



## APTAMER INFORMATION

### Human Serum Albumin (HSA) aptamer\_23G03 #372

#### 1a. Description:

- Identifiers: 23 G03 (Oligo #372)
- Number of DNA nucleotides: 39 bases (without 3'-6T), 45 bases (with 3'-6T)
- Molecular weight (includes 3'-biotin and 6T): 14,237.4 g/mol
- Target for selection: HSA protein, Sigma (Cat# A3782)

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

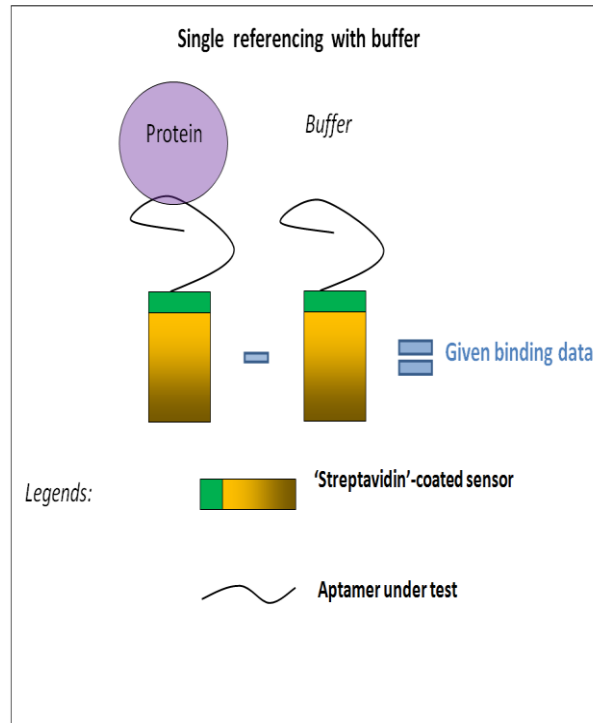
- Immobilized Ligand: HSA aptamer\_23G03 #372 with 3'-6T and biotin
- Analyte: HSA protein
- Buffer used for validation: 20 mM Tris, 100 mM NaCl, 0.005% Tween20 in nuclease free water, pH 7.4

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

We validate the binding data, by single reference method.

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

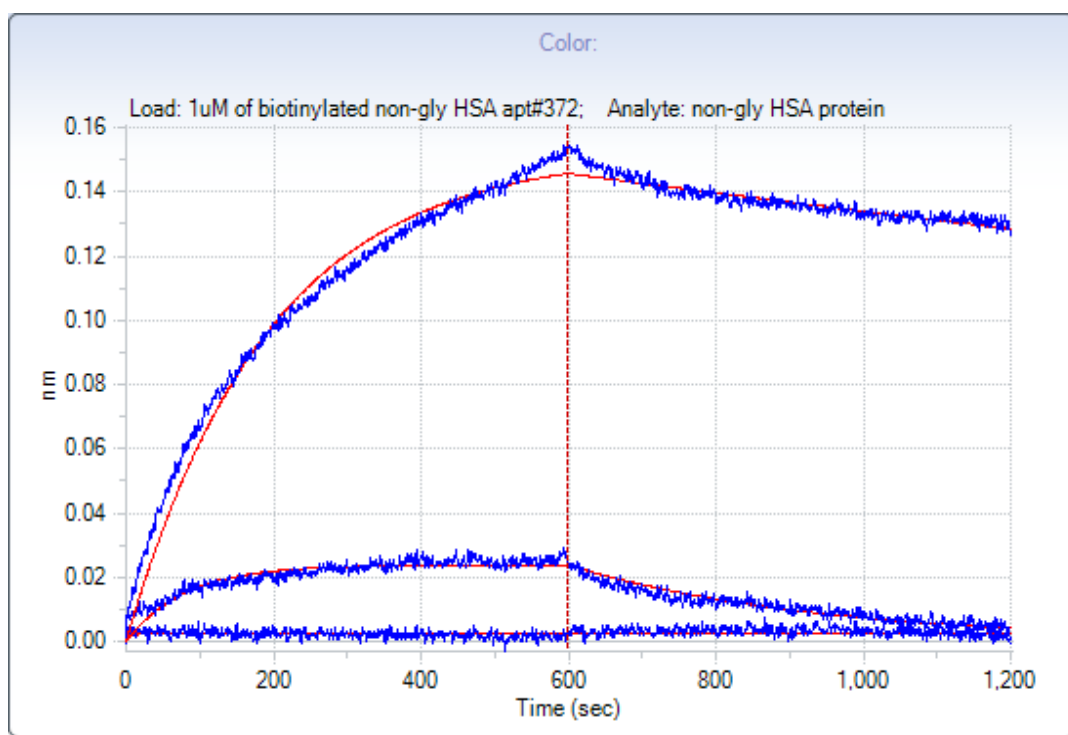




**Figure 1.** Diagram showing aptamer: protein binding validation scheme.



**1d. Single reference data:**



**Figure 2.** Association and dissociation graph of 1:1 fitting model of HSA aptamer (biotinylated) oligo #372 to HSA protein concentrations 500, 125 and 31.25 nM, by single reference method.

Table 1. $K_d$ , $R^2$ and $\chi^2$ values by Local fitting for single reference method. $K_d = 29.1$ nM						
Immobilized Aptamer	Analyte	Conc. (nM)	Response	$K_d$ (M)	Full $R^2$	Full $\chi^2$
HSA apt#372 biotin	HSA protein	500	0.1512	2.09E-08	0.985181	0.016463
HSA apt#372 biotin	HSA protein	125	0.0268	3.72E-08	0.933033	0.004003



