

Supplementary Informations 1

Reaching beyond HIV/HCV: Nelfinavir as a potential starting point for broad-spectrum protease inhibitors against dengue and chikungunya virus

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Active site identification of CHIKV NSP2 (PDB: 3TRK)

Output from SiteHound Web (<http://scbx.mssm.edu/sitehound/sitehound-web/Input.html>)

CYS 1013 A
TRP 1014 A
LYS 1045 A
ALA 1046 A
TYR 1047 A
SER 1048 A
VAL 1051 A
TYR 1079 A
ASN 1082 A
TRP 1084 A
LEU 1203 A
GLU 1204 A
LEU 1205 A
GLY 1206 A
ALA 1237 A
LYS 1239 A
GLN 1241 A
LEU 1243 A
ASP 1246 A

Output from MetaPocket (<http://projects.biotec.tu-dresden.de/metapocket/>)

RESI	ALA_A^1010^	ASN_A^1011^	CYS_A^1013^	ASN_A^1082^
HIS_A^1083^				
RESI	TYR_A^1079^	TRP_A^1084^	VAL_A^1012^	TRP_A^1014^
ASP_A^1081^				
RESI	LEU_A^1205^	TYR_A^1047^	ALA_A^1046^	SER_A^1048^
PRO_A^1049^				

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RESI      GLU_A^1204^  ASN_A^1202^  ASP_A^1044^  LYS_A^1045^
GLY_A^1206^
RESI      ASP_A^1246^  LEU_A^1207^  GLN_A^1241^  LEU_A^1203^
VAL_A^1051^
RESI      GLY_A^1245^  LEU_A^1243^  LEU_A^1192^  PRO_A^1191^
ALA_A^1040^
RESI      LYS_A^1239^  THR_A^1268^  ALA_A^1237^  GLY_A^1244^
GLU_A^1055^
RESI      ILE_A^1038^  GLN_A^1039^  ASP_A^1235^  LEU_A^1240^
GLU_A^1043^
RESI      ILE_A^1037^  VAL_A^1234^  HIS_A^1236^  GLN_A^1231^
ILE_A^1221^
RESI      ARG_A^1226^  THR_A^1223^  PRO_A^1224^  HIS_A^1222^
PHE_A^1225^
RESI      VAL_A^1272^  ASP_A^1266^  SER_A^1269^  CYS_A^1233^
GLY_A^1176^
RESI      ASN_A^1220^  TYR_A^1177^  GLU_A^1050^  LYS_A^1091^
ARG_A^1271^
RESI      ARG_A^1267^

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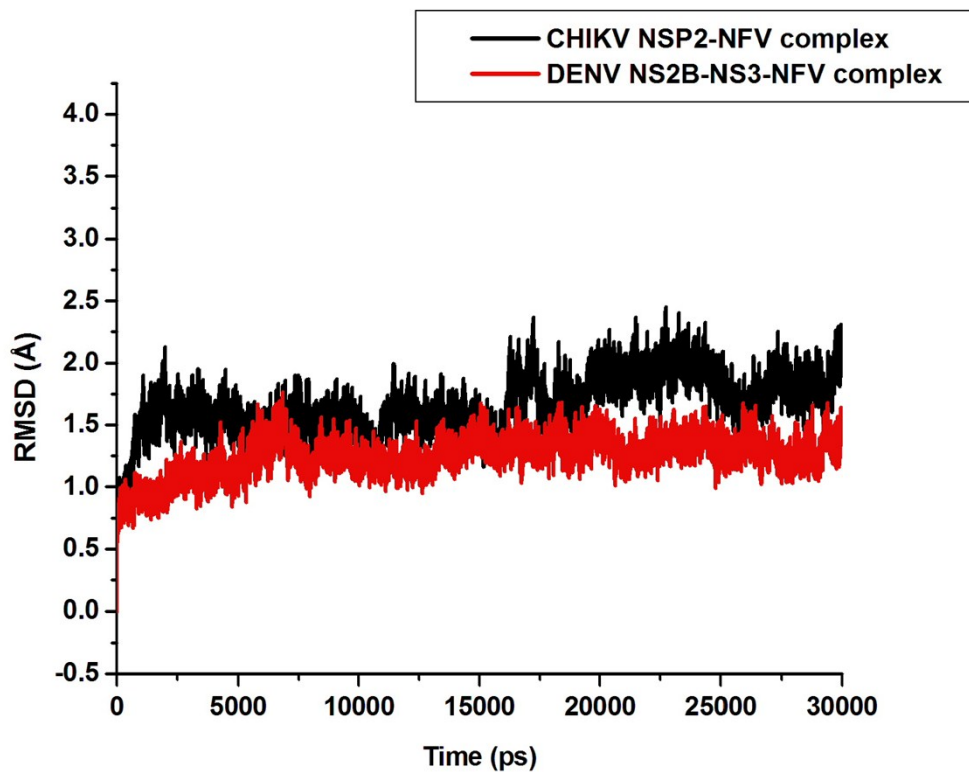


Figure S1. C- α RMSD fluctuation of CHIKV NSP2 and DENV NS2B-NS3 complexed with NFV during simulation time.

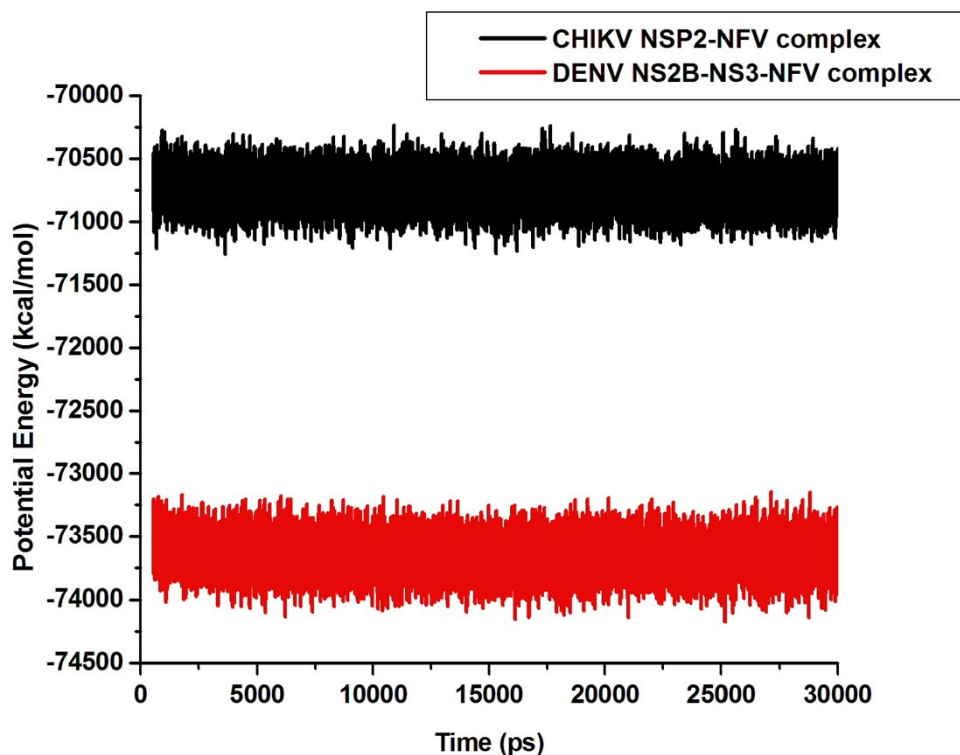


Figure S2. Potential energy fluctuation of CHIKV NSP2 and DENV NS2B-NS3 complexed with NFV during simulation time.

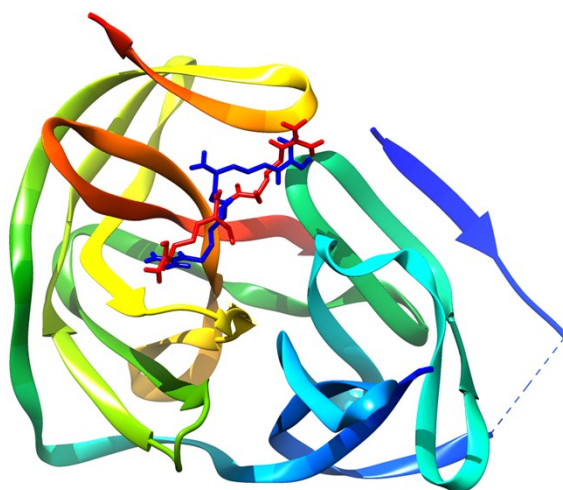


Figure S3. Redocking of the peptide inhibitor in the active site of DENV NS2B-NS3 protease. The co-crystal and docked ligand is highlighted in red and blue respectively. Due to its linear shape and peptide nature it is hard to derive a similar binding pose using molecular docking but its binding in almost similar cavity in proximity with the co-crystal ligand gives solid credibility to the preciseness of the docking.