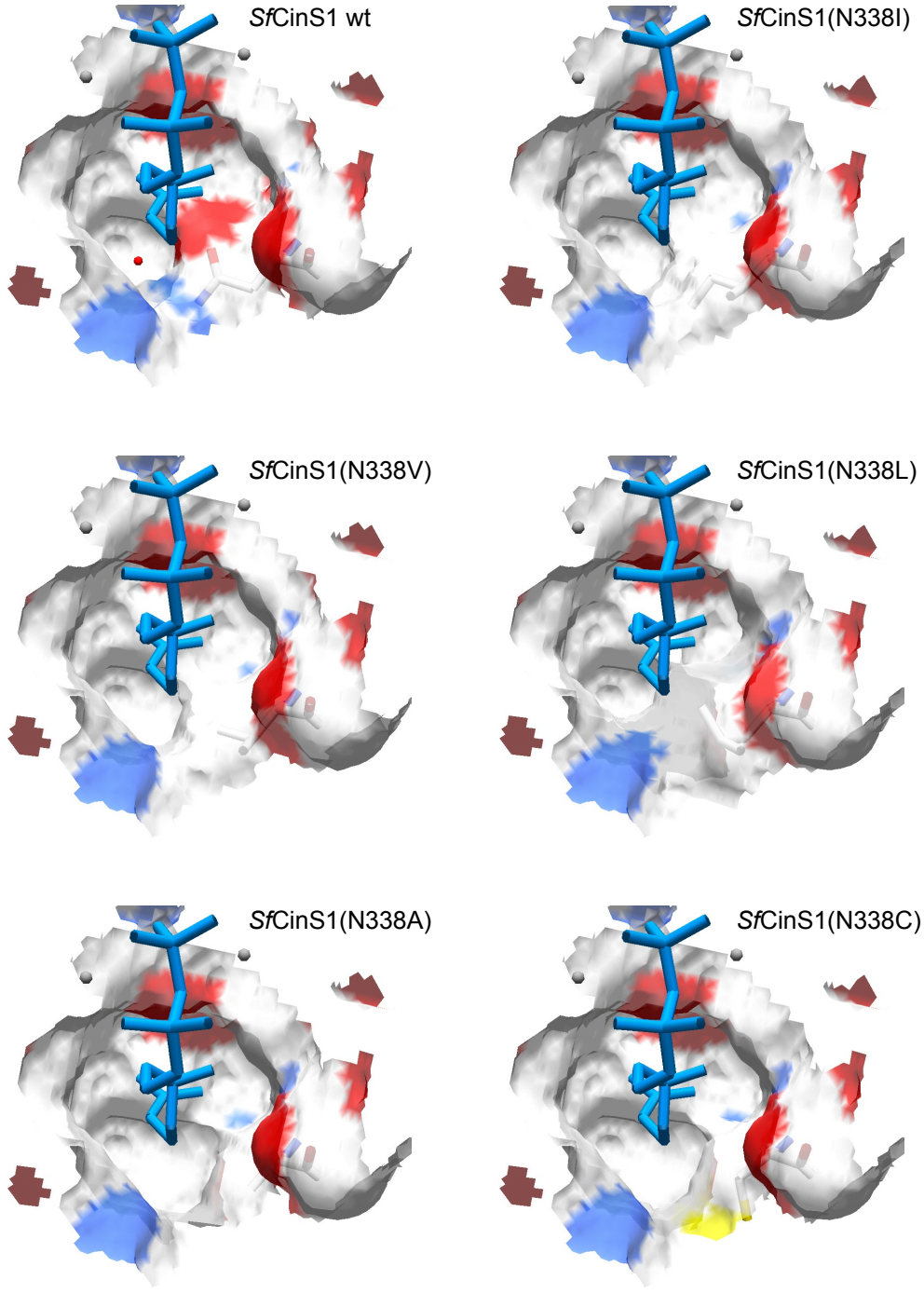

Supplemental Figure 1 online. Molecular model of the active site of some *Sf*CinS1 mutants. Molecular models were constructed in DeepView and the residues in a 6 Å radius of the mutated side-chain were energy minimised using the GROMOS96 forcefield as this is implemented in DeepView. The 3-aza-2,3-dihydrogeranyl diphosphate ligand of the *So*BPPS structure (PDB: 1N23) is superimposed.