Table 5 Free energy of protein–protein association

Complex	Insulin dimer	Trypsin–PTI	Haemoglobin αβ dimer
Dissociation constant K_D (molar)†	10^{-5}	10^{-13}	$\ll 10^{-8}$
Free energy of dissociation ΔG_D (kcalorie mol^{-1})†	7	18	>11
Translational/rotational free energy‡ $\Delta G^s{}_D$ (kcalorie mol^{-1})	23	27	27
Free energy required for association $\Delta G^t{}_D$ (kcalorie mol^{-1})§	30	45	>38
Surface area buried in the complex (Å^2)	1,130	1,390	1,720
Hydrophobic free energy (kcalorie mol^{-1})¶	28	35	43

*Data at neutral *p*H near 2'' °C from refs [12–14].
†$\Delta G_D = -kT \ln K_D$.
‡Calculated from the translational/rotational partition functions.
§$\Delta G^t{}_D = \Delta G^s{}_D + \Delta G_D$.
¶25 calorie mol^{-1} per Å^2 of buried surface area.