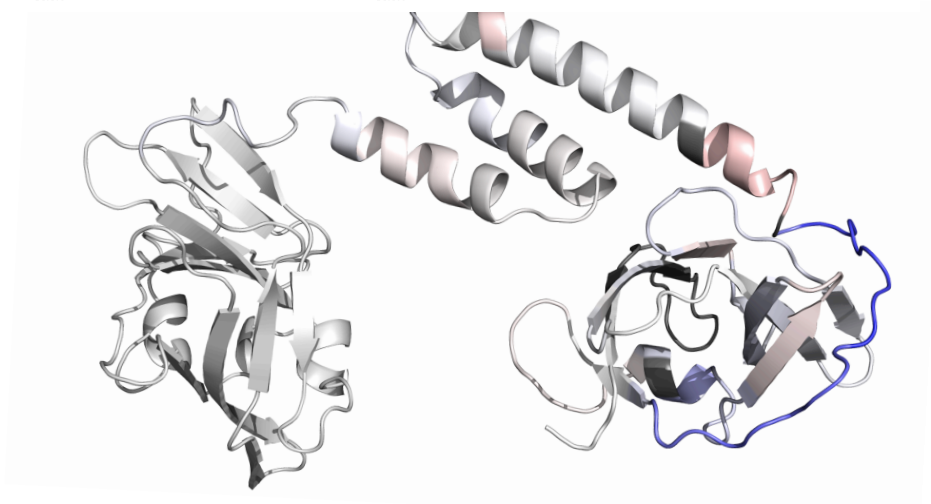


b.



Supplemental Figure 2. HDX-MS of IsdB-NEAT with STA-229

(a) Heat map showing the difference in relative deuterium-uptake of IsdB in complex with STA-229 Fab compared to unbound IsdB. The sequence of IsdB is shown and overlapping peptides are shown below. Shielded amino acids (blue) indicate potential binding-sites and are boxed. (b) The structure of crystalized IsdB is shown. Coloring represents the difference in deuterium-uptake in complex to that in the solitary IsdB from HDX. Scale ranges from -20 (blue) to +20 (red), black represents not observed regions.