Subdomain Interactions Foster the Design of Two Protein Pairs with ~80% Sequence Identity but Different Folds.
Subdomain Interactions Foster the Design of Two Protein Pairs with ∼80% Sequence Identity but Different Folds.

Abstract

<p>Metamorphic proteins, including proteins with high levels of sequence identity but different folds, are exceptions to the rule that sequence similarity is a reliable predictor of structure similarity. Most of these proteins adopt only one fold with many other topologies, which has implications for protein folding, evolution, and misfolding diseases.</p>