

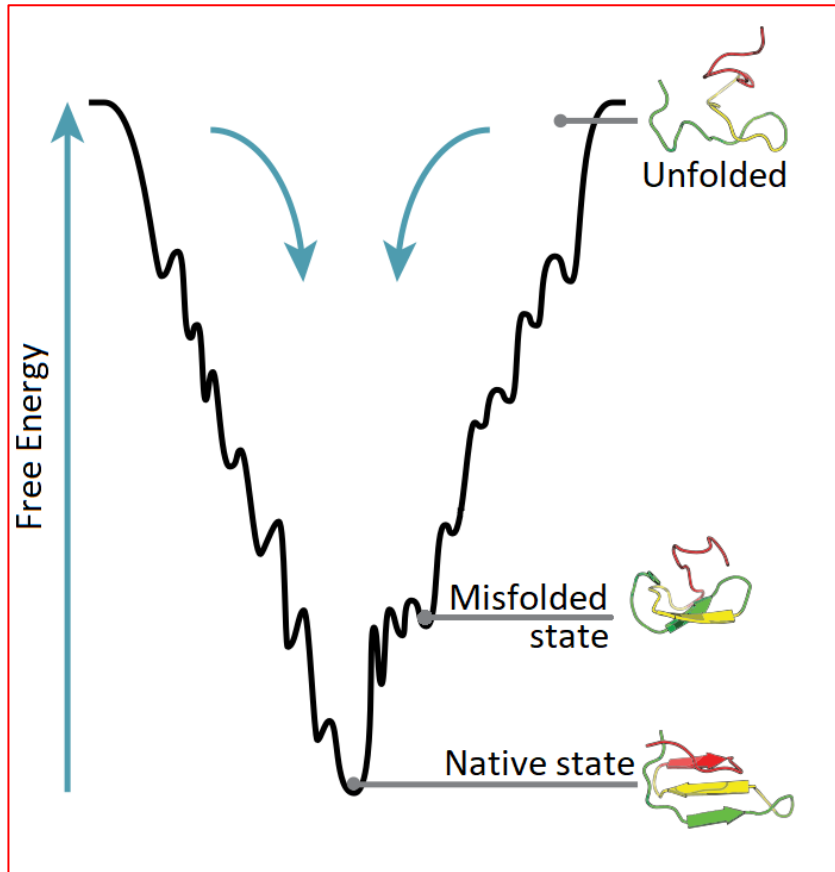
Exploration of possible structure-based models of the mechanism of action of AAA+ ATPases

Master's project defense - Antoine Maier

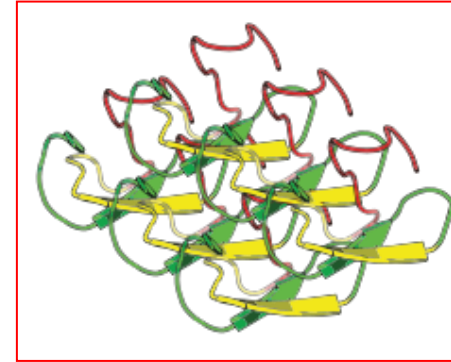
Supervisor: Prof. Paolo De Los Rios

External expert: Prof. Francesco Piazza

Protein (mis)folding



By Thomas Splettstoesser (www.scistyle.com) - Own work, CC BY-SA 3.0,
<https://commons.wikimedia.org/w/index.php?curid=28353539>
Adapted by Antoine Maier



Aggregate

Correlated

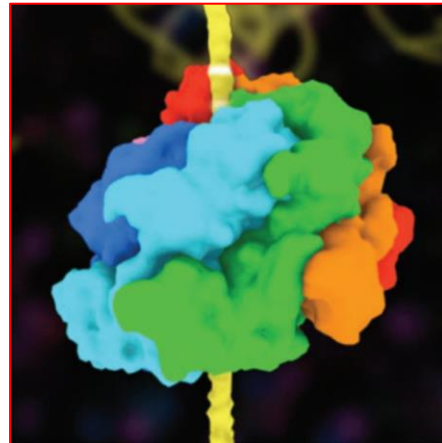
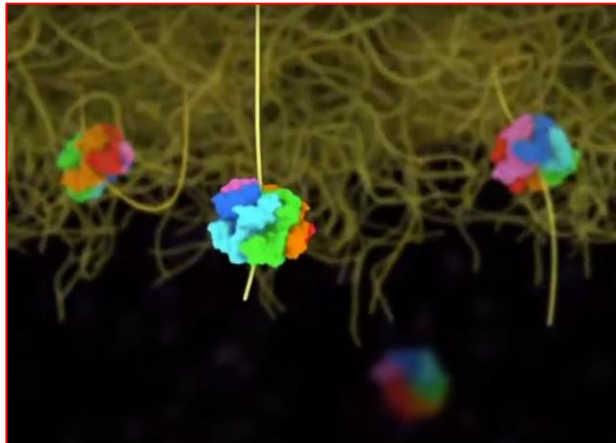
Protein misfolding diseases:

- Alzheimer's disease
- Parkinson's disease
- ...

Chaperones Hsp100

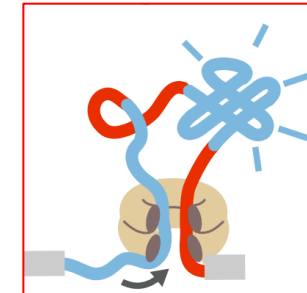
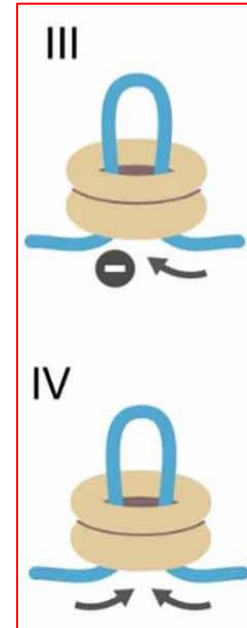
AAA+ ATPase, Hsp100 family

Hsp104



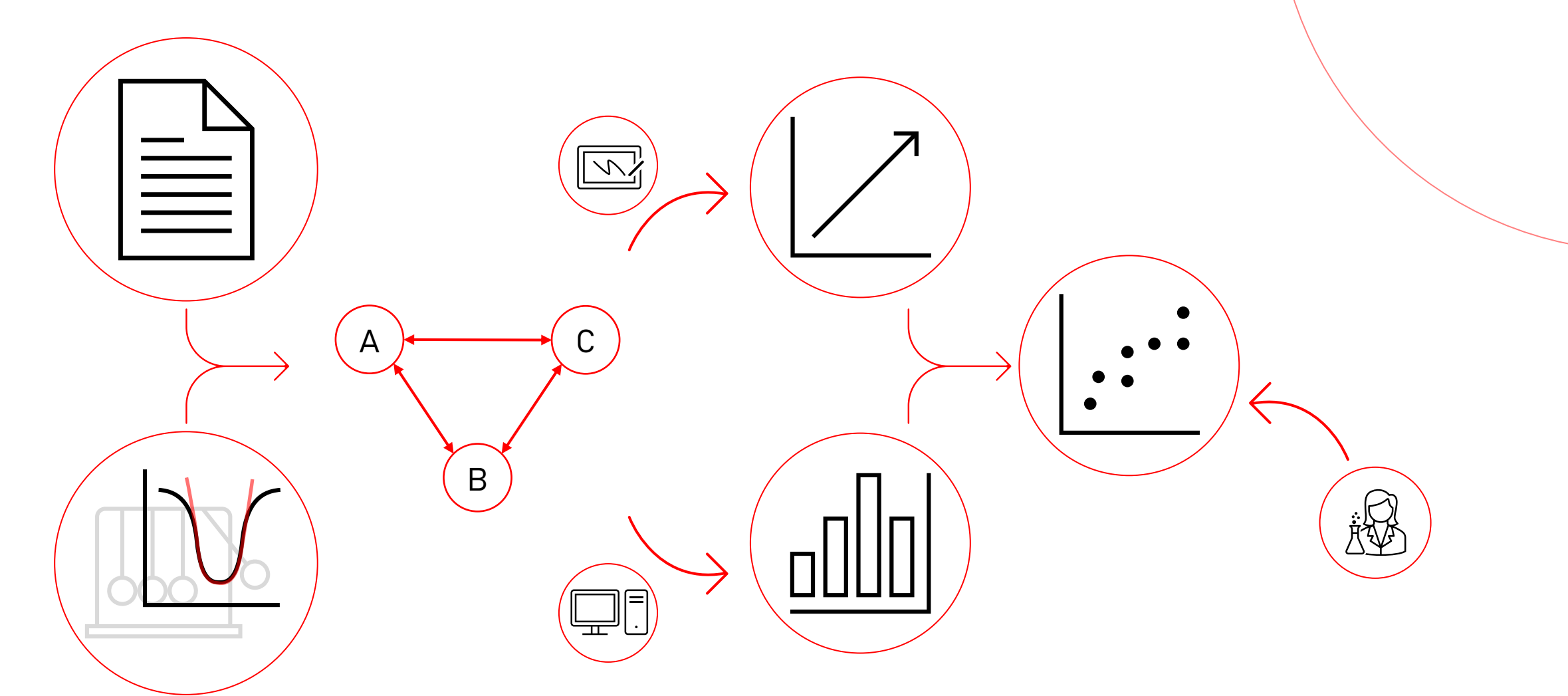
From animation related to "Ratchet-like polypeptide translocation mechanism of the AAA+ disaggregase Hsp104," Science, June 15, 2017. DOI: 10.1126/science.aan1052
URL: <https://www.youtube.com/watch?v=VXupZku6IEg>

ClpB



AVELLANEDA, Mario J. et al. Processive extrusion of polypeptide loops by a Hsp100 disaggregase. Nature. 2020, vol. 578, no. 7794, pp. 317–320. DOI: 10.1038/s41586-020-1964-y.

Introducing the method

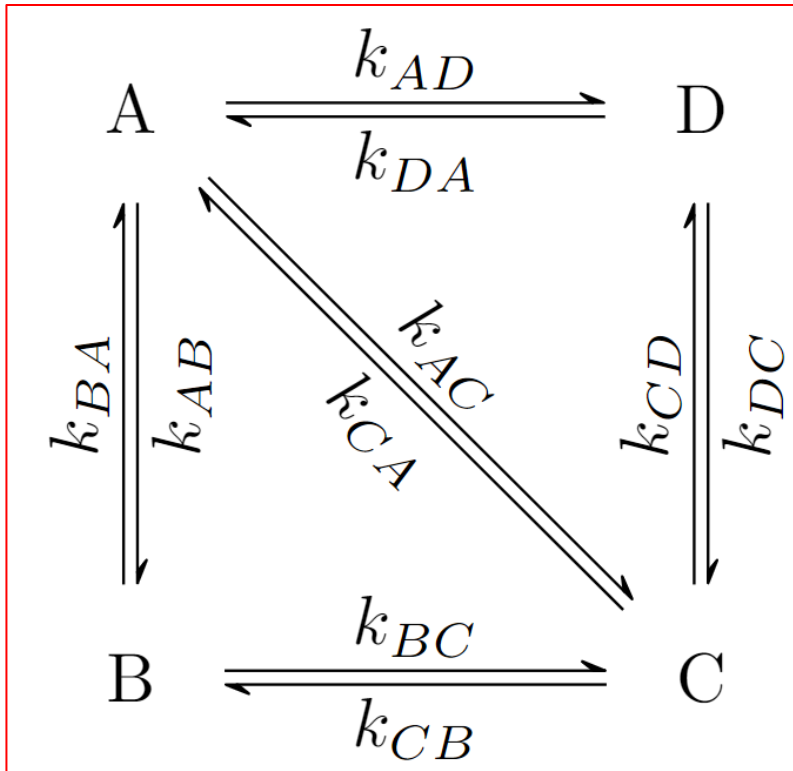




Theory

Kinetic scheme

Continuous time Markov chain



Master equation

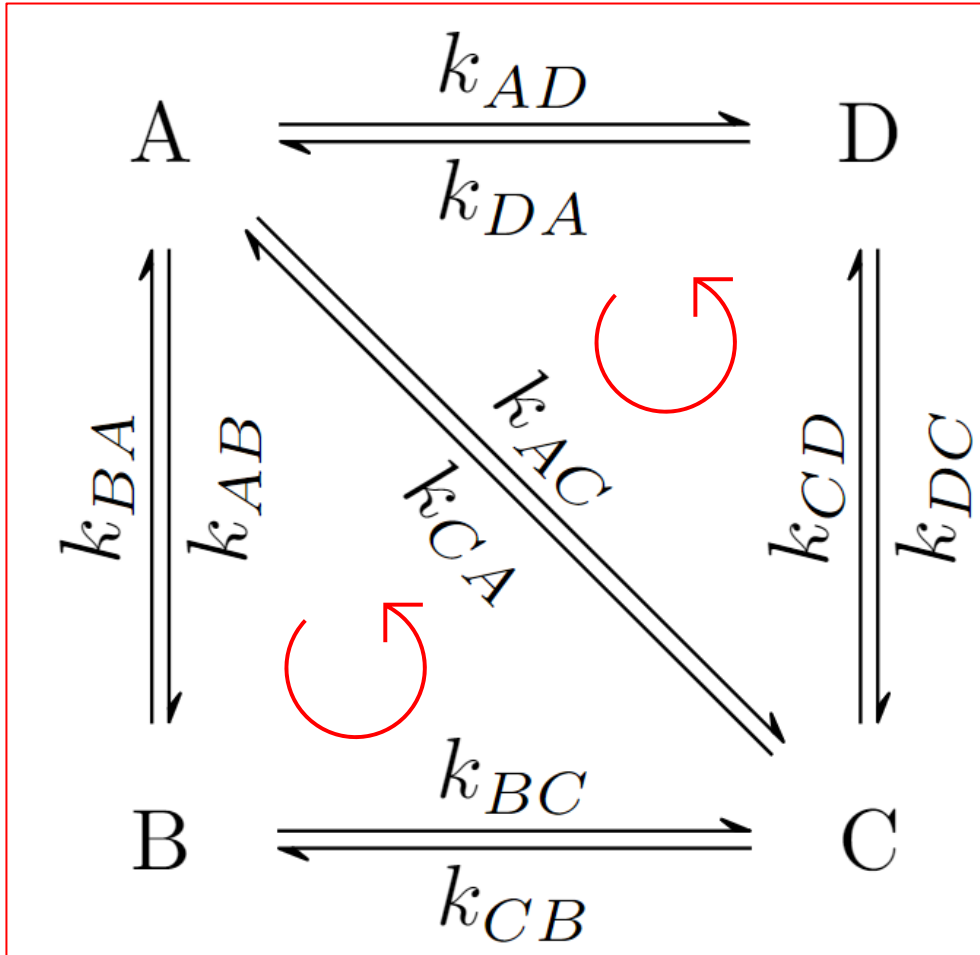
$$\dot{\mathbf{p}}(t) = \mathbf{M}\mathbf{p}(t)$$

$$M_{ij} = k_{ji} - \delta_{ij} \sum_{k=1}^N k_{ik}$$

Steady-state solution

$$\mathbf{M}\mathbf{p}^* = \mathbf{0}$$

Thermodynamic loop law



At equilibrium:

- Detailed balance

$$(p_i^* k_{ij})|_{eq.} = (p_j^* k_{ji})|_{eq.}$$

=> Thermodynamic loop law:

$$\left(\frac{\prod_{\text{clockwise}} k_{ij}}{\prod_{\text{counterclockwise}} k_{ji}} \right) \Big|_{eq.} = 1$$

Out of equilibrium:

$$\frac{\prod_{\text{clockwise}} k_{ij}}{\prod_{\text{counterclockwise}} k_{ji}} = \exp \left(\frac{\Delta\mu}{T} \right)$$

Computing statistics

Using $w_{xy} = w_{\Delta x=y-x} = \sum_{(i \rightarrow j) \in R_{\Delta x}} p_i(t) k_{ij}$

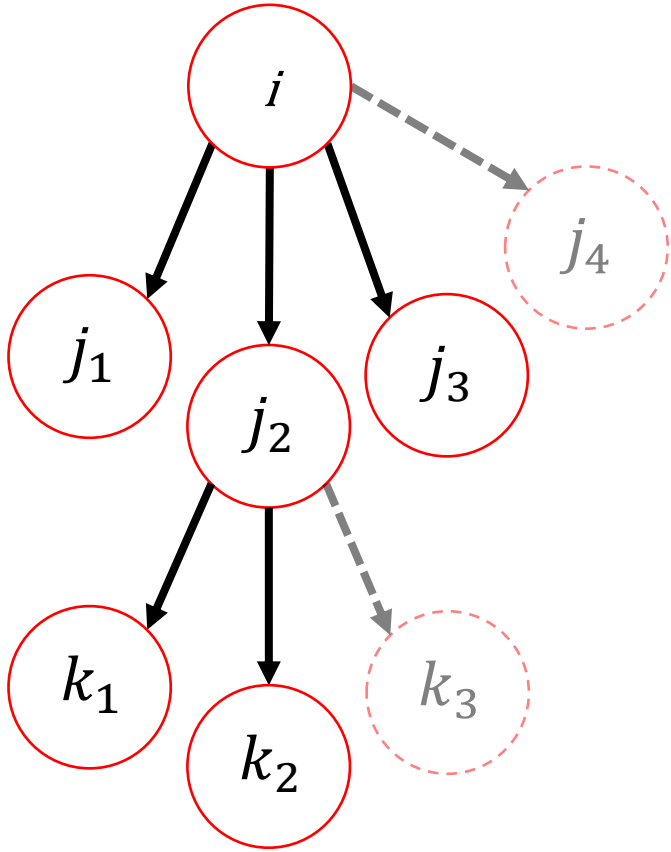
- $\langle X(t) \rangle = t \sum_{\Delta x, R_{\Delta x}} \Delta x p_i(t) k_{ij} (+ \langle X(0) \rangle)$

- $\text{Var}(X(t)) = t \sum_{\Delta x, R_{\Delta x}} (\Delta x)^2 p_i(t) k_{ij} (+ \text{Var}(X(0)))$

$$\frac{d}{dt} \langle X^k(t) \rangle = \sum_{x, y \in \mathbb{N}} p_x(t) w_{xy} (y^k - x^k)$$

(+ characteristic function)

Gillespie algorithm



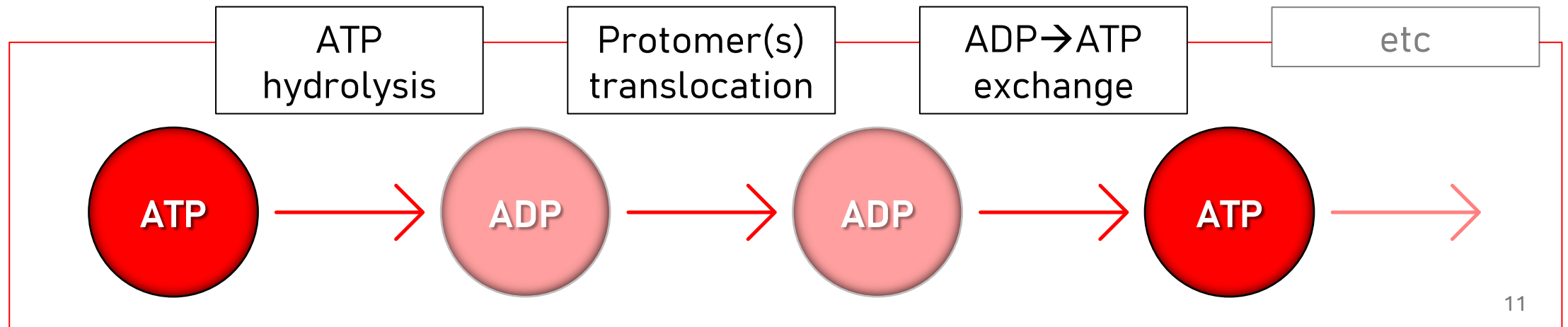
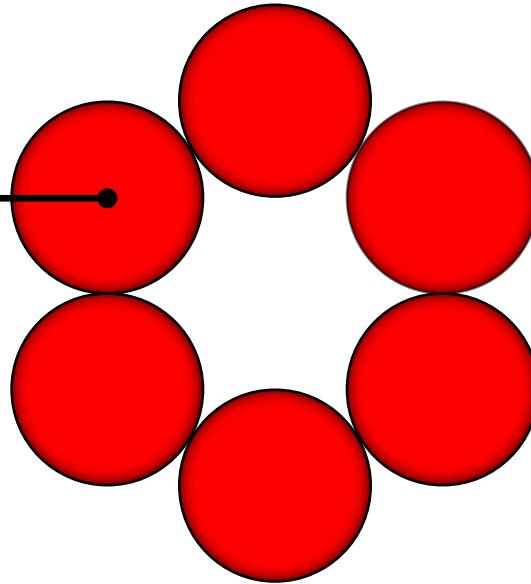
$$\tau \sim \text{Exp}(k_i) \quad k_i := \sum_j k_{ij}$$

$$j^* \sim \text{WeightedSampling} \left(\frac{k_{ij^*}}{k_i} \right)$$

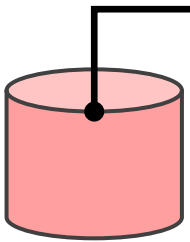
Translocation models

Coarse-grained modeling

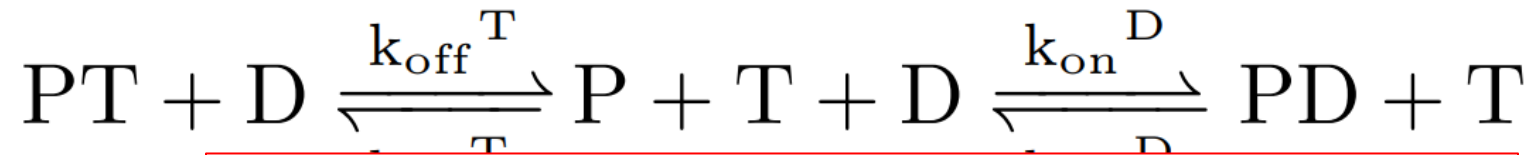
ATP- or ADP-bound



Nucleotide exchange



- ATP [T]
- ADP [D]
- Protein [P]



$$[\dot{P}] = 0$$

$$\frac{k_{DT}}{k_{TD}} = \frac{k_{DT}}{k_{TD}} \bigg|_{eq.} \left(\frac{[T]}{[D]} \bigg/ \frac{[T]}{[D]} \bigg|_{eq.} \right)$$

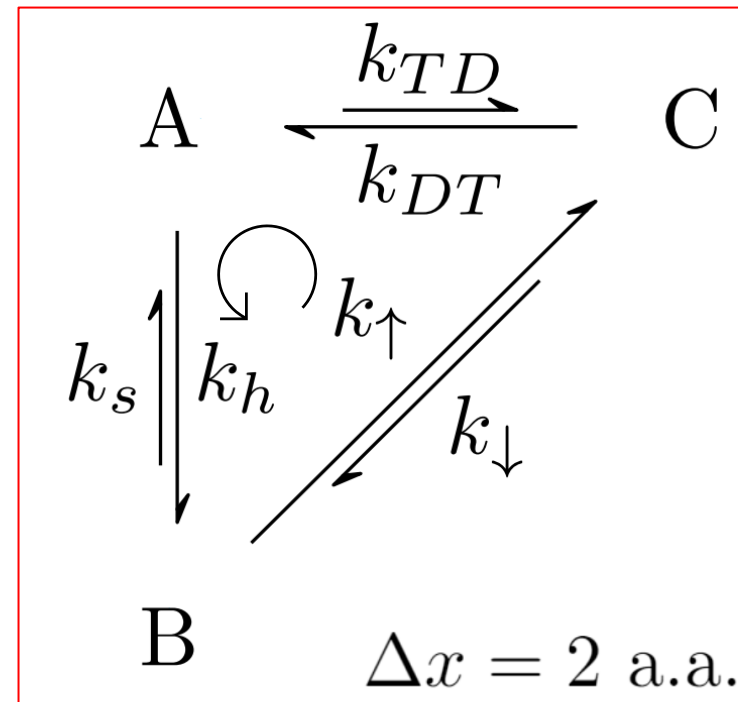
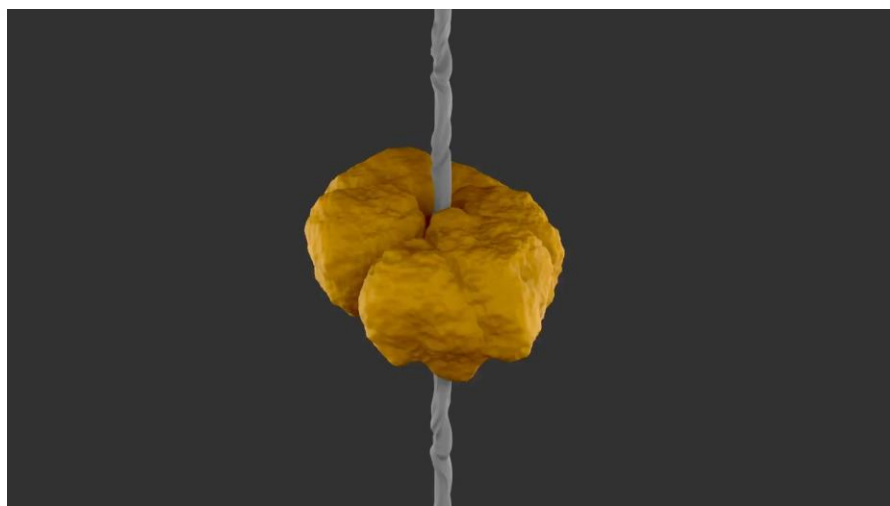
$$\frac{d[PT]}{dt} =$$

$$\Delta\mu \propto \log \left(\frac{[T]}{[D]} \bigg/ \frac{[T]}{[D]} \bigg|_{eq.} \right) [P]$$

Sequential Clockwise/2-Step Residue (SC/2R)



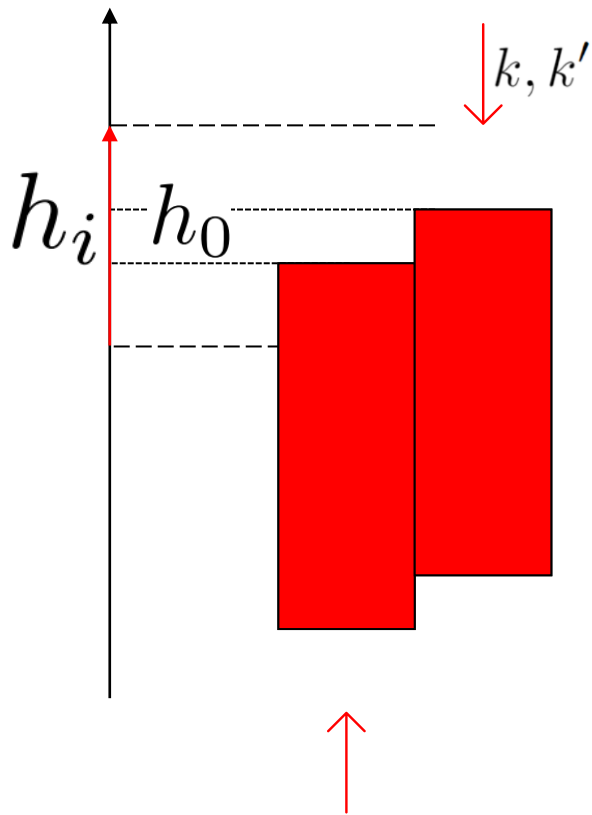
Spiraling in Control:
Structures and Mechanisms
of the Hsp104 Disaggregase



$$r_{ATP} \propto \left(1 - \frac{[T]}{[D]} \Big|_{eq.} / \frac{[T]}{[D]} \right) \prod_{\curvearrowright} k$$

$$\langle v \rangle = \Delta x \cdot r_{ATP}$$

Random Protomer Concertina Locomotion (RPCL)

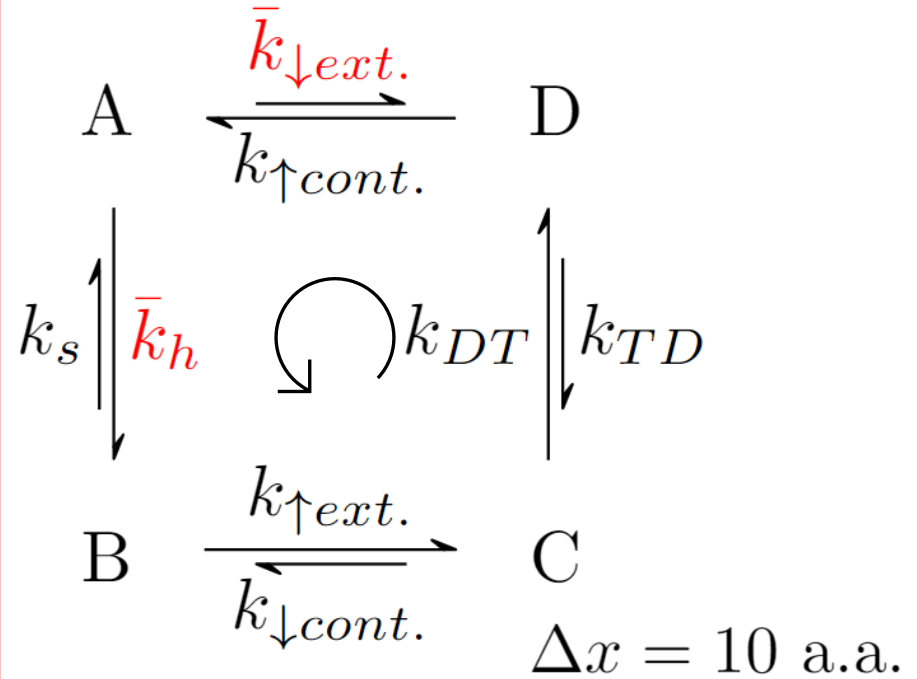
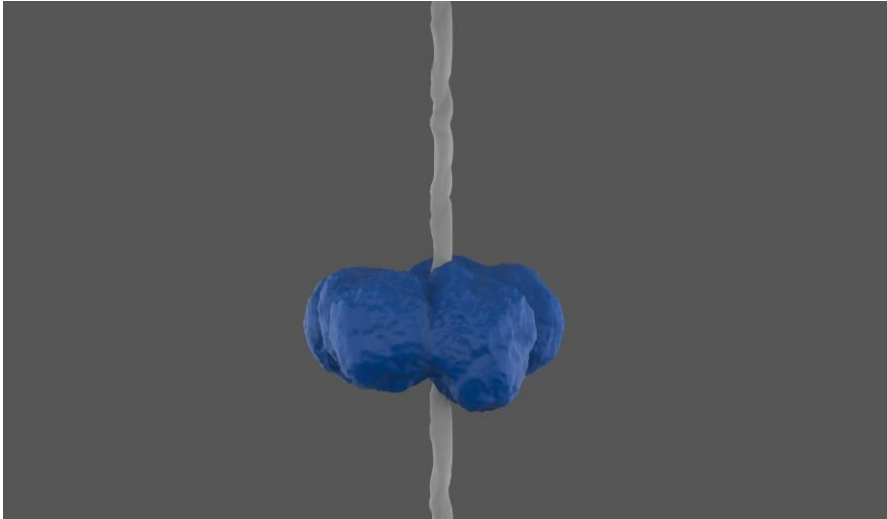


$$\mathcal{L} = \frac{1}{2}k \sum_{i=1}^{N-1} (h_i - h_0)^2 + \frac{1}{2}k'(h_N - h_0)^2 - \lambda \sum_{i=1}^N h_i$$
$$\Rightarrow \begin{cases} h_{i \neq N} = h_0 \frac{k - k'}{(N-1)k' + k}, \\ h_N = -(N-1)h_{i \neq N} \end{cases}$$

- *Hsp104 form[s] a closed hexameric ring.*
- *[...] the cryo-EM is at a lower resolution in this region, indicating conformational flexibility*
- *[...] we identified an additional [...] conformation of Hsp104 in which all six subunits are [...] in an evenly spaced helical spiral*

SHORTER, James; SOUTHWORTH, Daniel R.
Spiraling in Control: Structures and Mechanisms of the Hsp104 Disaggregase.
Cold Spring Harbor Perspectives in Biology. 2019, vol. 11, no. 8, a034033.
DOI: 10.1101/cshperspect.a034033.

Random Protomer Concertina Locomotion (RPCL)

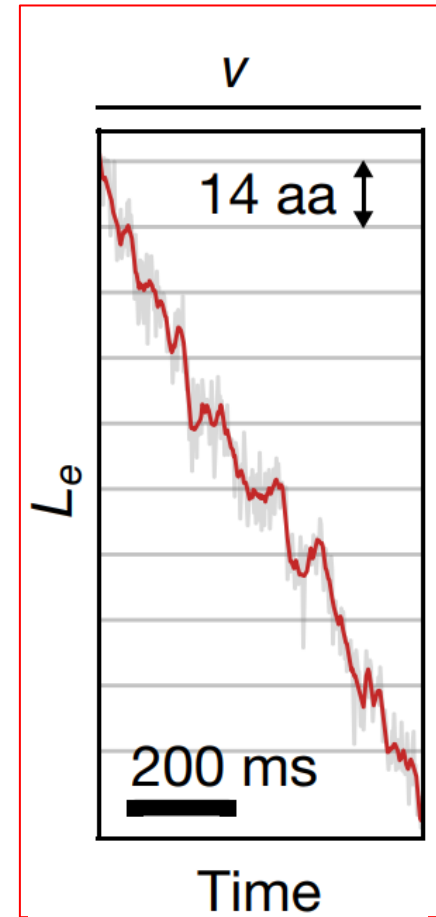
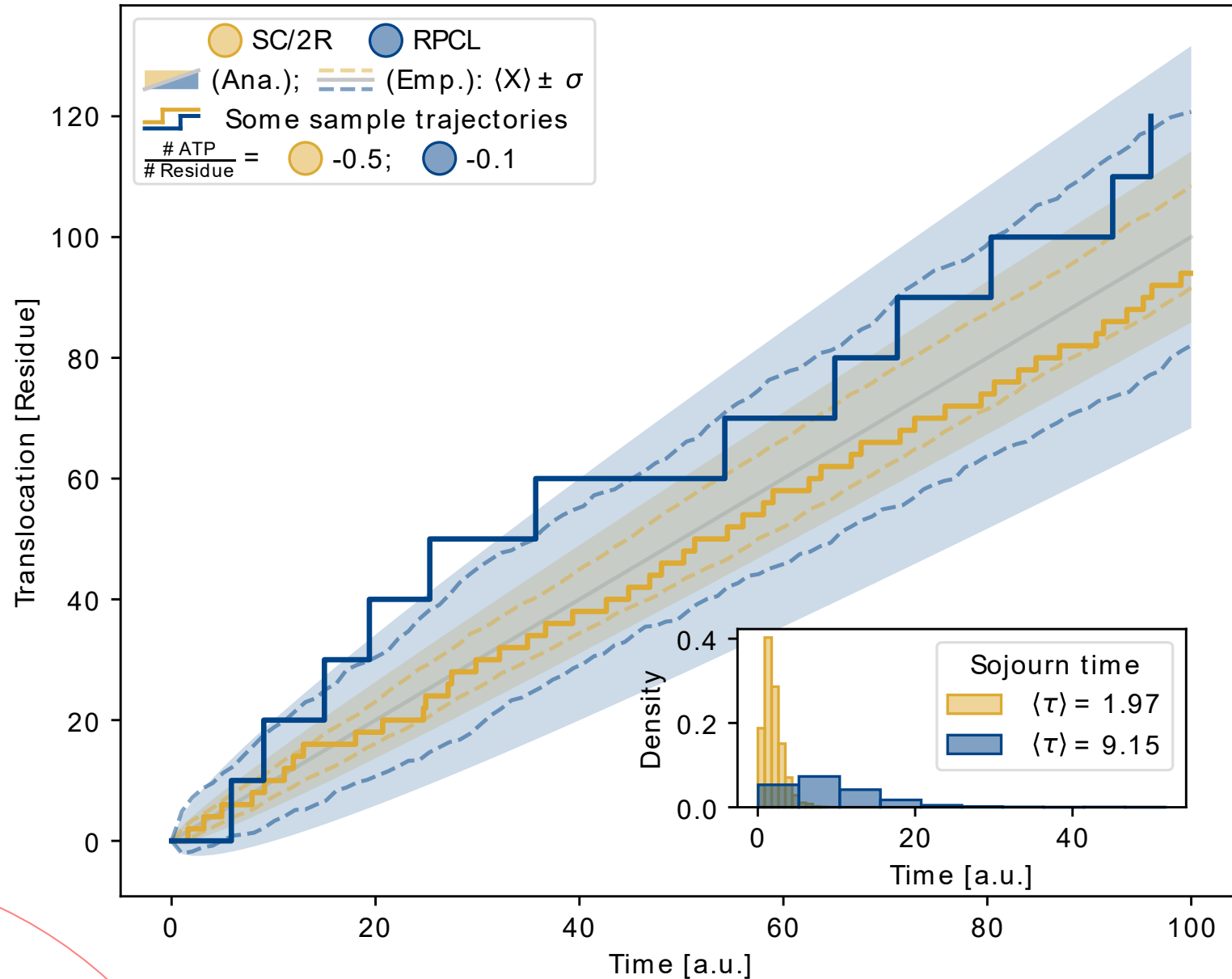


$$r_{ATP} \propto \left(1 - \frac{[T]}{[D]} \Big|_{eq.} / \frac{[T]}{[D]} \right) \Pi_{\curvearrowright}^k$$

$$\langle v \rangle = \Delta x \cdot r_{ATP}$$

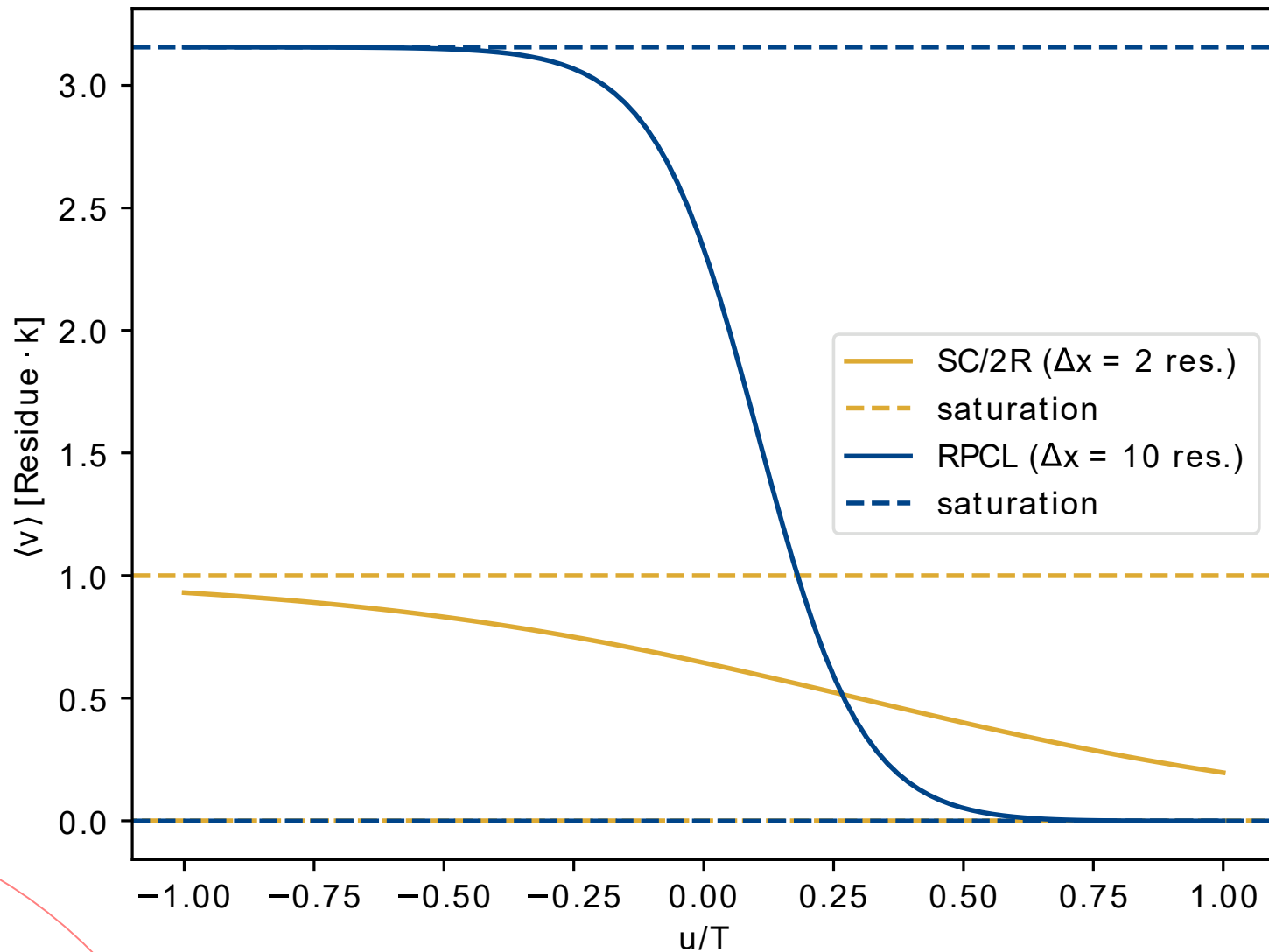
Numerical experiments

Comparing dynamics

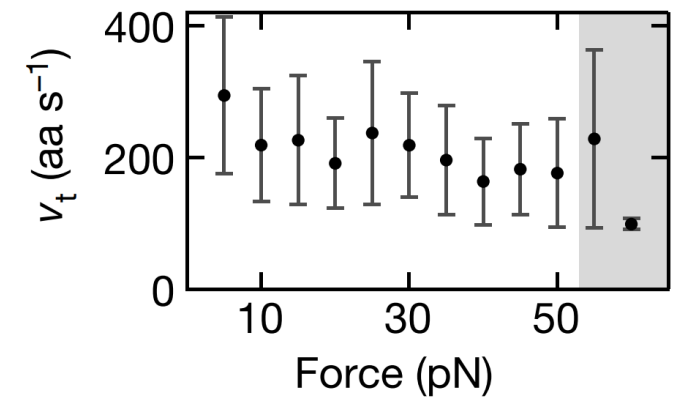


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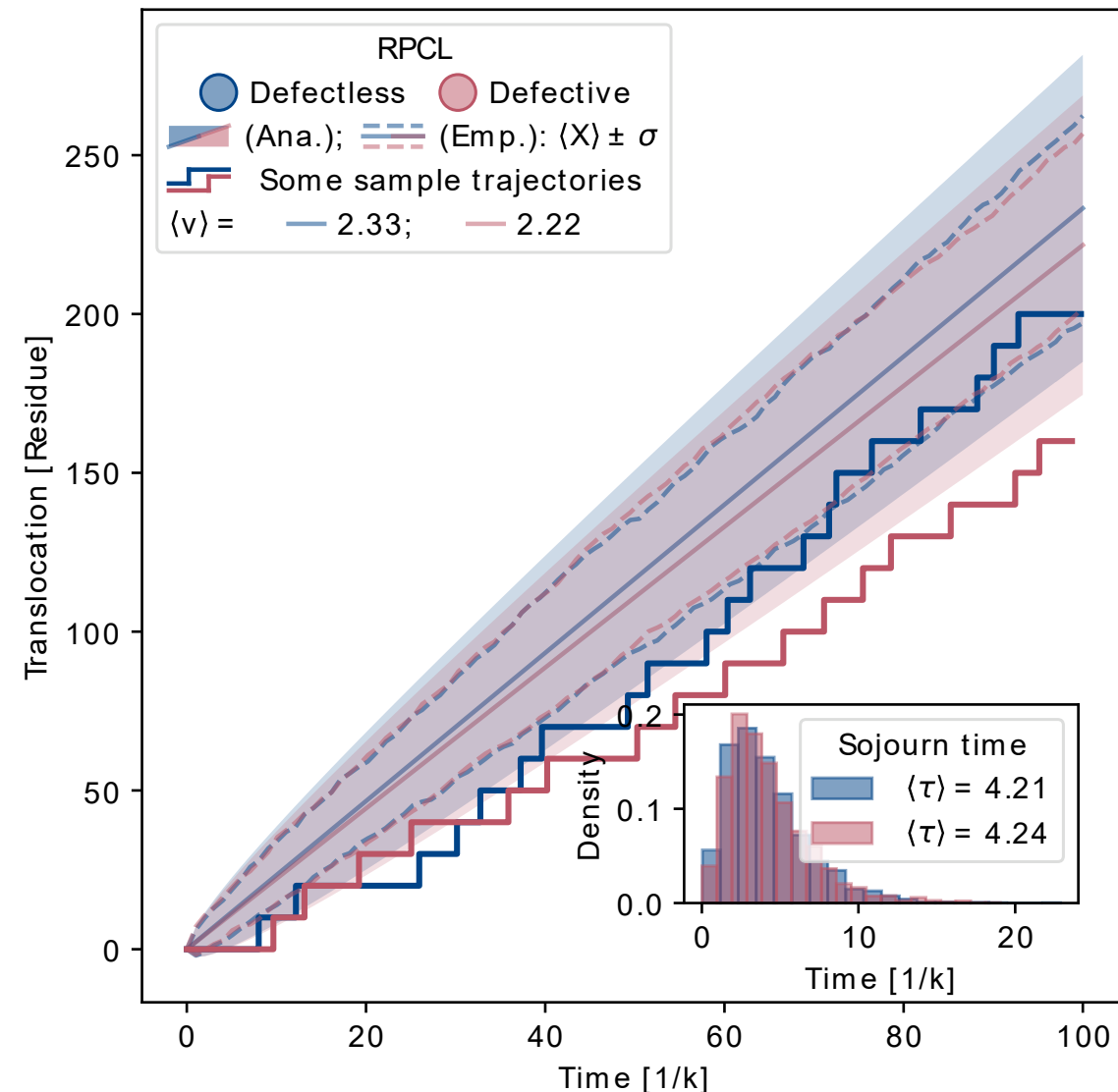
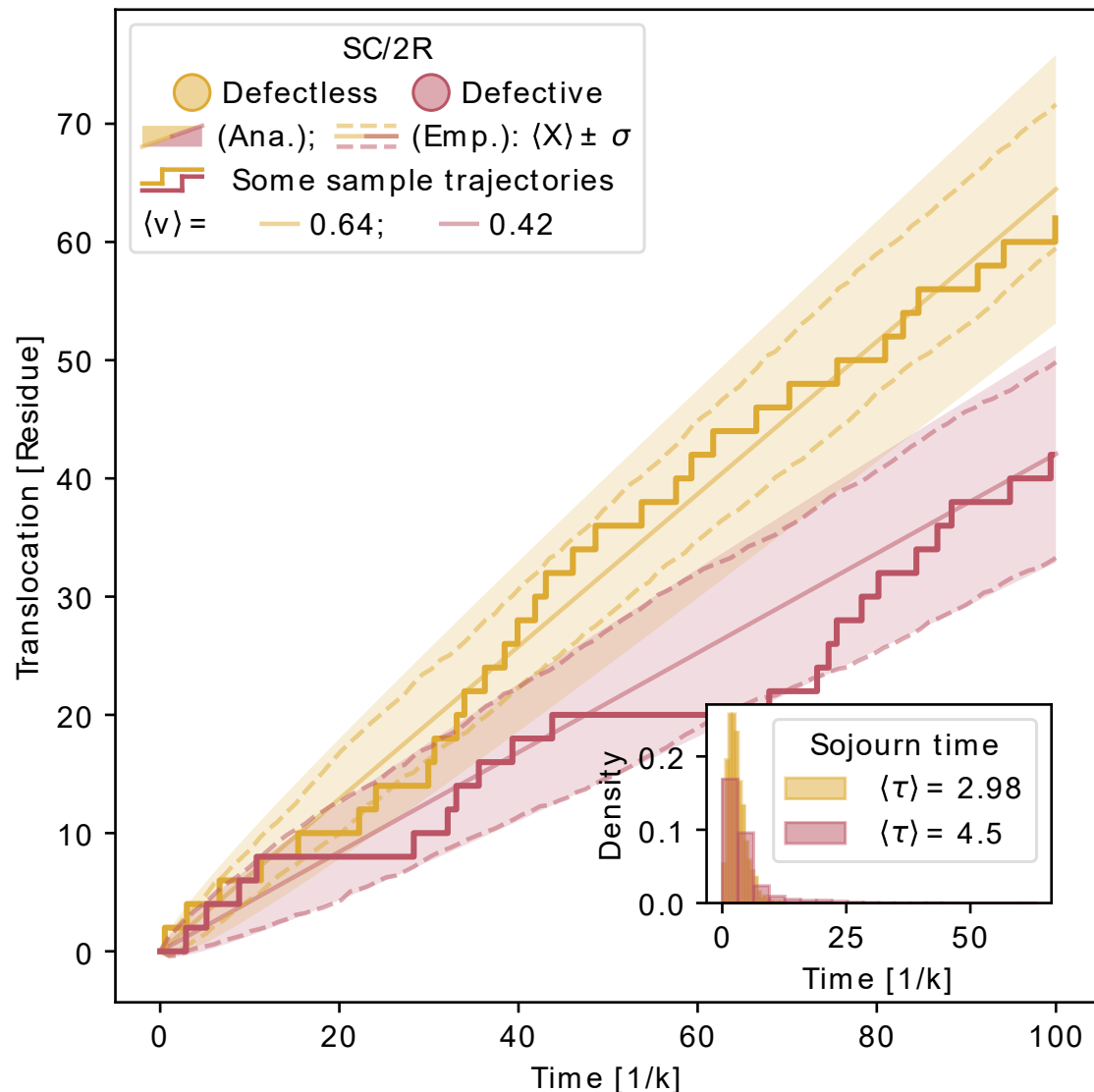
$$k \mapsto ke^{-\beta u \Delta x}$$



Pulling on the substrate



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 Nature. 2020, vol. 578, no. 7794, pp. 317–320.
 DOI: 10.1038/s41586-020-1964-y.



Defective protomer



[...] indicating that Hsp104 power stroke can be generated by ATP hydrolysis in a single subunit.

Conclusion

SC/2R vs RPCL

	SC/2R	RPCL
Compatible with cryo-EM observed contracted and extended configurations	Yes	Yes



Thank you for
your attention!

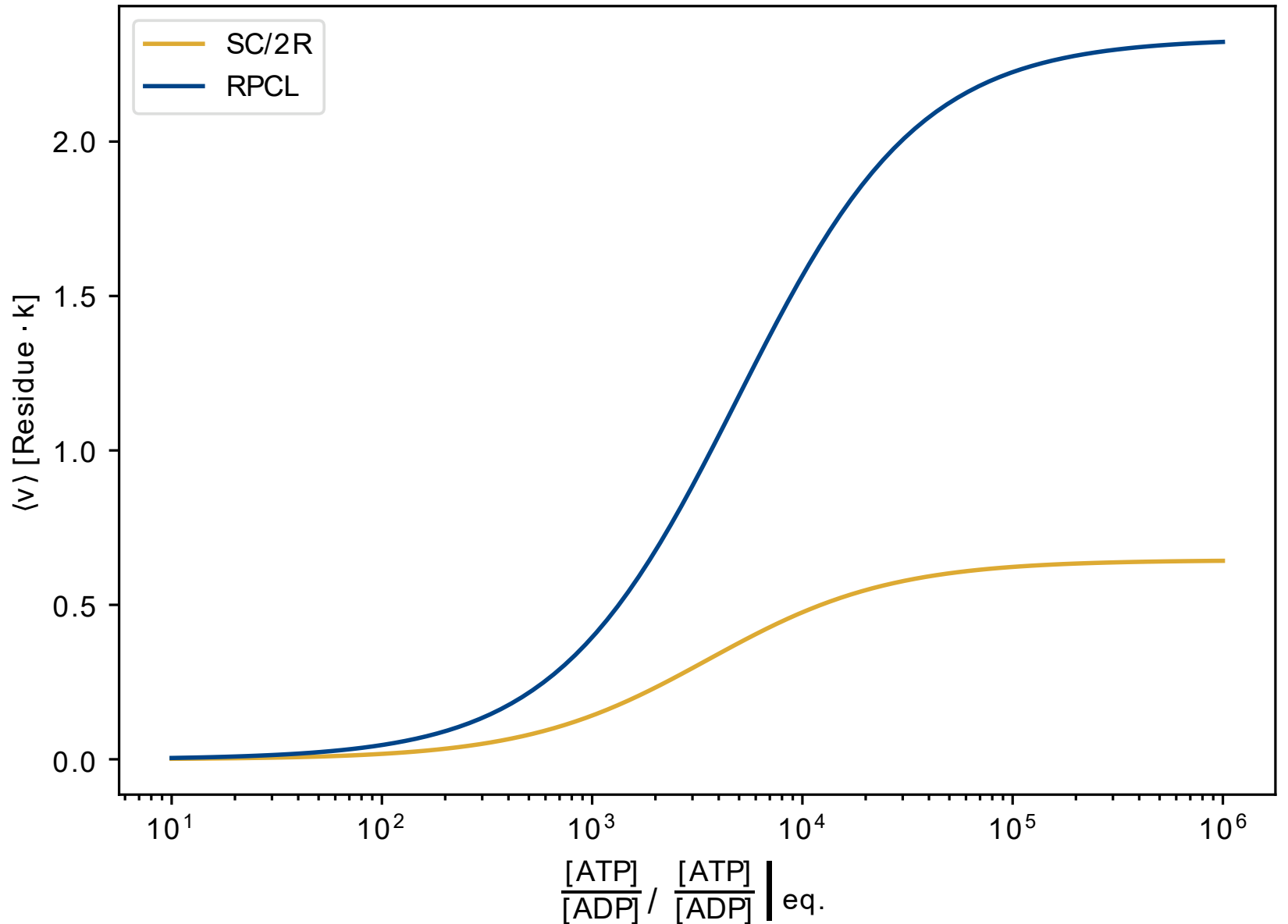
Concertina locomotion



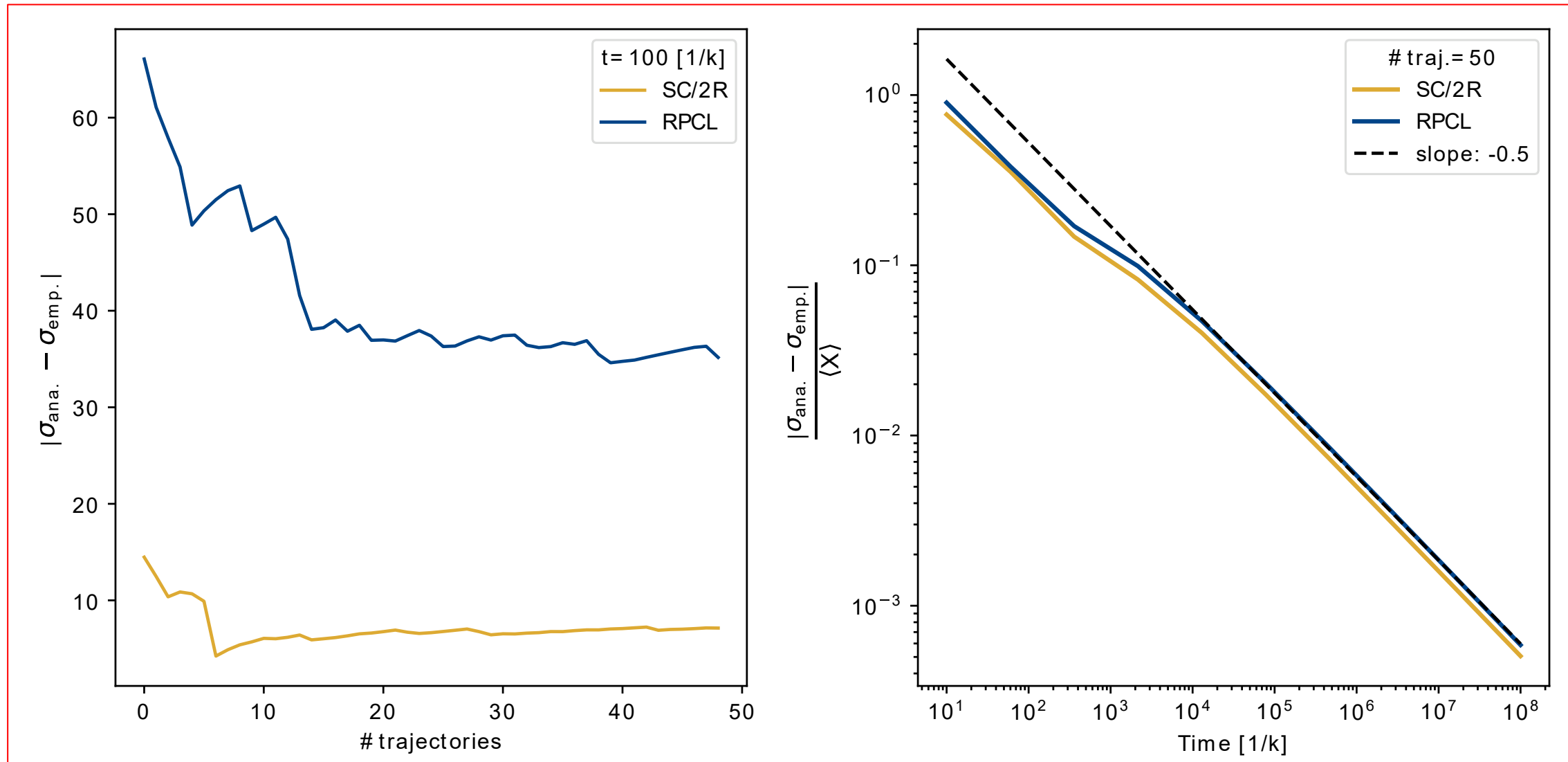
knowerzone. Snakes can climb trees. TikTok.
2023-10-18. Available from
<https://www.tiktok.com/@knowerzone/video/7291299264095931681>



Relation
between $\langle v \rangle$
and $\frac{[ATP]}{[ADP]}$

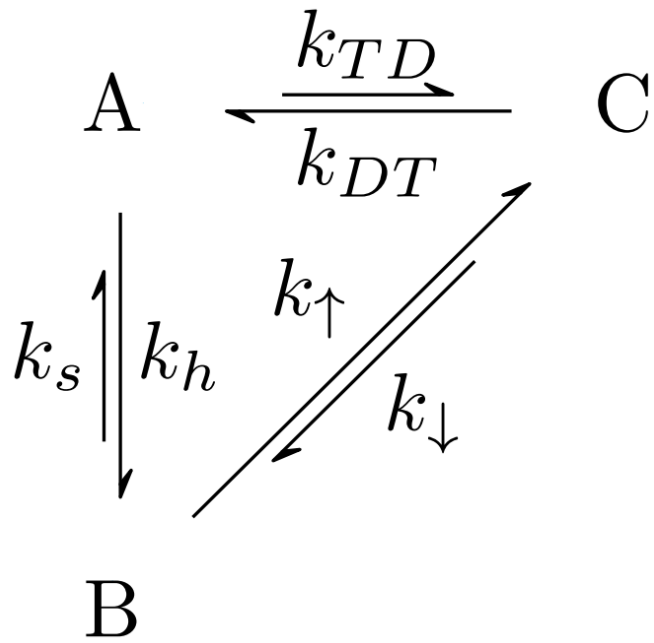


Translocated length: Error between empirical and analytical standard deviations



Saturating velocities for large forces

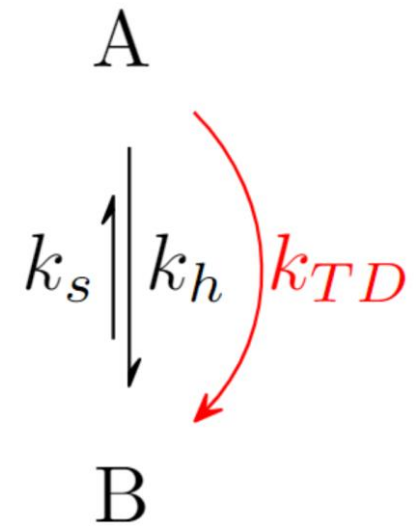
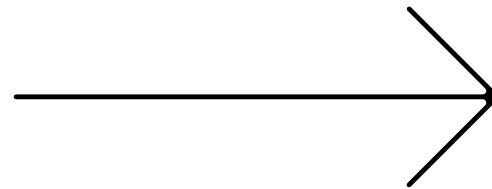
SC/2R



$$\begin{cases} p_A \propto k_s k_{DT} + k_{\downarrow} k_s + k_{\uparrow} k_{DT} \\ p_B \propto k_h k_{\downarrow} + k_{DT} k_h + k_{TD} k_{\downarrow} \\ p_C \propto k_{\uparrow} k_{TD} + k_s k_{TD} + k_h k_{\uparrow} \end{cases}$$

$$u \rightarrow \infty$$

$$\Rightarrow \begin{cases} k_{\uparrow} \rightarrow 0 \\ k_{\downarrow} \rightarrow \infty \end{cases}$$



$$\begin{cases} p_A \propto k_s \\ p_B \propto k_h + k_{TD} \\ \langle v \rangle \propto -\Delta x k_s k_{TD} \end{cases}$$

