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POS-29 - Impact of Insertion and Deletion Mutations on Protein Thermodynamics

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Insertion and deletion mutations are common events in protein evolution but occur much less frequently than point mutations. Due to this, the effects of insertions and deletions on the biophysical properties of proteins are much less studied and understood.

A continuous three-letter protein model was used to study the effects of these mutations on the folding and stability of proteins. Thermodynamic behaviour was calculated using simulated tempering Monte Carlo methods.

As an initial sequence, we used a 35-amino acid sequence that folds into a stable native state with both α - and β -structure. We generated and simulated all 25 unique insertion mutations and all 73 unique deletion mutations for this initial sequence. In particular, this allowed us to assess the effects of the mutations on structure and stability.

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