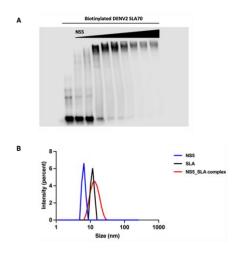
Structure and dynamics of the dengue virus nonstructural 5 (NS5) protein across serotypes



Fingers

Palm Thumb
10 sec

1 min
10 min
1 hr - 2hr

RdRp

Thumb
10 min
1 hr - 2hr

RdRp

Thumb
10 min
1 hr - 2hr

RdRp

RdRp

Thumb
10 min
1 hr - 2hr

RdRp

RdRp

Thumb
10 min
1 hr - 2hr

RdRp

RdRp

RdRp

Thumb
10 min
1 hr - 2hr

RdRp

RdR

Figure 1: Stoichiometric analysis of the NS5-SLA binding interactions. A) EMSA analysis of biotin-tagged SLA saturated with full-length DENV2 NS5. Only one band was observed in all concentrations of the NS5-SLA complex. B) Hydrodynamic radius analysis of particle size of full-length DENV2 NS5, SLA and the NS5-SLA complex.

Figure 2: HDX-MS studies of full-length DENV2 NS5 with SLA. A) Regions of protection and deprotection on DENV2 NS5 upon SLA binding mapped in blue and red respectively over the deuteration course, PDB ID: 5ZQK. B) Difference plot showing the changes in percent deuterium incorporation in DENV2 NS5 peptides upon binding SLA. C) Regions of protection and deprotection mapped on corresponding peptides in DENV3 NS5-SLA cryoEM structure, PDB ID: 8GZP.

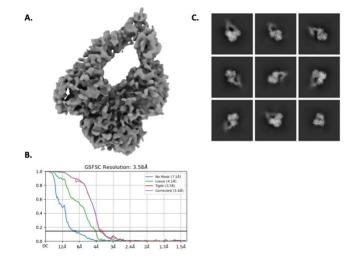


Figure 3: CryoEM single particle analysis of the DENV2 NS5-SLA complex. A) Final density map of the DENV2 NS5-SLA complex after multiple iterations of 3D reconstructions and homogenous refinements. B) Fourier shell correlation (FSC) plot showing the average map resolution of 3.58 Å. C) Class averages from 2D classification done before 3D reconstruction.

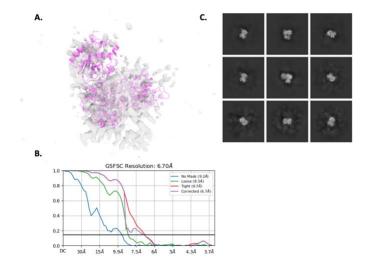


Figure 4: CryoEM single particle analysis of apo DENV2 NS5. A) Best density map obtained after 3D reconstruction and homogenous refinement. A structure of apo DENV2 NS5 in the closed form is fit into the map, PDB ID: 6KR2. B) Fourier shell correlation (FSC) plot showing the average map resolution of 6.70 Å. C) Class averages from 2D classification done before 3D reconstruction.