

# Investigation of C-terminal Domain of SARS Nucleocapsid Protein - Duplex DNA Interaction Using Transistors and Binding-Site Models

## Supplementary Materials

The two-binding-site model is developed and shown from equation (6) ~ (11) in the main article. Following the two-binding-site model, similarly to equation (11), the surface coverage ratio of the three-binding-site model can be shown as the following equation.

$$\alpha = \alpha_1 c_1 + \alpha_2 c_2 + \alpha_3 c_3$$

Where  $\frac{1}{1 + \frac{K_{D1}}{[L]}} = \alpha_1$ ,  $\frac{1}{1 + \frac{K_{D2}}{[L]}} = \alpha_2$ ,  $\frac{1}{1 + \frac{K_{D3}}{[L]}} = \alpha_3$ ,  $c_1 \equiv \frac{\Delta I_{\max 1}}{\Delta I_{\max}}$ ,  $c_2 \equiv \frac{\Delta I_{\max 2}}{\Delta I_{\max}}$  and

$$c_3 \equiv \frac{\Delta I_{\max 3}}{\Delta I_{\max}}$$

The three-binding-site model was used to fit with the experimental results (surface coverage ratio) as shown in the following figure.

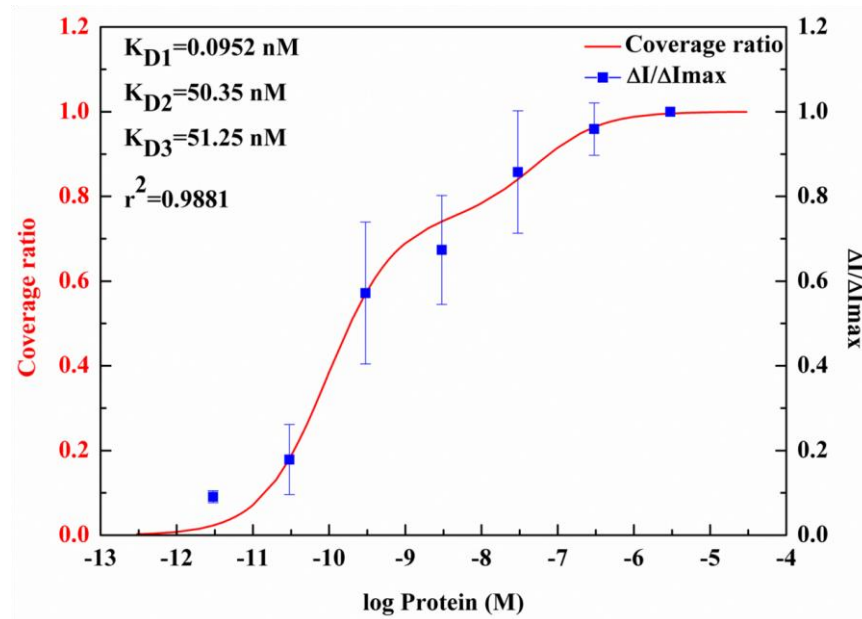


Figure I. Surface coverage ratio from experimental results fitted with three-binding-site model.

The fitting results from the three-binding-site model are shown as below.

$$K_{D1} = 0.0952nM, \quad c1 = 0.7498$$

$$K_{D2} = 50.35nM, \quad c2 = 0.1251$$

$$K_{D3} = 51.25nM, \quad c3 = 0.1251$$

Compared with the fitting results from the two-binding-site model, as shown below,

$$K_{D1} = 0.0955nM, \quad c1 = 0.7504$$

$$K_{D2} = 51.23nM, \quad c2 = 0.2492$$

the  $K_{D1}$  (0.0952nM) extracted from the three-binding-site model was found almost the same as the  $K_{D1}$  (0.0955nM) extracted from the two-binding-site model. The  $K_{D2}$  (50.35nM) and  $K_{D3}$  (51.25nM) extracted from the three-binding-site model are very close, and their values are also the same as the  $K_{D2}$  (51.23nM) extracted from the two-binding-site model. The coefficient  $c1$  of the three-binding-site model is almost the same as the one  $c1$  extracted from the two-binding-site model. Also, the coefficient  $c2$  and  $c3$  of the three-binding-site model is  $\frac{1}{2}$  of  $c2$  extracted from the two-binding-site model. We therefore can conclude that the curve fitted with the three-binding-site model has actually the same mathematical function as the one fitted with the two-binding-site model. Thus, in this study, the two-binding-site model was chosen for the fitting.

#### Sensor stability in buffer solution

We have tested the sensor stability in buffer solution more than 1700 seconds and it shows no current change. The sensor was initially started testing in buffer solution and showed great stability. Additional drop of buffer solution was added at 800 seconds and 1200 seconds, both showing no current changes. The result from sensor stability in buffer solution is shown as below.

