

Table S1. DALI statistics on structural alignment of *TkTIDE* with and the other structural homologues.

	Z-score	RMSD (Å)	Sequence Identity (%)
5NJ9 (TldE)	35.5	2.6	21
5NJ9 (TldD)	32.7	3.6	20
1VL4	41.1	2.1	21
3TV9	35.5	2.6	20
1VPB	4.8	2.5	21
3QTD	36.5	2.4	23

The low RMSDs and the high Z-scores indicate that the *TkTldE* structure is the closest to the structure.

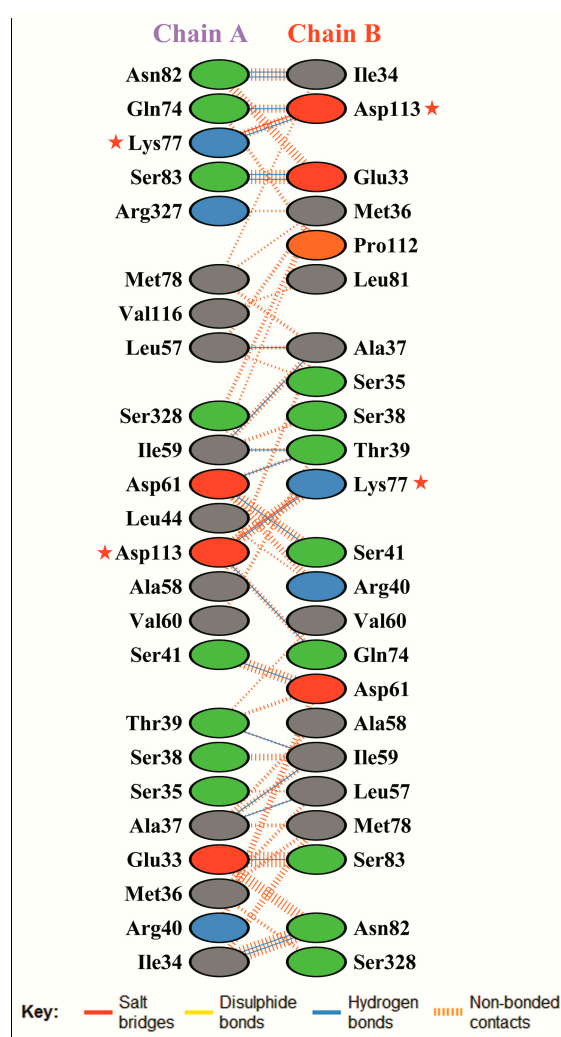


Figure S1. The dimer interface of *TkTldE*. Asp113 and Lys77 forming the salt bridge were labelled by stars. The interaction plot was generated by PDBsum.