# Mechanizm translokacji łańcuchów w obiektach biologicznych

## stan bieżący badań, wyniki i nadchodzące zagadnienia


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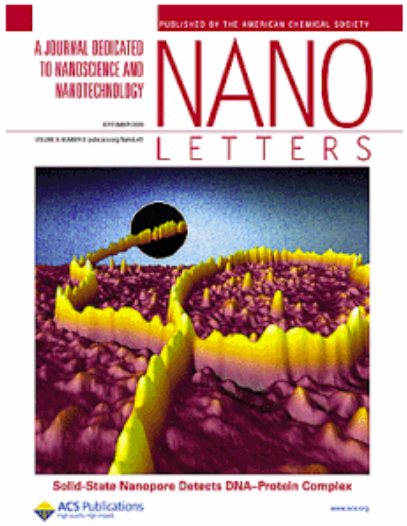
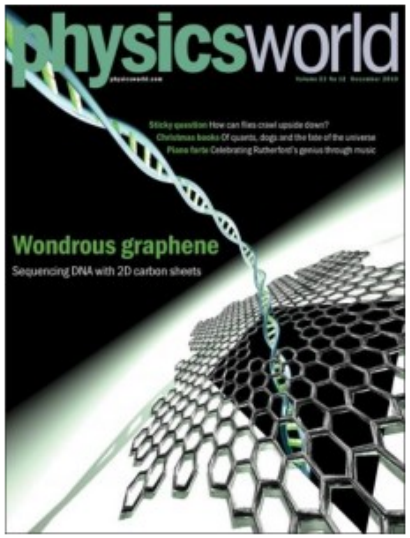
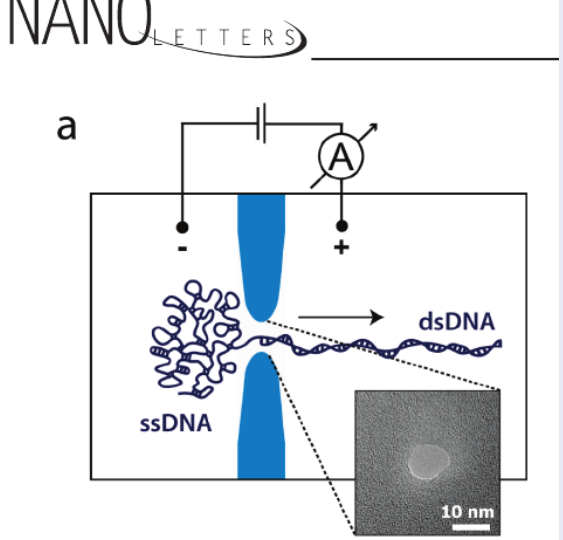
# Jaki jest mechanizm sterujący transportem protein?

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REVIEW

## Protein Translocation Across Biological Membranes

**William Wickner[1*] and Randy Schekman[2*]**

Subcellular compartments have unique protein compositions, yet protein synthesis only occurs in the cytosol and in mitochondria and chloroplasts. How do proteins get where they need to go? The first steps are targeting to an organelle and efficient translocation across its limiting membrane. Given that most transport systems are exquisitely

# Nasze badania i ważne (o)publikowane wyniki

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An IOP and SISSA journal

## Translocation of reptating chains

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**Abstract.** Voltage-driven translocation is modeled with the Rubinstein–Duke rules for hopping reptons in one- and two-dimensional lattices. The chain is driven through the pore by a bias potential promoting the transition of stored length in one direction. Coupling states give a semi-periodicity of the process that enables us to relate the properties to the stationary state of the master equation. The exact solution for short chains and Monte Carlo simulations for longer chains are used to calculate displacements, velocities and the translocation time.

**Keywords:** classical Monte Carlo simulations, other numerical approaches, polymer dynamics, stochastic processes (theory)

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## Translocation of polymers in a lattice model

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**Abstract**

Voltage-driven polymer translocation is studied by means of a stochastic lattice model. The model incorporates the voltage drop over the membrane as a bias in the hopping rate through the pore and exhibits the two main ingredients of the translocation process: the driven motion through the pore and the diffusive supply of chain length towards the pore on the cis-side and the drift away from the pore on the trans-side. The translocation time is either bias limited or diffusion limited. In the bias-limited regime the translocation time is inverse proportional to the voltage drop over the membrane. In the diffusion-limited regime the translocation time is independent of the applied voltage, but it is rather sensitive to the motion rules of the model. We find that the whole regime is well described by a single curve determined by the initial slope and the saturation value. The dependence of these parameters on the length of the chain, the motion rules and the repton statistics are established. Repulsion of reptons as well as increase of chain length decrease the throughput of the polymer through the pore. As for free polymers, inclusion of a mechanism for hernia creations/annihilations leads to cross-over from reptation to Rouse dynamics. For the Rouse chain that is experimentally the more relevant case the power-law dependence of the translocation time on the chain length is found.

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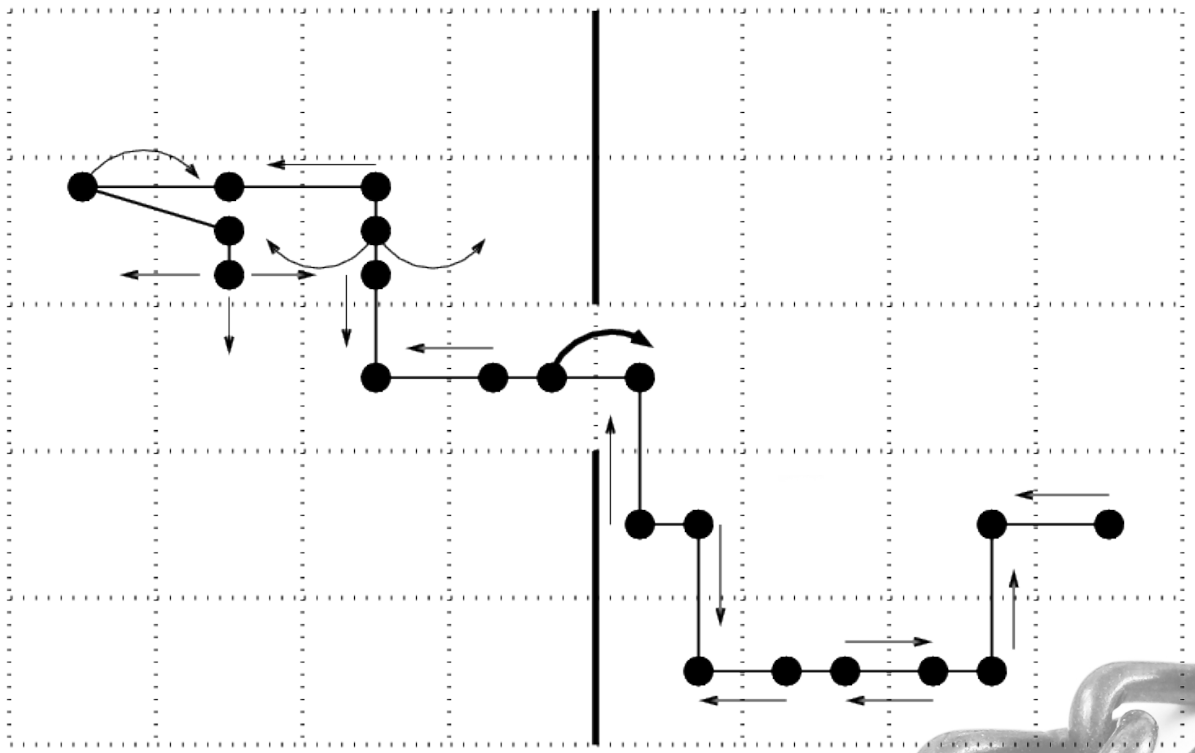
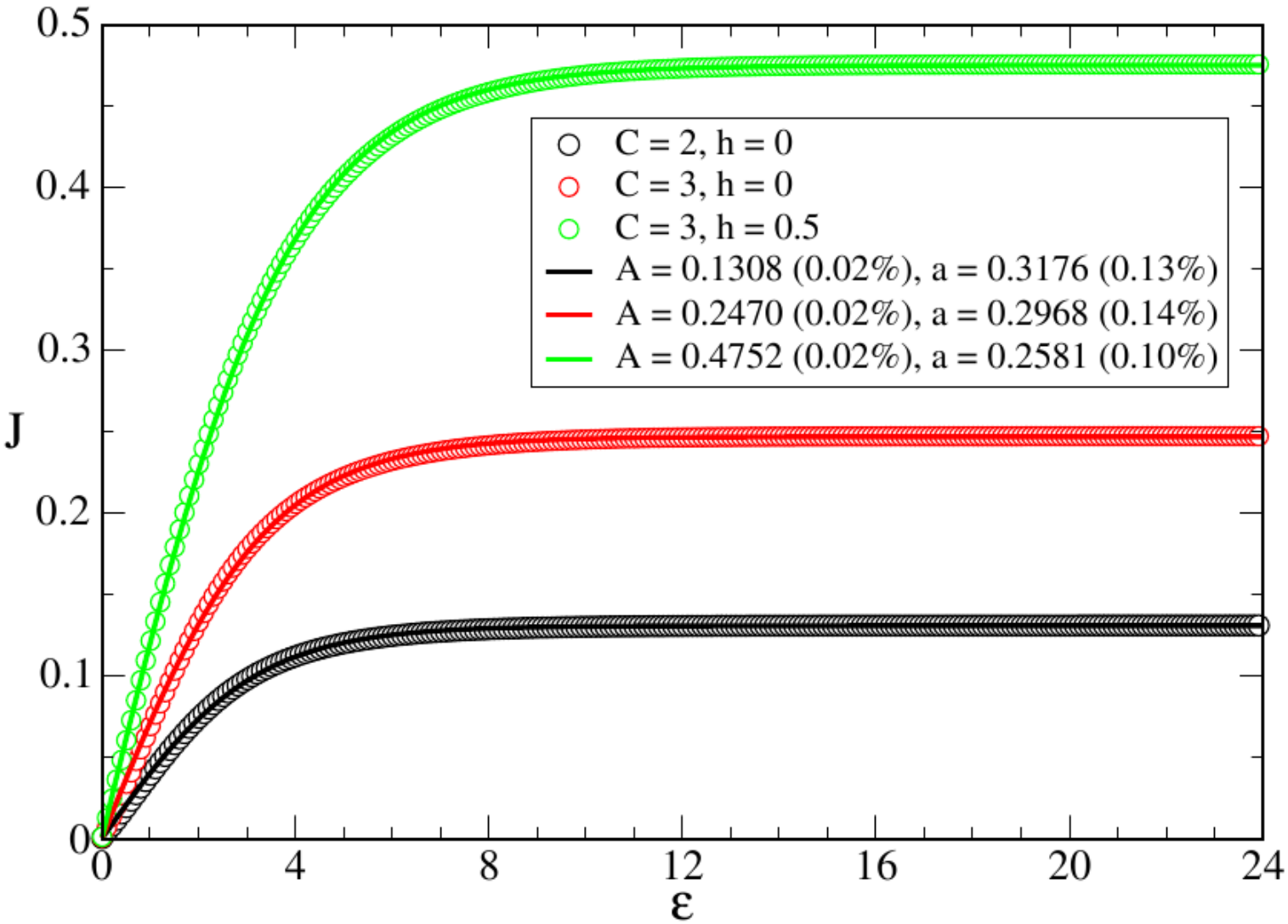
# Model transportu przez błonę

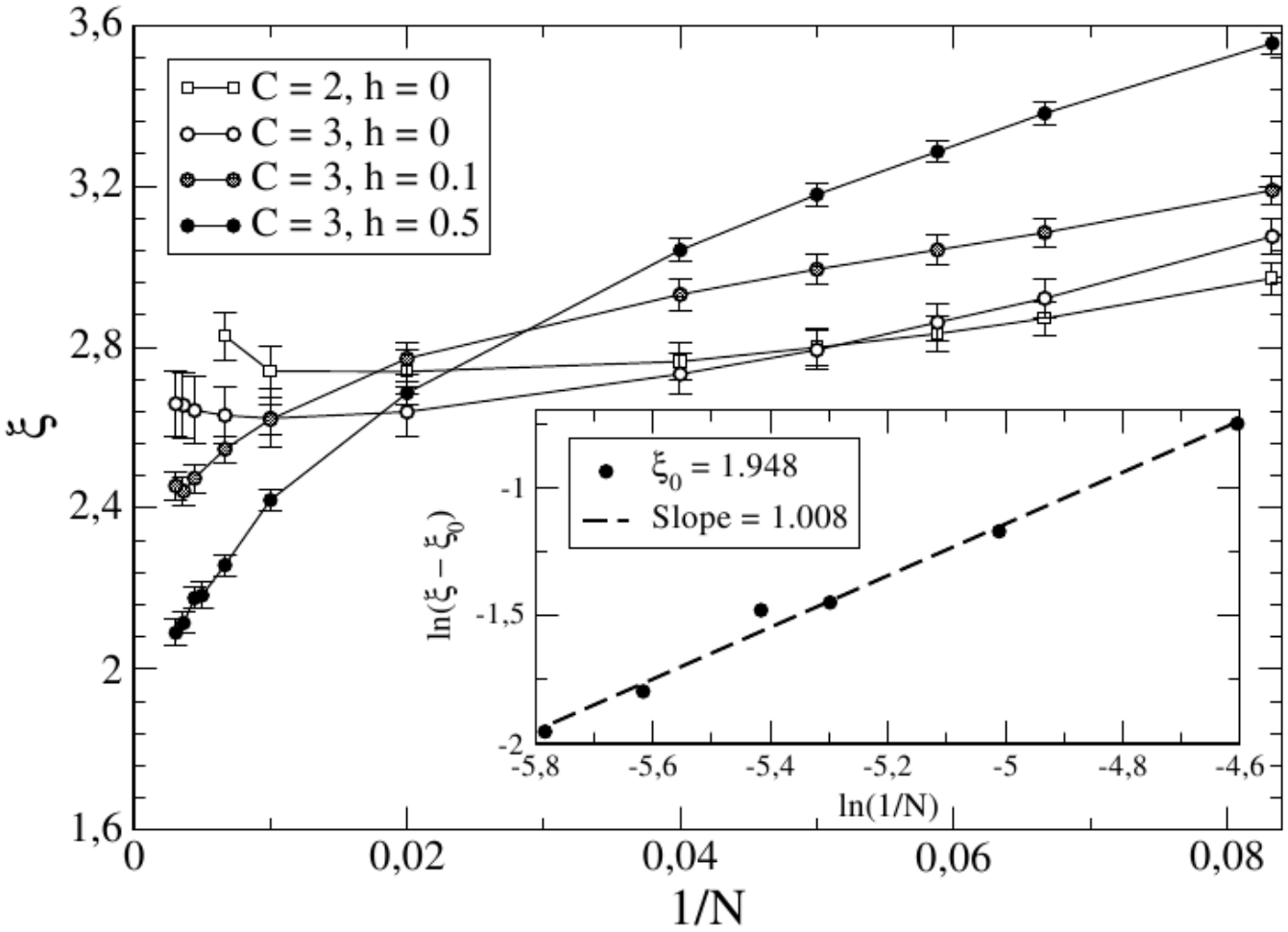


- N + 1 reptonów w położeniach: $(x_0, y_0), (x_1, y_1), ...(x_N, y_N)$
- Odległość pomiędzy reptonami zawsze: 0 lub 1
- Kilka nieskomplikowanych reguł ruchu

# $J(\epsilon) = A \cdot tanh(a \cdot \epsilon)$ fit

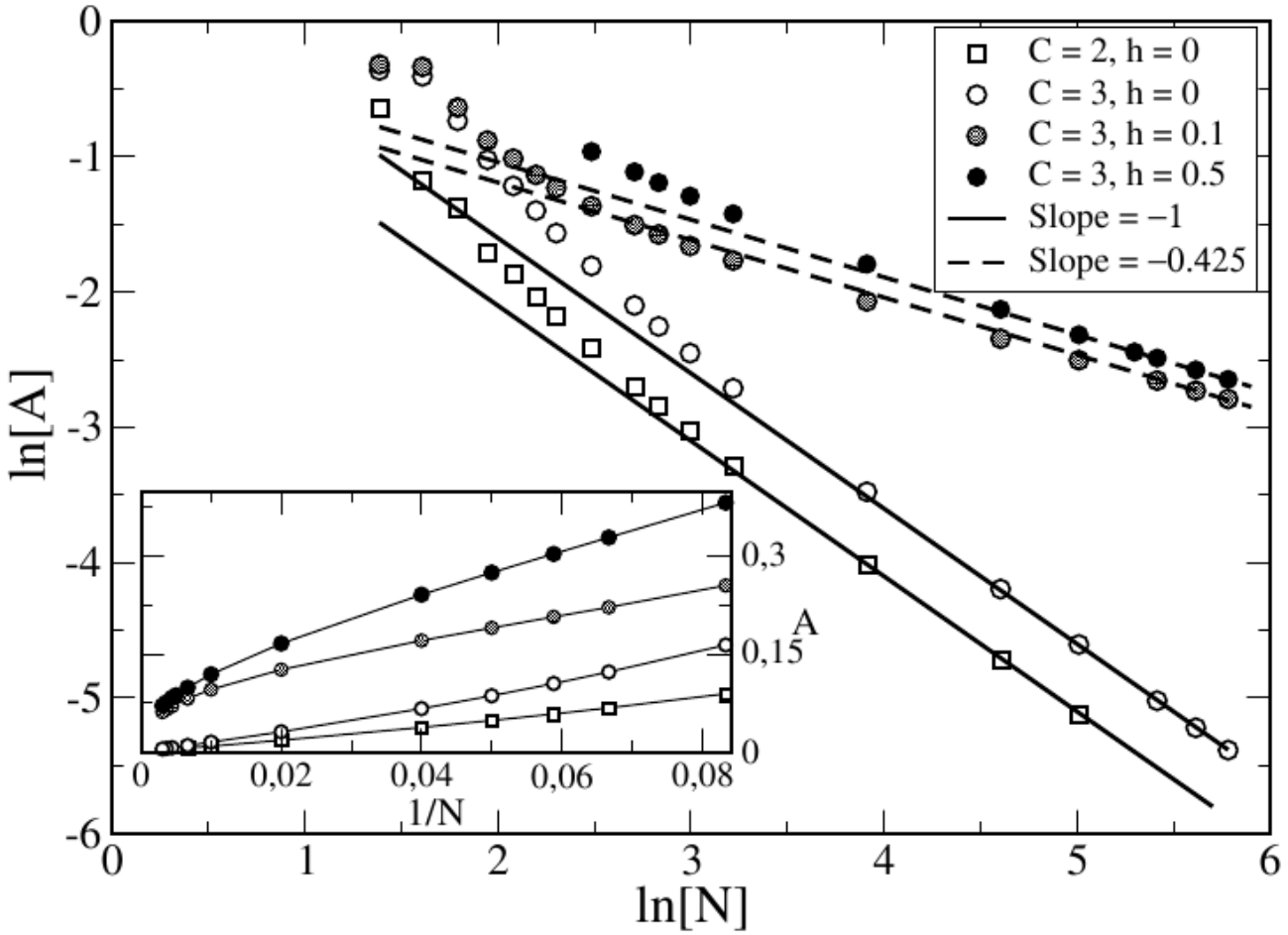


# Obszar ruchu sterowanego (zasilanego)




320 miliardów indywidualnych rekonfiguracji MC

# Transport ograniczany dyfuzyją




Jeden punkt: 10 zadań, każde to zazwyczaj 40 procesów MPI

# Czas translokacji dla obszaru ruchu zasilanego

$$A(h) = A_0(h)N^{-(\alpha-1)} + \ldots,$$

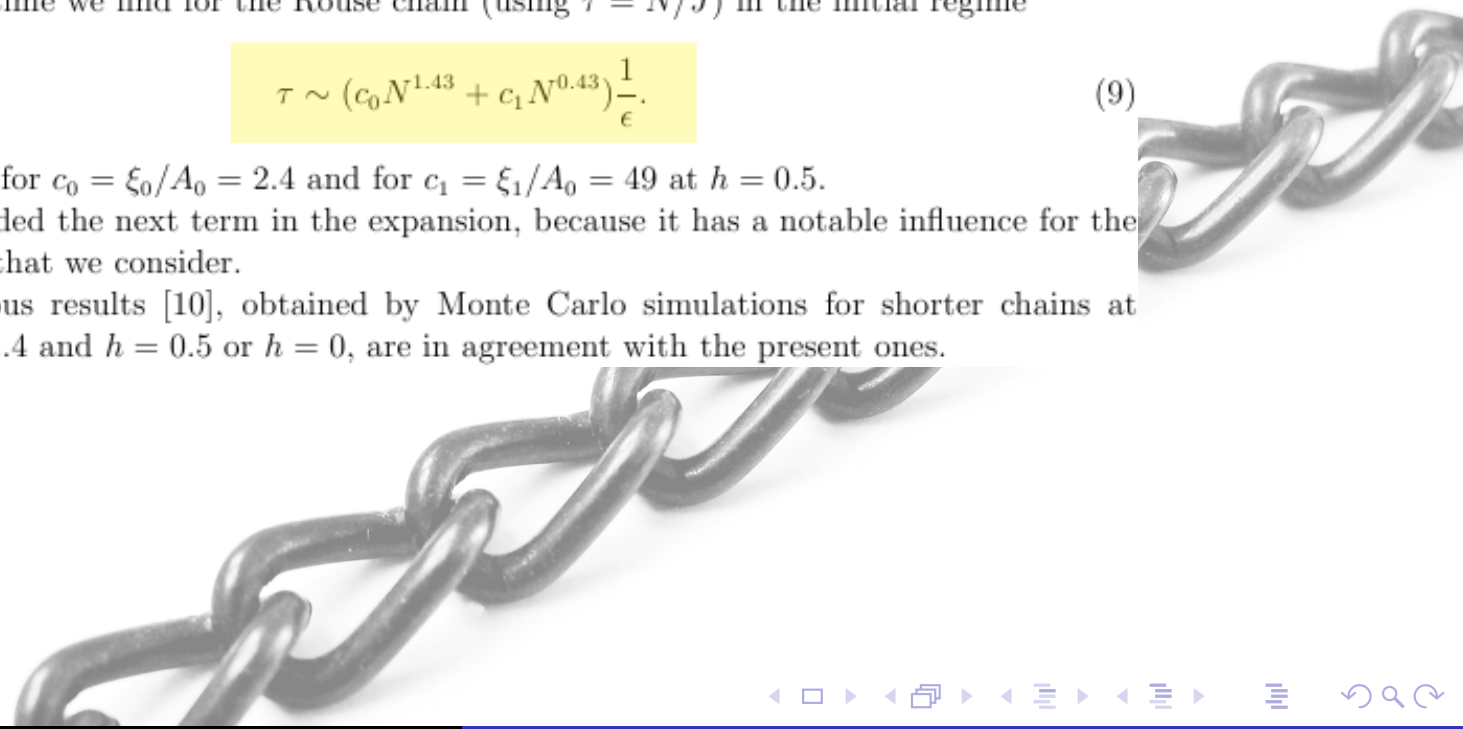
$$\xi(h) = \xi_0(h) + \xi_1(h)N^{-x} + \ldots$$

As argued, the Rouse chain is experimentally the more relevant case. Translated to the translocation time we find for the Rouse chain (using $\tau = N/J$) in the initial regime

$$\tau \sim (c_0 N^{1.43} + c_1 N^{0.43})\frac{1}{\epsilon}. \tag{9}$$

where we find for $c_0 = \xi_0/A_0 = 2.4$ and for $c_1 = \xi_1/A_0 = 49$ at $h = 0.5$.
We have included the next term in the expansion, because it has a notable influence for the chain lengths that we consider.

Our previous results [10], obtained by Monte Carlo simulations for shorter chains at $\epsilon = 2\ln(2) \sim 1.4$ and $h = 0.5$ or $h = 0$, are in agreement with the present ones.




Dziękuję!