Table S3. Distance measurements in known 3D structures.

Subunit (PDB ID)	Residue 1	Residue 2	Cα distance (Å)
Ubp8 (3MHH)	15	22	10.5
	181	T200	23.7*
Sgf29 (3MP8)	134	181	8.8
	151	177	9.1
	200	237	16.1
	220	237	16.1
	134	237	25.6
	177	237	36**
Gcn5 bromodomain (1E6I)	422	429	10.5
	415	422	10.8
	R329	385	13.1*
Gcn5 HAT domain (1YGH)	126	133	8.9
	111	153	16.6
TBP (1YTB)	133	156	8.7
	83	97	12.8
	83	145	15.2
	83	167	49.6**
DUB (3MHH)	Ubp8 K22	Sgf73 K33	11.8
	Ubp8 K22	Sgf73 K40	15

* One of the lysines is missing in the structure. Distance to the Cα of the adjacent residue (R329 instead of K328 in Gcn5 bromodomain; T200 instead of K201 in Ubp8) was measured.
** Distances that are larger than the 30Å cut-off.