

## Atomistic simulations of peptide unfolding and translocation by AAA+ biological nanomachines

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Bacterial proteases utilize powerful AAA+ ATPase ring nanomachines to unfold and translocate substrate proteins (SPs) through a narrow central channel. Mechanical forces, required to mediate these actions, are imparted through flexible central channel loops which comprise conserved aromatic and hydrophobic amino acids. In the course of repetitive ATP-driven cycles, which involve sequential intra-ring conformational changes, these loops execute large scale motions along the channel axis to promote SP translocation. To elucidate the unfolding and translocation of peptides with different secondary structures (random coil, helical, or beta-hairpin) by the ClpY ATPase, we perform molecular dynamics simulations using an implicit solvent model. We find that translocation of the unstructured peptide proceeds on a fast timescale, while unfolding of peptides with helical and hairpin structure imposes the rate-determining step. We also investigate the effect of order of intra-ring sequential allosteric motions on the peptide translocation. Our simulations indicate that the ATP-binding site location at the interface between two ClpY subunits provides an intrinsic directional bias for SP translocation. We find that allosteric motions which involve activation of the subunit nearest to the ATP-binding site result in the most efficient translocation mechanism.

### Biography

George Stan has completed his Ph.D in Physics in 1999 from the Pennsylvania State University and postdoctoral studies in computational biophysical chemistry from University of Maryland and the National Institutes of Health. He is an Assistant Professor of Chemistry at the University of Cincinnati. His research is focused on computational modeling of the action of biological nanomachines and bionanomaterials and he has published more than 25 papers in reputed journals.

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