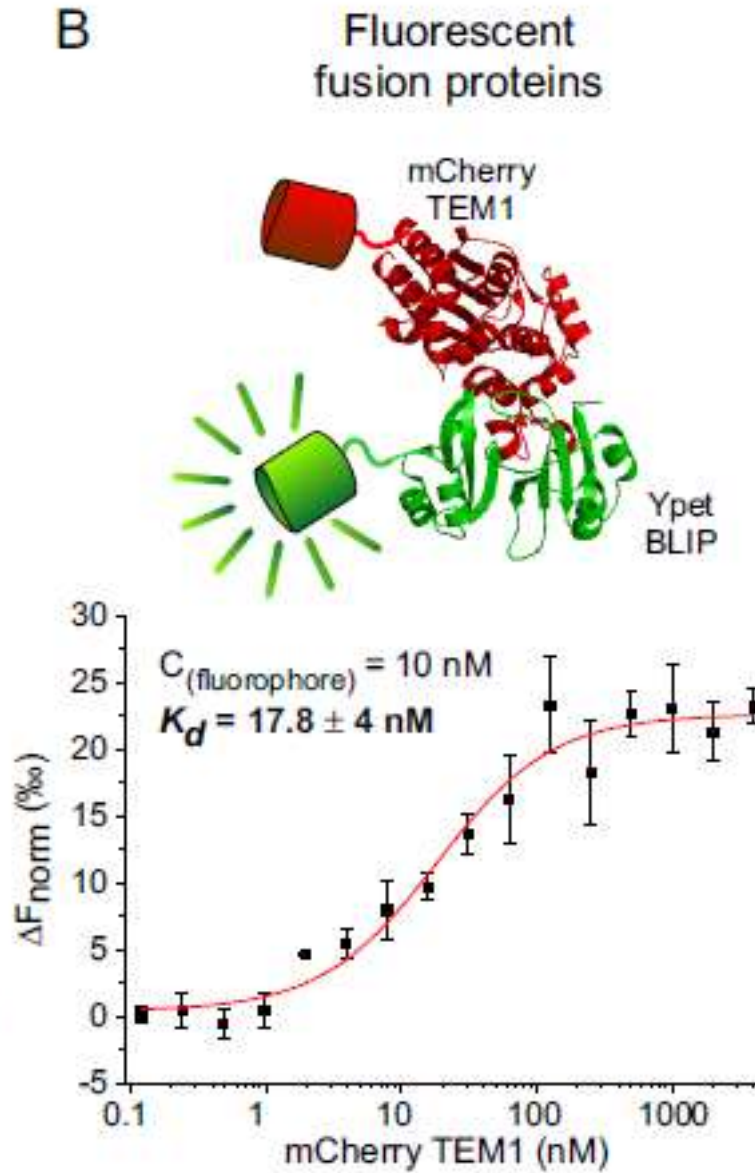
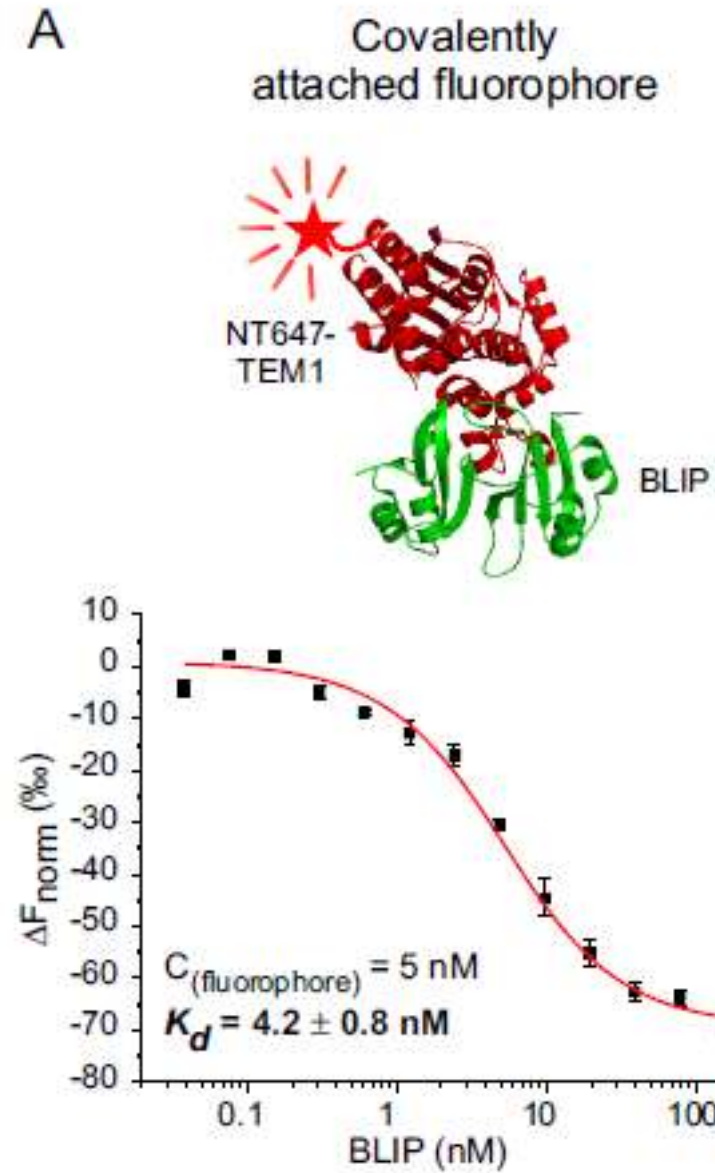


Competitive Assay with Compounds



Material was kindly provided by Dr. Krishna Saxena,
University Frankfurt, Germany

► Competition experiments are essentially label-free and site-specific







Nature: "Molecular basis of nitrate uptake by the plant nitrate transporter NRT1.1." Parker and Newstead, *Nature*, **2014**, 507, 68-72



RNA Biology: "Microscale thermophoresis provides insights into mechanism and thermodynamics of ribozyme catalysis." Gaffarogullari E. C., *et al.* *RNA Biology*, **2013**, 10, 1-7



Methods: "Microscale thermophoresis quantifies biomolecular interactions under previously challenging conditions." Seidel S. A., *et al.* *Methods*, **2013**, 59, 301-315



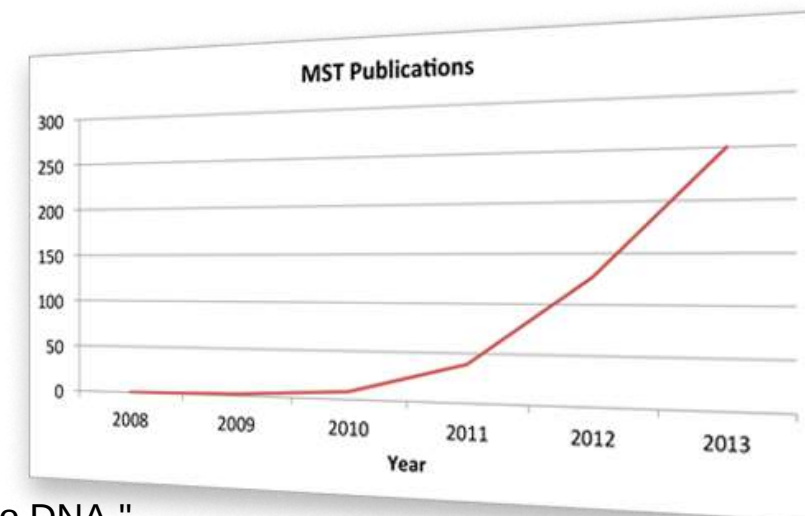
Nature: "Receptor binding by a ferret-transmissible H5 avian influenza virus." Xiong X., *et al.* *Nature*, **2013**, 497, 392-396



Cell: "Inhibition of basal FGF receptor signaling by dimeric Grb2." Lin C. C., *et al.* *Cell*, **2012**, 149, 1514-1524



J Biol Chem: "Mechanisms of unphosphorylated STAT3 transcription factor binding to DNA." Timofeeva O. A., *et al.* *J Biol Chem*, **2012**, 287, 14192-14200



... and many more! www.nanotemper-technologies.com/publications/

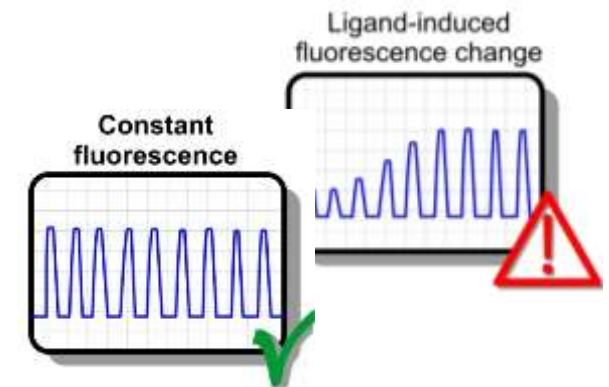
Assay Setup

- ▶ Sample labeling and important pre-tests
- ▶ Serial dilution and loading of capillaries
- ▶ NT.Analysis and NT.Control Software



Assay optimization

- ▶ Aggregation
- ▶ Fluorescence changes
- ▶ Noise level



- ▶ Concentration of **fluorescent molecule**: in the same range or lower than the expected K_d
- ▶ Highest concentration of **ligand**: ≥ 20 fold above the expected K_d
- ▶ Final **sample volume** per titration point: $\geq 20 \mu\text{l}$
- ▶ Use **small tubes** for the serial dilution: e.g. PCR strips, tubes
- ▶ Dilution buffer **should not vary in composition** in serial dilution: e.g. DMSO
- ▶ **Accurate pipetting** is essential
- ▶ **Mix with pipette** instead of vortexing
- ▶ Do not touch **capillaries in the center**

Monolith NT.115:

- ▶ Label one binding partner using a NT fluorescent dye
- ▶ Expression of a fusion protein (GFP, YFP...)
- ▶ Synthetic fluorescent samples (nucleic acids, peptides)
- ▶ Different methods: *in vitro* translation, incorporation of unnatural amino acids...



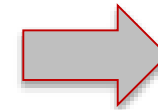
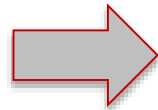
Protein labeling:

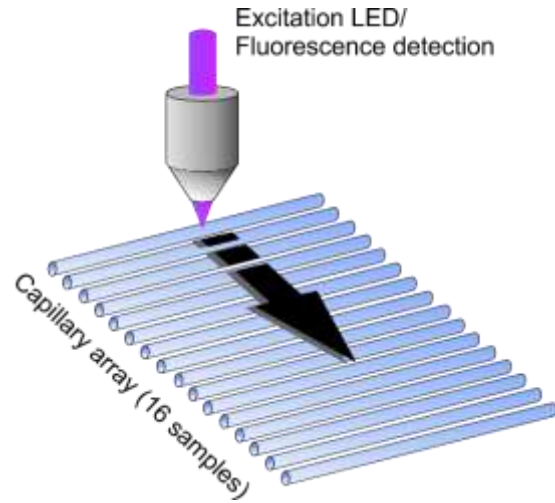
- ▶ NanoTemper Protein Labeling Kits are optimized for MST
- ▶ Use only high purity samples (>95%)
- ▶ Amine-reactive vs. cysteine-reactive labeling
- ▶ Efficient removal of free dye



Aim

- ▶ Check protein labeling efficiency
- ▶ Select proper capillary (Standard treated, Hydrophilic, Hydrophobic and Premium coated)





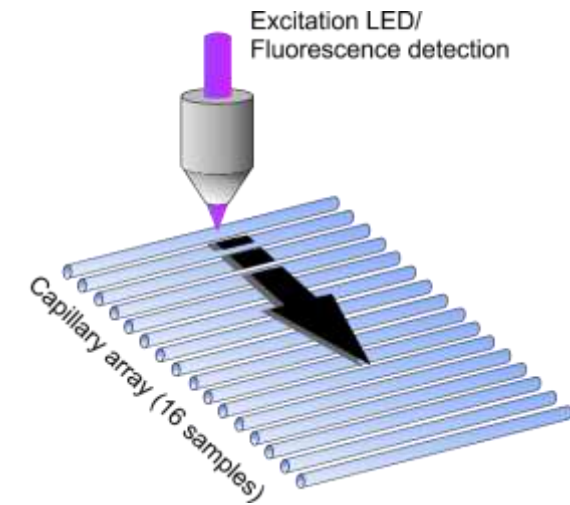
Fluorescence intensity: 200 – 1500 counts

Fluorescence signal < 200 counts:

- ▶ Increase LED power
- ▶ Increase fluorophore concentration
- ▶ Optimize labeling efficiency

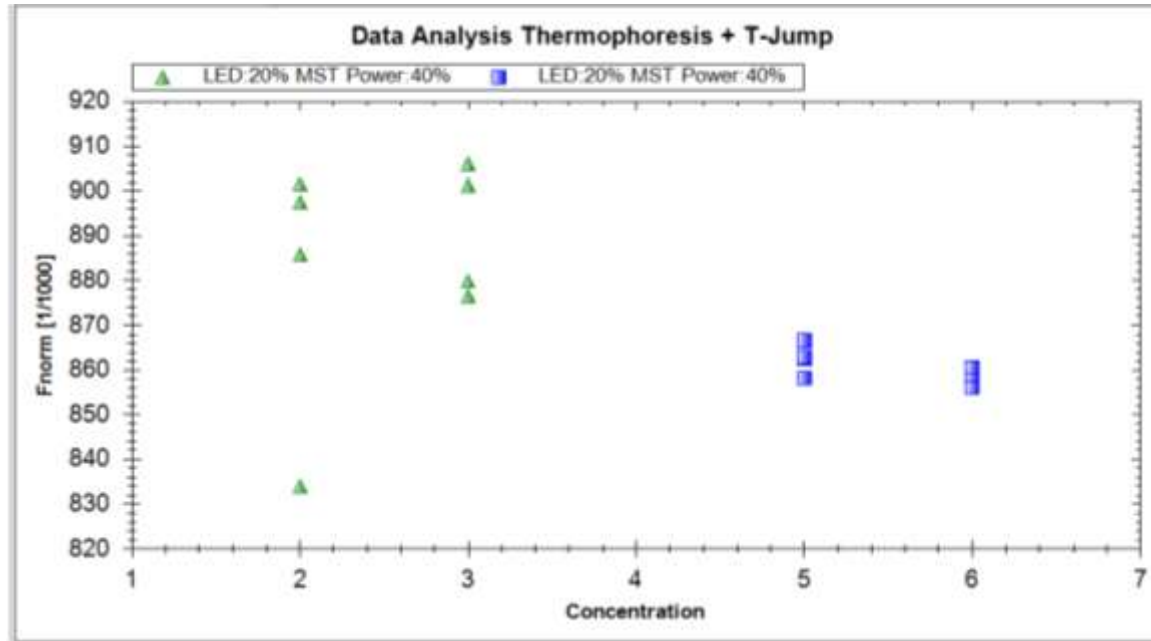
Fluorescence signal > 1500 counts:

- ▶ Decrease LED power
- ▶ Dilute sample
- ▶ Check for presence of free dye



Split peaks or shoulders:

- ▶ Change capillary type
(Standard or Premium coated)
- ▶ Optimize buffer

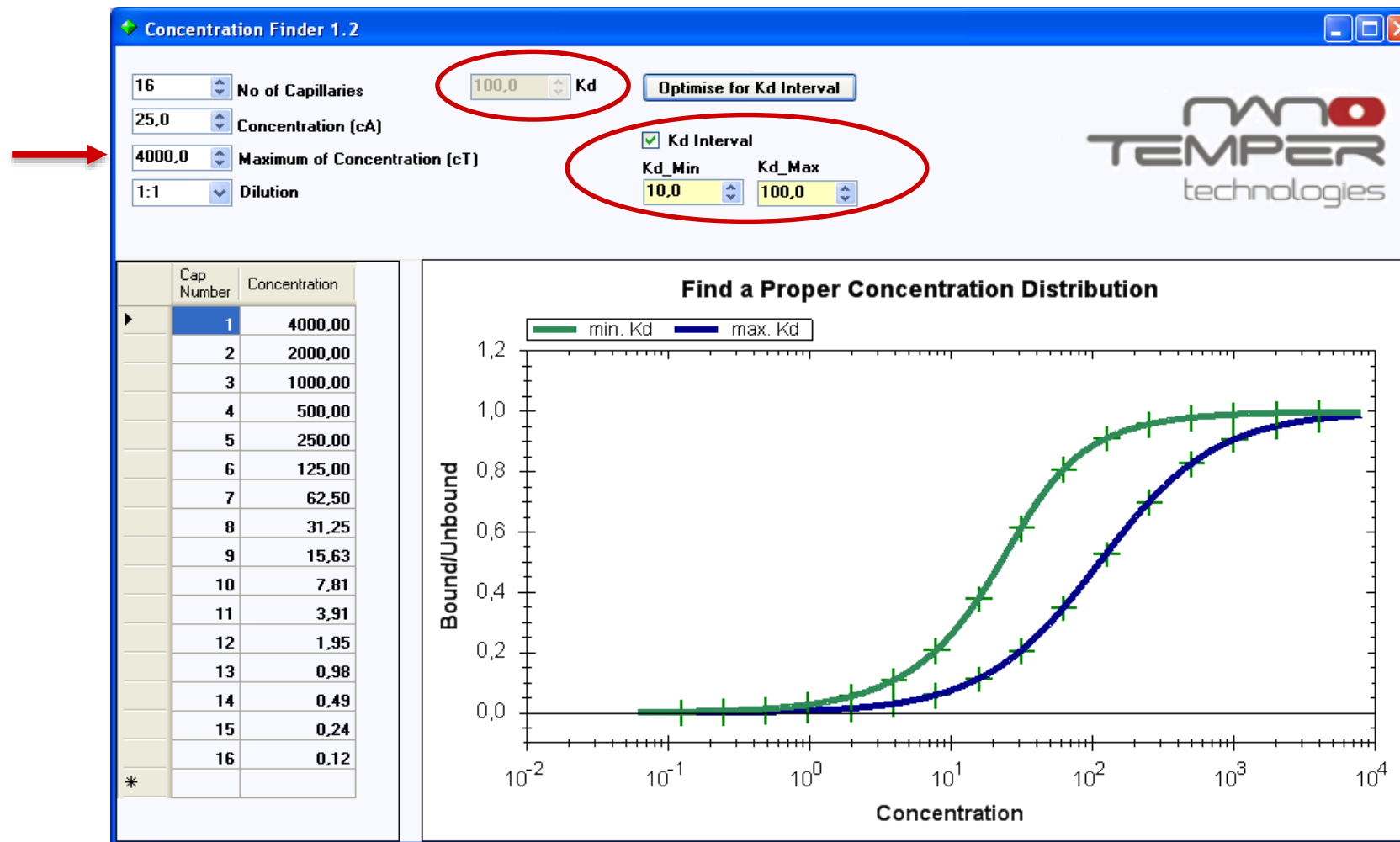


Capillary: std. premium std. premium

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 Assay buffer MST optimized buffer

- ▶ Load same sample in your assay buffer (4 capillaries each) and measure with 40 % MST power
- ▶ Noise level ≤ 6 -8 units
- ▶ Test different types of capillaries
- ▶ Test/improve buffer conditions
 - ▶ By adding detergents such as Tween 20, Pluronic-F127,...
 - ▶ By changing pH or ionic strength...



► Note: This tool can be accessed via NT.Control Software or NanoTemper website

Ligand

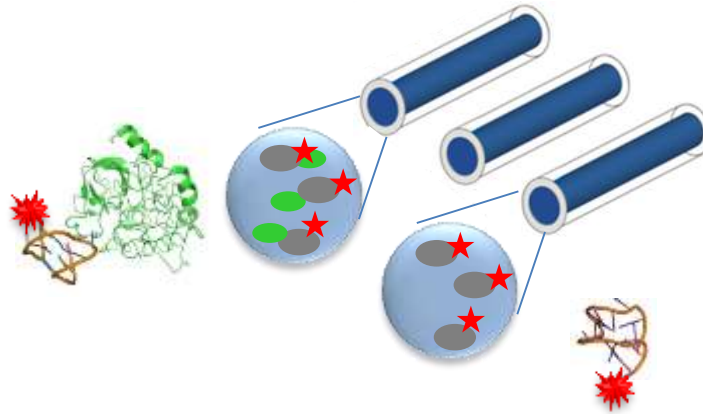
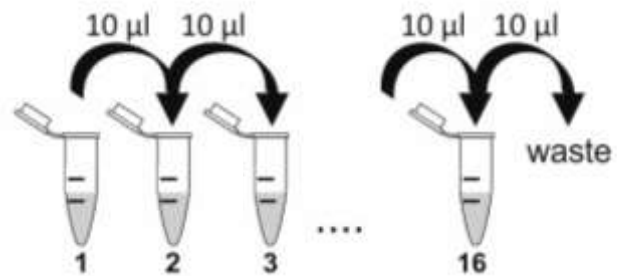
20 μ l



10 μ l buffer



Ligand dilution

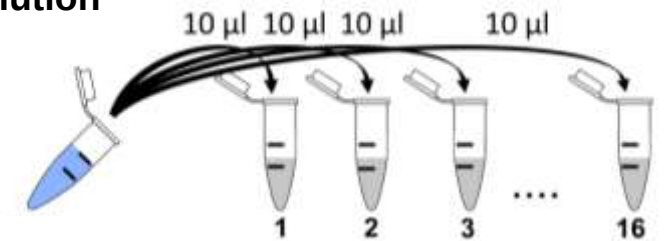


Fluorescent Molecule

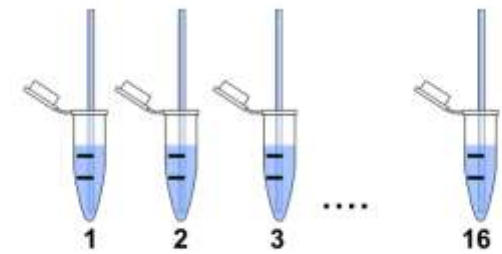
200 μ l stock

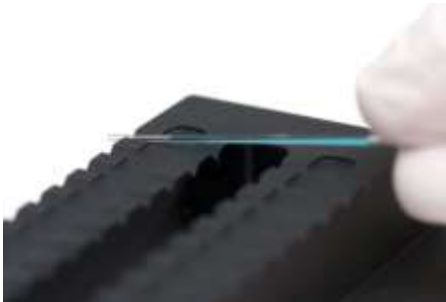
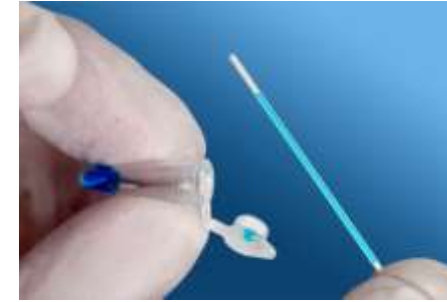


Serial dilution

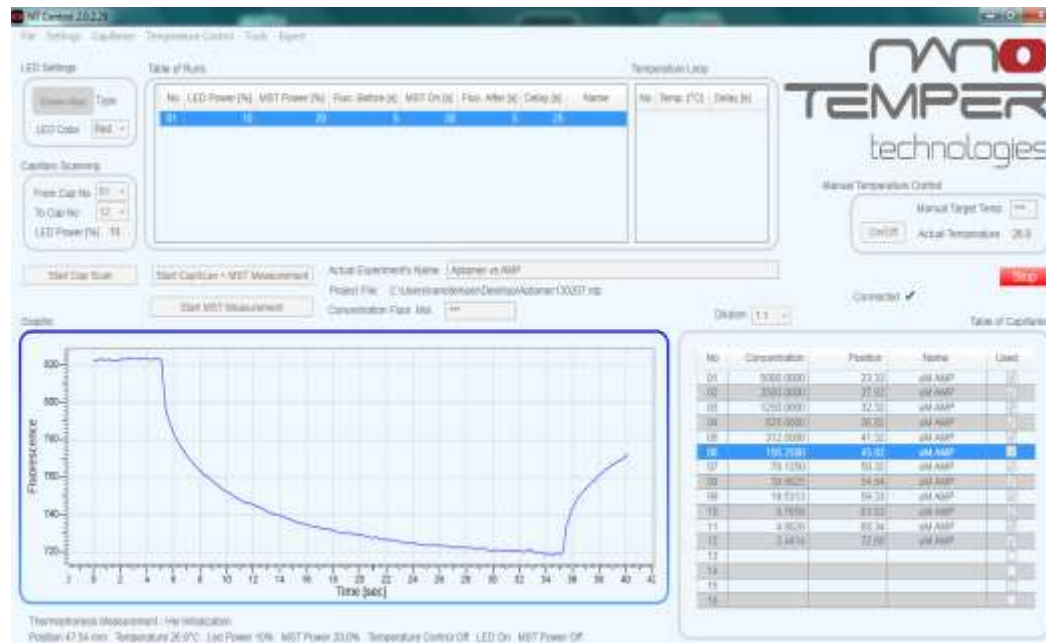


Fill capillary



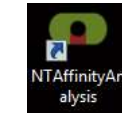


Running MST Experiments: NT.Control Software



- ▶ Adjust LED power to excite the fluorescent molecule
- ▶ Set MST power to induce the temperature gradient

Analyzing MST Data: NT.Analysis Software



- ▶ Fit curves to determine K_d or EC_{50}
- ▶ Export your data

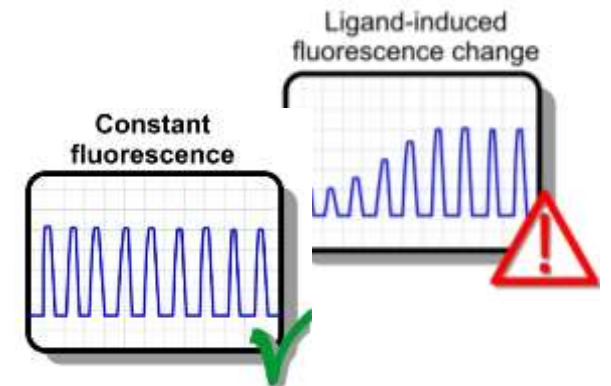
Assay Setup

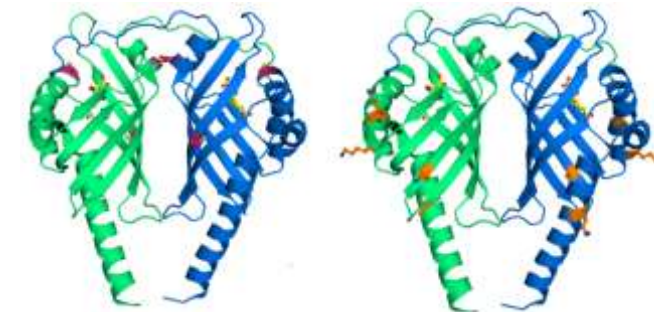
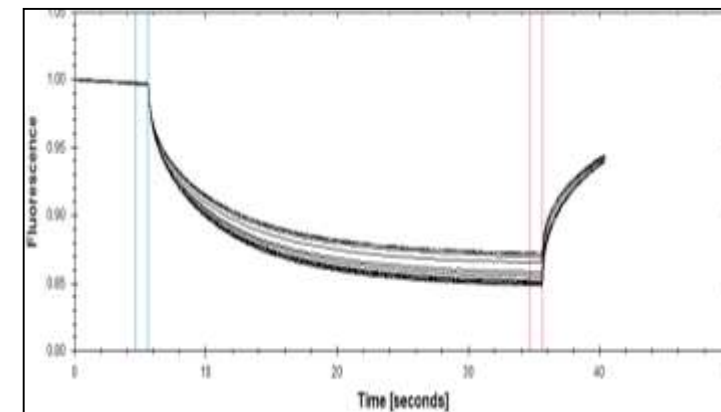
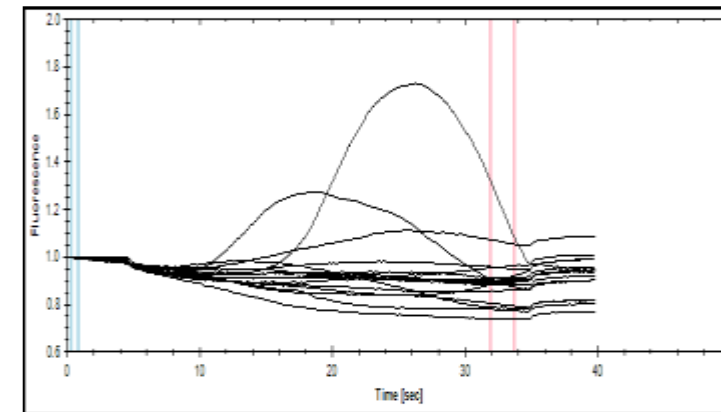
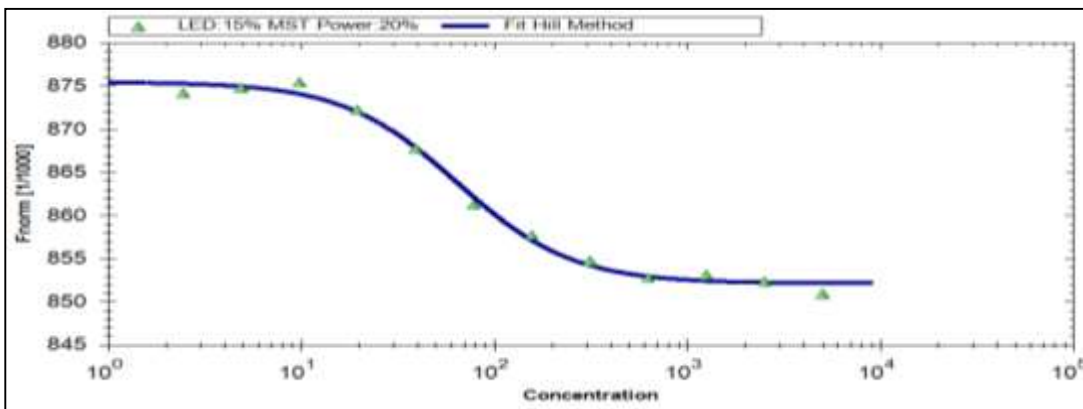
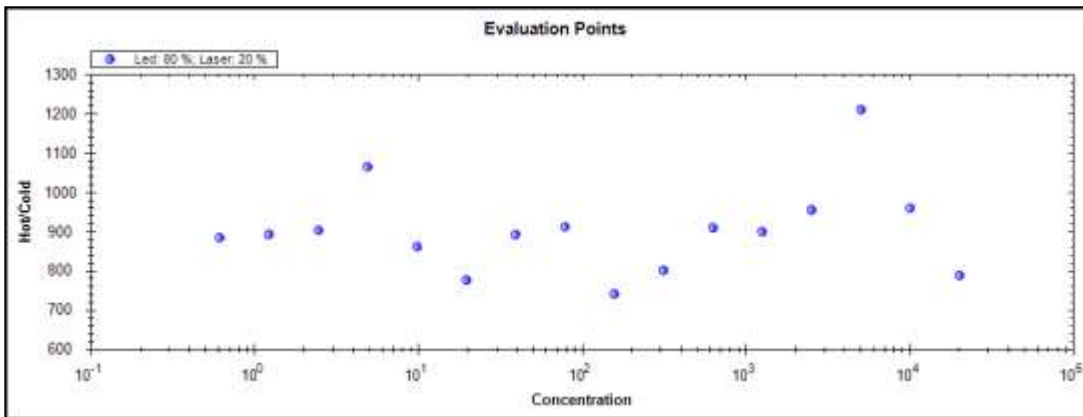
- ▶ Sample labeling and important pre-tests
- ▶ Serial dilution and loading of capillaries
- ▶ NT.Analysis and NT.Control Software



Assay optimization

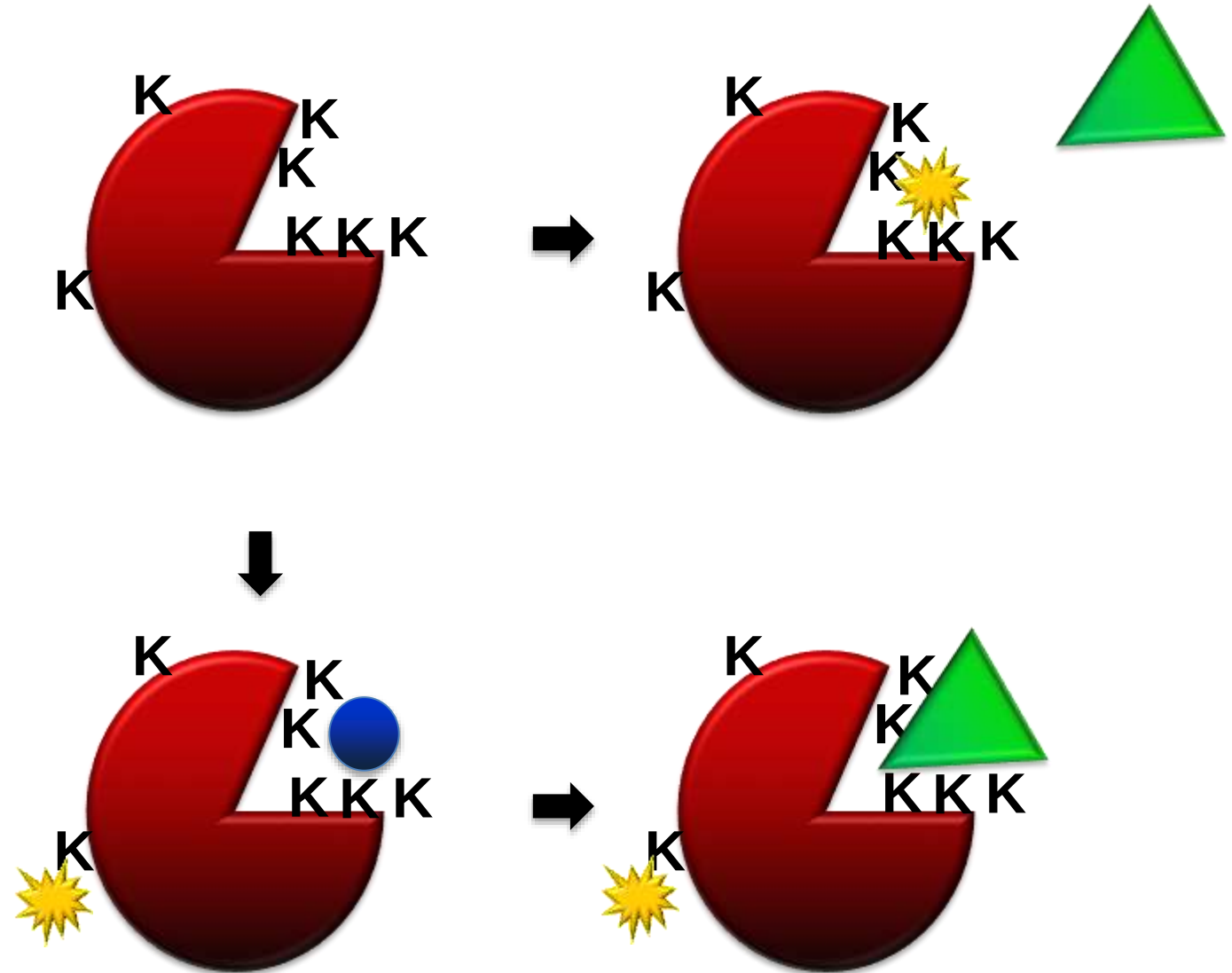
- ▶ Aggregation
- ▶ Fluorescence changes
- ▶ Noise level



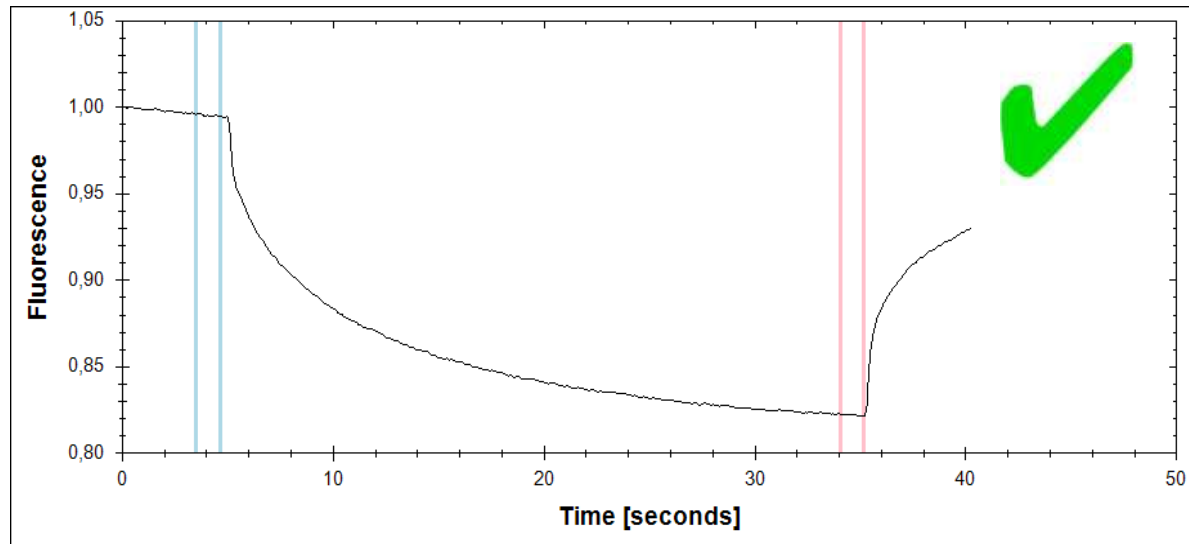


► 4 lysines are involved in binding

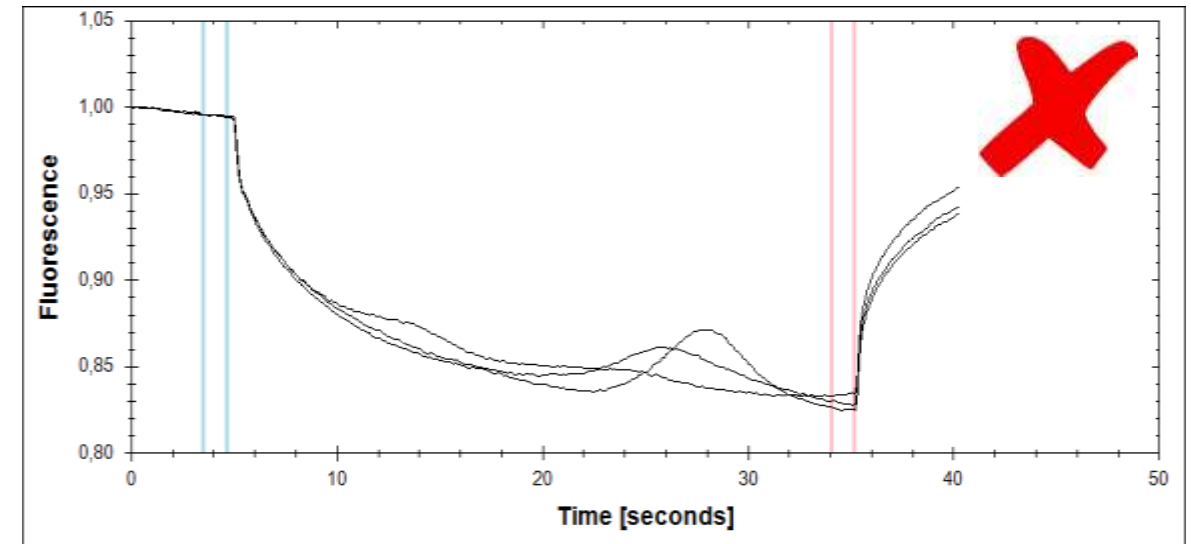
- ▶ Alternative labeling strategies
 - ▶ Different coupling chemistry (maleimide labeling)
 - ▶ Different dye
 - ▶ Fusion protein (GFP, YFP,...)
 - ▶ **Protection of binding site**
 - ▶ Site-specific label (unnatural amino acids, *in vitro* translation...)
- ▶ Alternative assay strategies
 - ▶ Competition experiment



No aggregation



Aggregation

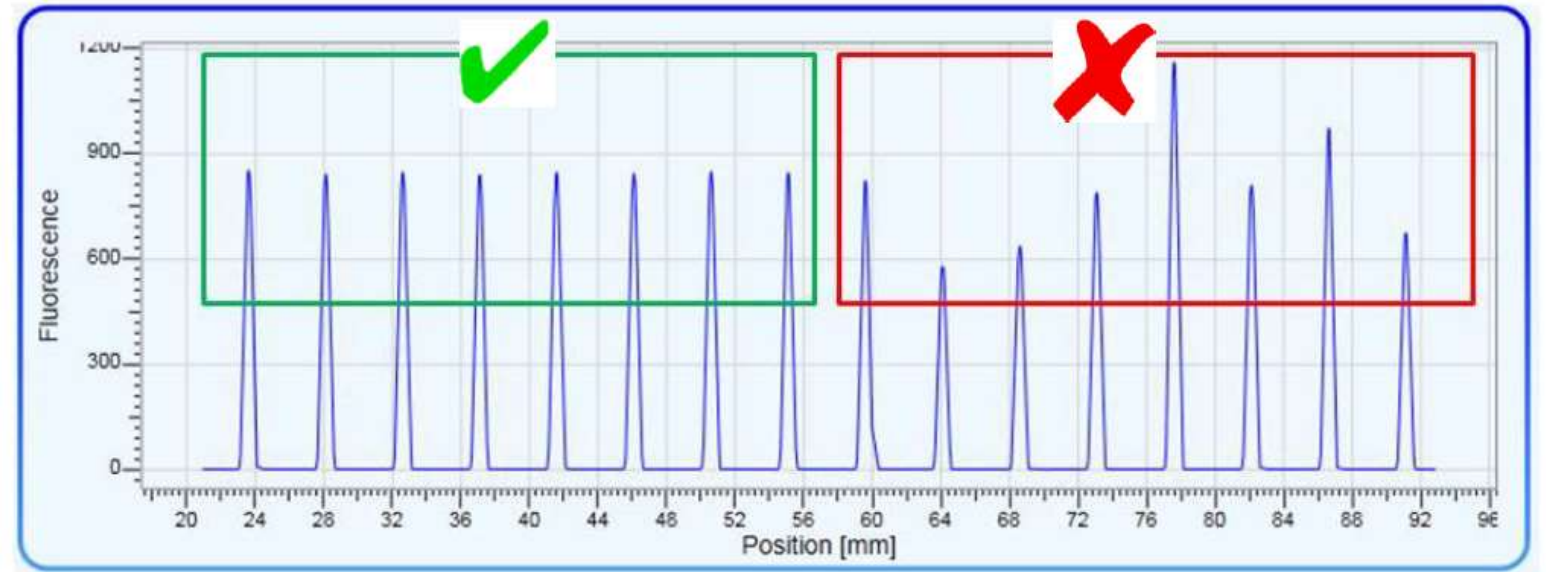


Buffer optimization is necessary:

- ▶ Detergents and additives (Tween-20, Pluronic F-127, BSA etc.)
- ▶ Centrifugation
- ▶ pH, ionic strength ...
- ▶ Concentration of organic solvents (DMSO)

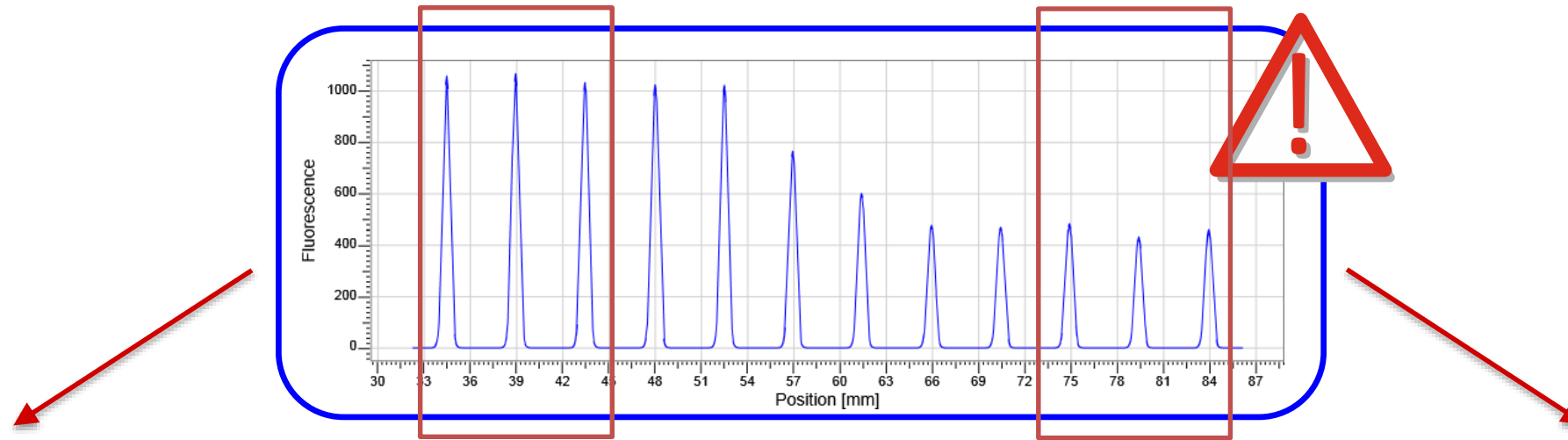
Random fluorescence changes

- ▶ Inaccurate pipetting
- ▶ Low sample quality
- ▶ Leads to increased noise level
- ▶ Buffer optimization necessary



< ±10 %

> ±10 %



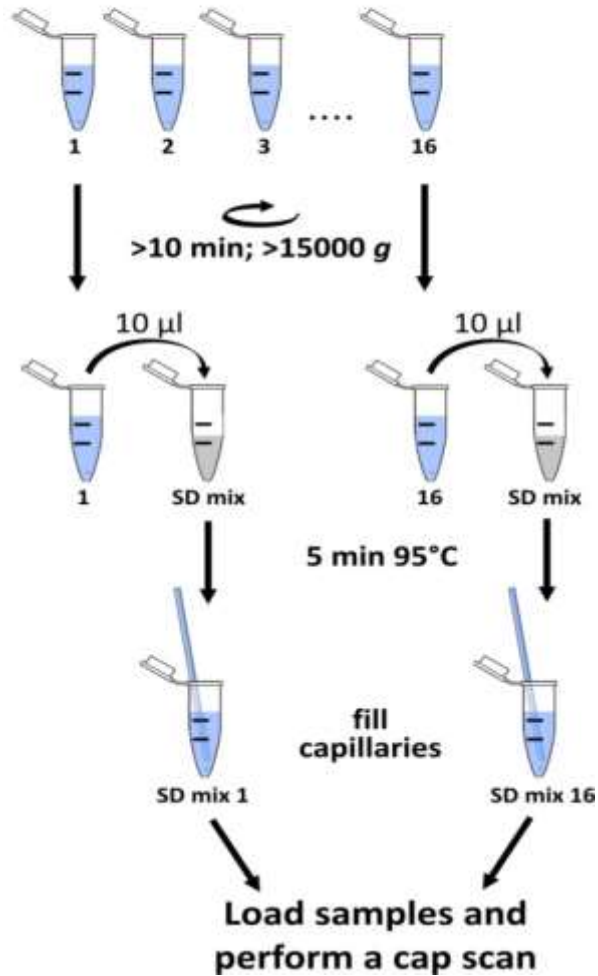
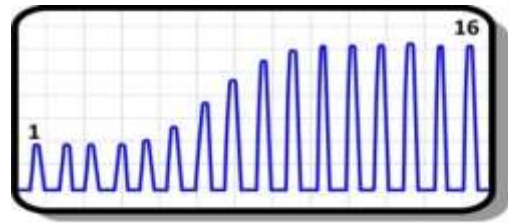
- ▶ Fluorescence quenching or enhancement induced by ligand binding

- ▶ Ligand-induced surface adsorption or
- ▶ Aggregation

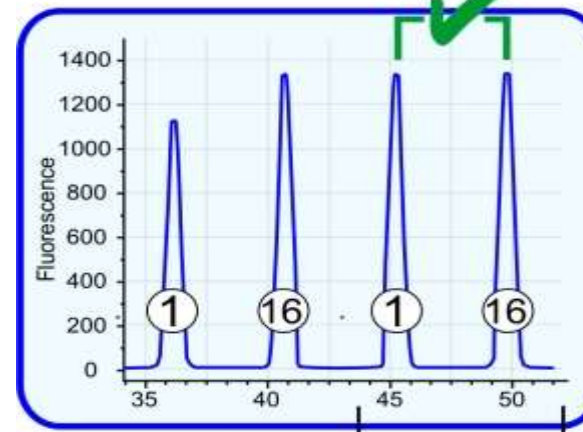


→ Perform SDS-denaturation (SD) test

Binding or Material Loss? How to perform the SD-Test

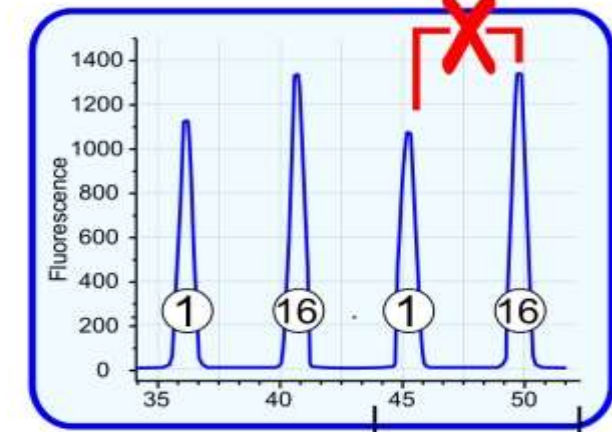


Specific, ligand-induced
fluorescence change



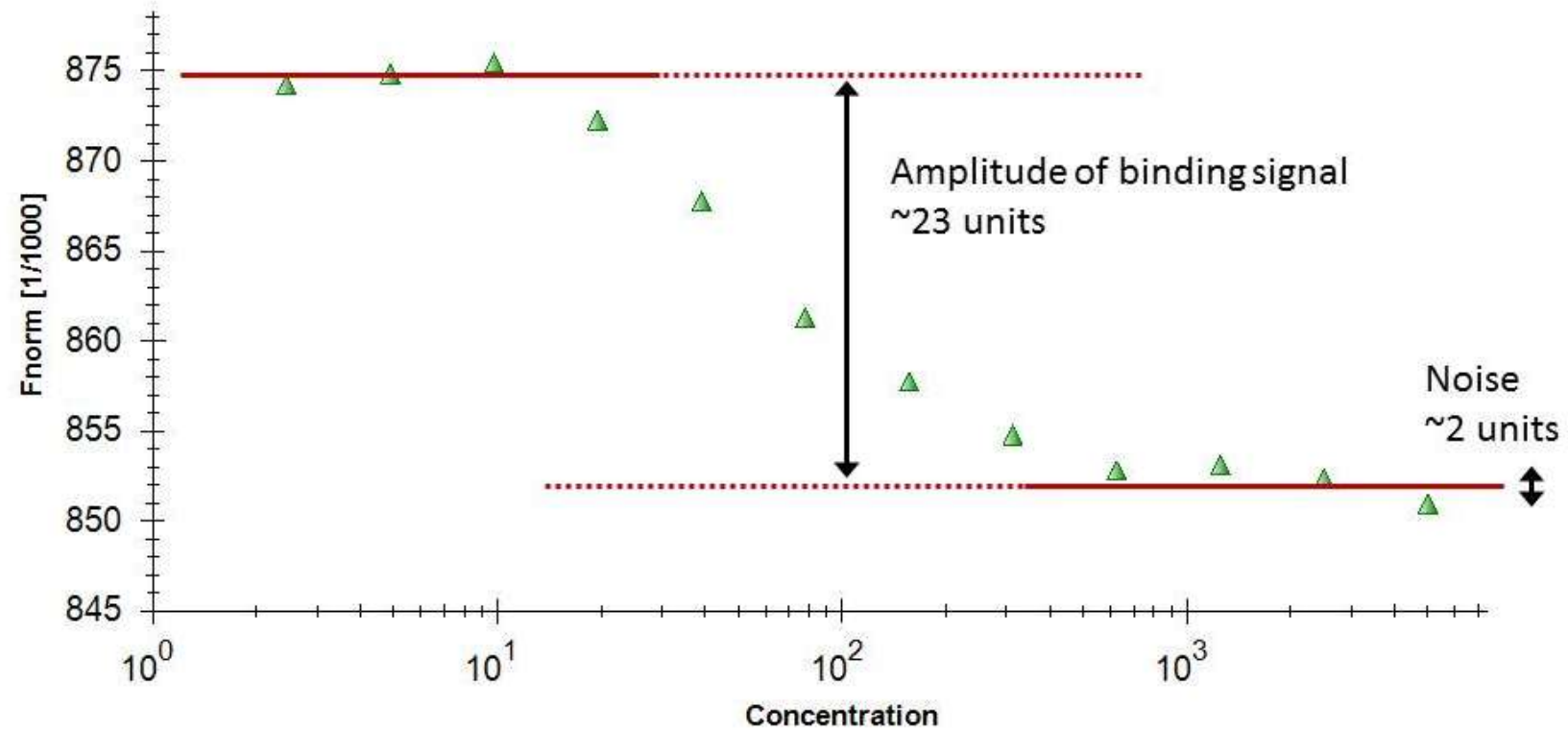
Use fluorescence change
of K_d -determination.

Fluorescence change due
to loss of fluorescent molecule

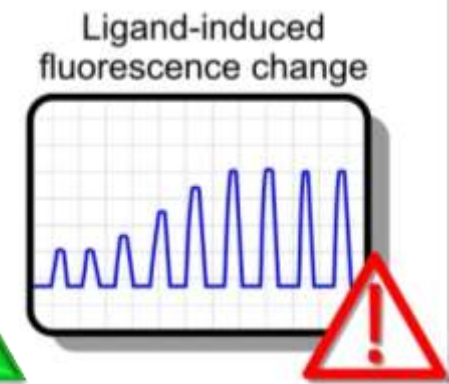
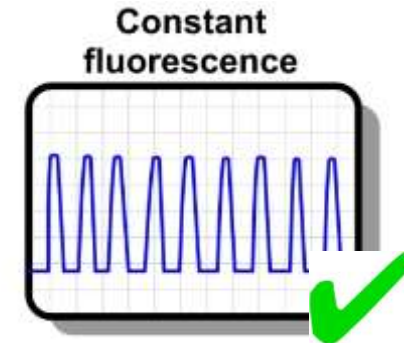
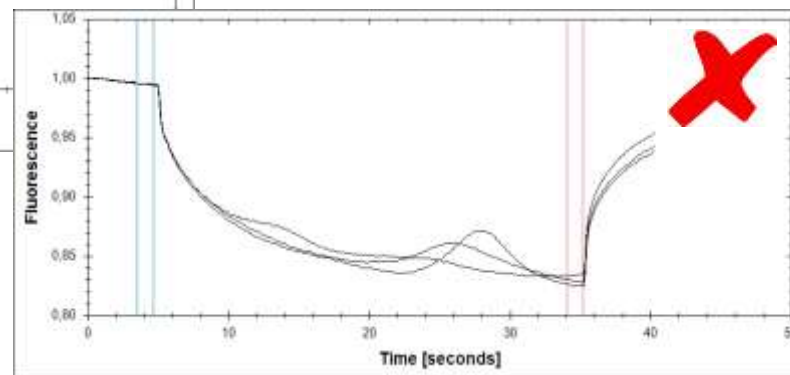
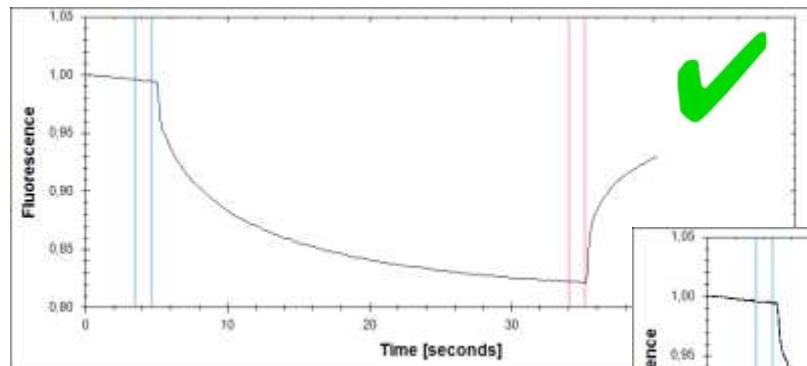
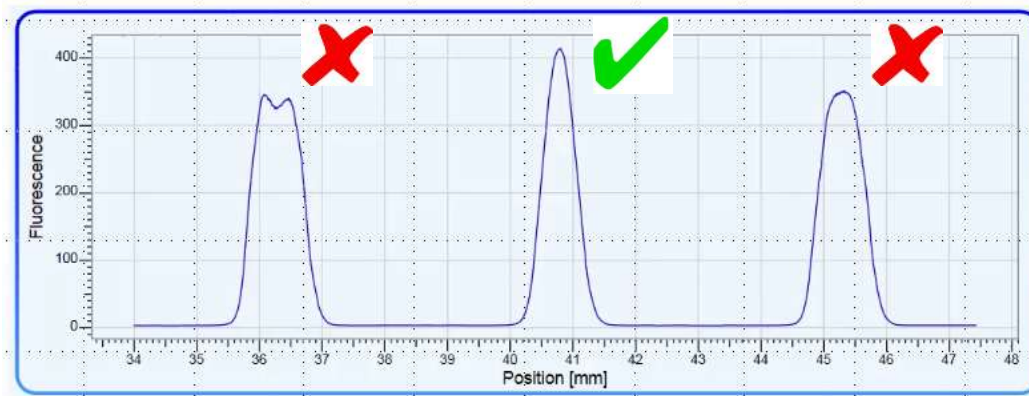


Assay optimization.

What is an acceptable Noise Level?

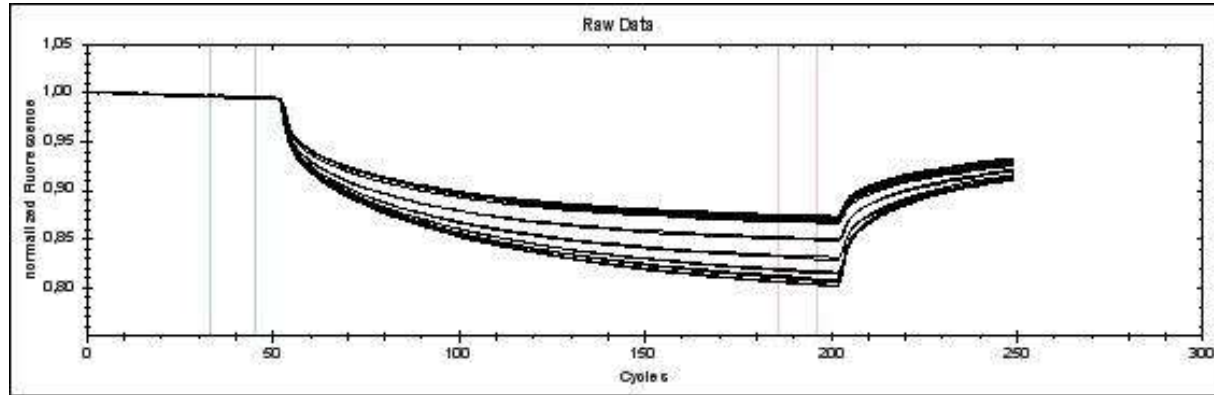


- ▶ Amplitude should be at least 3-fold above the noise level

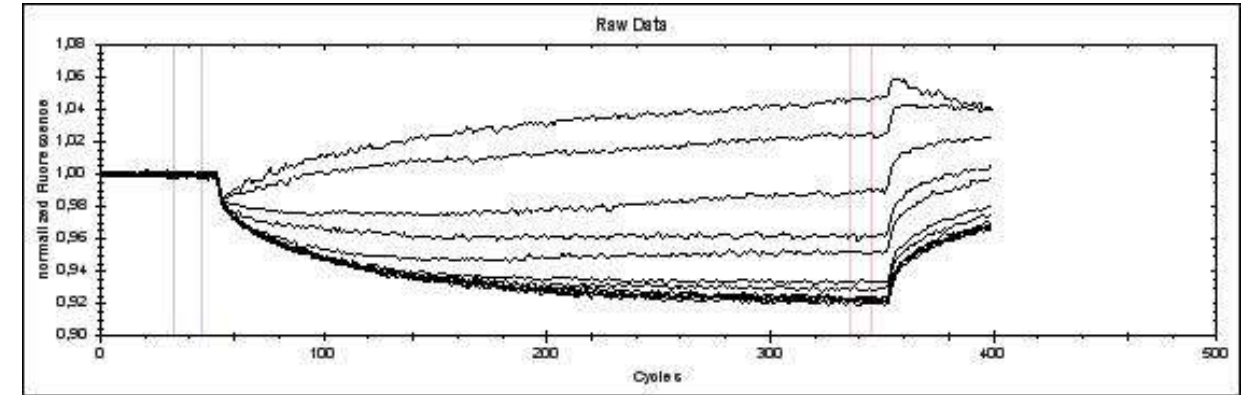


- Easy and straight forward assay optimization

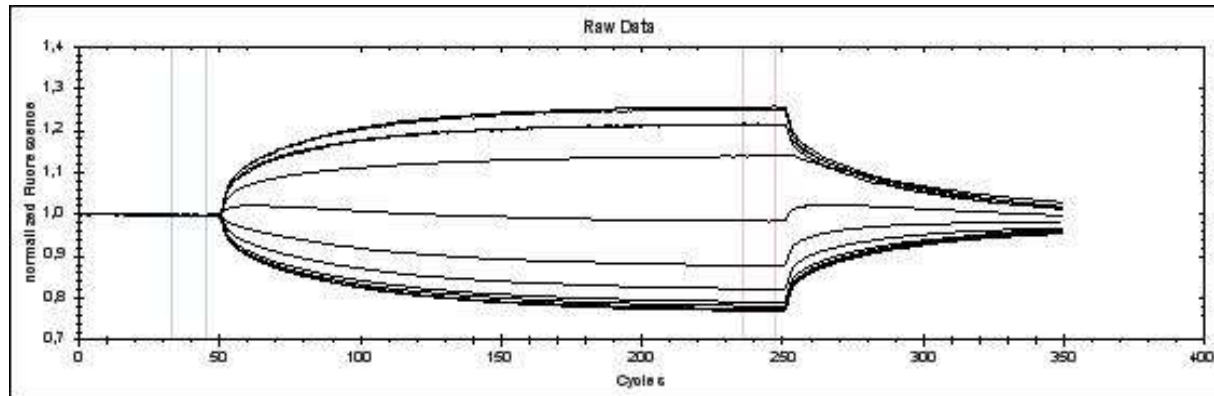
T-Jump (+) and thermophoresis (+)



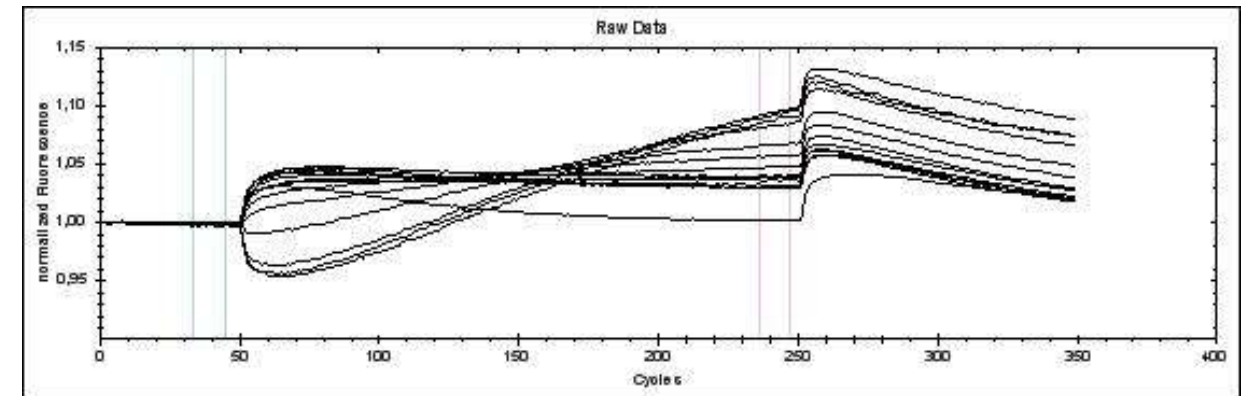
T-Jump (+) and thermophoresis (+/-)



T-Jump (+/-) and thermophoresis (+/-)



T-Jump (+/-) and thermophoresis (+/-)



▶ **NanoTemper Technologies support:**

From Scientists for Scientists

▶ **Individual support:**

Discuss your approach and your data

▶ **Experienced Application Scientists:**

Help with challenging samples

▶ **MST User Trainings:**

Intensive courses using your own samples

Please feel free to contact us:

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