

## Monolith Protocol MO-P-062

# Lysozyme – Aptamer (competitive assay)

Lysozyme is an enzyme that prevents bacterial infections by attacking peptidoglycan, a component of certain bacterial cell walls. Peptidoglycan is composed of the repeating amino sugars N-acetylglucosamine (NAG) and N-acetylmuramic acid (NAM), which are crosslinked by peptide bridges. Lysozyme hydrolyzes the bond between NAG and NAM, increasing the bacteria's permeability and causing the bacteria to burst. It is widely distributed in plants and animals. The majority of the lysozyme used in research is purified from hen egg whites. The DNA aptamer for lysozyme binds lysozyme with high affinity.

protein – DNA interaction | aptamer

## A1. Target/Fluorescent Molecule

Lysozyme

[uniprot.org/uniprot/B8YK79](https://uniprot.org/uniprot/B8YK79)

## A2. Molecule Class/Organism

Glycoside hydrolase

*Gallus gallus* (Chicken)

## A3. Sequence/Formula

KVFGRCELAA AMKRHGLDNY RGYSLGNWVC AAKFESNFNT QATNRNTDGS TDYGILQINS RWWCNDGRTP GSRNLCNIPC  
SALLSSDITA SVNCAKKIVS DGNGMNAWVA WRNRCKGTDV QAWIRGCRL

## A4. Purification Strategy/Source

Sigma-Aldrich GmbH

[L6876](#)

## A5. Stock Concentration/Stock Buffer

32 µg lyophilized powder

## A6. Molecular Weight/Extinction Coefficient

14.3 kDa

37,970 M<sup>-1</sup>cm<sup>-1</sup> (ε<sub>280</sub>)

## A7. Dilution Buffer

25 mM Histidine buffer, pH 5.0, 0.01% Pluronic® F-127

### A8. Labeling Strategy

Self-competition assay<sup>1</sup> with Cy5-labeled lysozyme-binding aptamer (Cy5-LBA)  
(metabion international AG)

5' **Cy5** TTT TTT ATC AGG GCT AAA GAG TGC AGA GTT ACT TAG 3'

### A9. Labeling Procedure

N/A

### A10. Labeling Efficiency

N/A

### B1. Ligand/Non-Fluorescent Binding Partner

Lysozyme-binding aptamer (LBA)

### B2. Molecule Class/Organism

DNA aptamer

### B3. Sequence/Formula

5' ATC AGG GCT AAA GAG TGC AGA GTT ACT TAG 3'

### B4. Purification Strategy/Source

metabion international AG

### B5. Stock Concentration/Stock Buffer

100  $\mu$ M  
ddH<sub>2</sub>O

### B6. Molecular Weight/Extinction Coefficient

11,678 Da  
356,800 M<sup>-1</sup>cm<sup>-1</sup> ( $\epsilon_{260}$ )

<sup>1</sup> NHS-labeling of lysozyme interferes with aptamer binding due to lysines in the binding interface, while lysozyme at high concentrations tends to form fibrils or aggregates. A self-competition assay with unlabeled LBA allows to work with a low concentration of lysozyme while avoiding the need to label lysozyme with a fluorescent dye.

## B7. Serial Dilution Preparation

### Direct binding assay

1. Resuspend 32 µg lysozyme in 112 µL of dilution buffer to obtain a 20 µM solution.
2. Mix 2 µL of 100 µM Cy5-LBA with 98 µL of dilution buffer to obtain 100 µL of a 2 µM Cy5-LBA solution.
3. Mix 4 µL of 2 µM Cy5-LBA with 196 µL of dilution buffer to obtain 200 µL of a 40 nM Cy5-LBA solution.
4. Prepare a PCR-rack with 16 PCR tubes. Transfer 20 µL of the 20 µM lysozyme solution into tube **1**. Then, transfer 10 µL of dilution buffer into tubes **2** to **16**.
5. Prepare a 1:1 serial dilution by transferring 10 µL from tube to tube. Mix carefully by pipetting up and down. Remember to discard 10 µL from tube **16** to get an equal volume of 10 µL for all samples.
6. Add 10 µL of 40 nM Cy5-LBA to each tube from **16** to **1** and mix by pipetting.
7. Incubate for 5 minutes at room temperature in the dark before loading capillaries.

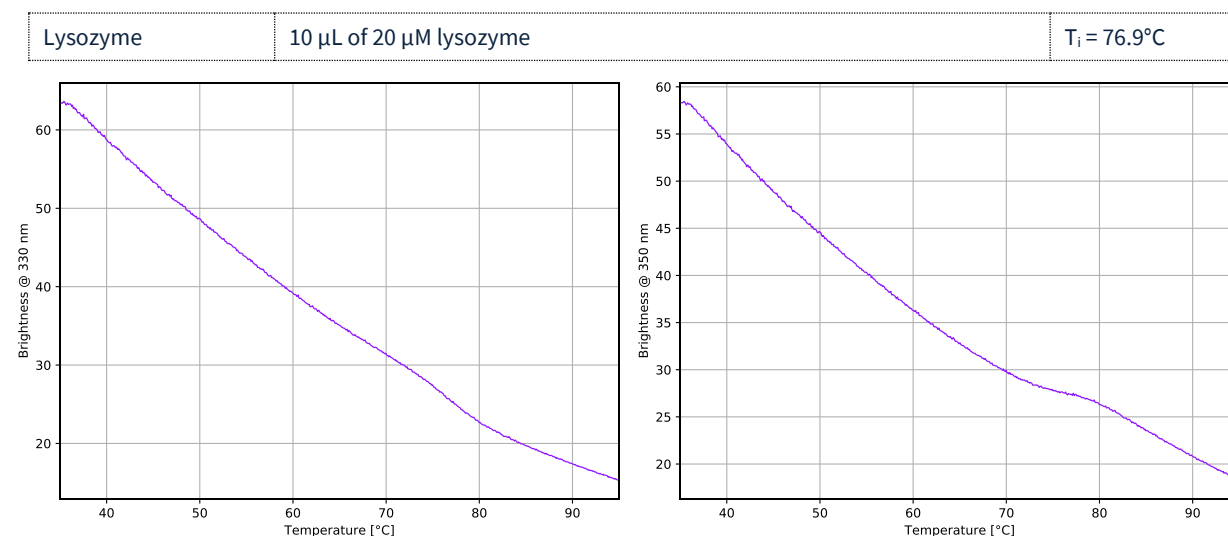
### Self-competition assay

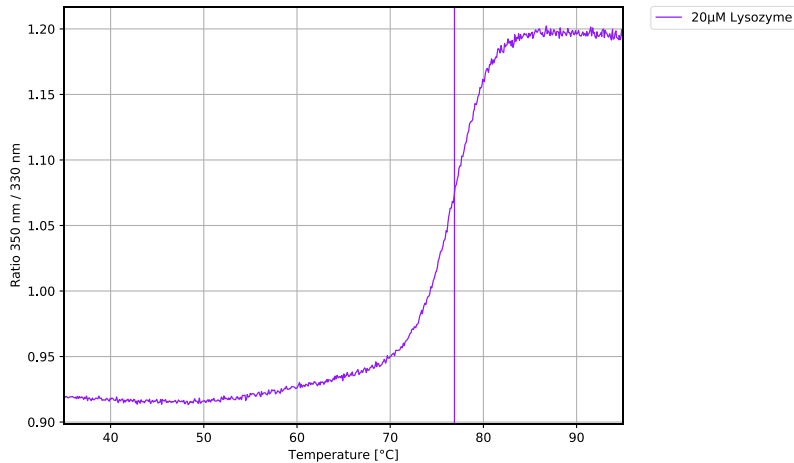
1. Mix 6 µL of 2 µM Cy5-LBA with 194 µL of dilution buffer to obtain 200 µL of a 60 nM Cy5-LBA solution.
2. Prepare a PCR-rack with 16 new PCR tubes. Mix 3.6 µL of a 100 µM LBA solution with 16.4 µL of dilution buffer in tube **1**. Then, transfer 10 µL of dilution buffer into tubes **2** to **16**.
3. Prepare a 1:1 serial dilution by transferring 10 µL from tube to tube. Mix carefully by pipetting up and down. Remember to discard 10 µL from tube **16** to get an equal volume of 10 µL for all samples.
4. Add 10 µL of 60 nM Cy5-LBA to each tube from **16** to **1** and mix by pipetting.
5. Mix 2 µL of 20 µM lysozyme with 18 µL of dilution buffer to obtain 20 µL of a 2 µM lysozyme solution.
6. Mix 6 µL of 2 µM lysozyme with 194 µL of dilution buffer to obtain 200 µL of a 60 nM lysozyme solution.
7. Add 10 µL of 60 nM lysozyme to each tube from **16** to **1** and mix by pipetting.
8. Incubate for 5 minutes at room temperature in the dark before loading capillaries.

## C. Applied Quality Checks

Validation of the structural integrity of lysozyme using Tycho NT.6:

[nanotempertech.com/tycho](https://nanotempertech.com/tycho)





## D1. MST System/Capillaries

Monolith NT.115 Red (NanoTemper Technologies GmbH)

Premium Capillaries Monolith NT.115 (MO-K025, NanoTemper Technologies GmbH)

## D2. MST Software

MO.Control v1.6 (NanoTemper Technologies GmbH)

[nanotempertech.com/monolith-mo-control-software](https://nanotempertech.com/monolith-mo-control-software)

## D3. MST Experiment (Assay Buffer/Concentrations/Temperature/MST Power/Excitation Power)

### Direct binding assay

25 mM Histidine buffer, pH 5.0, 0.01% Pluronic® F-127

20 nM Cy5-LBA | 10 μM – 305 pM lysozyme | 22°C | medium MST power | 20% excitation power

### Self-competition assay

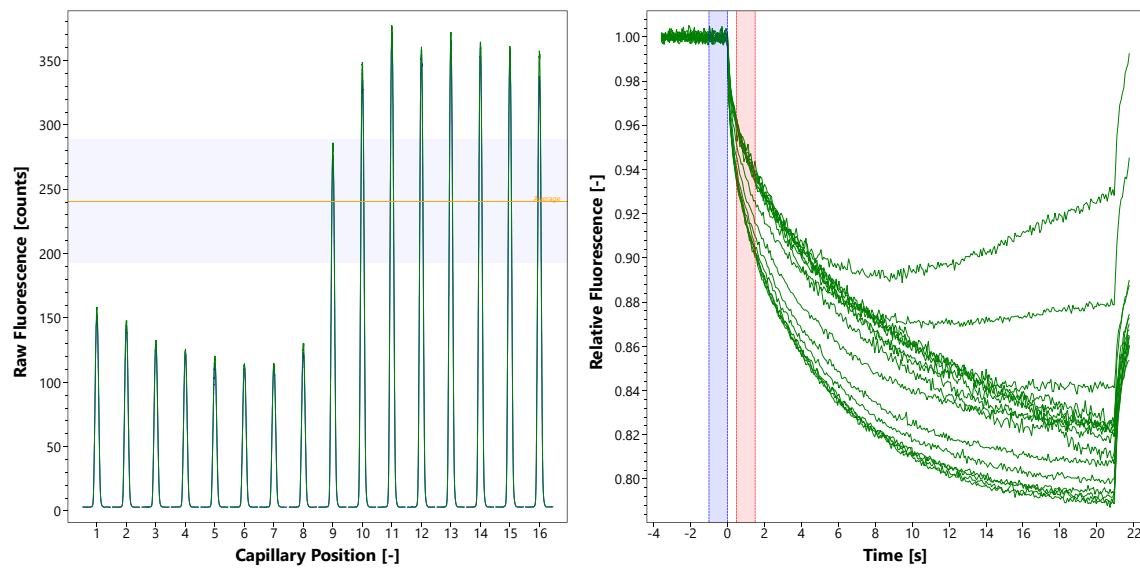
25 mM Histidine buffer, pH 5.0, 0.01% Pluronic® F-127

20 nM lysozyme, 20 nM Cy5-LBA | 6 μM – 183 pM LBA | 22°C | medium MST power | 20% excitation power

## D4. MST Results (Capillary Scan/Time Traces/Dose Response)

### Direct binding assay

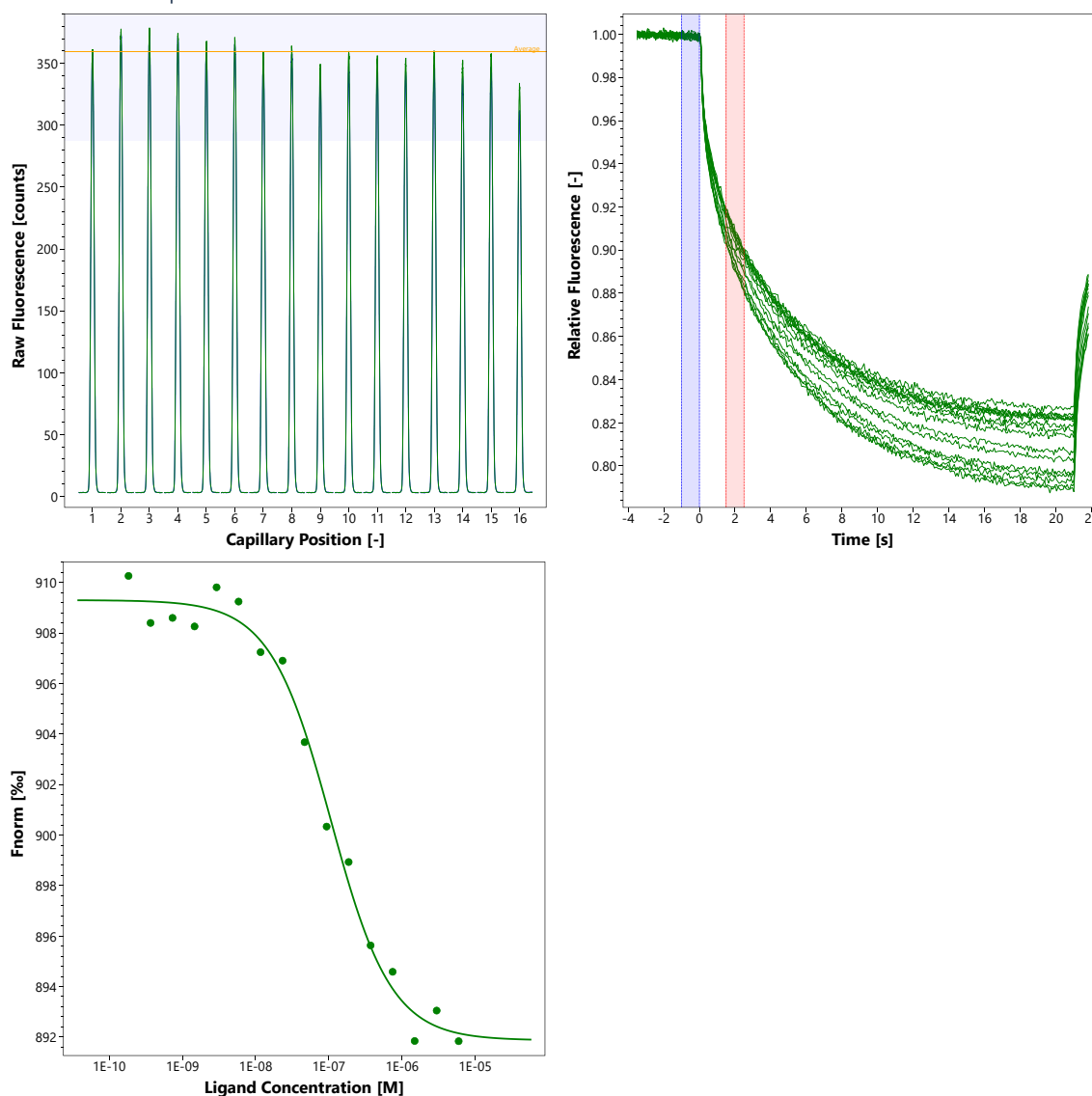
$$K_d = N/A^2$$



<sup>2</sup> Binding cannot be evaluated in the direct binding assay due to strong ligand-induced fluorescence changes that may be caused by lysozyme aggregation or fibrillation at high concentration. Therefore, an intermediate concentration of 20 nM (capillary #10) is chosen to form a complex between Cy5-LBA and lysozyme. Next, unlabeled LBA is added in a self-competition assay format to compete with Cy5-LBA for lysozyme binding.

## Self-competition assay

$EC_{50} = 97.2 \text{ nM}$  |  $K_i = 53.0 \text{ nM}^3$



## D5. Reference Results/Supporting Results

$K_d = 49.5 \text{ nM}$       Frontal analysis continuous microchip electrophoresis (FACMCE)  
[Girardot et al., Journal of Chromatography A, 1218 \(2011\) 4052–4058](#)

## E. Contributors

Andreas Langer<sup>4</sup>

<sup>3</sup> For calculation of  $K_i$ , it was assumed that the affinities of lysozyme for LBA and Cy5-LBA are identical (see also the NanoTemper 'FAQ Competitive Binding Assay').

<sup>4</sup> NanoTemper Technologies GmbH, München, Germany | [nanotempertech.com](http://nanotempertech.com)