Base Pair
BIOTECHNOLOGIES

APTAMER INFORMATION
CMVgB_40

Description:

- *Identifiers*: CmvgB_40
- *Number of DNA nucleotides*: 32 bases
- *Target for selection*: **CMV gB**

Aptamer was selected from a randomized 32-mer library against the CMV gB molecule. Proprietary methods were then used to select the aptamer.

Aptamer folding instruction before use:

Once the aptamer is in its working concentration, it needs to be heated to 85-90 °C for 2 minutes, and then cooled to room temperature before use.

1b. Validation data with Peptide #3 by MST (Microscale Thermophoresis) method:

- *Buffer used for validation:* 1X PBS, pH = 7.4, 1 mM $MgCl_2$
- *Average K_d* = 17.2± 2.1 nM

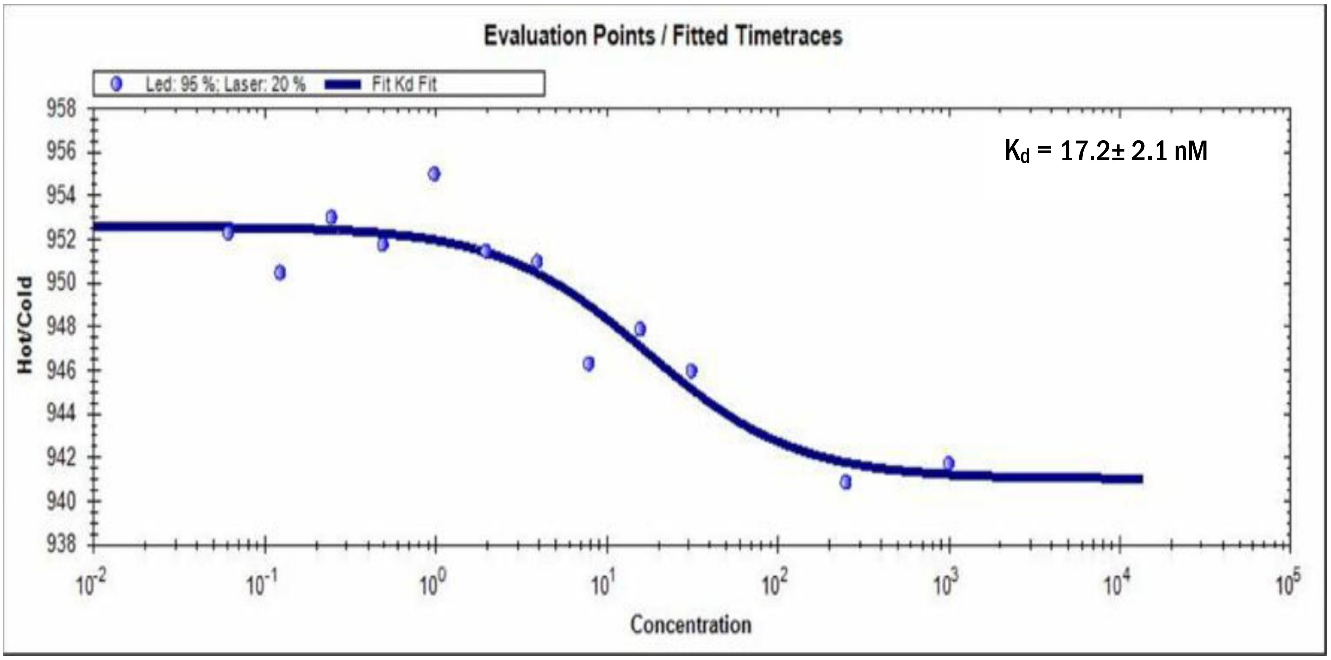

Figure 1. Aptamer-CMV gB binding. The thermophoresis is plotted versus the titrated CMV gB concentration.

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