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Title: Nascent Folding of Proteins Across the Three Domains of Life

We study the nascent behavior of three model coarse-grained proteins in six rigid all-atom structures representing ribosomes that come from three domains of life. The synthesis of the proteins is implemented as a growth process [1]. The geometry of the exit tunnel is quantified and shown to differ between the domains of life: both in volume and the size of constriction sites [2]. This results in different characteristic times of capture within the tunnel and various probabilities of the escape. One of the proteins studied is the bacterial YibK which is knotted in its native state [3]. A fraction of the trajectories results in knotting and the probability of doing so is largest for the bacterial ribosomes. Relaxing the condition of the rigidity of the ribosomes should result in a better avoidance of trapping and better proper folding [4].

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