

Supplementary information

Unveiling the Interactions of Non-structural Protein-W61 with nucleoprotein: and as a Potential Therapeutic Target in Severe Fever with Thrombocytopenia Syndrome Virus (SFTSV) Replication

Supplementary Table 1. Bacterial strains and plasmids use in this study

Strains/plasmid	Description	References
<i>Escherichia coli</i>		
DH5α	F ^{-endA1} , glnV44, thi-1, recA1, relA1, gyrA96, deoR, nupG, Φ80dlacZΔM15 Δ(lacZYA-argF)U169, hsdR17(rK-mK ⁺),	Lab stock
BL21(DE3)pLysS	F ⁻ , ompT, hsdS _B (rB ⁻ , mB ⁻), dcm, gal, λ (DE3), pLysS, Cm ^r	Lab stock
JOL2643	DH5α containing pcDNA-NP	This study
JOL2644	DH5α containing pcDNA-NS	
JOL2645	DH5α containing pcDNA-NSC5S	
JOL2646	DH5α containing pcDNA-NSW61Y	
JOL2647	DH5α containing pcDNA-NSS207T	
Plasmids		
pcDNA3.1-CMV	CMV promoter, MCS, f1 ori, SV40 promoter, Neomycin ^R pUC ori, Amp ^R	Lab stock
pcDNA-NP	pcDNA harboring NP of SFTSV	This study
pcDNA-NSs	pcDNA harboring NS of SFTSV	
pcDNA-NSsC5S	pcDNA harboring NSC5S mutant of NSs	
pcDNA- NSsW61Y	pcDNA harboring NSW61Y mutant of NSs	
pcDNA- NSsS207T	pcDNA harboring NSS207T mutant of NSs	
pET28a(+)	IPTG-inducible, T7 expression vector, C-terminal 6× histidine tag, Kan ^R	Lab stock
pET28a-NP	pET28a(+)harboring NP optimized genes	This study
pET28a-NSs	pET28a(+)harboring NS genes	

7 **Supplementary Table 2. Primers use in this study**

primers	Description (5' - 3')	References
pcDNA-NP-F	CCCAAGCTTGCCACCATGGCAGAGT	
pcDNA-NP-R	CGGAATTCTTACAGGTTTCTGTAAGCAGCA	
pcDNA- NSs-F	CCCAAGCTTATGTCGCTGAGCAA	
pcDNA-NSs-R	CGAAGCTTTTAGACCTCCTTCG	This study
pET28-NSs-F	CGGAATTCATGTCGCTGAGCAAATGCT	
pET28-NSs-R	GGAAGCTTGTGGTGGTGGTGG	
pET28-NP-F	CGGAATTCATGTCCGAGTGGAGC	
pET28-NP-R	GGAAGCTTCAGGTTCCGGTAAG	
Sseg-F-3	GGGTCCCTGAAGGAGTTGTAAA	Y. Sun et al. Journal of Clinical Virology 53 (2012) 48–53
Sseg-R-3	TGCCTTCACCAAGACTATCAATGT	
<i>Site-directed mutagenesis</i>		
NSst16a-F	ATGTCGCTGAGCAAAAGCTCCAACGTTGACCTCA AATC	This study
NSst16a-R	GATTTGAGGTCAACGTTGGAGCTTTTGCTCAGCGA CA	
NSsg182a-g183t-F	GGATTTTTTGGGTTGCCAAATAAATATACTGTGTTG GTCATCTTGCCC	
NSsg182a-g183t-R	GGGCAAGATGACCAACACAGTATATTTATTTGGCA ACCCAAAAAATCC	
NSst619a-F	CTTGAACCACCACTTATTCATTCTACCTCATTGCG TAAG	
NSst619a-R	CTTACGCAATGAGGTAGAAGTGAATAAGTGGTGGT TCAAG	

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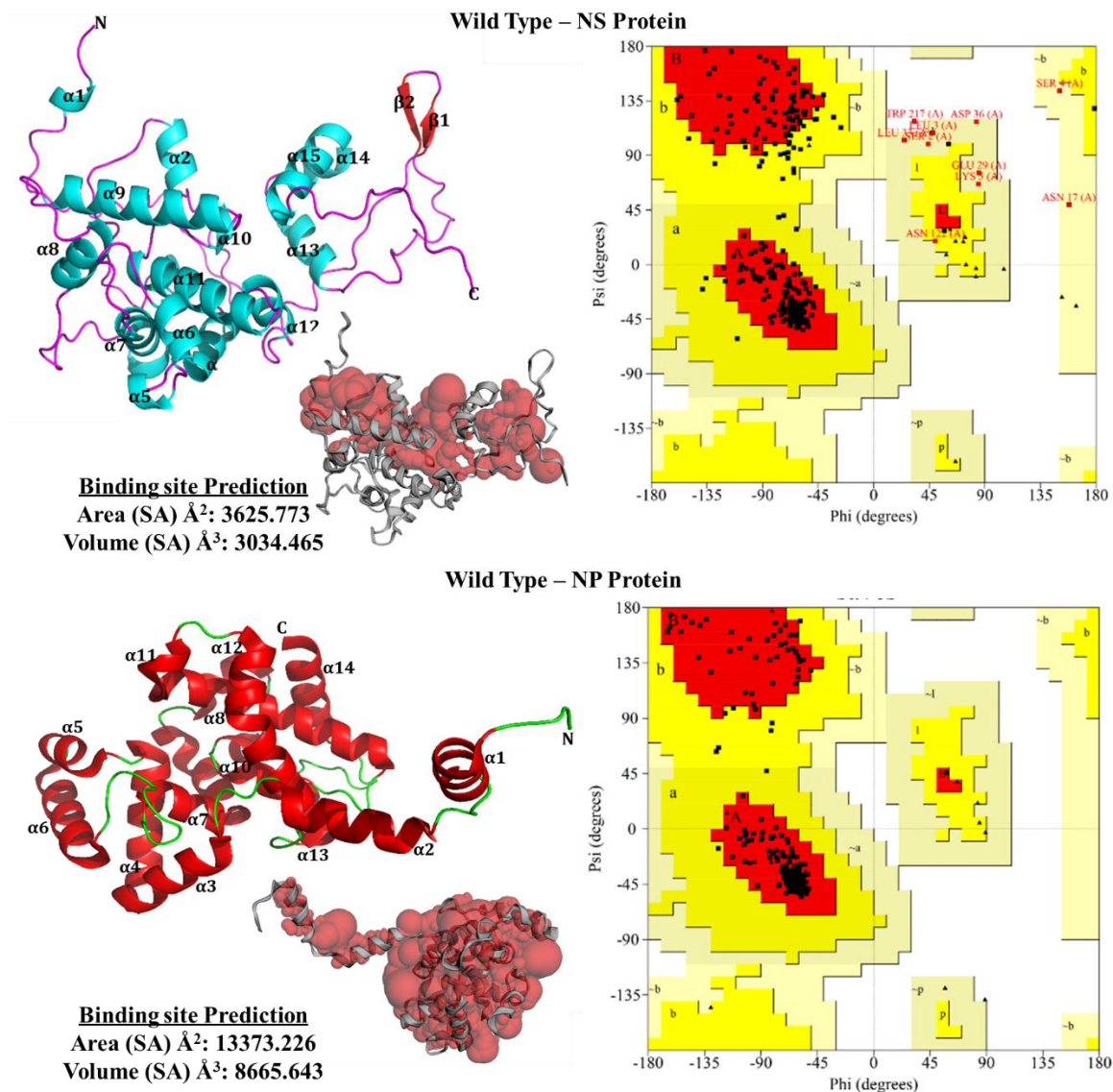
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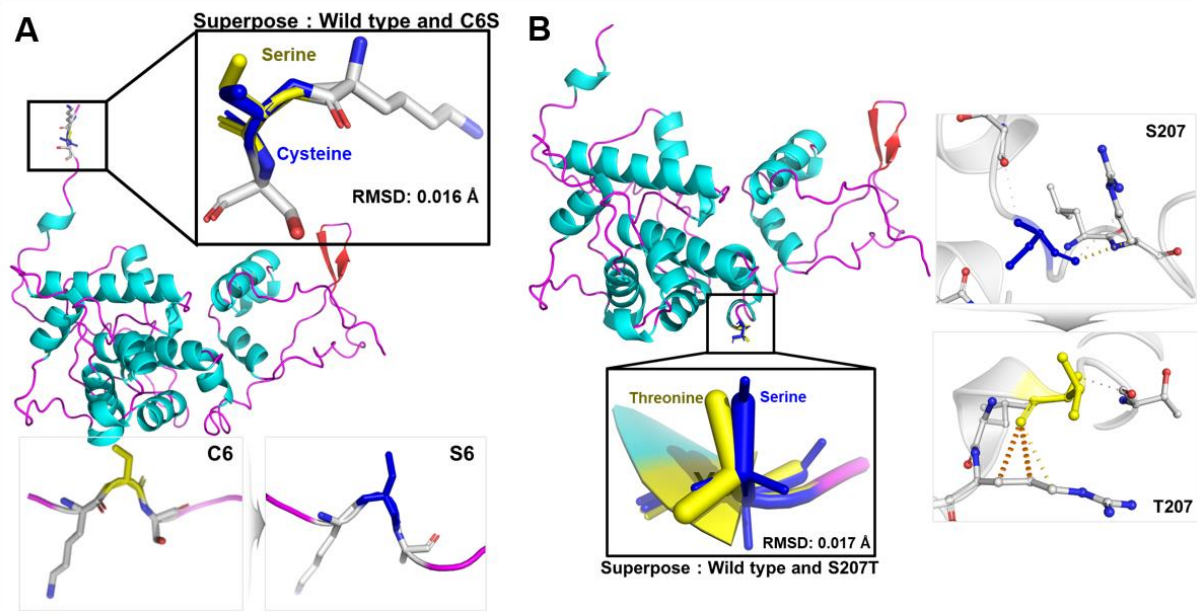
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S segment	1	2	3	4	5	6	7	8	9	10	11	12
CB2												
CB1	95.30											
CB3	95.02	96.45										
KADGH	96.11	96.11	96.05									
KAGNH	95.82	95.93	96.22	96.02								
KAGWH3	95.76	96.16	95.88	96.68	97.37							
KAGNH4	96.33	96.56	96.51	97.37	97.94	98.28						
KAJNH2	95.36	95.59	95.53	97.77	95.88	96.28	96.79					
KAGBH5	95.70	96.11	95.93	96.74	97.54	99.03	98.45	96.51				
KAGBH6	95.70	96.33	95.59	96.39	97.31	98.22	98.00	95.99	98.17			
KACNH3	95.07	96.74	98.00	96.39	96.22	95.99	96.68	95.76	96.05	95.82		
KASJH	95.99	94.96	94.79	95.48	95.48	95.76	96.33	94.79	95.88	95.65	94.79	

Supplementary Table 3. Pairwise comparison of nucleotide sequence alignment of complementary sequences within S segment of completely sequenced twelve Korean SFTSV isolates belonging to different genotypes. The lower comparison gradient indicated the percentage identity between two strains. Pairwise comparison was performed using CLC genomics workbench 22 software.



Supplementary Figure 1. Prediction of the 3D structure and Ramachandran plot analysis of the NSs and NP protein. The 3D structure of NSs and NP protein was modelled using AlphaFold and performed quality verification using the PROCHECK program. Ramachandran Plot analysis of the refined model of the NSs and NP proteins showing the number of residues located in a favourable region.



Supplementary Figure 2. Prediction of the NSs mutants docking structure (A) Molecular docking of NSsC6S with NP and (B) Molecular docking of NSsS207T with NP.