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## Introduction

- Optimer reagents were developed to the SARS-CoV-2 virus to address the COVID-19 pandemic.
- As the pandemic has evolved mutations in SARS-CoV-2 have resulted in the emergence of variant strains with prevalent and virulent strains showing mutations in the S protein.
- To ensure accurate diagnostics all tests should recognise both the WT and subsequent strains of SARS-CoV-2.



## Methods

- Optimer reagents were developed to the S1 and S2 subunits of the WT SARS-CoV-2 protein.
- SARS-CoV-2 variant S proteins from WHO variants of concern and irradiated virus particles were assessed for Optimer binding via biolayer interferometry.

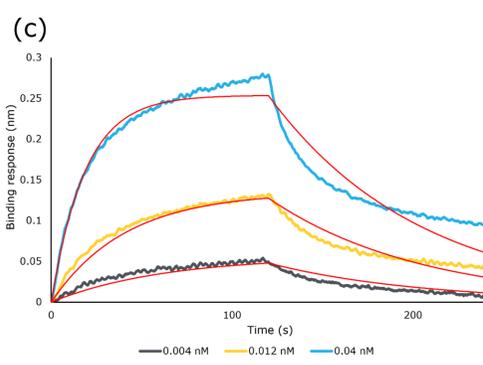
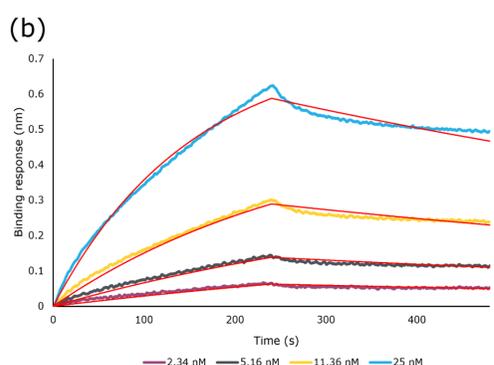
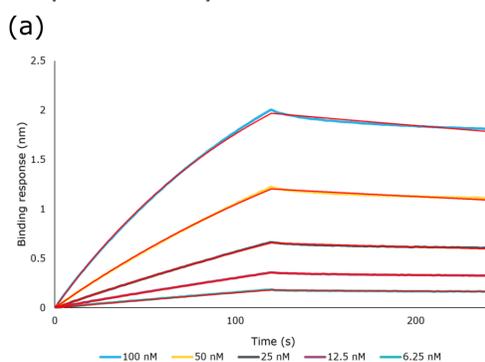
Mutation	Variant	Sample Type Analysed		
		S1 Protein	Virus Particles	
			S1 Optimer	S2 Optimer
WT	WT	✓	✓	✓
B.1.1.7	Alpha	✓	✓	✓
B.1.351	Beta	✓	✓	✓
P.1	Gamma	✓		
B.1.617.2	Delta	✓		
B.1.1.529	Omicron	✓		

**Table 1: The SARS-CoV-2 S protein variant forms analyzed for Optimer binding performance.** Seven different variants of the SARS-CoV-2 S protein were investigated representing examples of the most prevalent and virulent mutations internationally.

## Results

### Optimers bind the SARS-CoV-2 S protein variants

- Optimer reagents developed to the WT SARS-CoV-2 S1 protein subunit are able to bind each of the mutant SARS-CoV-2 strain S proteins by BLI.



**Figure 1: SARS-CoV-2 S1 Optimers bind S protein variants of concern by BLI.** BLI streptavidin probes were coated with 20 nM biotinylated Optimer, washed and interaction measured in 80  $\mu$ L sample volume over the S protein concentration range shown. Exemplar plots are shown for (a) WT (b) B.1.617.2 (c) B.1.1.529 S1 proteins.

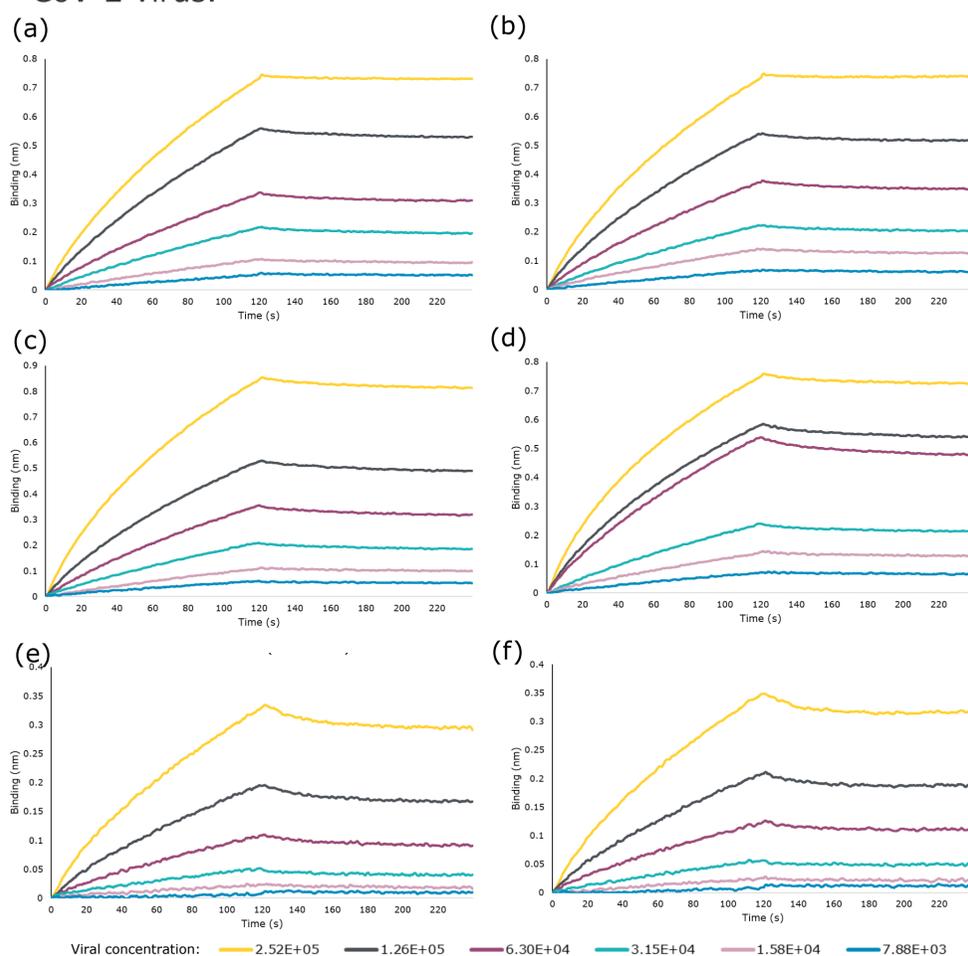
### Comparable binding for all SARS-CoV-2 variants

Mutation	Variant	$K_D$ (nM)
WT	WT	$10.7 \pm 0.07$
B.1.1.7	Alpha	$7.16 \pm 0.13$
B.1.351	Beta	$5.24 \pm 0.09$
P.1	Gamma	$15.4 \pm 0.14$
B.1.617.2	Delta	$5.68 \pm 0.04$
B.1.1.529	Omicron	$10.85 \pm 0.09$

**Table 2: Affinity of the S1 Optimer to the SARS-CoV-2 variants show similar binding kinetics to the WT and all S protein variants of concern.** Values determined by BLI analysis of Optimer-coated probes monitored across concentration gradients of each of the SARS-CoV-2 variant S proteins.

### Optimers bind SARS-CoV-2 irradiated virus particles

- Both S1 and S2 Optimer reagents bind to irradiated virus particles of SARS-CoV-2.
- Optimer reagents show similar binding performance to the B.1.1.7 and B.1.351 SARS-CoV-2 variants as to the WT SARS-CoV-2 virus.



**Figure 2: SARS-CoV-2 S1 and S2 Optimers bind irradiated SARS-CoV-2 virus by BLI.** WT SARS-CoV-2 binding (a) S1 Optimer (b) S2 Optimer. B.1.1.7 SARS-CoV-2 binding (c) S1 Optimer (d) S2 Optimer. B.1.1351 binding (e) S1 Optimer (f) S2 Optimer. BLI streptavidin probes were coated with 20 nM biotinylated Optimer, washed and interaction measured in 80  $\mu$ L of in buffer over the viral concentration range shown.

## Summary

- The Optimer platform can be used to reliably develop research and diagnostic tools to support ongoing disease monitoring.
- Comparable binding of the SARS-CoV-2 S1 and S2 Optimer reagents suggest that the Optimer epitope is not near the mutating site.
- Comparable performance for all variants simplifies assay optimization and maximises the likelihood of ongoing detection of COVID-19 infections.
- Optimer performance is maintained with regards to the SARS-CoV-2 variants for reliable research and diagnostic performance.