



#### **JEDI Program/JDI01**

#### **Compound Screening for SARS-CoV-2 Proteins Using MST/Dianthus**

**SARS-CoV-2 Spike protein** 

TRIC (Dianthus), MST

June 18, 2021



#### **Status**



#### TRIC:

- Assay optimization was performed on the Dianthus for Spike using ACE2 as control.
  - ➤ Binding of Fc-tagged ACE2 was observed with low nM affinity, when proteins were prepared with dialysis. However, aggregation was also observed and could not be prevented by different detergents or PEG-8000.
  - ➤ No binding of untagged ACE2 was observed.

#### Labelled MST:

- In parallel, assay optimization was performed on the Monolith NT.115.
  - ➤ In contrast to previous measurements, no binding of untagged ACE2 was observed.
  - ➤ However, binding of Fc-tagged ACE2 was observed with low nM affinity, when proteins were prepared with dialysis.
- ➤ Overall, labelled MST (NT.115 instrument) is feasible with Spike using Fc-tagged ACE2 as positive control and preparing proteins via dialysis (not microspin columns).
- > TRIC (Dianthus) assay optimization is very challenging and would require more efforts and protein.



## TRIC (Dianthus)

SARS-CoV-2 Spike (DYG4)

#### TRIC Assay Conditions

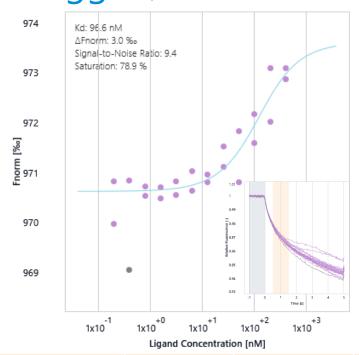


Fluor. Molecule	50 nM S (SARS-CoV-2) (DYG4, PD14787-1)									
Fluorophore	25 nM RED-tris-NTA 2 <sup>nd</sup> gen.									
	100 nM protein / 50 nM dye	100 nM protein / 50 nM dye								
<b>Labelling conditions</b>	Incubation time: 30 min									
	Centrifugation: 10 min at 15000g									
Instrument	Dianthus NT.23PicoDuo									
	LED Power: 14 % (nano detector)									
<b>Measurement parameter</b>	TRIC settings: 1 - 5 - 1 (s) (initial fluorescence	e – MST on time – back-diffusion)								
	Duplicates									
Assay buffer	20 mM Hepes pH 7.5, 150 mM NaCl, 0.05% Twe	en, 0.1% PEG-8k								
	ACE2 Fc-tagged	DYF1 (PD13357-1)	400 – 0.20 nM (12 conc.)							
Tituent	ACE2 untagged DYF3/4 (PD14701-1 / PD15147-1) 500 – 0.24 nM (12 conc									
Titrant	Preparation 1x with Micro Bio-Spin P-6 Gel									
	Columns and 1x with dialysis tubes									

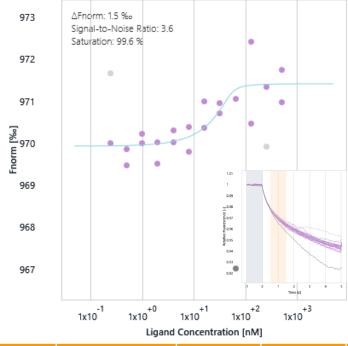


## RED-tris-NTA 2<sup>nd</sup> gen. labelled SARS-CoV-2 Spike vs. ACE2 (Fc-tagged, DYF1 and untagged, DYF3)





ACE2 Fc-tagged



ACE2 untagged

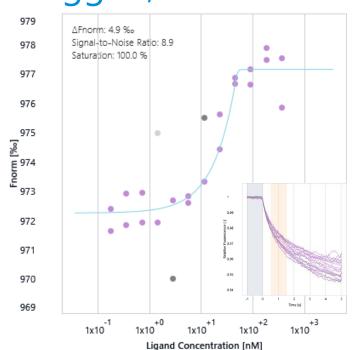
	Fluorophore	Fluor. Molecule	Titrant	K <sub>D</sub> [M]	Lower confidence [M]	Upper confidence [M]	ΔFnorm [‰]	Signal / Noise	TRIC On [s]	Comment
F	RED-tris-NTA 2 <sup>nd</sup> gen.	DYG4	ACE2 Fc-tagged	9.7E-08	2.9E-08	3.2E-07	3.0	9.4	1.5	Micro Bio-Spin P-6 Gel Columns
F	RED-tris-NTA 2 <sup>nd</sup> gen.	DYG4	ACE2 untagged	-	-	-	-	-	1.5	Micro Bio-Spin P-6 Gel Columns, No binding

- RED-tris-NTA 2<sup>nd</sup> gen. labelled Spike binds ACE2 Fc-tagged with a determined K<sub>D</sub> of 97 nM. However, aggregation was observed at later TRIC on time.
- RED-tris-NTA 2<sup>nd</sup> gen. labelled Spike does not bind ACE2 untagged. Aggregation was observed at later TRIC on time.

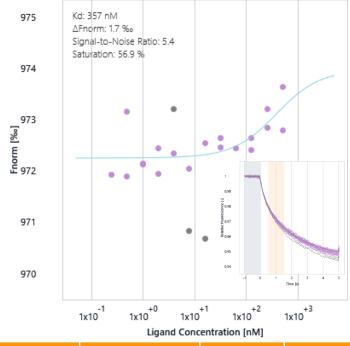


## RED-tris-NTA 2<sup>nd</sup> gen. labelled SARS-CoV-2 Spike vs. ACE2 (Fc-tagged, DYF1 and untagged, DYF3)





ACE2 Fc-tagged



ACE2 untagged

Fluorophore	Fluor. Molecule	Titrant	K <sub>D</sub> [M]	Lower confidence [M]	Upper confidence [M]	ΔFnorm [‰]	Signal / Noise	TRIC On [s]	Comment
RED-tris-NTA 2 <sup>nd</sup> gen.	DYG4	ACE2 Fc-tagged	< 1.0E-9	-	-	-	8.9	1.5	Dialysis tube, strong binder
RED-tris-NTA 2 <sup>nd</sup> gen.	DYG4	ACE2 untagged	-	-	-	-	-	1.5	Dialysis tube, No binding

- RED-tris-NTA  $2^{nd}$  gen. labelled Spike binds ACE2 Fc-tagged with a determined  $K_D < 1$  nM. However, aggregation was observed at a later TRIC on time.
- RED-tris-NTA 2<sup>nd</sup> gen. labelled Spike does not bind ACE2 untagged.



### TRIC Assay Conditions

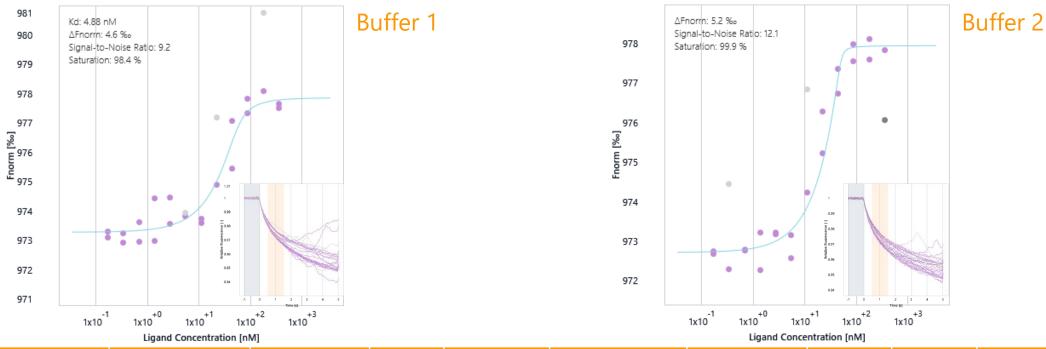


Fluor. Molecule	50 nM S (SARS-CoV-2) (DYG4, PD14787-1)								
Fluorophore	25 nM RED-tris-NTA 2 <sup>nd</sup> gen.	25 nM RED-tris-NTA 2 <sup>nd</sup> gen.							
	100 nM protein / 50 nM dye								
<b>Labelling conditions</b>	Incubation time: 30 min								
	Centrifugation: 10 min at 1500	00g							
Instrument	Dianthus NT.23PicoDuo								
	LED Power: 12 % (nano detector)								
<b>Measurement parameter</b>	TRIC settings: 1 - 5 - 1 (s)	(initial fluorescence – MST on	time – back-diffusion)						
	Duplicates								
Assay buffer	Buffer 1: 20 mM Hepes pH 7.5	5, 150 mM NaCl, 0.05% Pluron	ic						
Assay buffer	Buffer 2: 20 mM Hepes pH 7.5	Buffer 2: 20 mM Hepes pH 7.5, 150 mM NaCl, 0.05% Pluronic, 0.1% PEG-8k							
Titrant	ACE2 Fc-tagged	DYF1 (PD13357-1)	400 – 0.20 nM (12 conc.)						
Titialit	ACE2 untagged	DYF4 (PD15147-1)	500 – 0.24 nM (12 conc.)						



## RED-tris-NTA 2<sup>nd</sup> gen. labelled SARS-CoV-2 Spike vs. ACE2 Fc-tagged (DYF1)





Fluorophore	Fluor. Molecule	Titrant	K <sub>D</sub> [M]	Lower confidence [M]	Upper confidence [M]	ΔFnorm [‰]	Signal / Noise	TRIC On [s]	Comment
RED-tris-NTA 2 <sup>nd</sup> gen.	DYG4	ACE2 Fc-tagged	4.9E-09	7.3E-10	3.3E-0	4.6	9.2	1.5	Dialysis tube
RED-tris-NTA 2 <sup>nd</sup> gen.	DYG4	ACE2 Fc-tagged	< 1.0E-09	-	-	-	12.1	1.5	Dialysis tube, stong binder

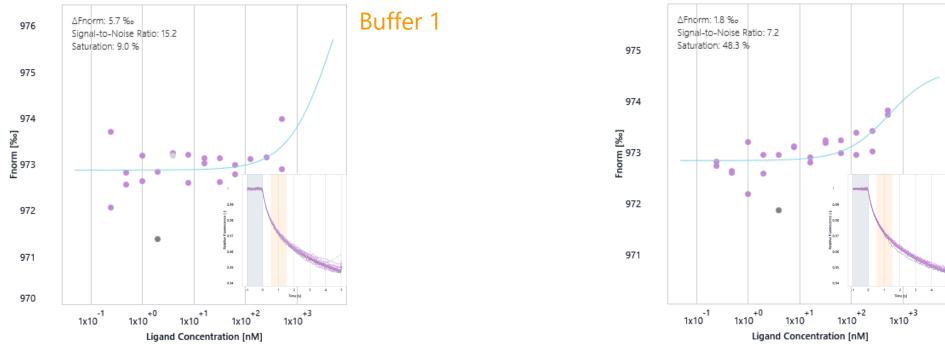
• RED-tris-NTA  $2^{nd}$  gen. labelled Spike binds ACE2 Fc-tagged with a determined  $K_D$  of 4.9 nM in buffer 1 and with a determined  $K_D$  < 1 nM in buffer 2. However, aggregation was observed at later TRIC on time in both buffers.



### RED-tris-NTA 2<sup>nd</sup> gen. labelled SARS-CoV-2 Spike vs. ACE2 untagged (DYF4)



**Buffer 2** 



						-3					
Flu	ıorophore	Fluor. Molecule	Titrant	K <sub>D</sub> [M]	Lower confidence [M]	Upper confidence [M]	ΔFnorm [‰]	Signal / Noise	TRIC On [s]	Comment	
RED-tri	s-NTA 2 <sup>nd</sup> gen.	DYG4	ACE2 untagged	-	-	-	-	-	1.5	Dialysis tube, no binding	
RED-tri	s-NTA 2 <sup>nd</sup> gen.	DYG4	ACE2 untagged	-	-	-	-	-	1.5	Dialysis tube, no binding	

 RED-tris-NTA 2<sup>nd</sup> gen. labelled Spike does not bind ACE2 untagged in buffer 1 or buffer 2. In addition, aggregation was observed at later TRIC on time.



### Labelled MST

SARS-CoV-2 Spike (DYG4)

### MST labelled assay conditions

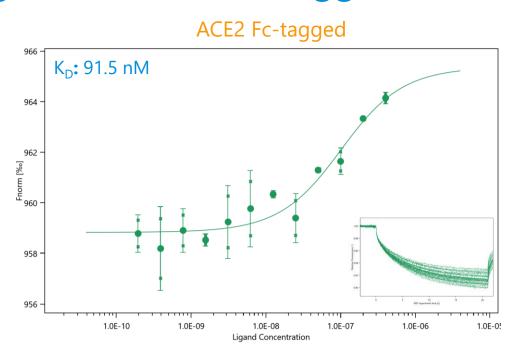


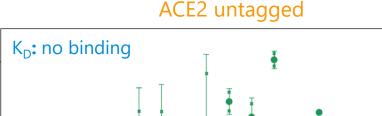
Fluor. Molecule	50 nM S (SARS-CoV-2) (DYG4, PD14787-	50 nM S (SARS-CoV-2) (DYG4, PD14787-1)								
Fluorophore	25 nM RED-tris-NTA 2 <sup>nd</sup> gen.									
	100 nM protein / 50 nM dye									
<b>Labelling conditions</b>	Incubation time: 30 min									
	Centrifugation: 10 min at 15000g									
Instrument	Monolith NT.115 (02)									
Capillary type	Monolith™ NT.115 Series MST Premium	Coated Capillaries								
	LED Power: 30 %	LED Power: 30 %								
Measurement	MST Power: 40 %									
parameter	MST settings: 3 – 15 – 1 (s) (initial flu	orescence – MST on time – back-diff	usion)							
	Duplicate									
Assay buffer	20 mM Hepes pH 7.5, 150 mM NaCl, 0.0	5% Tween, 0.1% PEG-8k								
	ACE2 Fc-tagged	DYF1 (PD13357-1)	400 – 0.20 nM (12 conc.)							
The same	ACE2 untagged DYF3/4 (PD14701-1 / PD15147-1) 500 – 0.24 nM (12 conc.)									
Titrant	Preparation 1x with Micro Bio-Spin P-6									
	Gel Columns and 1x with dialysis tubes									



## RED-tris-NTA 2<sup>nd</sup> gen. labelled SARS-CoV-2 Spike vs. ACE2 (Fc-tagged, DYF1 and untagged, DYF3)







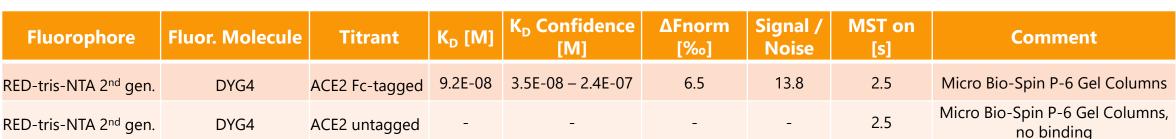
1.0E-08

Ligand Concentration

1.0E-07

1.0E-06

1.0E-05



1.0E-10

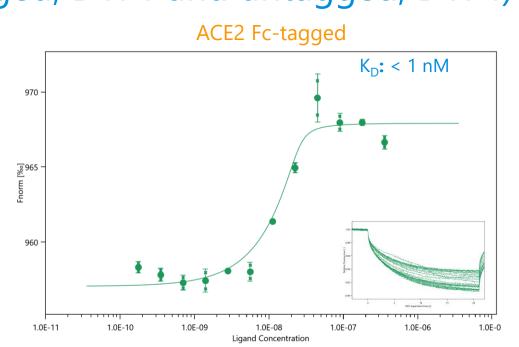
1.0E-09

- RED-tris-NTA 2<sup>nd</sup> gen. labelled Spike binds ACE2 Fc-tagged with a determined K<sub>D</sub> of 91.5 nM.
- RED-tris-NTA 2<sup>nd</sup> gen. labelled Spike does not bind ACE2 untagged.

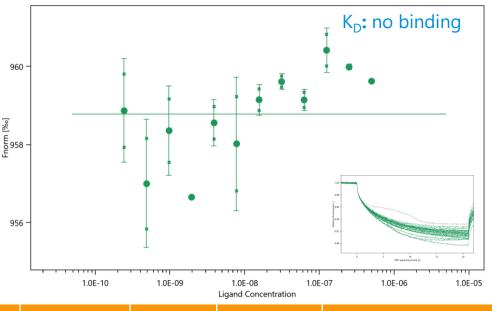


## RED-tris-NTA 2<sup>nd</sup> gen. labelled SARS-CoV-2 Spike vs. ACE2 (Fc-tagged, DYF1 and untagged, DYF4)





#### ACE2 untagged



Fluorophore	Fluor. Molecule	Titrant	K <sub>D</sub> [M]	K <sub>D</sub> Confidence [M]	ΔFnorm [‰]	Signal / Noise	MST on [s]	Comment
RED-tris-NTA 2 <sup>nd</sup> gen.	DYG4	ACE2 Fc-tagged	< 1.0E-09	2.4E-11 – 2.2E-08	10.8	11.3	2.5	Dialysis tube, saturation curve, strong binder
RED-tris-NTA 2 <sup>nd</sup> gen.	DYG4	ACE2 untagged	-	-	-	-	2.5	Dialysis tube, no binding

- RED-tris-NTA 2<sup>nd</sup> gen. labelled Spike binds ACE2 Fc-tagged with a determined  $K_D < 1$  nM. Due to the high protein concentration in the assay setup, the  $K_D$  cannot be determined accurately.
- RED-tris-NTA 2<sup>nd</sup> gen. labelled Spike does not bind ACE2 untagged.



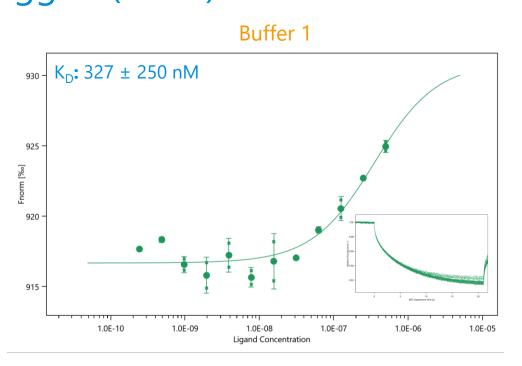
### MST labelled assay conditions

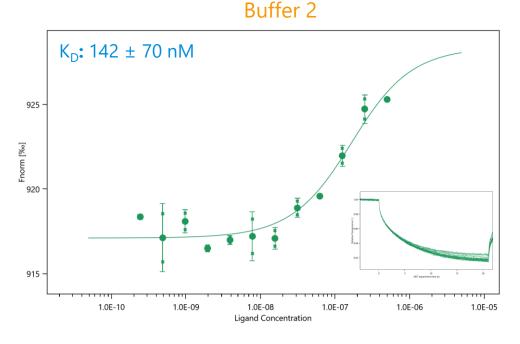


Fluor. Molecule	50 nM S (SARS-CoV-2) (DY	G4, PD14787-1)						
Fluorophore	25 nM RED-tris-NTA 2 <sup>nd</sup> gen.							
	100 nM protein / 50 nM dy	⁄e						
<b>Labelling conditions</b>	Incubation time: 30 min							
	Centrifugation: 10 min at 1	5000g						
Instrument	Monolith NT.115 (02)							
Capillary type	Monolith™ NT.115 Series N	MST Premium Coated Capil	laries					
	LED Power: 40 %							
Measurement	MST Power: 40 %							
parameter	MST settings: 3 – 15 – 1 (s)	(initial fluorescence – N	MST on time – back-diffusion)					
	Duplicate							
Assay buffer	Buffer 1: 20 mM Hepes pH	7.5, 150 mM NaCl, 0.05% F	Pluronic					
Assay buller	Buffer 2: 20 mM Hepes pH	7.5, 150 mM NaCl, 0.05% F	Pluronic, 0.1% PEG-8k					
Titrant	ACE2 untagged	DYF4 (PD15147-1)	500 – 0.24 nM (12 conc.)					

# RED-tris-NTA 2<sup>nd</sup> gen. labelled SARS-CoV-2 Spike vs. ACE2 untagged (DYF4)







Fluorophore	Fluor. Molecule	Titrant	K <sub>D</sub> [M]	K <sub>D</sub> Confidence [M]	ΔFnorm [‰]	Signal / Noise	MST on [s]	Comment
RED-tris-NTA 2 <sup>nd</sup> gen.	DYG4	ACE2 untagged	3.3E-07	2.5E-07	14.2	17.3	20	Buffer 1
RED-tris-NTA 2 <sup>nd</sup> gen.	DYG4	ACE2 untagged	1.4E-07	7.0E-08	11.3	16.8	20	Buffer 2

RED-tris-NTA 2<sup>nd</sup> gen. labelled Spike binds ACE2 untagged with a determined K<sub>D</sub> of 327 nM in buffer 1 and 142 nM in buffer 2.

#### Next steps



- Nanobody and Spike protein tests at Pasteur (proteins will be shipped next week).
  Depending on the outcome, test/optimize labelled MST with nanobodies as positive control
- Potentially: test Spike protein from Pasteur (if it can be supplied)
- Assay setup is ready with Spike and Fc-tagged ACE2 (positive control) using labelled MST (NT.115) → discuss if MST is an option (not covered by current contract, additional Spike required)
- Alternatively, further assay optimization using the Dianthus, which we estimate to be very challenging for this protein target







**Crelux GmbH** a WuXi AppTec company

Dr. Saskia Villinger Senior Scientist and Deputy Head of Biophysics & Screening Am Klopferspitz 19a 82152 Martinsried Germany

Saskia.Villinger@wuxiapptec.com www.crelux.com www.wuxiapptec.com

