

Abstract Submitted
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Translation with secondary structure: Dynamic blockages in totally asymmetric simple exclusion process LEAH SHAW, College of William and Mary — The totally asymmetric simple exclusion process (TASEP) is often used as a model for protein synthesis, with the lattice and particles representing the mRNA and ribosomes, respectively. Here we model the effect of secondary structure (folding) of the mRNA by introducing a dynamic blockage region in the lattice. If the region is unoccupied by particles, the blockage can close and prevent upstream particles from moving into it, representing the folding of that section of mRNA. Reopening of the blockage, allowing particles to pass, represents unfolding. We study the effects of the blockage size, closing/opening probabilities, and TASEP parameters on the particle current and blockage switching rates.

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