

**Table 2.** Conformation change upon formation of large interfaces

Code	Complex	B (Å <sup>2</sup> )	Type of change
<i>A. Large protease complexes</i>			
1bth	Thrombin E192Q-PTI	2380	Enzyme: large loops movements. PTI: no change.
4htc	Thrombin-hirudin	3350	Enzyme: no change. Hirudin: C-terminal tail becomes ordered.
1tbq	Thrombin-rhodniin	3510	Enzyme: no change. Rhodniin has two domains with a flexible linker.
1toc	Thrombin-ornithodorin	3510	Enzyme: no change. Ornithodorin has two domains with a flexible linker.
1dan	Factor VIIA-soluble tissue factor	3770	Factor VIIA is an extended molecule made of five domains that wrap around Tissue Factor. Tissue factor: no change.
<i>B. Antibody-antigen complexes</i>			
1kb5	Fab Désiré-1-TCR Fv domain	2340	No structure of free components.
<i>C. Others</i>			
(*3)	$\beta$ -Lactamase-BLIP	2560	Enzyme: no change. BLIP: bending of saddle-shaped inhibitor.
1dfj	RNase A-RNase inhibitor	2600	Enzyme: no change. Horseshoe shaped inhibitor opens up to fit the enzyme in.
1dhk	$\alpha$ -Amylase-bean inhibitor	3080	Enzyme: large loop movements. No free inhibitor structure.
1udi	U-DNA glycosylase-inhibitor	2020	Enzyme: no change. No free inhibitor structure.
1tx4	Rho-Rho GAP	2280	Rho: loop becomes ordered. Rho GAP: a 10 residue loop becomes ordered.
1efu	EFtu-EFts, <i>E. coli</i>	3660	EFtu: domains and loops move, a $\alpha$ -helix refolds. No free EFts structure.
1aip	EFtu-EFts, <i>T. thermophilus</i>	2940	EFtu: domains move, a $\alpha$ -helix and loops shift. EFts: N-terminal residues become ordered.
1gg2	G <sub>1<math>\alpha</math>1-G<sub>1<math>\beta</math>1<math>\gamma</math>2</sub></sub>	2360	G <sub>1<math>\alpha</math></sub> : a $\alpha$ -helix rotates, loops move; N- and C-terminal residues become ordered or refold. No free G <sub>1<math>\beta</math><math>\gamma</math></sub> structure.
1got	Transducin G <sub>1<math>\alpha</math></sub> -G <sub>1<math>\beta</math><math>\gamma</math></sub>	2500	See the text.
2trc	G <sub>1<math>\beta</math><math>\gamma</math></sub> -phosducin	4660	G <sub>1<math>\beta</math><math>\gamma</math></sub> : loops move. Phosducin is an extended molecule that wraps around G <sub>1<math>\beta</math><math>\gamma</math></sub> .
1fin	CDK2-cyclin A	3400	Kinase: domains move, a $\alpha$ -helix rotates, a loop moves. No free cyclin structure.
2btf	Actin-profilin	2090	Actin: domain rotation relative to actin-DNase complex. Profilin: no change.
1hwg	HGH receptor-HGH	4200	Receptor dimerizes. Large helix movements in HGH.
1tco	FKBP12-Calcineurin	2470	No change in FKBP12. No structure of free calcineurin.