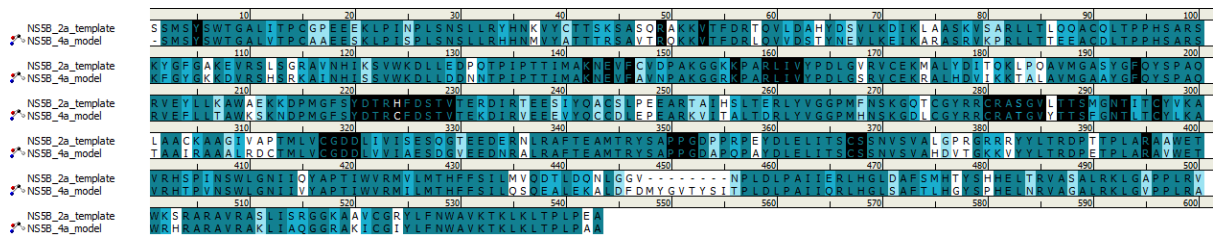
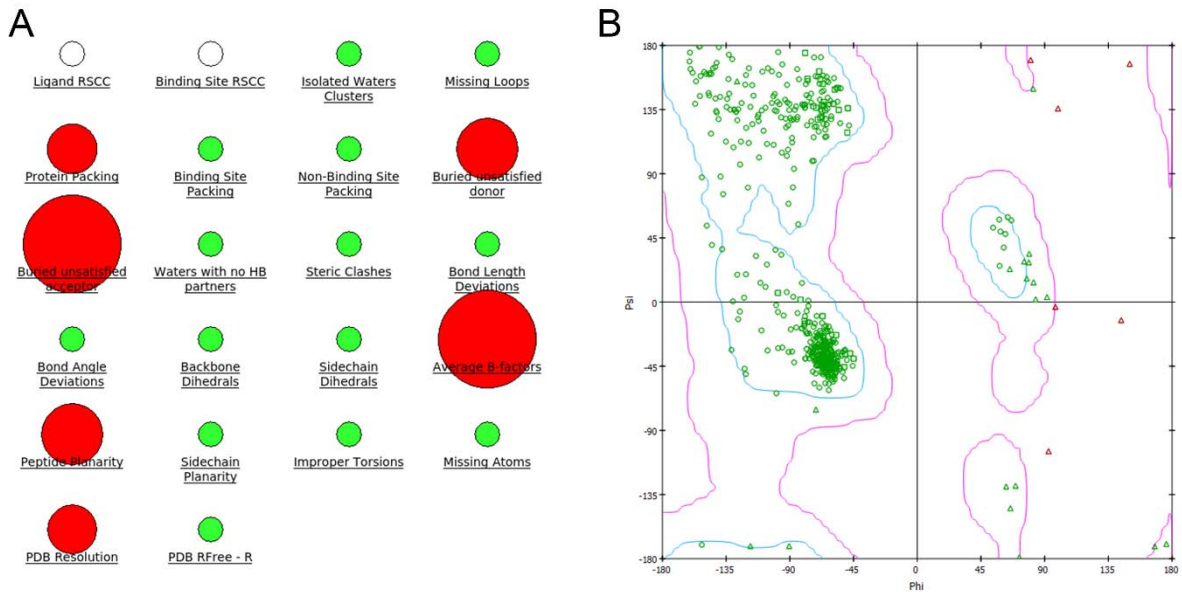


Supplementary Figures

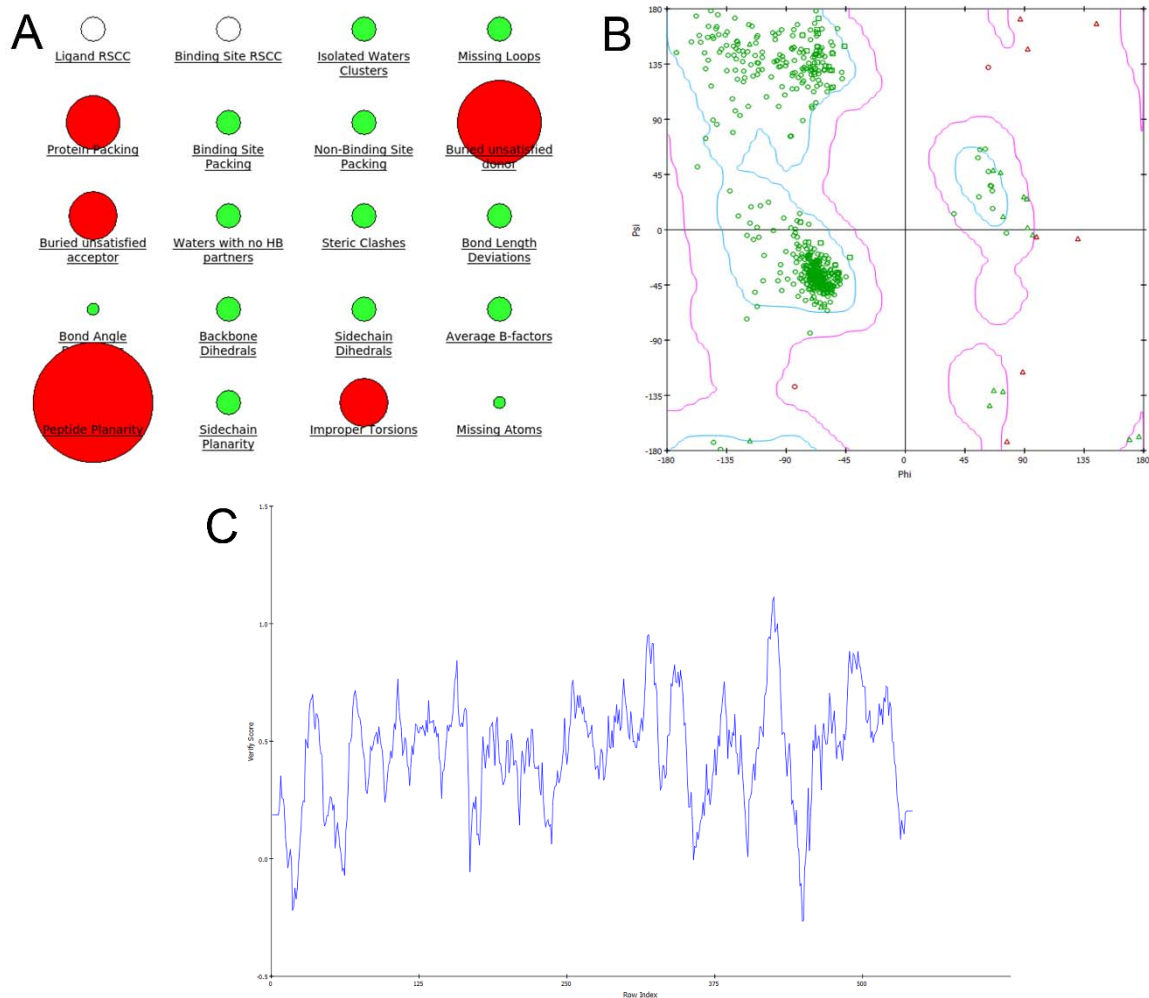
Molecular Characterization of Hepatitis C Virus for Developed Antiviral Agents Resistance Mutations and New Insights into In-Silico Prediction Studies



Supplementary Figure 1 Sequence alignment of template sequence (PDB ID: 4WTA, HCV genotype 2a) and model sequence (Uniprot entry O39929). Amino acids colored based on similarity. Residues within 8 Å of the nucleotide binding site are highlighted in black. Image prepared using BIOVIA Discovery Studio



Supplementary Figure 2 The 4WTA template structure quality report. A) Template Protein Reliability Report; B) Template Ramachandran Plot



Supplementary Figure 3 HCV genotype 4a NS5B homology model quality report. A) Protein Reliability Report; B) Homology Model Ramachandran Plot; C) Profile-3D scores for homology model residues