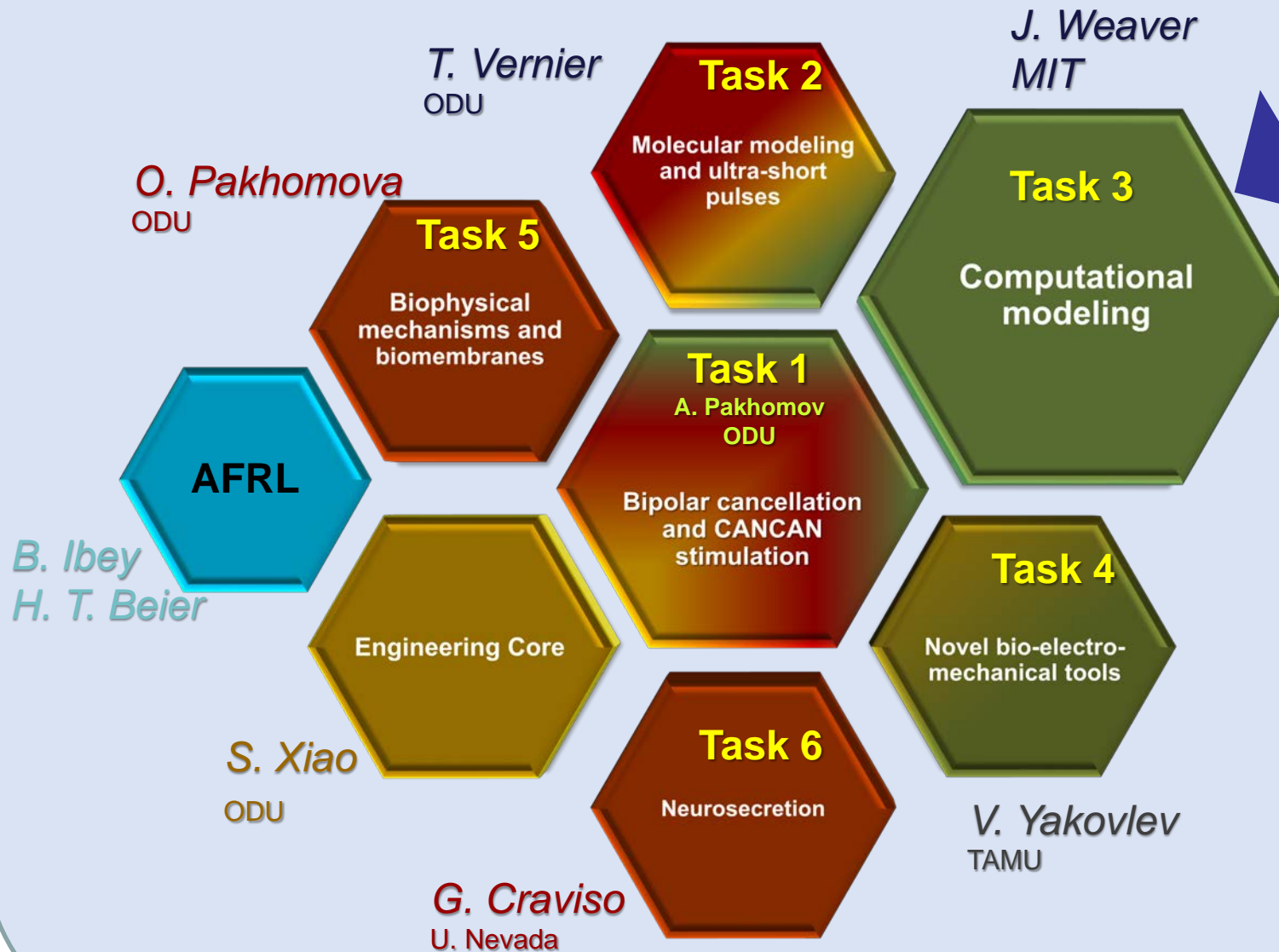


Synergy for Task 3: Computational modeling





Task 3

Computational
modeling

*J. Weaver
MIT*

Science generally involves experiments & theory/models.

Biophysics is central to understanding how electric fields alter structure or modulate processes, and includes cell membrane electroporation (EP). Maybe straightforward to explain bipolar cancellation (BPC). **Not so!**

TP = Transient pore (lipidic); CP = Complex pore (hybrid)

Standard Model failed. A new Cell EP model is able to account for key responses of the experimental groups (Pakhomov, Pakhomova, Craviso, Vernier).

Our models use Xiao waveforms and will benefit from Yakovlev electromechanics tools.

Task 3 – Why is our modeling essential?

Task 3

Computational modeling

We show biophysical mechanism that can account for BPC.

- Based on cytoplasmic molecules
- Decreased tracer uptake by a 2nd pulse of opposite polarity
- Partial recovery of uptake with a delay between pulses

New updated extended cell model:

- Field-driven insertion of cytoplasmic molecules into TPs
- Describes both membrane- and cell-level interactions
 - short-lived transient pores (lifetime 100 ns)
 - long-lived complex pores (lifetime 100 s)
- Quantifies electrodiffusion of tracer molecules post-pulse
 - dominant in uptake experiments that last several orders of magnitude longer than the pulse duration

Occluding molecules yield complex pores (CPs)

- lifetimes up to ~1,000 s

Partial occlusion hinders tracer molecule transport into cell (measured)

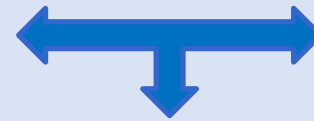
*J. Weaver
MIT*

Synergy

40 year old “standard model”
of electroporation
is inadequate



Continuum & MD multi-scale



Molecular modeling
and ultra-short
pulses

Vernier group experimental results:

- CPs (post-pulse tracer) drift
- calcein efflux data validates post-pulse transport

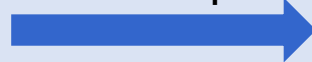
New EP model under
continual development.
Capable of bipolar
cancellation. Results in
new biophysical
phenomena.

**Biophysics:
effects
mechanisms
limitations**

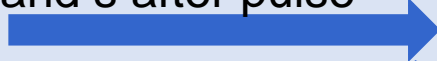
4

Computational
modeling

Waveforms are
model inputs



Post-pulse U_m : ms
and s after pulse

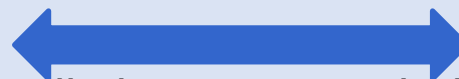


U_m during pulse



- Experimental Data: Tracer uptake from BPC from experimental groups tests the theoretical/computational model
- Modeling suggests experiments

Bipolar cancellation poses a challenge to
biophysics. New discoveries of biophysical
mechanisms were needed. BPC in turn can
be applied to new and exciting applications.



Engineering
Core

Novel bio-
electro-
mechanical
tools

AFRL

Biophysical
mechanisms
and
biomembranes

Neurosecretion

Bipolar
cancellation
and CANCAN
stimulation

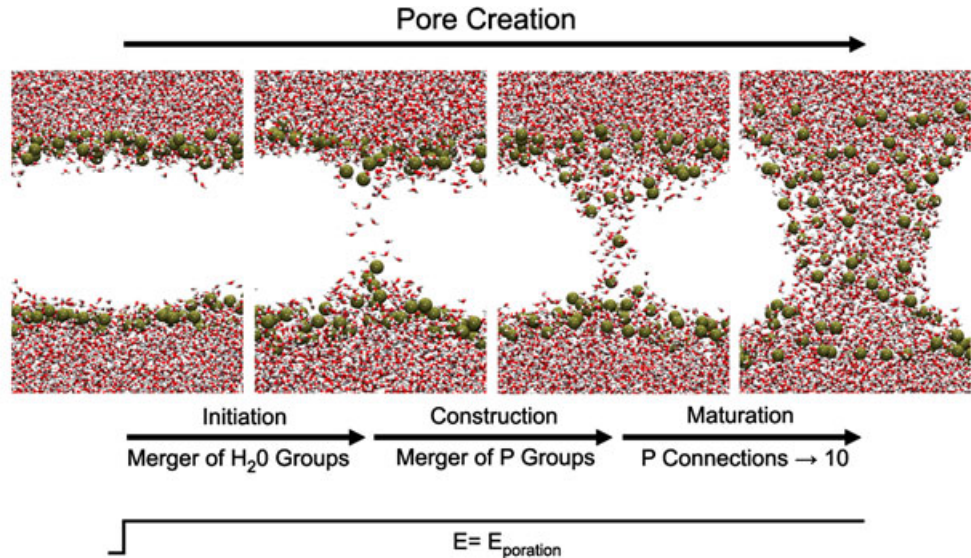
Traditional/Transient Pores (TPs)

(as revealed by molecular dynamics – MD)

Pore birth

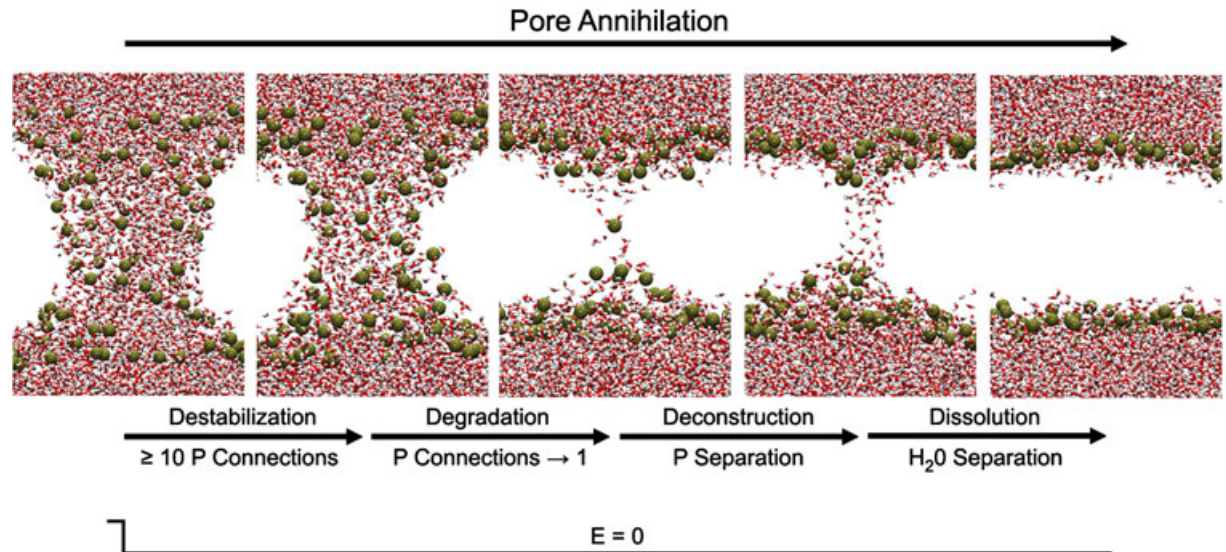
Pore lifetime is more important

100 ns lifetime pores vanish before observations



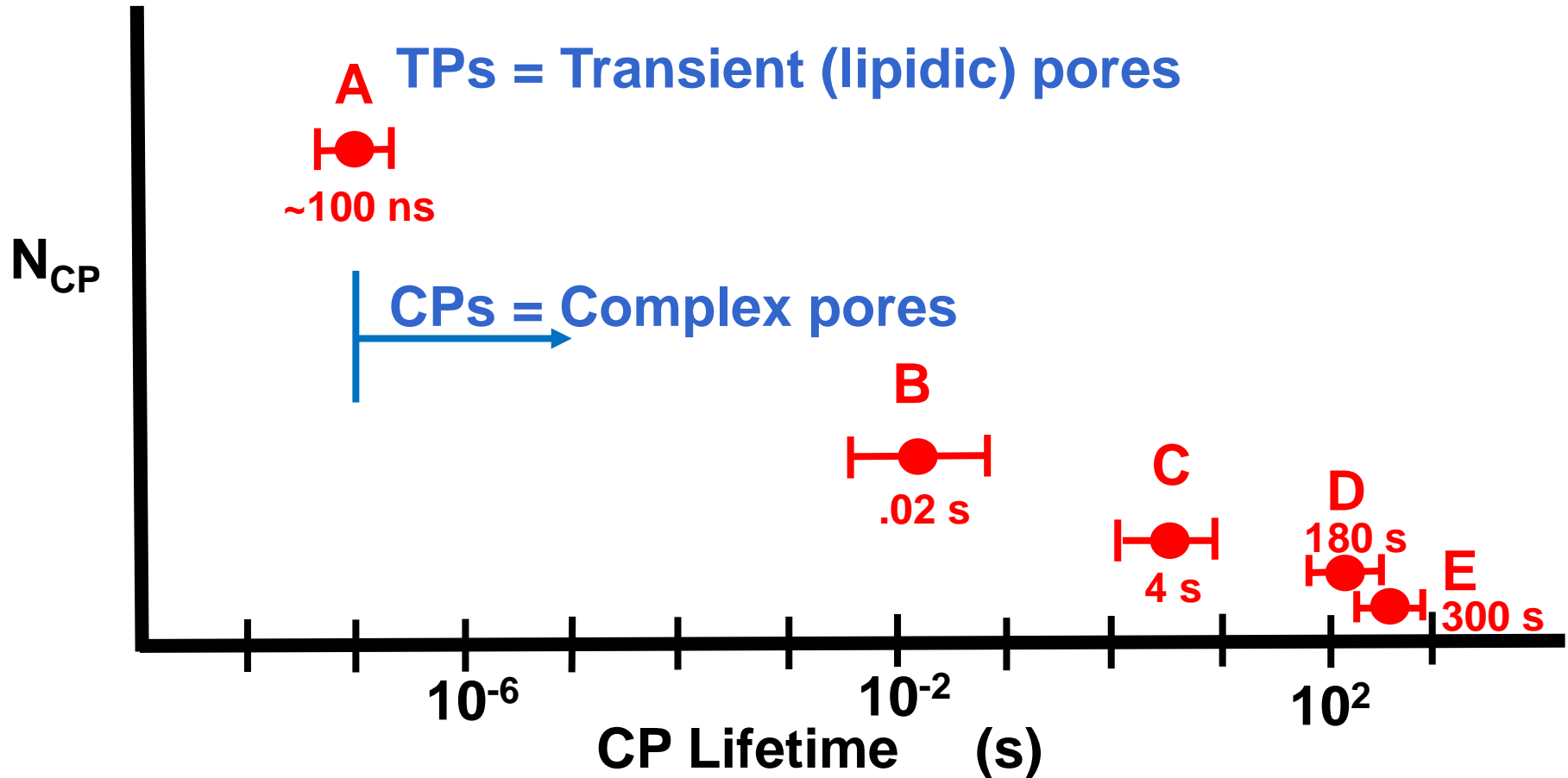
Pore death

~100 ns lifetimes



(Levine and Vernier JMB 2010)

Broad Lifetime Distribution Concept



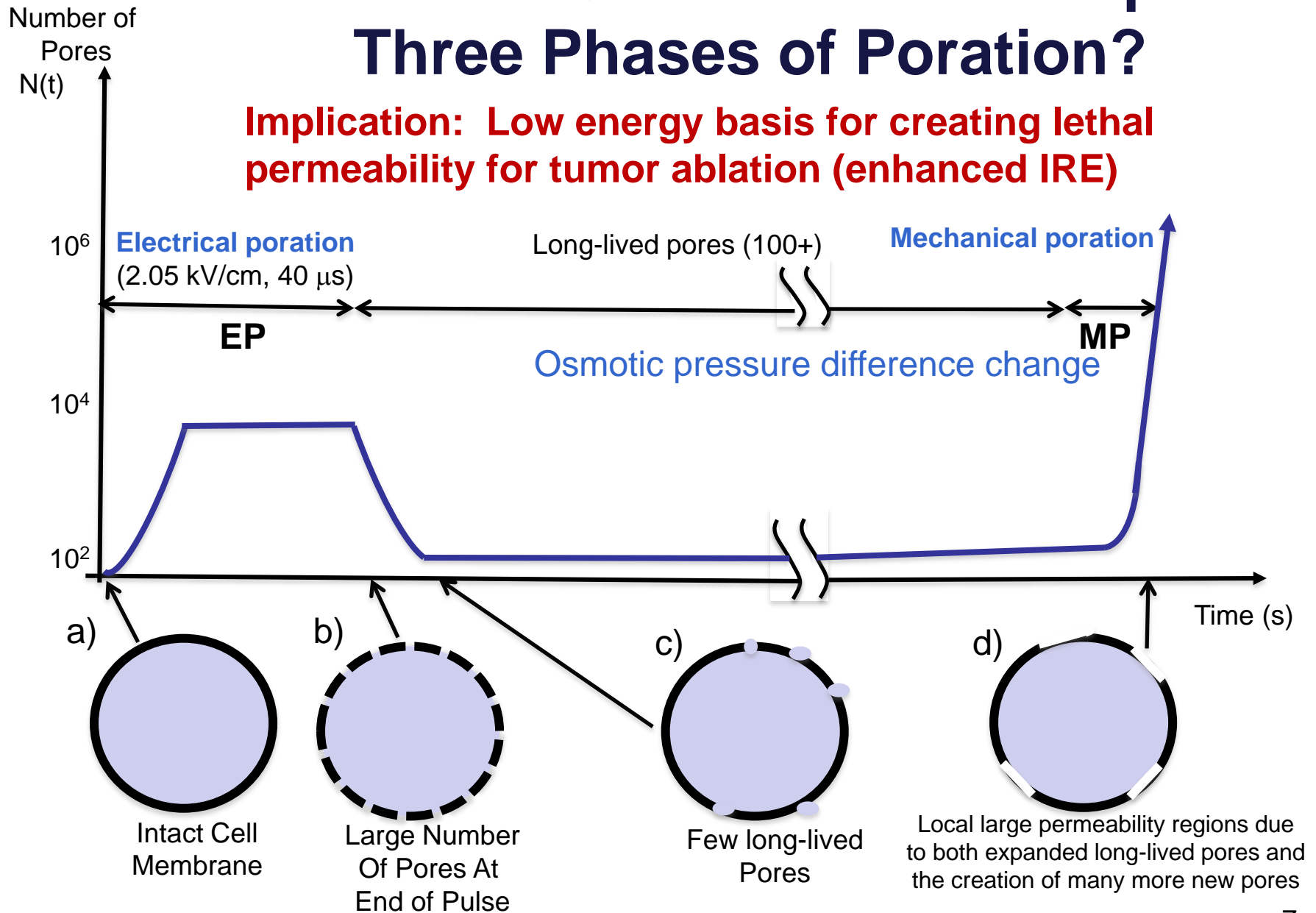
Guess-estimates are based on order of magnitude TP numbers, and experiments with ~1 to 300 s observation times

Further experiments are essential.

(Stern et al., arXiv 25 AUG 2017)

What Else Can New Model Explain: Three Phases of Poration?














Implication: Low energy basis for creating lethal permeability for tumor ablation (enhanced IRE)




























Crowded cytoplasm: Simulation demonstration














(McGuffee & Elcock, PLoS Comp. Biol. 2010)

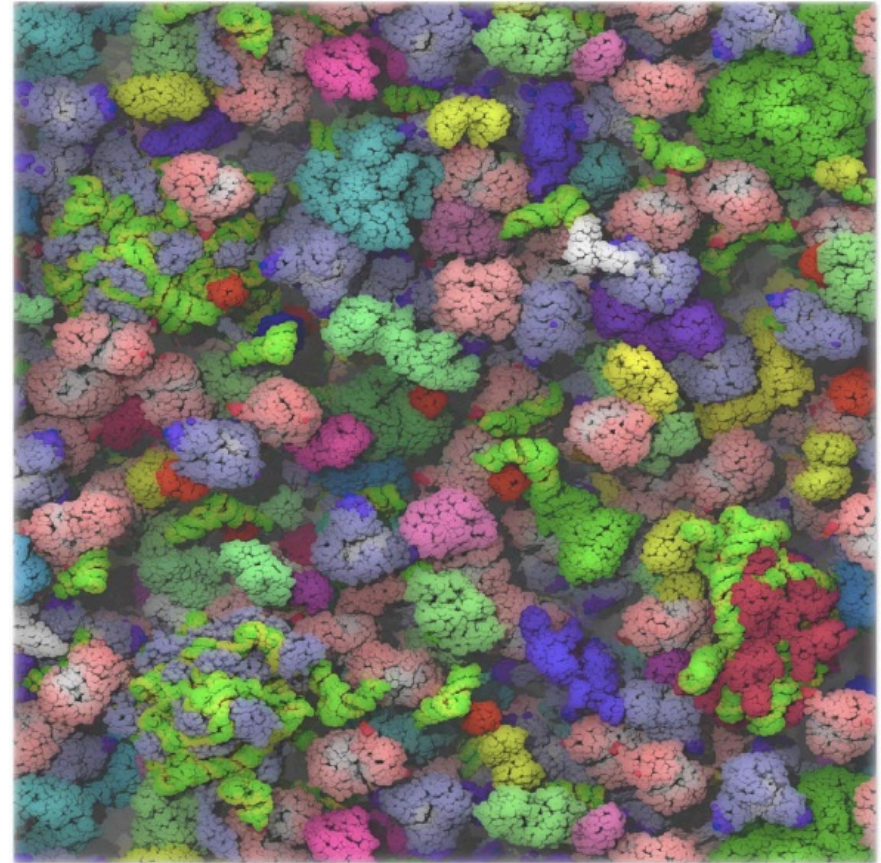
Prior cell EP models treat cytoplasm as simple aqueous electrolyte

	Name	Mw	#
	Adk	24	14
	AhpC	187	7
	Asd	80	4
	Bcp	11	8
	CspC	7	72
	CysK	64	13
	DapA	125	2
	DnaK	41	11
	Efp	20	14
	Eno	91	18
	Fba	78	6
	Frr	21	7
	FusA	69	22

	Name	Mw	#
	GapA	142	10
	GlnA	621	1
	GltD	94	3
	GlyA	91	15
	GpmA	55	4
	Hns	5	7
	Hup	15	12
	IcdA	92	43
	IlvC	54	18
	Mdh	65	13
	MetE	84	213
	Mop	845	2

	Name	Mw	#
	PanB	140	2
	Pgk	41	26
	Pnp	190	3
	Ppa	116	9
	PpiB	18	7
	PurA	94	4
	PurC	42	7
	Pyr	308	3
	RpiA	46	3
	Rpo	260	4
	SerC	79	11
	SodA	46	13
	SodB	42	9

	Name	Mw	#
	Suc	142	4
	Tig	48	9
	TpiA	54	5
	Tsf	61	12
	TufA	84	181
	Upp	45	11
	UspA	31	7
	50S	1,355	10
	30S	788	10
	tRNA-C	24	37
	tRNA-Q	24	37
	tRNA-F	25	37
	GFP	26	8



In new, extended model we recognize the complex cytoplasm.

We hypothesize complex pores (CPs), and estimate some CP functions.

Typical cytoplasmic proteins + GFP shown (color for distinction).
These contact or are close to the PM, so interactions are expected.