

Figure S2. Cluster analysis segments the structures that the protein samples during the simulation into sub-groups according to an adjustable RMSD cut-off value that reflects the extent of similarity between the structures. The analysis was performed using the Gromos algorithm (RMSD cut-off of 1 Å). Cluster index of wildtype and mutant EAL region of KIT protein during simulation. a) wildtype cluster index in time slab I b) wildtype cluster index in time slab II c) mutant cluster index in time slab I and d) mutant cluster index in time slab II. Time slab I is between 0-50 ns and time slab II is between 50-100 ns.

