Supplementary Figure 3. Human wild-type SDH homology model, showing the 3D positions of hot-spot residues involved in tumour-associated mutations. The left image shows the surface of the complex. The right image shows hot-spot residues as spheres with a faint background of the surface image. The peripheral hot-spot residues are coloured purple and the non-peripheral hot-spot residues are coloured mauve. Subunits A, B, C, D are coloured green, cyan, magenta, and yellow respectively. The hot-spot mutations have no obvious structurally deleterious features, and are located close to each other on the periphery of the complex near the binding of a finger of membrane subunit C to soluble subunit B. Thus one possible speculation is that this region binds an assembly factor. Image created using PyMOL (DeLano 2009).