

Translocation and degradation of repeat proteins by the protease ClpXP

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ClpXP is a protease included in the AAA+ family in charge of the unfolding, translocation and degradation of certain tagged proteins inside cells of several organisms in the bacterial kingdom, proving fundamental in the maintenance of equilibrium inside them [1]. This task is accomplished through the binding and subsequent hydrolyzation of ATP.

The protease itself is divided into two different subunits, each of them in charge of different parts of the overall degradation process: these are ClpX, an hexameric ring that leads to the unfolding and translocation of proteins it comes in contact with, and ClpP, an heptameric chamber in which the proteins are translocated to in order to be degraded back into aminoacids.

The way in which ClpXP differentiates itself from other AAA+ proteases comes in the fact that it does not present a continuous work output leading of a progressive translocation process; the protease works on a series of dwell and burst phases, the latter being characterized by sudden decreases on the length of the protein [2].

In this work we aim to build a time-discrete probabilistic model that correctly describes the dynamics of the protease, ranging from the ATP binding and hydrolyzation to the degradation processes observed in experiments, taking as a base the widely known WSME model [3, 4] and considering the following Hamiltonian:

$$\mathcal{H}^{(1,n)}(m_i) = -T \sum_{i=1}^n q_i (1 - m_i) + \sum_{i < j} h_{ij} \prod_{k=i}^j m_k \quad (1)$$

In which n is the length of protein remaining outside ClpXP, and its characterized by enthalpic and entropic contribution to its stability, marked by h_{ij} and q_i .

The results of the model regarding ATP consumption rates and time taken for the degradation of different repeat proteins will then be compared to their experimental counterparts.

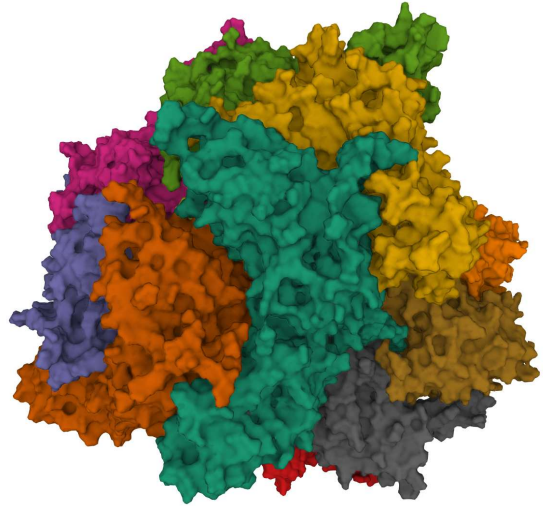


Fig. 1. ClpXP protease (6PO3).

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