

Kinetics in High Serum

Creoptix™ WAVE



Summary

Analysis of molecular interactions in complex matrices like blood serum is of great interest. Label-free surface-based biosensors are typically put under stress by such complex matrices due to potential deleterious effects on the microfluidics, and high non-specific binding of the matrix components (e.g. serum albumines) to the surface. Here we show that the innovative disposable microfluidics of the **Creoptix™ WAVE** system provides very high tolerance against blood serum both with regard to clogging but also regarding kinetic analysis.

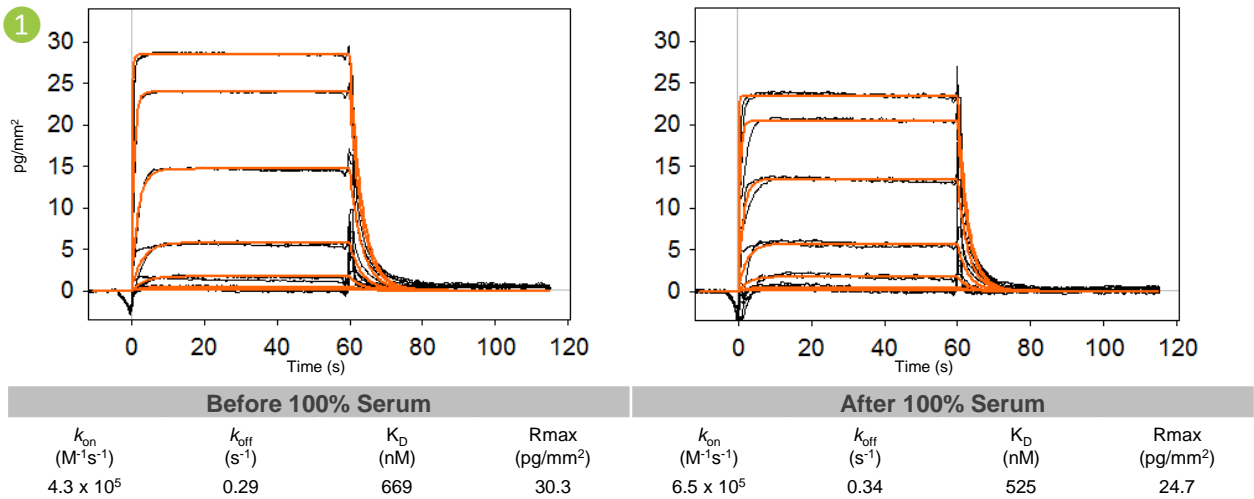


Figure 1: Sensorgrams of the interaction between a biotinylated ssDNA of 34nt (ligand, MW: 10.9KDa) and a complementary ssDNA of 7nt (analyte, MW: 2089Da) before (left) and after (right) injection of untreated and undiluted blood serum (i.e. 100% serum). The expected affinity for the binding is of $0.56\mu M$ in HBS-EP+ buffer. The buffer used in this experiment is Hepes 50mM pH7.4, $MgCl_2$ 10mM. Dilution series from $10\mu M$ to $2.4nM$ (4-fold dilutions) in duplicates were injected (60s) for each kinetic measurement at the flow of $30\mu l/min$. In between the two kinetic measurements two injections of untreated undiluted blood serum (100%) were performed ($30\mu l/min$, 60s).

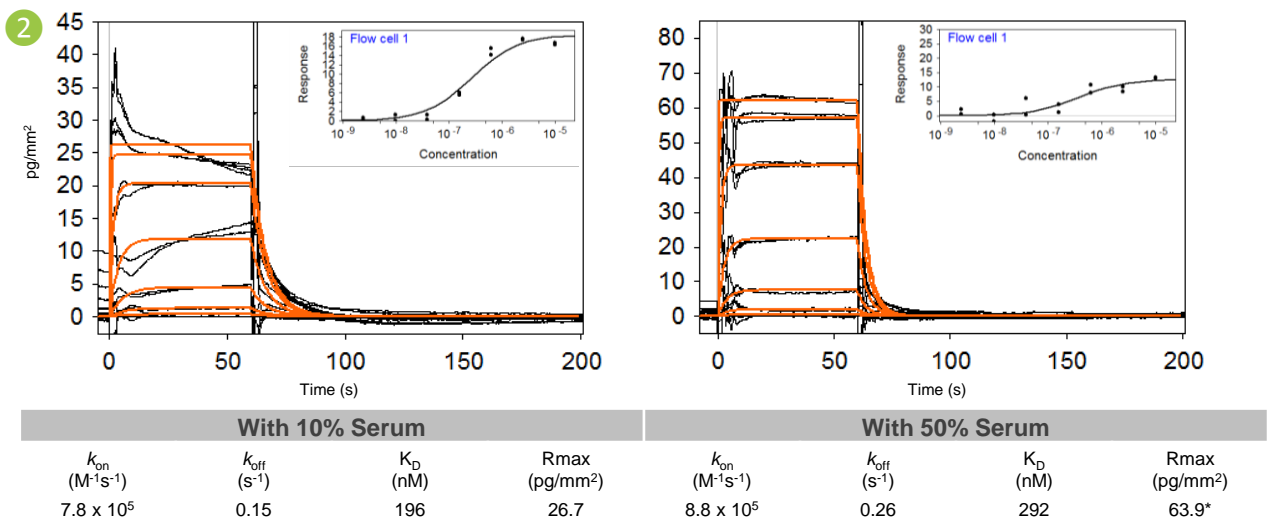


Figure 2: Sensorgrams of the interaction between a biotinylated ssDNA of 34nt (ligand, MW: 10.9KDa) and a complementary ssDNA of 7nt (analyte, MW: 2089Da) before (left) and after (right) injection of untreated and undiluted blood serum (i.e. 100% serum). The expected affinity for the binding is of $0.56\mu M$ in HBS-EP+ buffer. The buffer used in this experiment is PBS-EP 0.5% BSA. Dilution series from $10\mu M$ to $2.4nM$ (4-fold dilutions) in duplicates in serum concentrations of 0, 10, 20 and 50 %, respectively were injected (60s) for each kinetic measurement at the flow of $30\mu l/min$ (data for 0 and 20% not shown). The figure shows that serum concentrations tested up to 50% do not affect the performance of the system. (*: high value due to refractive index correction)