

ELECTRONIC SUPPLEMENTARY INFORMATION

On-Chip Bioorthogonal Chemistry Enables Immobilization of In Situ Modified Nanoparticles and Small Molecules for Label-Free Monitoring of Protein Binding and Reaction Kinetics

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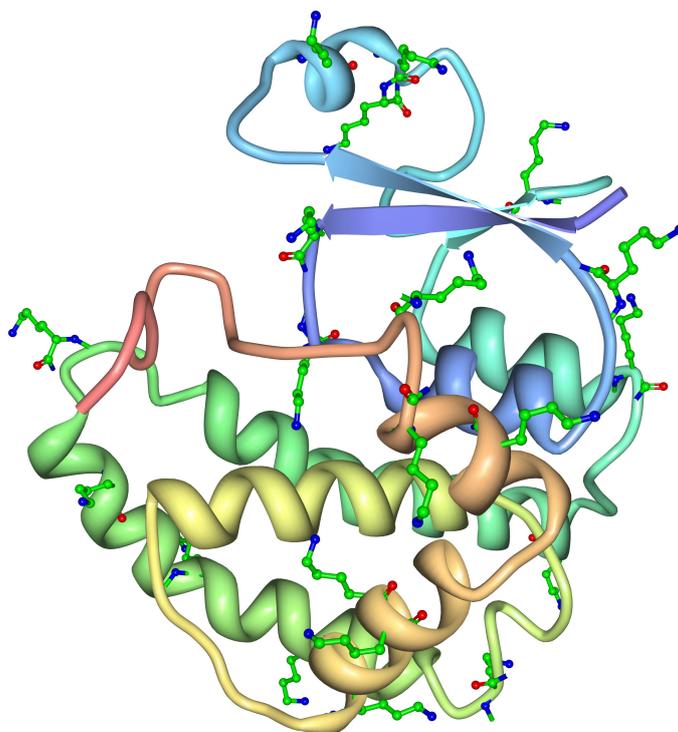
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Determination of GST conjugate stability and loading:

Fig. S1. GST amino acid sequence and crystal structure showing lysine residues

PDB ID: 1Y6E

```
1  spilgywkik glvqptrlll eyleekyeeh lyerdegdkw rnkkfelgle fpnlpyyidg  
61  dvkltqsmal iryiadkhnmlggcpkerae ismlegavld irygvsvriay skdfetlkvd  
121 flsklpemlk mfedrlchkt ylngdhvthp dfmlydaldv vlymdpmcld afpklvcfkk  
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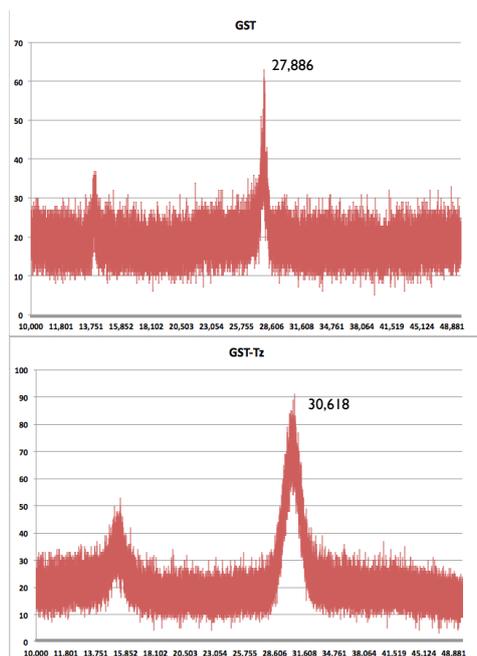


Fig. S2. MALDI-TOF spectra showing the mass for GST and Tz-modified GST. The difference in mass is indicative of Tz loading.

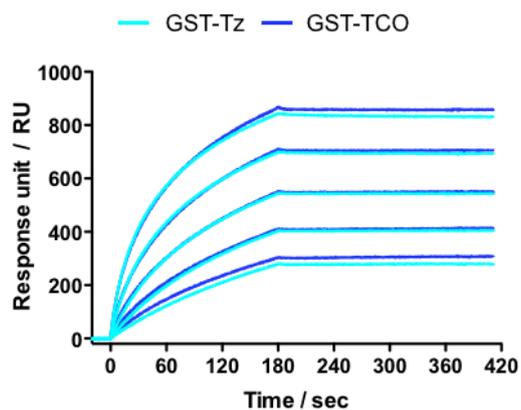
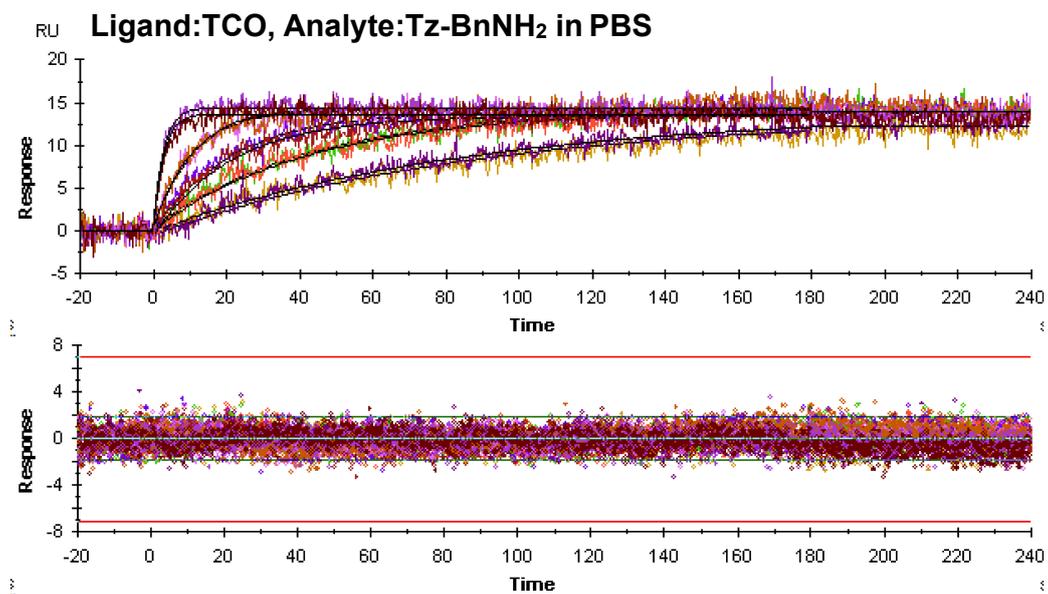


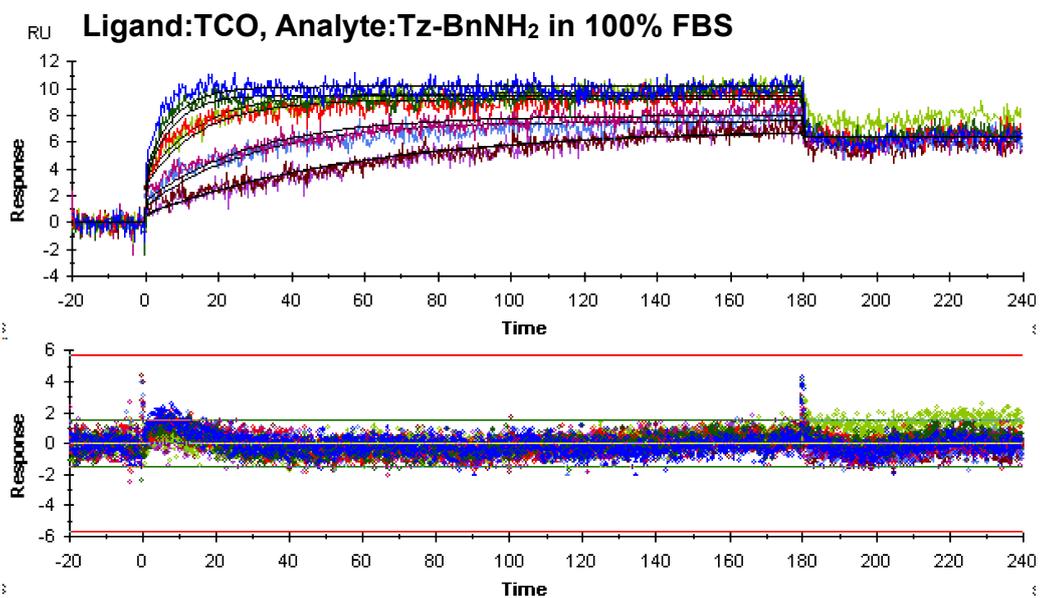
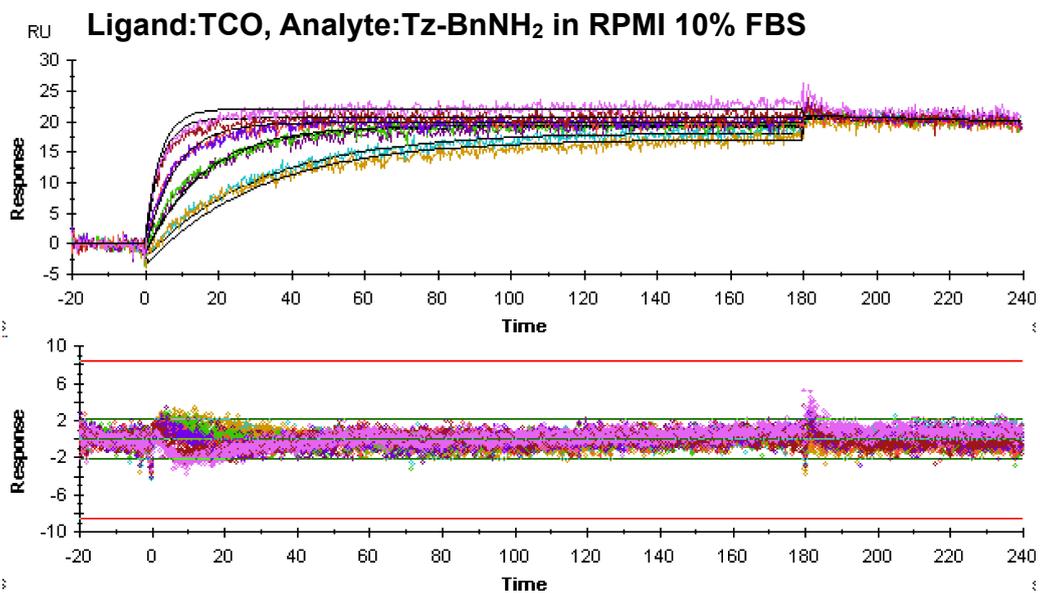
Fig. S3 Overlay of sensograms showing GST-Tz and GST-TCO capture and stability.

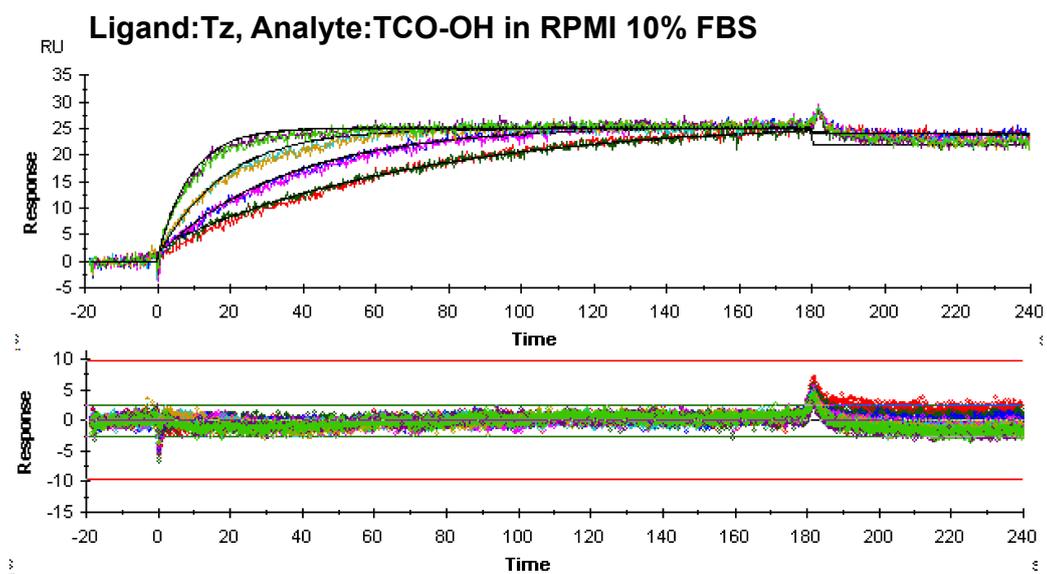
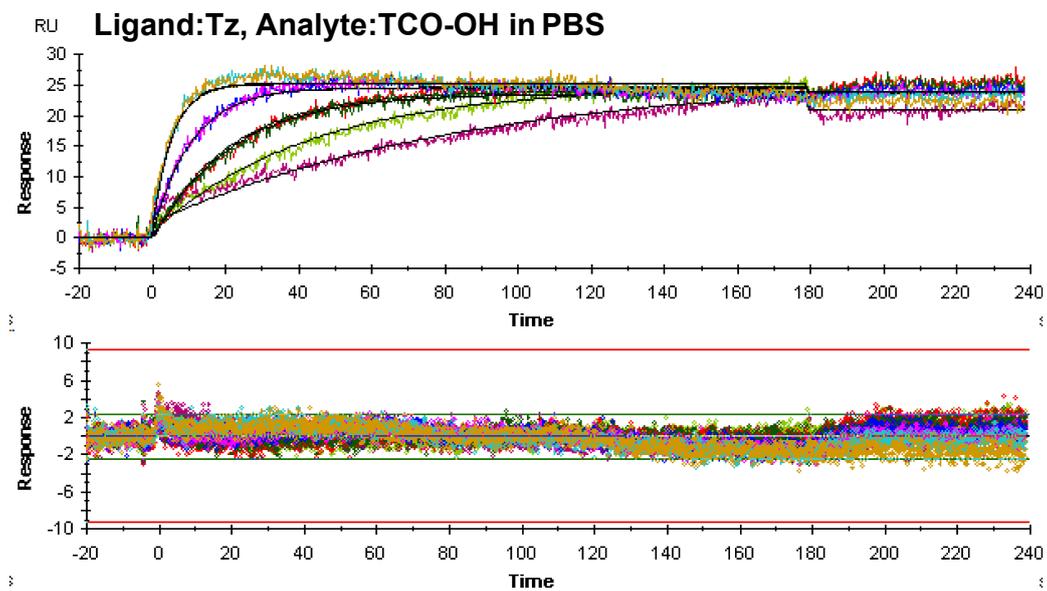
Measurements of small molecule cycloaddition rates:

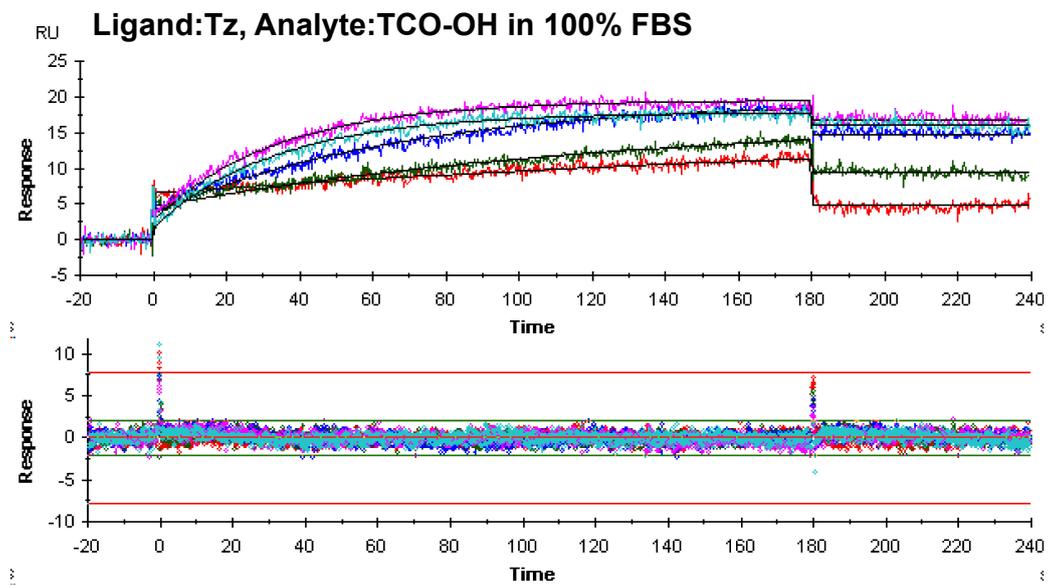
Table S1. Summary of cycloaddition (association) rate constants, k_a for small molecules in various buffer conditions.

Buffer	Analyte	Ligand	k_a M ⁻¹ s ⁻¹	SEM
PBS	Tz-BnNH ₂	TCO	34,062	1,536
RPMI, 10% FBS	Tz-BnNH ₂	TCO	23,740	180
100% FBS	Tz-BnNH ₂	TCO	11,943	2,987
PBS	TCO-OH	Tz	18,880	1,570
RPMI, 10% FBS	TCO-OH	Tz	12,775	925
100% FBS	TCO-OH	Tz	2,415	111





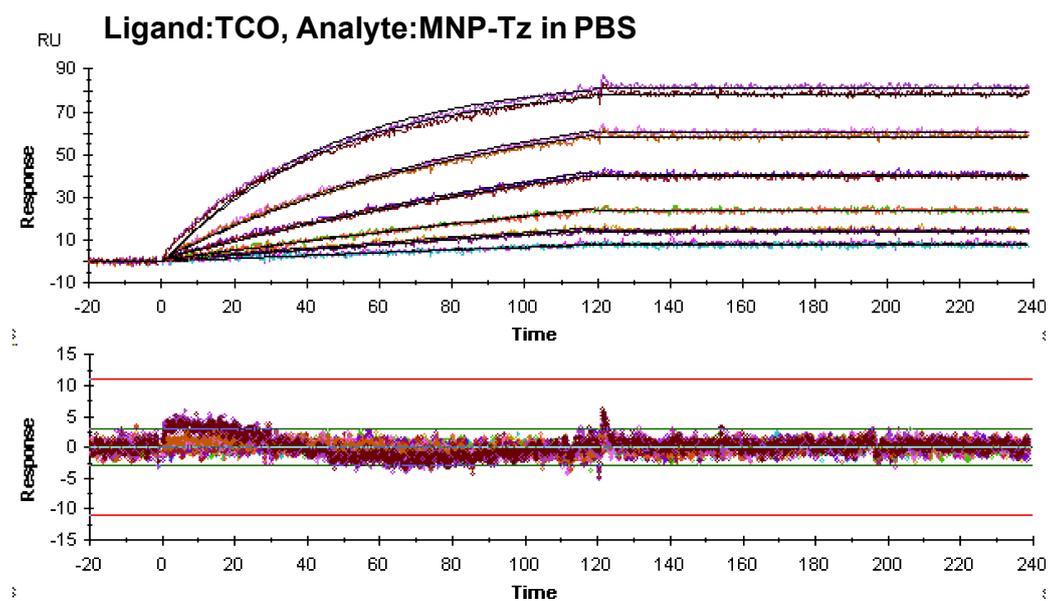


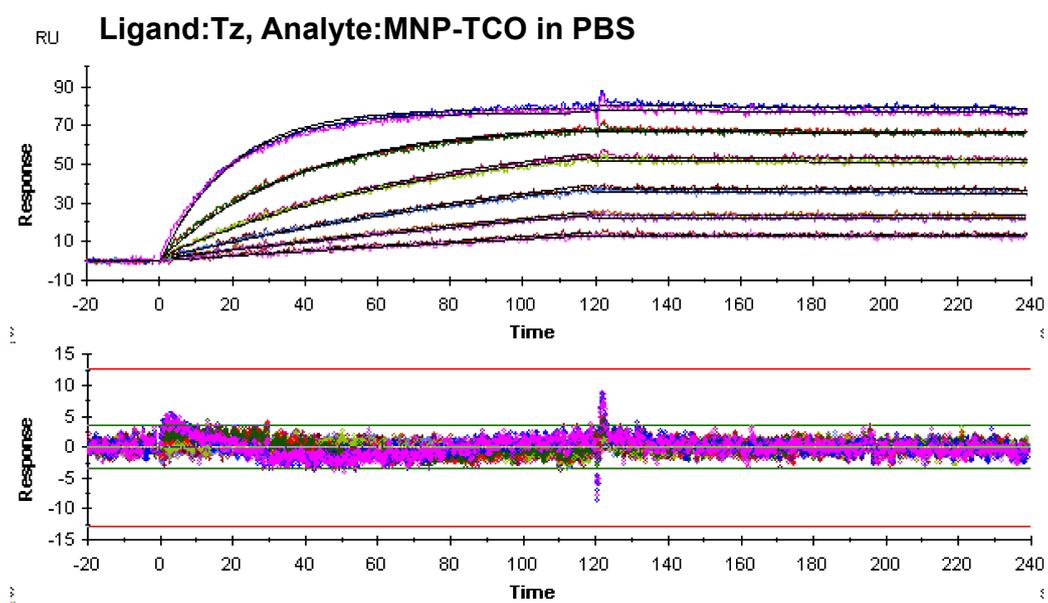
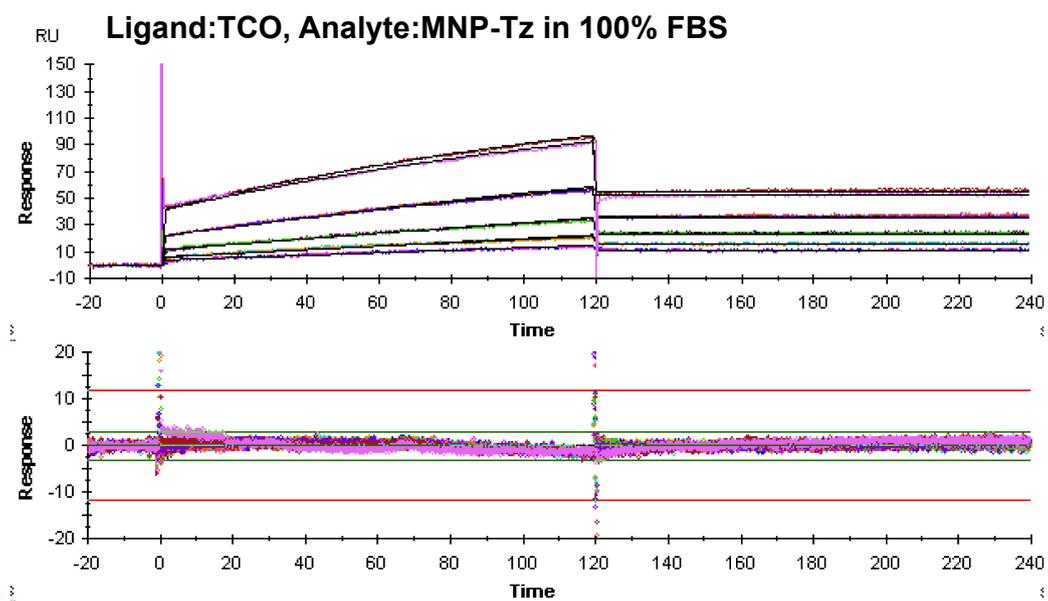


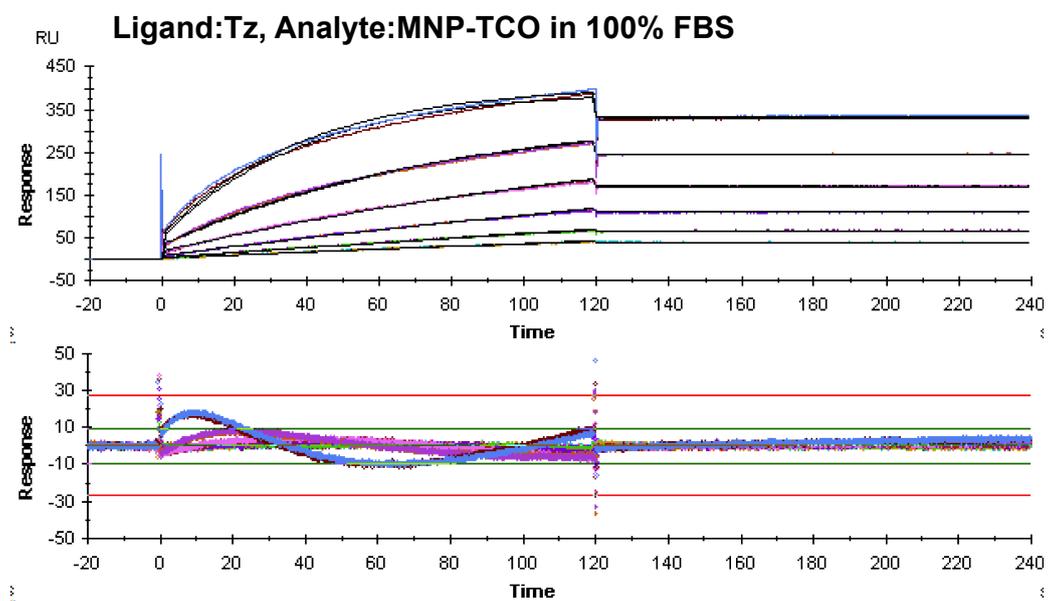
Measurements of MNP-conjugate cycloaddition rates:

Table S2. Summary of cycloaddition (association) rate constants, k_a for MNPs in various buffer conditions.

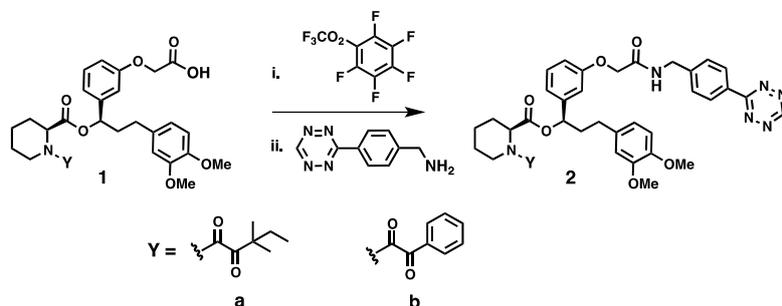
Buffer	Analyte	Ligand	k_a M ⁻¹ s ⁻¹	SEM
PBS	MNP-Tz	TCO	89,573	4,412
100% FBS	MNP-Tz	TCO	28,705	1,145
PBS	MNP-TCO	Tz	235,440	4,554
100% FBS	MNP-TCO	Tz	118,200	5,500



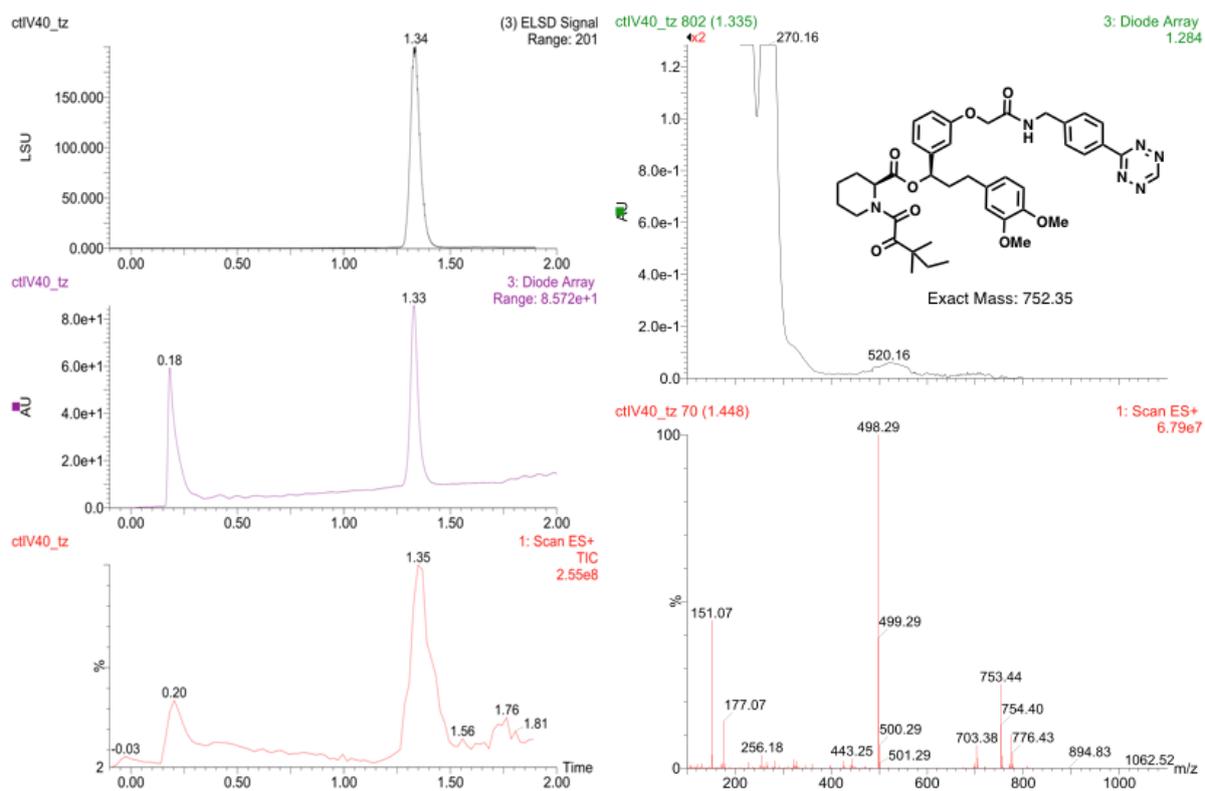




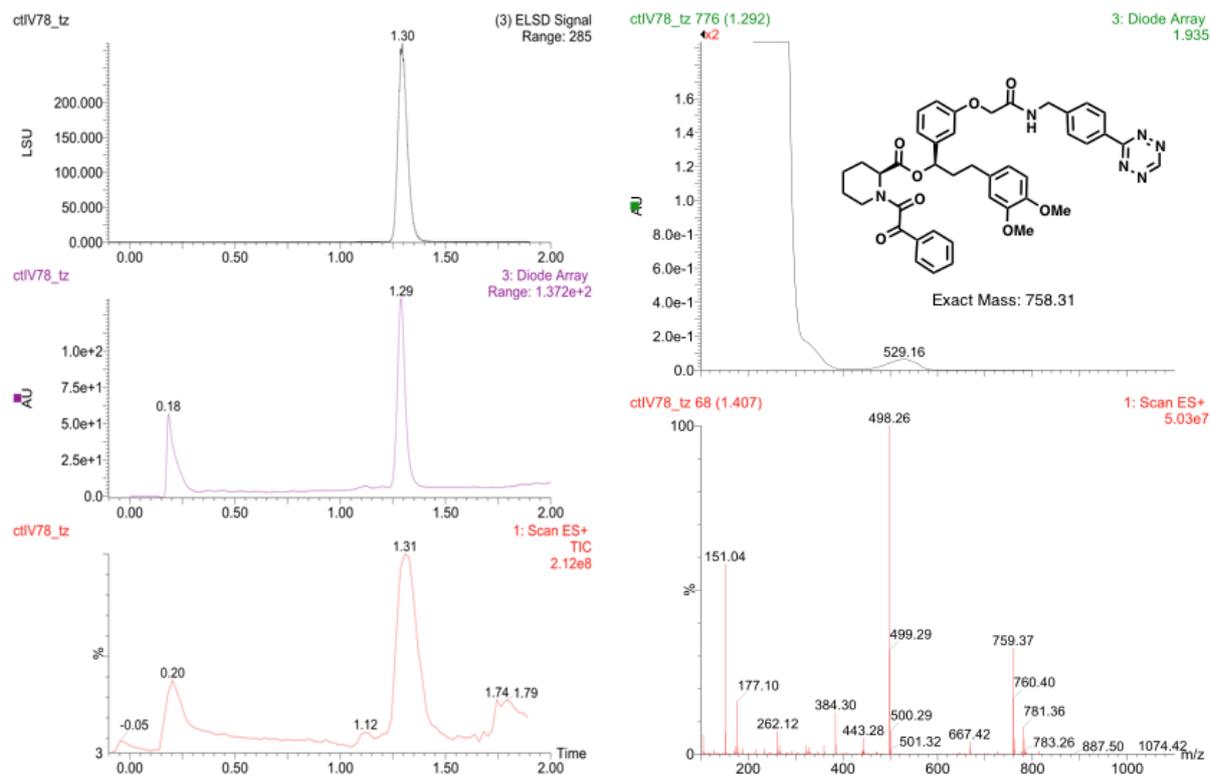
Analytical LC/MS chromatograms and spectra for FKBP12 binding ligands:



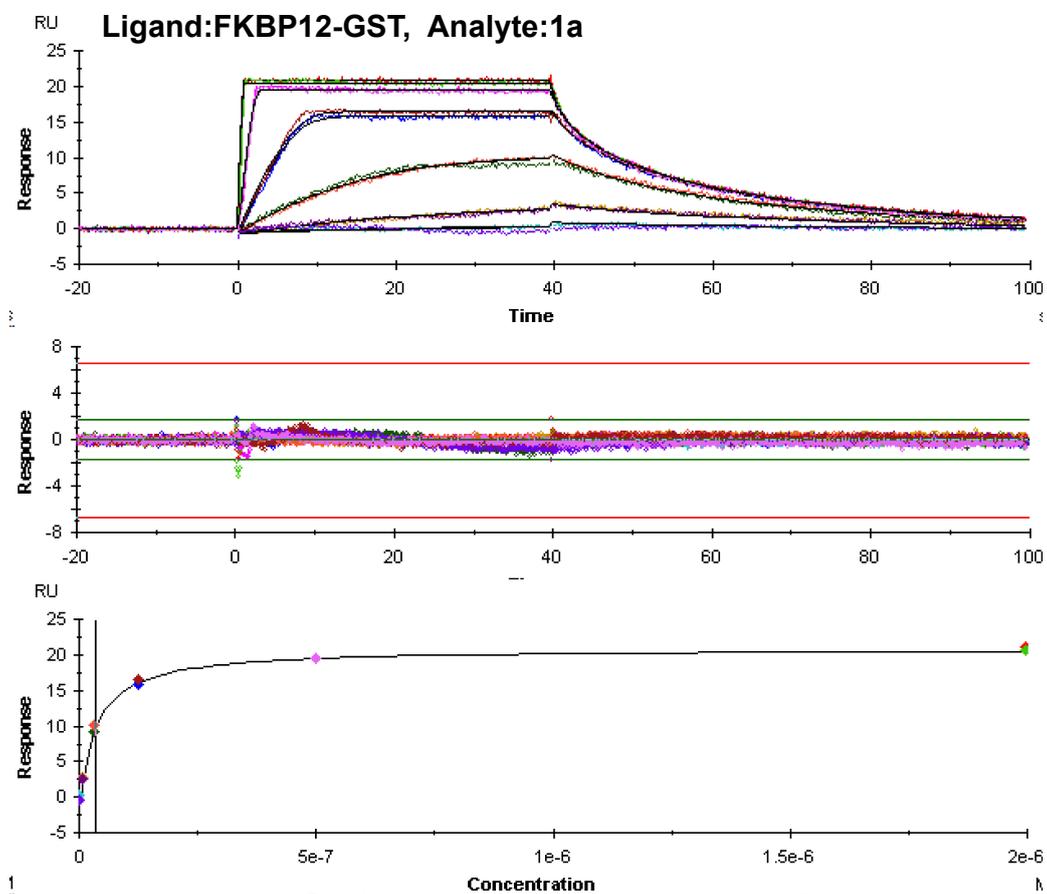
(S)-(R)-1-(3-(2-((4-(1,2,4,5-tetrazin-3-yl)benzyl)amino)-2-oxoethoxy)phenyl)-3-(3,4-dimethoxyphenyl)propyl 1-(3,3-dimethyl-2-oxopentanoyl)piperidine-2-carboxylate (2a).



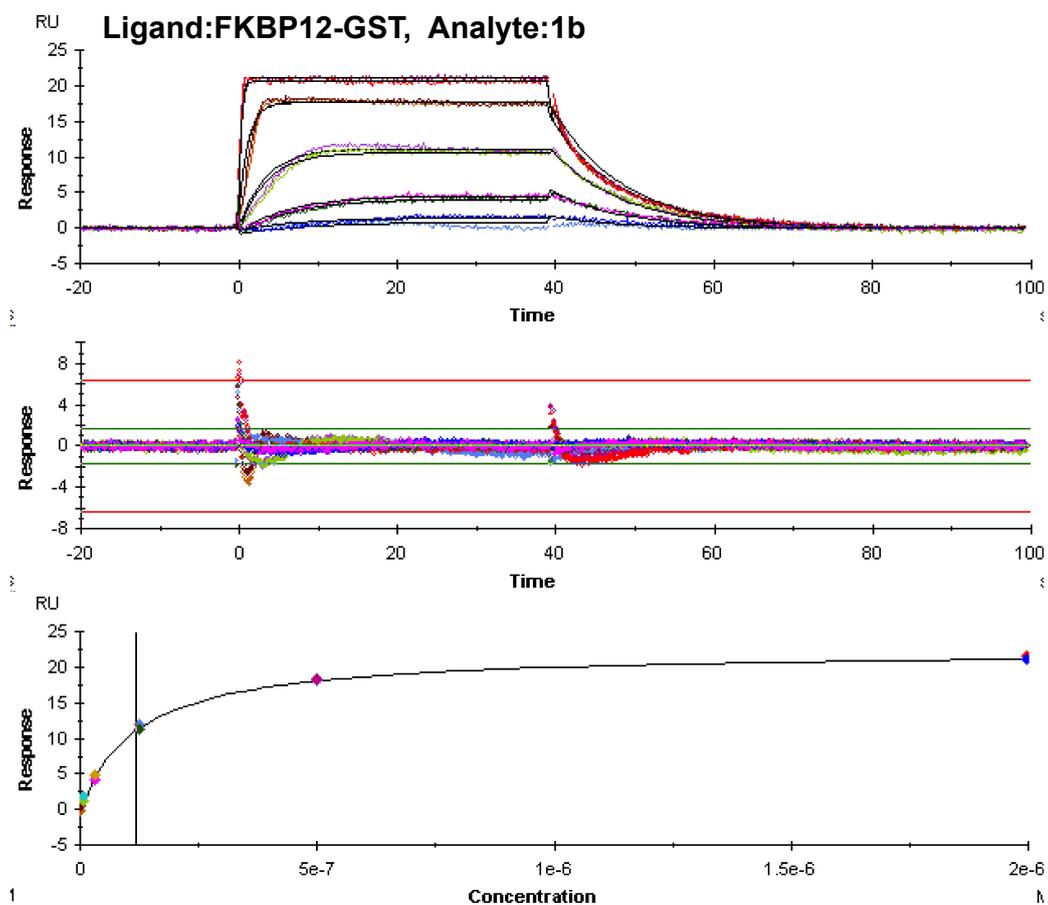
(*S*)-(*R*)-1-(3-(2-((4-(1,2,4,5-tetrazin-3-yl)benzyl)amino)-2-oxoethoxy)phenyl)-3-(3,4-dimethoxyphenyl)propyl 1-(2-oxo-2-phenylacetyl)piperidine-2-carboxylate (2b).



The binding of small-molecules 1 to immobilized FKBP12:

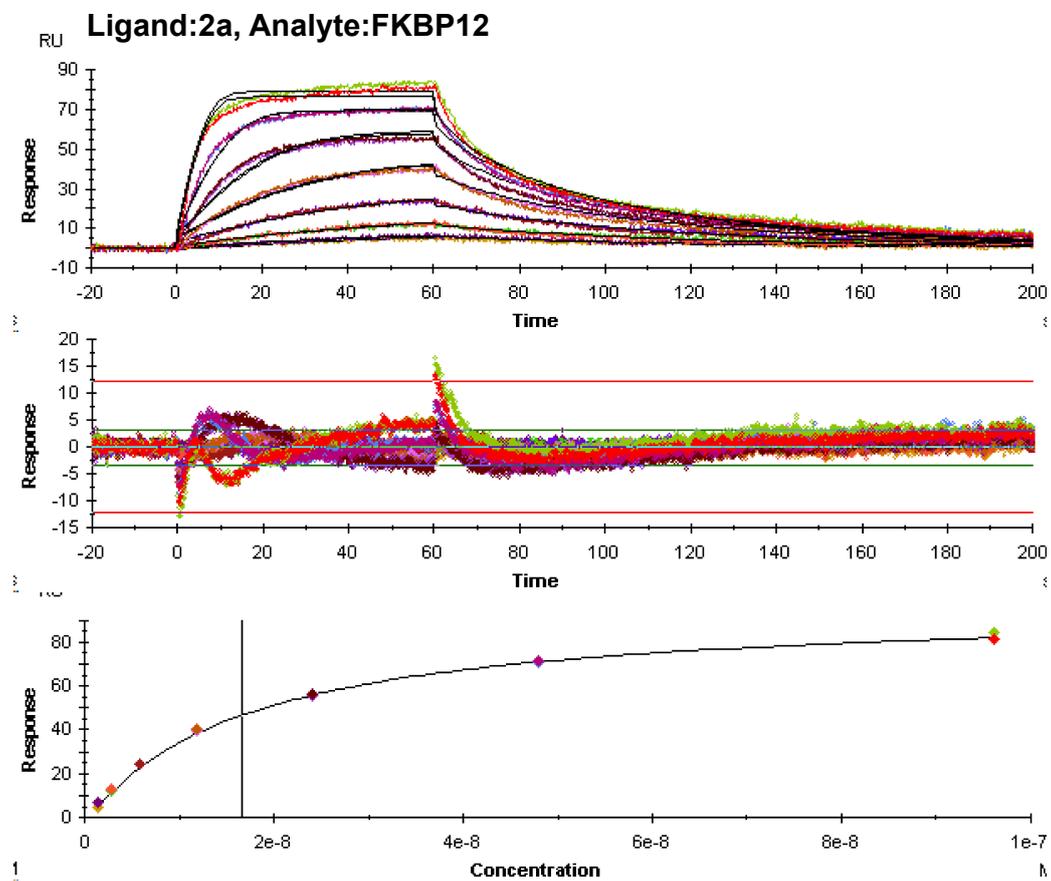


Kinetic analysis: $k_a = 1.83 \times 10^7 \text{ M}^{-1}\text{s}^{-1}$, $k_d = 0.553 \text{ s}^{-1}$, $K_D = 30.3 \text{ nM}$, $\chi^2 = 0.08$
Steady state analysis: $K_D = 34.2 \text{ nM}$, $\chi^2 = 0.14$

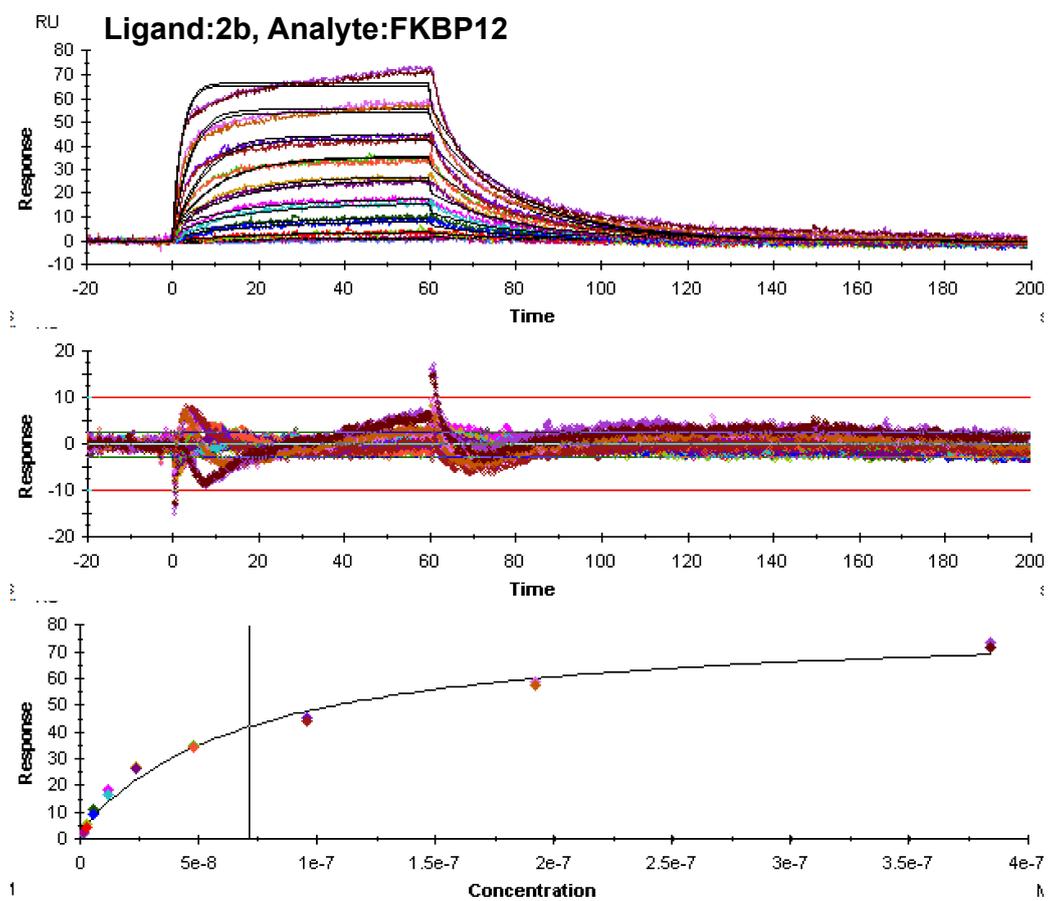


Kinetic analysis: $k_a = 1.48 \times 10^6 \text{ M}^{-1}\text{s}^{-1}$, $k_d = 0.114 \text{ s}^{-1}$, $K_D = 76.8 \text{ nM}$, $\chi^2 = 0.20$
Steady state analysis: $K_D = 117 \text{ nM}$, $\chi^2 = 0.13$

The binding of FKBP12 to immobilized small molecules 2:

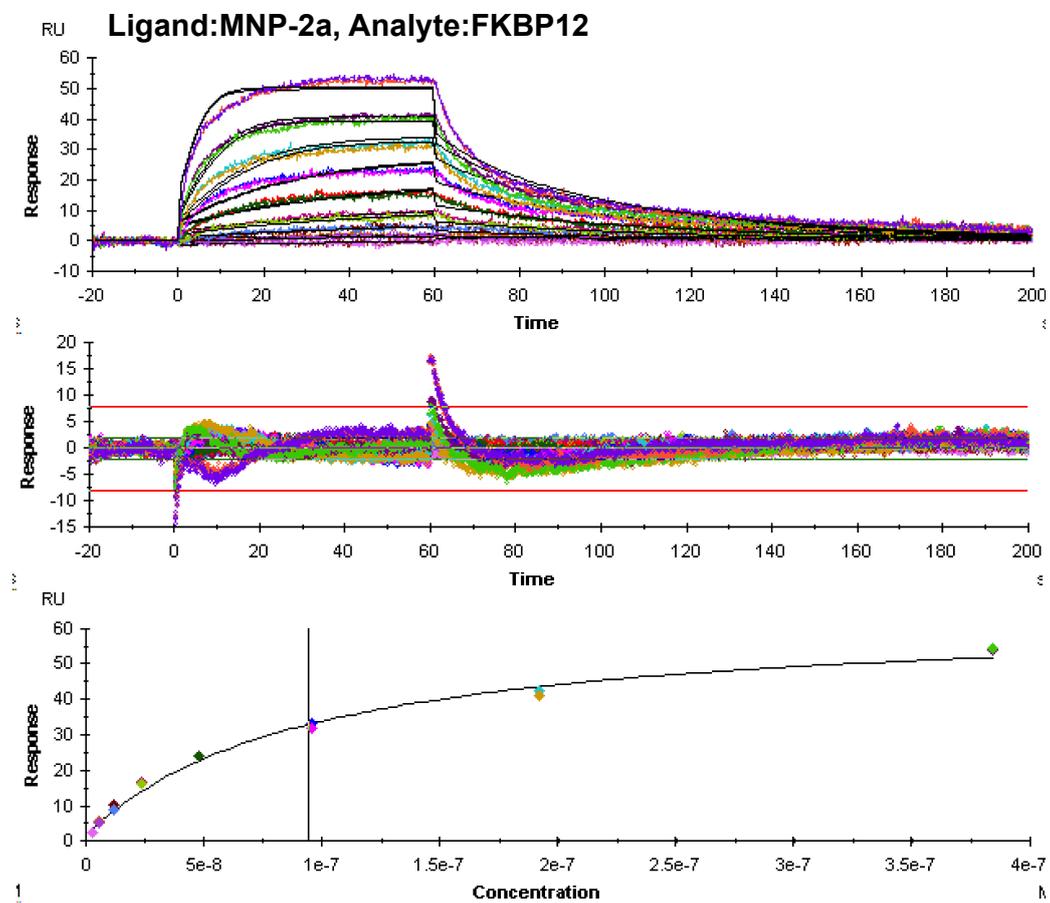


Kinetic analysis: $k_a = 5.98 \times 10^6 \text{ M}^{-1}\text{s}^{-1}$, $k_d = 5.55 \times 10^{-2} \text{ s}^{-1}$, $K_D = 11.0 \text{ nM}$, $\chi^2 = 3.49$
Steady state analysis: $K_D = 16.7 \text{ nM}$, $\chi^2 = 0.89$

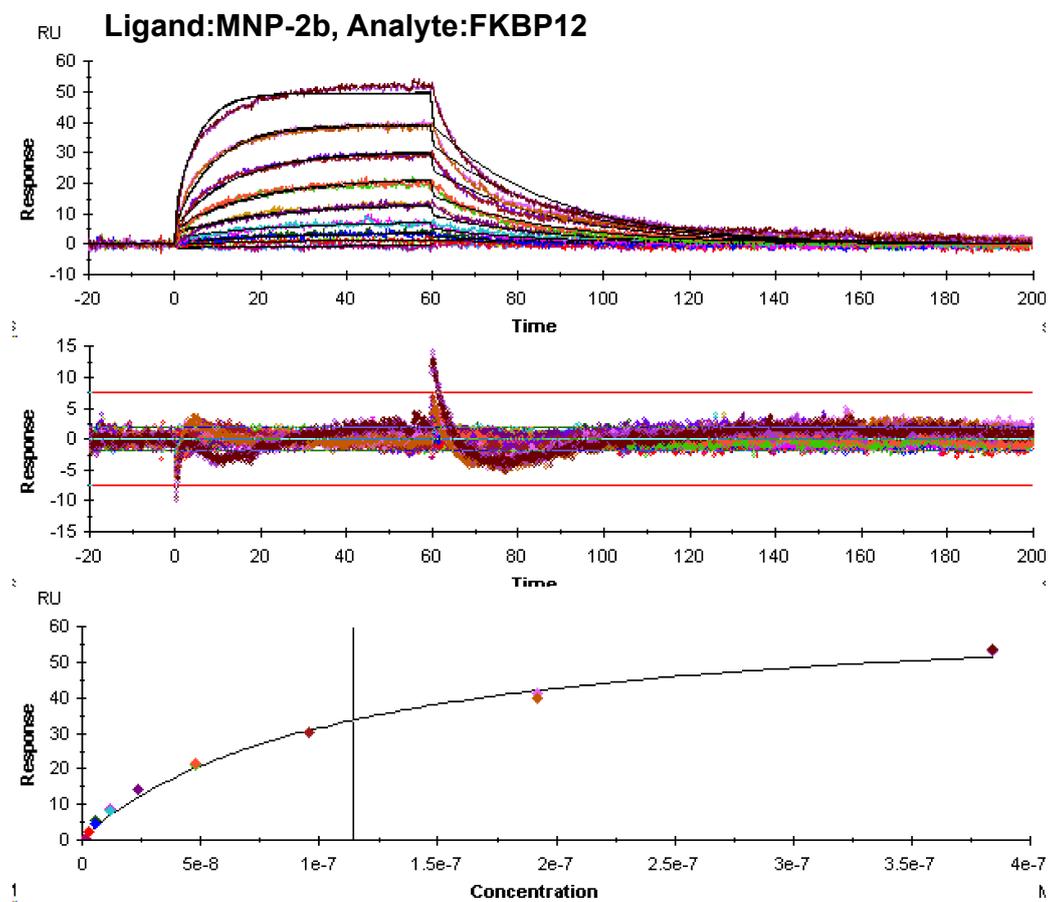


Kinetic analysis: $k_a = 1.22 \times 10^6 \text{ M}^{-1}\text{s}^{-1}$, $k_d = 6.36 \times 10^{-2} \text{ s}^{-1}$, $K_D = 52.3 \text{ nM}$, $\chi^2 = 3.37$
Steady state analysis: $K_D = 71.6 \text{ nM}$, $\chi^2 = 8.75$

On-Chip nanoparticle derivatization and binding of FKBP12:



Kinetic analysis: $k_a = 8.82 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$, $k_d = 3.76 \times 10^{-2} \text{ s}^{-1}$, $K_D = 42.6 \text{ nM}$, $\chi^2 = 2.61$
Steady state analysis: $K_D = 94.2 \text{ nM}$, $\chi^2 = 2.61$



Kinetic analysis: $k_a = 3.91 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$, $k_d = 3.63 \times 10^{-2} \text{ s}^{-1}$, $K_D = 92.7 \text{ nM}$, $\chi^2 = 1.56$
Steady state analysis: $K_D = 114 \text{ nM}$, $\chi^2 = 1.89$