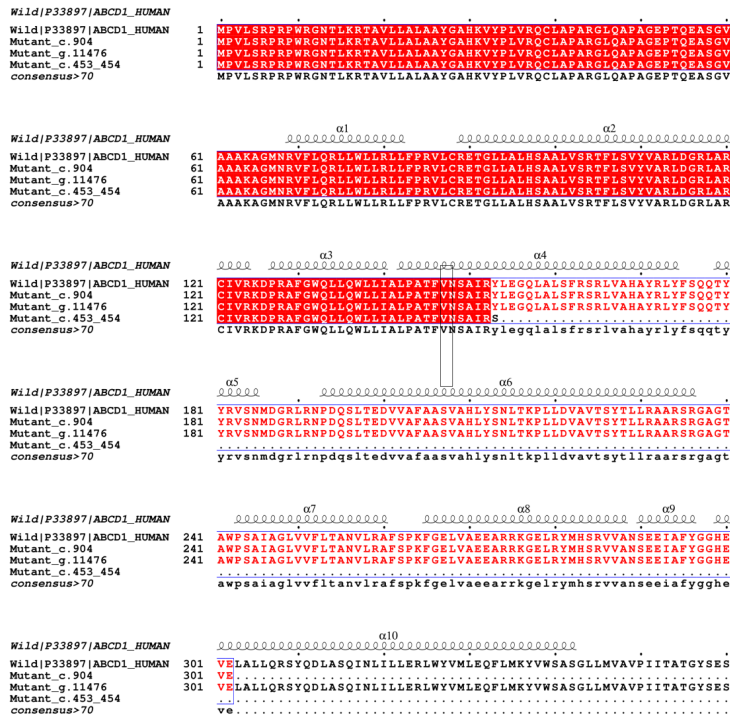
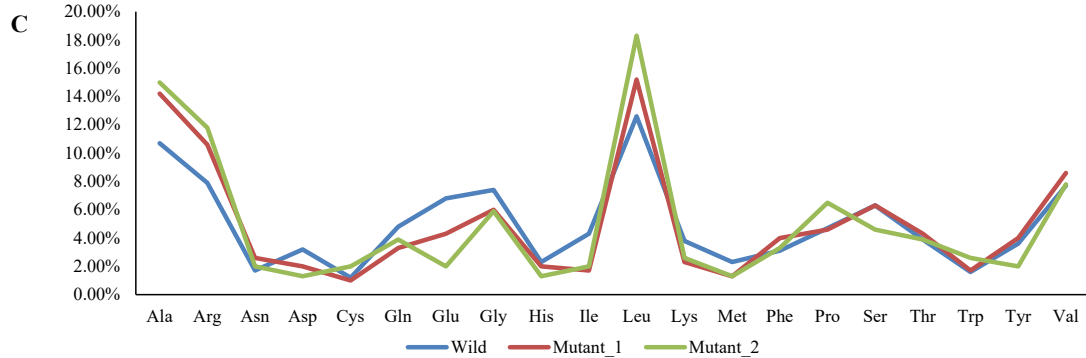
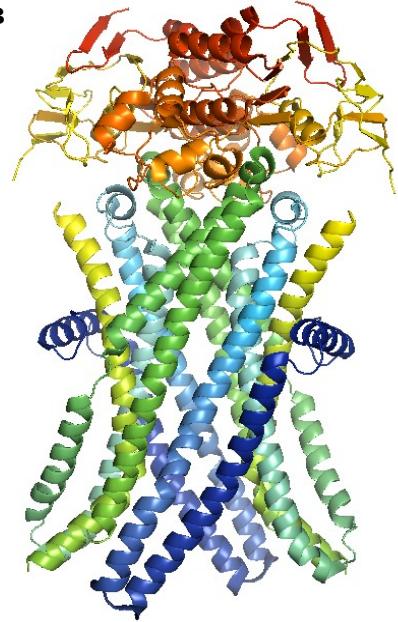


A



B



Supplementary Fig. 1. (A) Multi-sequence alignment of wild and mutant protein sequences of *ABCD1* gene. The position of single residue change in the mutant corresponding to c.453_454 [in CGTT] is depicted within the box. (B) 3D structure of *ABCD1* gene in its dimer form consisting of Chain A and Chain B derived from PDB :7RRA. (C) Percent amino acid composition among wild and mutant protein sequences of *ABCD1* gene.