



Supplementary Fig. 2. Structural comparison between wild and mutant forms of *ABCD1* gene. (A) Wild *ABCD1*, chain A derived from 7RRA. (B) Mutant 3D structure corresponding to c.904 [G>T]; p.E302* mutation with the information of secondary structure and estimated accessibility of each residue of the mutant sequence. (C) Ramachandran plot analysis modelled mutant structure showing more than 89.6 per cent residues in the favoured region, suggesting a good quality model. (D) Superimposition of mutant structure with wild *ABCD1*, reflecting a complete change in the mutant structure. (E) 3D structure corresponding to c.453_454 [ins CGTT]; p.Tyr153Serfs*43 mutation. (F) Ramachandran plot analysis of the modelled mutant structure showing more than 97 per cent residues in the favoured region. (G) Superimposition of mutant structure with wild *ABCD1*, reflecting a complete change in the mutant structure with RMS.