

## Supplementary Information

# The Importance of Epigallocatechin as a Scaffold for Drug Development against Flaviviruses

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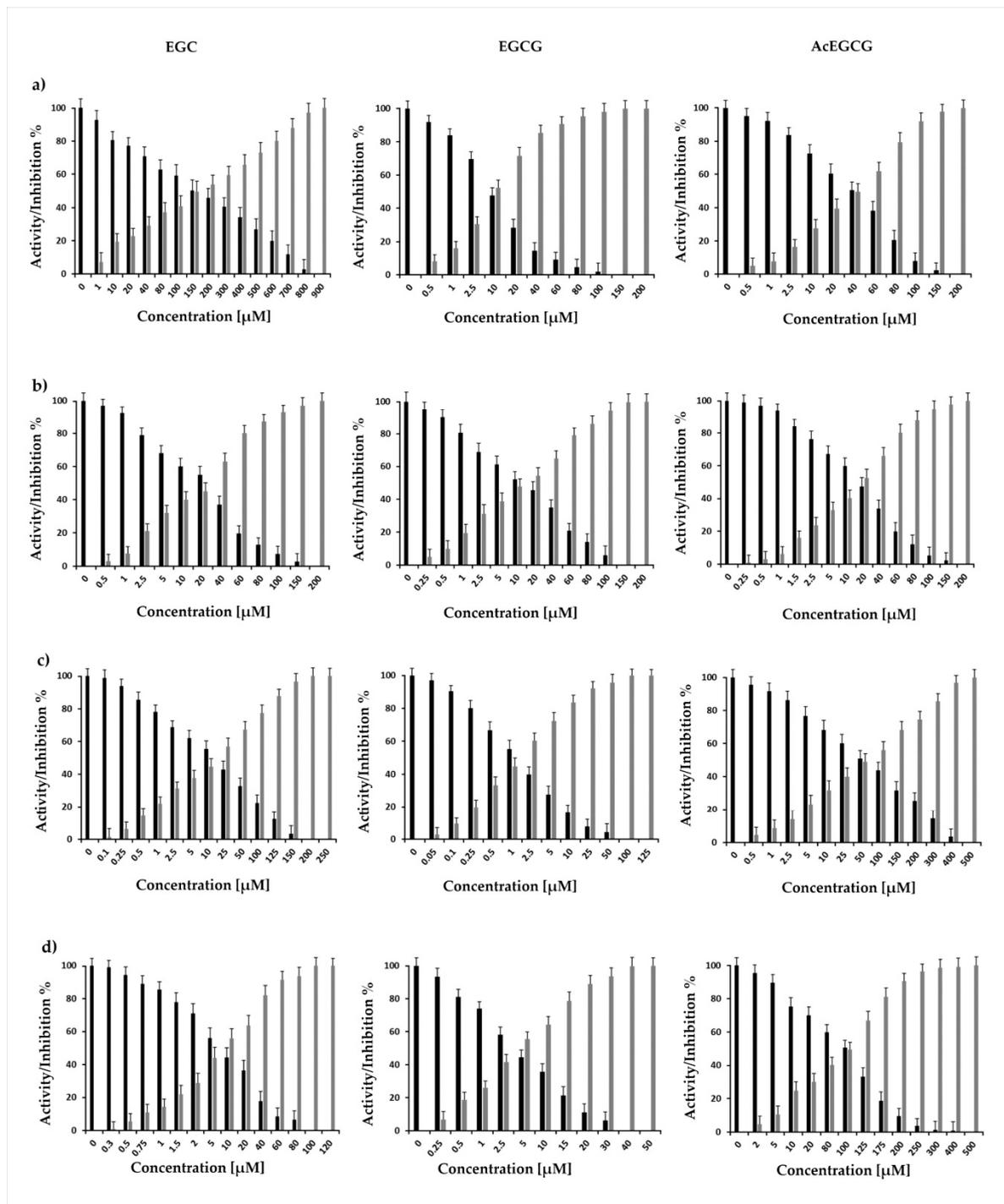
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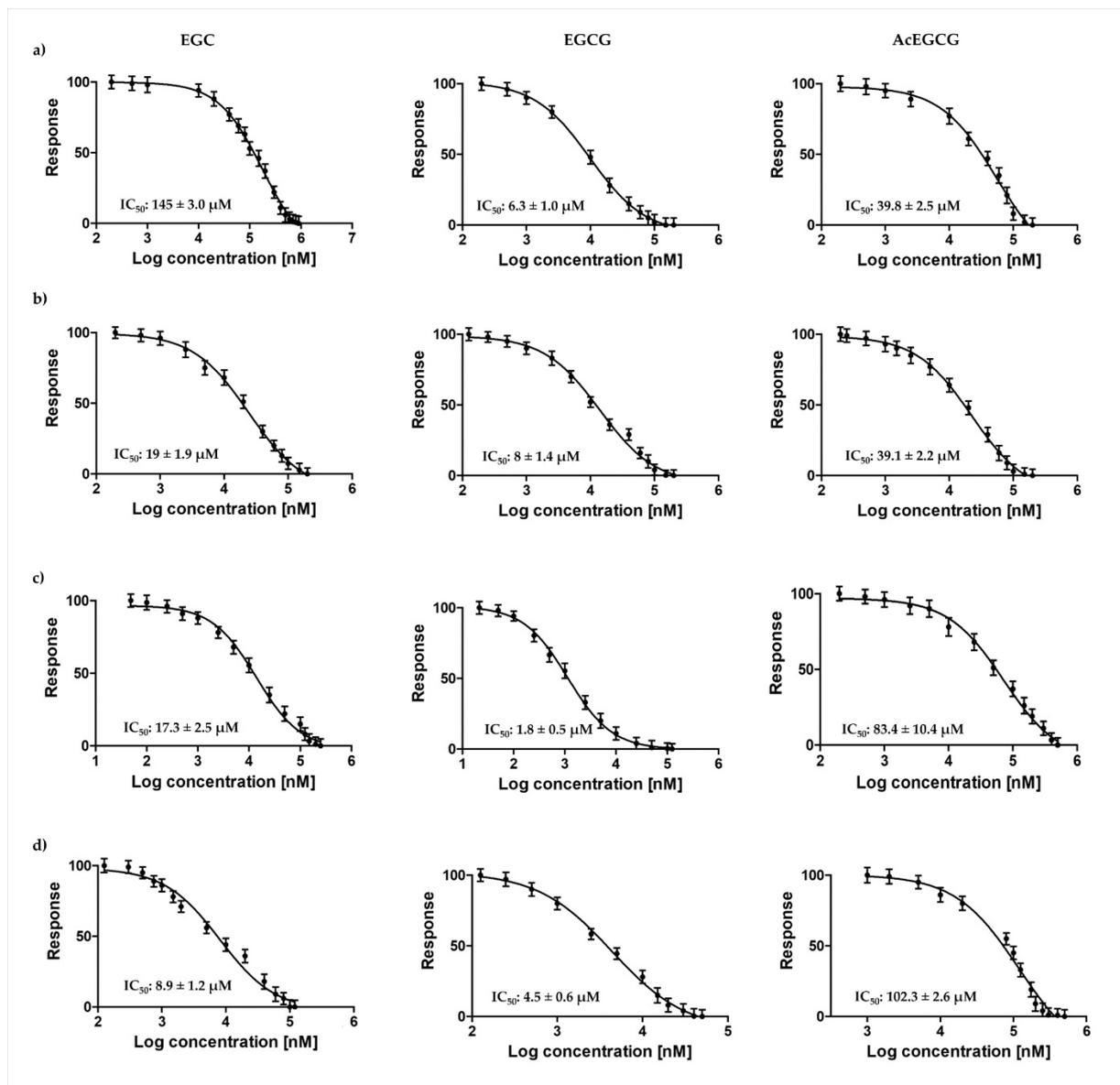
**Table S1.** Range of the epigallocatechin molecules concentrations.

Epigallocatechin molecules concentration (µM)		
EGC	EGCG	AcEGCG

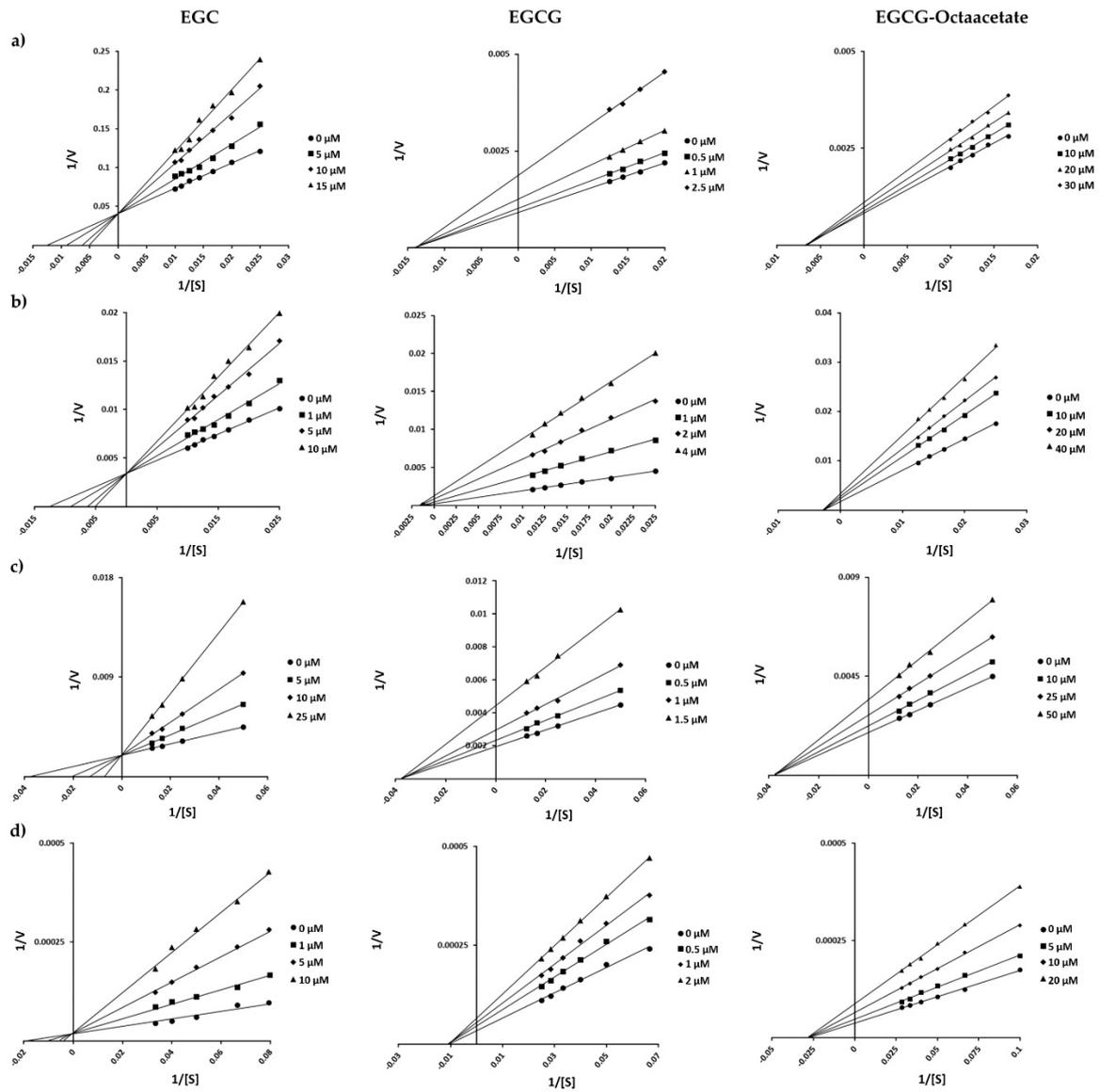
<b>DENV2</b>	1.31; 1.97; 2.96; 4.44	0.58; 0.88; 1.32; 1.97	1.95; 2.9; 4.38; 9.87; 14.81
<b>YFV</b>	1.75; 2.63; 3.95; 5.92; 8.88; 13.33	0.39; 0.58; 1.31; 1.97; 2.9; 4.44	1.97; 2.9; 4.44; 6.66; 10
<b>WNV</b>	1.56; 3.12; 6.25; 12.5	1.3; 1.95; 2.9; 4.38; 6.5	4.38; 6.5; 9.9; 14.81; 22.2
<b>ZIKV</b>	4; 8; 16; 32; 64	0.58; 0.88; 1.32; 1.97	2.92; 4.39; 6.58; 9.87; 14.81; 22.22; 33.33



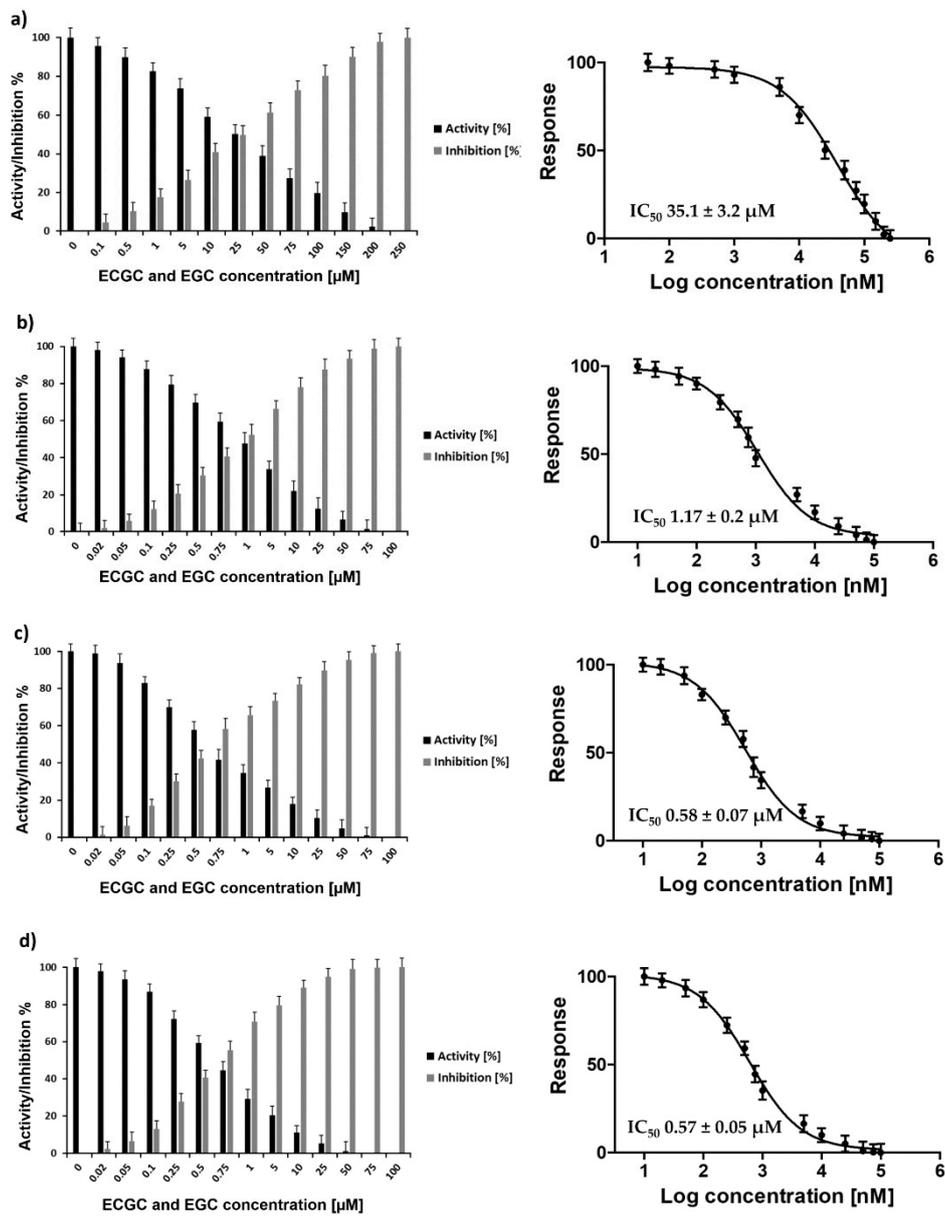
**Figure S1.** Inhibition effect of the Epigallocatechin molecules over the NS2B/NS3 proteases of (a) DENV, (b) YFV), (c) WNV, and (d) ZIKV. Data showed are the mean  $\pm$  SD from three independent measurements (n=3).



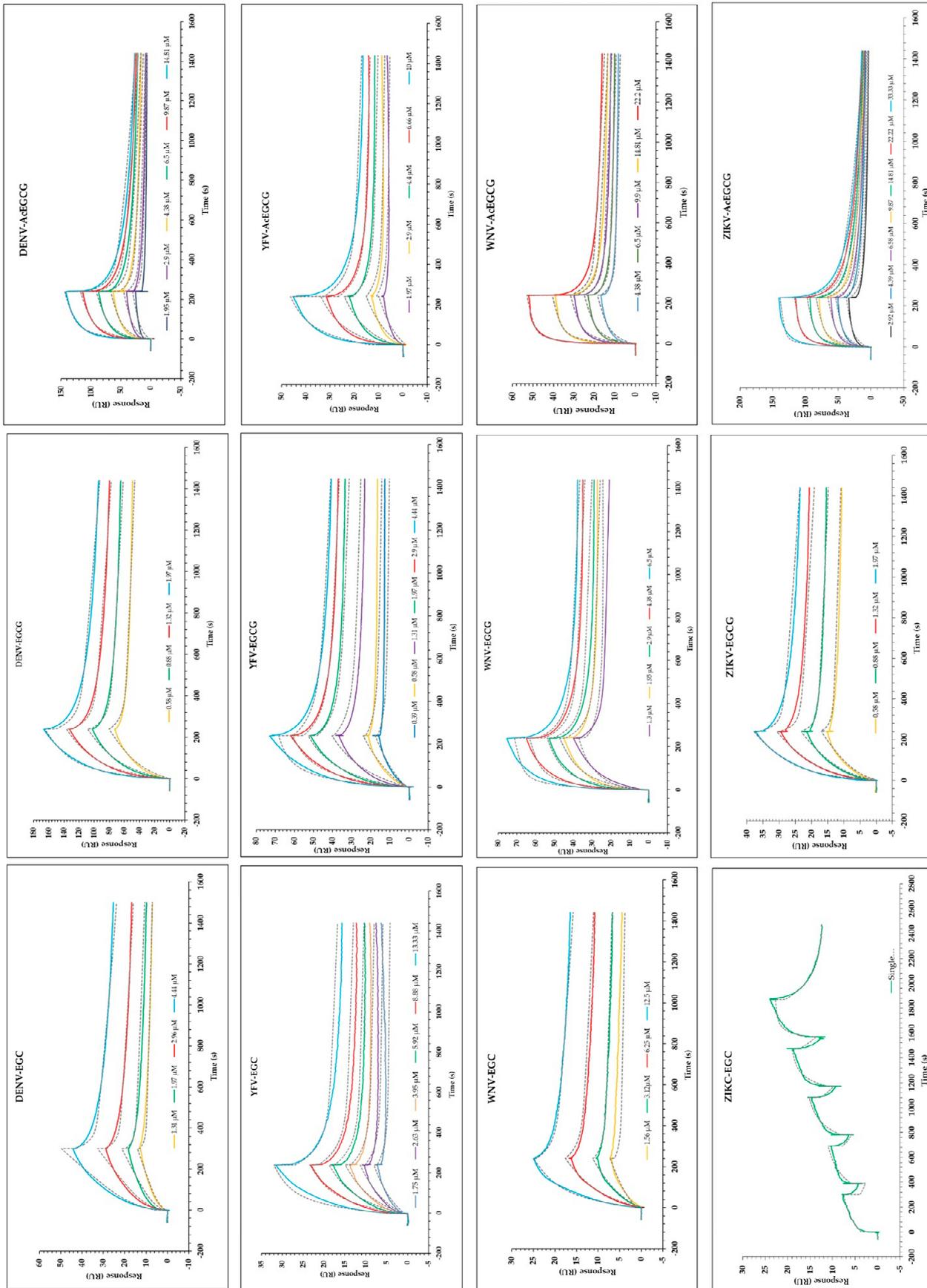
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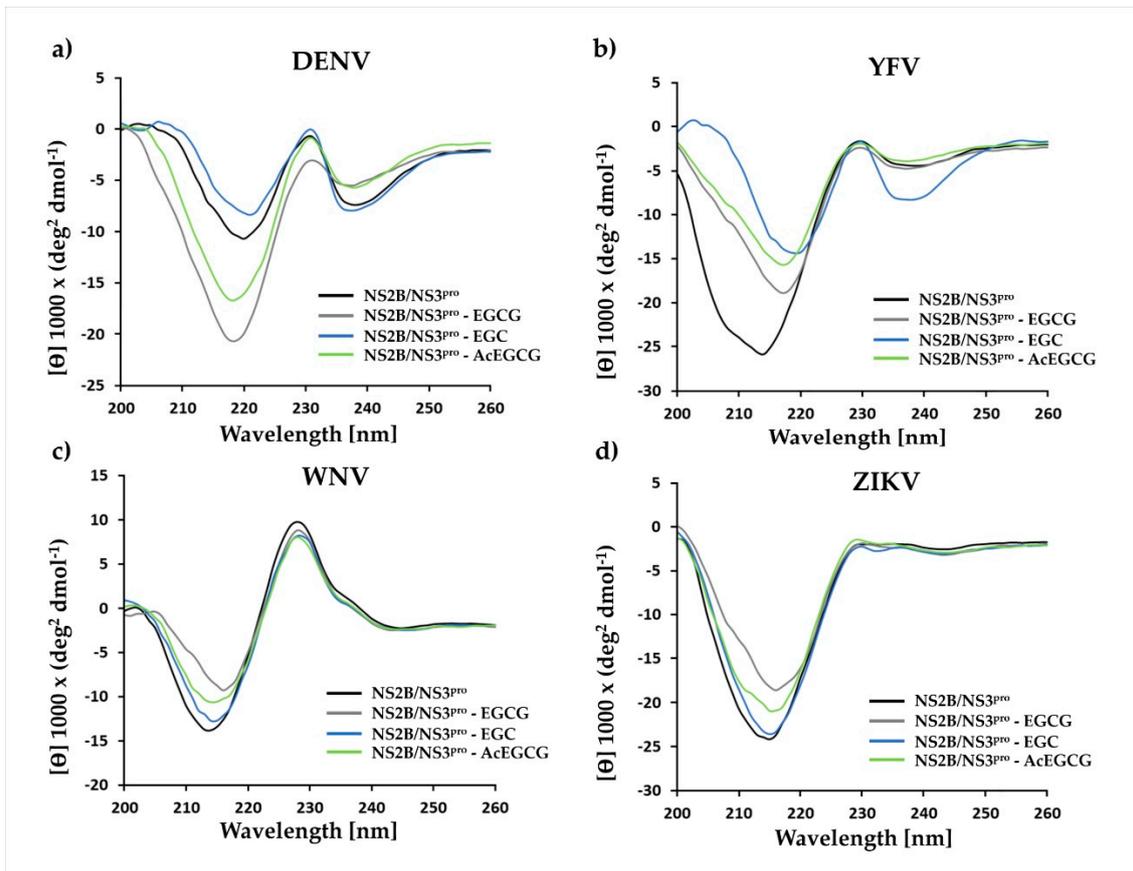
**Figure S3.** Inhibition mode of the Epigallocatechin molecules over the NS2B/NS3 proteases of (a) DENV, (b) YFV, (c) WNV, and (d) ZIKV. Data showed are the mean  $\pm$  SD from three independent measurements ( $n=3$ ).



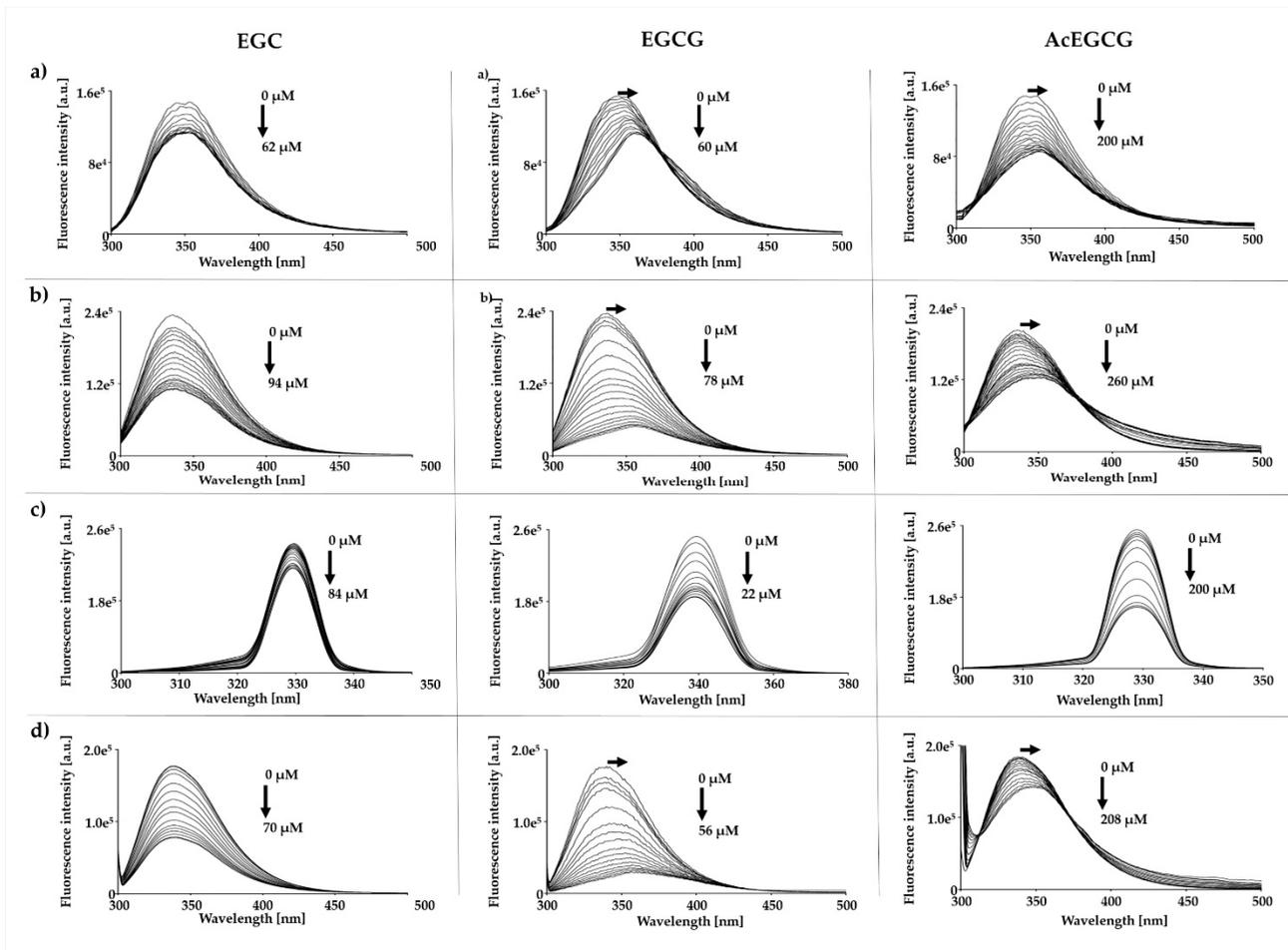
**Figure S4.** Inhibition effect of the Epigallocatechin molecules combination over the NS2B/NS3 protease of (a) DENV, (b) YFV, (c) WNV, and (d) ZIKV. Data showed are the mean  $\pm$  SD from three independent measurements ( $n=3$ ).



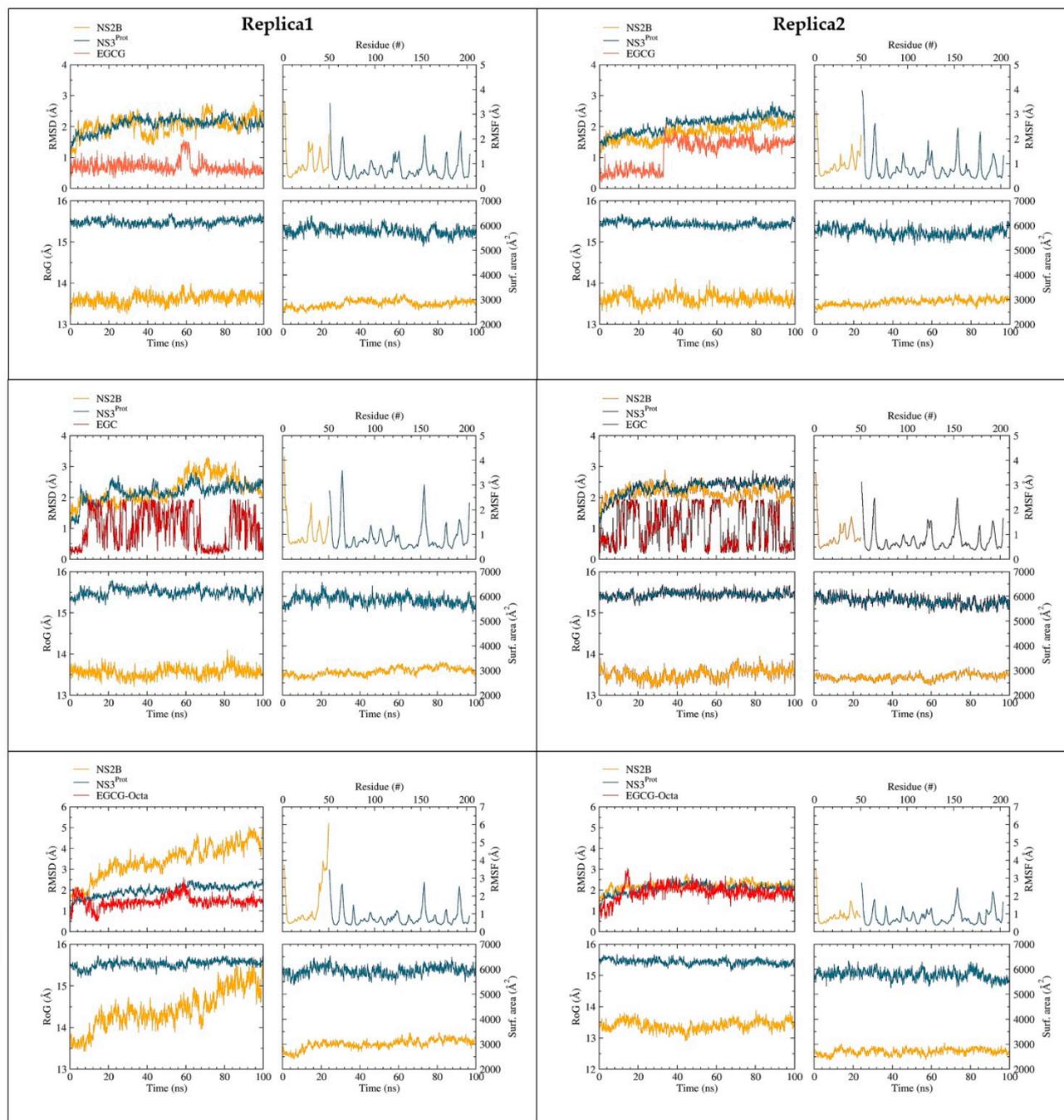
**Figure S5.** Dissociation constant ( $K_D$ ) determination of the epigallocatechin molecules binding to NS2B/NS3<sup>pro</sup>s using surface plasmon resonance (SPR). NS2B/NS3 proteases were immobilized on CM5 sensor chip and a range of the epigallocatechin molecules concentrations (Table S1) were passed over the surface. The final sensorgram is representative of two cycles.



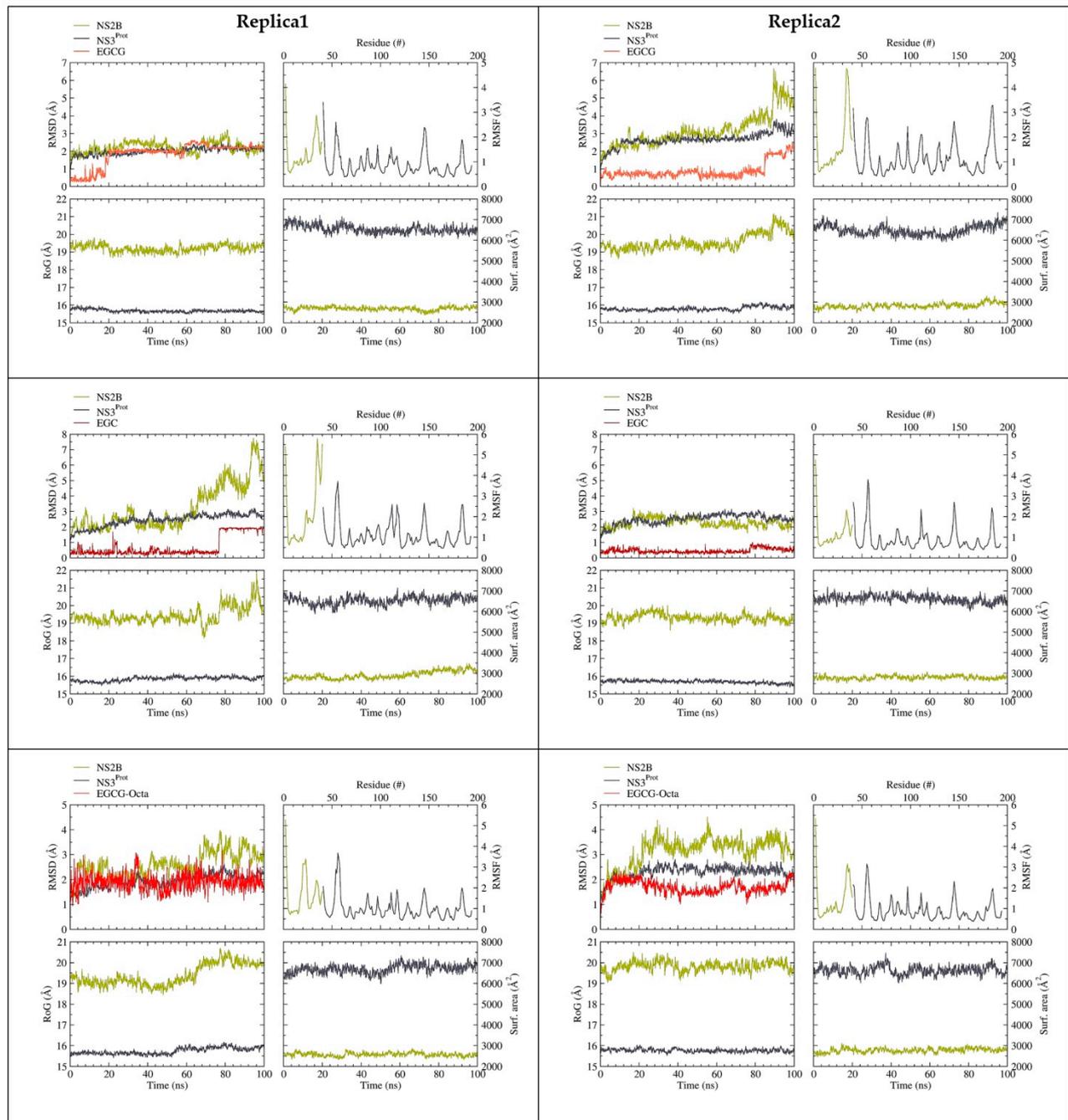
**Figure S6.** Ligand-induced changes in the CD spectrum of soluble NS2B/NS3 proteases of DENV, YFV, WNV and ZIKV in 20 mM K<sub>2</sub>HPO<sub>4</sub>/KH<sub>2</sub>PO<sub>4</sub> pH 7.5.



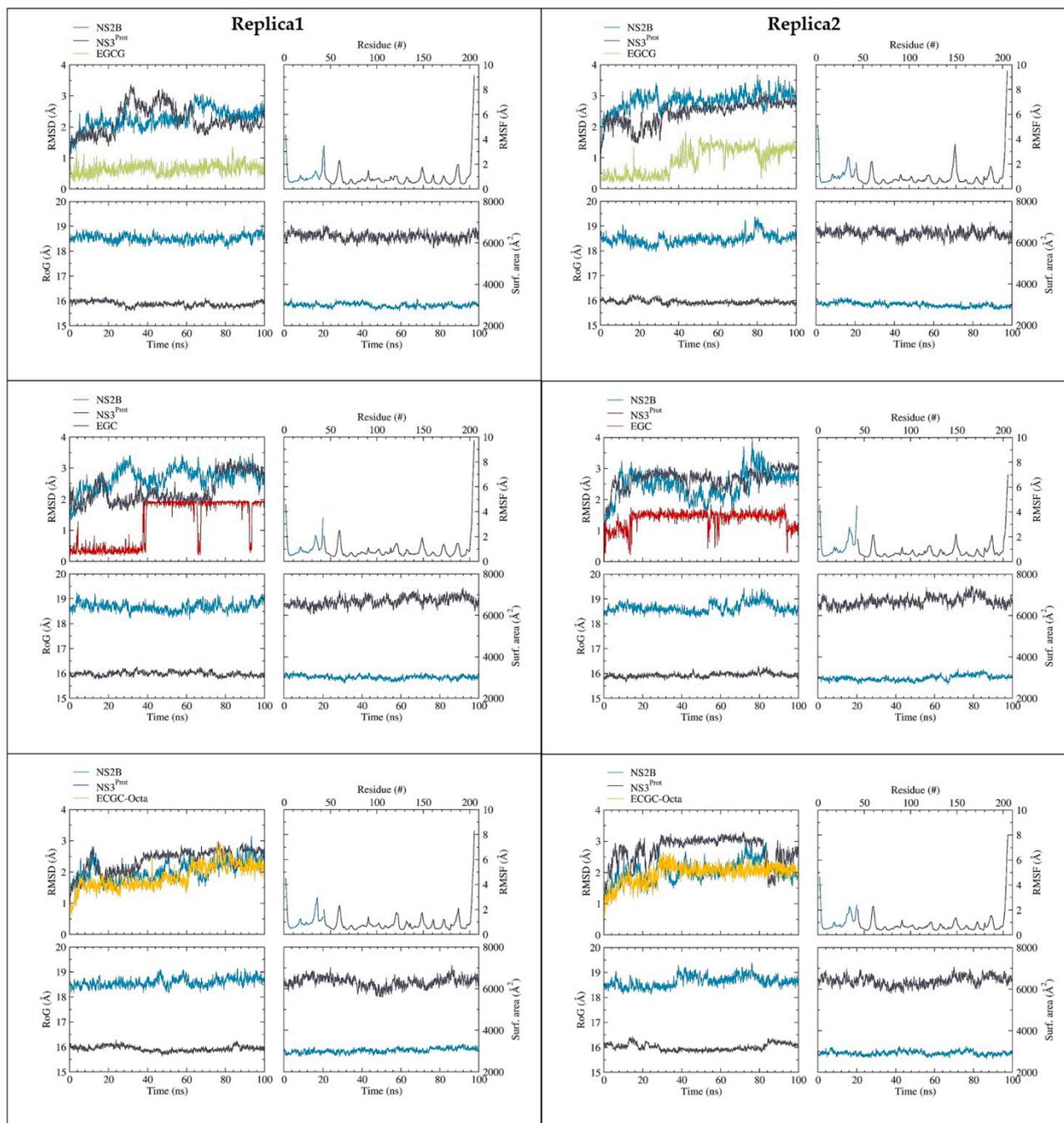
**Figure S7.** Fluorescence spectroscopy of Trp at 295 nm of the NS2B/NS3pros and the epigallocatechin molecules. a) DENV, (b) YFV), (c) WNV, and (d) ZIKV.



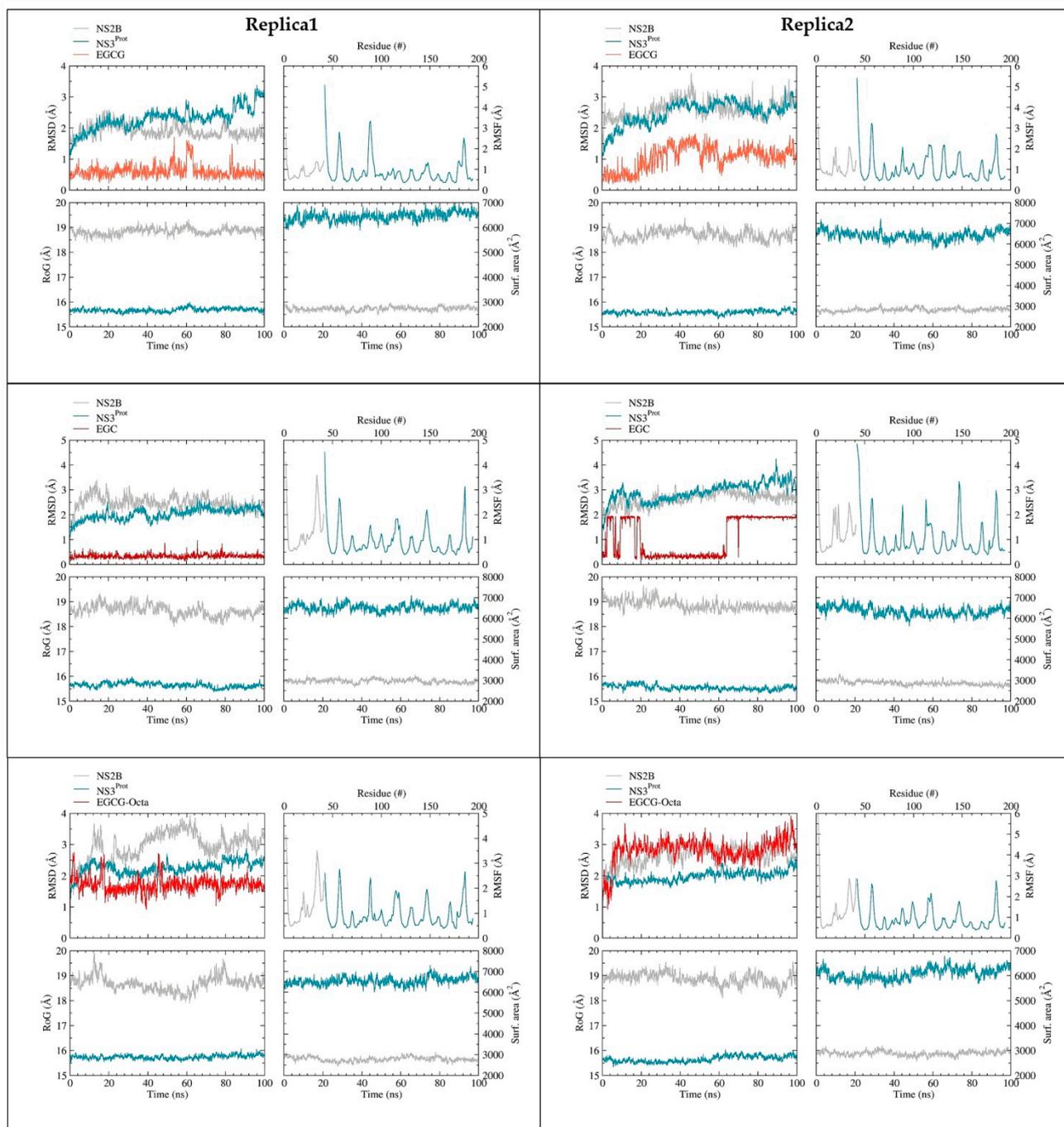
**Figure S8** RMSD values and RMSF profiles for the replicate 100 ns of MD simulations of NS2B/NS3 protease of DENV in complex with the epigallocatechin molecules. The RMSD time profiles concerning all backbone atoms of NS2B/NS3<sup>prost</sup> and the molecules (EGC, EGCG, and AcEGCG). The RMSF plot corresponds to the protein/molecules complex, and the replicates are specified.



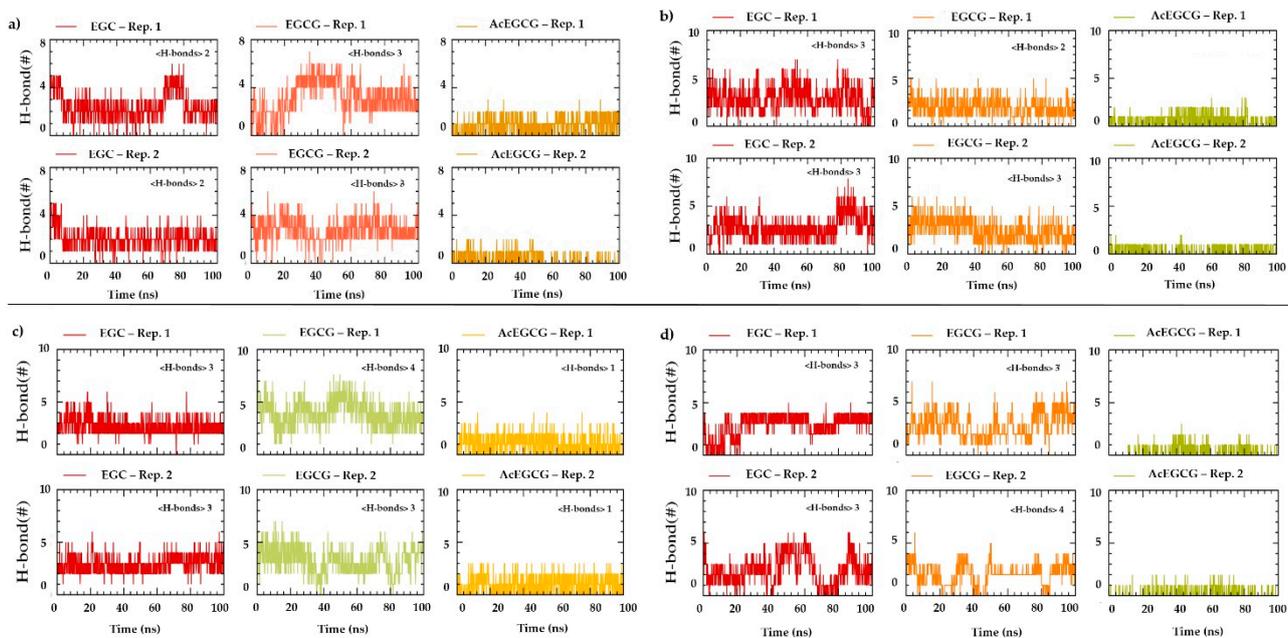
**Figure S9.** RMSD values and RMSF profiles for the replicate 100 ns of MD simulations of NS2B/NS3 protease of YFV in complex with the epigallocatechin molecules. The RMSD time profiles concerning all backbone atoms of NS2B/NS3<sup>Prot</sup> and the molecules (EGC, EGCG, and AcEGCG). The RMSF plot corresponds to the protein/molecules complex, and the replicates are specified.



**Figure S10.** RMSD values and RMSF profiles for the replicate 100 ns of MD simulations of NS2B/NS3 protease of WNV in complex with the epigallocatechin molecules. The RMSD time profiles concerning all backbone atoms of NS2B/NS3<sup>prot</sup> and the molecules (EGC, EGCG, and AcEGCG). The RMSF plot corresponds to the protein/molecules complex, and the replicates are specified.



**Figure S11.** RMSD values and RMSF profiles for the replicate 100 ns of MD simulations of NS2B/NS3 protease of ZIKV in complex with the epigallocatechin molecules. The RMSD time profiles concerning all backbone atoms of NS2B/NS3<sup>Prox</sup> and the molecules (EGC, EGCG, and AcEGCG). The RMSF plot corresponds to the protein/molecules complex, and the replicates are specified.



**Figure S12.** Numbers of H-bonds between the epigallocatechins and NS2B/NS3pro residues during the 100 ns MD simulations. The general criteria to determine the occurrence of the H-bond was a donor-acceptor distance  $\leq 3.5$  Å and a donor-H-acceptor angle  $\geq 120^\circ$ . <H-bonds> represents the average number of intermolecular H-bonds formed along each trajectory. a) Dengue, b) YFV, c) WNV, and d) ZIKV.