

Structural and biophysical characterization of protein folding.

The protein folding problem addresses how amino acid sequences determine protein structures [1]. The problem remains of fundamental importance in molecular biology as the number of new sequences identified continues to vastly outpace known protein structures. Progress in this area has enormous potential dividends including streamlining structure determination, facilitating rational protein design, and understanding how proteins misfold in disease states.

My lab's approach to the protein folding problem has been to structurally characterize equilibrium intermediates that result when the native state is disrupted by denaturants or mutagenesis [2]. An improved understanding of the structural properties of initial states in protein folding is critical to the development of accurate theoretical models. Residual structure in denatured states has the potential to affect protein stability (by raising or lowering the free energy difference from the native state), as well as folding kinetics (depending on whether intermediates are on- or off-pathway). The role of partially folded structure in aggregative misfolding is becoming increasingly recognized [3].

While our studies use a multi-faceted experimental approach, the principle technique in our work is NMR spectroscopy. NMR has the advantage of being able to characterize structure in a solution environment relevant to protein folding, and is unique among spectroscopic techniques in its ability to provide information at atomic resolution [4]. The model system we have used for most of our folding studies are three proteins

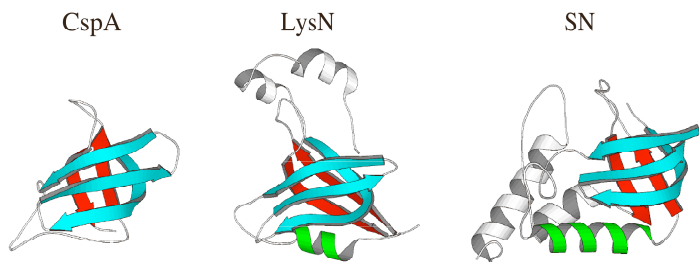


Fig. 1 : OB-fold proteins used for comparative protein folding studies. The structurally conserved β -barrel core of the OB-fold consists of a three-stranded β 1-3 menader (blue) and a two-stranded β 4-5 hairpin (red). Elements of structure that are unique to the individual proteins are left uncolored.

that lack sequence homology but share an 'OB-fold' β -barrel structure [5]. The presence of a shared structural motif together with divergent elements of structure makes it possible to ask whether the conserved structures are the most stable to unfolding. This is in fact what we found based on mutagenesis and hydrogen exchange experiments [6-8]. In

addition to OB-fold proteins, we have looked at the folding of α -helical coiled coils [9-11] and protein fragments such as the ribonuclease S-peptide [12,13]. These systems have the advantage of a small size, and of a relatively simple α -helical structure that can be used to benchmark the NMR methods used to study non-native proteins (e.g. relaxation experiments [13], through-hydrogen bond coupling constants [12], and residual dipolar couplings [14]).

Our studies and those of others have pointed to a large variety of folding intermediates [3,15-19]. These include sub-domains that retain part of the native tertiary structure independent of the rest of the protein, molten globules with native-like secondary structure but fluctuating side-chain structure, and highly disordered species that retain small amounts of native-like secondary structure. These results paint a picture of protein folding as a hierarchical assembly process, in which initially autonomous

elements of structure become increasingly interdependent as the protein folds [20]. Presumably, this reflects evolutionary constraints that favored unique functional native states over alternative conformations. Work on the OB-fold proteins in particular, suggests that the independent folding properties of a conserved β -barrel motif may be vestiges of evolutionary processes during which the autonomy of the motif was sacrificed to achieve a maximally cooperative integrated structure [6]. Partially formed structures are particularly prone to aggregation. This has been observed for all three of the OB-fold proteins under acid denaturing conditions. In all three proteins aggregation is initially promoted by the association of the conserved β 1-3 meander (Fig. 1), which corresponds to the most persistent structure under denaturing conditions [21-23].

Long-term goals:

- An unresolved issue in protein folding is whether a global folding topology persists under highly denaturing conditions [24]. We are using NMR residual dipolar couplings (RDCs) and distance restraints from engineered paramagnetic spin labels to test for the presence of conserved long-range structure in denatured states of OB-fold proteins.
- Insights from our protein folding studies will be used to develop strategies for modeling protein structures. A first effort in this direction has been the development of an approach for supplementing structure determination in cases where there are limited experimental data, with ‘hydrophobic distance restraints’ derived directly from the protein sequence. [25] Most work on structure prediction has focused on modeling new folds. If folds could be modeled reliably, there still remains the problem of how to go from a coarse fold-topology model to a usable high-resolution structure. Often, it is necessary to have multiple structures of a protein; for example, with and without an inhibitor. The problem of determining closely related structures is easily tractable by X-ray crystallography (through Fourier difference maps), but current NMR approaches can require months of data collection per structure. We are exploring the application of RDCs to this problem. We anticipate that RDC-based refinement methods could be of general use in modeling closely related structures, for example obtaining snapshots of structural changes over a range of solution conditions.

Recent Publications

- 1) Kammerer, R.A., Jaravine, V.A., Frank, S., Schulthess, T., Landwehr, R., Lustig, A., Garcia-Echeveria, C., Alexandrescu, A.T., Engel, J., & Steinmetz, M.O. (2001) "An interhelical salt bridge within the trigger site stabilizes the GCN4 leucine zipper". *J. Biol. Chem.* 276, 13685-13688.
- 2) Jaravine, V.A., Alexandrescu, A. T., & Grzesiek, S. (2001) "Observation of the closing of individual hydrogen bonds during TFE-induced helix formation in a peptide". *Protein Science* 10, 943-950.
- 3) Alexandrescu, A.T., Snyder, D.R., & Abildgaard, F. (2001) "NMR of hydrogen bonding in cold shock protein A and an analysis of the influence of crystallographic resolution on comparisons of hydrogen bond lengths", *Protein Sci.* 10, 1856-1868.
- 4) Alexandrescu, A.T., & Kammerer, R.A. (2003) "Structure and disorder in the ribonuclease S-peptide probed by NMR residual dipolar couplings", *Protein Sci.* 12, 2132-2140.
- 5) Matousek, W.M., & Alexandrescu, A.T. (2004) "NMR structure of the C-terminal domain of SecA in the free state" *Biochem. Biophys. Acta* 1702, 163-171.
- 6) Alexandrescu, A.T. (2004) "Strategy for supplementing structure calculations using limited data with hydrophobic distance restraints" *Proteins* 56, 117-129.
- 7) Sallum, C.O., Martel, D.M., Fournier, R.S., Matousek, W.M & Alexandrescu, A.T. (2005) "Sensitivity of NMR residual dipolar couplings to perturbations in folded and unfolded staphylococcal nuclease". *Biochemistry* 44, 6392-6403.

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