

# Influence of chain stiffness and sequence on knottedness in polymer globules

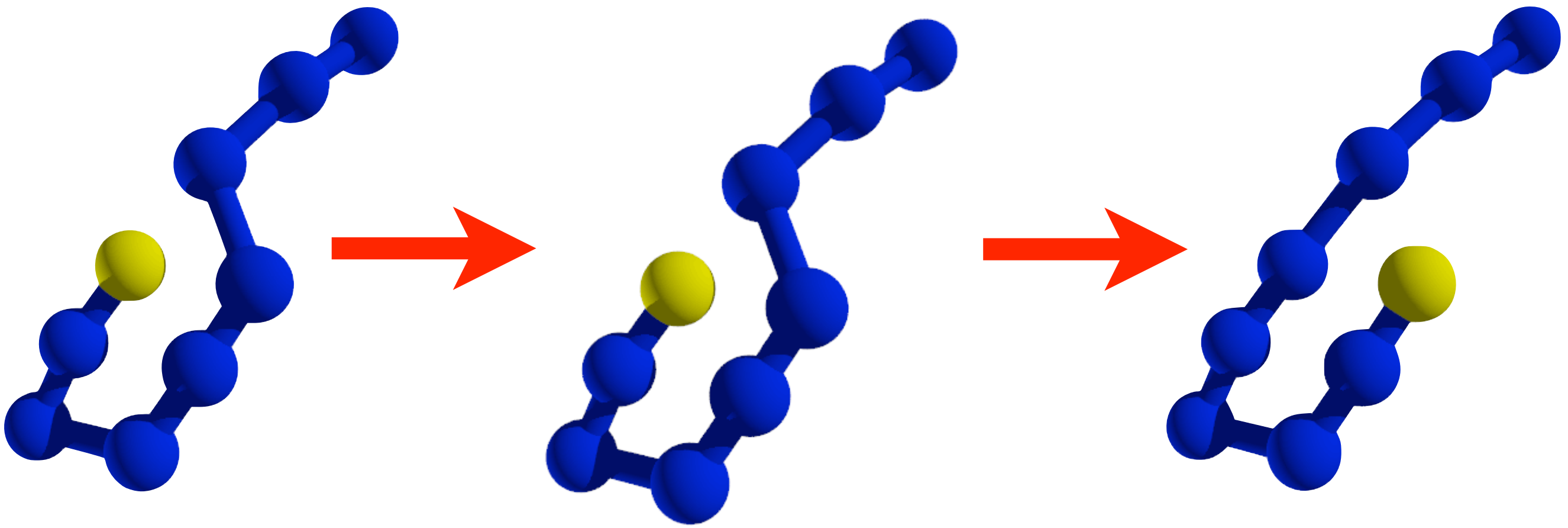
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<sup>2)</sup> Center for Simulational Physics, The University of Georgia, Athens

<sup>3)</sup> Polymer Institute, Slovak Academy of Sciences, Bratislava

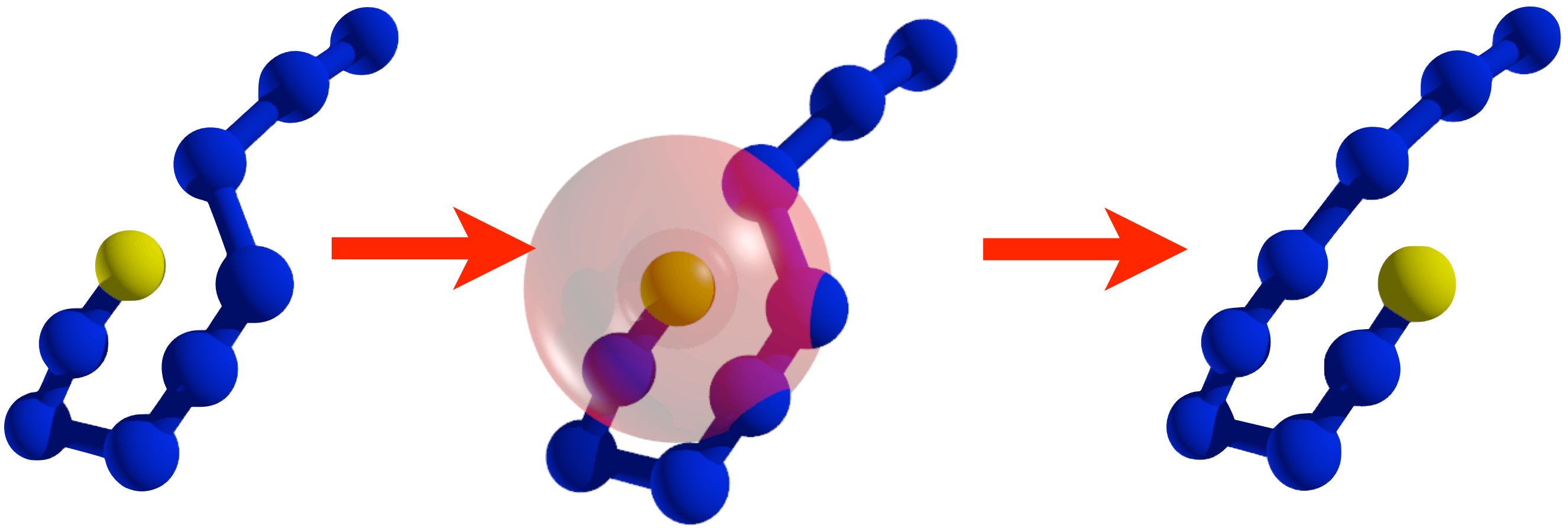
# Backbite move



Start

End

# Backbite move

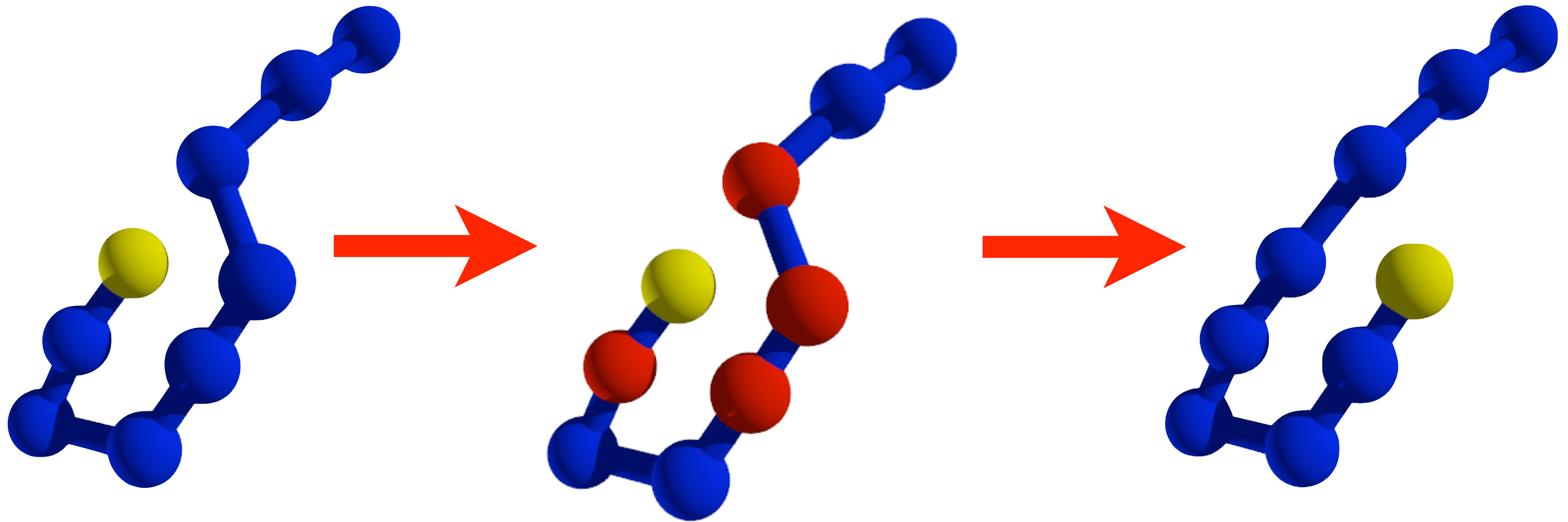


Start

End

for lattice models: M.L. Mansfield, J. Chem. Phys., **77**, 1554 (1982)

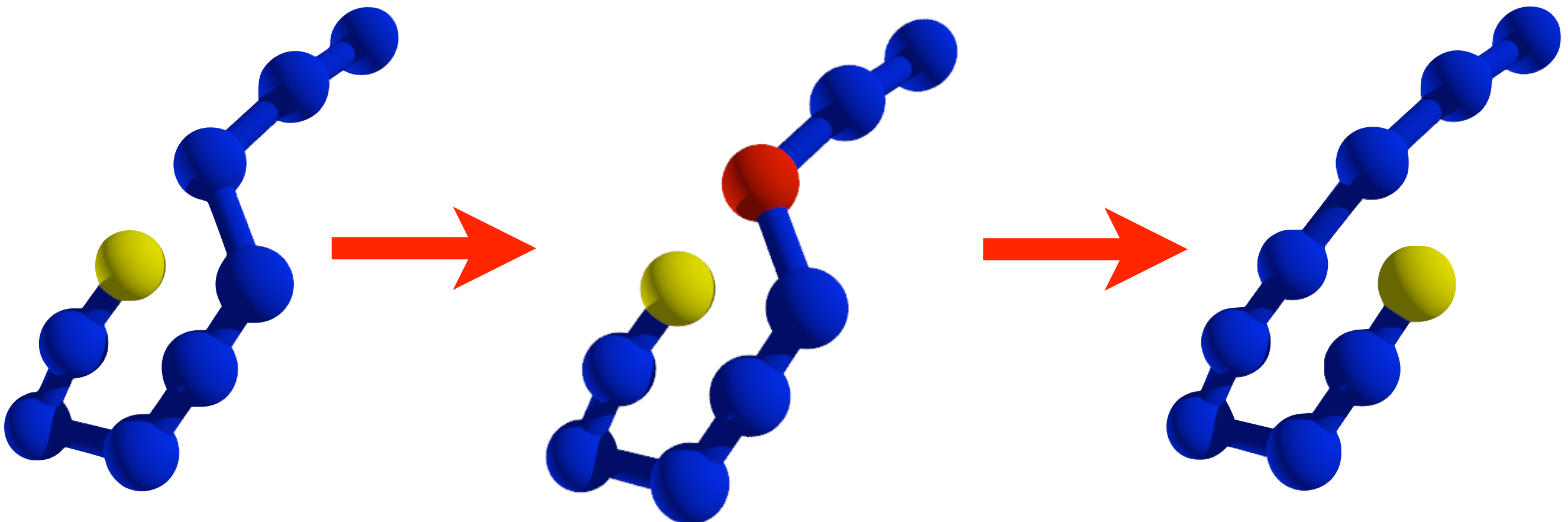
# Backbite move



Start

End

# Backbite move

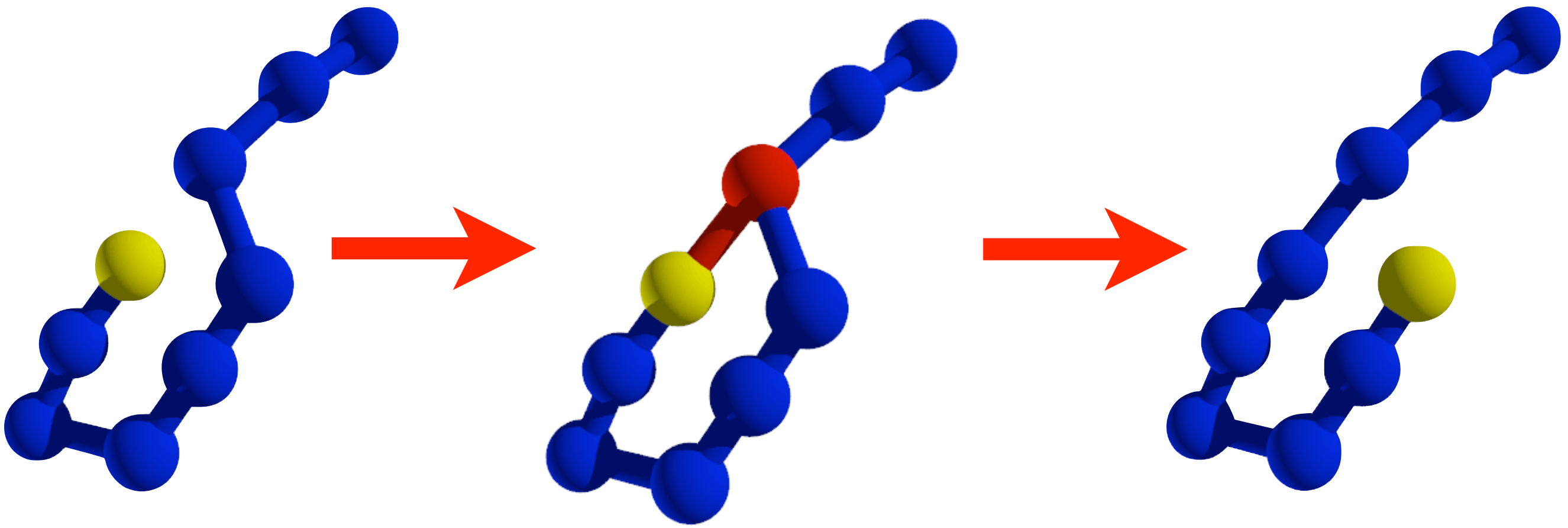


Start

End

for lattice models: M.L. Mansfield, J. Chem. Phys., **77**, 1554 (1982)

# Backbite move

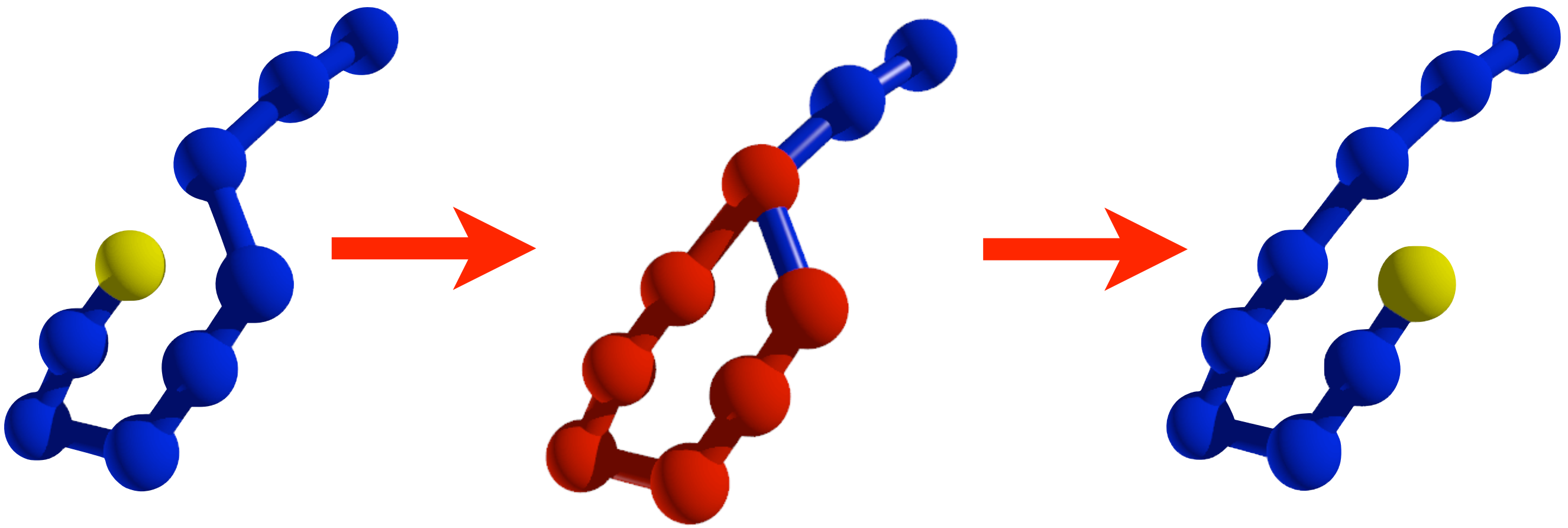


Start

End

for lattice models: M.L. Mansfield, J. Chem. Phys., **77**, 1554 (1982)

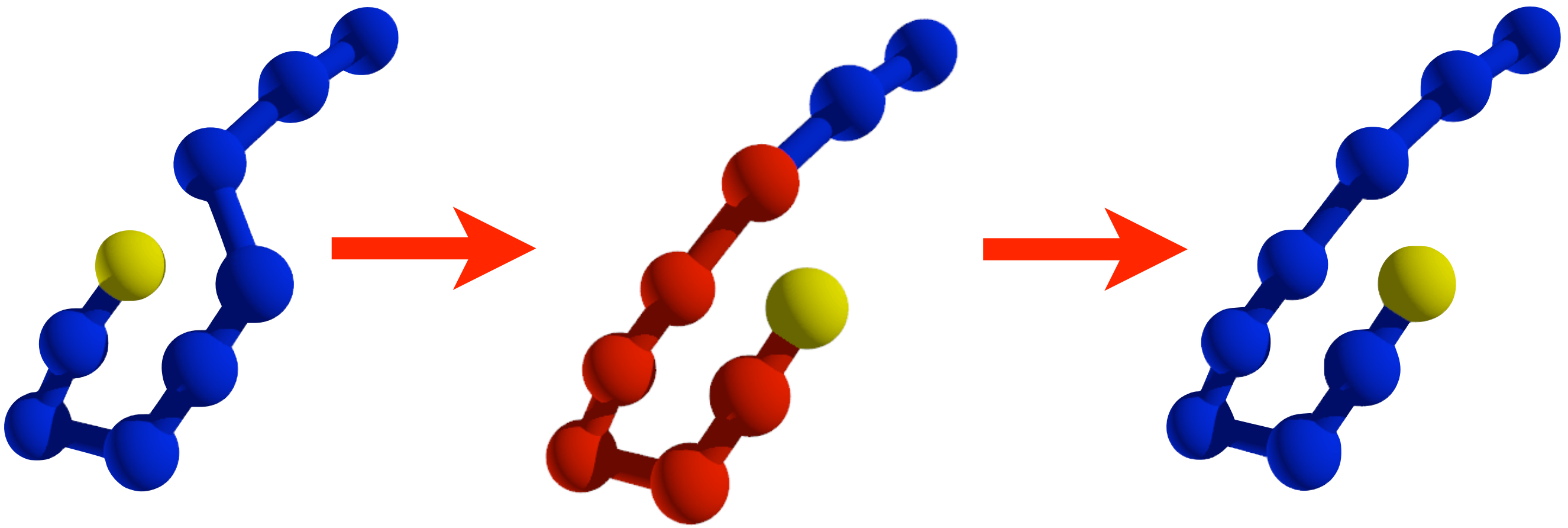
# Backbite move



Start

End

# Backbite move



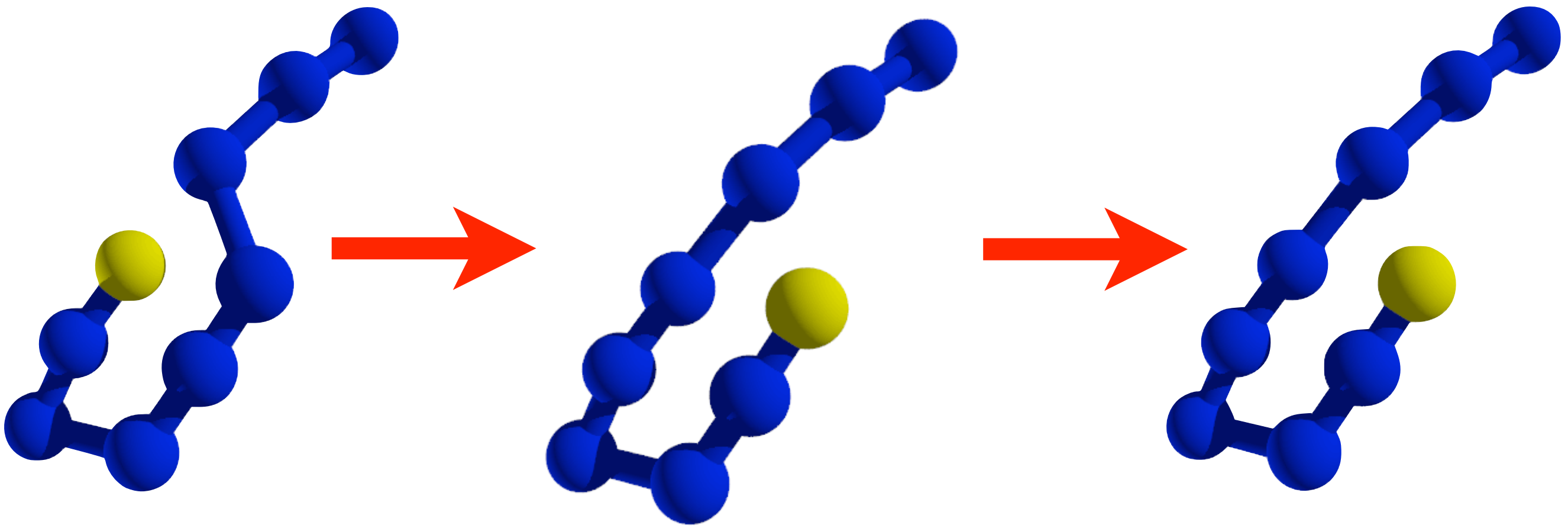
Start

End

for lattice models: M.L. Mansfield, J. Chem. Phys., **77**, 1554 (1982)



# Backbite move

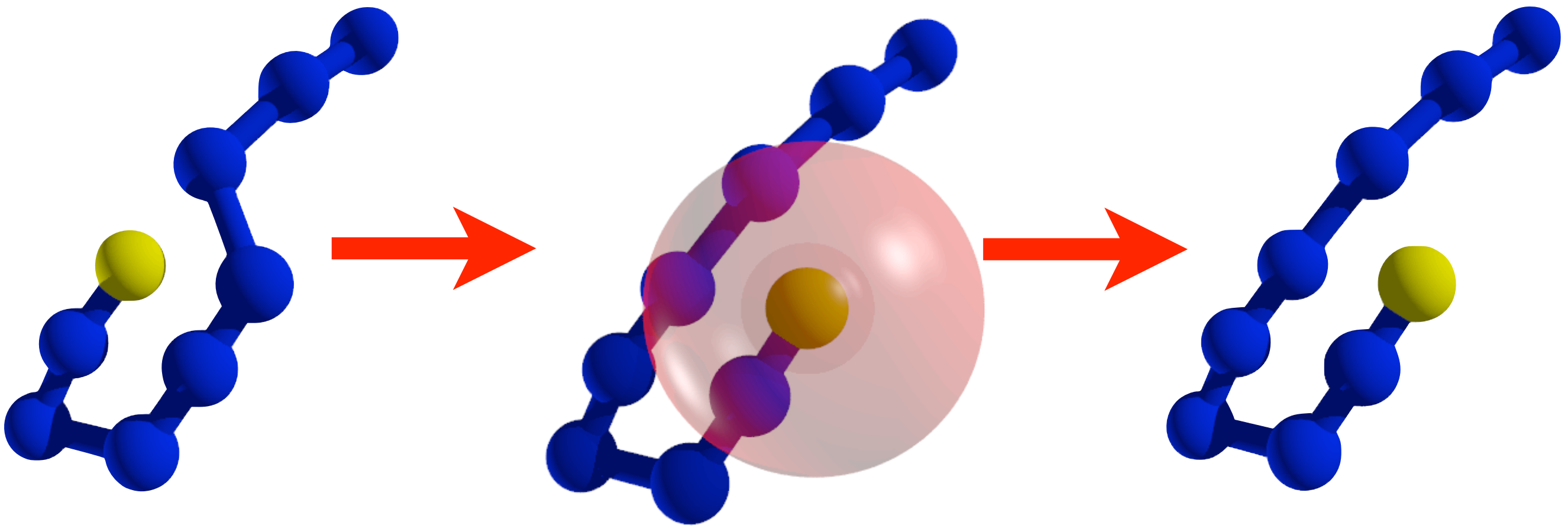


Start

End

for lattice models: M.L. Mansfield, J. Chem. Phys., **77**, 1554 (1982)

# Backbite move



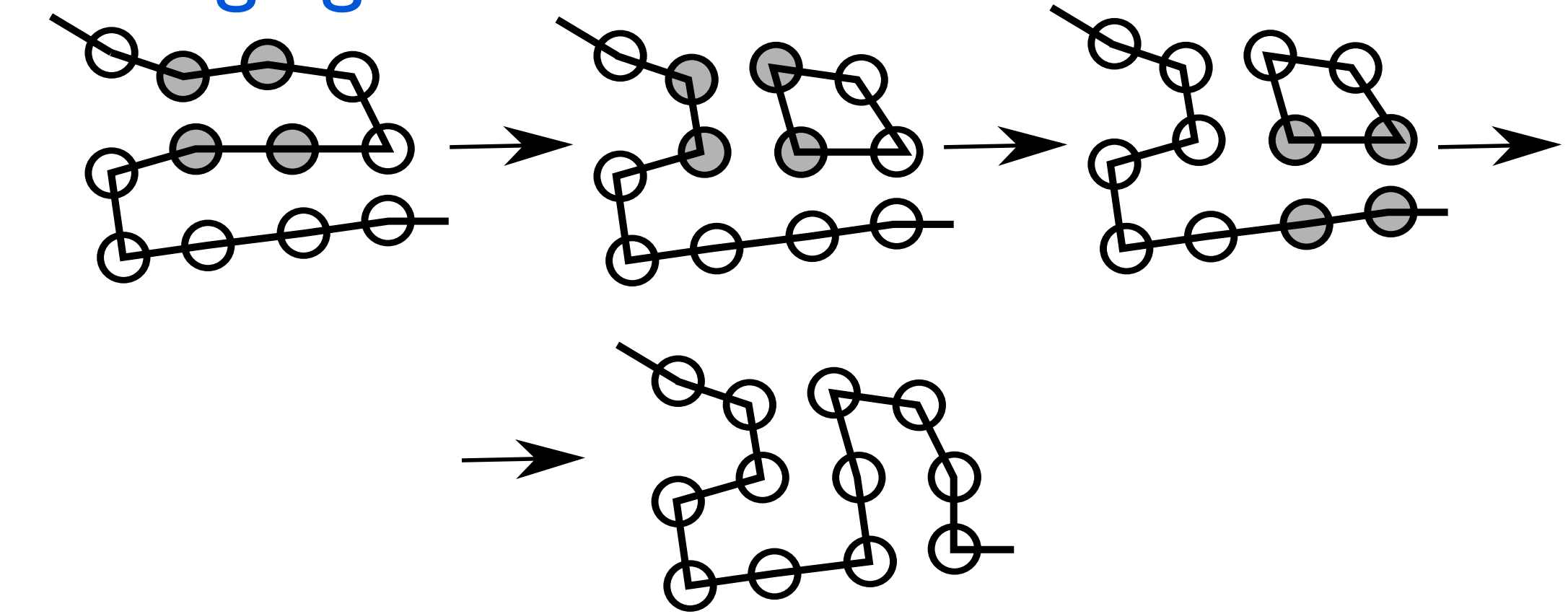
Start

End

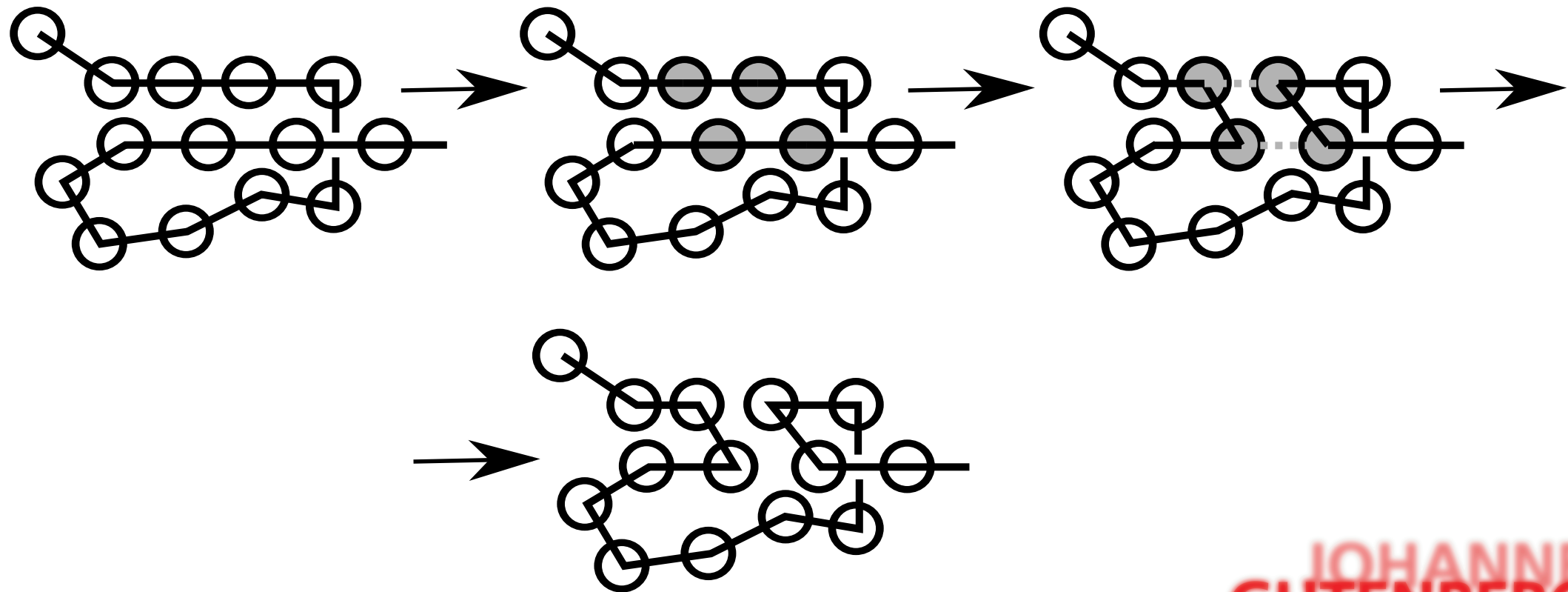
for lattice models: M.L. Mansfield, J. Chem. Phys., **77**, 1554 (1982)

# Internal rebridging

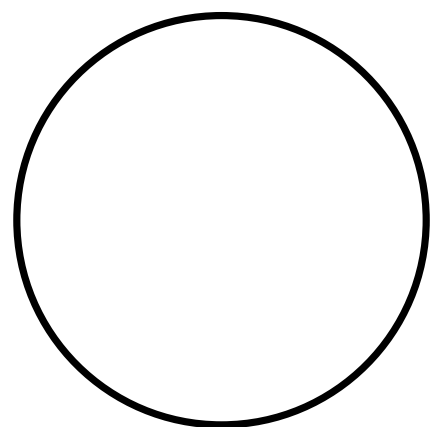
type I



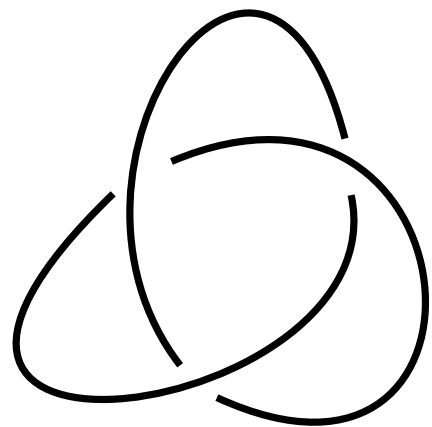
type II



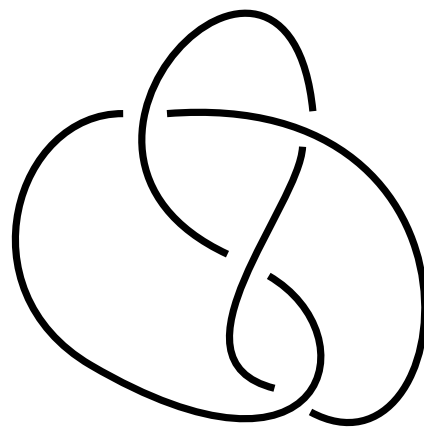
# Talking about topology: Knots



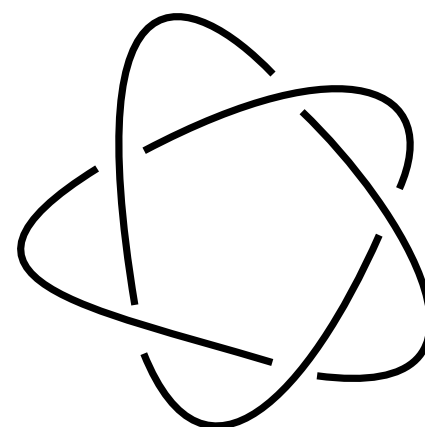
Unknot



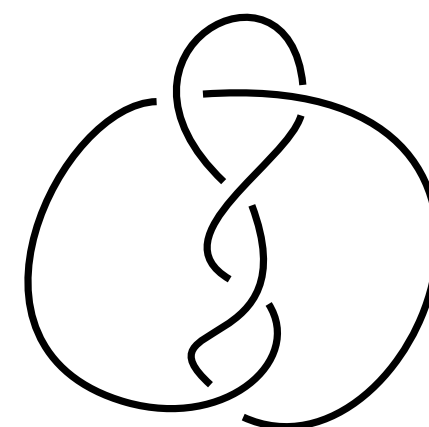
$3_1$



$4_1$



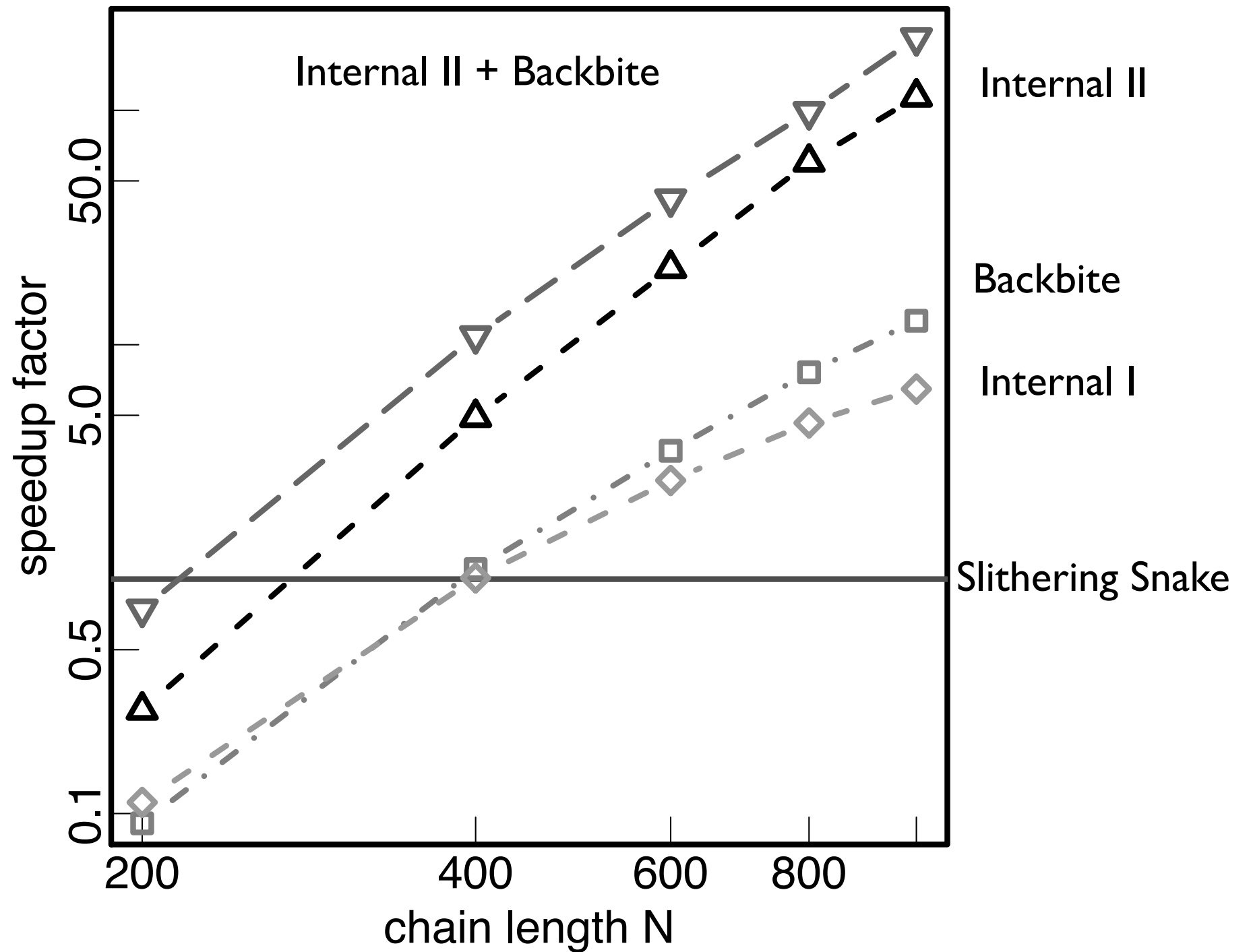
$5_1$



$5_2$

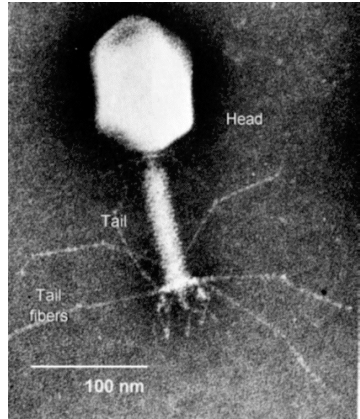
- topological property of closed curves in three dimensional space
- connect both ends to investigate the knottedness of open chains

# Performance

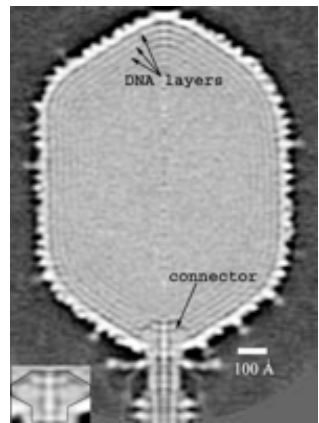


- bridging faster if  $N > 400$
- most efficient: Internal II

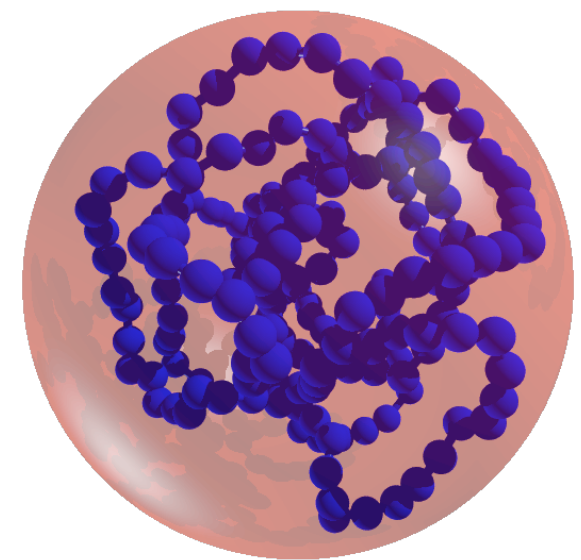
# Homopolymer - motivation - experimental results



- DNA inside viral capsids is coiled up
- one end is anchored in the loading channel



- can we understand the underlying knot avoiding mechanism?

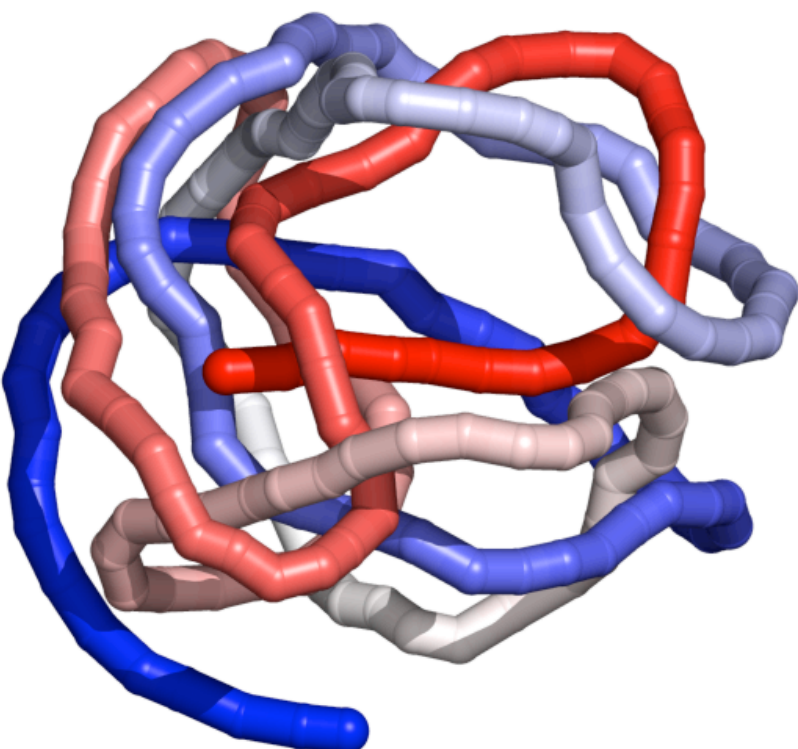




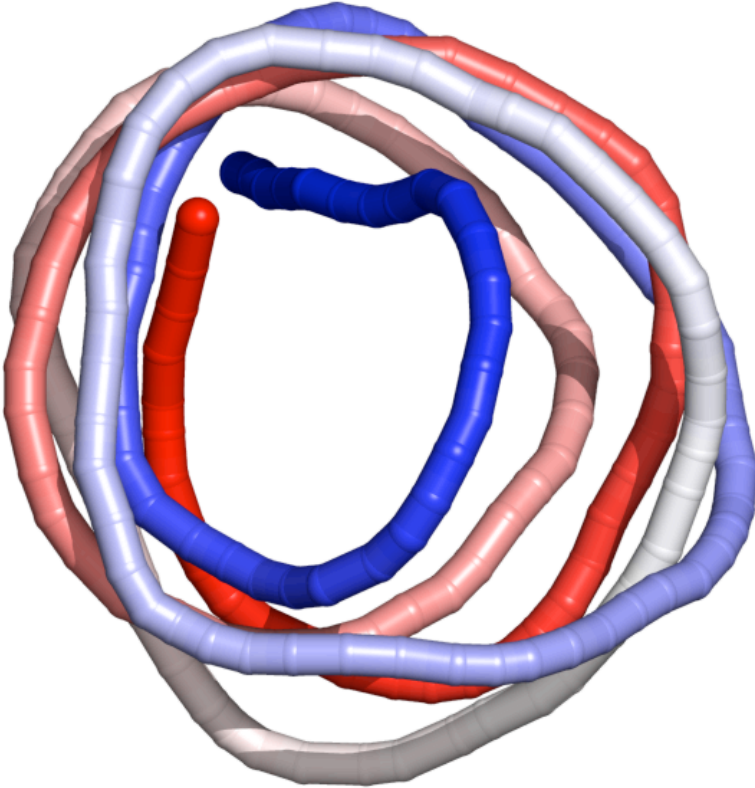
# Homopolymer - results $N=200$



$B=0$



$B=10$



$B=45$

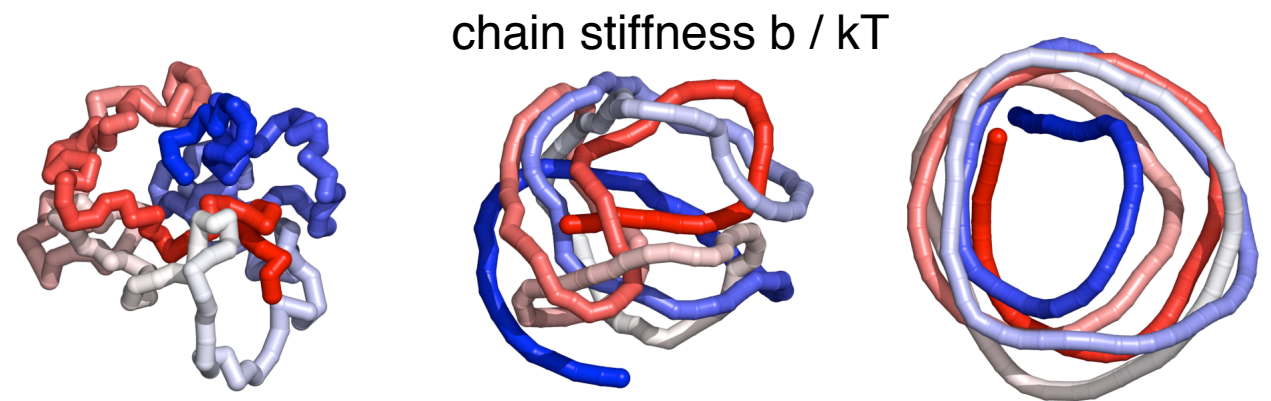
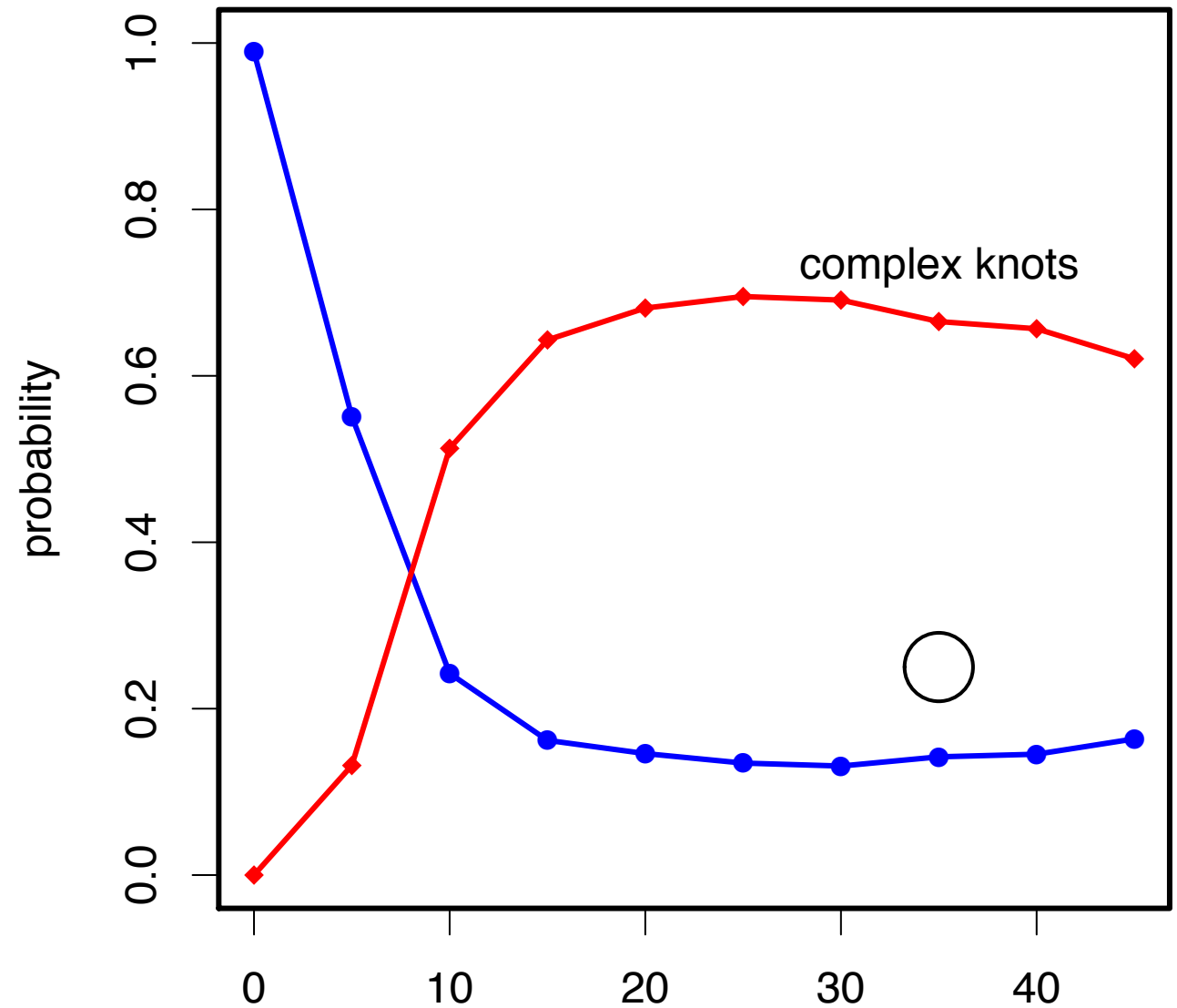
increasing bending rigidity ...



... global ordering...

# Homopolymer - results for $N=200$

...but semiflexible chains are „more knotted“ than flexible chains

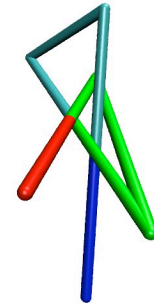
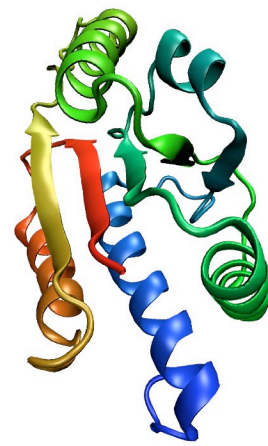




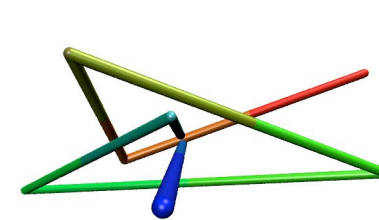
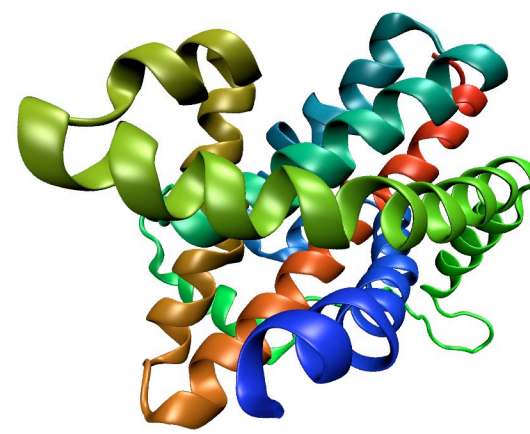
# Heteropolymer - motivation

#folds:

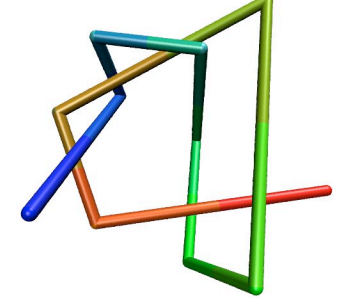
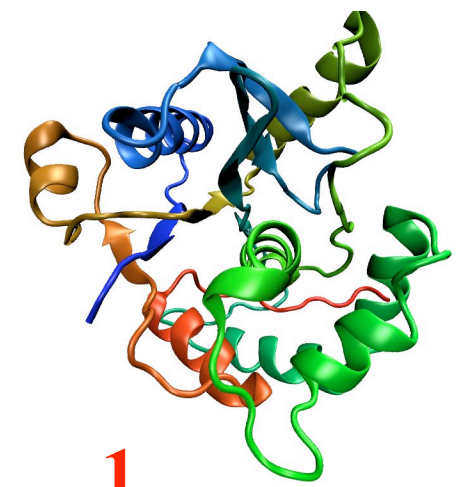
4



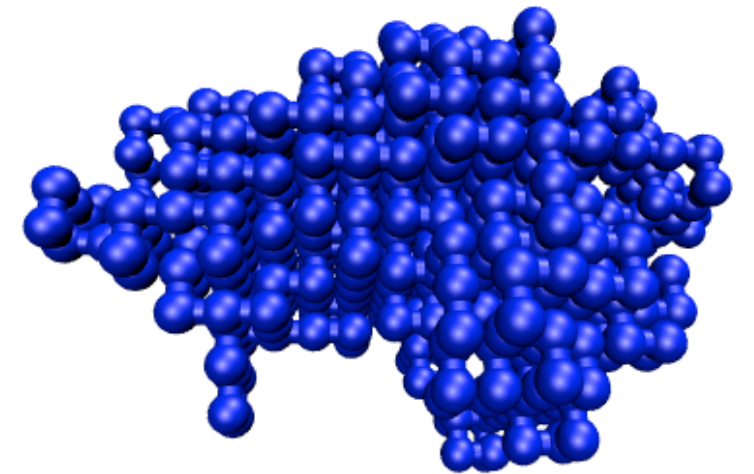
2



1



Probability of finding knots in proteins  $\sim 0.5\%$



But frequent in homopolymers  $\sim 50\%$  (N=500)

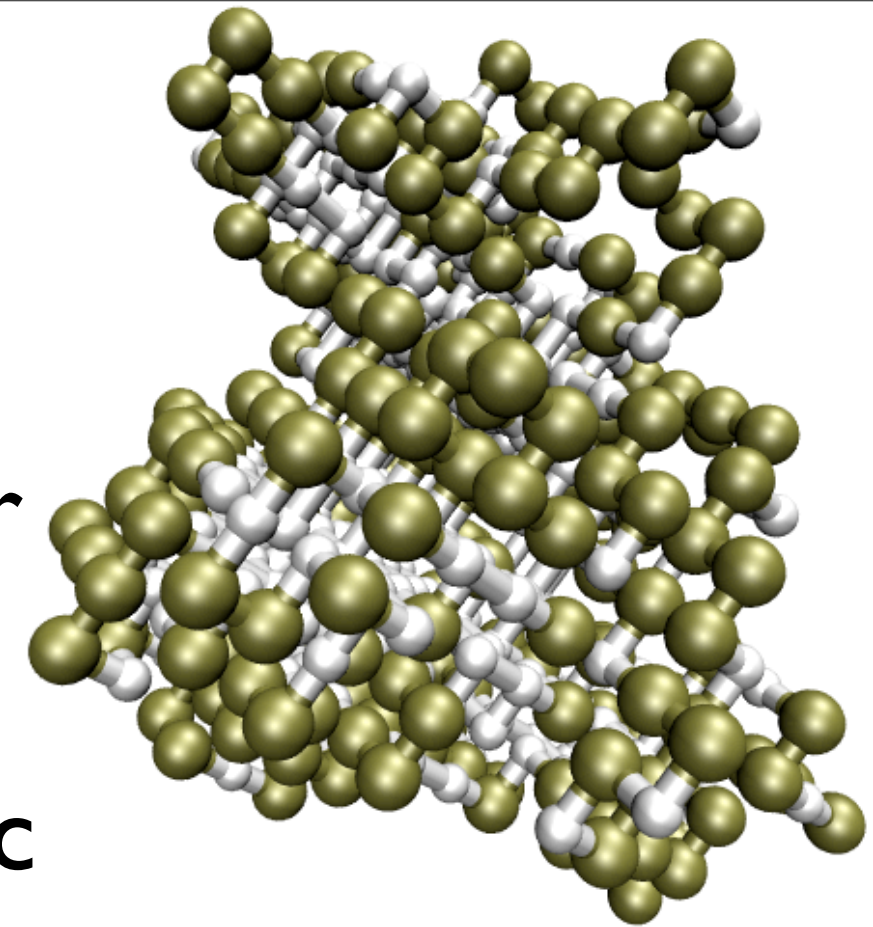
# HP-model

- lattice model
- excluded volume, only one monomer per site allowed
- two types of monomers: hydrophobic (H) and polar (P)
- effective interaction between neighbouring non bonded monomers:

$$\epsilon_{HH} = -1,$$

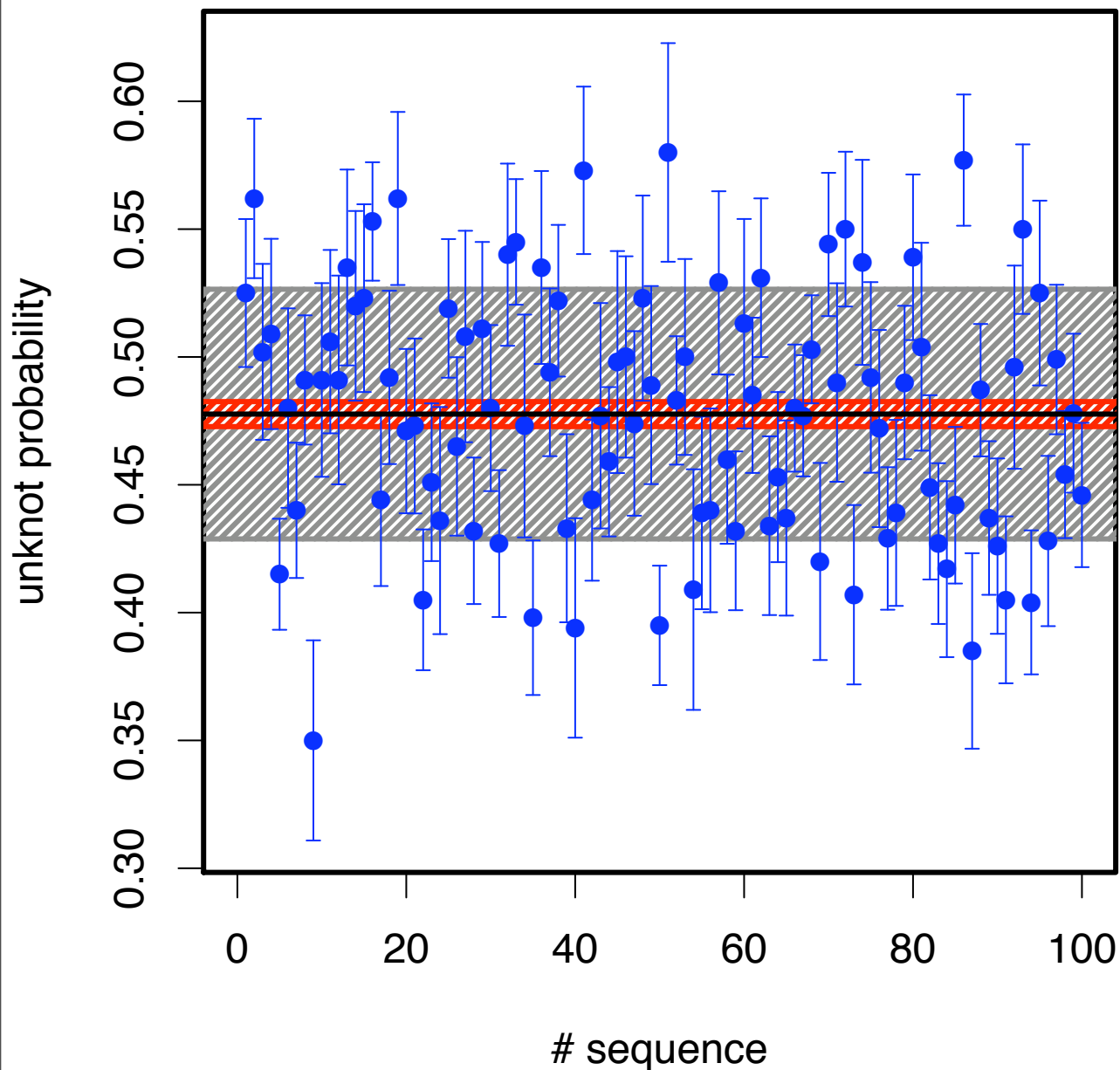
$$\epsilon_{HP} = 0,$$

$$\epsilon_{PP} = 0$$



simplest toy model for coarse-grained  
description of protein folding

# Heteropolymer - random sequences N=500

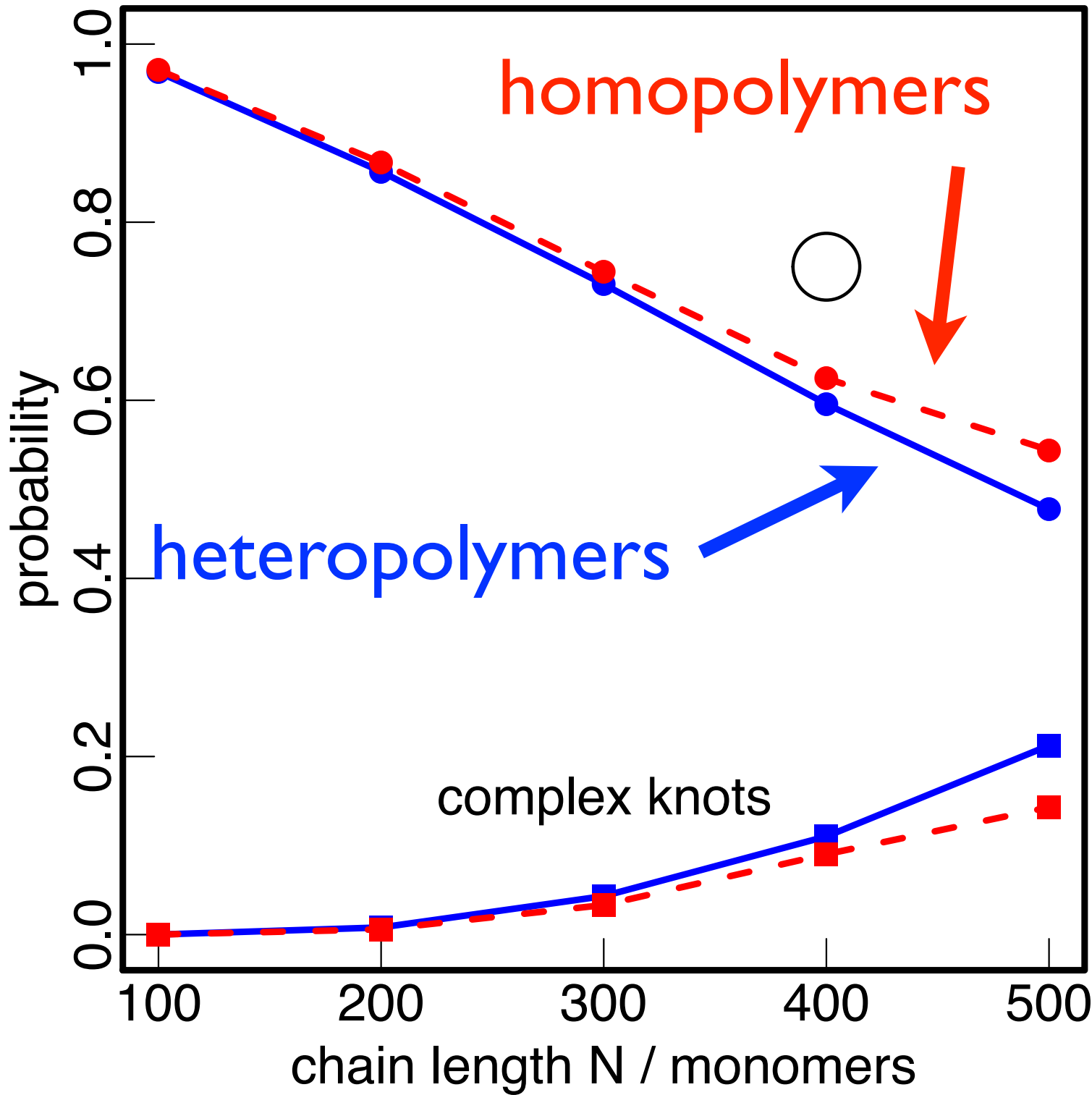


- H-P-P-H-P-H-H-H-P-P-...
- 50% H - 50 % P - like in real proteins

## Results

- knotting depends on exact sequence

# Heteropolymer - results



Knottedness in homo- and heteropolymers: similar

# Take home messages

3 types of bridging moves: **internal II most efficient**

## Applications:

- semiflexible homopolymers in spherical confinement: **rigidity ↑ knots ↑**
- random heteropolymers: **knotted similar to homopolymers**

Thank you!

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