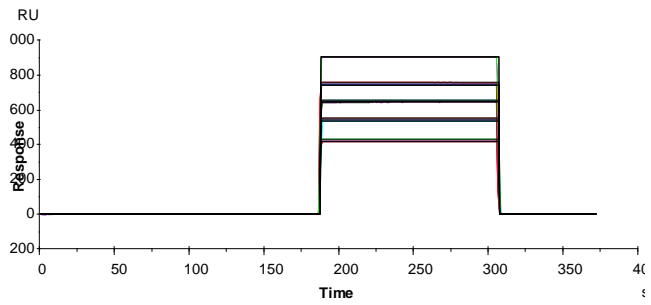
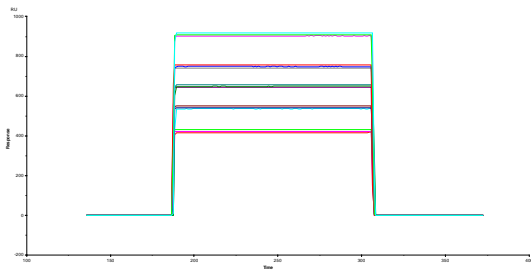


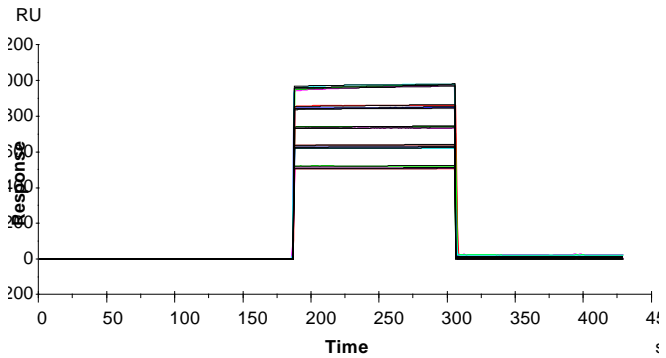
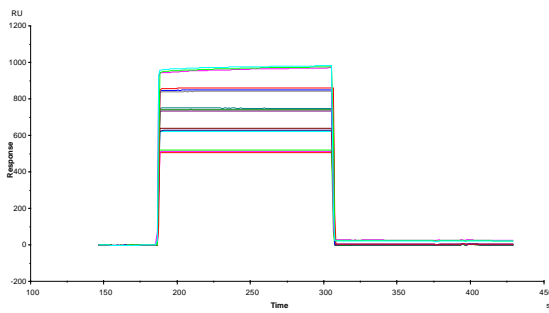
# Supplementary figure 1

## SPR data

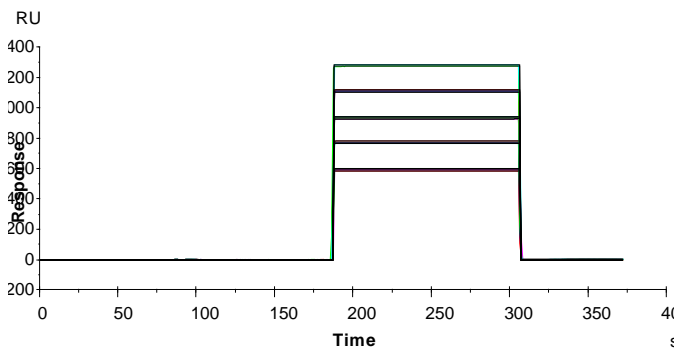
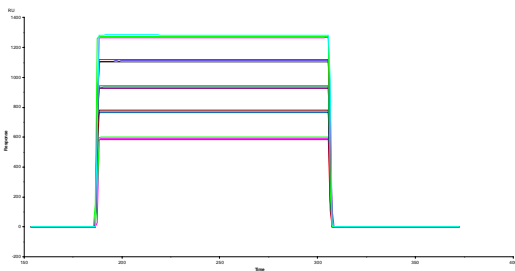
### RNase II\_CSD\_R



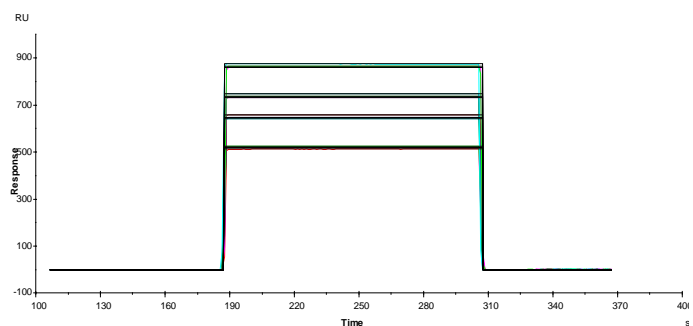
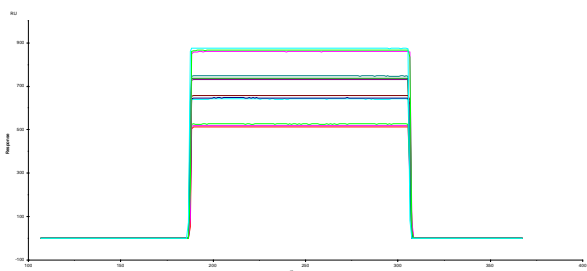
### RNase II\_RNB\_R



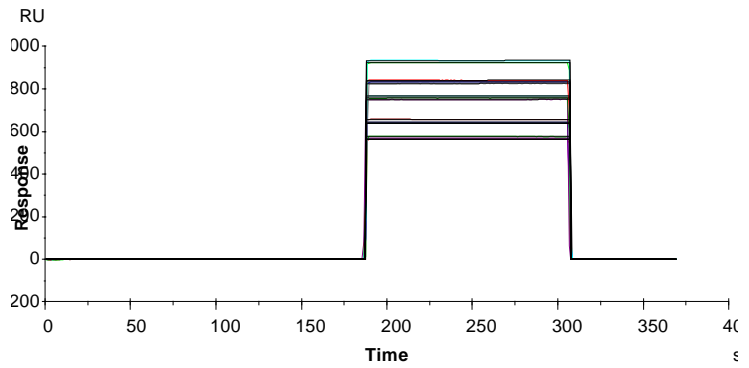
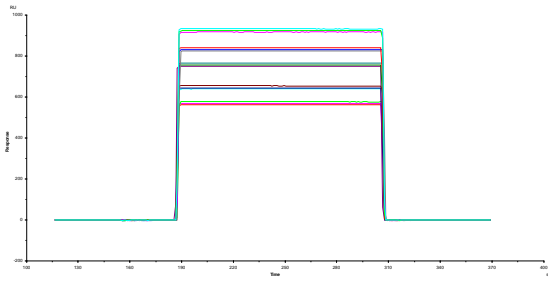
### RNase II\_S1\_R



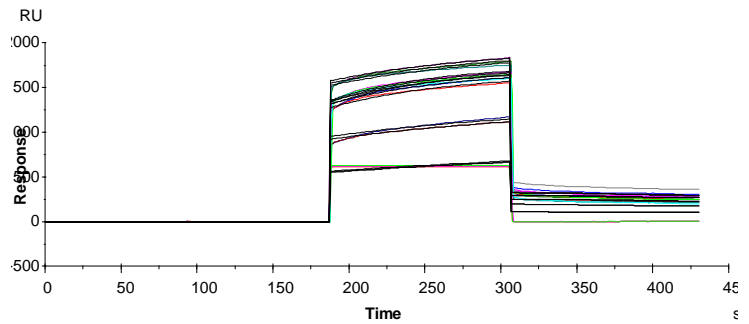
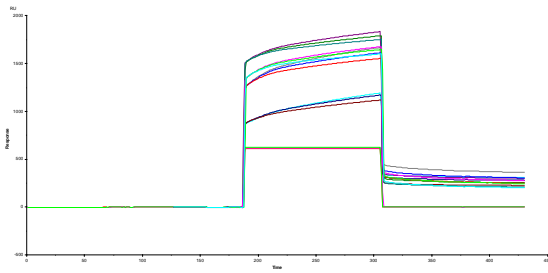
### RNase R\_CSD\_II



## RNase R\_RNB\_II



## RNase R\_S1\_II



**Surface Plasmon Resonance Analysis.** The graphics on left represent the raw data before the fitting and those on the right the data after fitting. All experiments included triple injections of each protein concentration (10, 20, 30, 40 and 50 nM) to determine the reproducibility of the signal and control injections to assess the stability of the RNA surface during the experiment. No target RNA was captured on flow cell 1 and as such this data was used to correct for refractive index changes and nonspecific binding. Rate constants and equilibrium constants were calculated using the BIA EVALUATION 3.0 software package, according to the fitting model 1:1 Langmuir Binding.