

S4 Table. Measurement of C_α-C_α distance between residue 227 and 371^δ from structural analysis of Cbl wildtype and mutant proteins

PDB ID	Cbl structure	C_α-C_α distance (Å)
2Y1M	WT closed, inactive	9.8
4A4C	WT open, active	46.4
5HKX	Y371E mutant	16.9
5J3X	Y371F mutant	9.5

^δResidues 227 (in the TKBD) and 371 (in the LHR) forms a hydrogen bond in Cbl wildtype closed inactive state, used here as points of reference to show the displacement of LHR following phosphorylation or mutation [C_α alpha-Carbon, WT wildtype, TKBD tyrosine kinase binding domain, LHR linker helix region]