

APTAMER INFORMATION

MRSA Round 5 aptamer2 #820

1a. Description:

- ***Identifiers:*** MRSA Round 5 aptamer2 (Oligo#820)
- ***Number of DNA nucleotides:*** 32 bases (without primers); 70 bases (with primers)
- ***Molecular weight (including primers and 3'-bioTEG):*** 22,058.6 g/ mol
- ***Target for selection:*** MRSA protein- Recombinant *Staphylococcus aureus* PBP2a, Ray Biotech [Cat # 230-00051].

Aptamer was selected from a randomized 32-mer library against MRSA protein. 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 MRSA protein by BLI (Bio-Layer Interferometry) method:

- ***Immobilized Ligand:*** MRSA Round 5 aptamer 2_ Oligo #820 (with primers and 3'-bioTEG)
- ***Analyte:*** MRSA protein
- ***Buffer used for validation:*** 1 X Kinetics buffer (1X PBS, pH = 7.4, 0.01% BSA, 0.002% Tween20),

1c. Kinetics Screening Assay using Streptavidin Biosensors :

We validate the binding data by,

- ***Single reference data:*** All curves are referenced to a sensor dipped in buffer alone (no protein) (see Figures 1, 2 and Table 1).

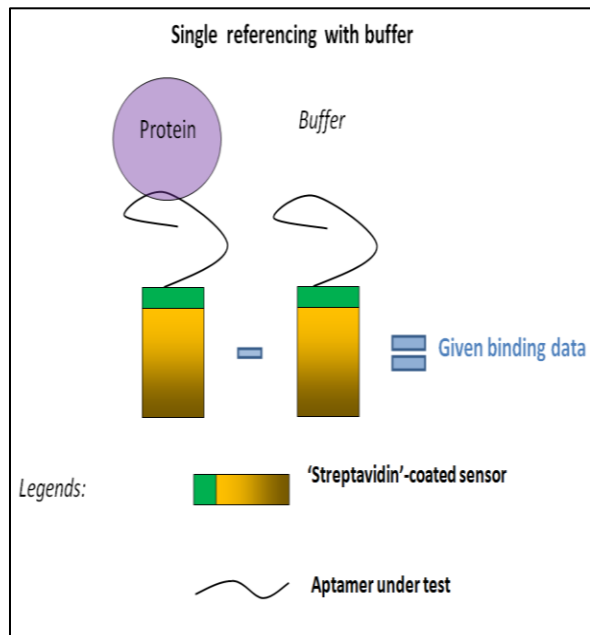


Figure 1. Diagram showing aptamer: protein binding validation scheme.

1d. Single reference data:

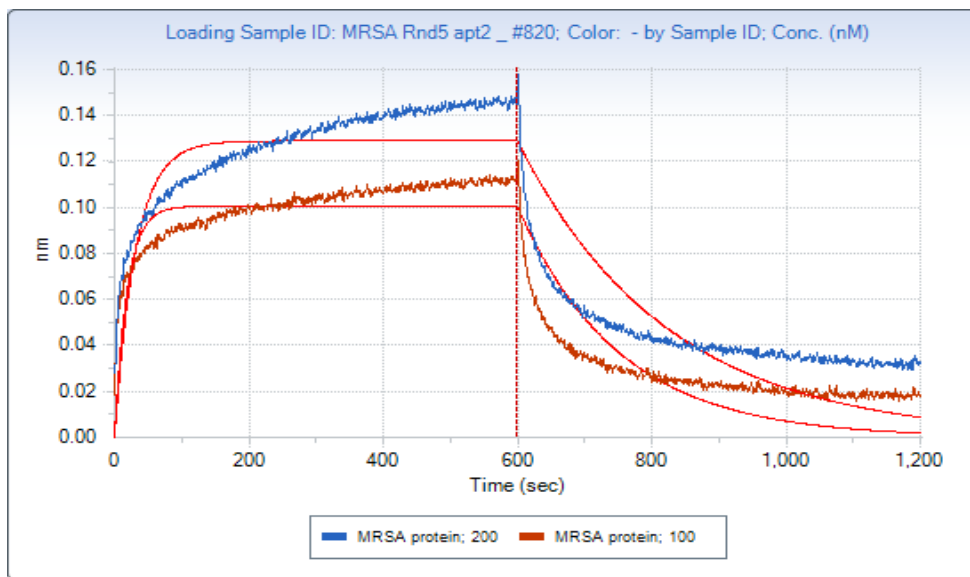


Figure 2. Association and dissociation graph of 1:1 fitting model of MRSA aptamer #820 (biotinylated) to MRSA protein concentration 200 and 100 nM.



Table 1. K_d , R^2 and χ^2 values by Local fitting for Referenced data. **Avg $K_d = 23.5$ nM**

Immobilized Aptamer	Analyte	Conc. (nM)	Response	K_d (M)	Full χ^2	Full R^2
MRSA Rnd5 apt2_#820	MRSA protein	200	0.1454	3.28E-08	0.303125	0.877093
MRSA Rnd5 apt2_#820	MRSA protein	100	0.1122	1.42E-08	0.158173	0.91171

