Design and extraction of energy parameters for protein folder recognition

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Abstract

Using the protein threading and perceptron learning, we designed the various forms of energy parameters for the recognition of native state of proteins. We proposed several forms of one and two body energy functions among amino acids in the physical and biological parameter spaces. We benchmarked our energy parameters to identify the native folder for a new set of proteins, and report a remarkably high (>95%) success ratio for identifying the native folder. We also discuss the implication of various parameters, and extend the possible application of these parameters.