

Molecular search in gene regulation

— Houston, 5th December 2019 —



Main protagonist: bacteria cells such as E.coli

Cell size: roughly $2\mu\text{m} \times 1/2\mu\text{m}$

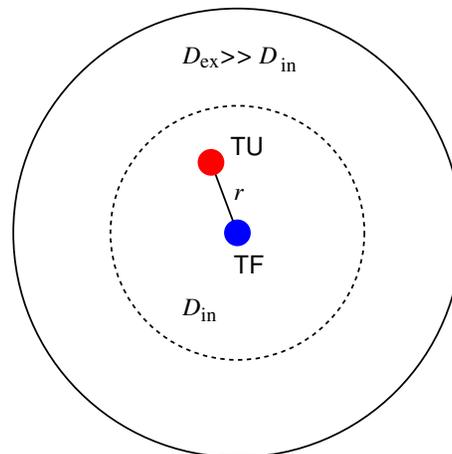
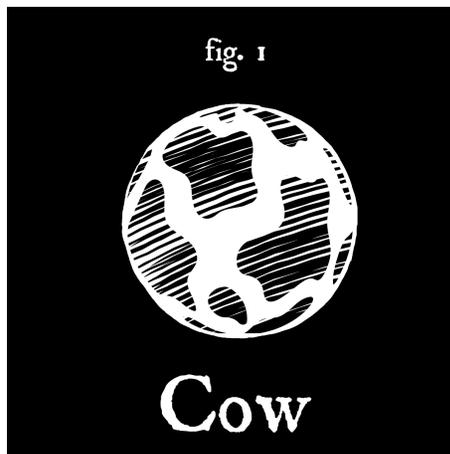
Cell volume: $\approx 1\mu\text{m}^3$

DNA length: 4.7×10^6 base pairs or $\approx 1.6\text{mm}$

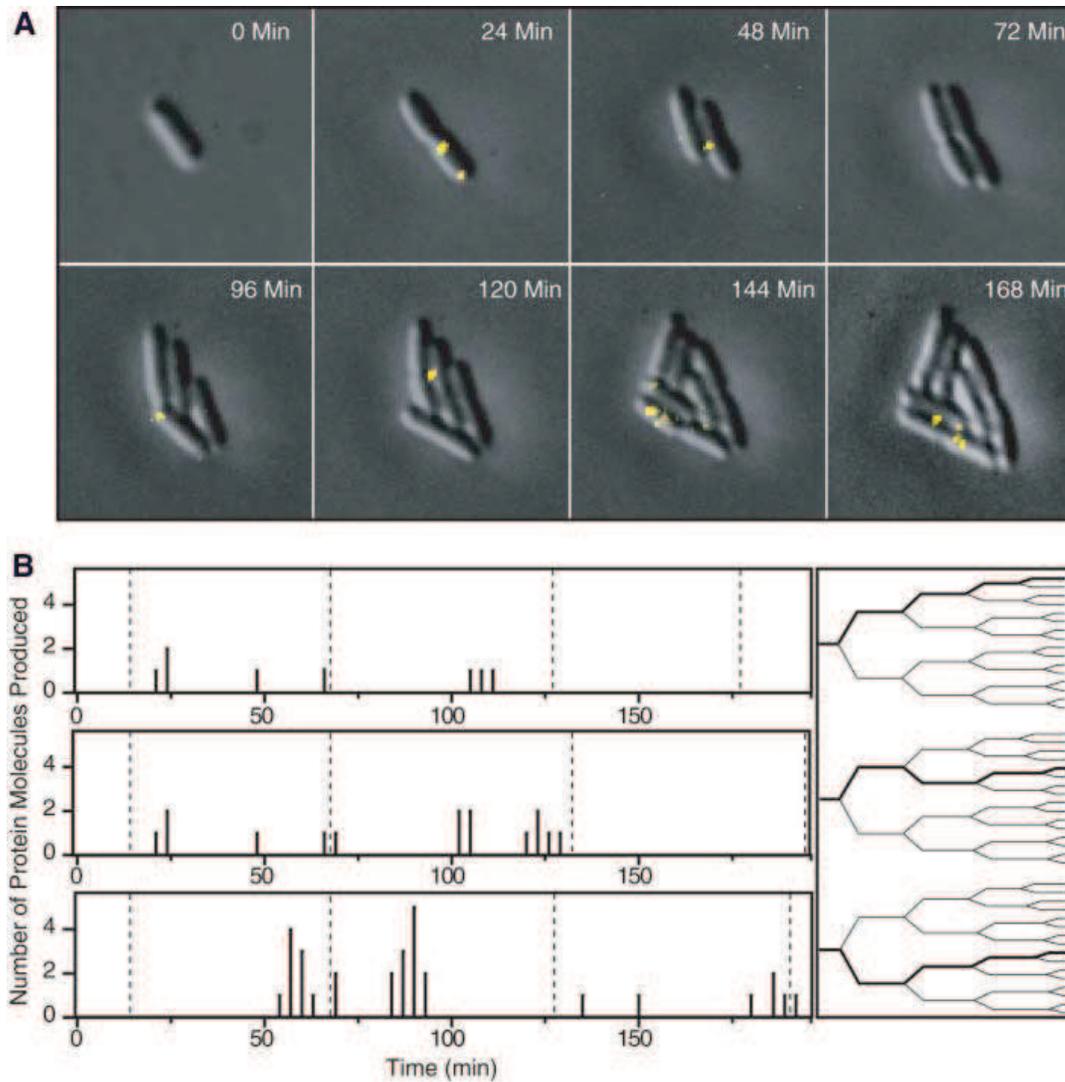
Number of proteins in cell: $\approx 2.4 \times 10^6$

Different proteins (# genes): 4,300

Some proteins occur only as few or few tens of copies/cell (nM concentrations)



Gene expression one molecule at a time



synthesised proteins (bursty) along three cell lineages, dashed lines marking cell divisions

Yu et al, Science (2006); I Golding et al, Cell (2005)

Smoluchowski search picture

Search rate for a particle with diffusivity D_{3d} to find an immobile target of radius a (assuming immediate binding):

$$k_{\text{on}}^S = 4\pi D_{3d} a$$

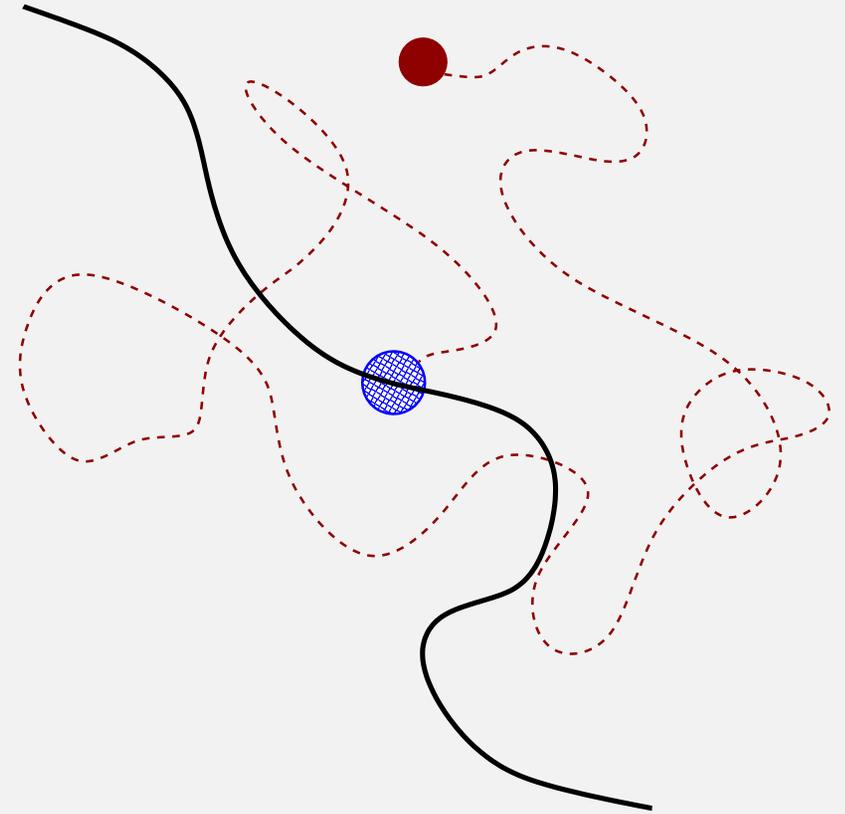
Protein-DNA interaction: $a \approx \{\text{few bp}\} \approx 1\text{nm}$
 $D_{3d} \approx 10\mu\text{m}^2/\text{sec}$ (typically $\varnothing_{\text{TF}} \approx 5\text{nm}$):

$$k_{\text{on}}^S \approx \frac{10^8}{(\text{mol/l}) \times \text{sec}}$$

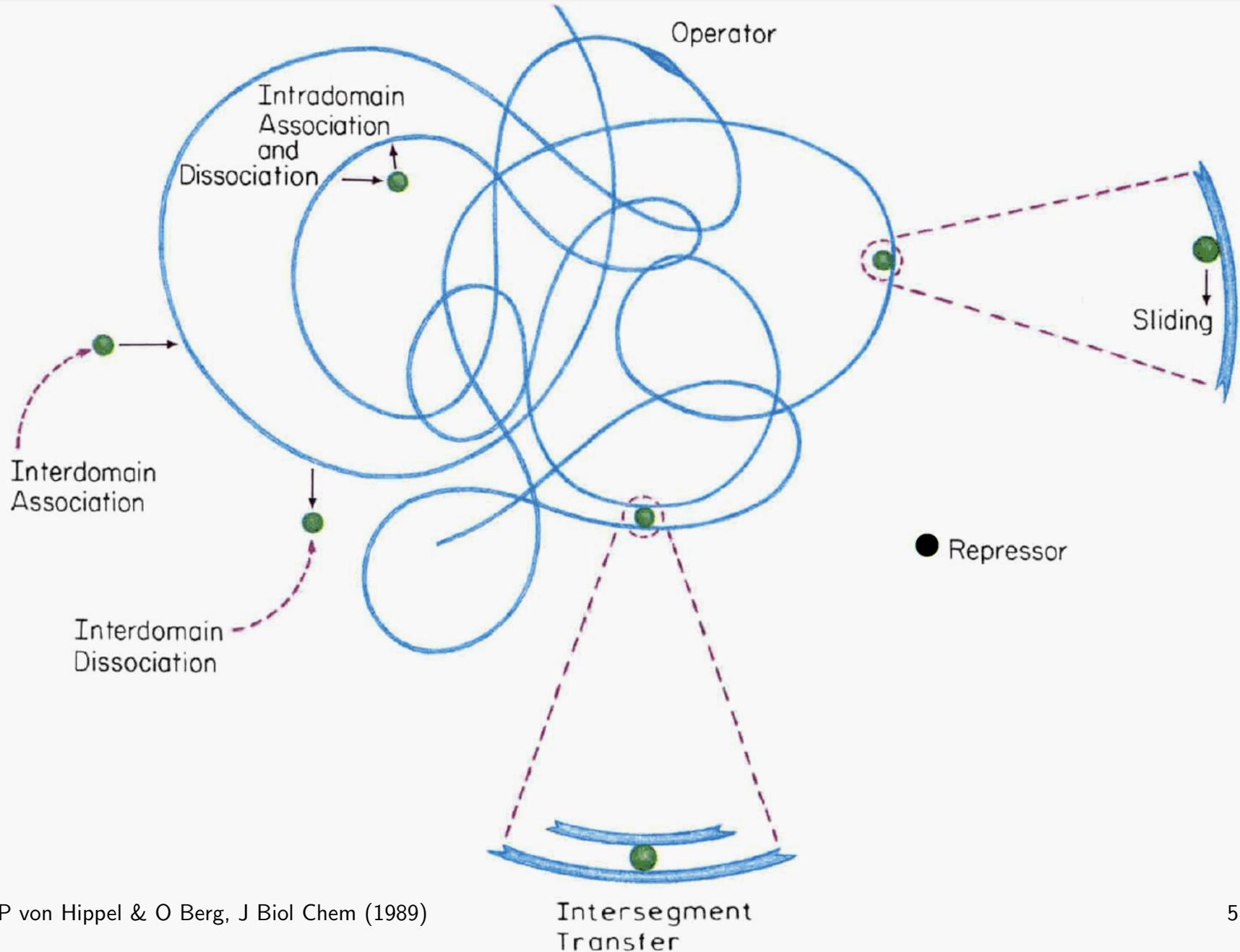
Lac repressor [AD Riggs, S Bourgeois, M Cohn, J Mol Biol 53, 401 (1970)]:

$$k_{\text{on}} \approx \frac{10^{10}}{(\text{mol/l}) \times \text{sec}}$$

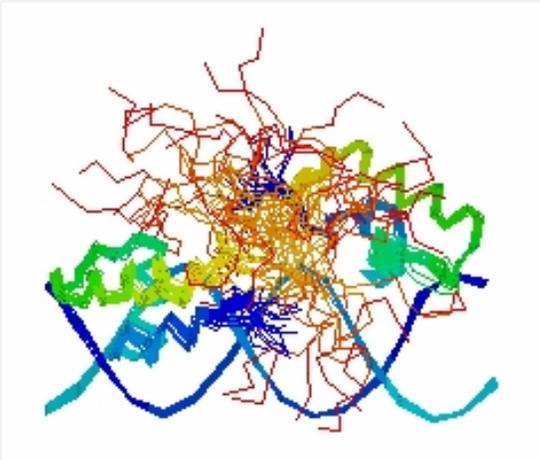
→ Facilitated diffusion picture



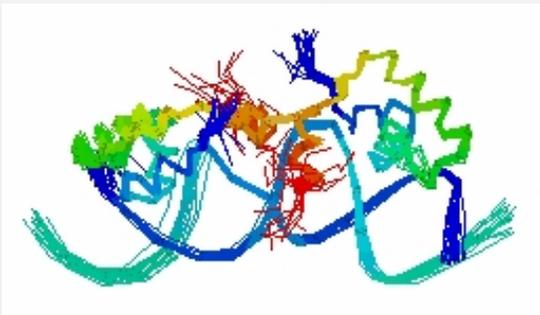
Facilitated diffusion: the Berg-von Hippel model



Non-specific binding energy based on *in vivo* data



Lac repressor, nonspecific binding

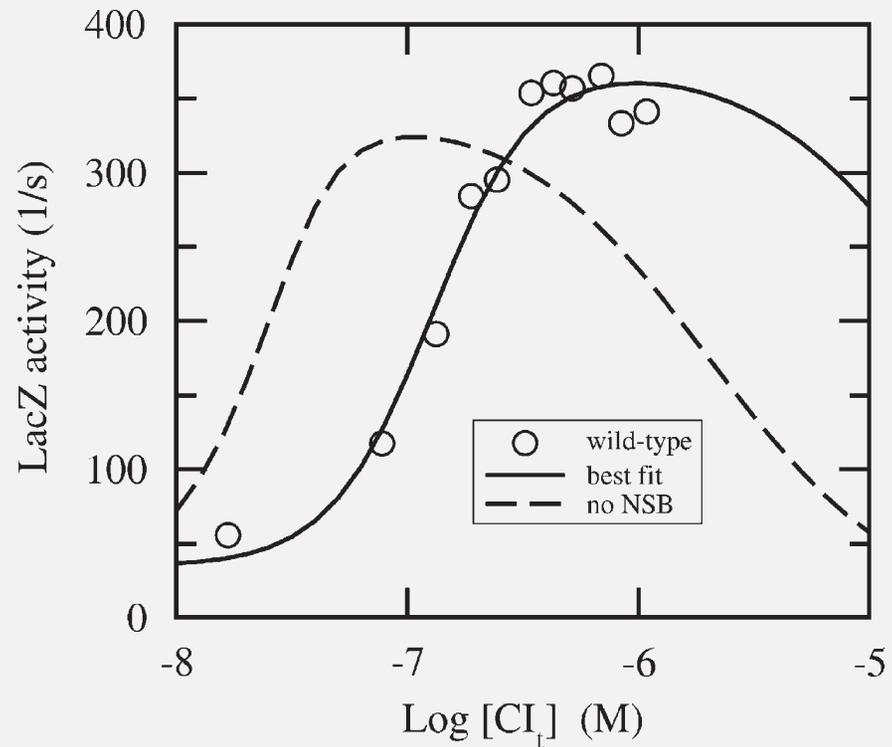


Lac repressor, specific binding

$$[X] = [X_{\text{free}}] + [X_{\text{@O}_P}] + [X_{\text{NSB}}]$$

$$\Delta G_{\text{NSB}}(\text{CI}) = -4.1 \pm 0.9 \text{ kcal/mol,}$$

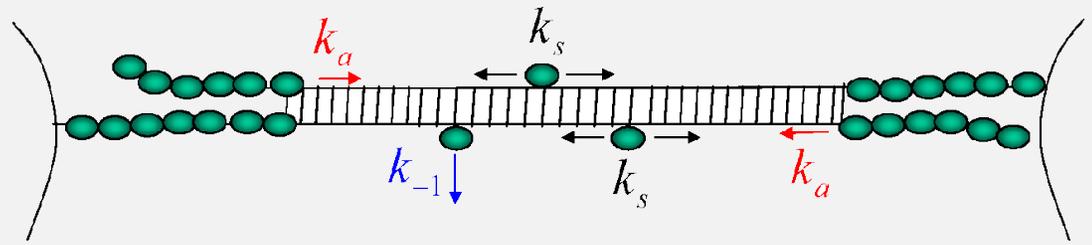
$$\Delta G_{\text{NSB}}(\text{Cro}) = -4.2 \pm 0.8 \text{ kcal/mol}$$



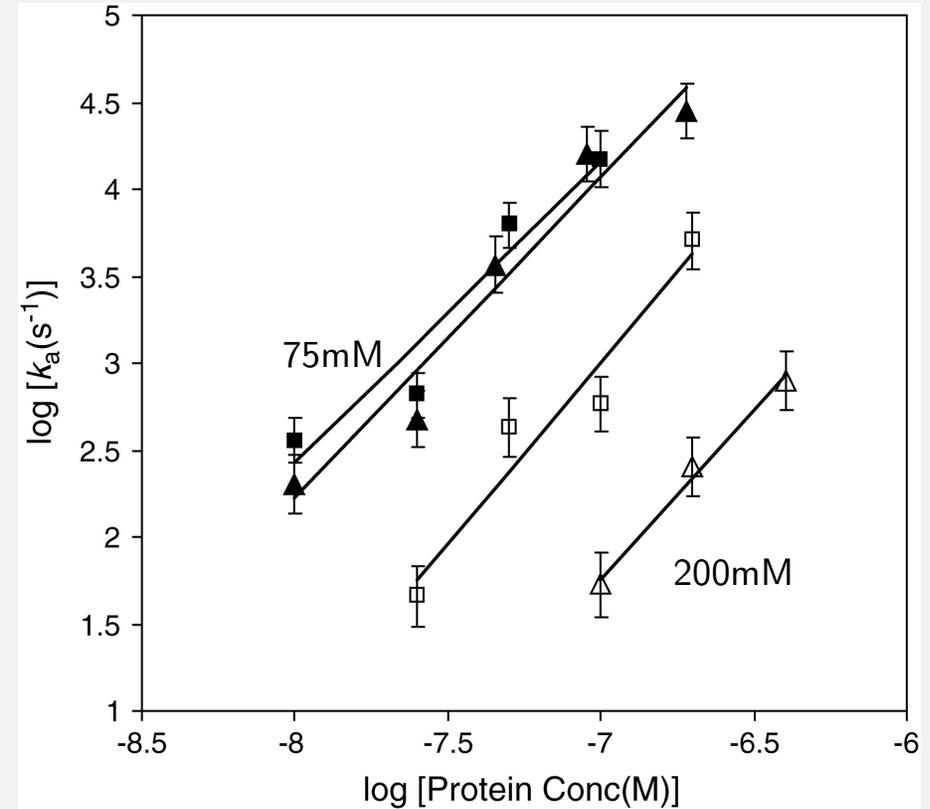
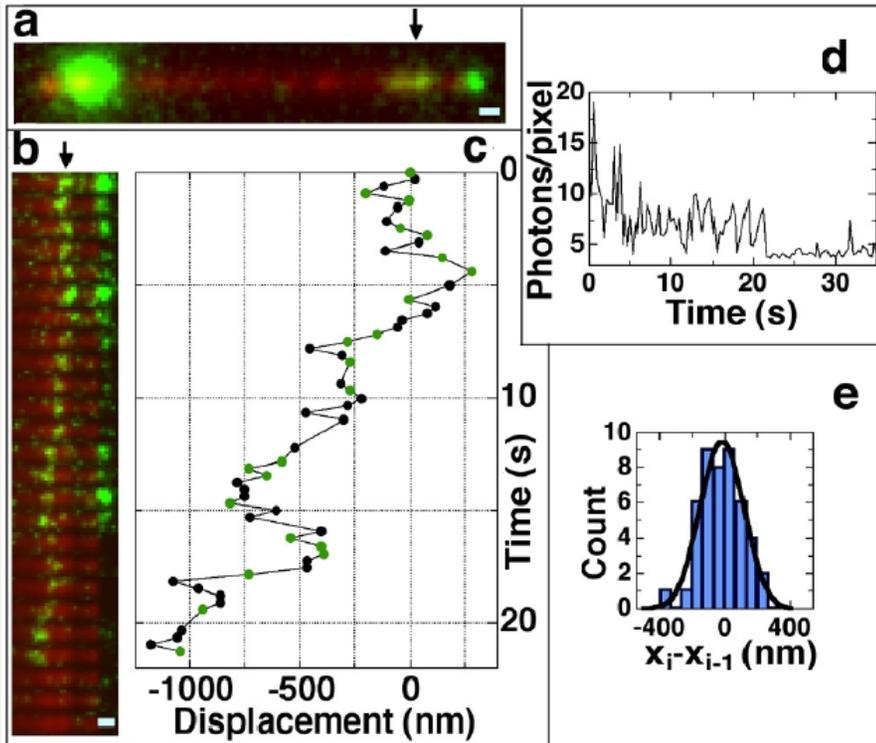
Proof of 1D search mode

McGhee & von Hippel isotherm

$$f = \frac{N\lambda}{L} \simeq K_{ns}\lambda C, \quad f \ll 1$$



$$k_a \simeq \begin{cases} C, & \text{1D/3D Berg \& von Hippel} \\ C^2, & \text{Pure 1D search} \end{cases}$$



$$\Delta = 1.74 \pm 0.35, 1.85 \pm 0.24, 2.08 \pm 0.39, 1.95 \pm 0.17$$

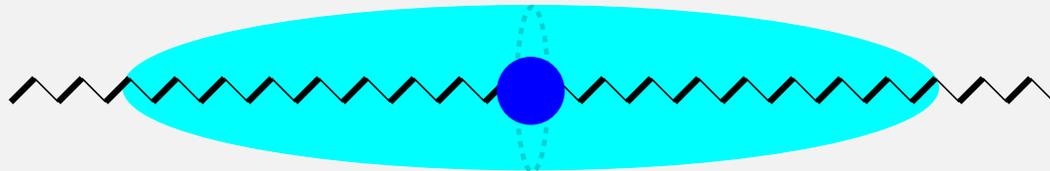
The antenna effect

Target search rate for cylindrical DNA model:

$$k_{\text{on}} \sim 4\pi D_{3d} \ell_{\text{sl}}^{\text{eff}} \times \frac{1}{\sqrt{\ln(\ell_{\text{sl}}^{\text{eff}} / r_{\text{int}})}}$$

Sliding length:

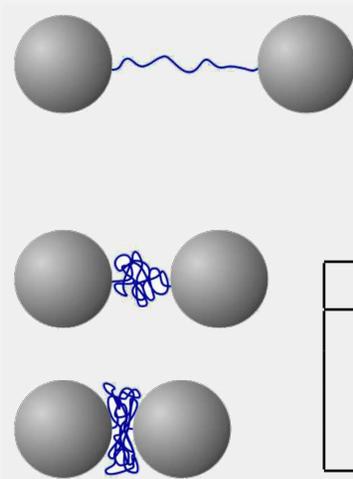
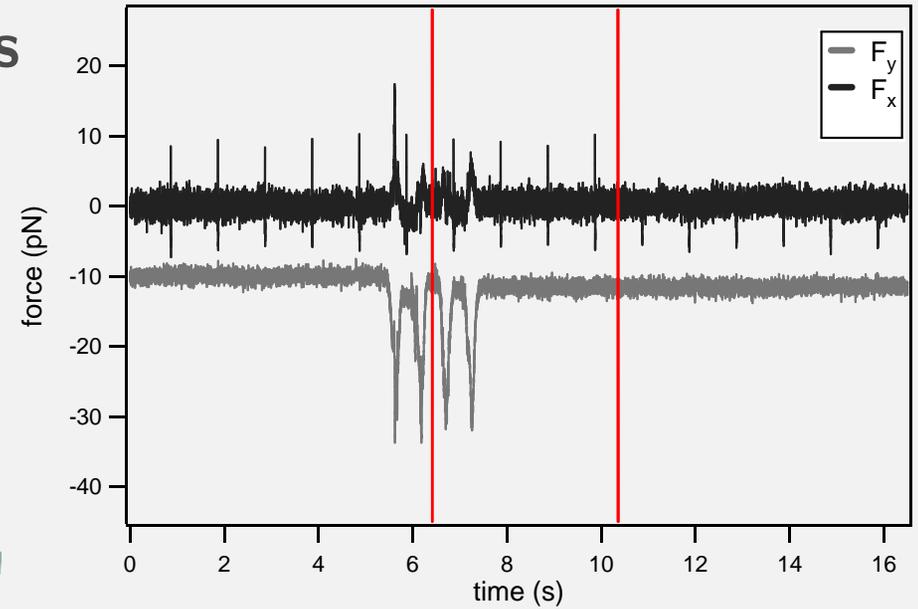
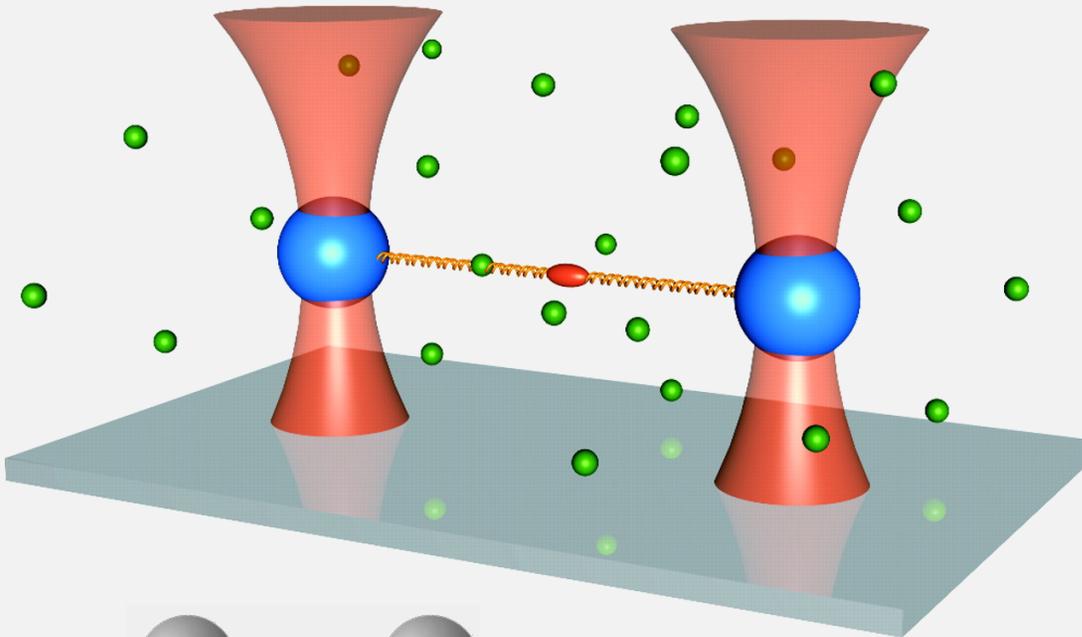
$$\ell_{\text{sl}} = \sqrt{\frac{D_{1d}}{k_{\text{off}}}}$$



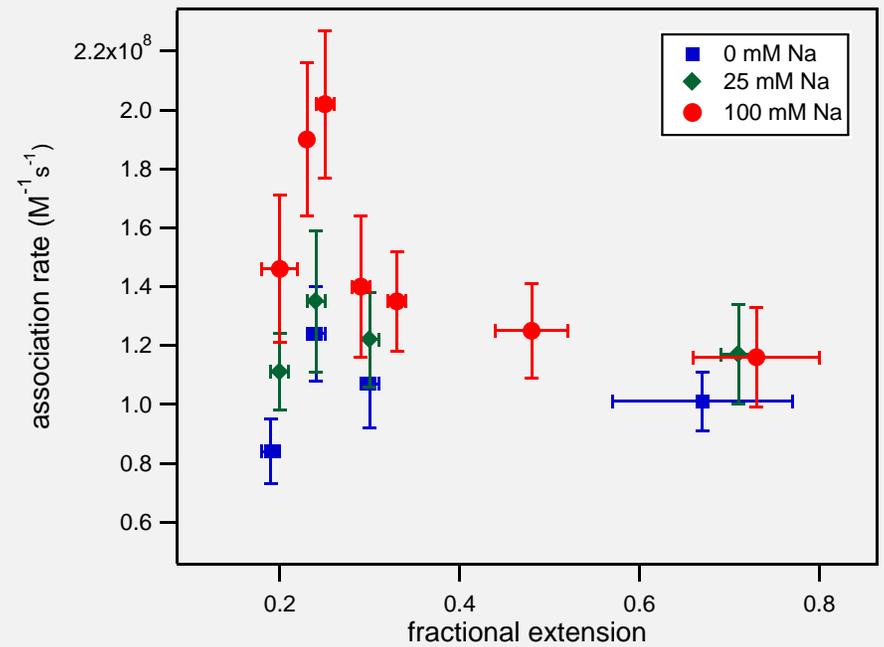
Effective sliding length:

$$\ell_{\text{sl}}^{\text{eff}} = \sqrt{\frac{k_{\text{on}}}{2\pi D_{3d}}} \times \ell_{\text{sl}} \quad \text{microhop correction:} \quad \sqrt{\frac{k_{\text{on}}}{2\pi D_{3d}}}$$

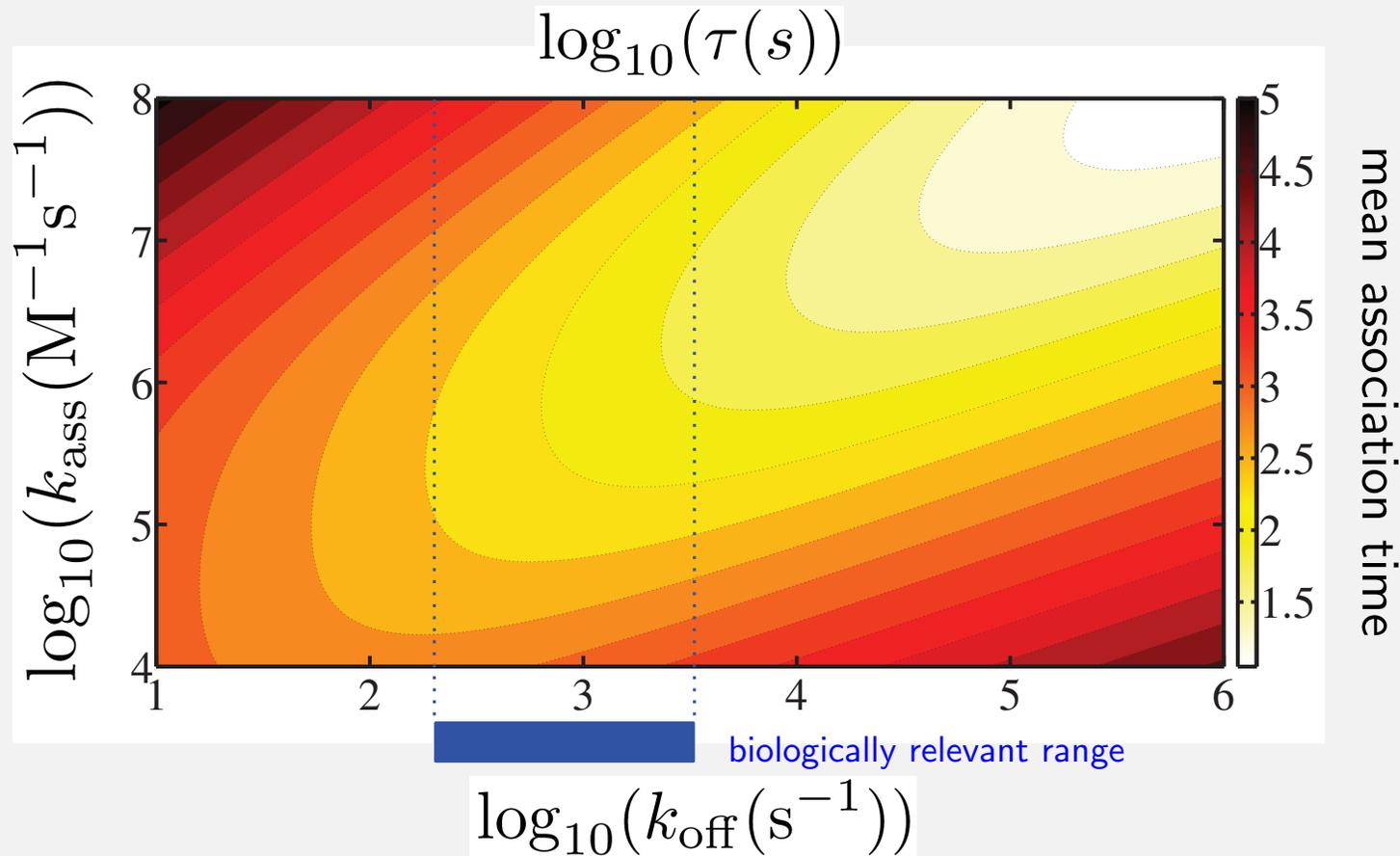
The rôle of DNA conformations



[NaCl]	R_{theory}	R_{measured}
0 mM	1.18	1.3 ± 0.2
25 mM	1.23	1.1 ± 0.2
100 mM	1.67	1.7 ± 0.3
150 mM	1.15	1.3 ± 0.4



In vivo gene regulation consistent with facilitated diffusion



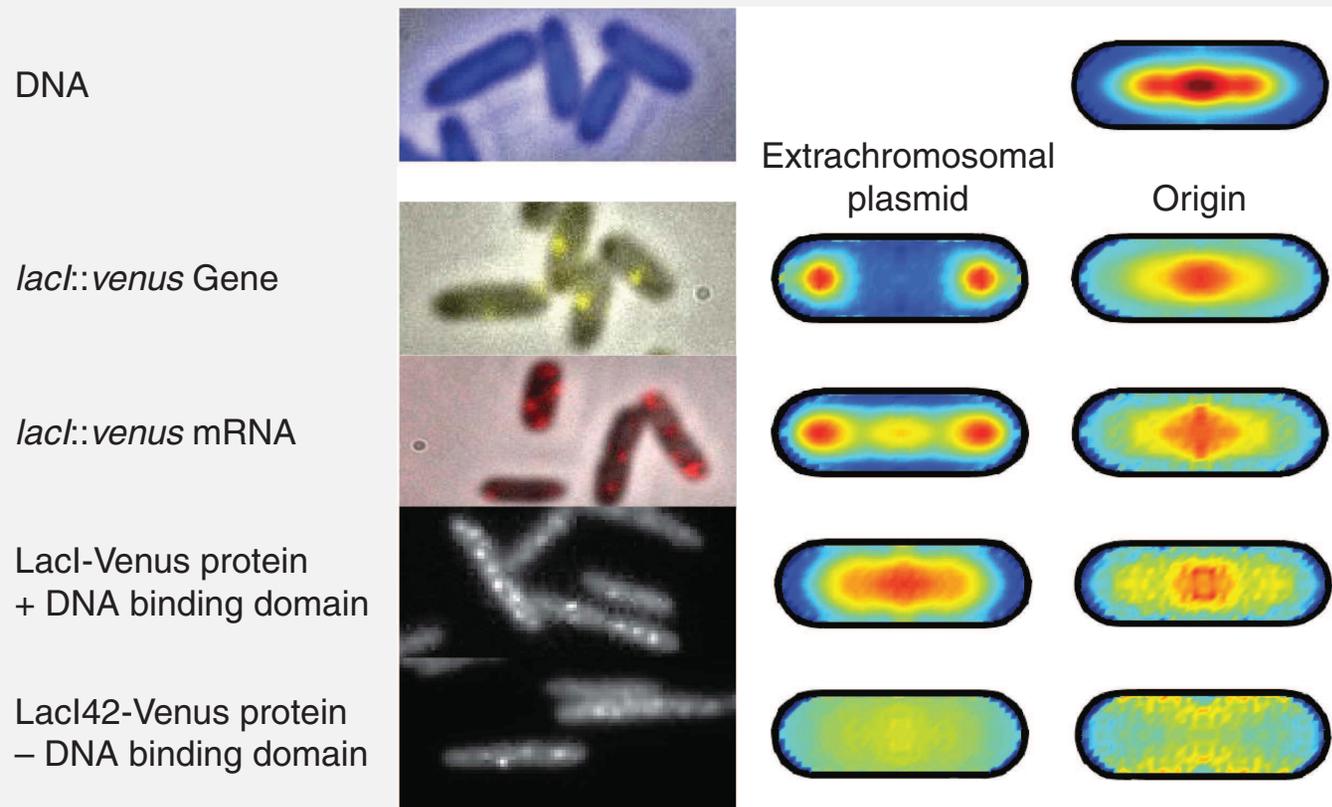
@ optimum the target association time is $\tau \approx 311\text{sec}$ (no fit parameter)

single molecule experiment: $\tau_{\text{exp}} = 354\text{sec}$ [Elf et al, Science (2007)]

Spatial aspects: do gene locations matter?

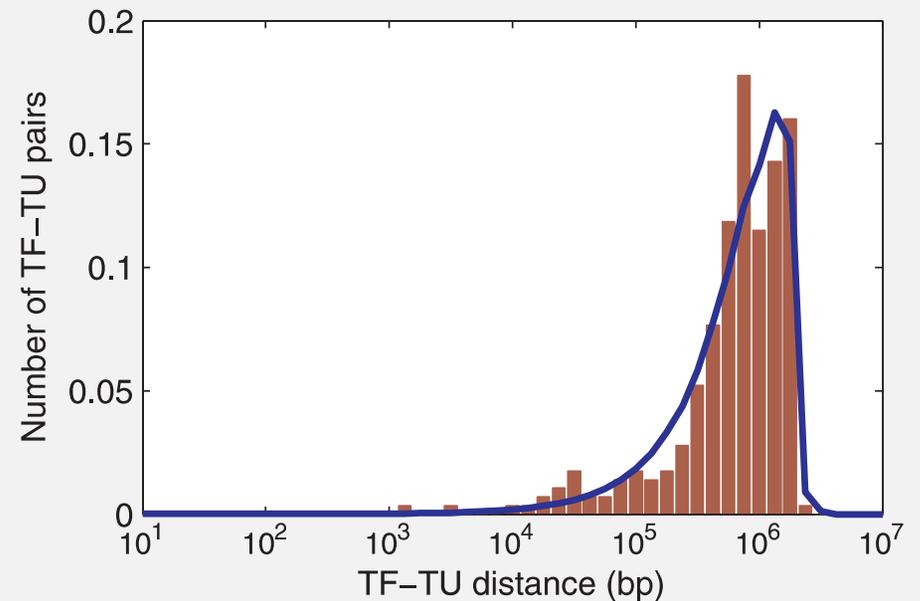
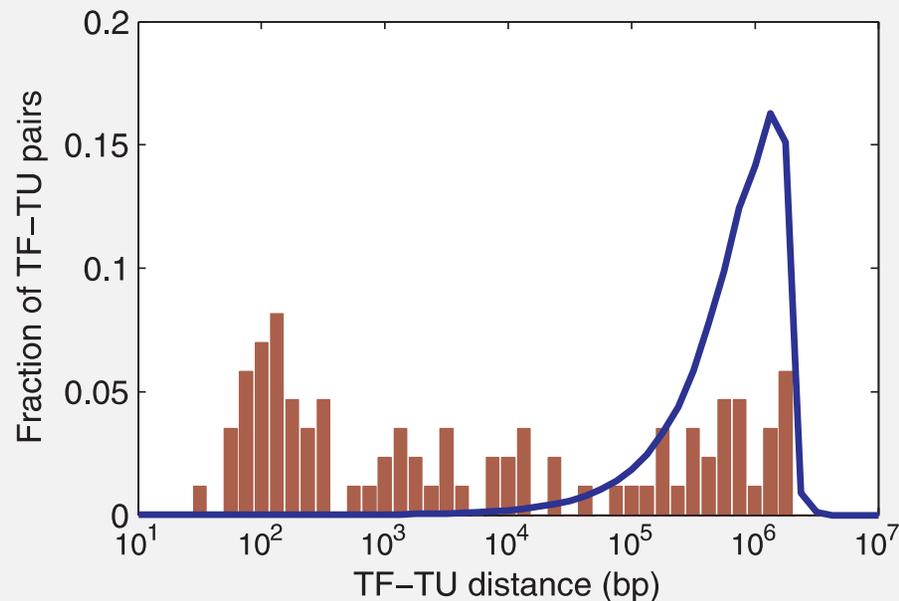
Képes: TF targets are typically located next to or at regular distances from the TF gene
→ TF gene-target pairs close in 3D

Kuhlman & Cox: • TF distribution highly heterogeneous • TF gene influences distribution:
localisation of TF near TF gene

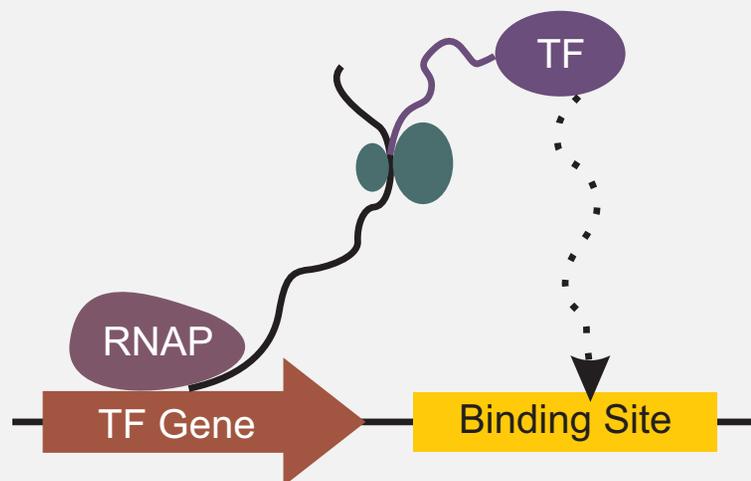


TF-regulation effects gene-proximity: rapid-search-hypothesis

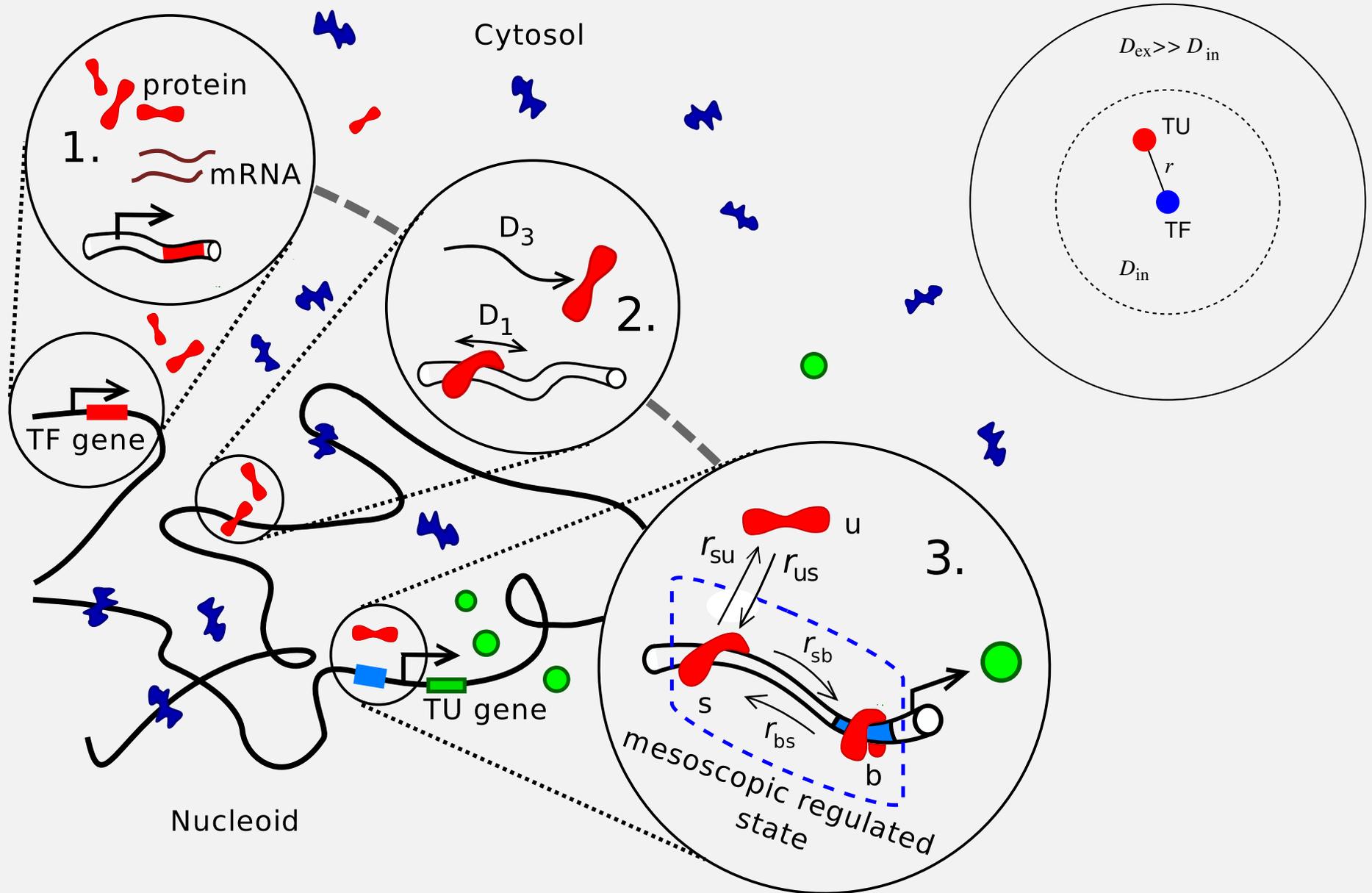
Gene-gene distance distribution for local TFs (regulate < 4 operons, left) and global (regulate ≥ 4 operons, right). Blue line: random location of genes



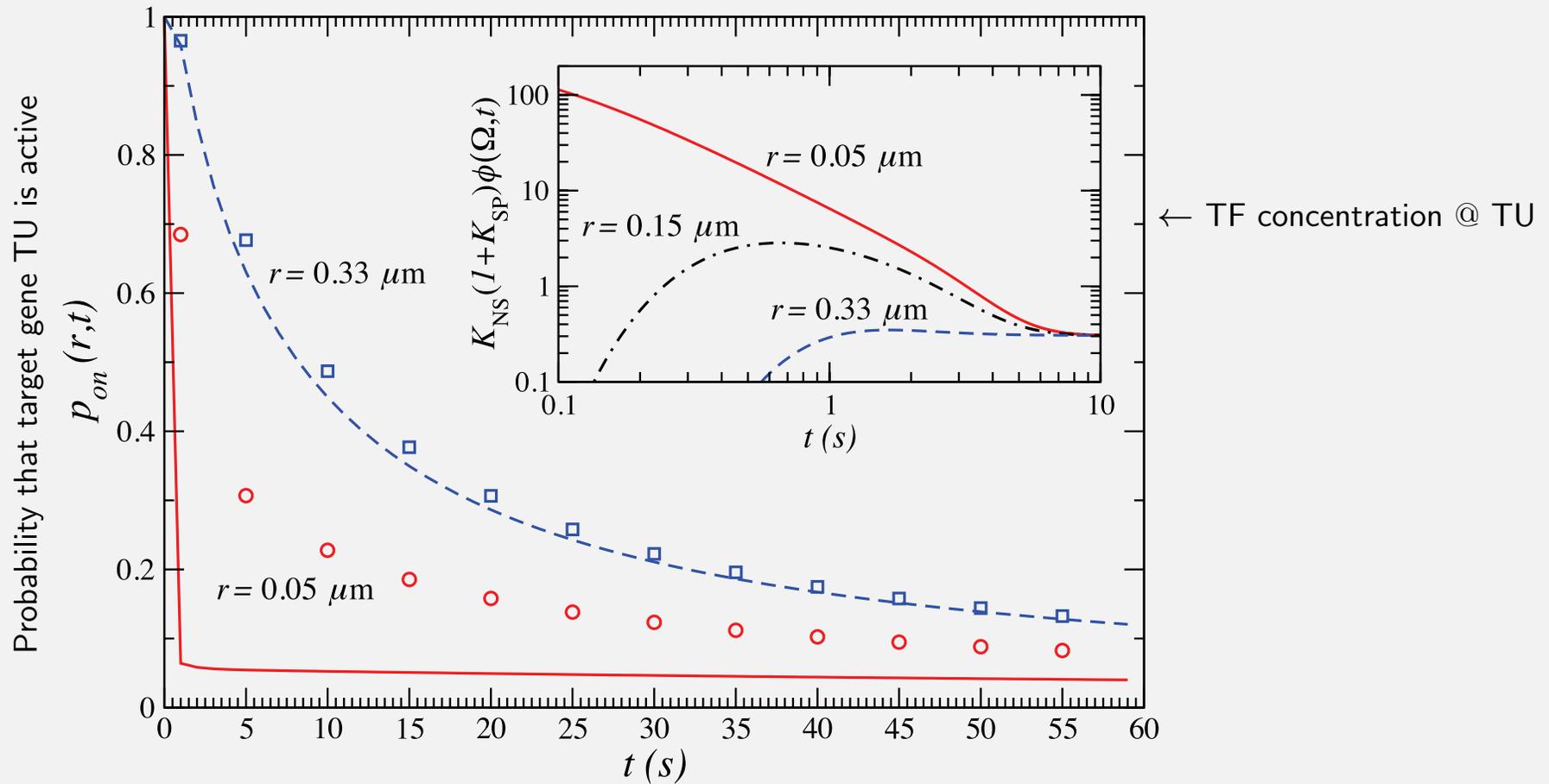
Kolesov et al, PNAS (2007)



Transient intracellular signalling is geometry-controlled



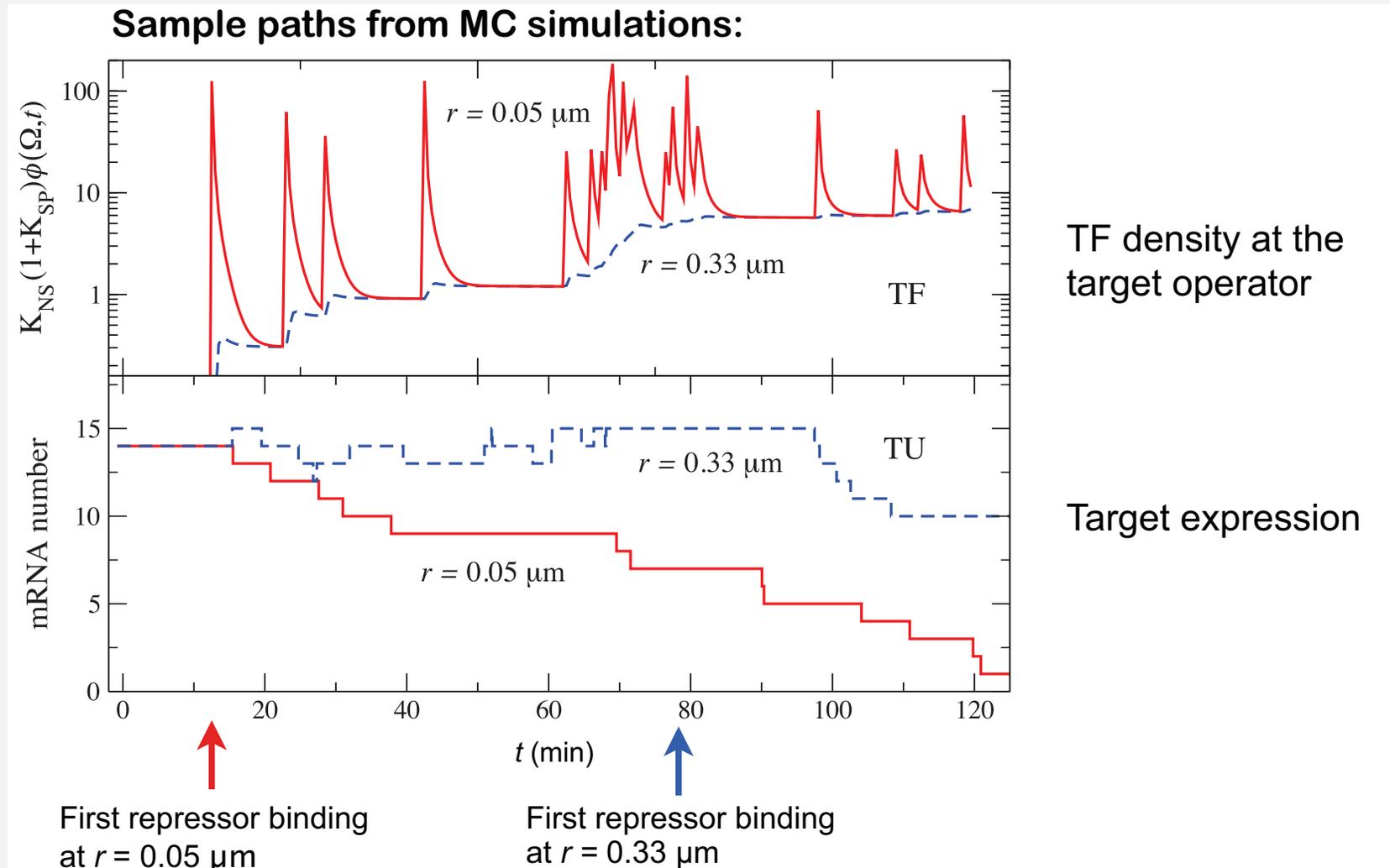
Result 1: transient response to repression



Mean field approximation (full & dashed lines):

$$p_{on}(r, t) = \left\langle \frac{1 + K_{NS}\rho_{TF}(r, t)}{1 + \tilde{K}\rho_{TF}(r, t)} \right\rangle \approx \frac{1 + K_{NS}\langle\rho_{TF}(r, t)\rangle}{1 + \tilde{K}\langle\rho_{TF}(r, t)\rangle}$$

Result 2: time dependence of gene response: bursts!

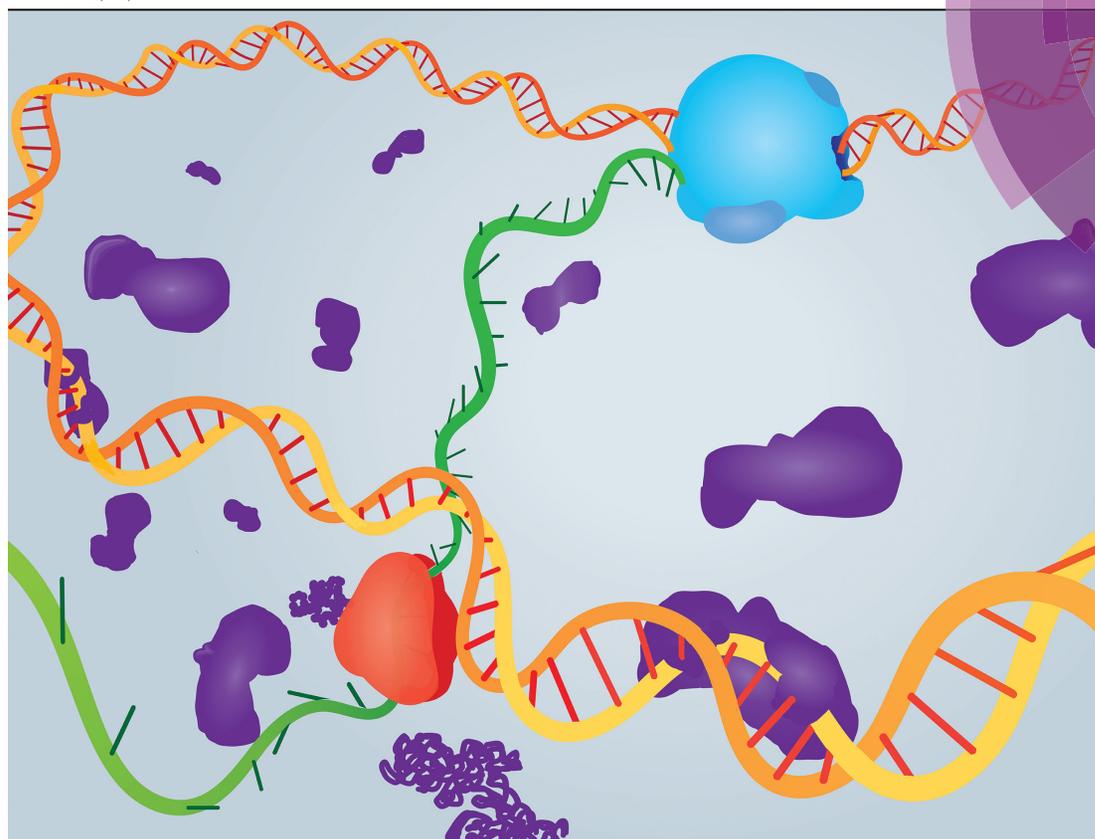


Numerical analysis confirms relevance of proximity effect

Volume 20 | Number 12 | 28 March 2018 | Pages 7899–8360

PCCP

Physical Chemistry Chemical Physics
rsc.li/pccp



ISSN 1463-9076

P Kar, AV Cherstvy & RM, PCCP (2018)

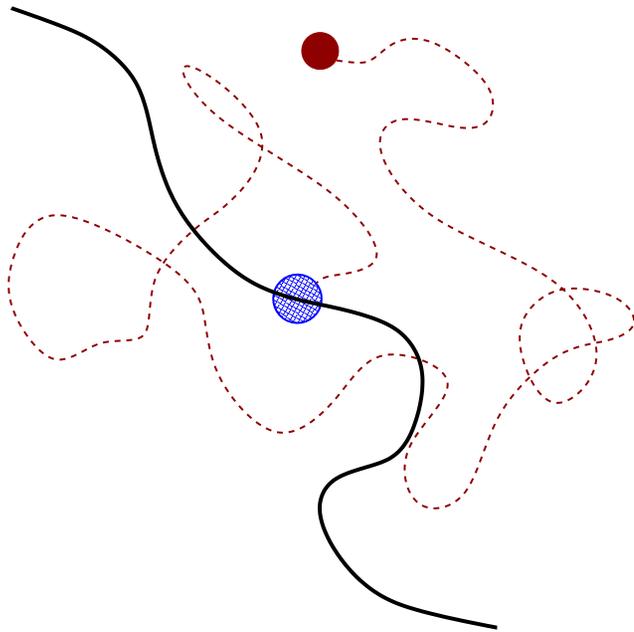


PAPER
Ralf Metzler *et al.*
Acceleration of bursty multiprotein target search kinetics on DNA by colocalisation

Brownian impromptu: from mere means to distributions

Search rate for particle with diffusivity D_{3d} to find an immobile target of radius a (assuming immediate binding):

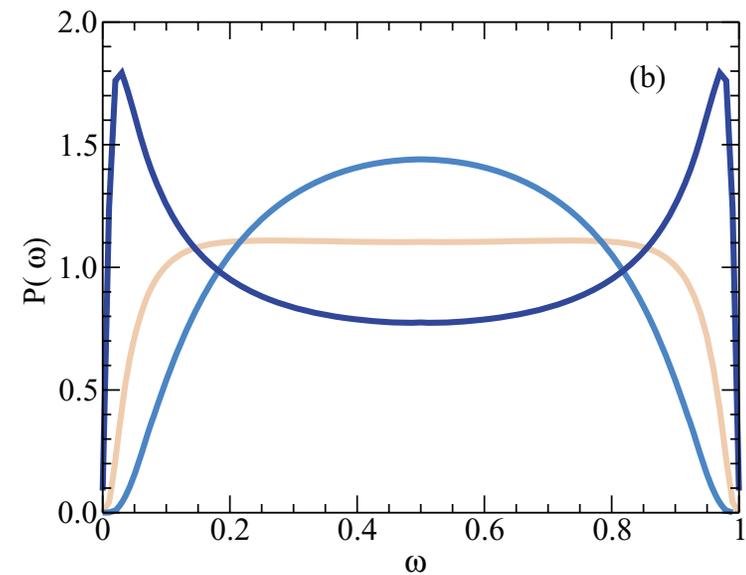
$$k_{\text{on}} = 4\pi D_{3d}a$$



Uniformity index for two independent first-passage times τ_1, τ_2 :

$$\omega = \frac{\tau_1}{\tau_1 + \tau_2}$$

$\curvearrowright \omega = 1/2$ means good reproducibility

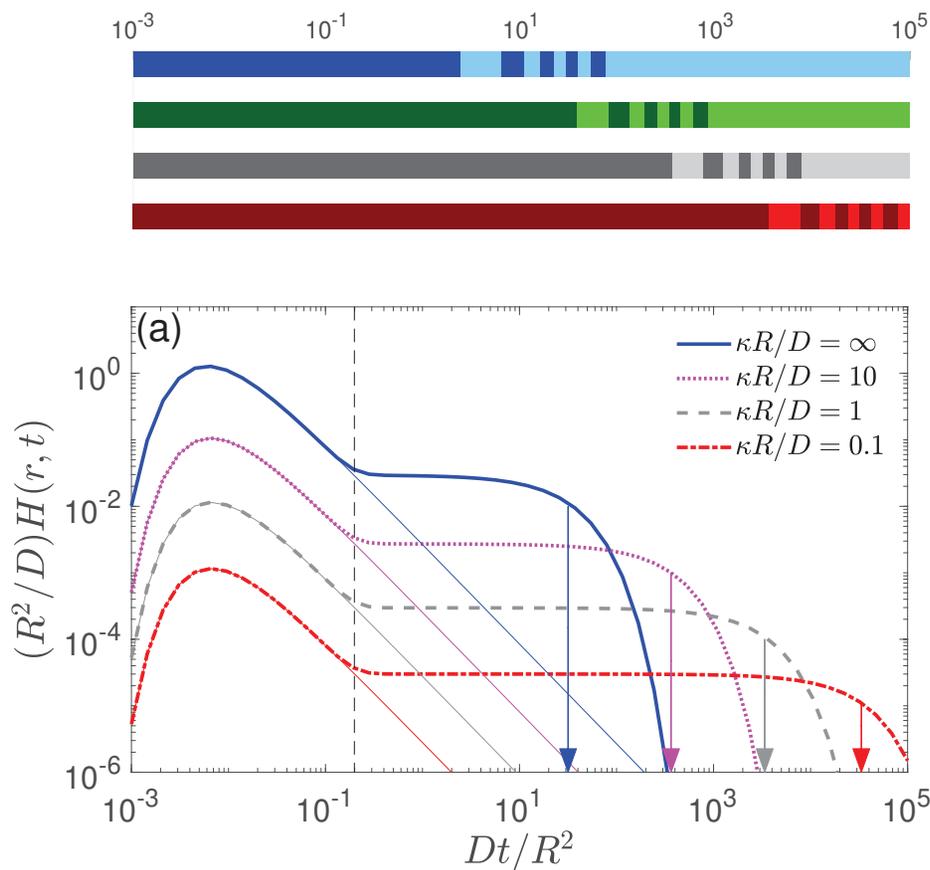


Beyond mere means: first-passage time distributions

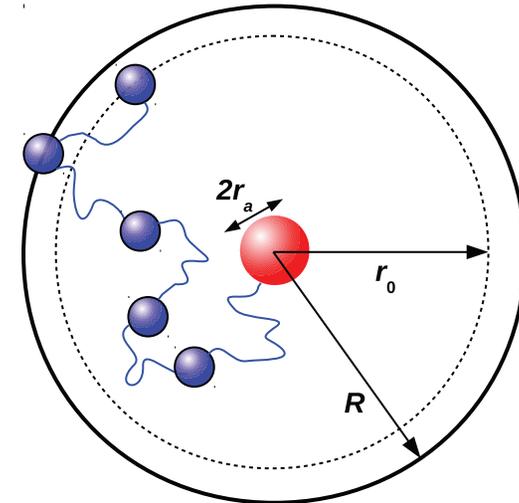
Even in μm -sized bacteria cells biochemical reactions are distance-dependent (geometry-controlled) [Kolesov et al, PNAS (2007); O Pulkkinen & RM, PRL (2013)]

Geometry- versus reaction-control in finite-reactivity scenario

Full first passage time density:

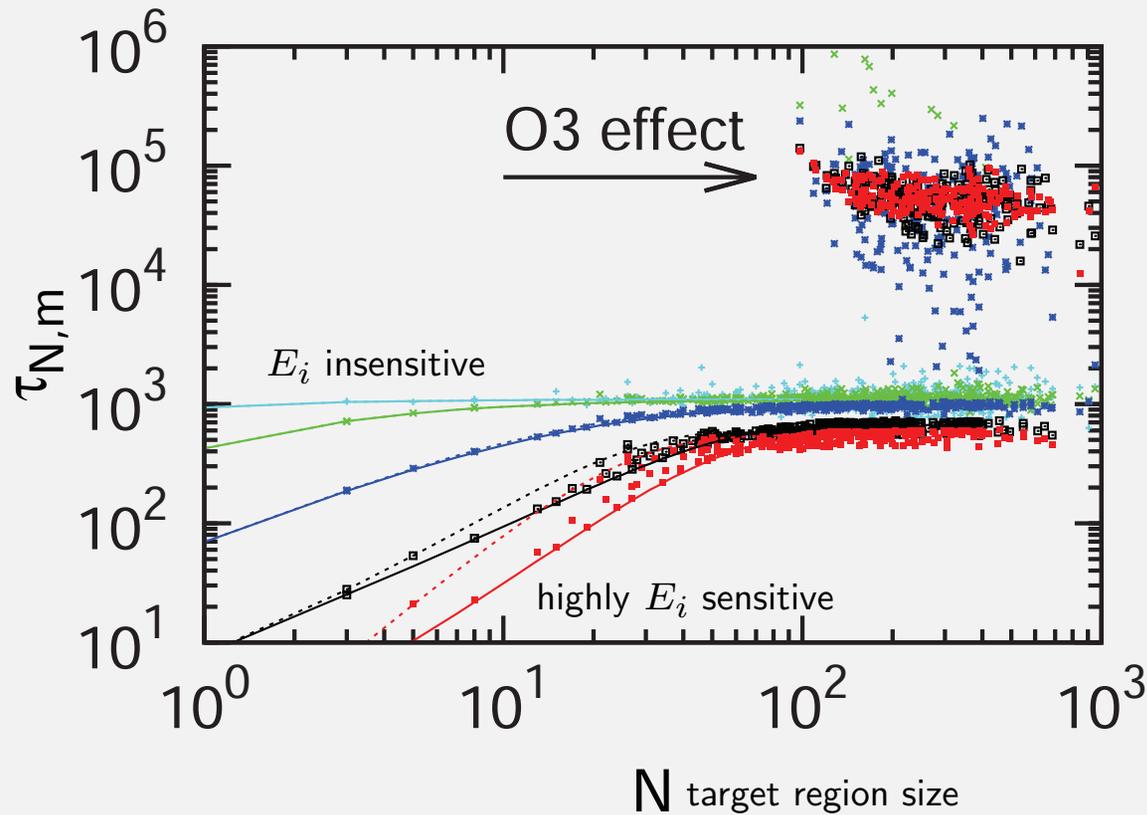
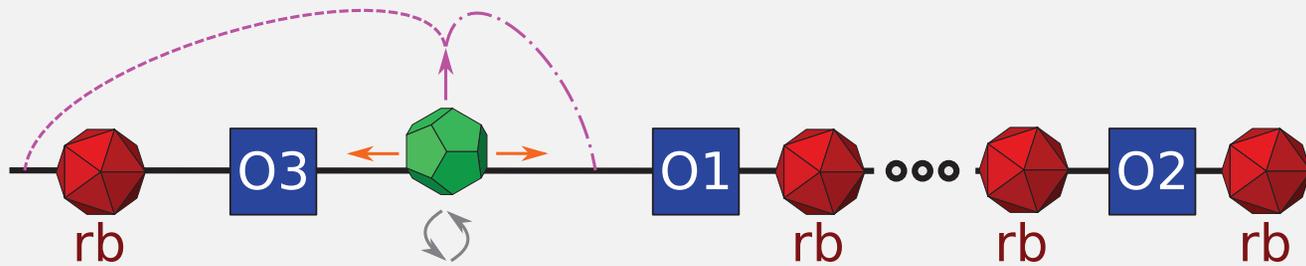


Direct vs indirect trajectories:



$$\langle t \rangle = \frac{(r_0 - r_a)(2R^3 - r_0 r_a [r_0 + r_a])}{6Dr_0 r_a} + \frac{R^3 - r_a^3}{3\kappa r_a}$$

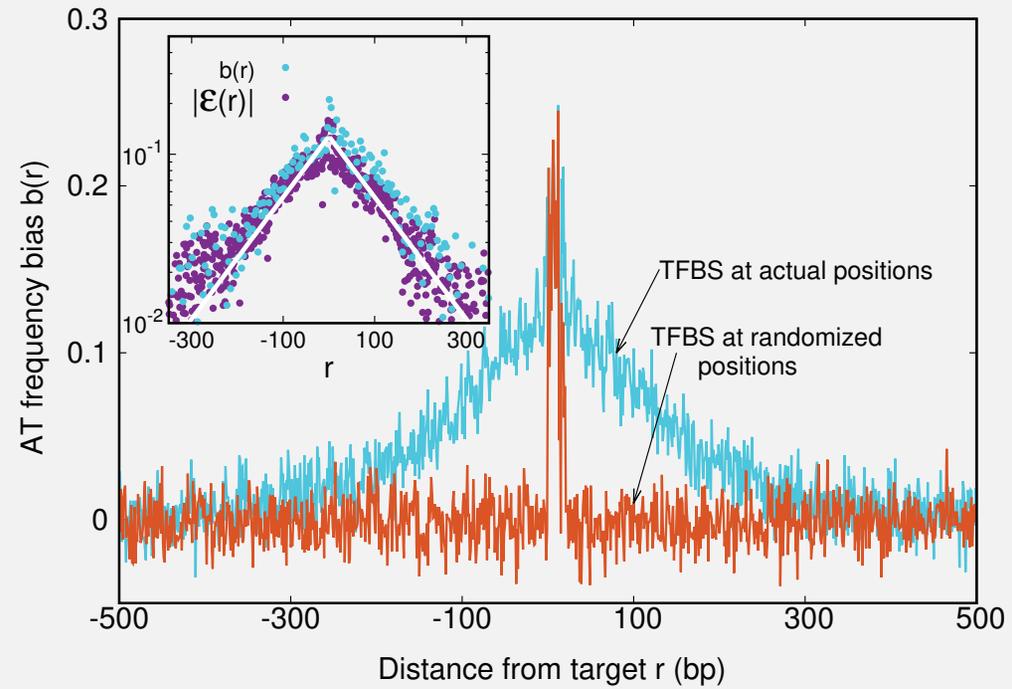
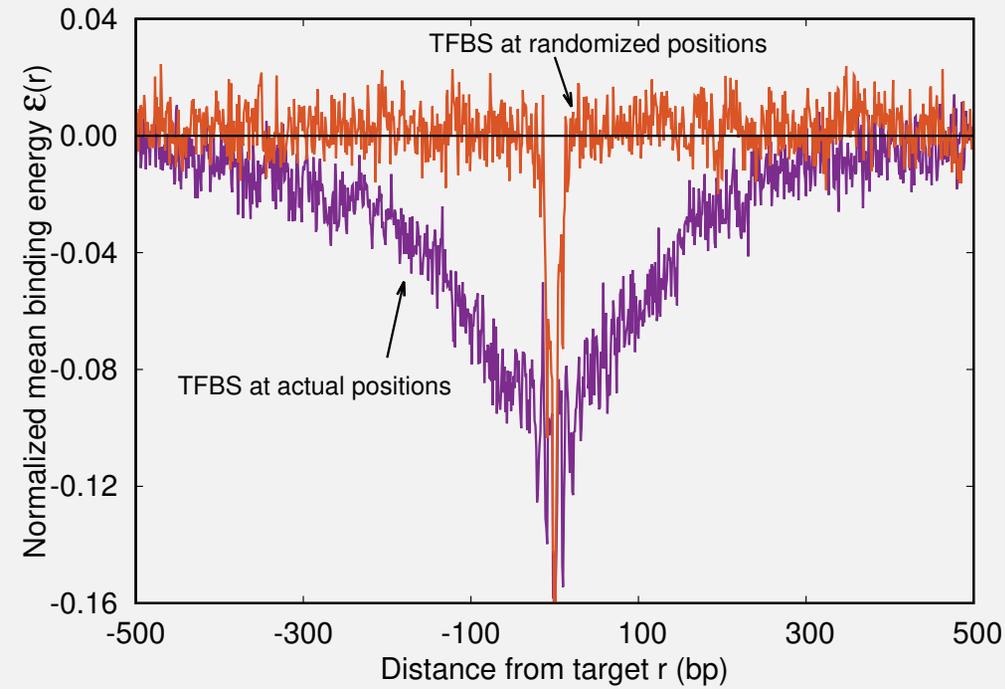
Sequence (binding energy) effects on target search time



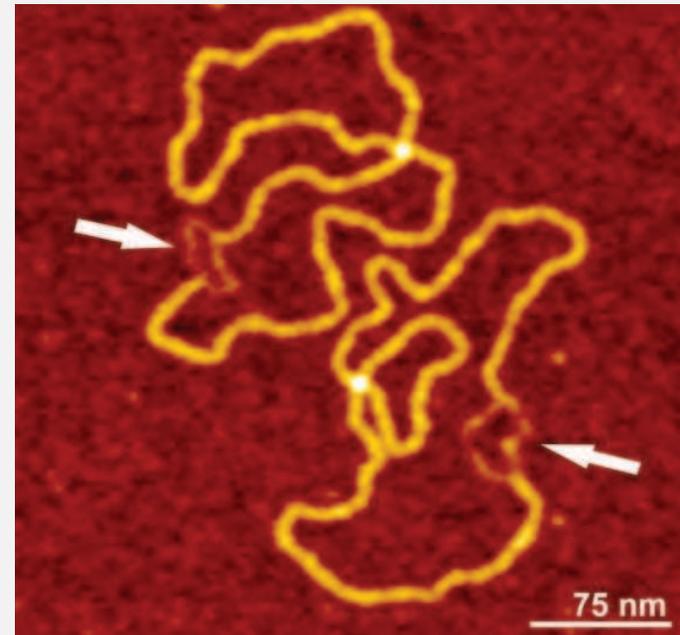
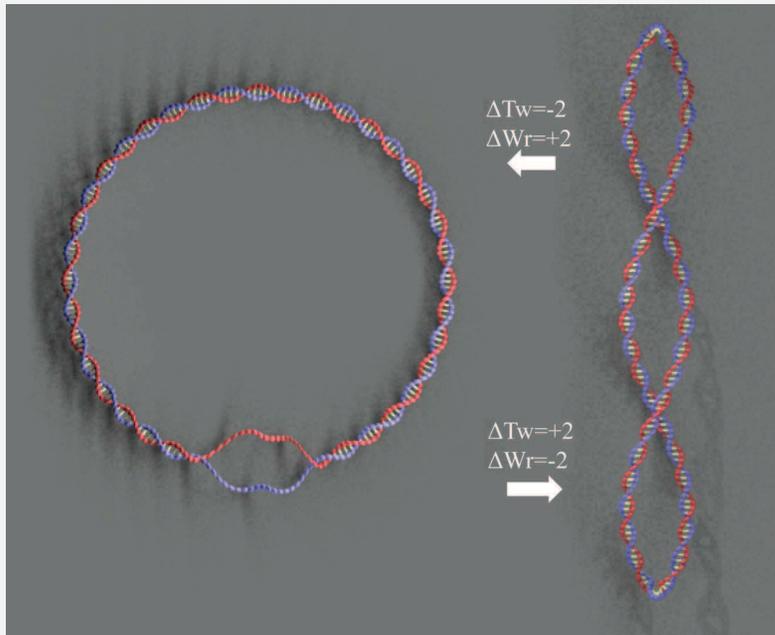
full line: centred target

dashed line: target @ boundary

Energetic funnel facilitated diffusion

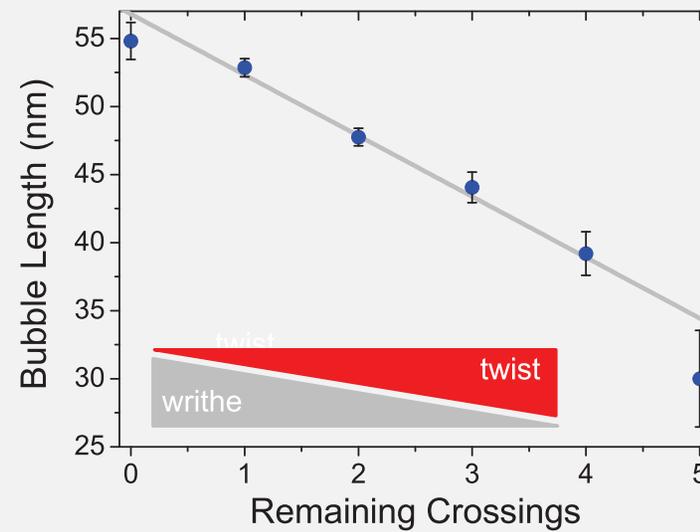


Weak regions at gene starts promote DNA denaturation

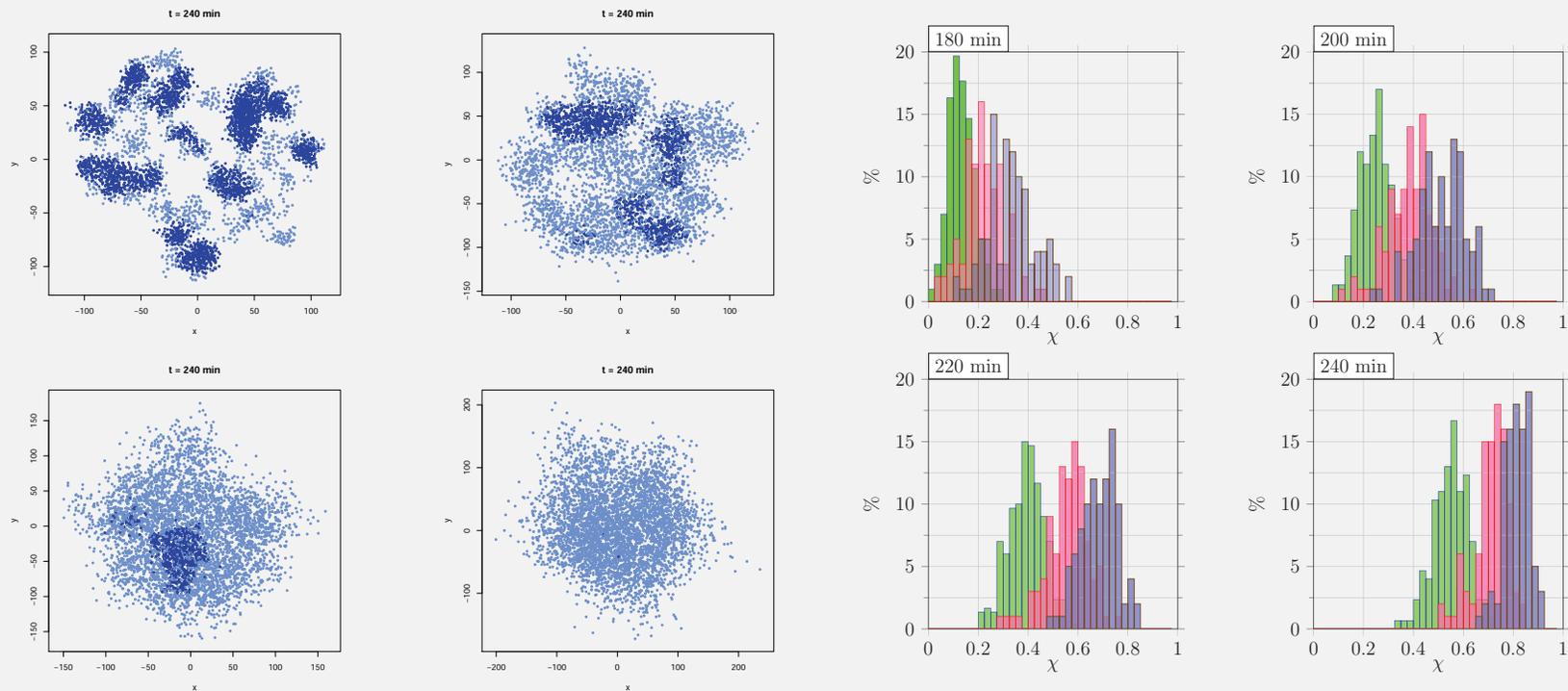
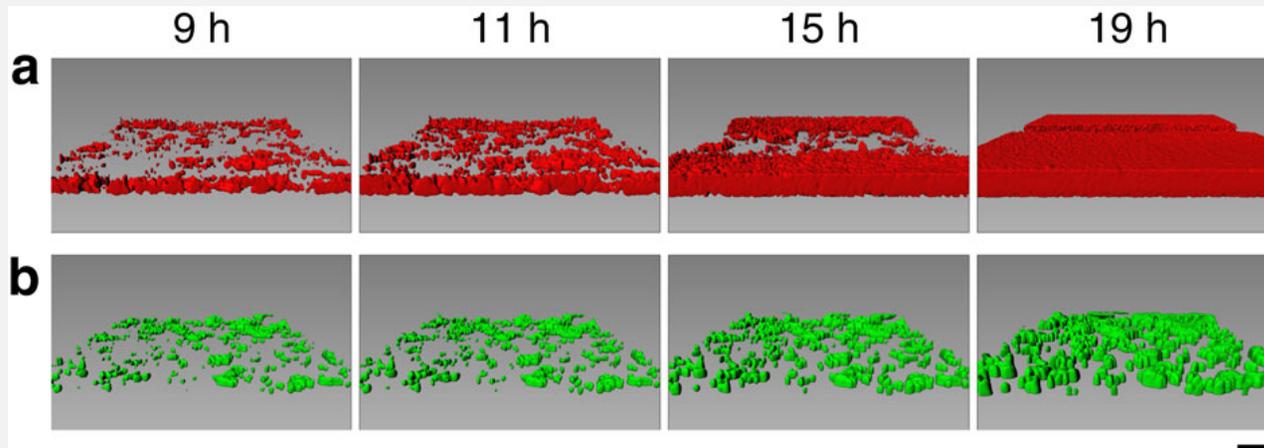


DNA superhelical density:

$$\sigma = \frac{Lk - Lk_0}{Lk_0} \approx -0.06$$



Quorum sensing dynamics in heterogeneous populations

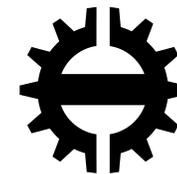


SH Hong et al, Nat Comm **3**, 613 (2011); O Kindler, O Pulkkinen, AG Cherstvy & RM, Sci Rep (2019)

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