

What did the Hiwi do besides making coffee?

Vibrational energy transport in the WW loop

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Target system

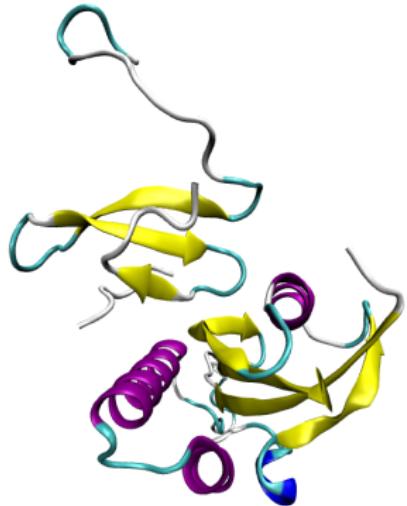
Simulation

MD results

Rate model

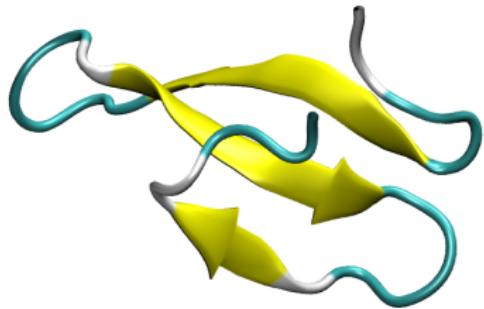
Conclusion and Outlook

WW loop



- found in peptidyl-prolyl isomerase (Pin1)
- 34 residues
- 3 anti-parallel β -sheets

WW loop

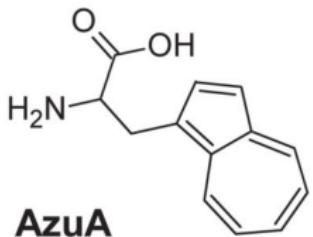


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- 3 anti-parallel β -sheets

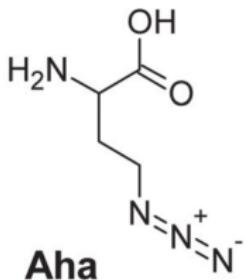
Heater and "thermometer"



Experimental monitoring of VET needs a pump-probe-pair

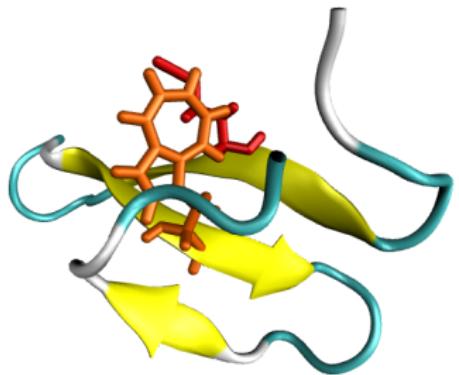


- excitable at 600 nm
- full vibrational decay on sub-picosecond time scale



- monitored at 2098 cm⁻¹
- sensitive to low frequency modes

Manipulated WW loop



- experimentally synthesized mutants
 - 8 AHA / 19 AZU
 - 8 AHA / 29 AZU
 - 17 AHA / 19 AZU
 - 26 AHA / 29 AZU
- simulated: 8 AHA / 19 AZU

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Simulation details

- 200 conformations from 100 K equilibrium simulation
 - cool down to 10 K
 - couple chromophore of AZU to 910 K and freeze rest of protein
 - 100 ps NEQ simulation with $\Delta t = 0.2 \text{ fs}$
- kinetic energies averaged over 200 trajectories

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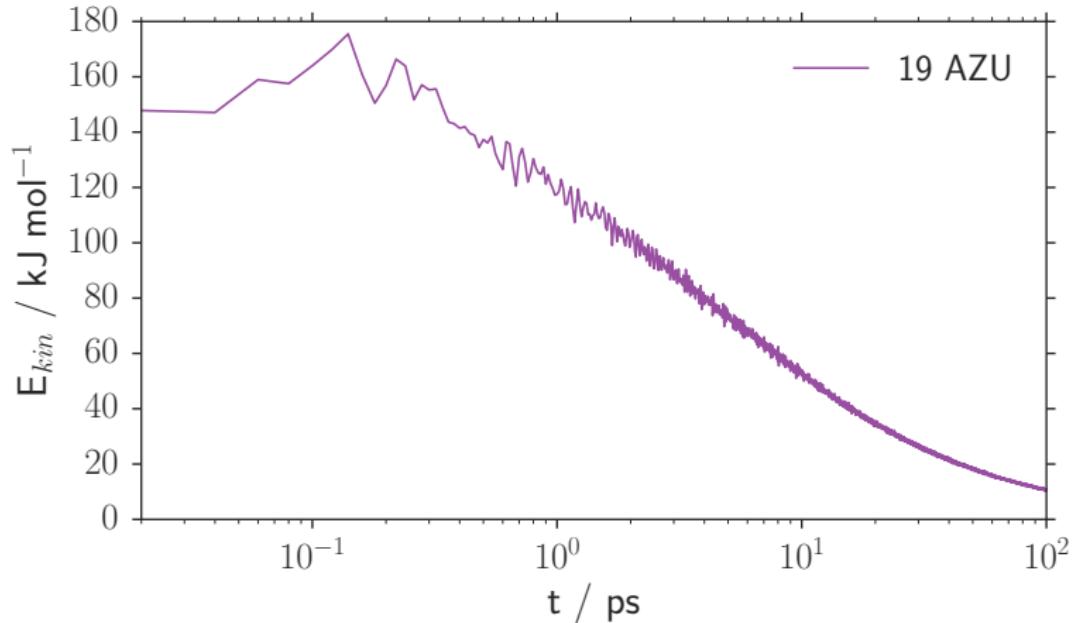
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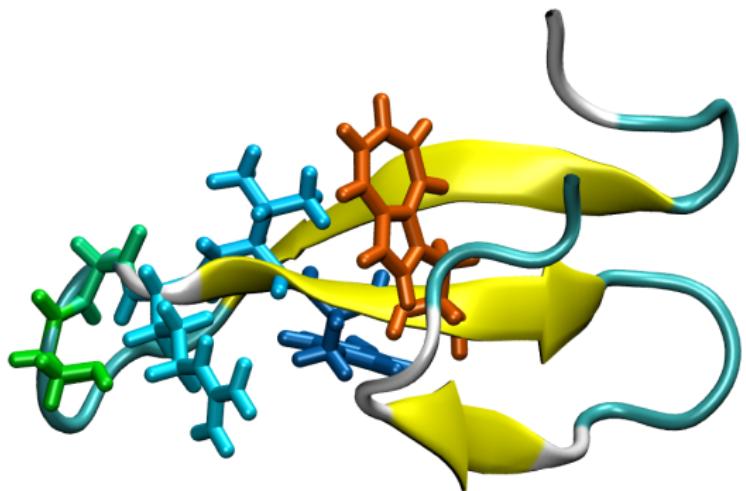
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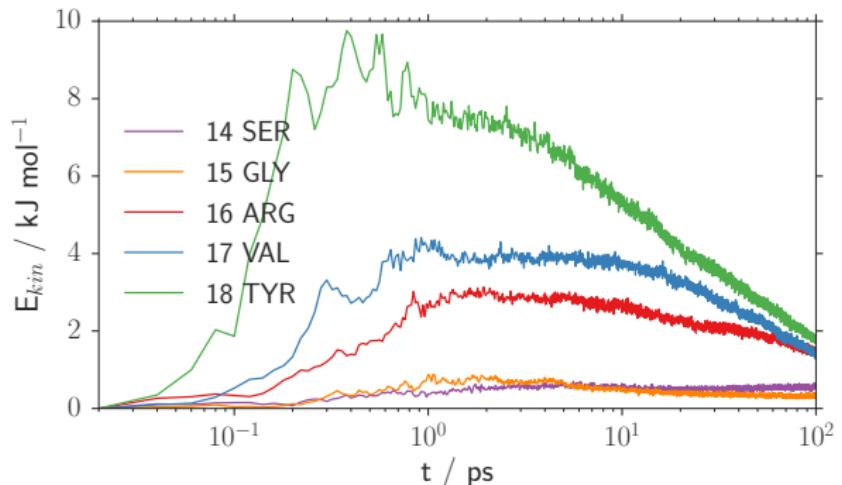


→ fitted decay time $\tau = 10.3 \text{ ps}$

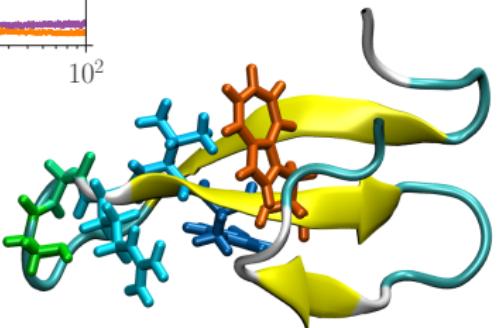
Upstream neighbours



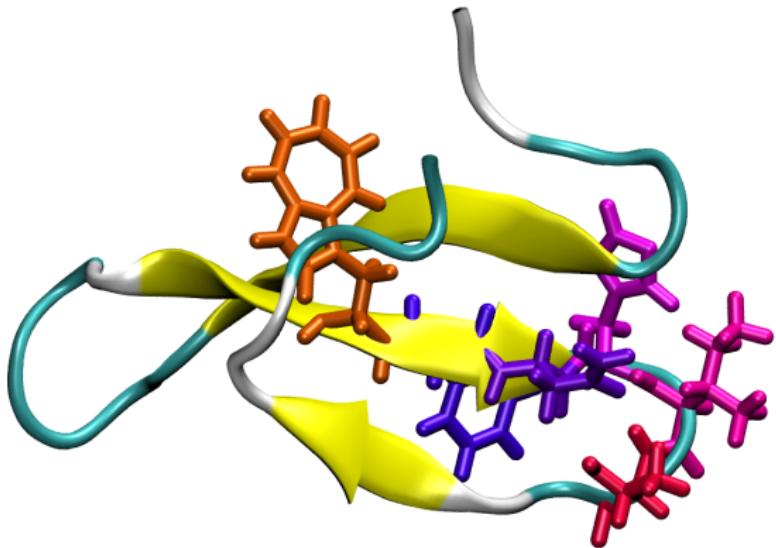
Upstream neighbours



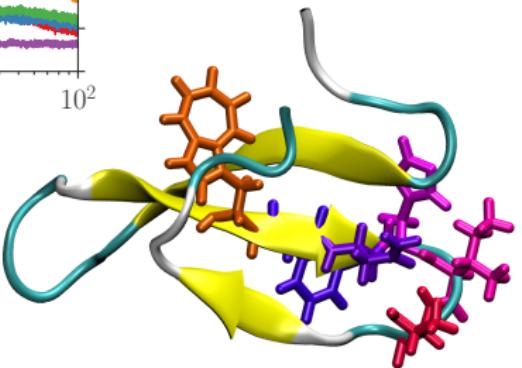
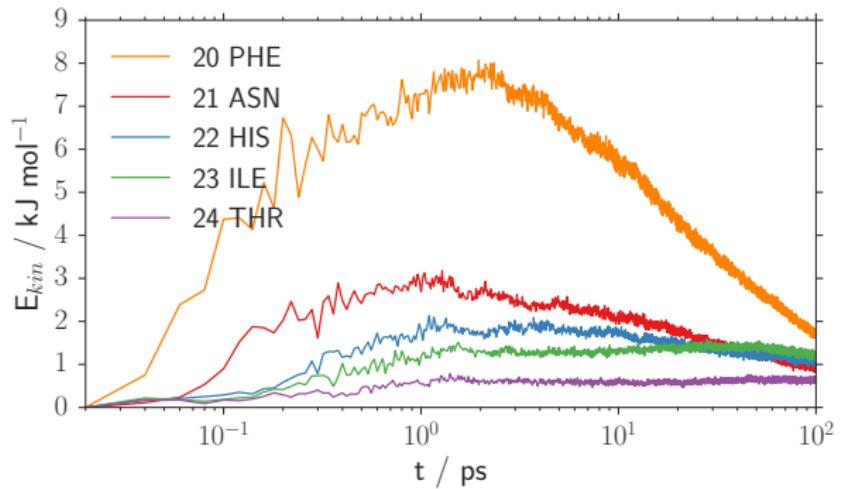
$\rightarrow \Delta E \approx 10 \frac{\text{kJ}}{\text{mol}}$ for direct neighbour



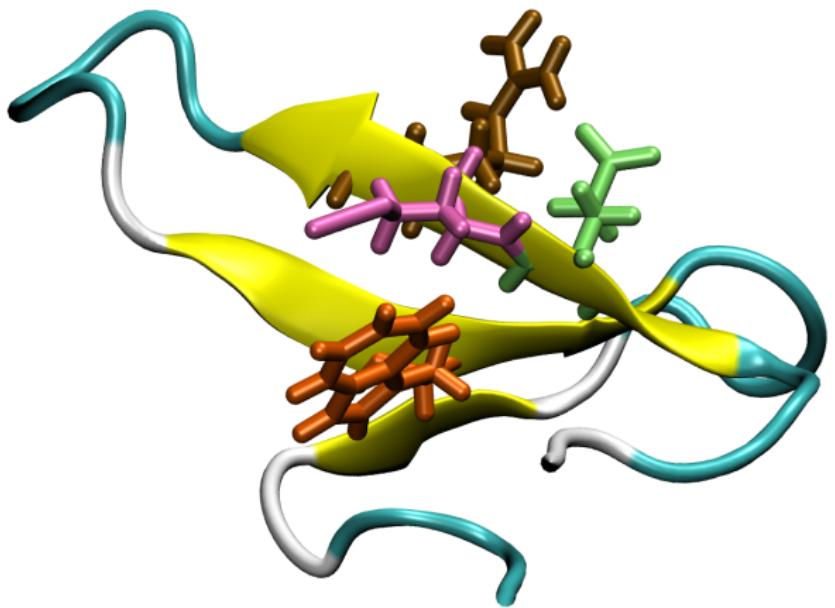
Downstream neighbours



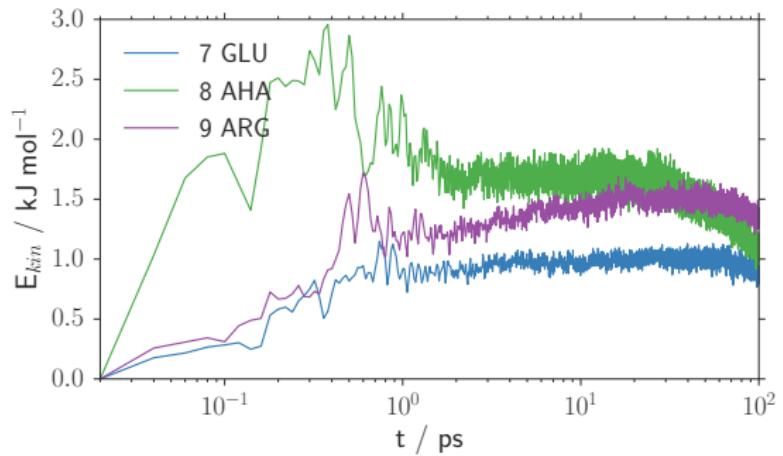
Downstream neighbours



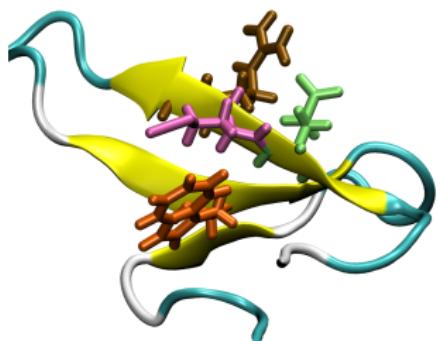
Beta sheet neighbours



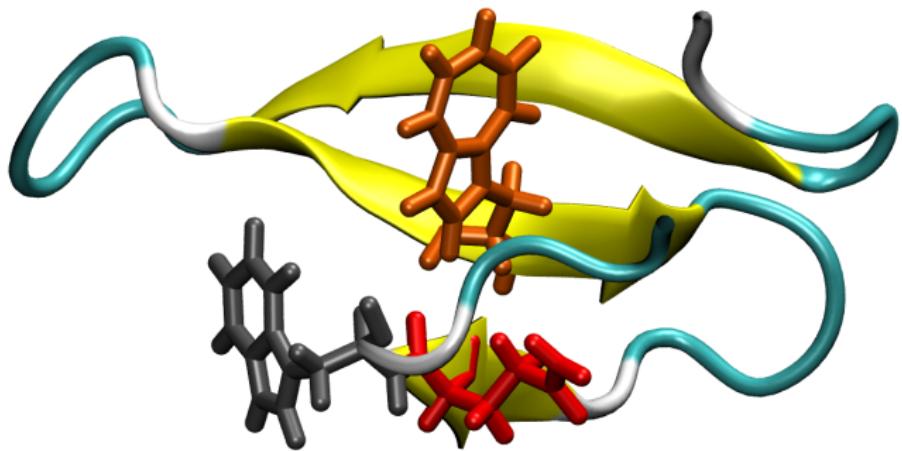
Beta sheet neighbours



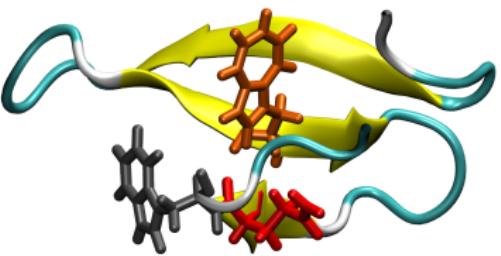
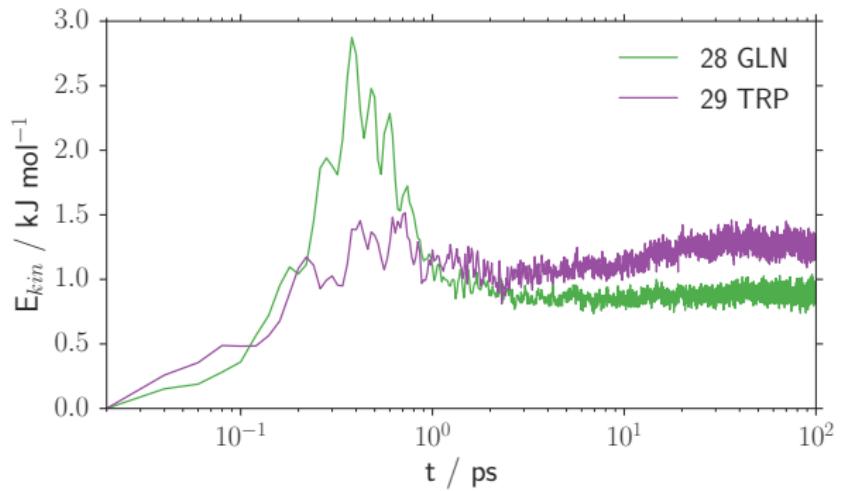
→ role of sidechain contacts



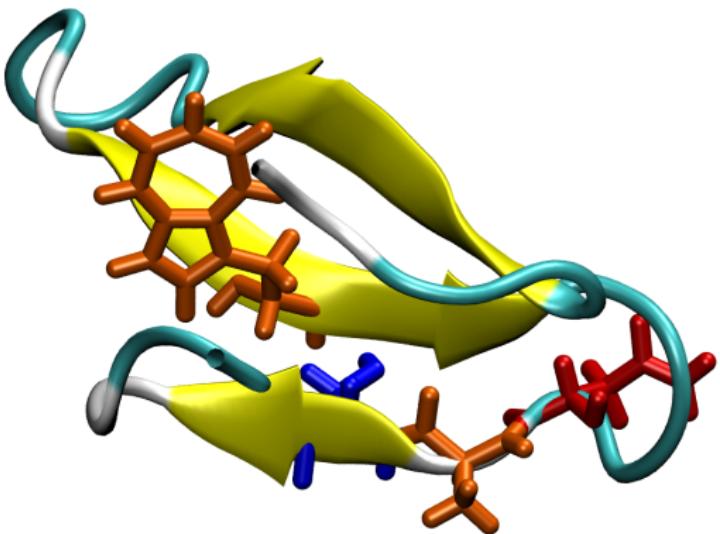
Beta sheet neighbours



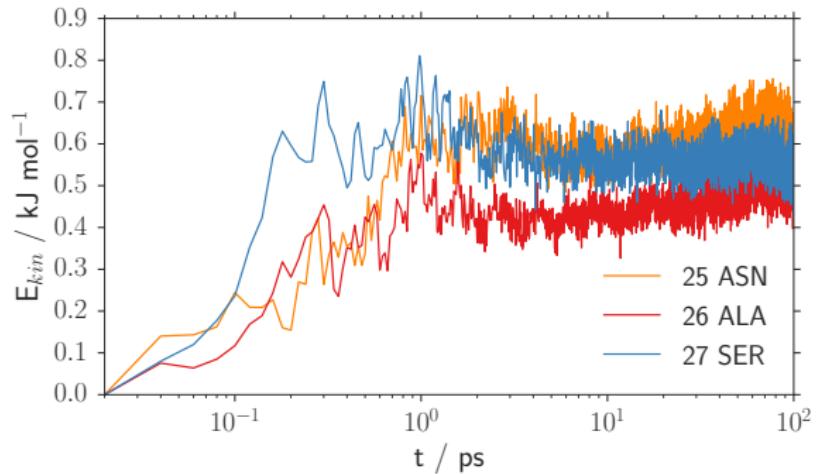
Beta sheet neighbours



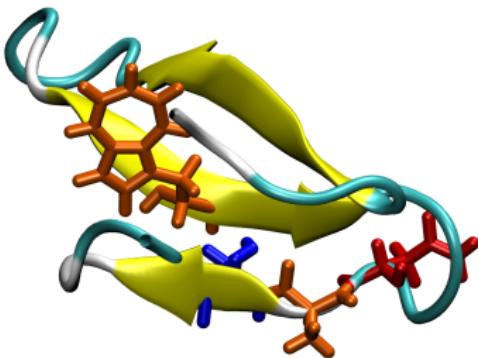
Beta sheet neighbours



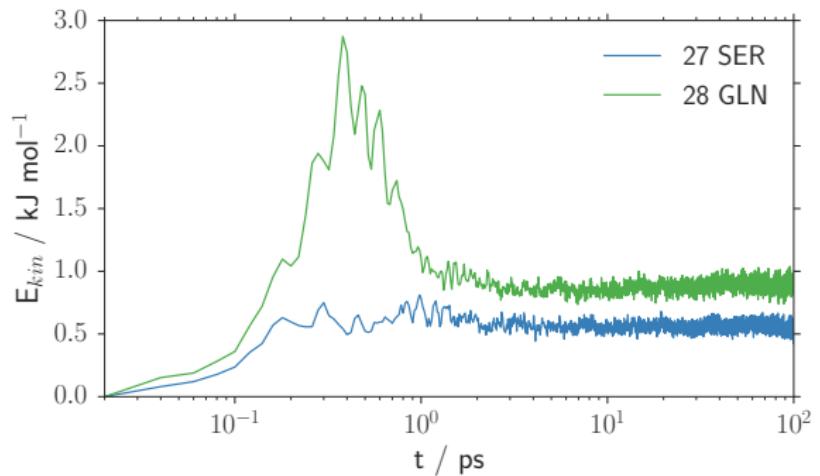
Beta sheet neighbours



→ ΔE one order of magnitude smaller than for direct neighbours



Beta sheet neighbours



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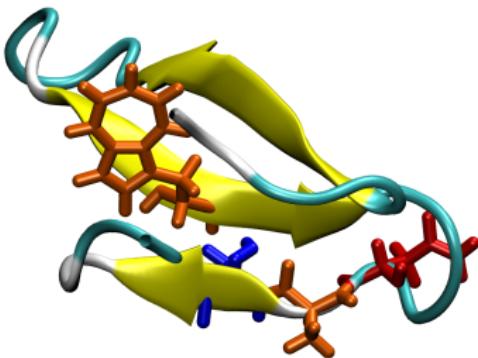


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How can the vibrational energy transport be expressed in a simple model?

→ transition rate model for residues

Master equation

Change in energy of residue i

$$\frac{dE_i}{dt} = \sum_j (k_{ji}E_j - k_{ij}E_i) - k_{i,S}E_i + k_{S,i}E_S,$$

with

- k_{ij} transition rate from residue i to residue j
- $k_{i,S}$ cooling rate from protein to solvent
- $k_{S,i}$ back rate from solvent to protein

Scaling rules

→ diffusion model and detailed balance condition for transition rates

Backbone rates

$$k_{ij}^B = \frac{D_B}{\langle \Delta x_{ij} \rangle^2} \sqrt{\frac{f_j}{f_i}}$$

Polar contact rates

$$k_{ij}^C = \frac{D_C}{\langle \Delta x_{ij}^2 \rangle} \sqrt{\frac{f_j}{f_i}}$$

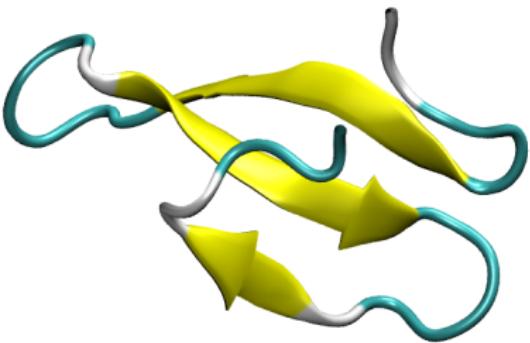
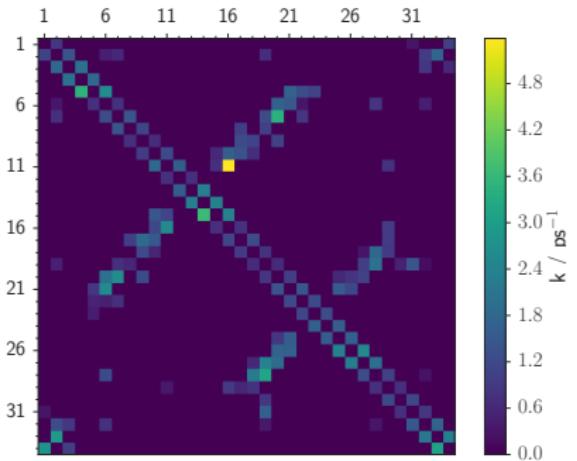
With

- f degrees of freedom
- Δx distance between closest atoms

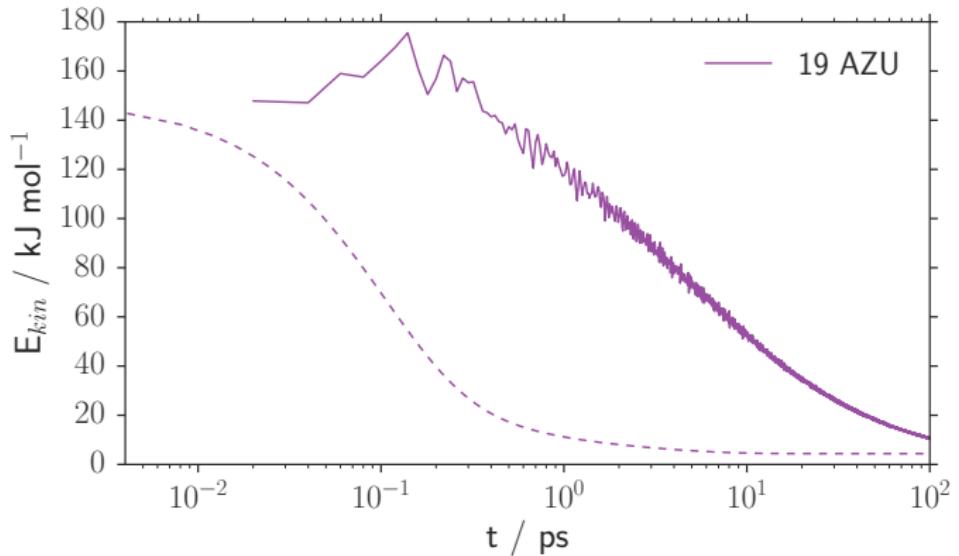
Can we apply the model, including the diffusion constants, globally
if T is constant?

Transition rates

■ Polar + backbone rates

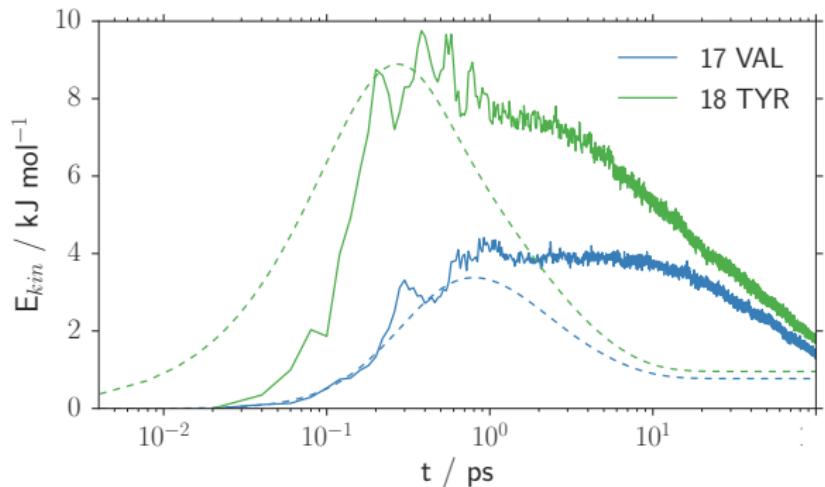


MEQ Results - Heater

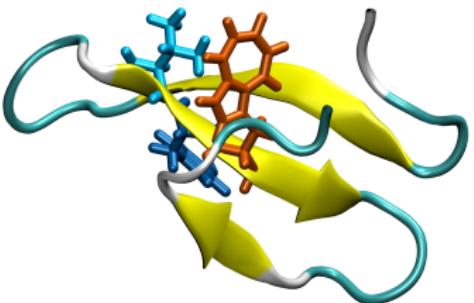


→ excited limbo state 19*?

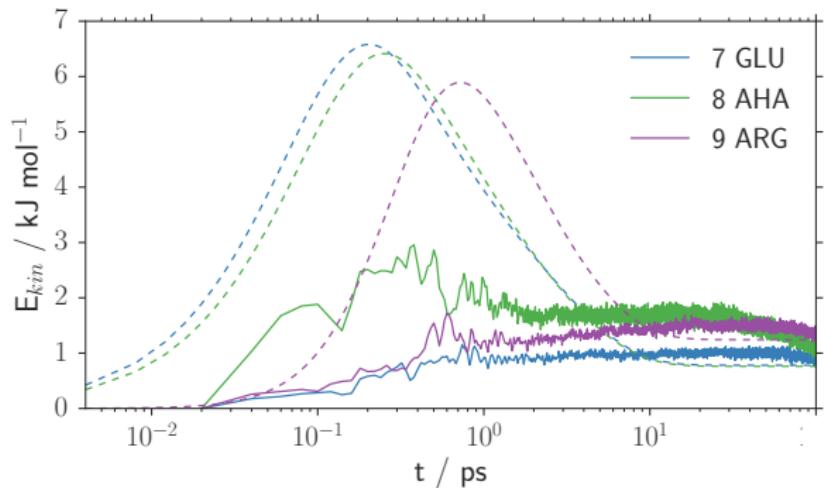
MEQ Results - Neighbours



→ shoulder to the right?



MEQ Results - Polar contacts



→ overestimation of D_C ?

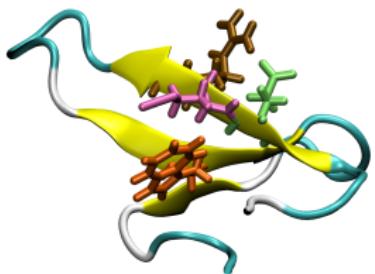


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■ MD results

- direct neighbours 18TYR and 20PHE receive 7-10 $\frac{\text{kJ}}{\text{mol}}$
- beta sheet “neighbours” 8AHA and 28GLN receive $\approx 3 \frac{\text{kJ}}{\text{mol}}$
- bottlenecks in backbone transport

■ Rate model

- decay process of AZU slower
- magnitude of energy transport good for direct neighbours
- polar contact rates too high

- Comparison to experiment
 - behaviour of AHA modes
 - propagation along sidechains
- Rate model
 - fit a model with excited limbo state 19*
 - fit diffusion constants D_C and D_B and compare to other systems

References I

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A donor-acceptor pair for the real time study of vibrational energy transfer in proteins.
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Scaling Rules for Vibrational Energy Transport in Globular Protein.
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-  [D. Leitner, S. Buchenberg, P. Brettel and G. Stock](#)
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Thanks for the attention!

