BasePair Biotechnologies, Inc.

HSA Aptamer Data Sheet

ATW0015

Aptamer to Human Serum Albumin

Selection Information

Target for Selection: Human Serum Albumin (HSA), Sigma Cat# A3782

Number of DNA Nucleotides: 39

Aptamers were selected from a randomized Base Pair 39-mer DNA library against the target protein. Proprietary methods were used to select this specific aptamer sequence.

Affinity Determination

Affinity Determination Method: Bio-Layer Interferometry (BLI)

Buffer Used for Affinity Determination: 20mM Tris, 100mM NaCl, 0.005% Tween 20, in nuclease-free water, pH 7.4

Average kD: 29.1 nM

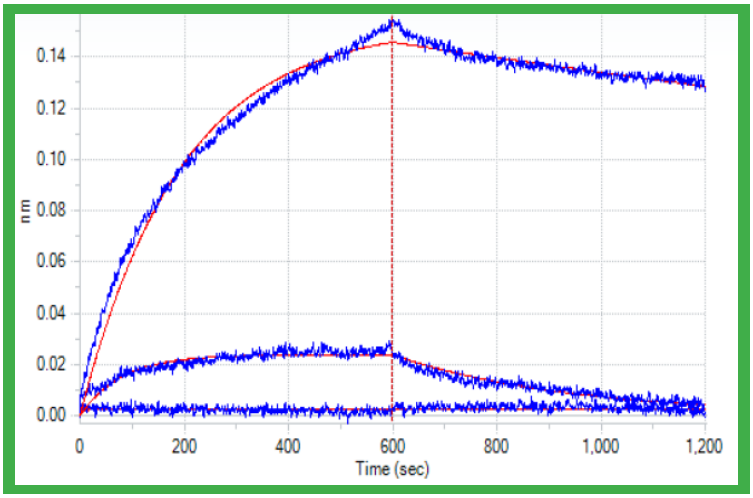

Figure 1. Aptamer-HSA Binding

Association and dissociation graph of 1:1 fitting model of HSA aptamer (biotinylated) 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. **Avg K_D = 29.1 nM**

Immobilized Aptamer	Analyte	Concentration	Response	Full X^2	Full R^2
ATW0015 + biotin	Hu HSA Protein	500	0.512	0.016463	0.985181
ATW0015 + biotin	Hu HSA Protein	125	0.0268	0.004003	0.933033

Aptamer Folding

For optimal binding, aptamers must be folded into their tertiary structure prior to use. Dilute to 10x working concentration in Folding Buffer, heat to 90-95°C for 5 minutes, then cool to room temperature (~15 minutes). Final application buffers used for dilution of aptamer to working concentration and washing should contain 1 mM MgCl2.