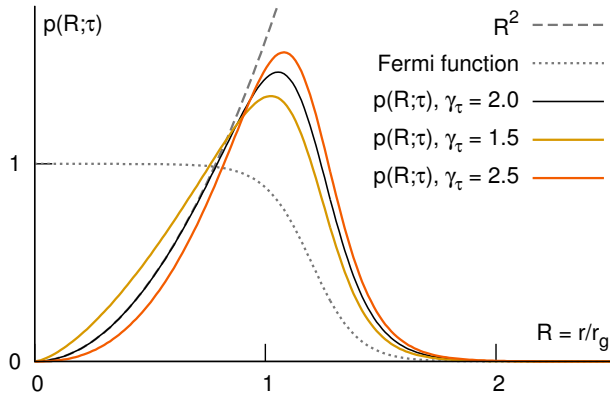




the (Lambert's) omega function, and the mean value can be estimated by $-A\beta^{-(\gamma+2)} \Gamma(\gamma+2) \text{Li}_{\gamma+2}(-\exp(\beta\mu))$, where Γ and Li are the (Euler's) gamma and (Jonquière's) polylogarithm functions.

Figure S2. Probability density function used in this work:

$$p(R; \tau) = \frac{A_\tau R^{\gamma_\tau}}{1 + \exp(\beta_\tau(R - \mu_\tau))}$$

for example values of γ_τ . Parameters: $\mu_\tau = 1.2$, $\beta_\tau = 10$; values of A_τ are chosen accordingly to normalize distributions. In general, when $\gamma_\tau < 2$, the function better fits histograms of atomic central distances for hydrophobic amino acids; when $\gamma_\tau > 2$, it better fits histograms of atomic distances for hydrophilic residues. For $\gamma_\tau = 2$ the function adopts the simplest form of a special case ($\alpha_\tau = 1$) demonstrated by Gomes et al. (*Proteins* **66**(2):304-20 (2007)). The location of the maximum is $\beta^{-1}(\gamma + W(\gamma \exp(\beta\mu - \gamma)))$, where W is