# **Supplementary Material**

# Oxidization increases the binding of EGCG to serum albumin revealed by kinetic data from label-free optical biosensor with reference channel

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## **Kinetic model equations**

#### Homogeneous binding site model

The homogeneous binding site model supposes that between the analyte (A, in our case EGCG or ox. EGCG) and the ligand (L, in our case BSA) only one type of bindig can occur, resulting in the ligand-analyte complex (LA). The process is reversible, involving association and dissociation, which are characterized by the kinetic constants  $k_a$  and  $k_d$ , respectively. The interaction of the ligand and analyte can be described with the following reaction scheme:

$$L_{k_d}^{k_a} + A \rightleftharpoons LA \tag{S1}$$

Based on the mass action law, the rate equations expressing the change of the concentration of L and LA can be written as:

$$\frac{d[L]}{dt} = -(k_a[L][A] - k_d[LA])$$

$$\frac{d[LA]}{dt} = (k_a[L][A] - k_d[LA])$$
(S2)

where *t* denotes the time, and [L], [A] as well as [LA] are the concentration of the related components. The dissociation constant ( $K_d$ ) that measures the strength of the L-A interaction can be determined by calculating the ratio  $k_a/k_d$ .

#### Heterogeneous binding site model

The heterogeneous binding site model can be used to model interacting L-A systems where L has two independent binding sites with different affinities to A.

Considering two types of binding sites which have different binding affinities (characterized by kinetic constants of  $k_{a1}$ ,  $k_{d1}$ ,  $k_{a2}$  and  $k_{d2}$ ), one can write the following scheme which hypothesizes two different ligands,  $L_1$  and  $L_2$ .

$$L_{1}^{k_{a1}} + A \rightleftharpoons L_{1}A$$

$$L_{2} + A \rightleftharpoons_{k_{d2}}^{k_{a2}}A$$
(S3)

The rate equations for the relevant components are:

$$\frac{d[L_1]}{dt} = -(k_{a1}[L_1][A] - k_{d1}[L_1A]) 
= \frac{d[L_1A]}{dt} = (k_{a1}[L_1][A] - k_{d1}[L_1A]) 
\frac{d[L_2]}{dt} = -(k_{a2}[L_2][A] - k_{d2}[L_2A]) 
= \frac{d[L_2A]}{dt} = (k_{a2}[L_2][A] - k_{d2}[L_2A])$$
(S4)

### Adsorption of EGCG to different type of surfaces

In order to characterize the adsorption characteristics of EGCG, we tested different type of chip surfaces using the GCI technique: PCP (thin polycarboxylate functionalization, quasi-planar surface, hydrophilic), PCP-L (quasi-planar polycarboxylate coating with lipid anchors, hydrophobic) as well as  $Ta_2O_5$  surface (bare chip). As demonstrated in Fig. S1, we found that the EGCG can adsorbed at a high level to all of the examined surfaces.

Considering the reproducibility and variability of the measurements, we determined the standard deviations of data obtained on the bound BSA and EGCG amounts. Based on three repeated experiments performed on different PCP chips, the bound surface mass of BSA was determined to be  $541 \pm 22$  pg/mm<sup>2</sup> (average  $\pm$  standard deviation), representing only a small variation in the

replicated measurements. Even using three types of surfaces (PCP, PCP-L and Ta<sub>2</sub>O<sub>5</sub>), relatively low value of standard deviation was obtained for EGCG binding, both on the measurement (*ch1*) and reference (*ch2*) channel (1786  $\pm$  44 pg/mm<sup>2</sup> on *ch1* and 1562  $\pm$  106 pg/mm<sup>2</sup> on *ch2*, respectively).



**Figure S1.** Kinetic surface mass curves representing the adsorption of ECGC to PCP-L, PCP and  $Ta_2O_5$  surfaces at EGCG concentrations of 2.18 mM and 17.5 mM.

# Kinetic measurement results demonstrating the performance of the Creoptix WAVE

To prove the performance of the novel GCI technique, we carried out reference measurements on the furosemide–carbonic anhydrase II (CAII) analyte–ligand pair, which is a widely used model system of small molecule bindig kinetic experiments. Our measurement results are presented in Fig. S2.



**Figure S2.** Kinetic measurement series performed to measure the binding characteristics of the small molecule furosemide (331 Da) to CAII protein. We fitted the obtained kinetic curves by the homogeneous binding site model and we determined a  $K_d = 2.2 \,\mu$ M value. Measured concentration series: 100  $\mu$ M, 33.3  $\mu$ M, 11.1  $\mu$ M, 3.70  $\mu$ M, 1.24  $\mu$ M, 0.41  $\mu$ M, 0.14  $\mu$ M (in the figure, only the 100  $\mu$ M, 3.70  $\mu$ M and 0.14  $\mu$ M concentrations are marked by their values).