Fig. 6. *(a)* Illustration of low- and high-entropy ensembles. Protein families typically have intermediate entropies. *(b)* Semi-log plot of the increase in the average entropy $\bar{S}$ as the reciprocal of the size n of the subset of randomly selected database sequences increases for dihydrofolate reductase (orange) and transformylase (blue) families. $\bar{S}_\infty$ was extrapolated by a least-squares fit of the data with the functional form $y = \bar{S}_\infty kn/(1 + kn)$. *(c)* Flowchart describing the procedure for determining T.