Figure S2. Probability density function used in this work:

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

for example values of \(\gamma_{\tau}\). Parameters: \(\mu_{\tau} = 1.2, \beta_{\tau} = 10\); values of \(A_{\tau}\) 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 the (Lambert’s) omega function, and the mean value can be estimated by \(-A\beta^{-1}(\gamma+2)\Gamma(\gamma+2)L_{\gamma+2}(-\exp(\beta\mu))\), where \(\Gamma\) and \(Li\) are the (Euler’s) gamma and (Jonqui`ere’s) polylogarithm functions.

Figure S3. Distributions of central distances of C\(_{\alpha}\) (A) and distal side chain atoms (B) of all amino acids. Curves for amino acids with hydrophobic side chains are green, polar charged – red and blue, polar uncharged – pink and violet.