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BIOTECHNOLOGIES

# APTAMER INFORMATION
# Hsp27 aptamer E05 # 481

## 1a. Description:

- *Identifiers*: E05 (Oligo#481)
- *Number of DNA nucleotides*: 40 bases (without 3′-6T); 46 bases (with 3′-6T)
- *Molecular weight (including 3′-6T and biotin):* 14,747.7 g/mol
- *Target for selection:* **Heat Shock Protein 27 (hsp27), Human Recombinant [Proscpec, cat# HSP-027]**

Aptamer was selected from a randomized 40-mer library against hsp27 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 hsp27 protein by BLI (Bio-Layer Interferometry) method:

- *Immobilized Ligand:* hsp27 aptamer #481 with 3′-6T and biotin
- *Analyte:* hsp27 protein
- *Buffer used for validation:* 20 mM Tris, 100 mM NaCl, 0.005% Tween20, in nuclease free water, pH 7.4

## 1c. Kinetics Screening Assay using Streptavidin Biosensors:

We validate the binding data by:

- Referenced data: All curves are referenced to a quenched sensor dipped in buffer alone (no analyte) (see Figure 1 and Table 1).



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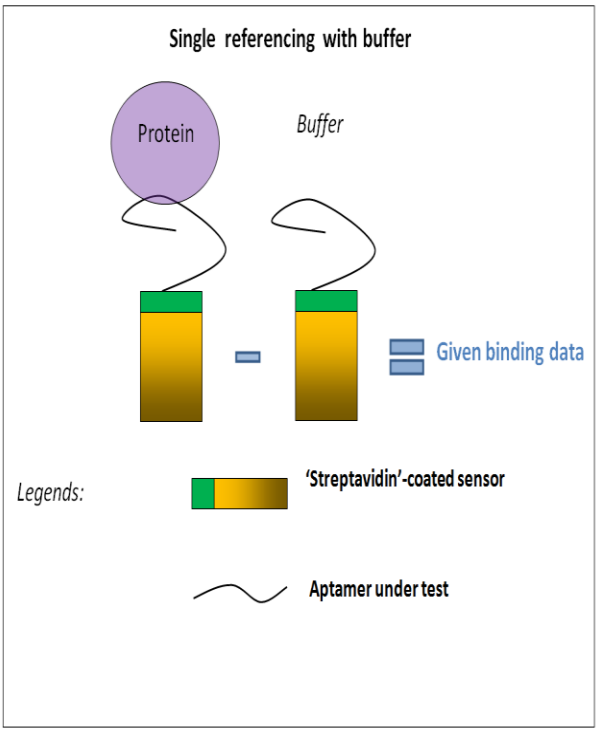


**Figure 1.** Diagram showing aptamer: protein binding validation scheme.

## 1d. Referenced data:

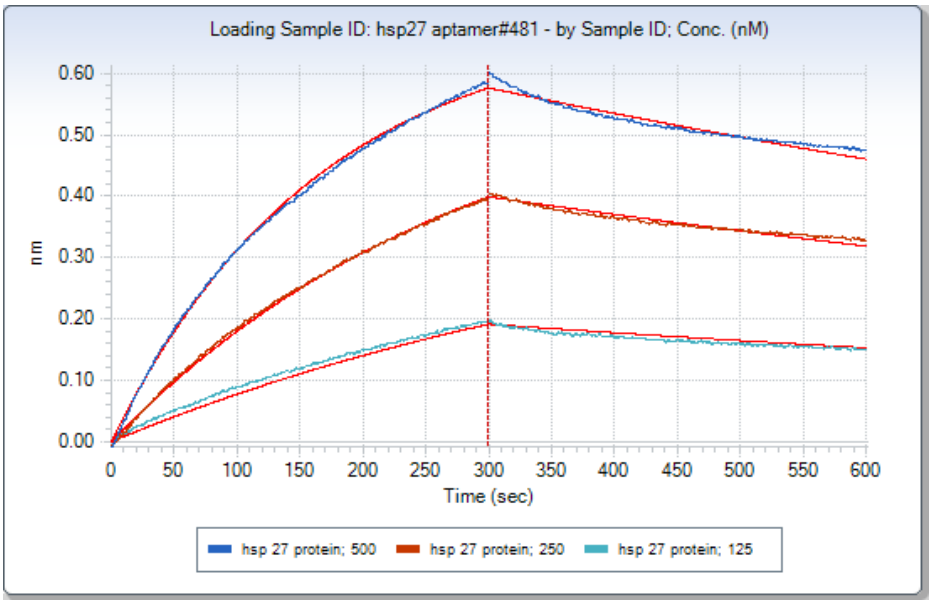


**Figure 2.** Association and dissociation graph of 1:1 fitting model of hsp27 aptamer #481 (biotinylated) to hsp27 protein concentration 500, 250 and 125 nM.



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**Table 1.** $K_d$, $R^2$ and $Chi^2$ values by Global fitting for Referenced data. **$K_d$ = 70.7 nM**

| Immobilized Aptamer | Analyte | Conc. (nM) | Response | $K_d$ (M) | Full $X^2$ | Full $R^2$ |
|---|---|---|---|---|---|---|
| hsp27 aptamer#481 | hsp 27 protein | 500 | 0.5779 | 7.07E-08 | 0.158513 | 0.997968 |
| hsp27 aptamer#481 | hsp 27 protein | 250 | 0.3887 | 7.07E-08 | 0.158513 | 0.997968 |
| hsp27 aptamer#481 | hsp 27 protein | 125 | 0.1927 | 7.07E-08 | 0.158513 | 0.997968 |



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