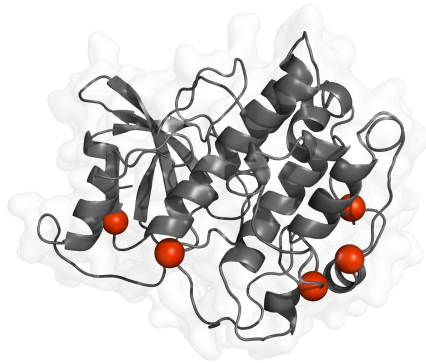


Additional File 6 Figure S2



Additional File 6 Figure S2. Structure model for DCLK3. Cancer mutations are highlighted as red spheres. The homology model was built based on templates 2W4OA, 2JC6A and 1A06A. Templates were identified by a psi-blast search with 5 iterations. Suitable templates were manually selected based on sequence similarity, alignment quality and predicted secondary structure. Alignments were refined using a contact-based target to multiple template alignment. Finally, models were built using distance geometry and subsequent simulated annealing refinement.