Additional File - 1

Equations and statistics used in the study

For every pair of proteins the $\Omega$ and the $Z$ score have been normalised as:

$$Score_{\text{norm}} = \frac{Score - Score_{\text{min}}}{Score_{\text{max}} - Score_{\text{min}}}$$  \hspace{1cm} (S.1)

where $Score$ can be either $\Omega$ or $Z$ score. The maximum and the minimum values across all the pairs used are represented with the respective subscripted acronym.

The variance to mean ration (VMR) for the $\Omega$ and the $Z$ score is defined for the protein pairs those sharing a given SCOP structural level.

$$VMR = \frac{\text{Variance}}{\text{Mean}}$$  \hspace{1cm} (S.2)

The coefficient of error defined for protein pairs sharing a given SCOP structural level.

$$CE = \frac{\text{Standard Deviation}}{\text{Mean}}$$  \hspace{1cm} (S.3)

The separation of secondary structure elements (SSEs) $i$ and $j$ in a protein $a$ is defined as:

$$\rho_{ij}^a = \sqrt{(COM_{Xi} - COM_{Xj})^2 + (COM_{Yi} - COM_{Yj})^2 + (COM_{Zi} - COM_{Zj})^2}$$

(S.4)
where $COM_{X(YZ)}$ refers to the $X(YZ)$-coordinate of the centre of mass.

The relative orientation of SSEs $i$ and $j$ in a protein $a$ is defined as:

$$\theta_{ij}^a = \cos^{-1} \frac{|V_i||V_j|}{\vec{V}_i \cdot \vec{V}_j}$$  \hspace{1cm} (S.5)

where $\vec{V}_{i(j)}$ refers to the vector passing thorough the terminal $C_\alpha$ atoms of the SSE $i(j)$.

The root mean square deviation (RMSD) of the separation among the sequential SSE pairs in proteins $a$ and $b$ is defined as:

$$\rho_{rmsd}^{ab} = \sqrt{\left(\rho_{12}^a - \rho_{12}^b\right)^2 + \left(\rho_{13}^a - \rho_{13}^b\right)^2 + \left(\rho_{23}^a - \rho_{23}^b\right)^2}$$  \hspace{1cm} (S.6)

The normalised separation RMSD for proteins $a$ and $b$ is defined as:

$$\rho_{nrm\text{sd}}^{ab} = \frac{\rho_{rmsd}^{ab} - \rho_{rmsd}^{min}}{\rho_{rmsd}^{max} - \rho_{rmsd}^{min}}$$  \hspace{1cm} (S.7)