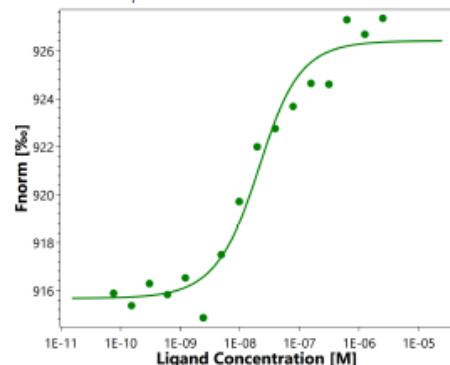


# Supplementary Information

Figure S1: Thermophoresis titration original data  
Green coffee

1.875 mg/ml coffee extract

Dose Response



Response Evaluation: On Time 2.5s

Kd model

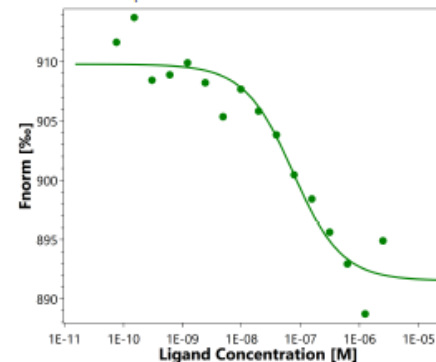
Unbound 915.7  
Bound 926.4  
Kd 13 nM  
TargetConc 15 nM

Response Amplitude: 10.7

Noise: 0.9

Signal to Noise Ratio: 12.3

Dose Response



Response Evaluation: On Time 20s

Kd model

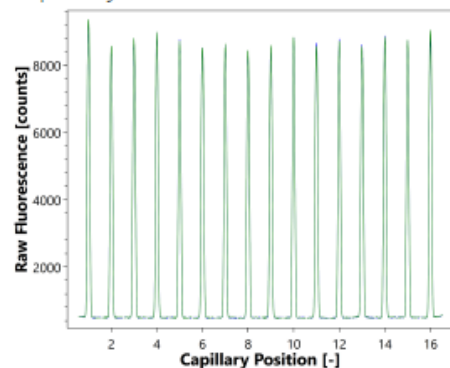
Unbound 909.8  
Bound 891.5  
Kd 67.5 nM  
TargetConc 15 nM

Response Amplitude: 18.2

Noise: 2.0

Signal to Noise Ratio: 9.2

Capillary Scans



Initial Fluorescence:

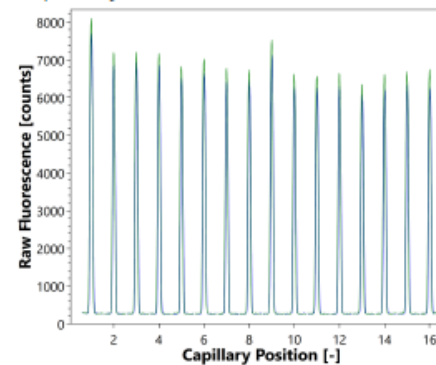
Average: 8695 counts

Variation: ±7.1%

No adsorption

No Ligand Induced  
Fluorescence Change

Capillary Scans



Initial Fluorescence:

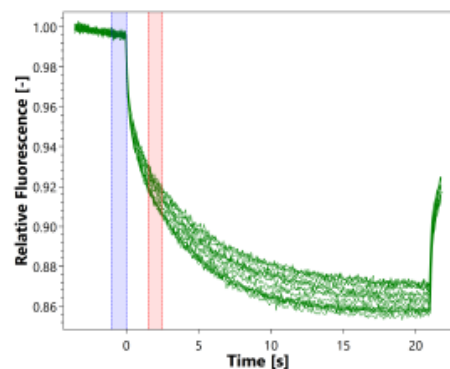
Average: 6899 counts

Variation: ±17.1%

Adsorption

No Ligand Induced  
Fluorescence Change

MST Traces



Cursor positions:

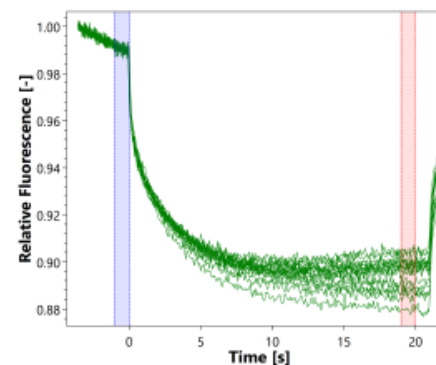
Cold Region: -1s - 0s

Hot Region: 1.5s - 2.5s

No Aggregation

No Ligand Induced  
Photobleaching Rate  
Change

MST Traces



Cursor positions:

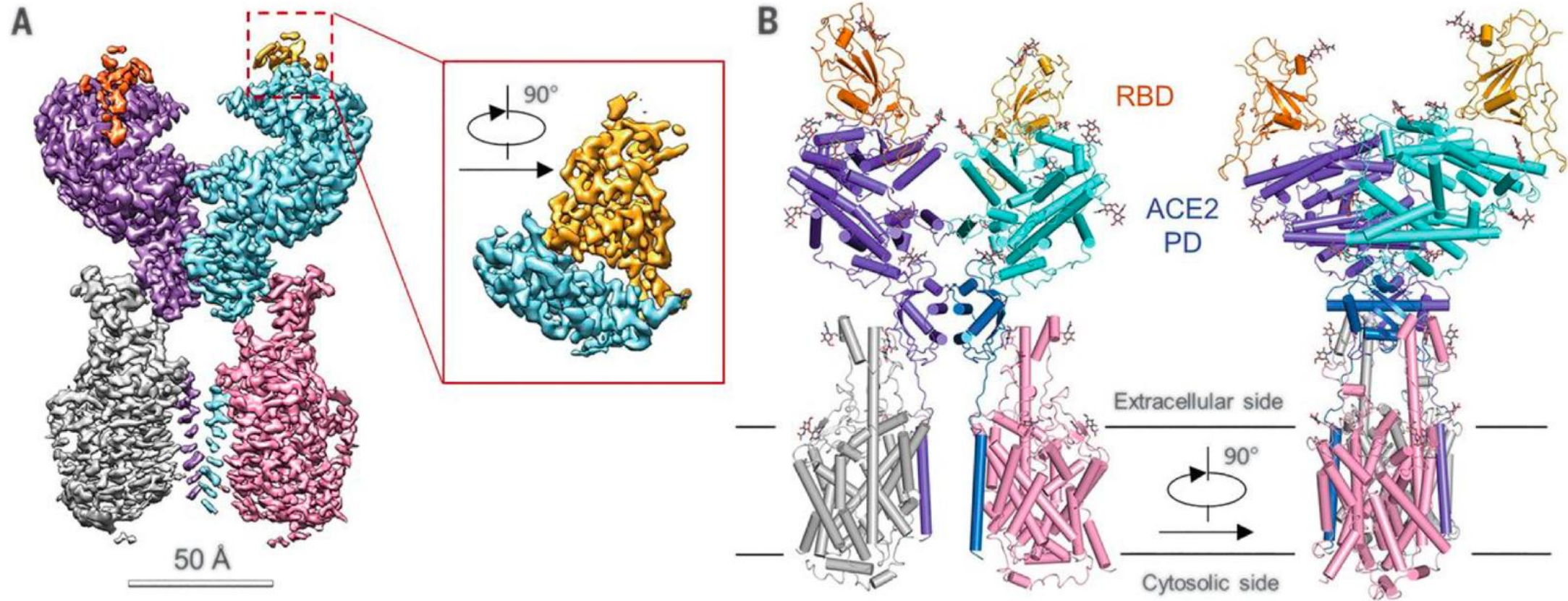
Cold Region: -1s - 0s

Hot Region: 19s - 20s

No Aggregation

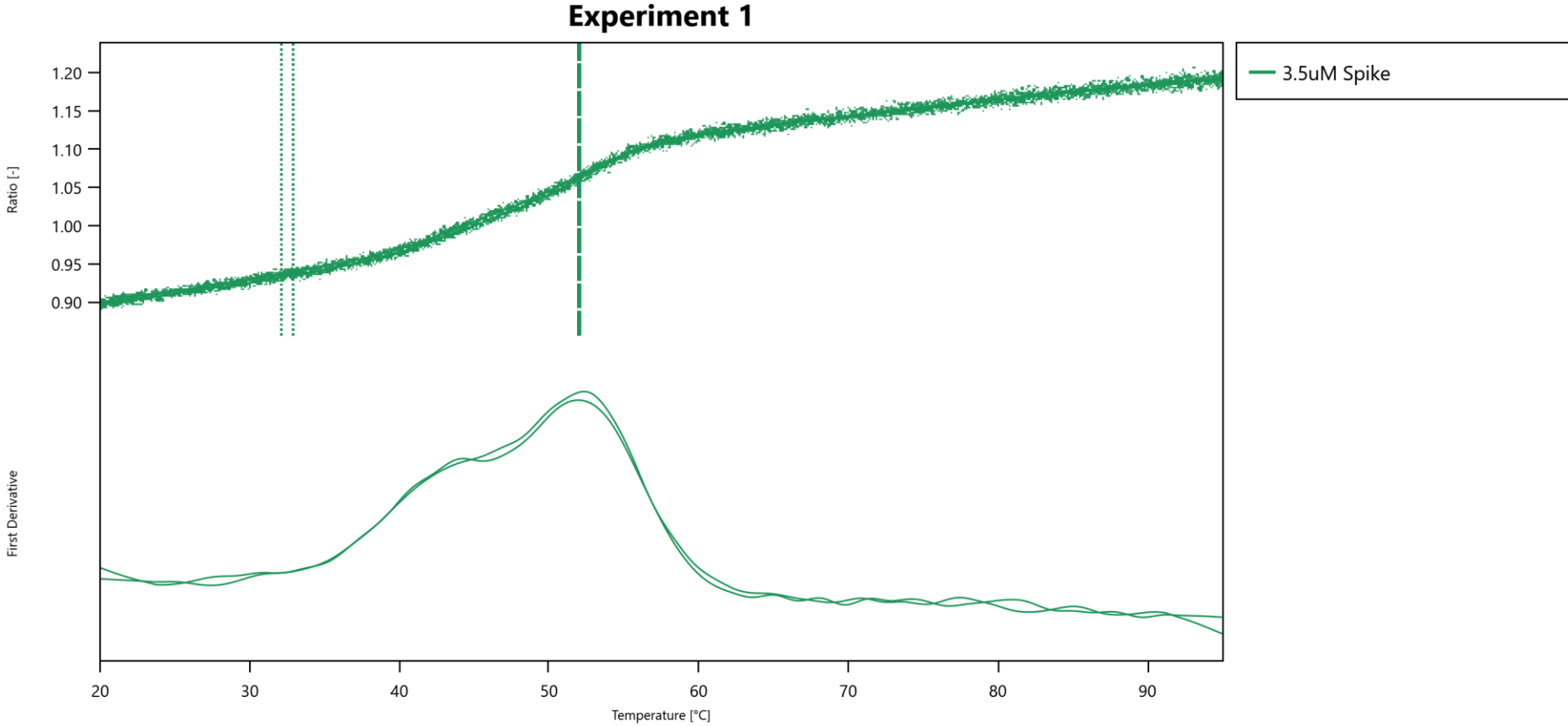
No Ligand Induced  
Photobleaching Rate  
Change

S2: Published structure of Spike protein ACE-2 complex



**Figure 1: Overall structure of the RBD-ACE2-B0AT1 complex. (A) Cryo-EM map of the RBD-ACE2-B0AT1 complex. (B) The overall structure of the RBD-ACE2-B0AT1 complex. The figure is taken from Yan et al. (2020).**

# S3: Thermal folding and unfolding of S-üprotein by nano-DSF



## S4: additional nano DSF curves with ACE-2 protein

