

Matthew Cordes The University of Arizona

Host: David Giedroc



How Evolution Can Remodel A Protein Fold

There are approximately 1200 known protein folds, but relatively little is known about the origin and evolution of this impressive structural diversity. Many protein folds may have arisen independently, while others evolved from preexisting folds through mutational remodeling of the topology. In the Cro protein family, an all alpha-helical fold has evolved into a mixed alpha-helix/beta-sheet fold through accumulation of substitution mutations and small indels. We have found that some designed hybrids of differently folded Cro proteins adopt intermediate structures with a range of helix and sheet content. This suggests that protein folds can be remodeled in multistep structural transitions. We have also accumulated evidence that the newer alpha-helix/beta-sheet fold initially contained strained conformations that were subsequently resolved by mutation. These findings suggest that the evolution of new protein folds could involve transitional forms.

For further details, contact Ms. Jill Campbell at 5-9749

QCB Seminar Series

Co-hosted by the Department of Chemistry and the Graduate Program in Biochemistry

FRIDAY
MAY 1

CHEMISTRY
C033
2:30 p.m.