

## Supplementary Information

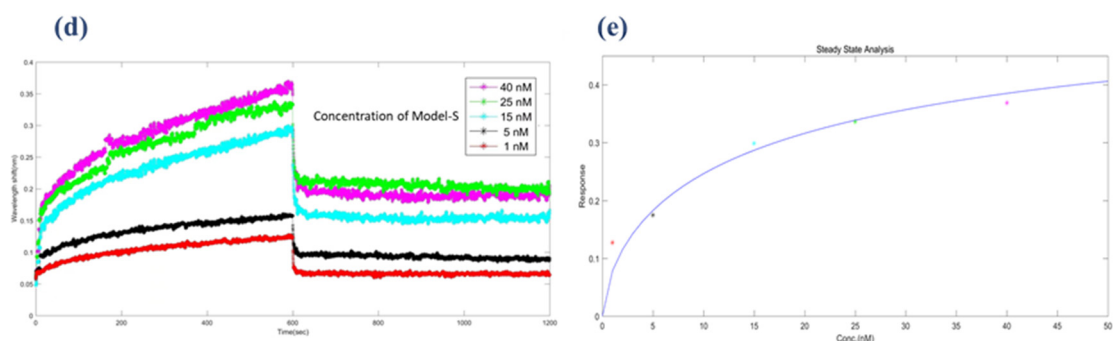
### S1. Sequencing validation for the S gene

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## S2. Affinity analysis of Model-S

The affinity analysis of Model-S was investigated by the molecular interaction instrument ForteBio Octet K2 (SARTORIUS, Germany). Below are the Figure 1 (d) and (e) from the manuscript and the related information was shown below in Table S1.

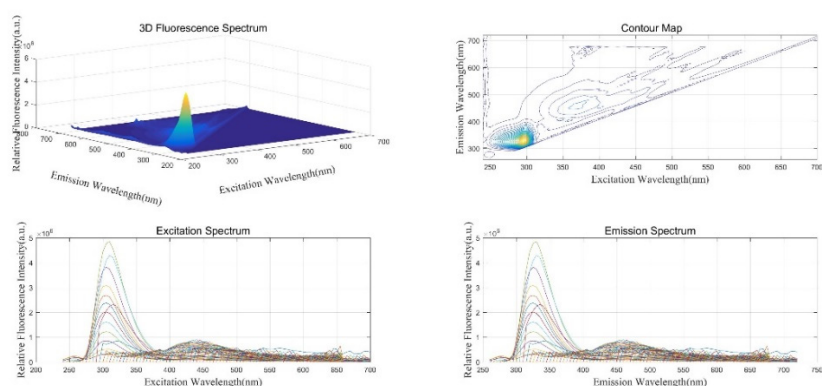


**Table S1.** Fitting results for the affinity analysis of Model-S

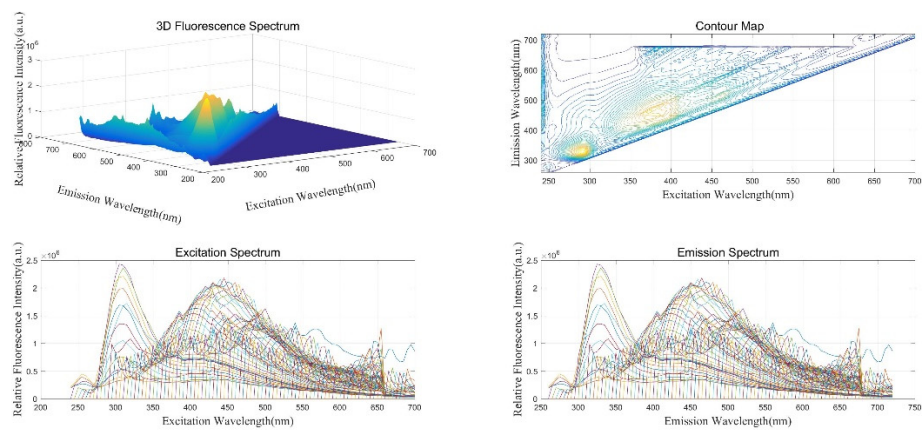
|   |  |                |
|---|--|----------------|
| $K_a = 1.426 \times 10^5 \text{ M}^{-1} \text{ s}^{-1}$<br>$K_d = 3.525 \times 10^{-4} \text{ s}^{-1}$<br>$KD = \frac{K_d}{K_a} = 2.473 \times 10^{-9} \text{ M}$<br>Affinity constant = $4.044 \times 10^8 \text{ M}^{-1}$ |  |                |
| Binding model   | 1:1 Model<br>(Fitting one analyte in solution binding to one binding site on the surface.) |                |
| Model equation  | $\text{Response} = \frac{R_{\max} \times \text{Conc.}}{KD + \text{Conc.}}$                 |                |
| Results   | $\chi^2/\text{DoF} = 0.0021$   | $R^2 = 0.9417$ |

## S3. Results from three-dimensional fluorescence spectroscopy for the nine samples.

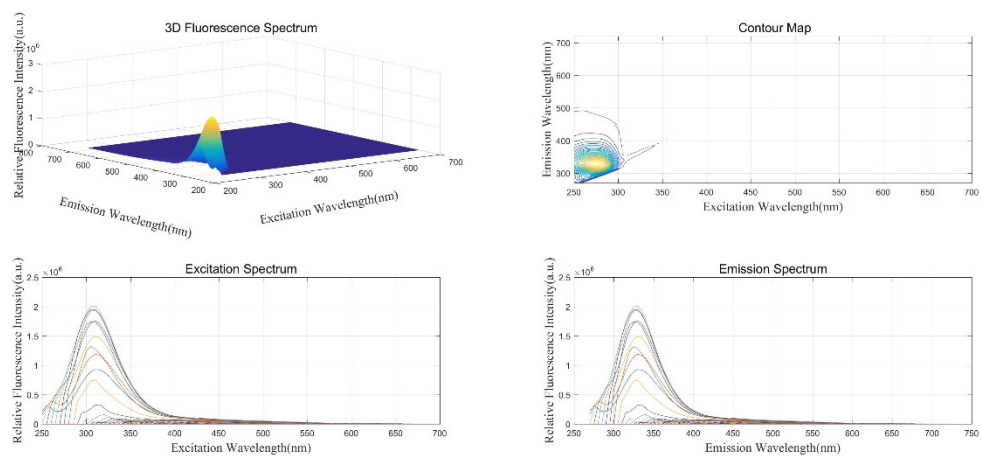
### (1) BSA



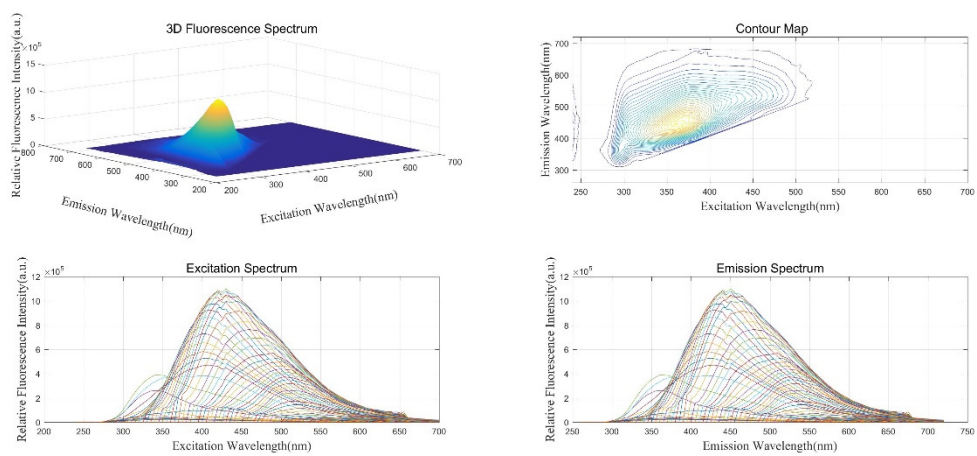
## (2) OVA



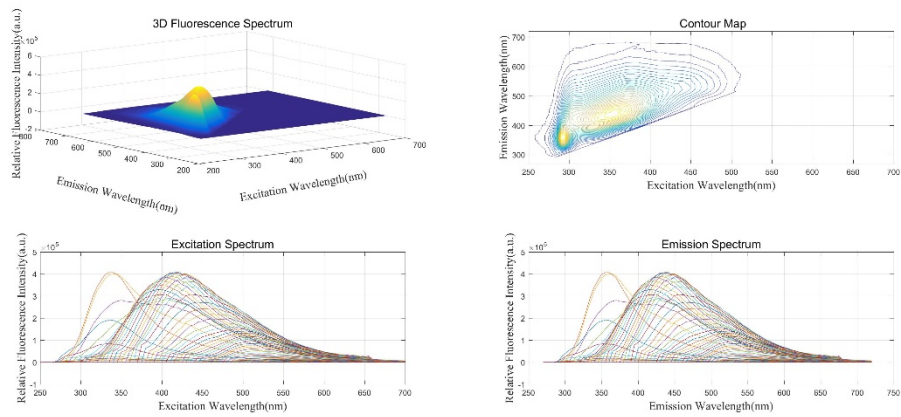
## (3) M13 phage



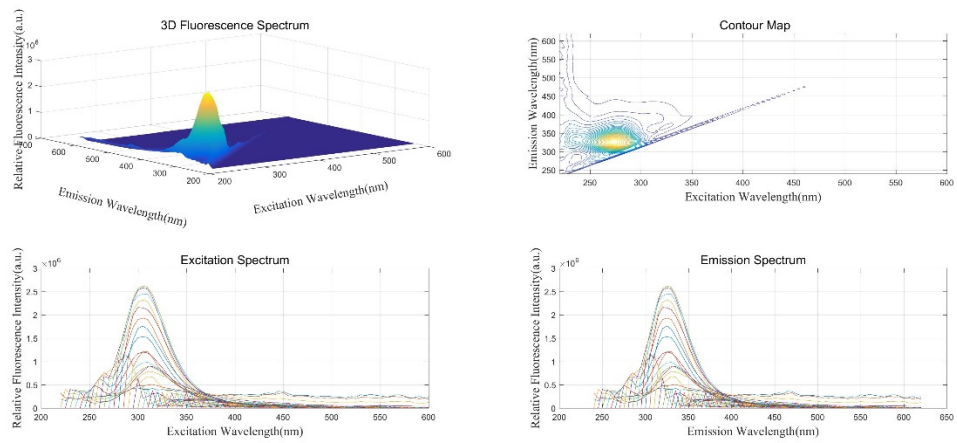
## (4) Model-N



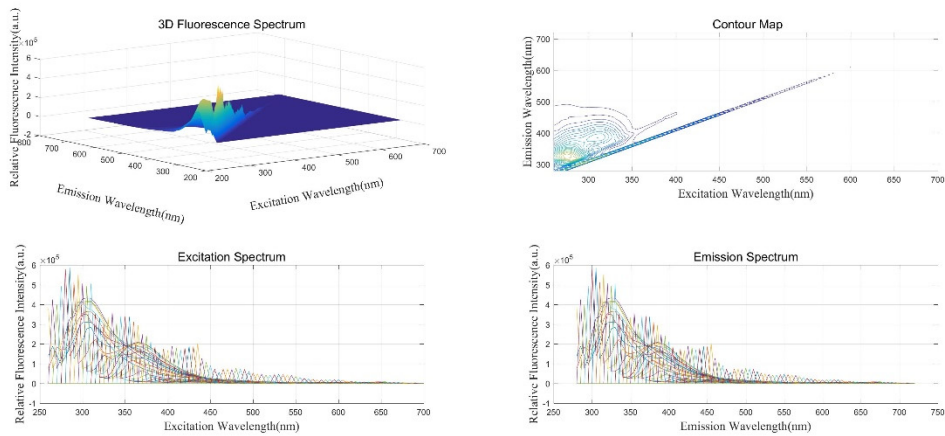
## (5) Model-S



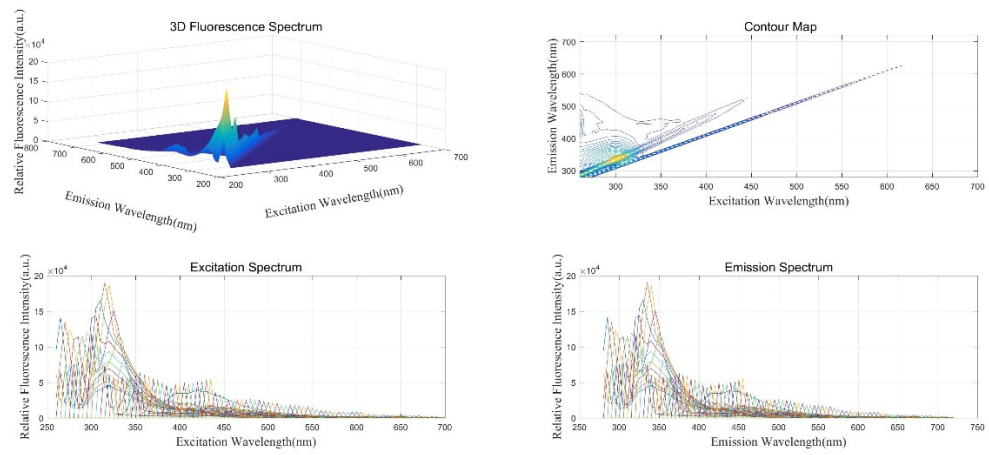
## (6) N protein



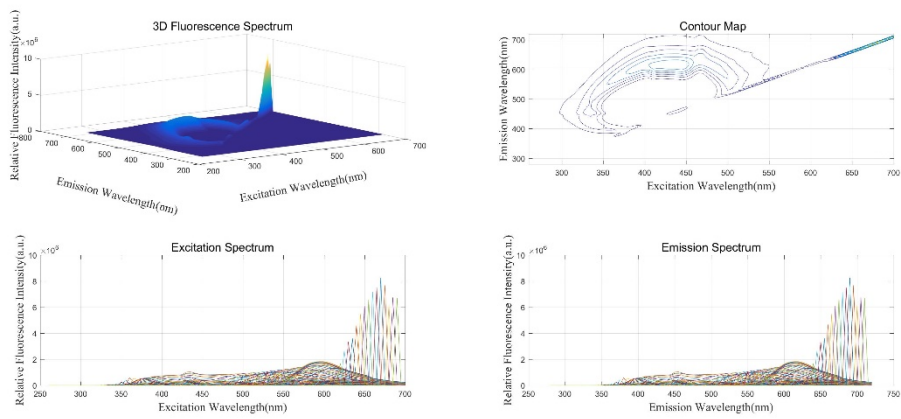
## (7) S1 protein



(8) S2 protein



(9) *E. coli* TG1



## S4. Results from Raman spectroscopy for the nine samples

