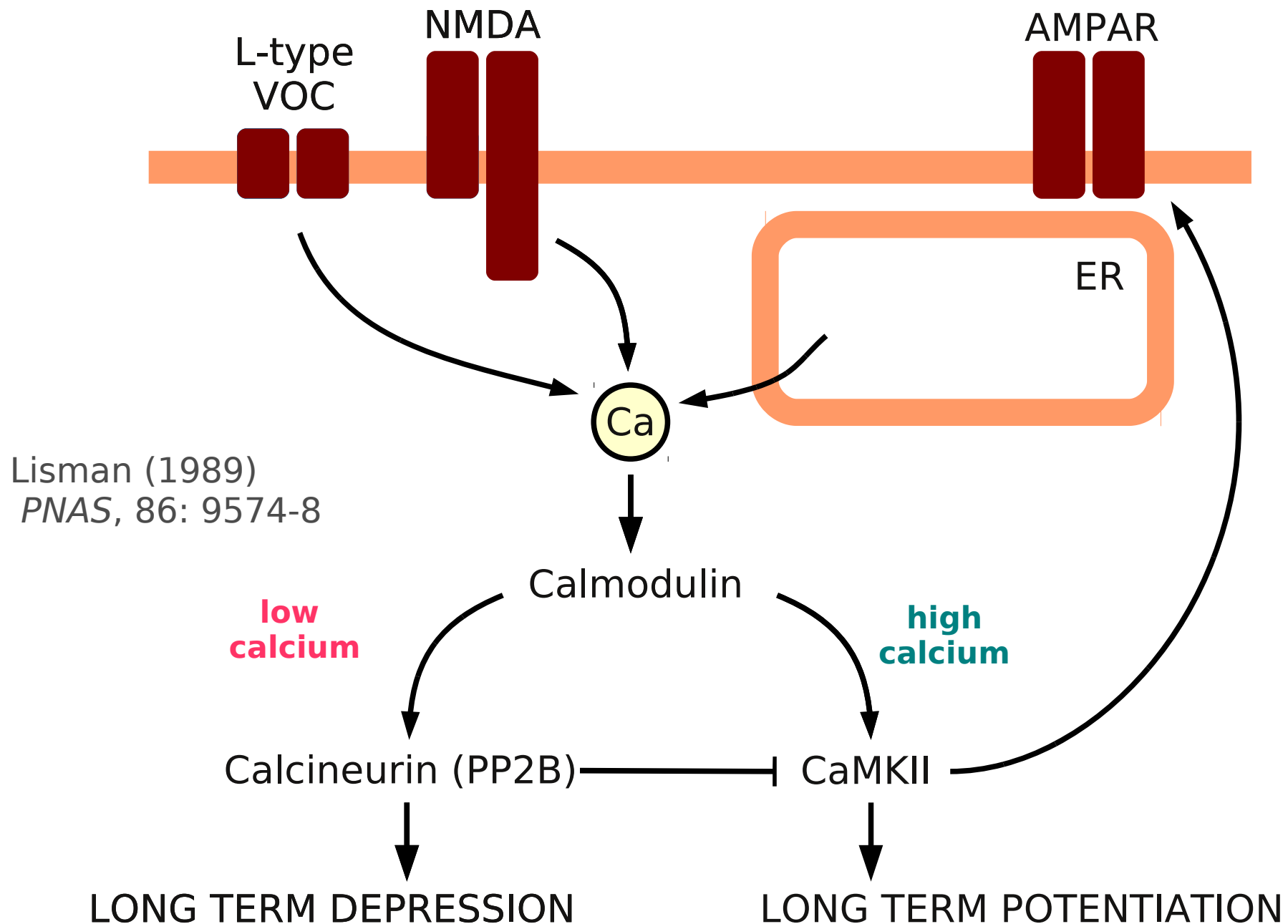


Modelling the behaviour of allosteric calcium sensors involved in synaptic plasticity

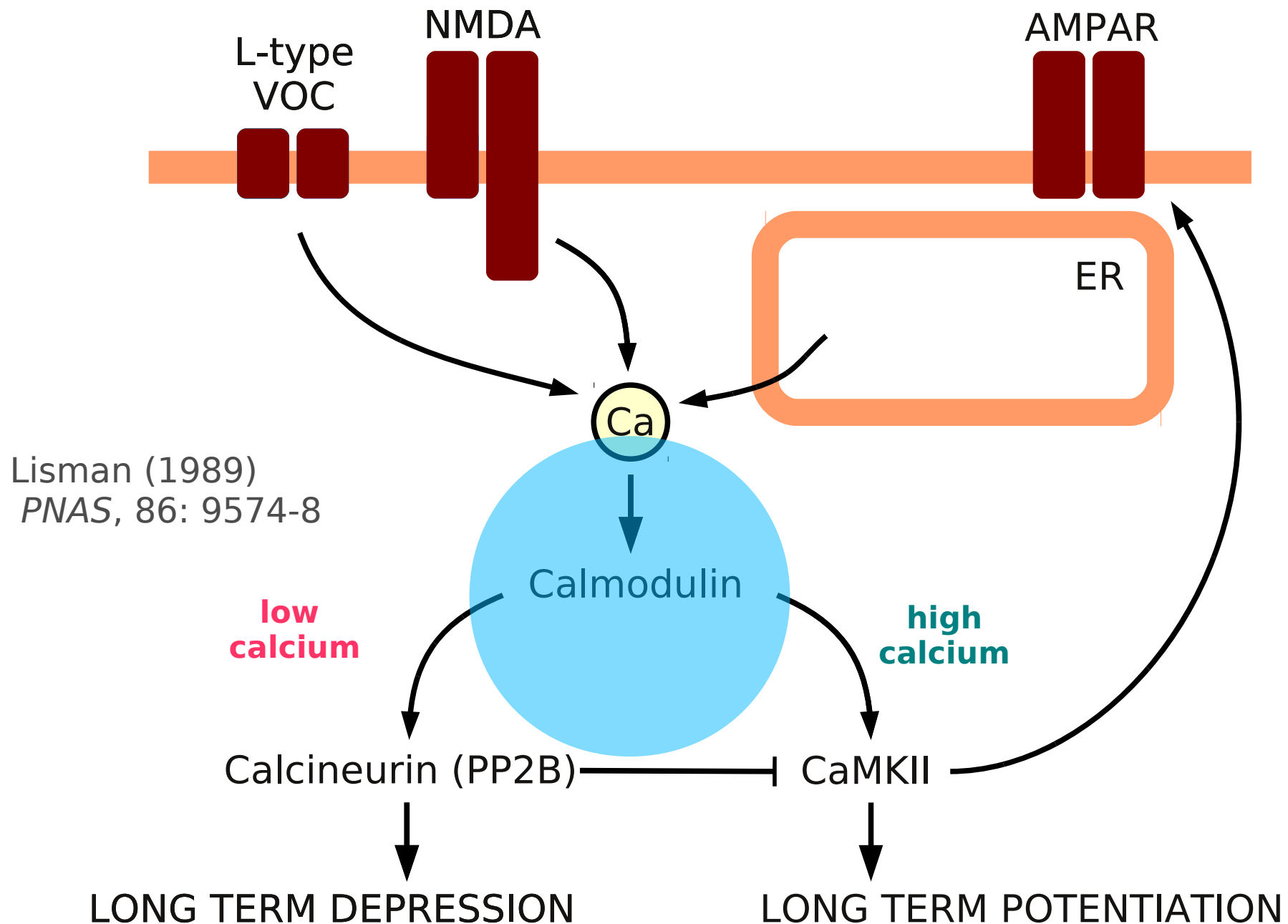
Cooperativity, sensitivity and all that

Nicolas Le Novère, EMBL-EBI

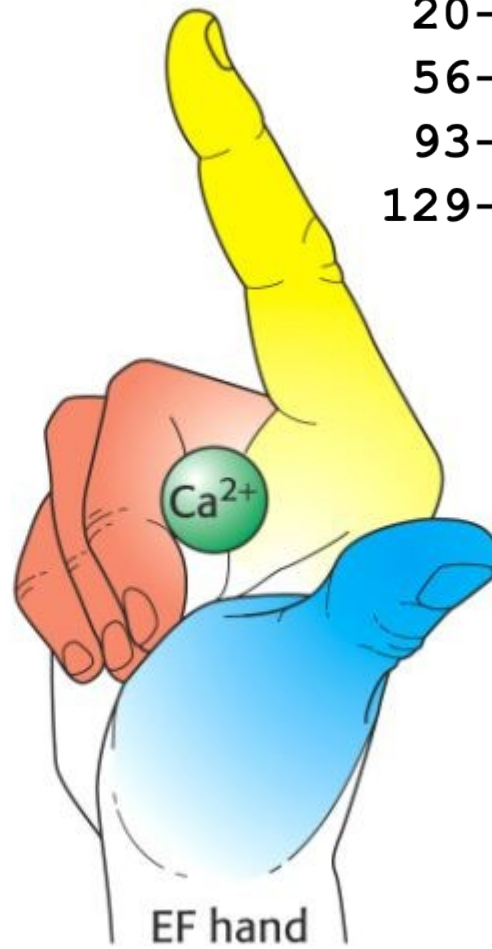
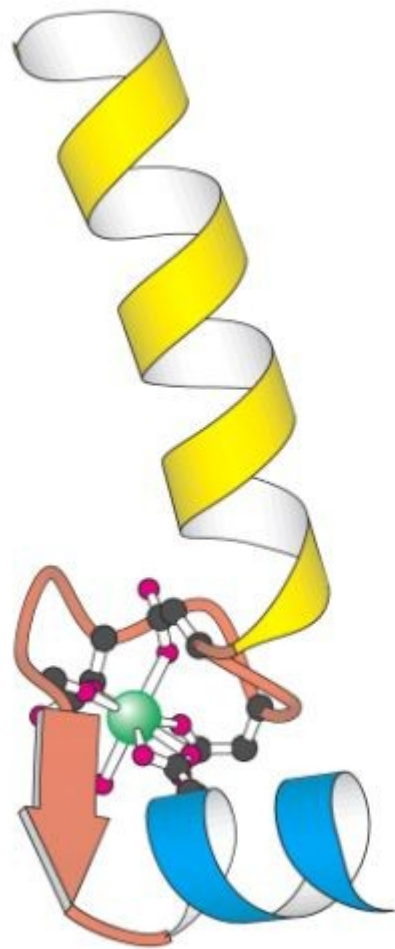
Calmodulin, the memory switch



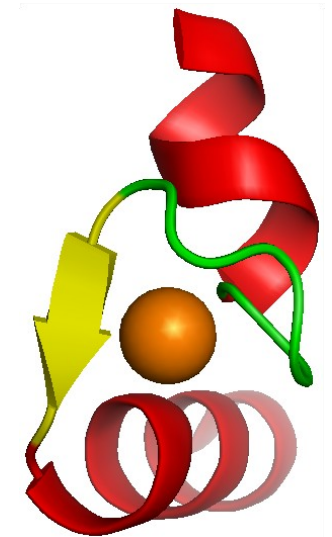
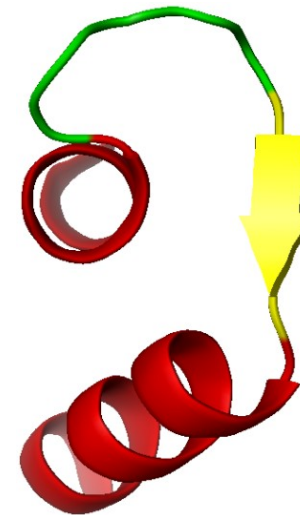
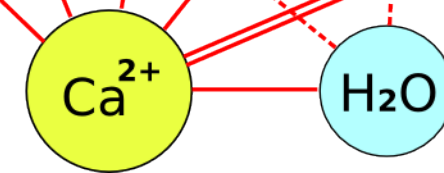
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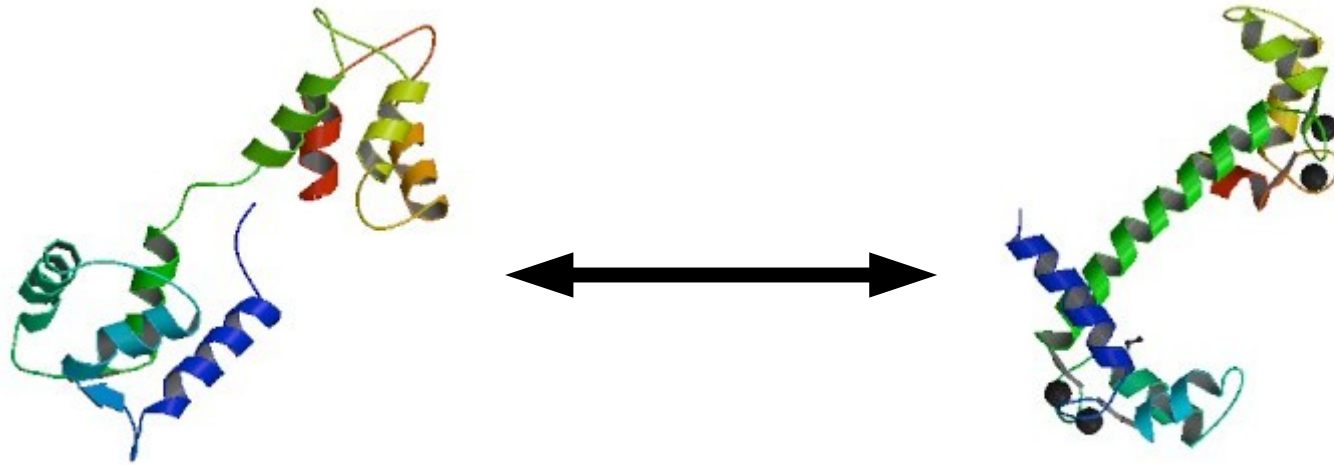
Structure of Calmodulin



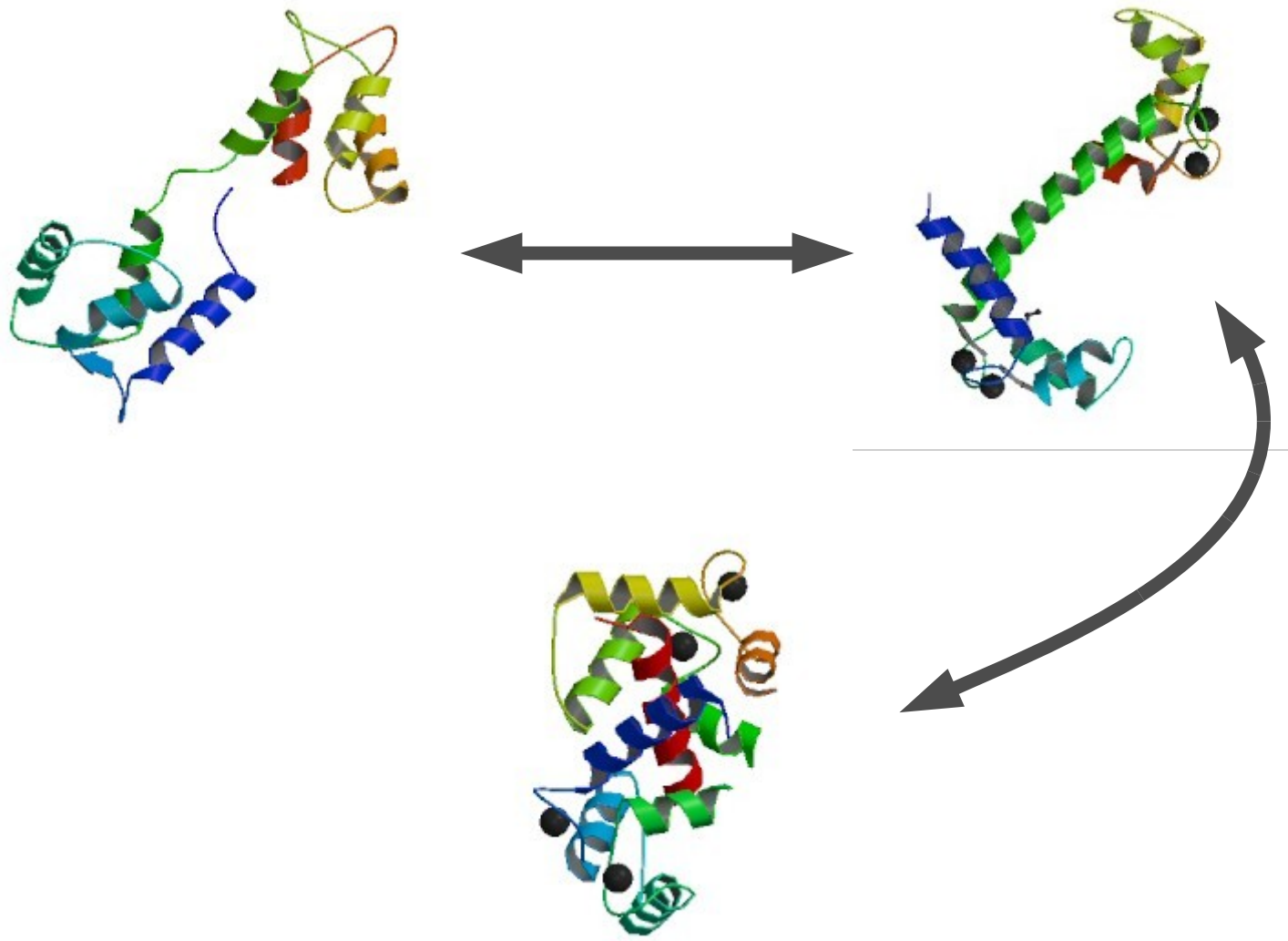
	X		Y		Z		-Y		-X		-Z		
20-	D	K	D	G	D	G	T	I	T	T	K	E	- 31
56-	D	A	D	G	N	G	T	I	D	F	P	E	- 67
93-	D	K	D	G	N	G	Y	I	S	A	A	E	-104
129-	D	I	D	G	D	G	Q	V	N	Y	E	E	-140



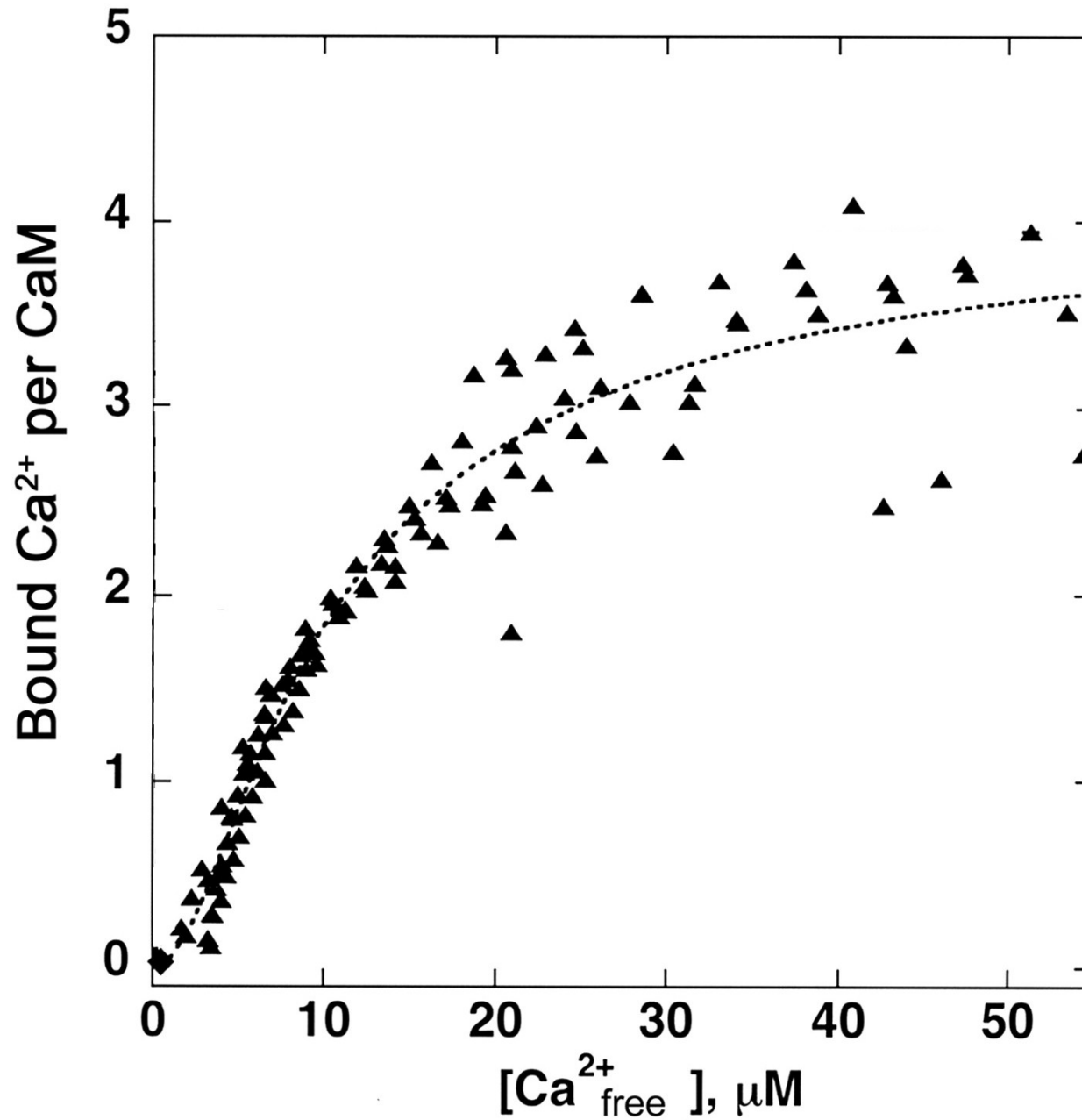
State transitions of calmodulin



State transitions of calmodulin

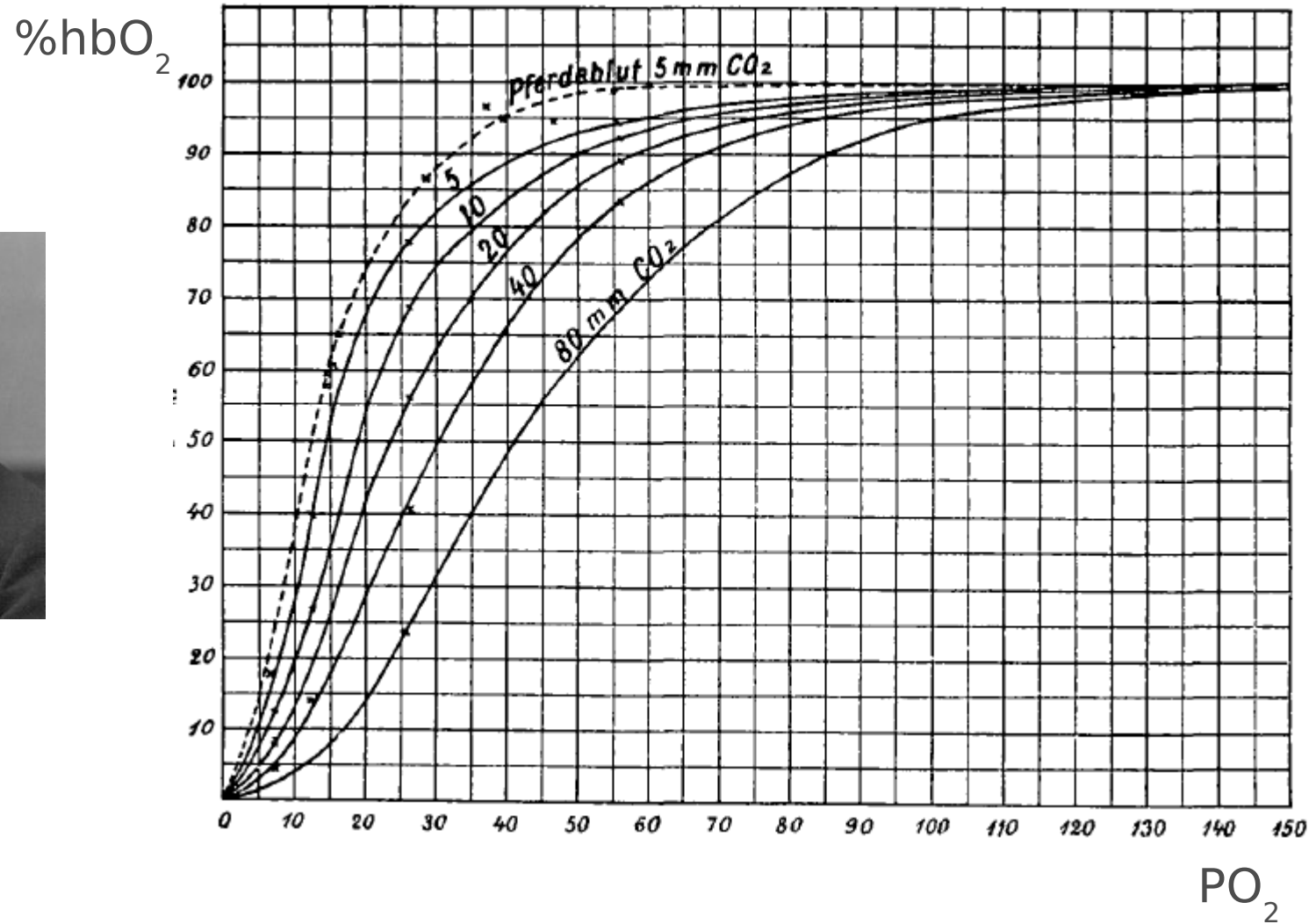


Calmodulin is ultra-sensitive



Shifman et al (2006)
PNAS, 103: 13968-13973

Origins of cooperativity: Bohr



Bohr C (1903) Theoretische behandlung der quantitativen verhältnisse bei der sauerstoff aufnahme des hämoglobins *Zentralbl Physiol* 17: 682

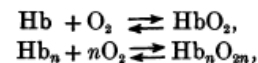
The possible effects of the aggregation of the molecules of hæmoglobin on its dissociation curves. By A. V. HILL.

In a previous communication Barcroft and I gave evidence which seemed to us to prove conclusively that dialysed hæmoglobin consists simply of molecules containing each one atom of iron. The molecular weight is therefore $Hb = 16,660$. These experiments have not been published yet, but I shall assume the results.

Other observers (Reid, Roaf, Hüfner and Gansser) working on different solutions have obtained divergent results. The method used by all of them was the direct estimation of the osmotic pressure, by means of a membrane permeable to salts, but not to hæmoglobin. The method involves a relatively large error, because the quantity measured is small. It is doubtful however whether this can explain the discordant results.

Our work led me to believe that the divergence between the results of different observers was due to an aggregation of the hæmoglobin molecules by the salts present in the solution, a consequent lowering of the number of molecules, and an increase in the average molecular weight as observed by the osmotic pressure method. To test this hypothesis I have applied it to several of the dissociation curves obtained by Barcroft and Camis with hæmoglobin in solutions of various salts, and with hæmoglobin prepared by Bohr's method.

The equation for the reaction would be



where Hb_n represents the aggregate of n molecules of Hb . I have supposed that in every solution there are many different sized aggregates, corresponding to many values of n .

If there were in the solution only Hb and Hb_2 the dissociation curve would be

$$y = \lambda \frac{K'x^2}{1 + K'x^2} + (100 - \lambda) \frac{Kx}{1 + Kx} \dots\dots\dots (A),$$

where $\lambda\%$ is as Hb_2 , $(100 - \lambda)\%$ as Hb , K' is the equilibrium constant of the reaction $Hb_2 + 2O_2 \rightleftharpoons Hb_2O_4$ and K that of $Hb + O_2 \rightleftharpoons HbO_2$: K has the value '125 (Barcroft and Roberts).

Origins of cooperativity: Hill

Hill (1910) *J Physiol* 40: iv-vii.



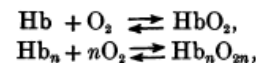
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Now it is unlikely that in either of these cases there is only Hb and Hb_2 : and as the calculation of the constants in these equations is very tedious I decided to try whether the equation

$$y = 100 \frac{Kx^n}{1 + Kx^n} \dots\dots\dots (B)$$

would satisfy the observations.

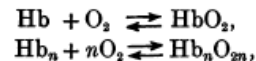
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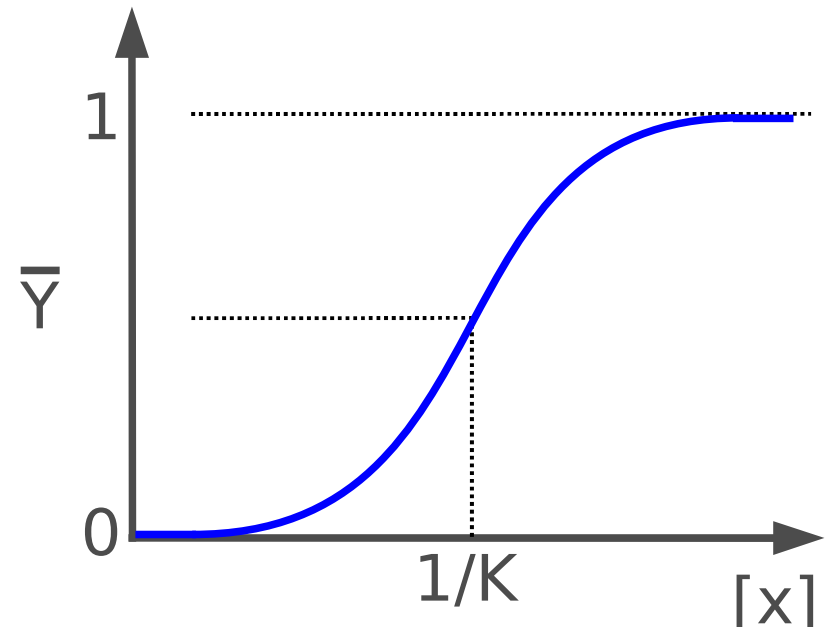
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$$\bar{Y} = \frac{K^n [X]^n}{1 + K^n [X]^n}$$

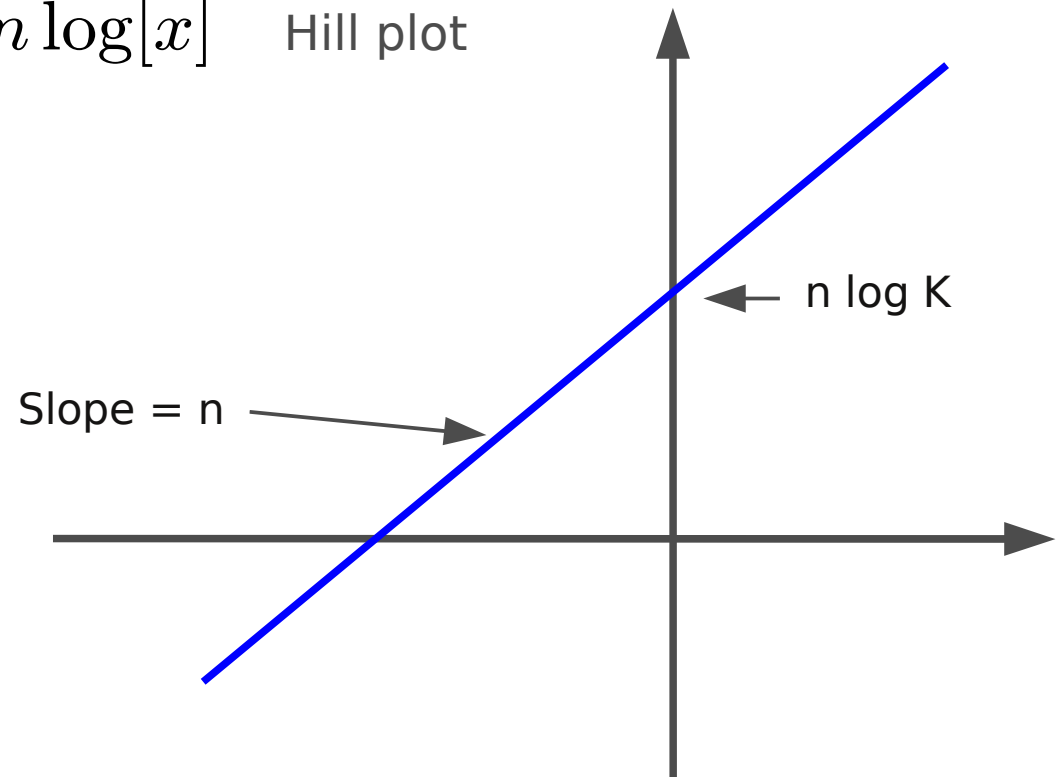
Hill equation

$$\log \frac{\bar{Y}}{1 - \bar{Y}} = n \log K + n \log [x]$$

Hill plot

Effect increases in function of the signal to the power of n:
 $n > 1$, ultra-sensitive
 $n < 1$, infra-sensitive

BUT cooperativity of ligand,
 not of binding sites: unique affinity



THE HEMOGLOBIN SYSTEM.

VI. THE OXYGEN DISSOCIATION CURVE OF HEMOGLOBIN.*

By G. S. ADAIR.

WITH THE COLLABORATION OF A. V. BOCK AND H. FIELD, JR.

(*From the Medical Laboratories of the Massachusetts General Hospital,
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(Received for publication, January 7, 1925.)

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$$\bar{Y} = \frac{1}{n} \frac{K_1[x] + 2K_2[x]^2 + 3K_3[x]^3 + 4K_4[x]^4}{1 + K_1[x] + K_2[x]^2 + K_3[x]^3 + K_4[x]^4}$$

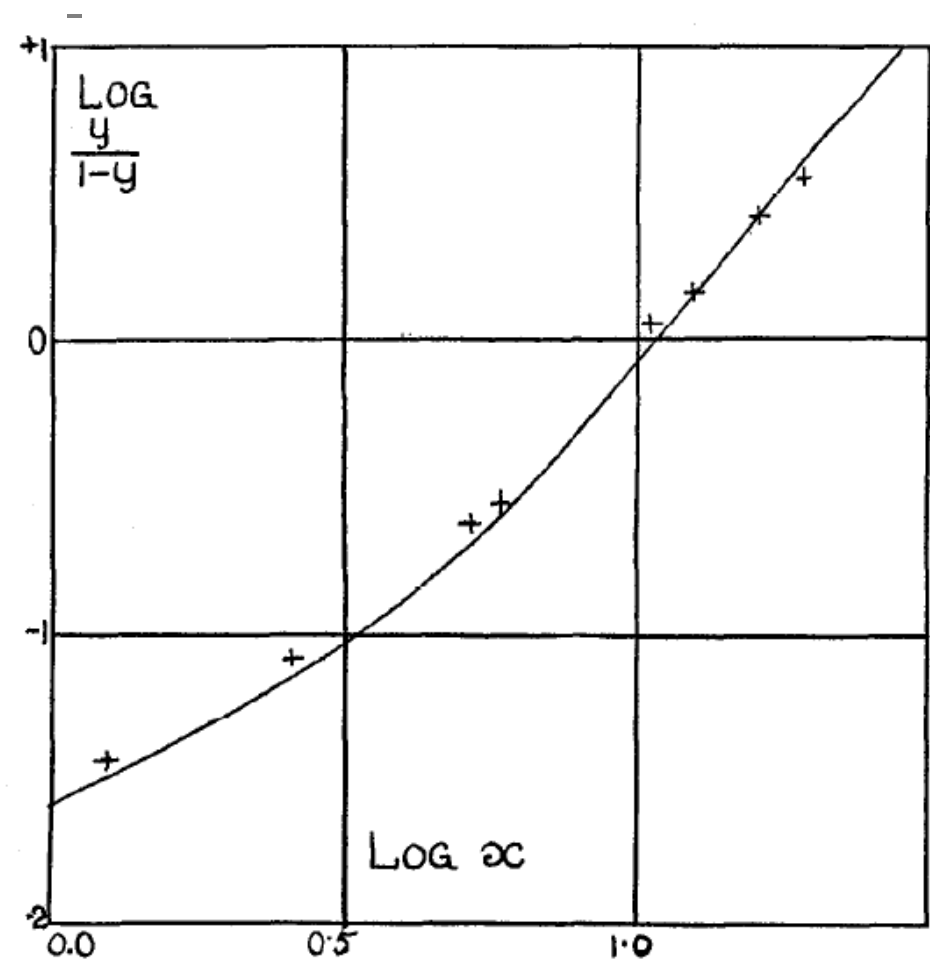


FIG. 2. Test of formula (6). Curve drawn from 6 experimental points from Table IV.

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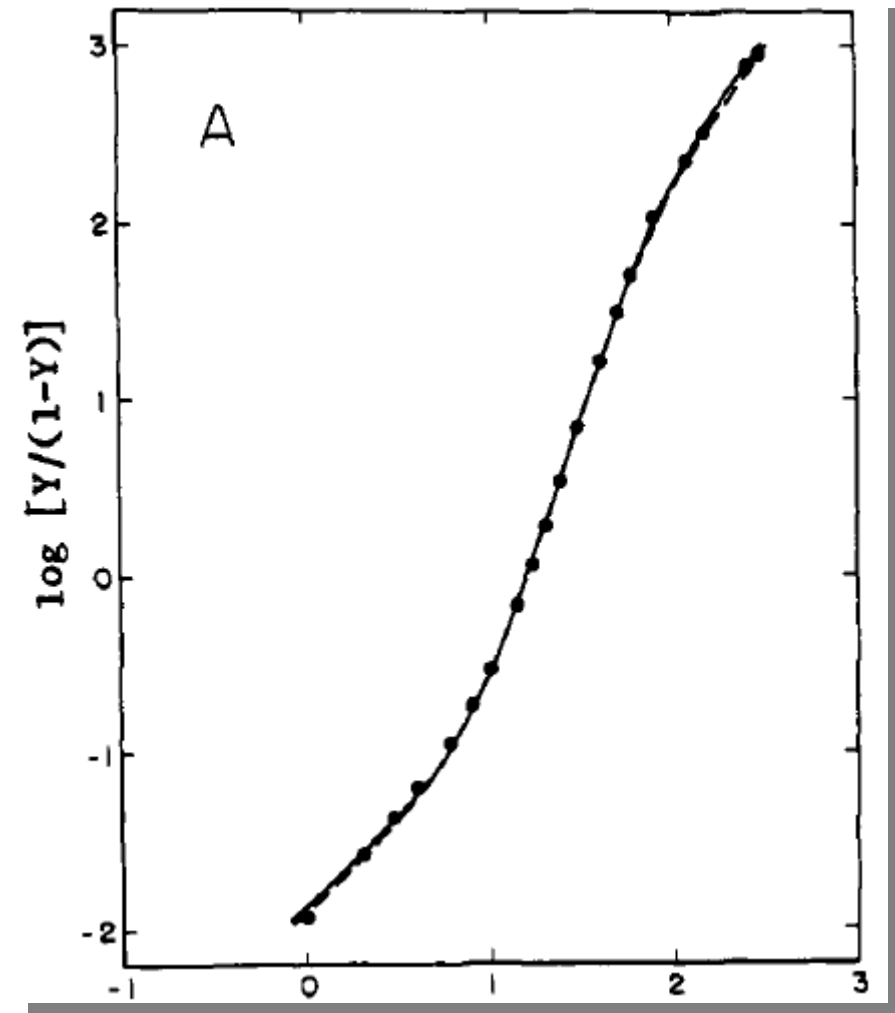
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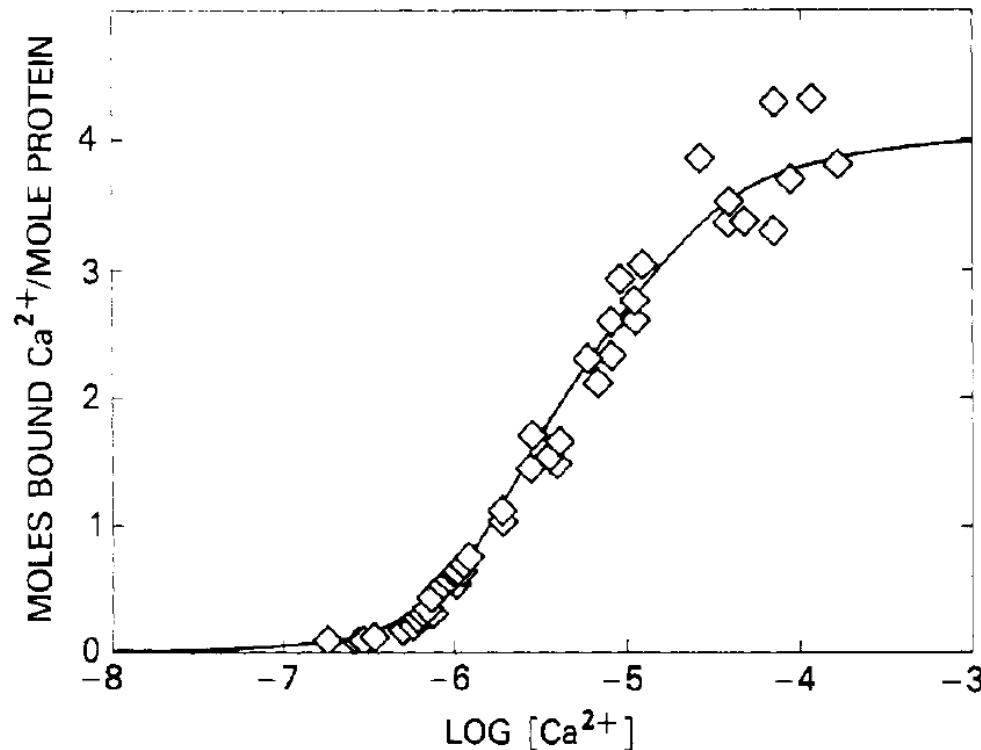


Imai (1973) *Biochemistry* 12: 798-808

Adair-Klotz model applied to Calmodulin

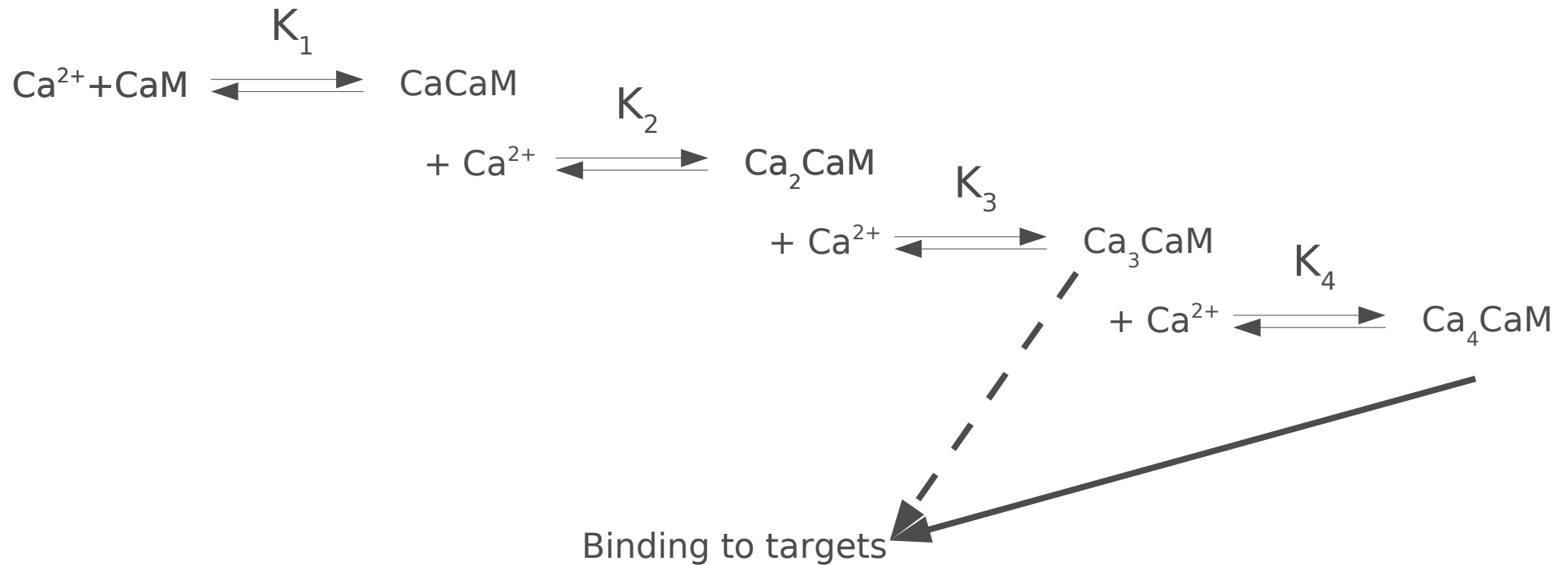
Klotz (1946) The Application of the Law of Mass Action to Binding by Proteins. Interactions with Calcium. *Arch Biochem*, 9:109-117.

$$\bar{Y} = \frac{1}{n} \frac{K_1[Ca] + 2K_1K_2[Ca]^2 + 3K_1K_2K_3[Ca]^3 + 4K_1K_2K_3K_4[Ca]^4}{1 + K_1[Ca] + K_1K_2[Ca]^2 + K_1K_2K_3[Ca]^3 + K_1K_2K_3K_4[Ca]^4}$$

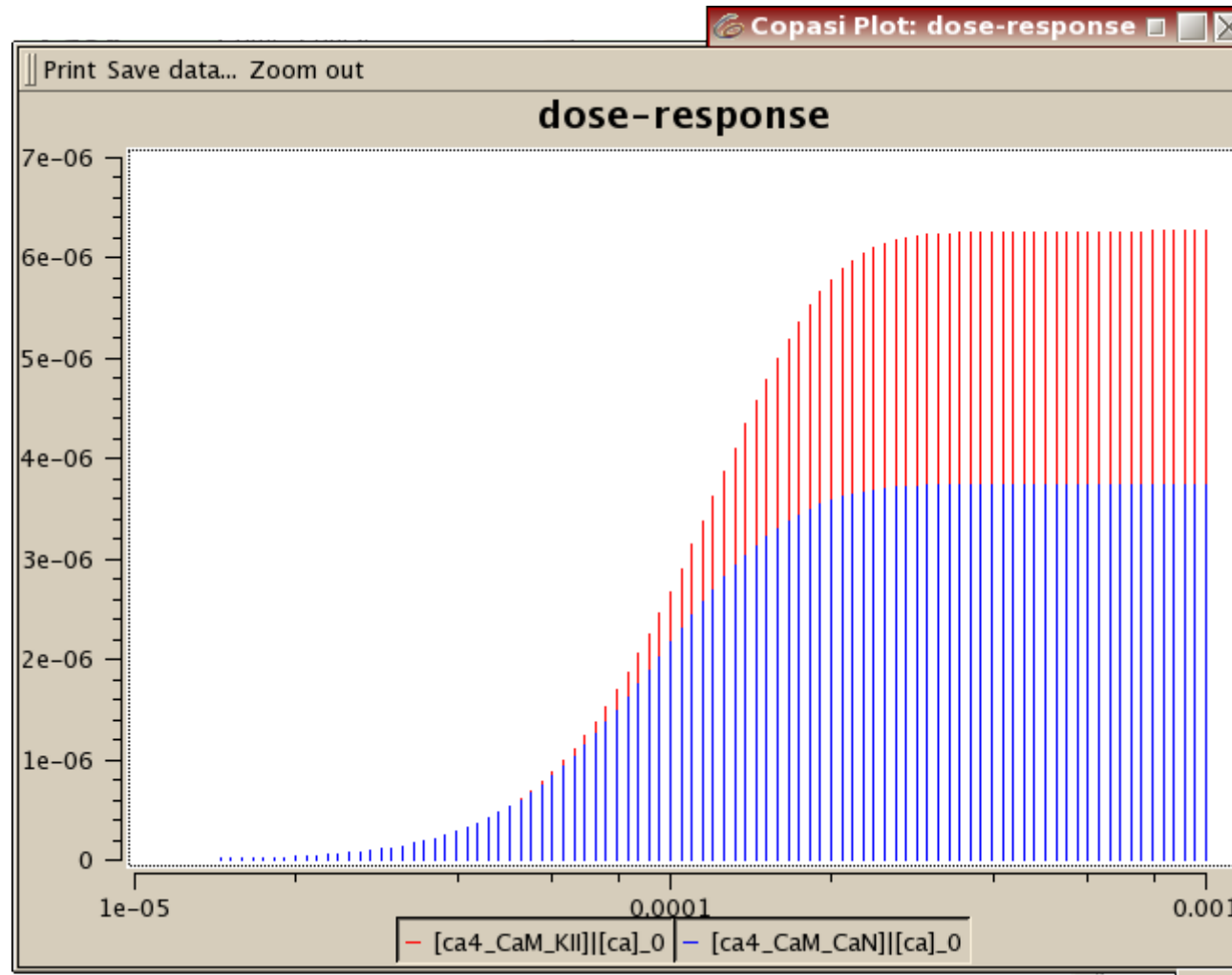


Crouch and Klee (1980)
Biochemistry, 19: 3692-3698

Corresponding induced-fit model



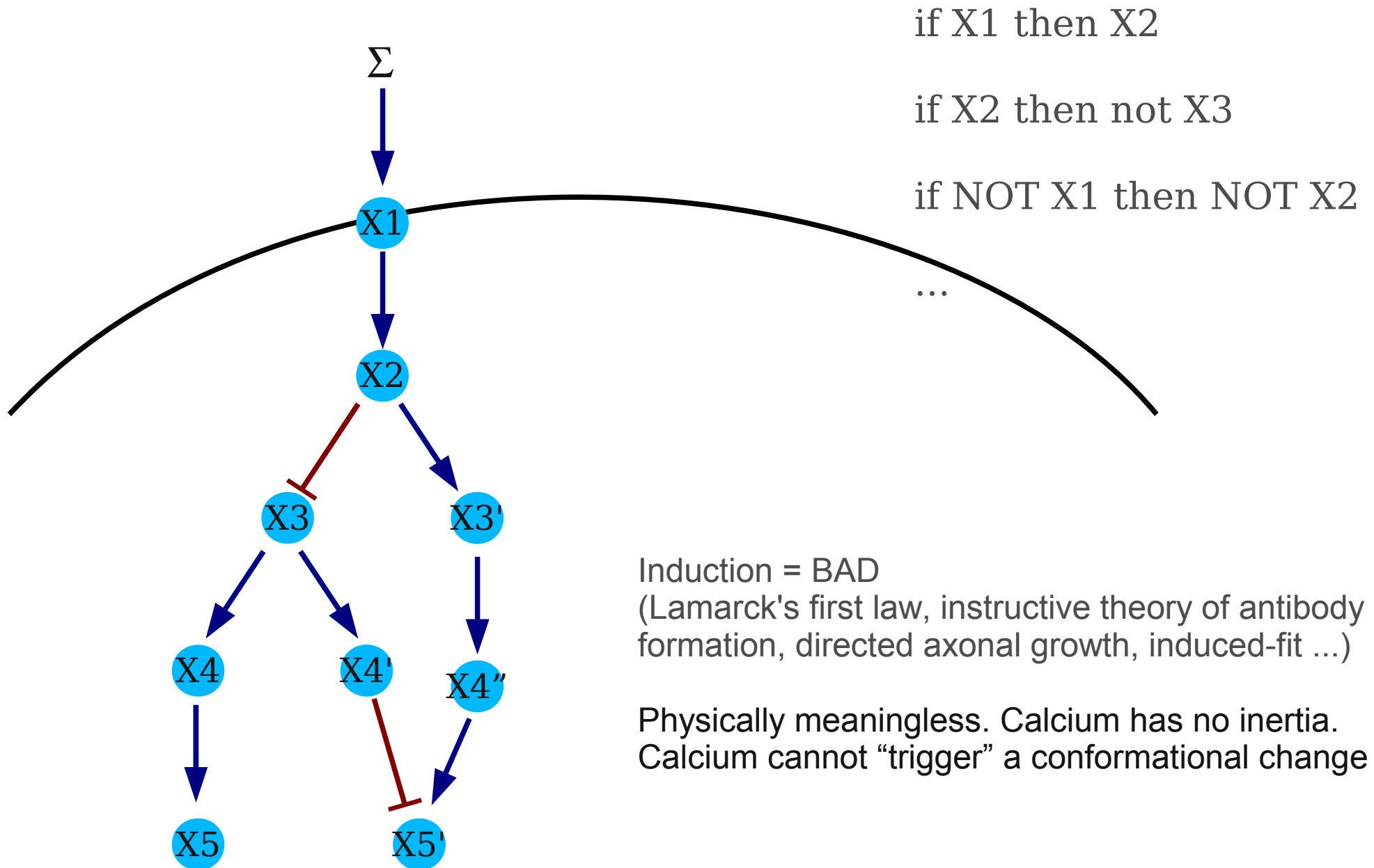
That does not work ...



We knew it would not work

- Calmodulin bound to three calcium activates calcineurin
 - Kincaid and Vaughan (1986). *PNAS*, 83: 1193-1197
- Calmodulin bound to two calcium can bind CaMKII
 - Shifman et al (2006). *PNAS*, 103: 13968-13973
- Calmodulin affinity for calcium increases once bound to CaMKII
 - Shifman et al (2006) [but many previous reports on other targets: e.g. Burger et al (1983). *JBC*, 258: 14733-14739 ; Olwin et (1984). *JBC* 259: 10949-10955]
- Calcium activates both LTP and LTD through calmodulin
 - Lisman (1989) *PNAS*, 86: 9574-9578
 - High $[Ca^{2+}]$ (high freq) $\cong$ CaMKII ; Low $[Ca^{2+}]$ (low freq) $\cong$ Calcineurin

Mistake: signals, activity flow and induction

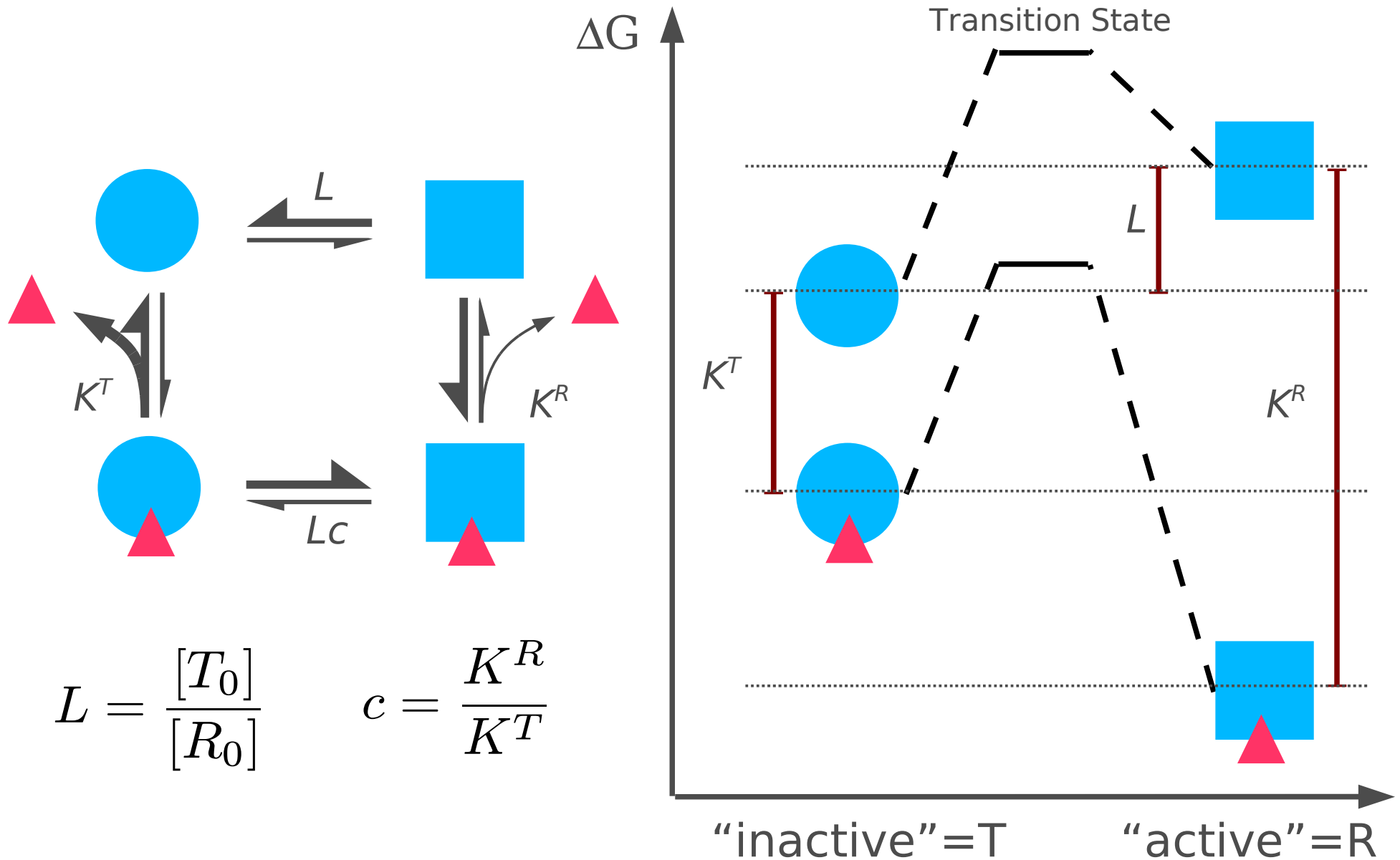


Allostery and state selection

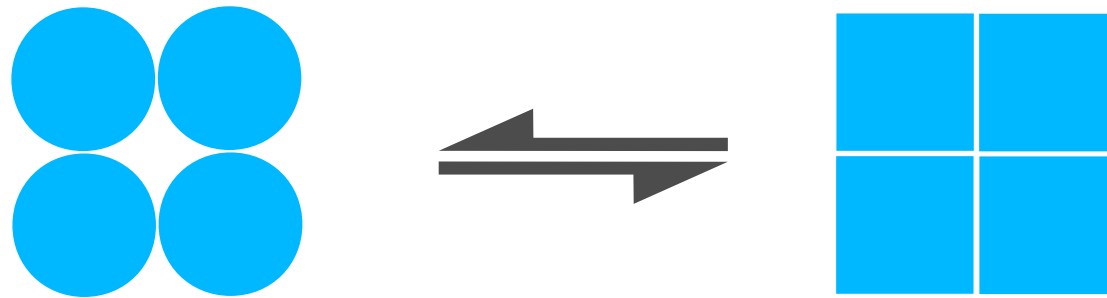
- ➔ Monod, Wyman, Changeux (1965). On the nature of allosteric transitions: a plausible model.
J Mol Biol, 12: 88-118



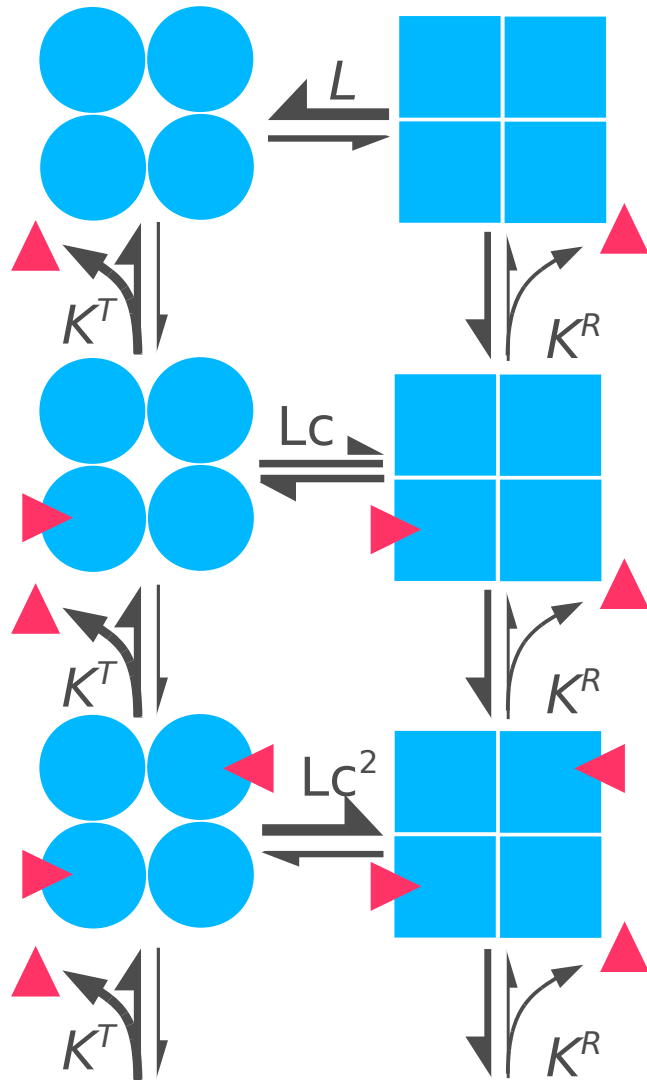
Modulation of thermal equilibria $\neq$ induced-fit



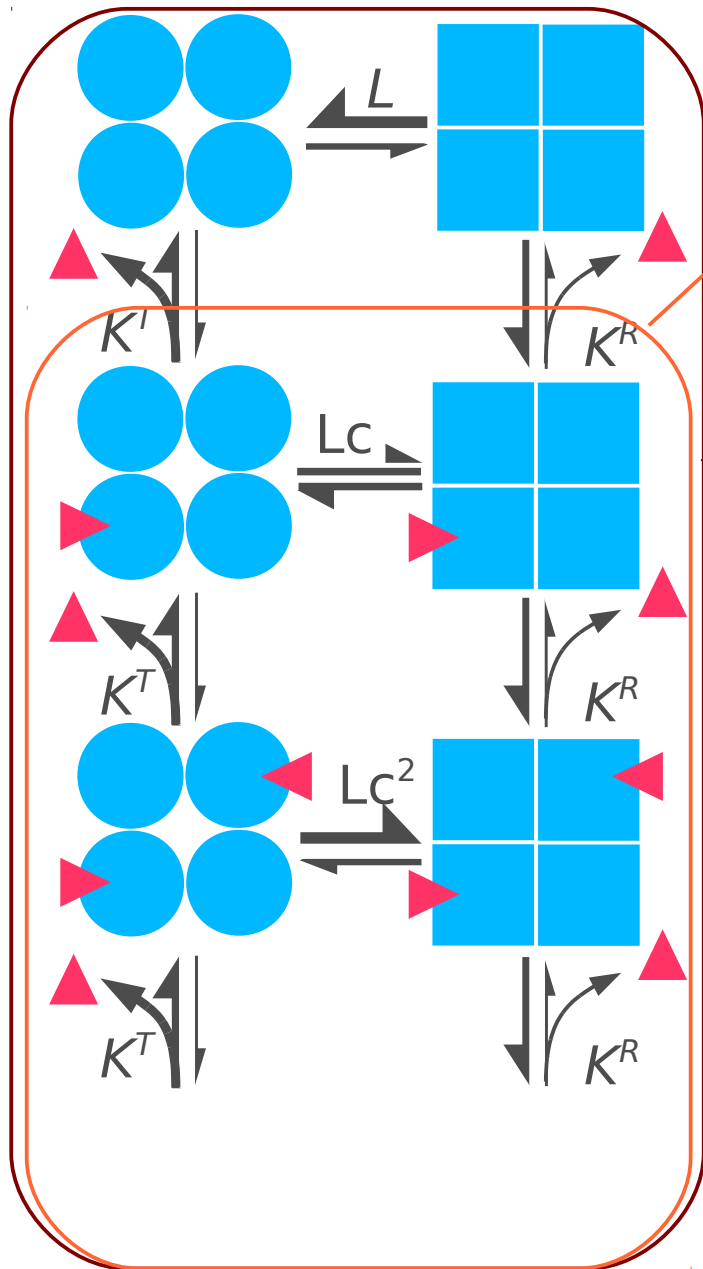
Concerted transitions $\neq$ sequential model



Monod-Wyman-Changeux model

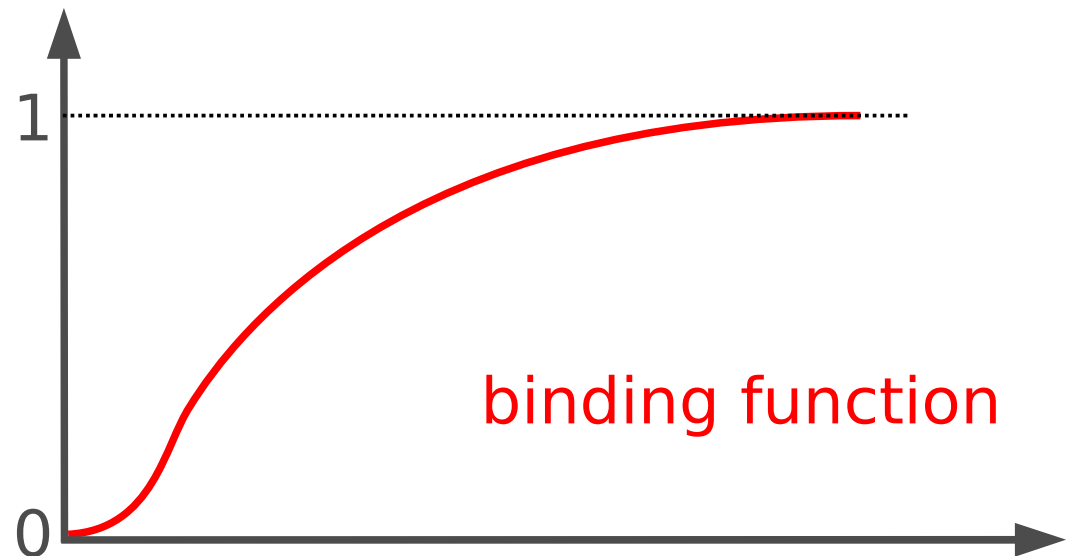


Monod-Wyman-Changeux model

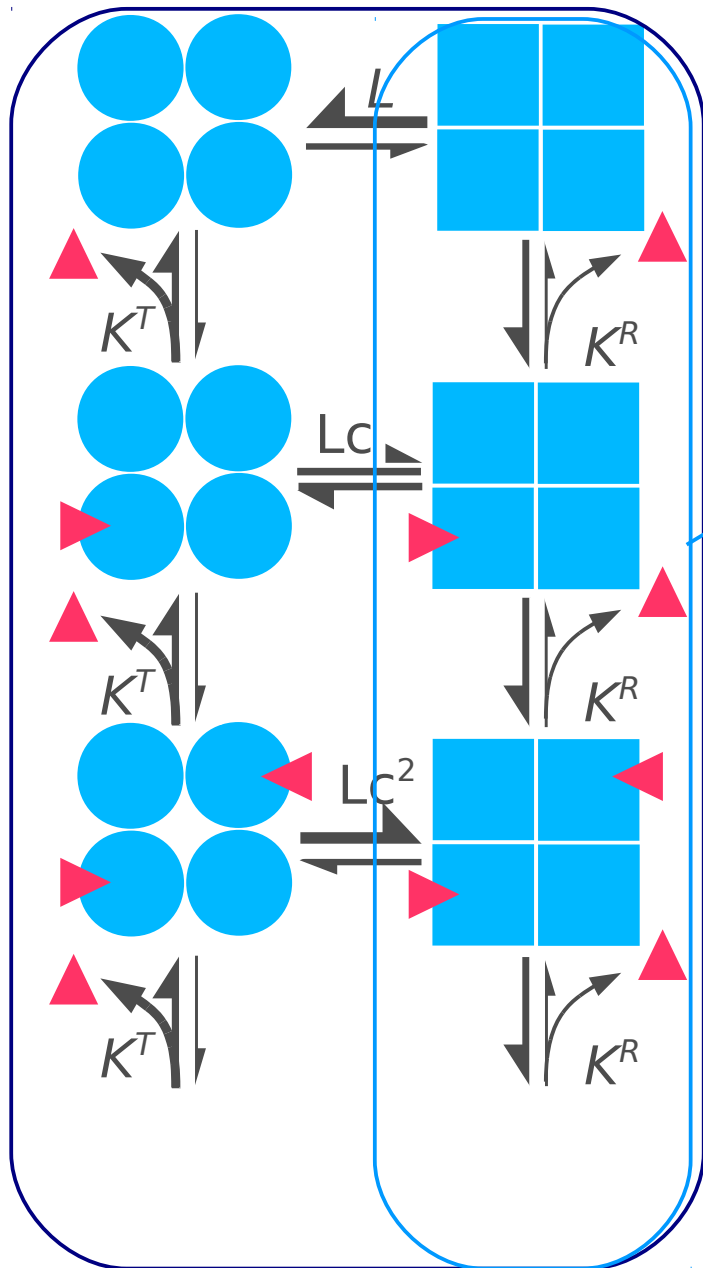


$$\alpha = \frac{[x]}{K^R}$$

$$\bar{Y} = \frac{\alpha(1 + \alpha)^{n-1} + Lc\alpha(1 + c\alpha)^{n-1}}{(1 + \alpha)^n + L(1 + c\alpha)^n}$$



Monod-Wyman-Changeux model



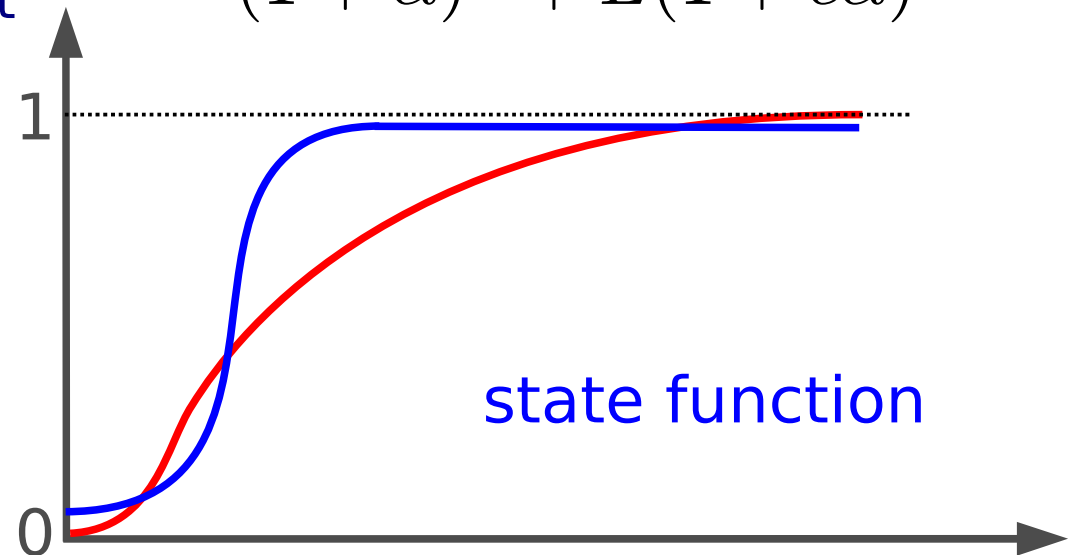
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this

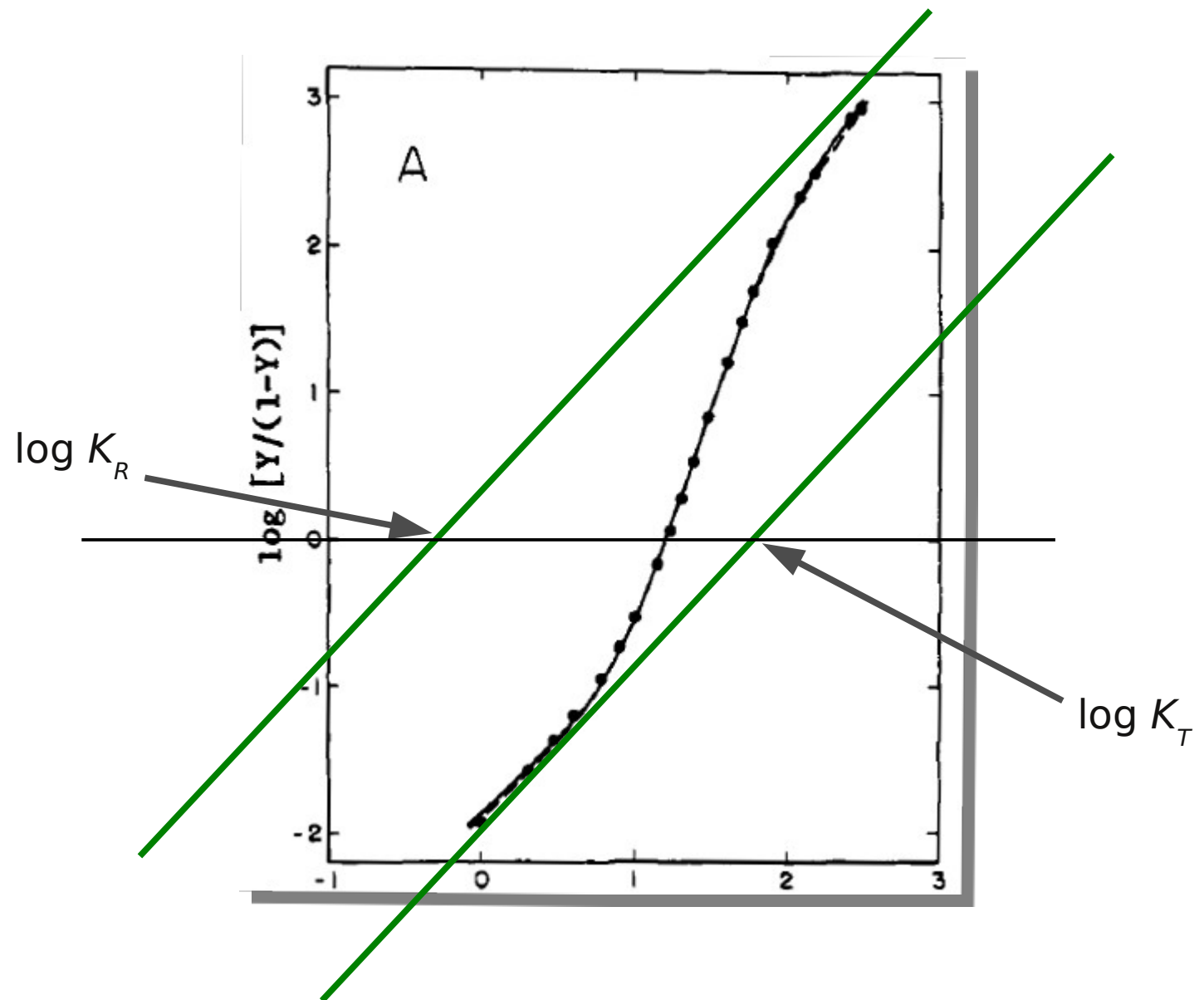
that

$$\bar{R} = \frac{(1 + \alpha)^n}{(1 + \alpha)^n + L(1 + c\alpha)^n}$$

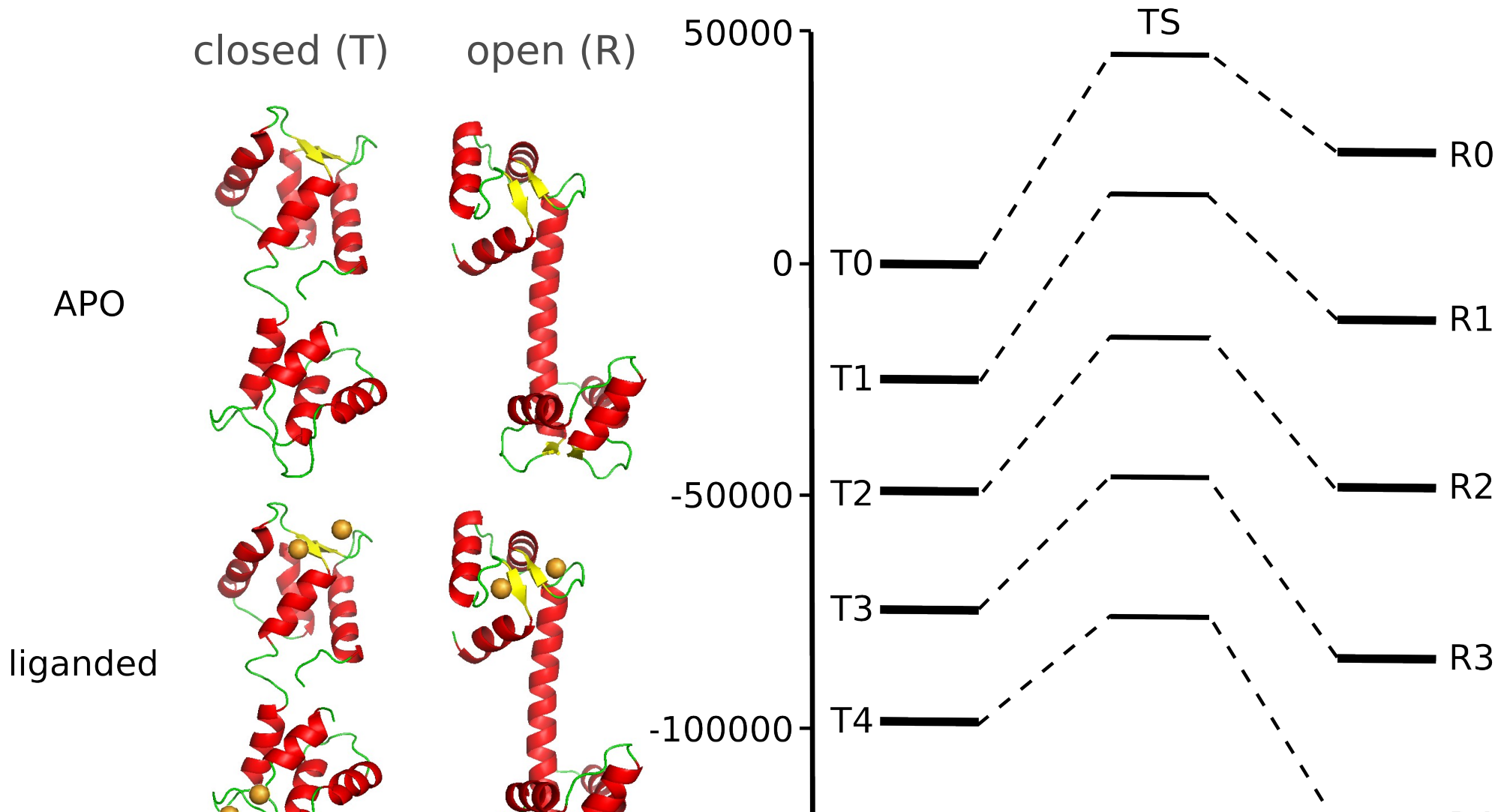


state function

“Hill” Plot for MWC model

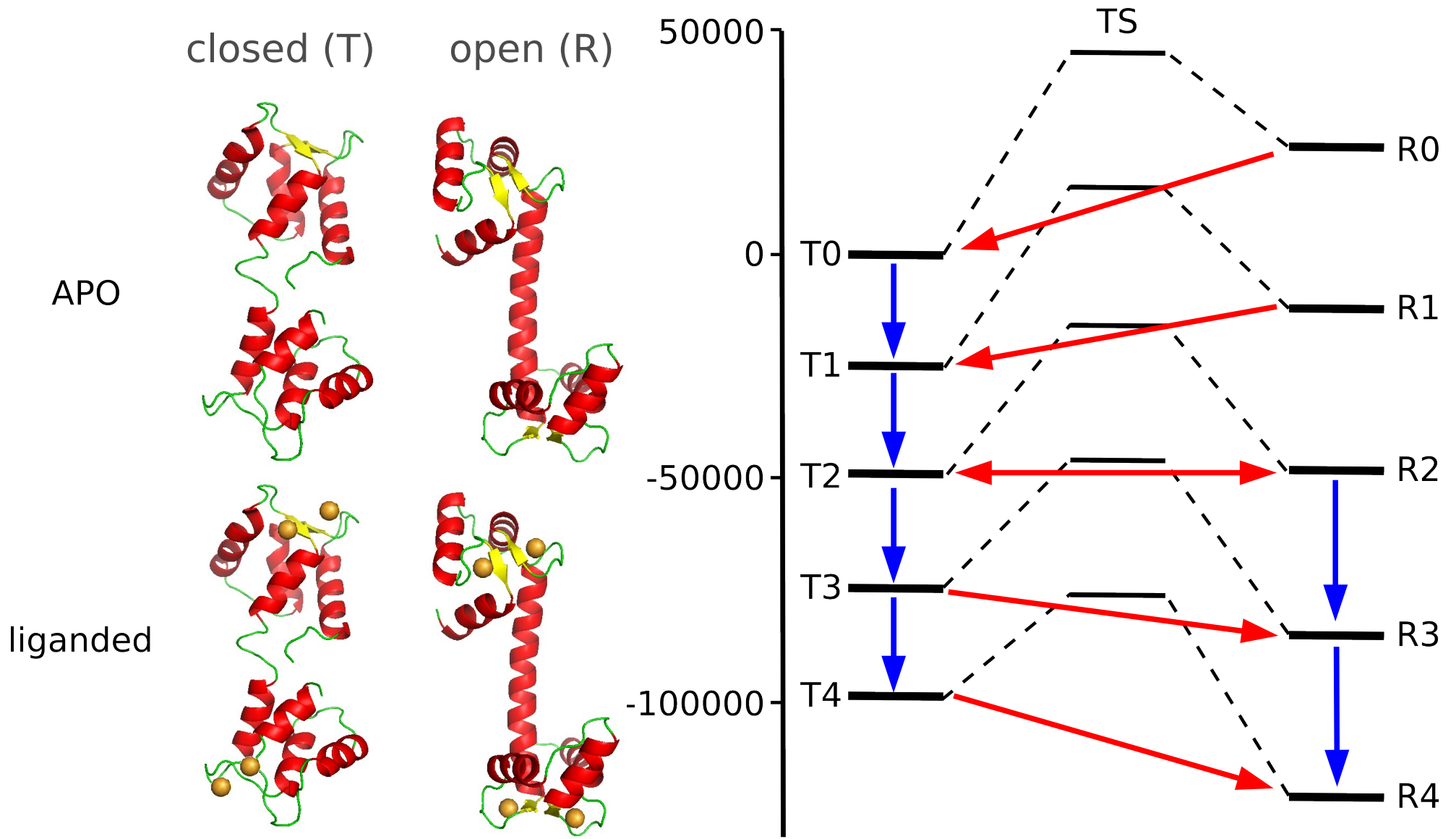


Concerted transition

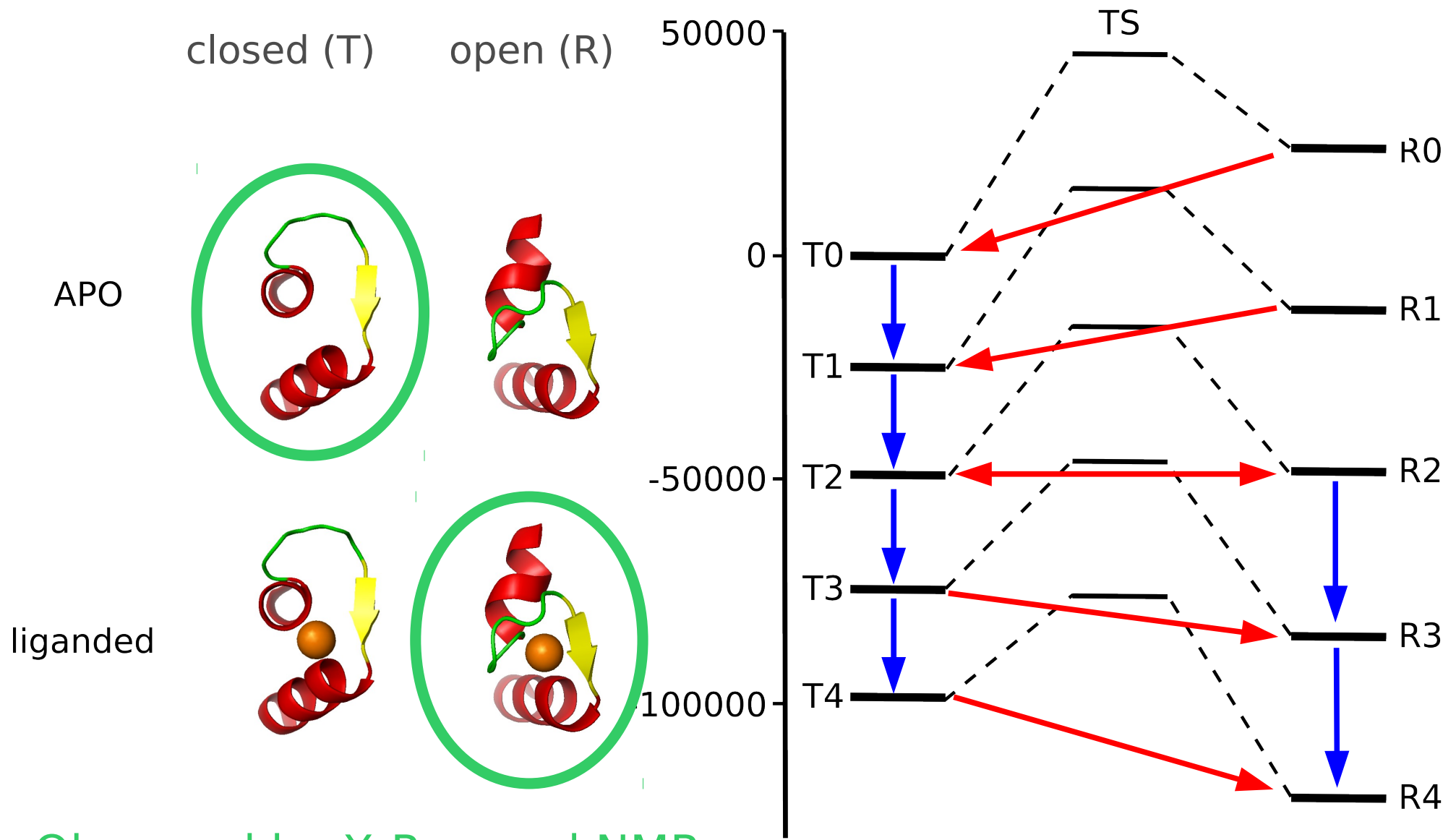


Stefan MI, Edelstein SJ, Le Novère N (2008) An allosteric model of calmodulin explains differential activation of PP2B and CaMKII. *Proc Natl Acad Sci USA*, 105:10768-10773

Concerted transition

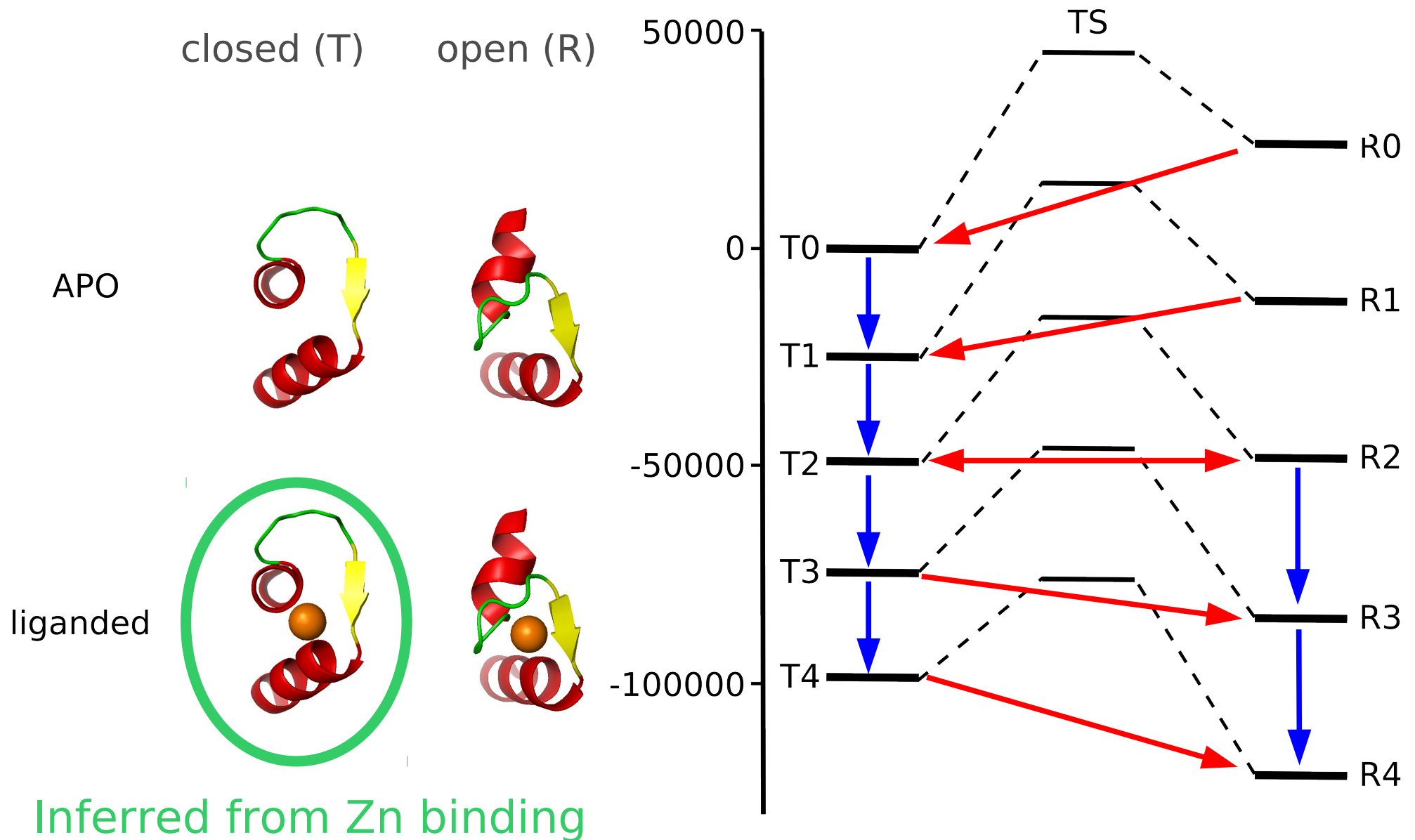


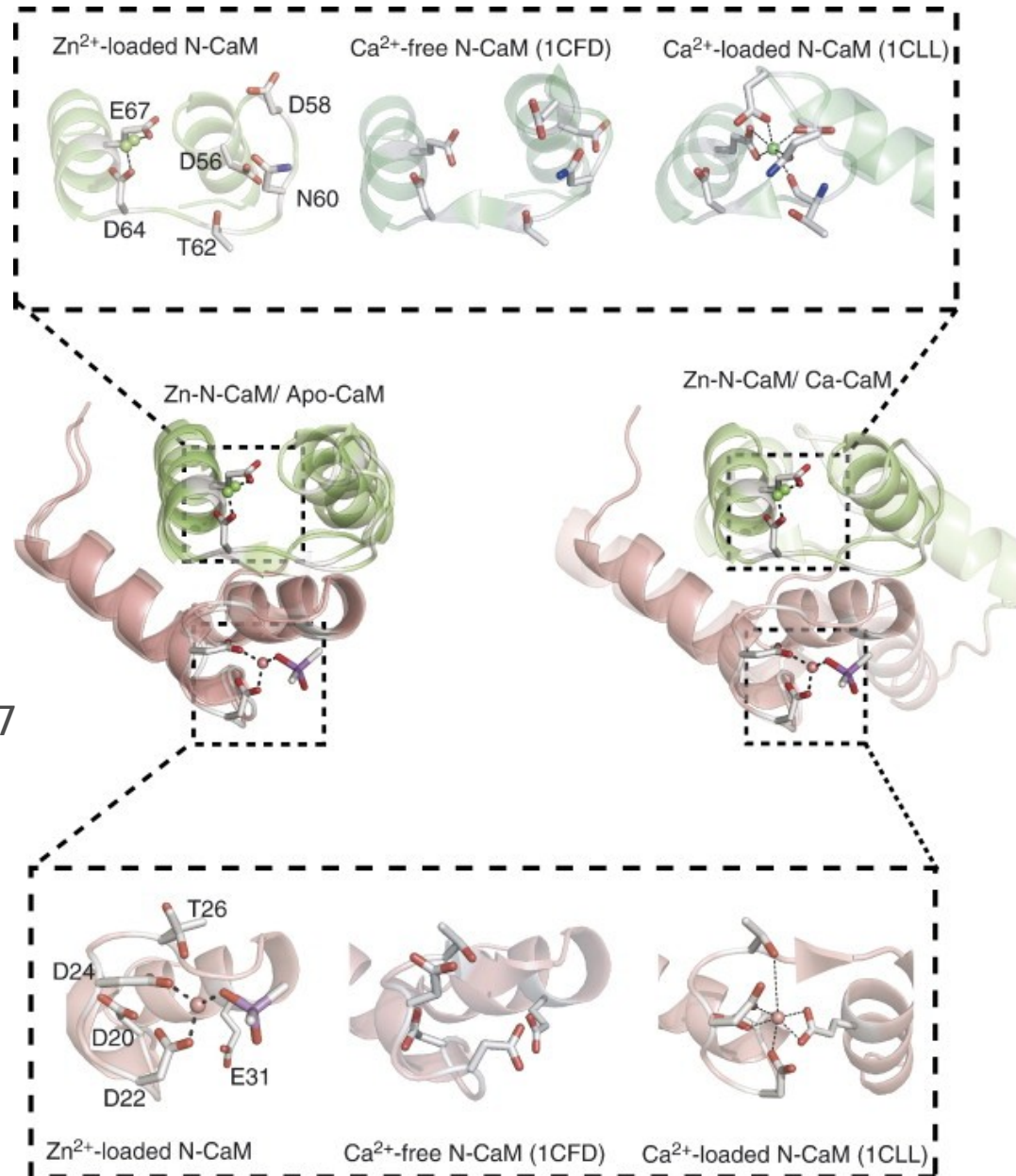
Observation Vs. Prediction



Observed by X-Ray and NMR

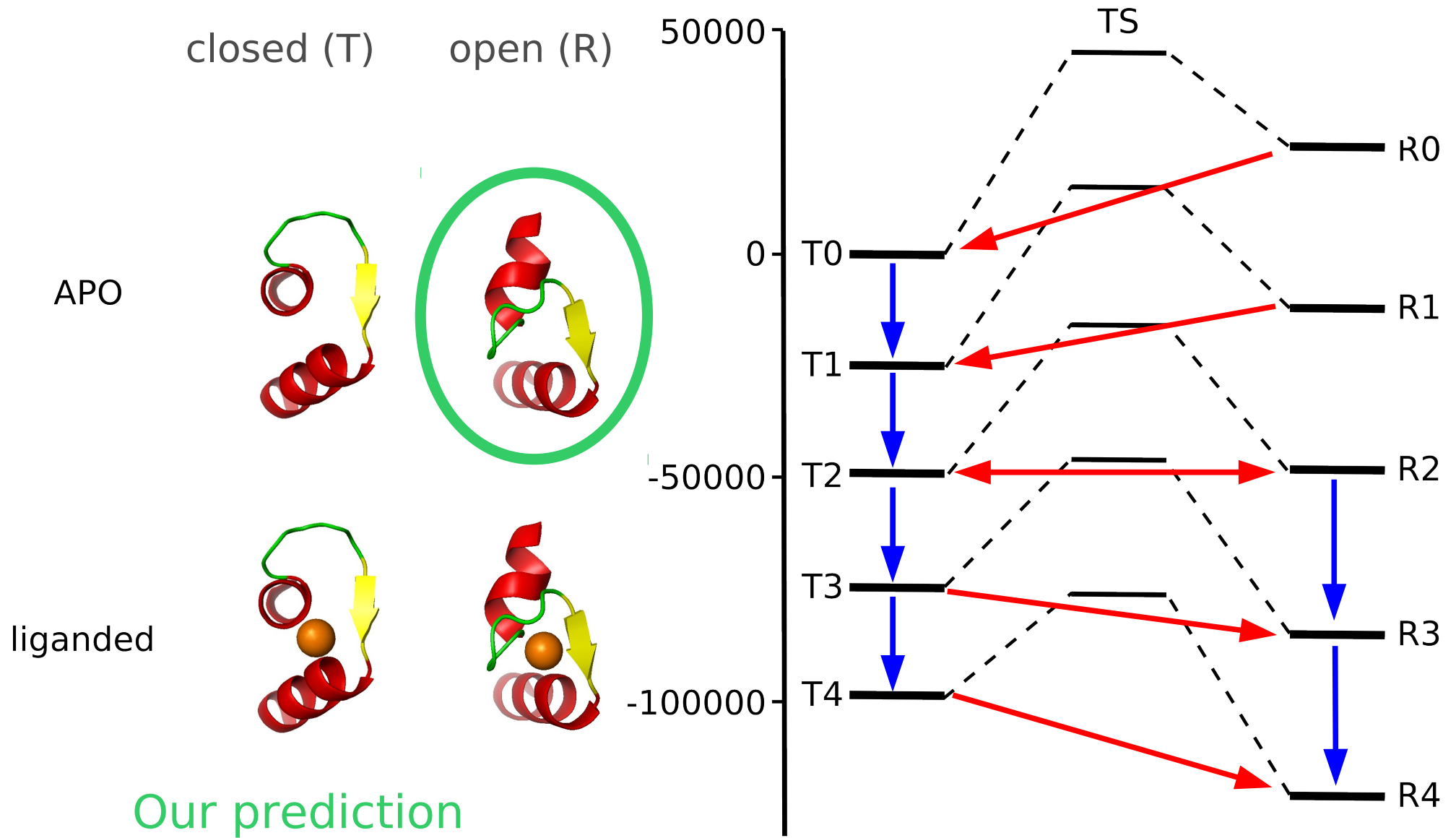
Observation Vs. Prediction





Warren *et al.* (2007).
J Mol Biol 374: 517-527

Observation Vs. Prediction



Extended MWC model necessary for Calmodulin

Based on Rubin and Changeux
(1966) *J Mol Biol*, 21: 265-274

$$\bar{Y} = \frac{\alpha(1 + \alpha)^{n-1} + L \left(\frac{1 + d\beta}{1 + \beta} \frac{1 + e\gamma}{1 + \gamma} \right)^n c\alpha(1 + c\alpha)^{n-1}}{(1 + \alpha)^n + L \left(\frac{1 + d\beta}{1 + \beta} \frac{1 + e\gamma}{1 + \gamma} \right)^n (1 + c\alpha)^n}$$

Extended MWC model necessary for Calmodulin

$$\bar{Y} = \frac{\frac{1}{n} \sum_i \left(\alpha_i \prod_{j \neq i} (1 + \alpha_j) \right) + L \prod_k \left(\frac{1 + e_k \gamma_k}{1 + \gamma_k} \right) \sum_i \left(c_i \alpha_i \prod_{j \neq i} (1 + c_j \alpha_j) \right)}{\prod_i (1 + \alpha_i) + L \prod_k \left(\frac{1 + e_k \gamma_k}{1 + \gamma_k} \right) \prod_i (1 + c_i \alpha_i)}$$

Any number of different sites per protomer.
Several protomers can be carried by one subunit

- $\alpha_i = [\text{ligand}] / K_{i,\text{lig}}^R$
- $\gamma_k = [\text{modulator}] / K_{k,\text{mod}}^R$
- $c_i = K_{i,\text{lig}}^R / K_{i,\text{lig}}^T$
- $e_k = K_{k,\text{mod}}^R / K_{k,\text{mod}}^T$

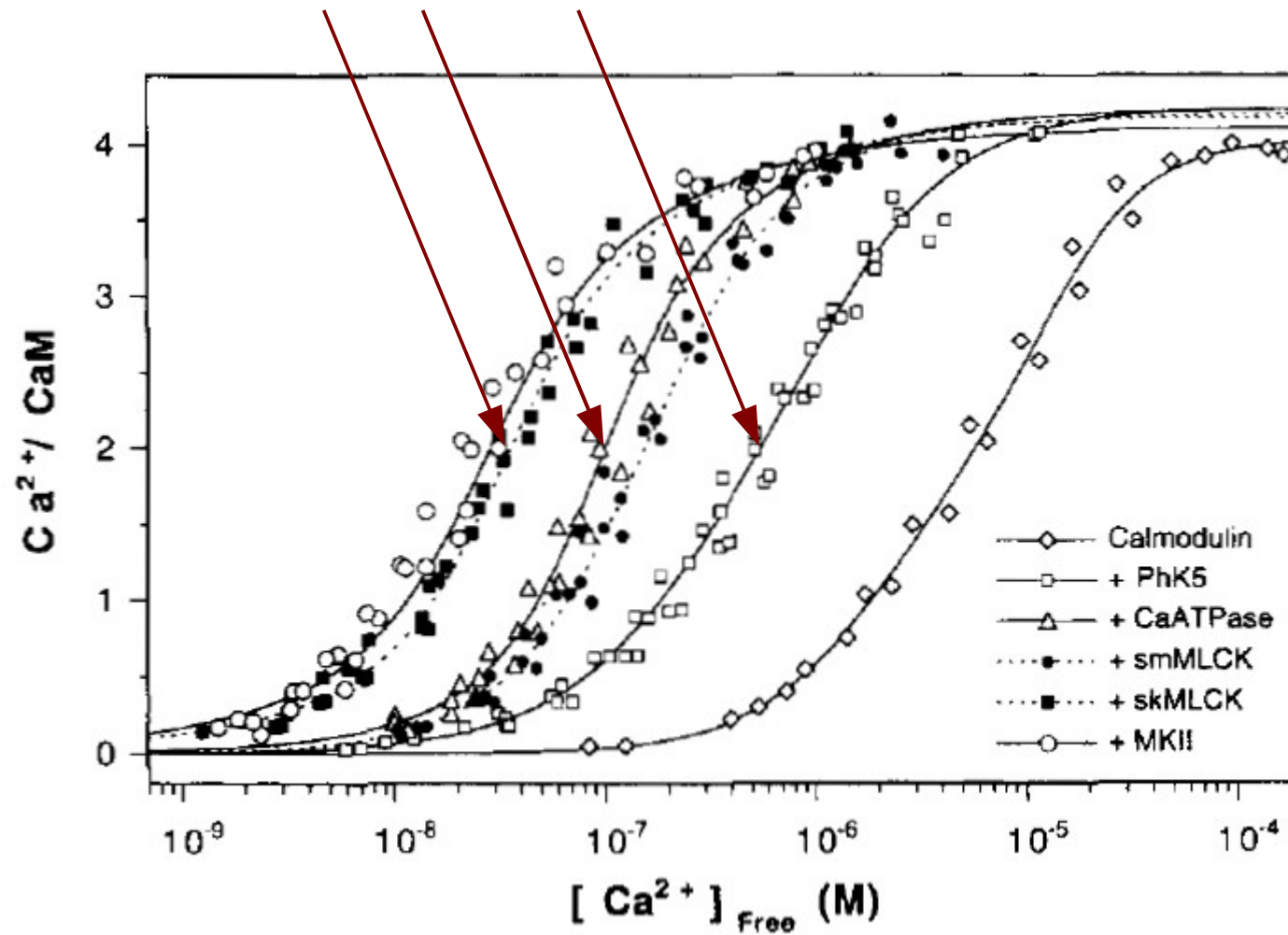
Stefan M.I., Edelstein S.J., Le Novère N.
Computing phenomenologic Adair-Klotz constants from microscopic MWC parameters.
BMC Systems Biology (2009), 3: 68

Simplification of the model for finding L and c

- Hypothesis for the whole model: free energy of conformational transition is evenly distributed: c is unique
- Additional simplification to determine L : affinities are identical

$$\bar{Y} = \frac{\alpha(1 + \alpha)^3 + L\left(\frac{1 + \gamma e}{1 + \gamma}\right)c\alpha(1 + c\alpha)^3}{(1 + \alpha)^4 + L\left(\frac{1 + \gamma e}{1 + \gamma}\right)(1 + c\alpha)^4}$$

Targets as allosteric effectors



Peersen et al. (1997) *Prot Sci*, 6: 794-807

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- Model constraints for the determination of c and L
 - Ca binding in presence of target: none, skMLCK, PhK5, CaATPase (Peersen et al (1997) Prot Sci 6: 794-807). Concentration at 50% saturation.
 - 100 000 parameter sets plus least-square
 - 13 identical minima. e for skMLCK is 10^{-15} , which can be taken as skMLCK binding only to R state.

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$L=20670$
 $c=3.96.10^{-3}$

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Relaxation of the model for finding *K_i*

- Determination of individual affinities:

$$\bar{Y} = 0.25 \frac{\sum_i \left(\alpha_i \prod_j (1 + \alpha_j) \right) + L \sum_i \left(c \alpha_i \prod_j (1 + c \alpha_j) \right)}{\prod_i (1 + \alpha_i) + L \prod_i (1 + c \alpha_i)}$$

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- Determination of individual affinities:

$$\bar{Y} = 0.25 \frac{\sum_i \left(\alpha_i \prod_j (1 + \alpha_j) \right) + L \sum_i \left(c \alpha_i \prod_j (1 + c \alpha_j) \right)}{\prod_i (1 + \alpha_i) + L \prod_i (1 + c \alpha_i)}$$

- Model constraints for calcium dissociation constants
 - Complete CaM (Bayley et al (1996) *Prot Sci* 5: 1215-1228)
 - N and C term Mutants (Shifman et al (2006) *PNAS*, 103: 13968-13973)
 - R-only – skMLCK (Peersen et al (1997) *Prot Sci* 6: 794-807)
 - Concentration at 25% and 50% saturation.
 - Systematic logarithmic sampling of the affinity space (coarse-grained, 50 values per affinity, then refined 66 values per affinity) = 25 millions parameter sets

Relaxation of the model for finding K_i

- Determination of individual affinities:

$$\bar{Y} = 0.25 \frac{\sum_i \left(\alpha_i \prod_j (1 + \alpha_j) \right) + L \sum_i \left(c \alpha_i \prod_j (1 + c \alpha_j) \right)}{\prod_i (1 + \alpha_i) + L \prod_i (1 + c \alpha_i)}$$

$$K_A^R = 8.32 \cdot 10^{-6}$$

$$K_B^R = 1.66 \cdot 10^{-8}$$

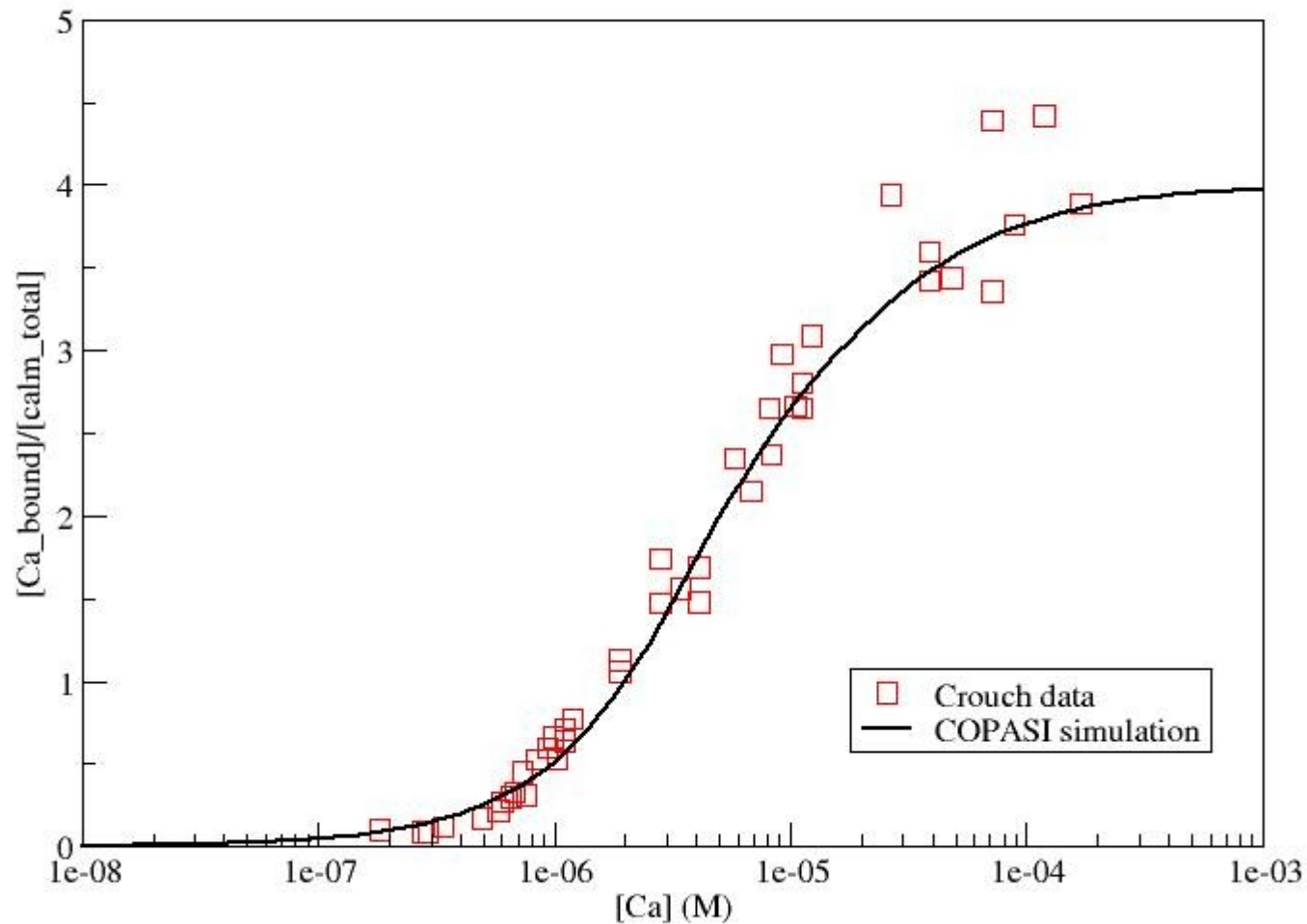
$$K_C^R = 1.74 \cdot 10^{-5}$$

$$K_D^R = 1.45 \cdot 10^{-8}$$

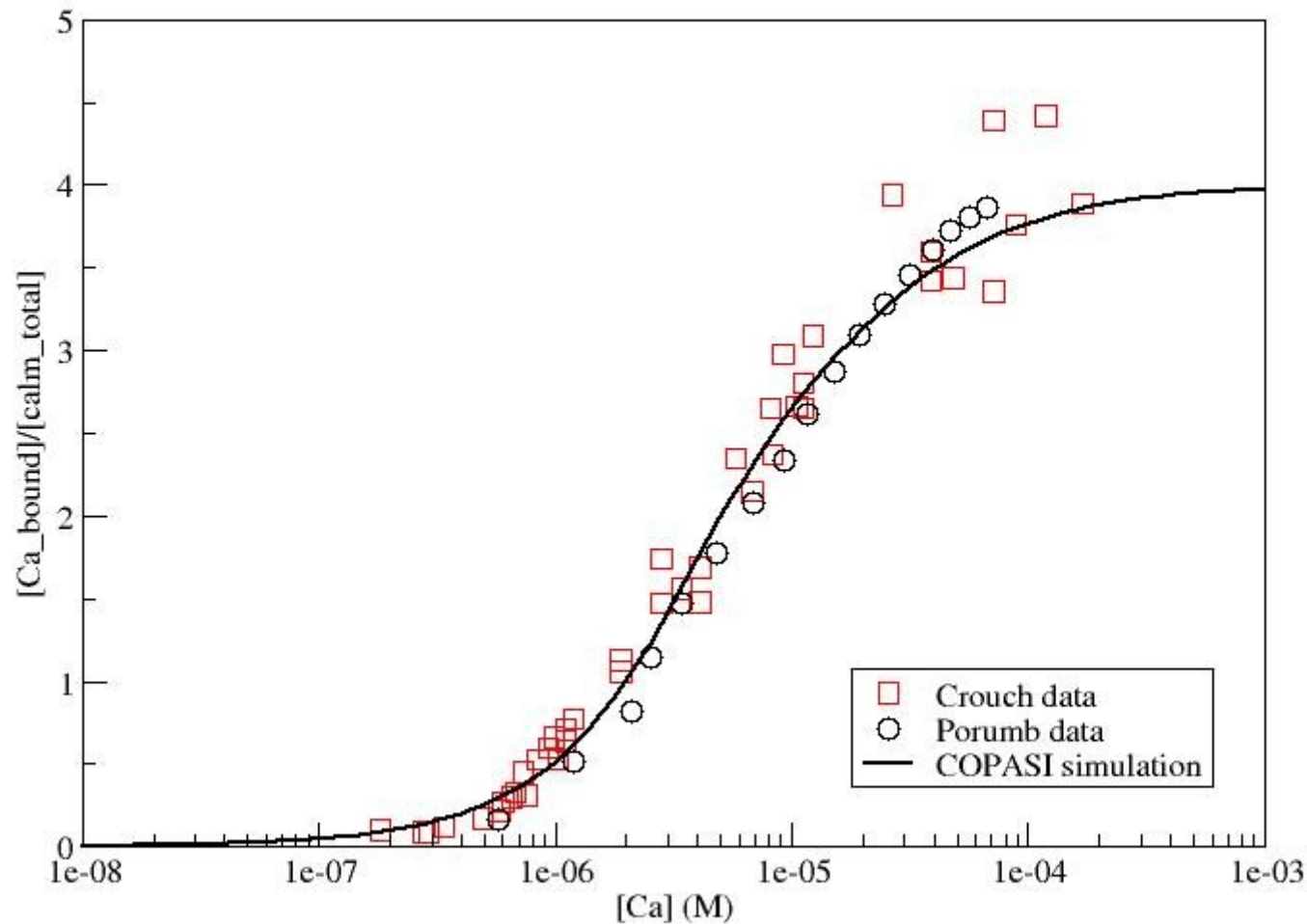
- Model constraints for calcium dissociation constants

- Complete CaM (Bayley et al (1996) *Prot Sci* 5: 1215-1228)
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- R-only – skMLCK (Peersen et al (1997) *Prot Sci* 6: 794-807)
- Concentration at 25% and 50% saturation.
- Systematic logarithmic sampling of the affinity space (coarse-grained, 50 values per affinity, then refined 66 values per affinity) = 25 millions parameter sets

Comparison with experiments



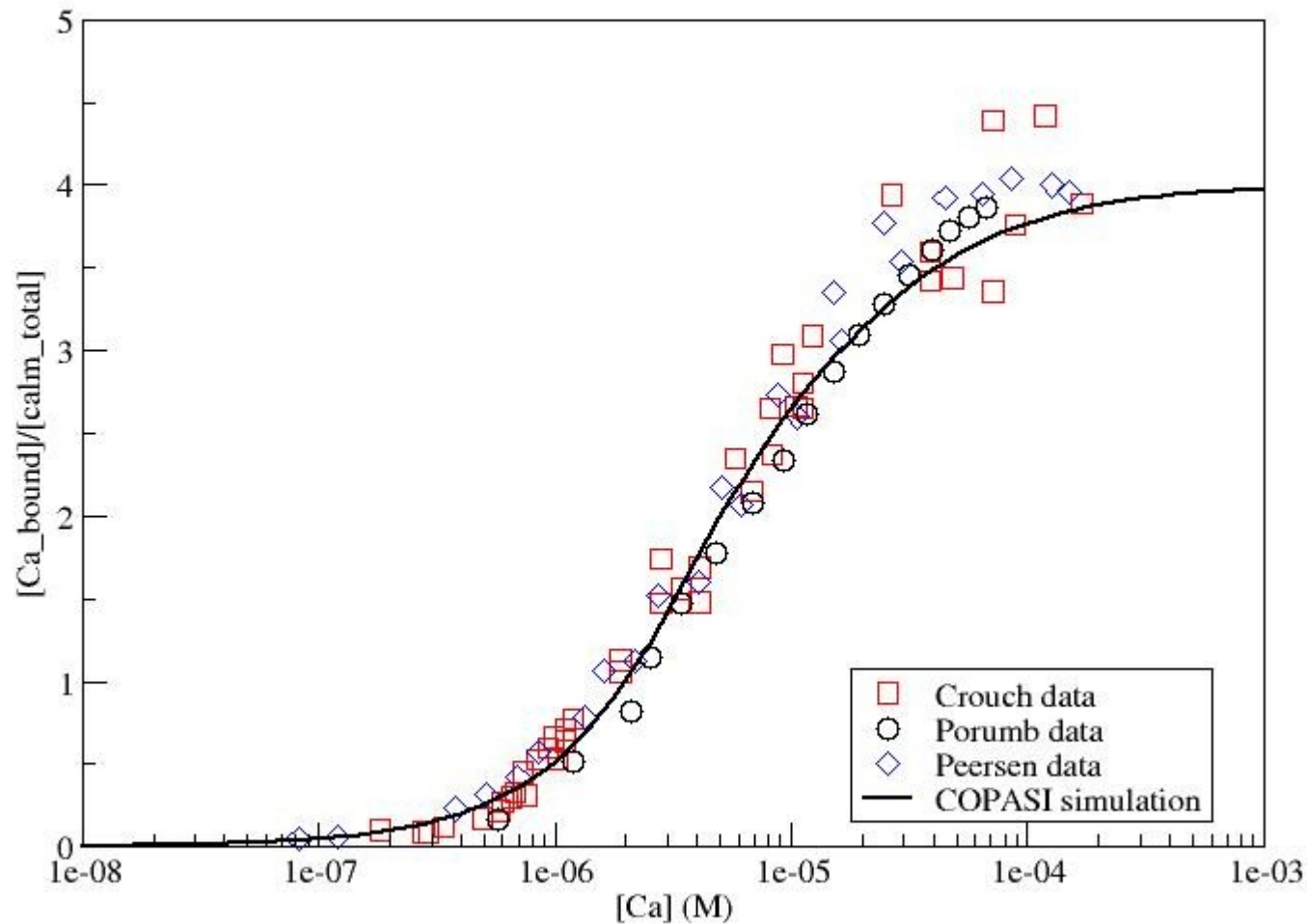
Comparison with experiments



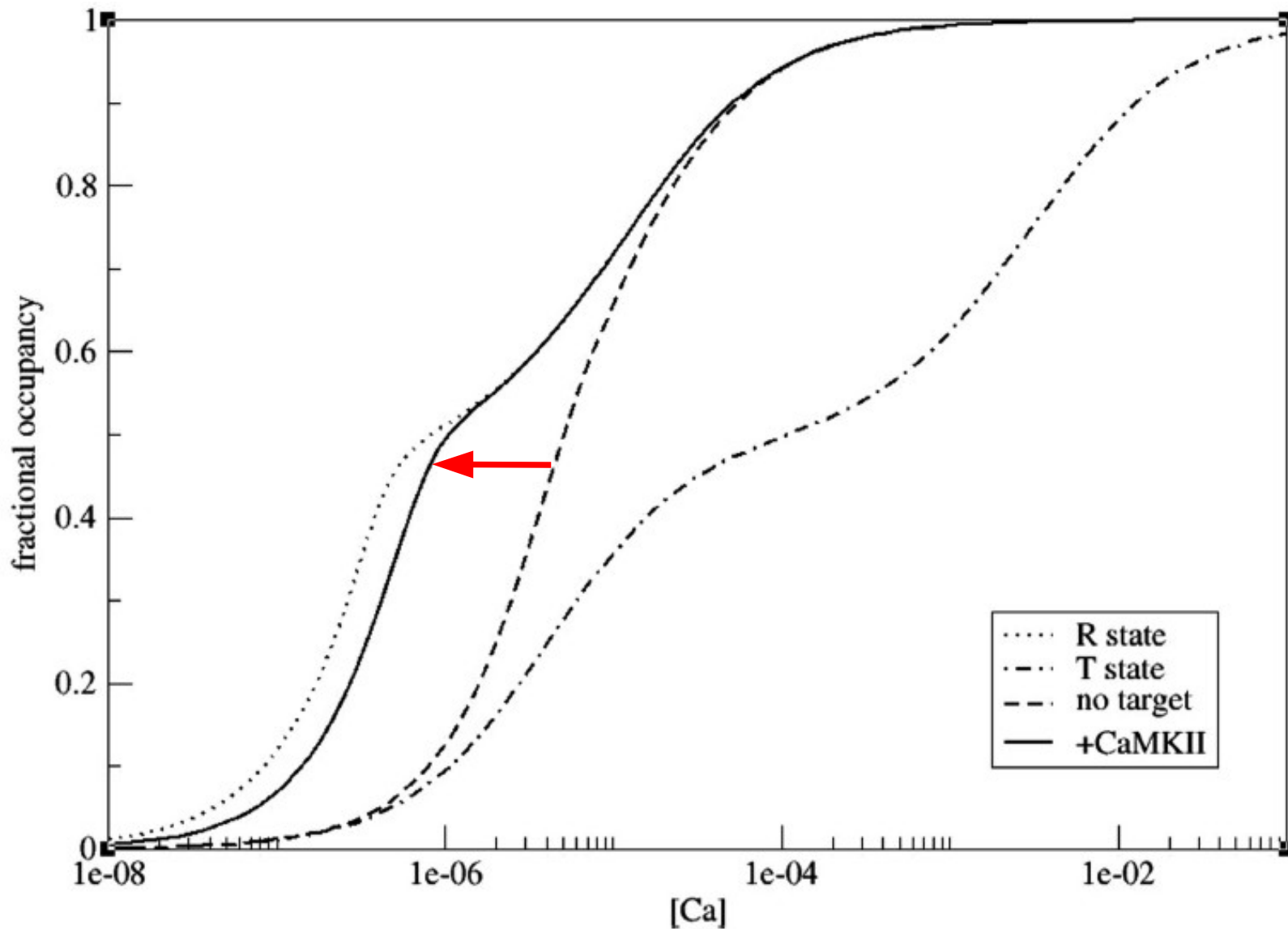
Porumb et al (1994) Anal Biochem 220: 227-237

Synapse Symposium, 1-3 July 2010

Comparison with experiments



Binding to target increases the affinity for Ca^{2+}



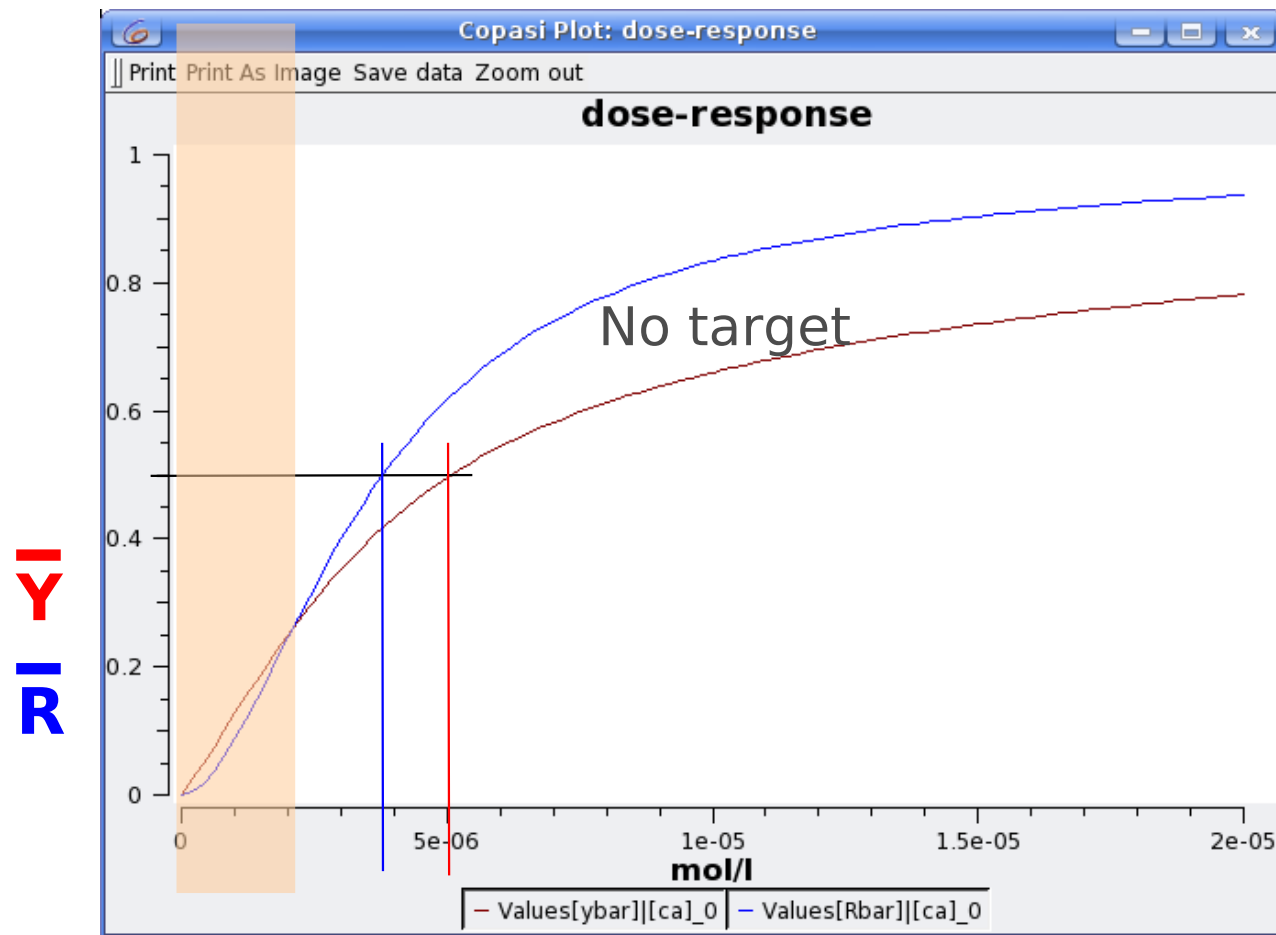
Activity of unsaturated calmodulin

- Fractional activity depends on the number of calcium ions bound. E.g.:

$$\frac{R_2}{T_2} = \frac{1}{L \cdot c^2}$$

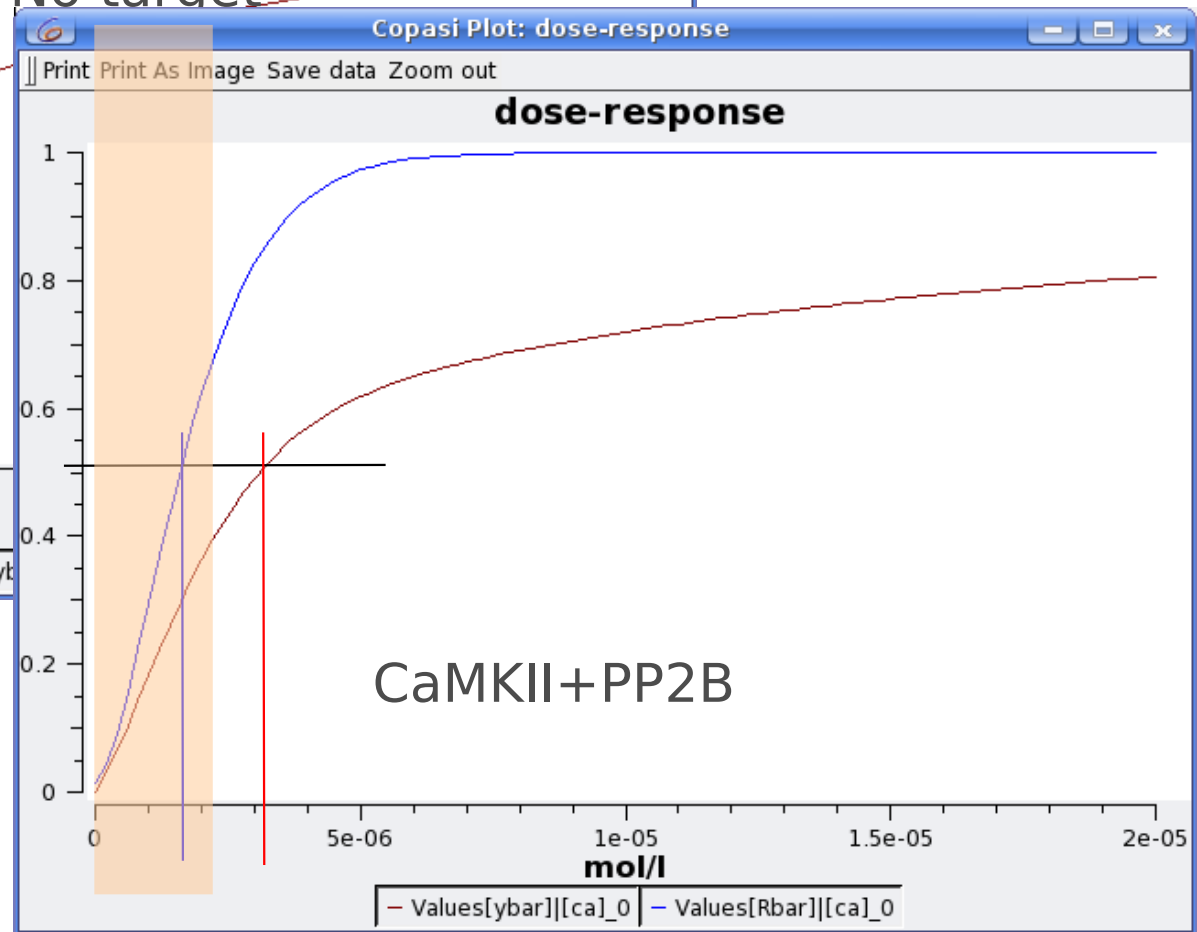
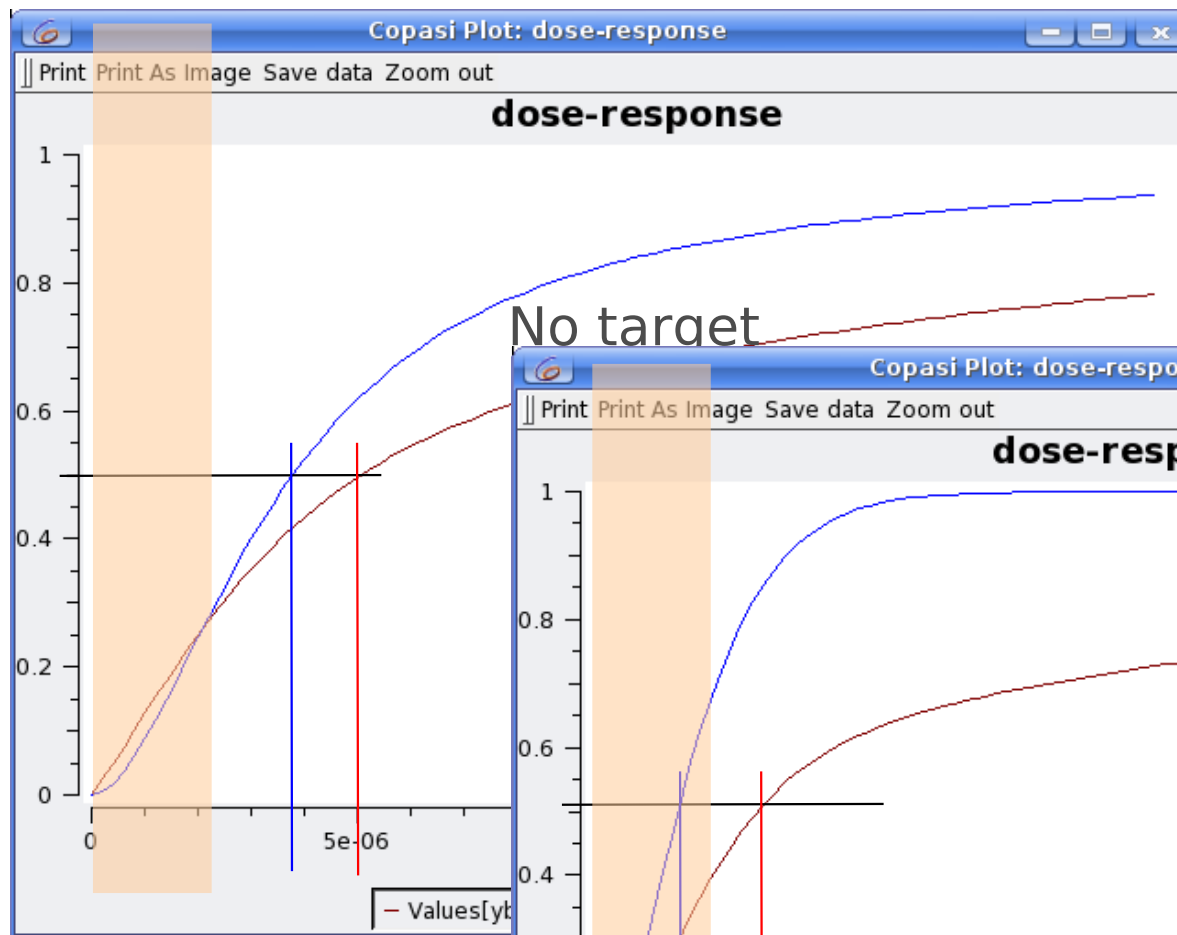
- $R_0/T_0 = 1/20000$ (1/L)
- $R_1/T_1 = 1/170$
- $R_2/T_2 = 0.69$ → half-saturation = equi-probability
- $R_3/T_3 = 80$
- $R_4/T_4 = 10000$

But ... efficacy of a calcium spike?

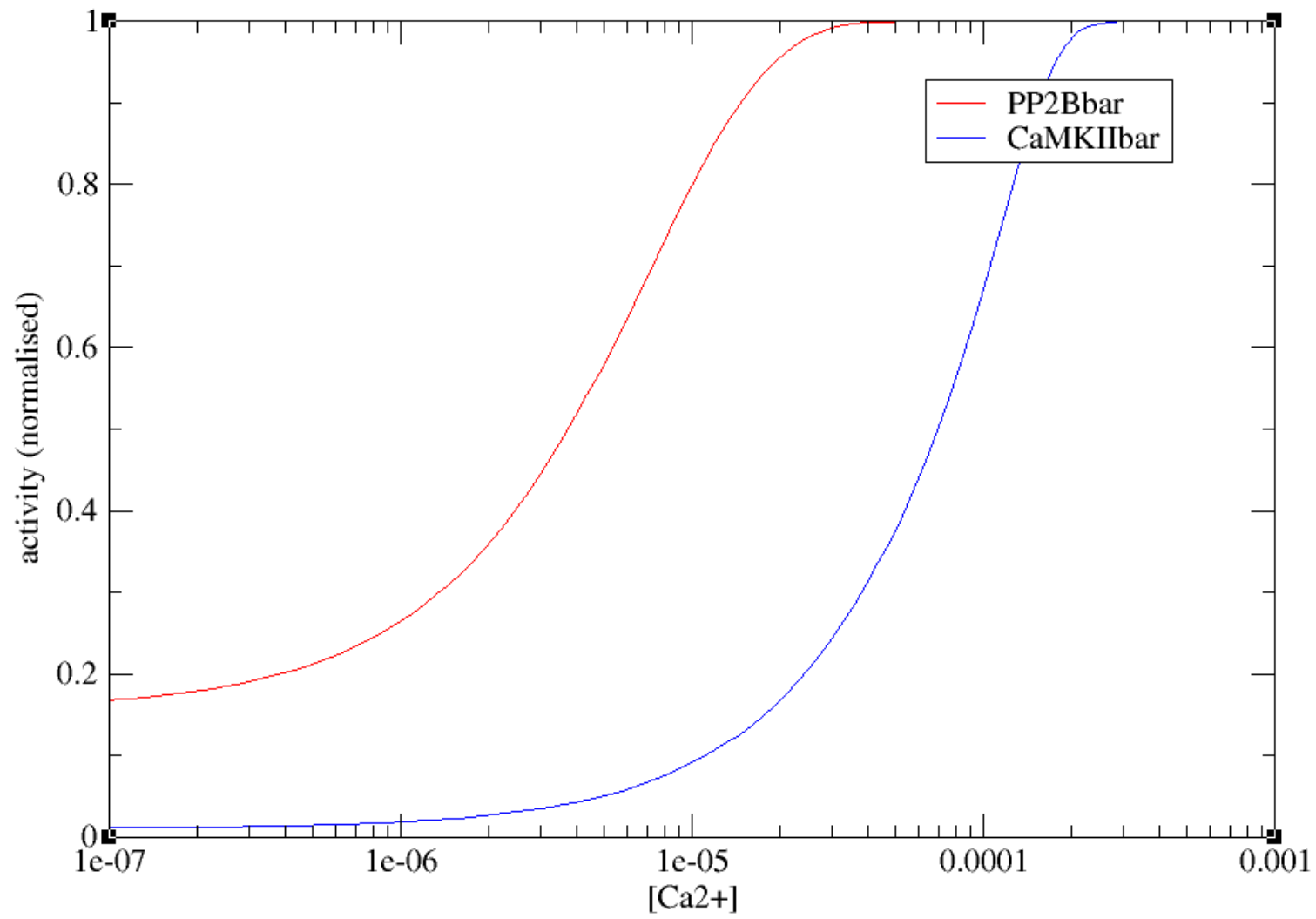


This is Systems Biology!

Y
I
R

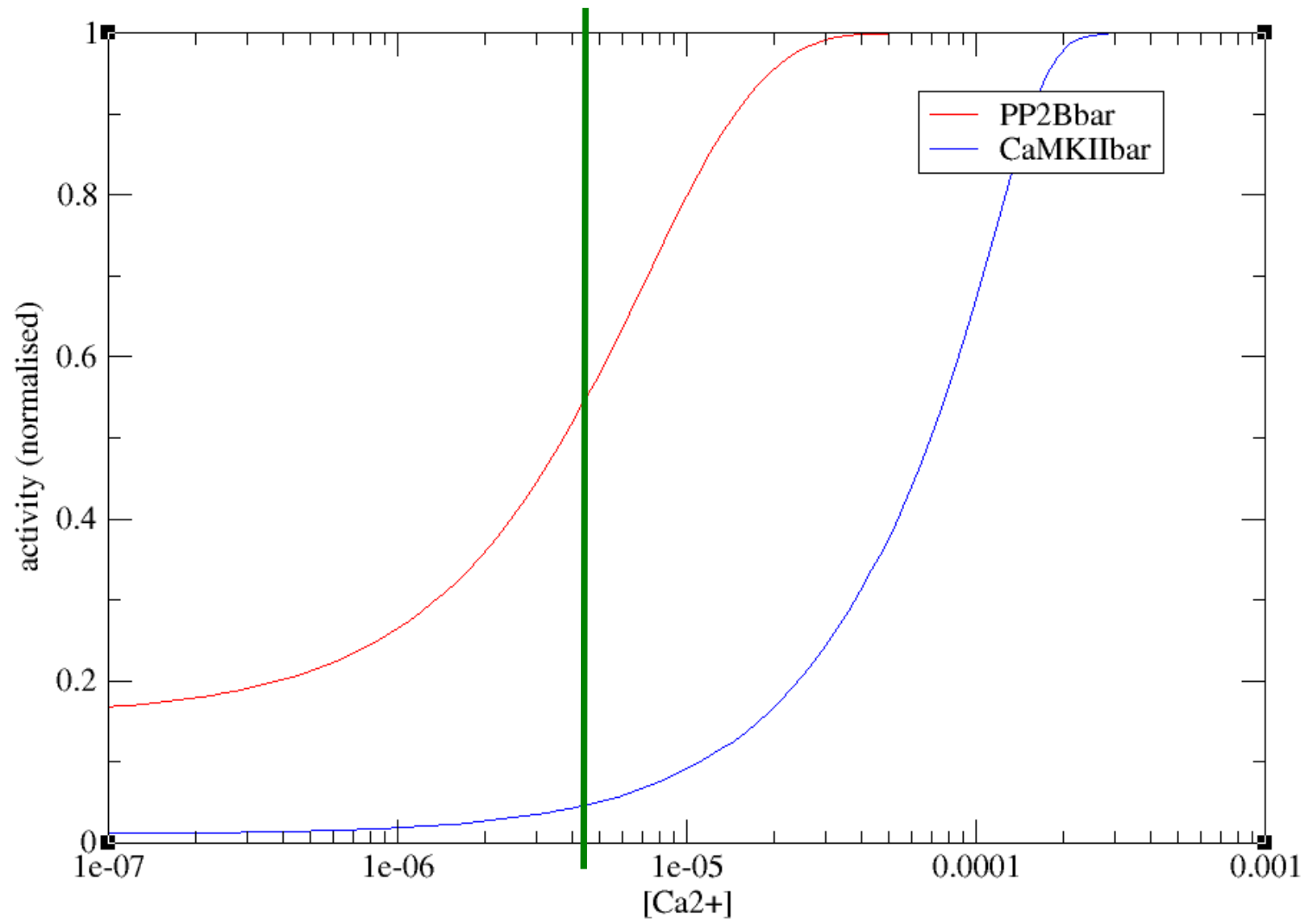


Bidirectional synaptic plasticity

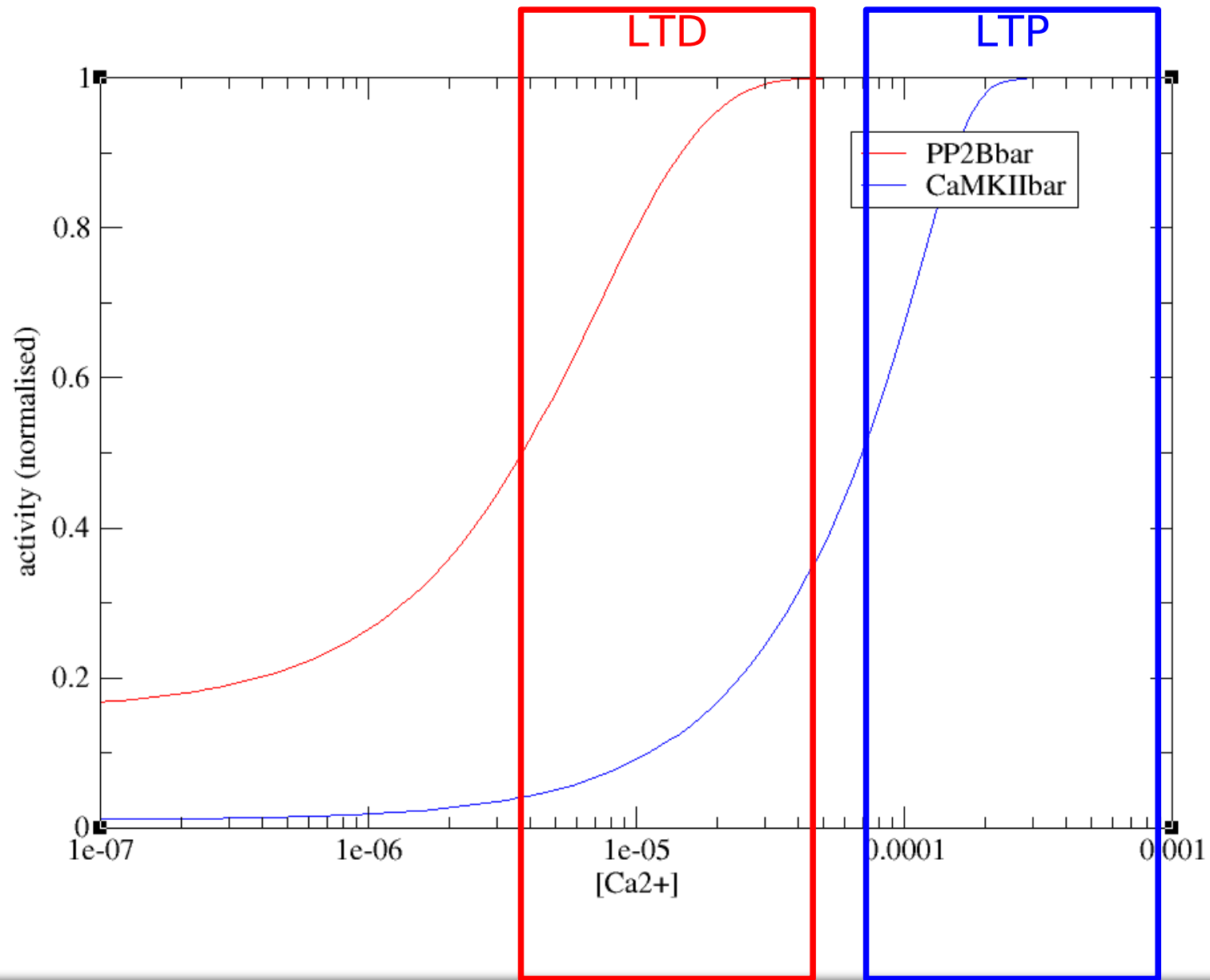


Bidirectional synaptic plasticity

half saturation of calmodulin

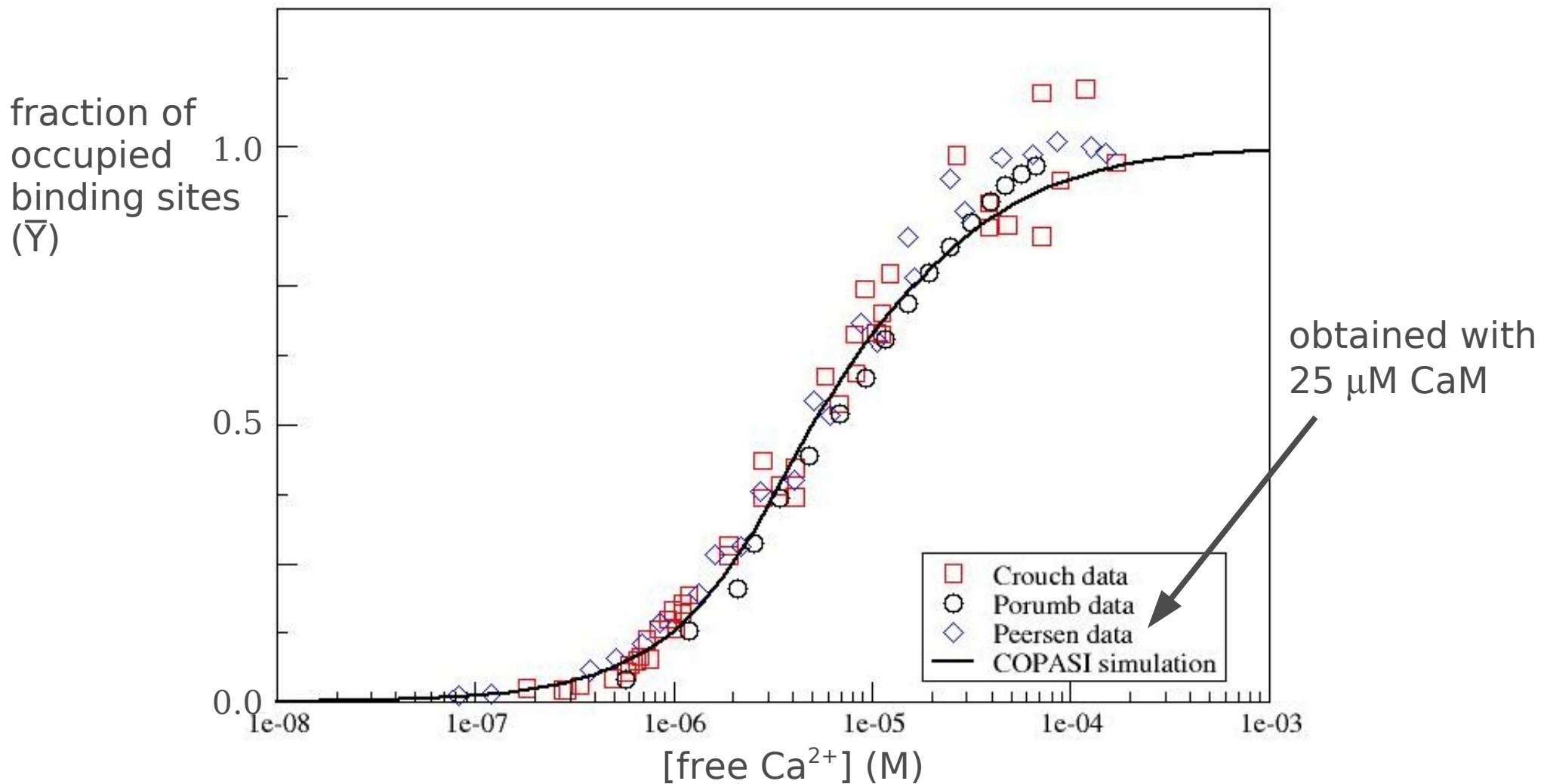


Bidirectional synaptic plasticity



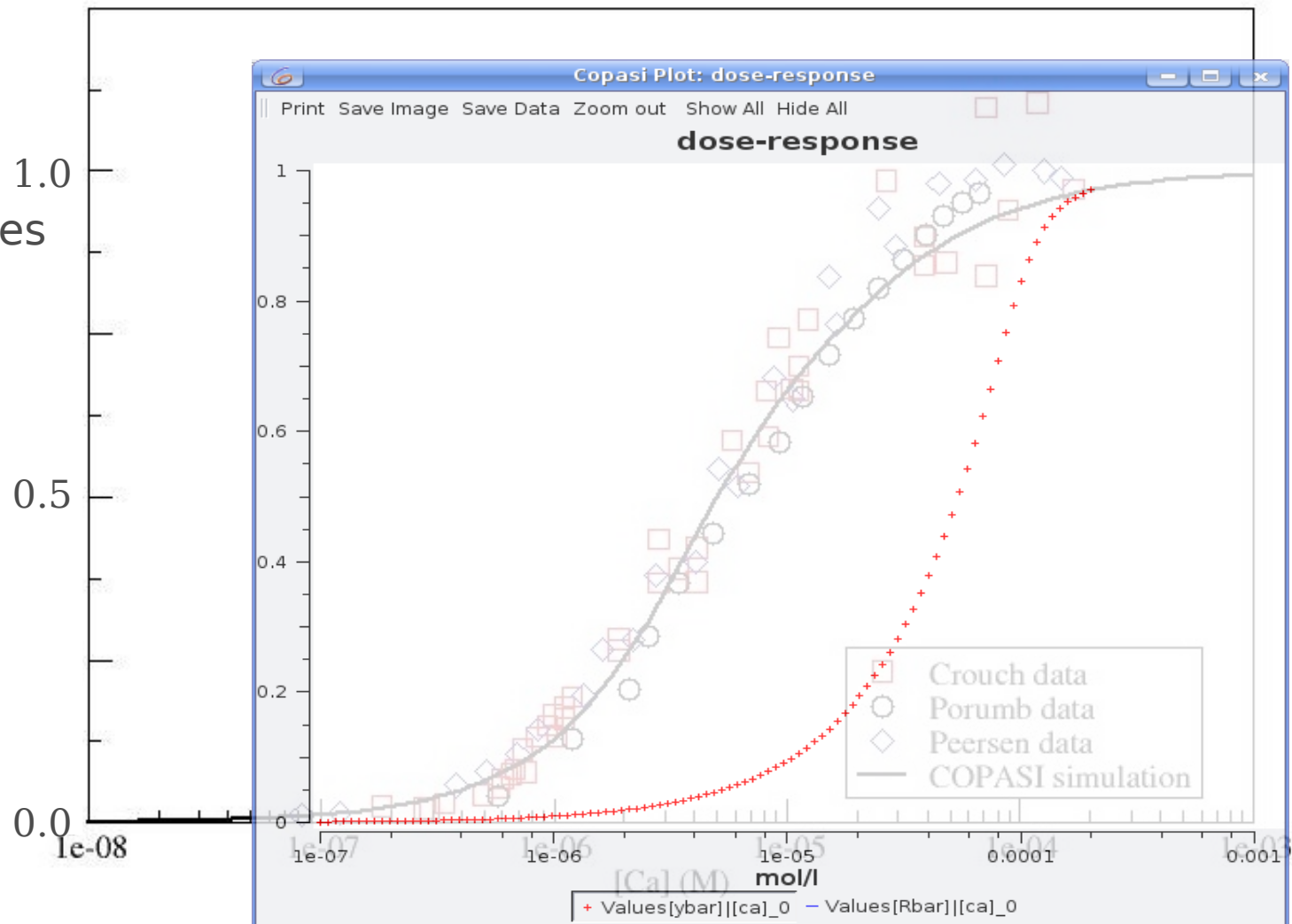
- We designed an allosteric model of Calmodulin, based on only two states for the EF hands, both binding calcium with different affinities, and a concerted transition for all 4 EF hands. We parametrised the model with experimental data-sets.
 - The model fits independent experimental datasets.
 - The affinity of CaM for calcium increases upon binding of the target.
 - CaM can be significantly in the open state even with less than 4 calcium bounds.
 - CaM can bind its targets even when with less than 4 calcium bounds.
- The model displays an activation of the sole PP2B at low concentration of calcium, while high concentrations activate both PP2B and CaMKII.

Allosteric model of Calmodulin function



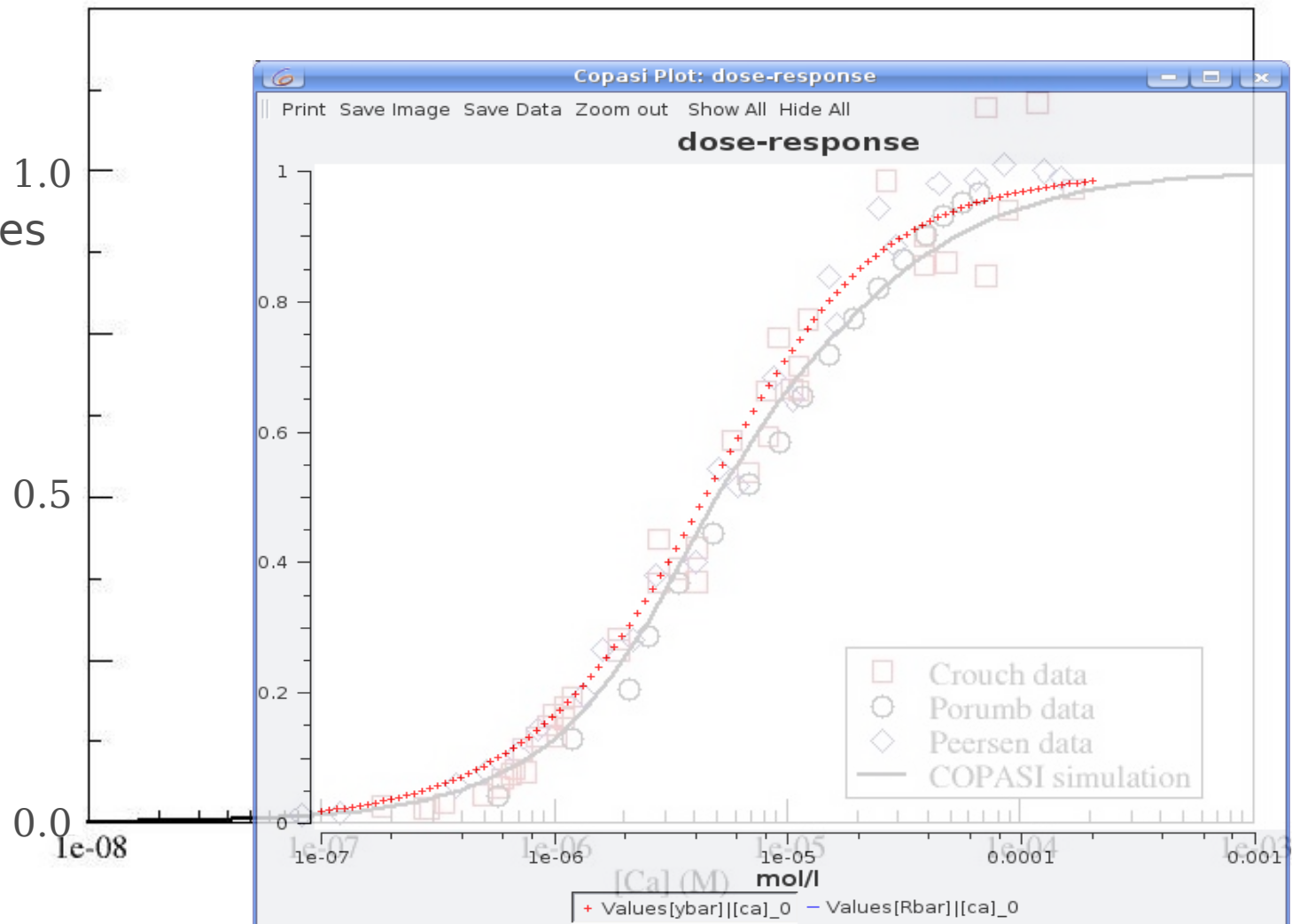
Calcium dose-response on 25 μM Calmodulin

fraction of
occupied
binding sites
($\bar{Y}$)



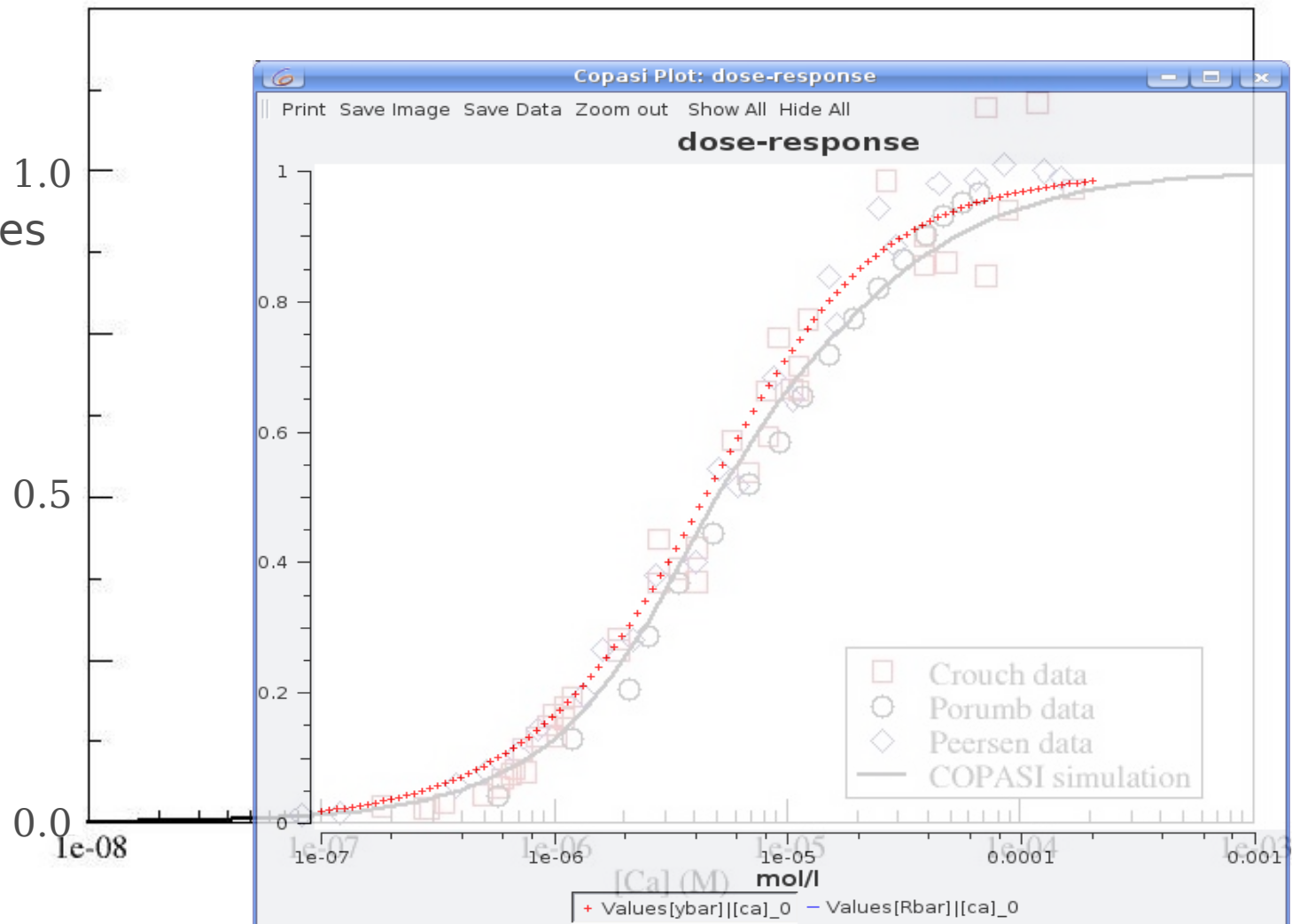
Calcium dose-response on 0.1 μM Calmodulin

fraction of
occupied
binding sites
($\bar{Y}$)



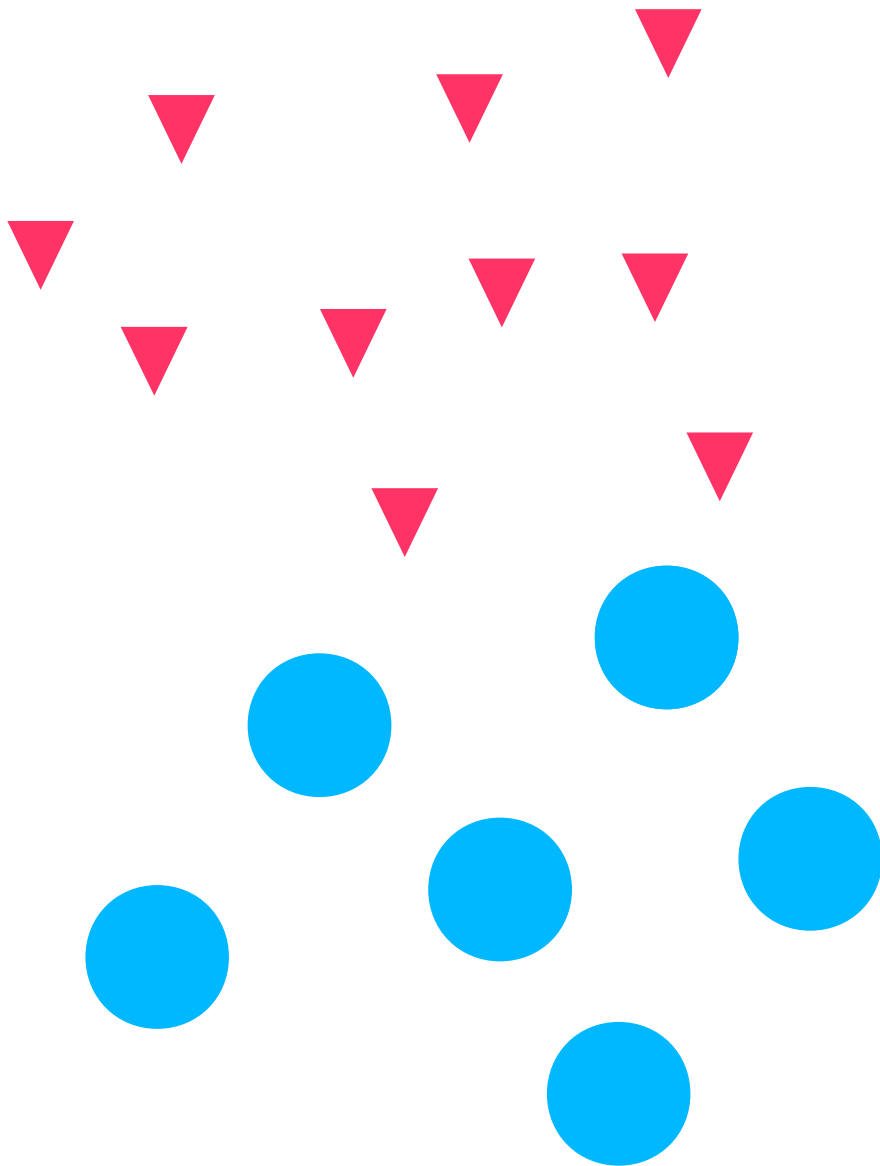
Calcium dose-response on 0.1 μM Calmodulin

fraction of
occupied
binding sites
($\bar{Y}$)



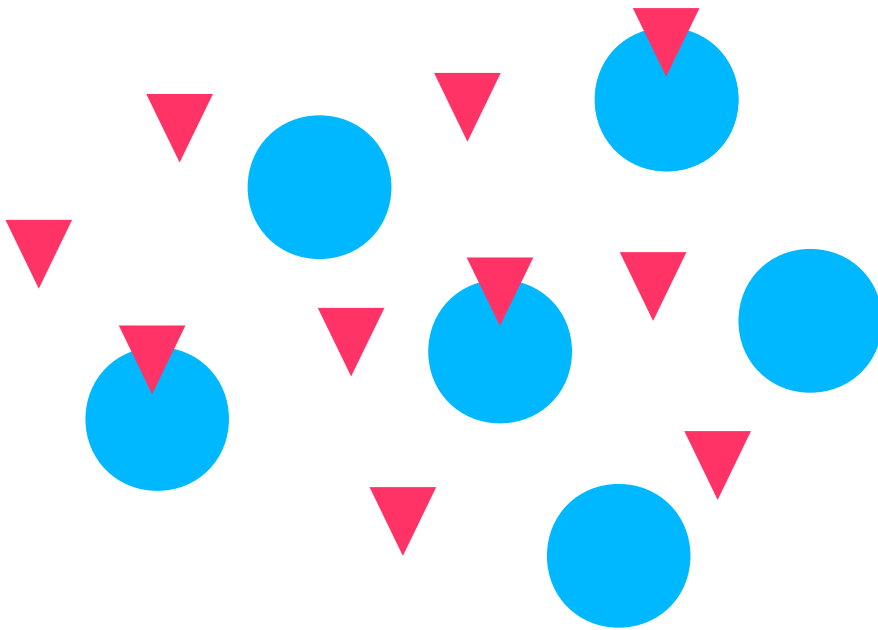
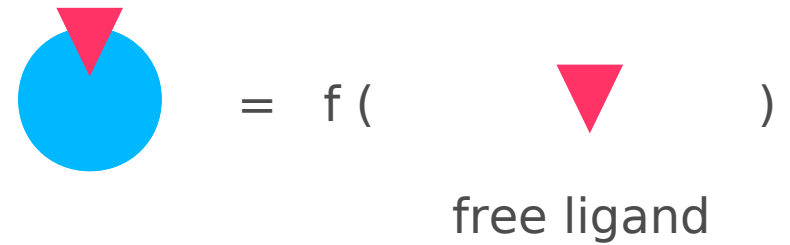
Edelstein S.J., Stefan M.I, Le Novère N. Ligand depletion in vivo modulates the dynamic range and cooperativity of signal transduction. PLoS One (2010), 5(1): e8449

What is ligand depletion?



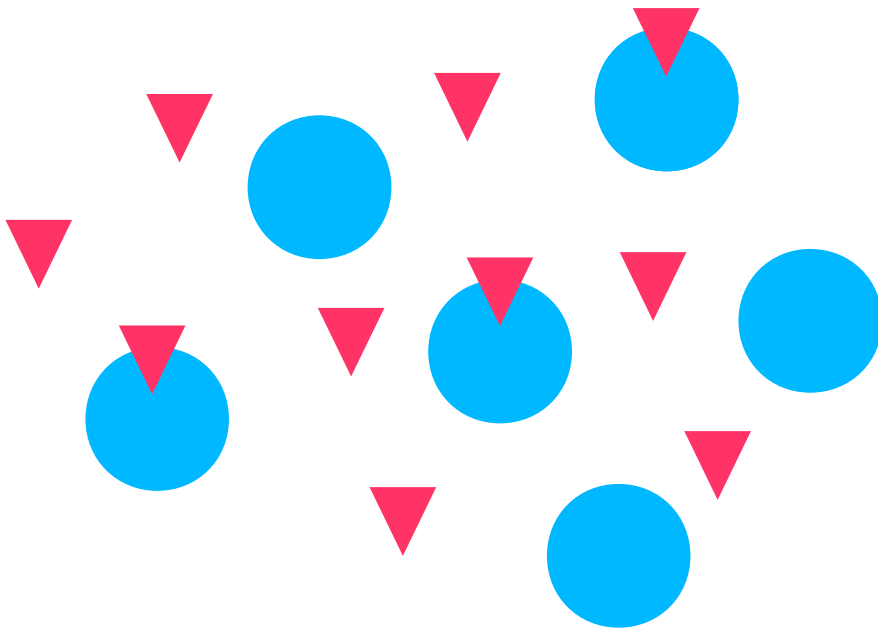
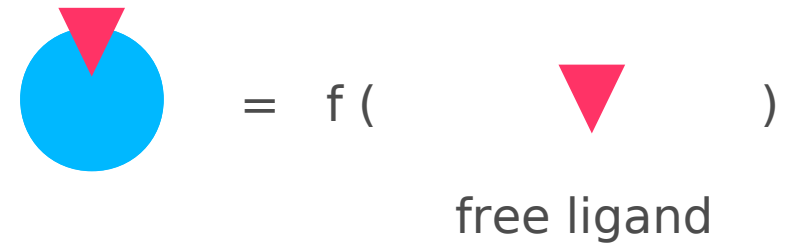
What is ligand depletion?

Chemistry (mass-action law)

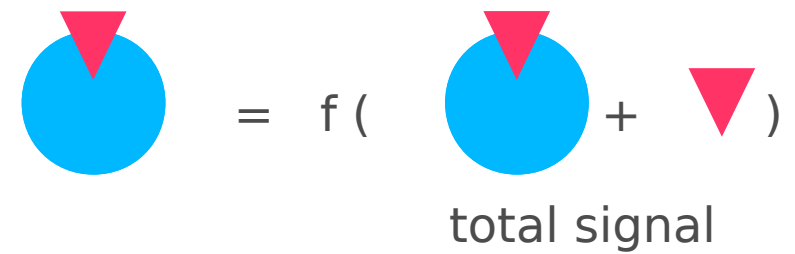


What is ligand depletion?

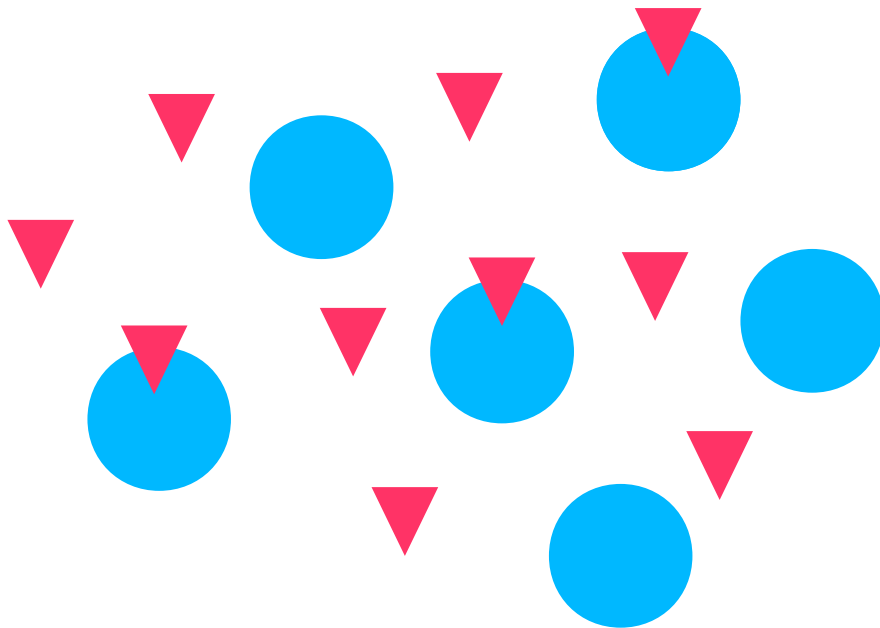
Chemistry (mass-action law)



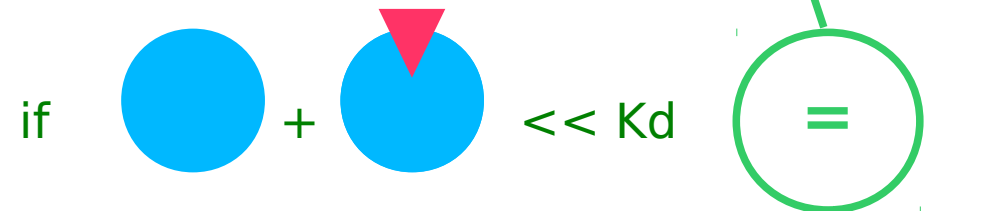
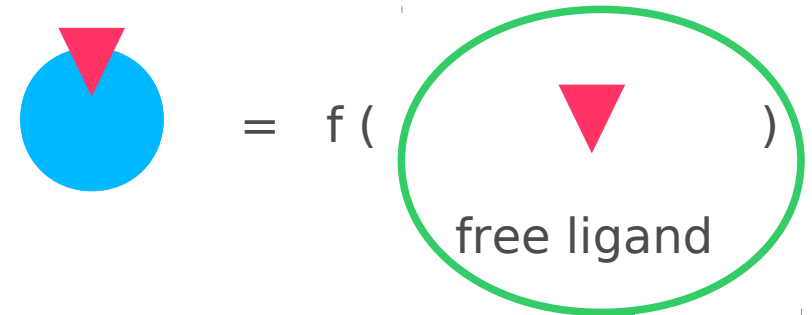
Cellular signalling



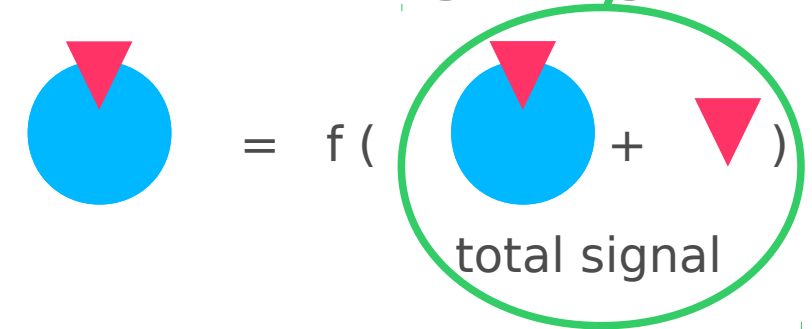
What is ligand depletion?



Chemistry (mass-action law)

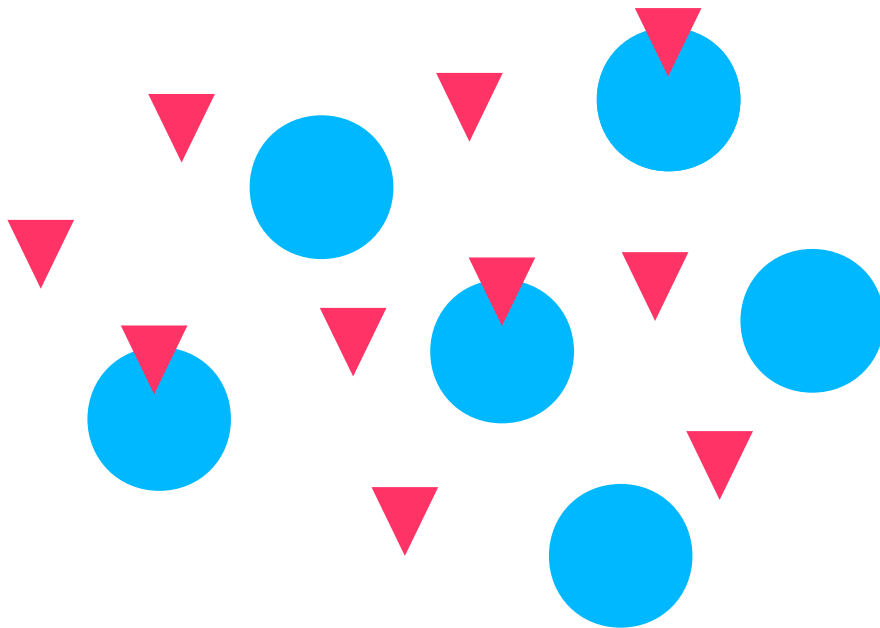


Cellular signalling

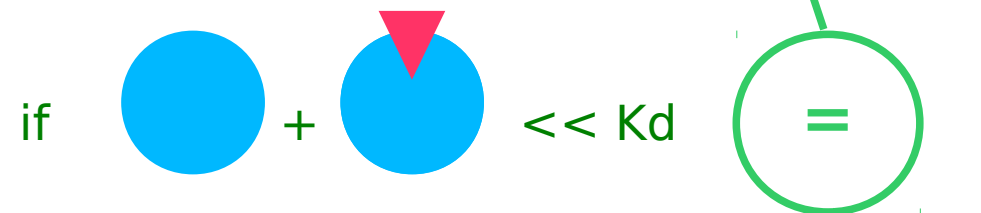
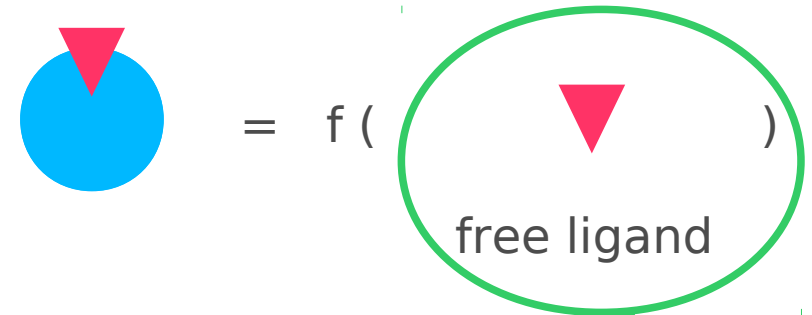


What is ligand depletion?

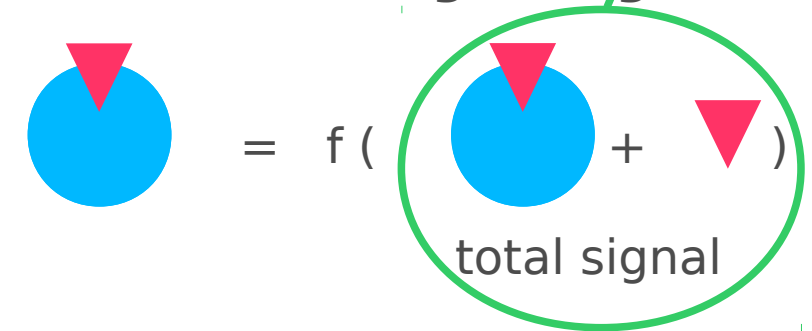
This is generally not the case in signalling:
Concentrations of sensors are in micromolar range, as are the dissociation constants.



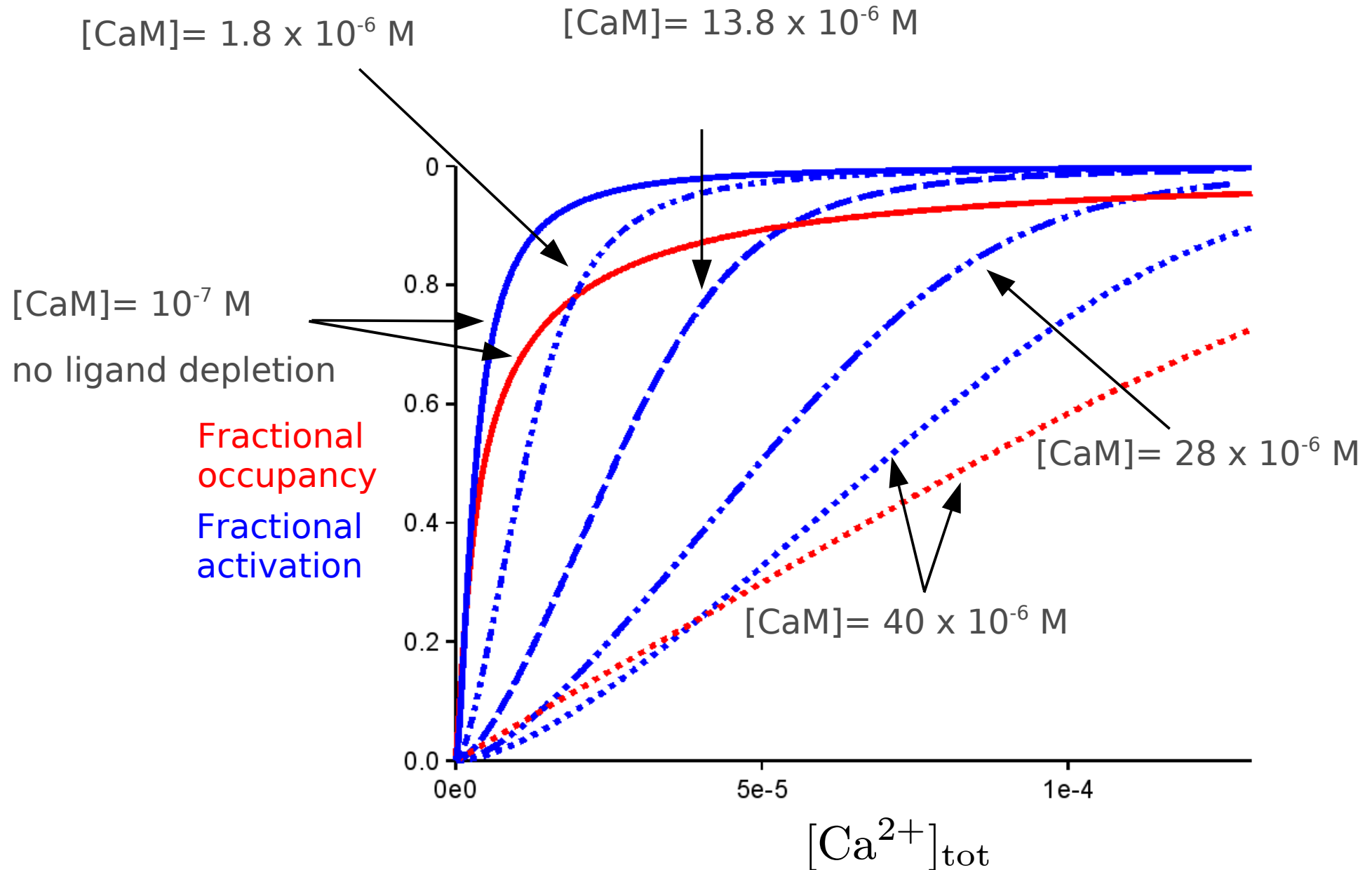
Chemistry (mass-action law)



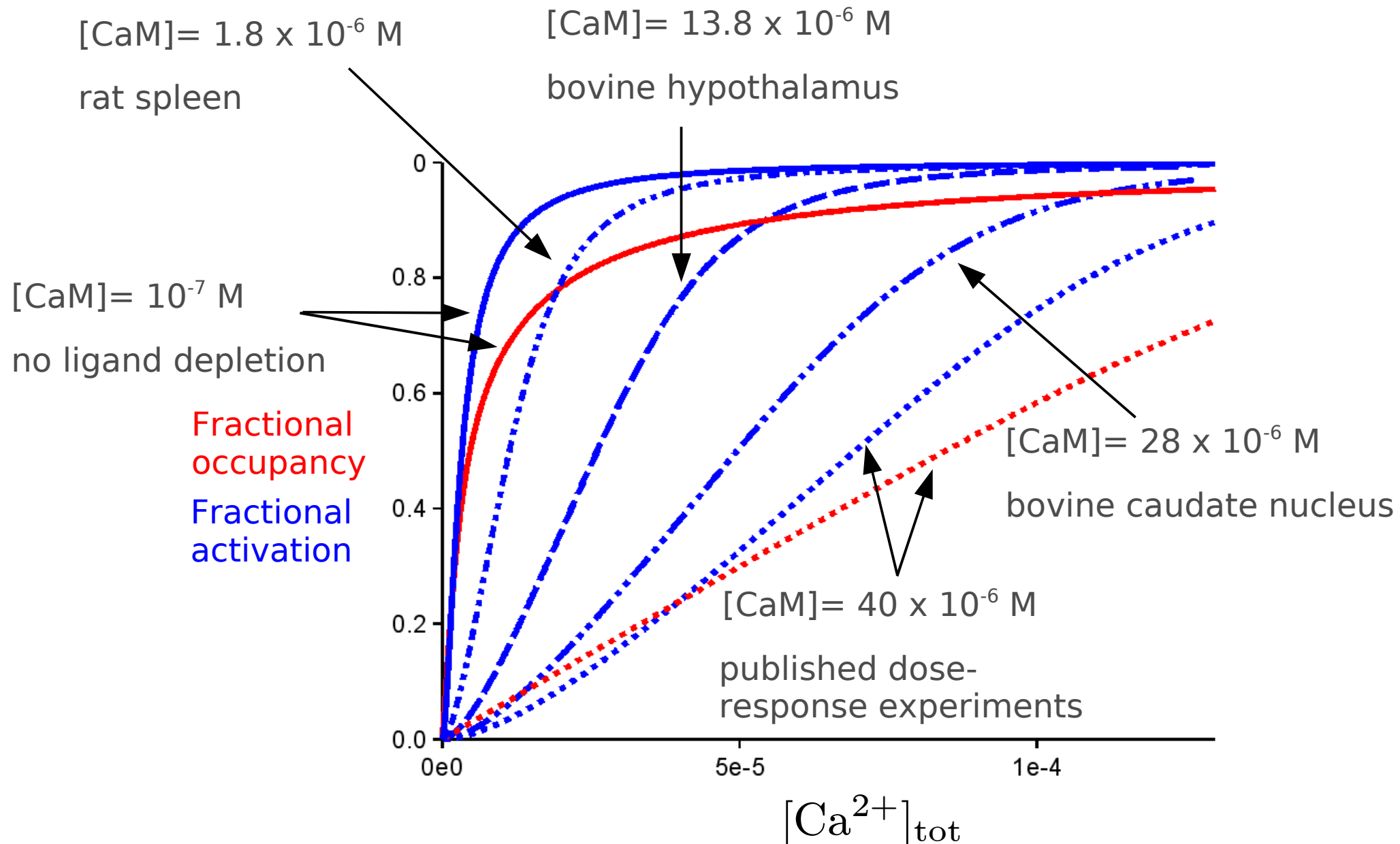
Cellular signalling



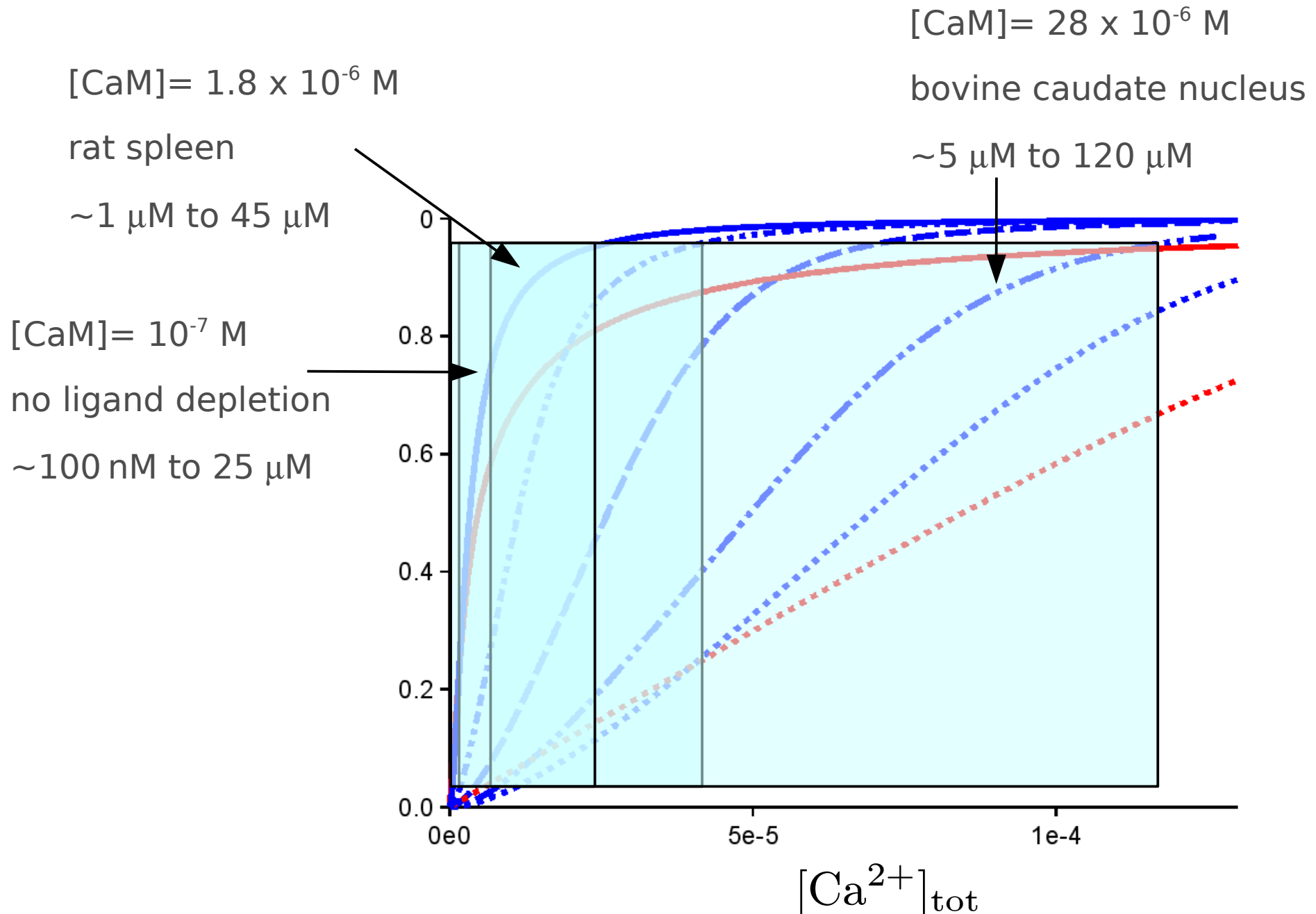
Dose-response depends on Calmodulin concentration



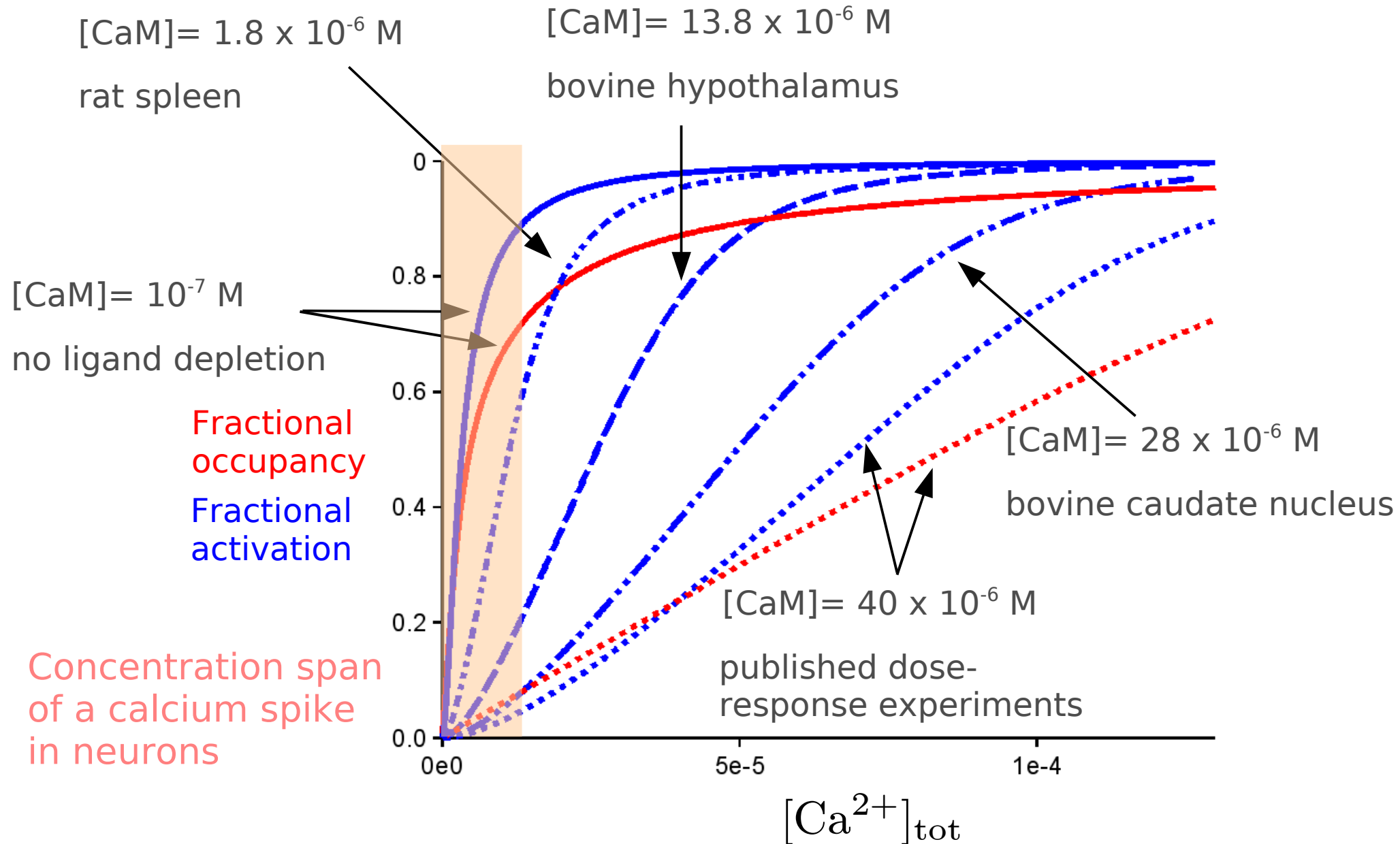
Dose-response depends on Calmodulin concentration



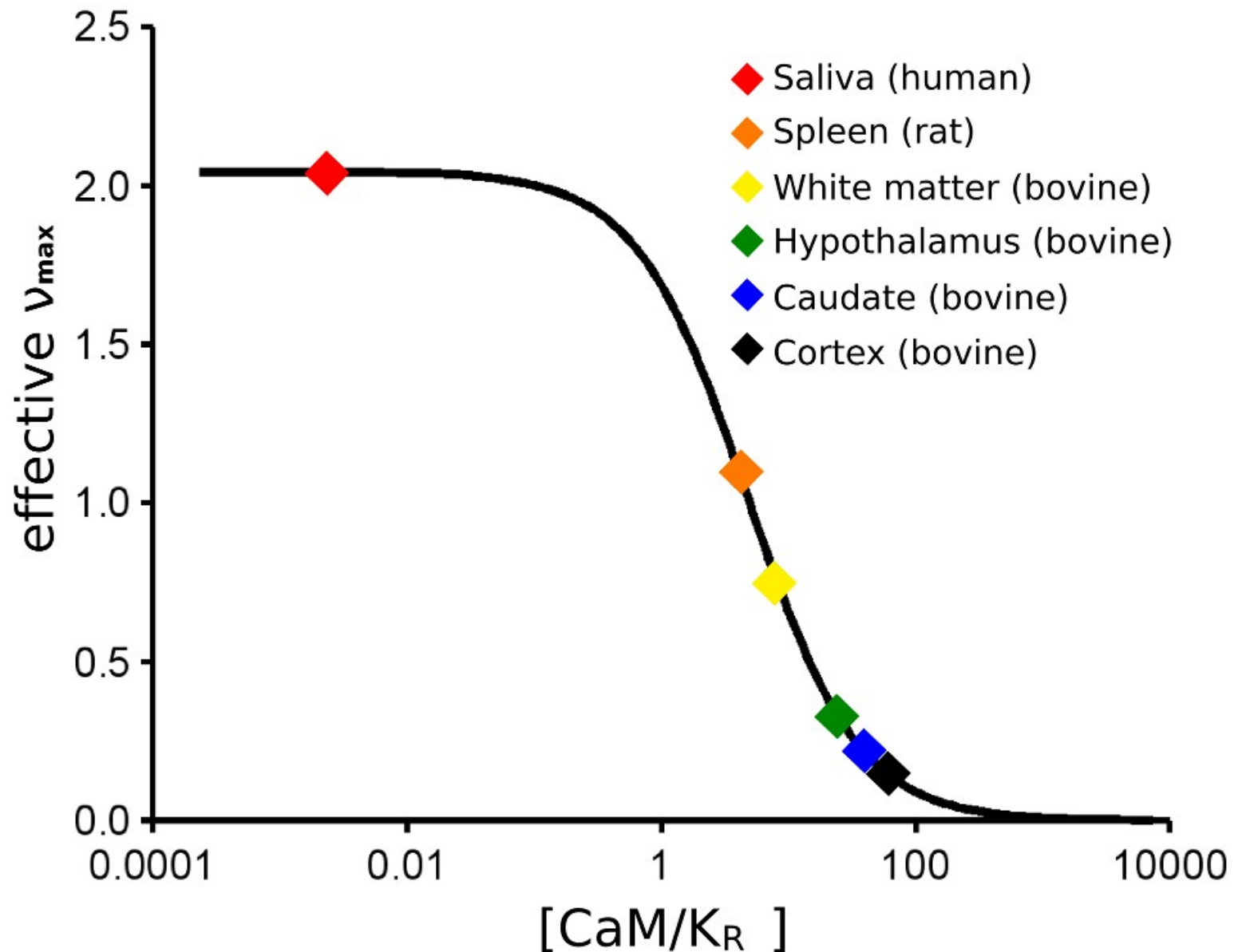
Ligand-depletion modifies sensitivity



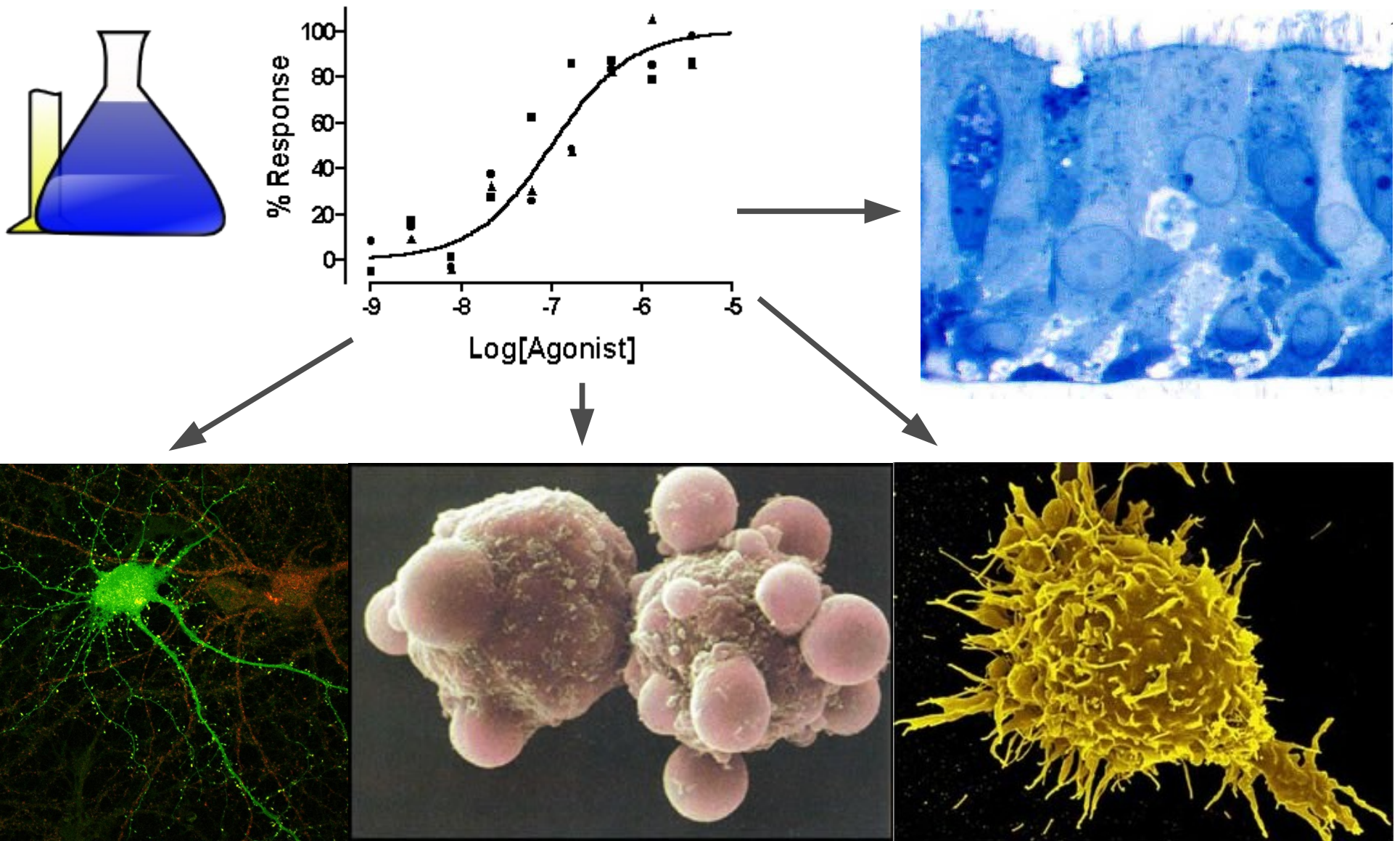
But we cannot build a large $[Ca^{2+}]$ in neurons ...



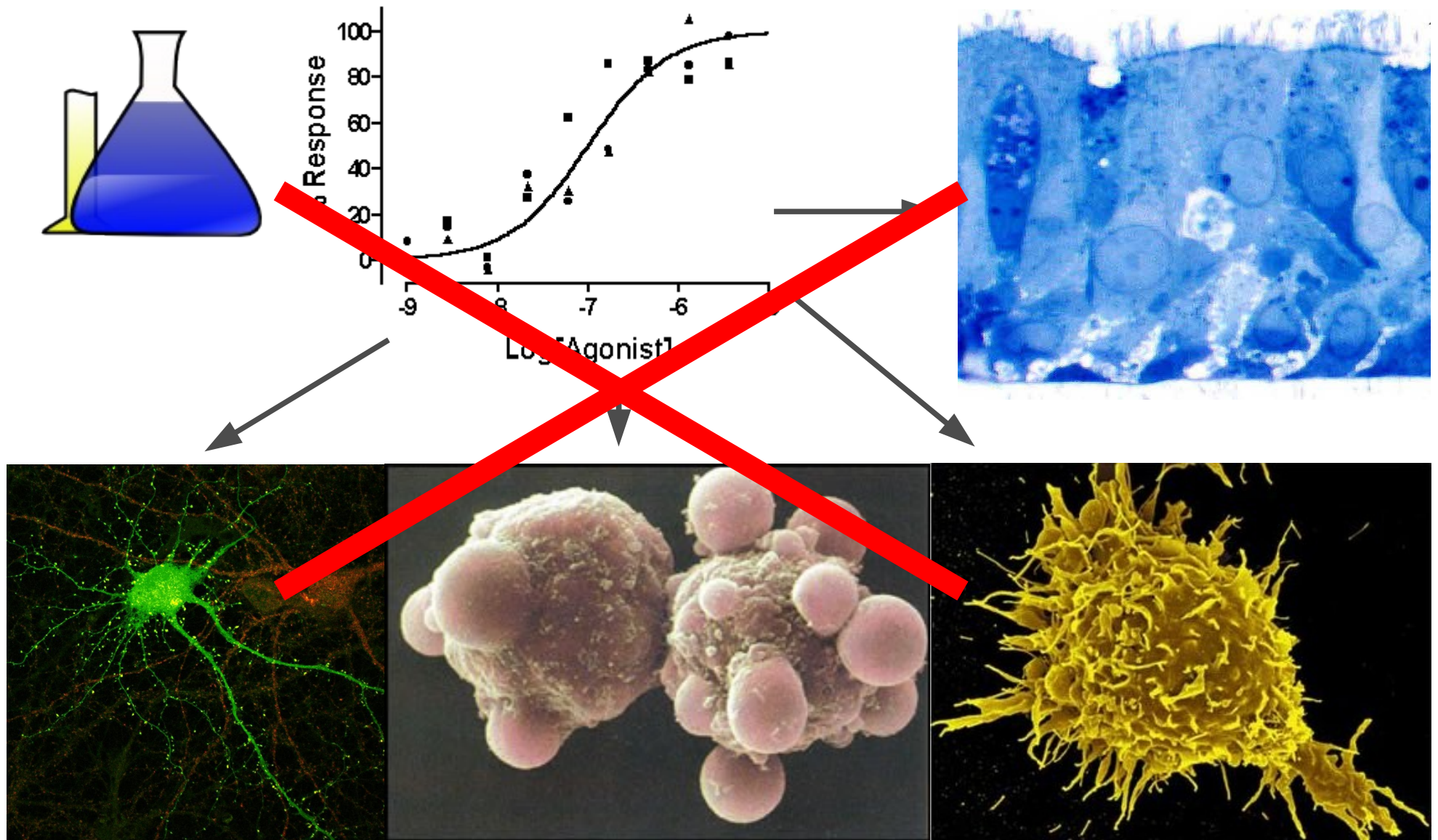
Ligand-depletion decreases effective cooperativity



How general is a dose-response?



A “dose-response” cannot be reused directly!



- Dose-responses are the basic characterisations of “systems”, but also at the core of pharmacological treatments. Here we show that:
 - A “dose-response” cannot be reused directly in models of signalling systems. Instead one needs to build “mechanistic” models and run parameter-fitting approaches.
 - Ligand depletion decreases the effective cooperativity of transducers *in situ*
 - Ligand depletion increases the dynamic range
- Modifying the concentration of the sensor may be a powerful way to quickly adapt to a new environment, and switch from a measurement mode to a detection mode.

Acknowledgements

- Developers of COPASI
 - Sven Sahle
 - Stefan Hoops
 - Ursula Kummer
 - Pedro Mendes
- Developers of Scilab
- Annalisa Pastore
- Stephen Martins

See poster P43
for more details
on ligand depletion

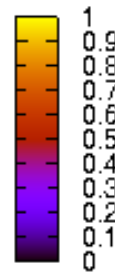
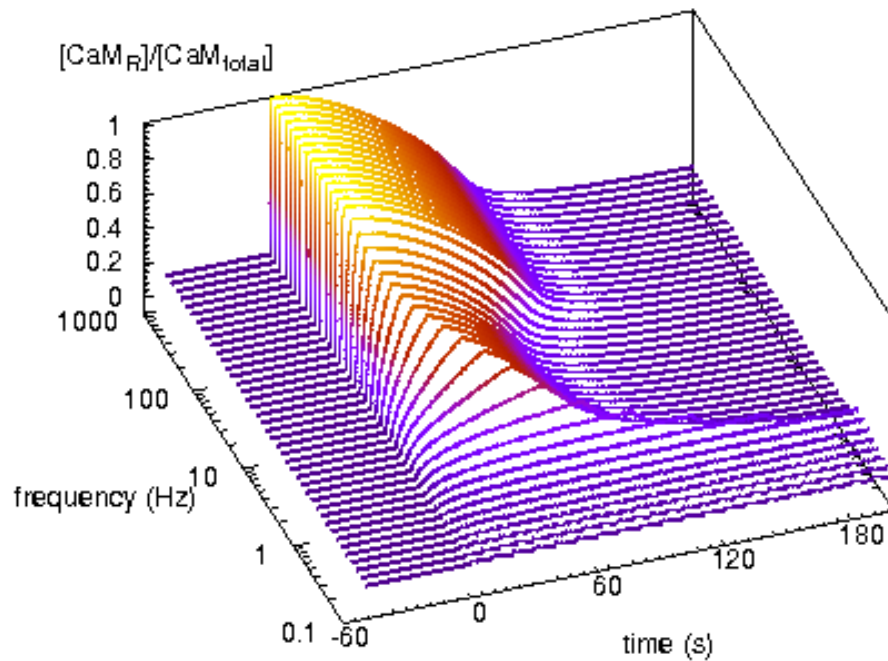


Melanie Stefan

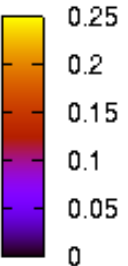
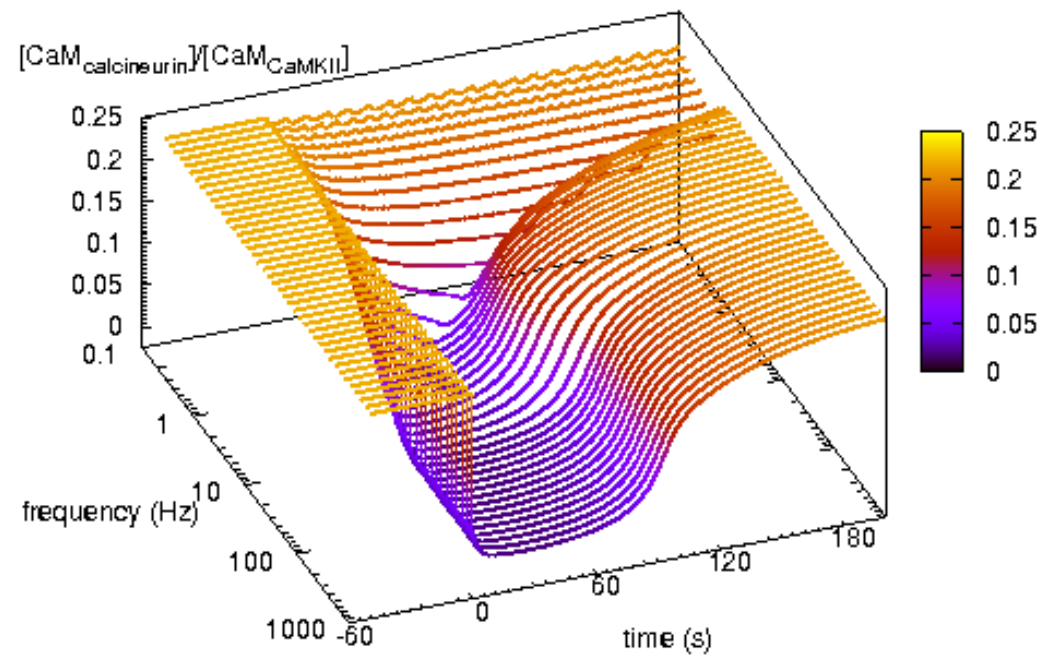


Stuart Edelstsein

More on the effect of calcium spike frequency, amplitude and duration



See poster P31
by Dr Lu Li



2 Post-doctoral fellowships at EMBL-EBI

Modelling synaptic signalling pathways

- *SynSys* is a European consortium that will 1) provide a quantitative description of protein complexes, interactomes and networks in the mammalian glutamatergic synapse, 2) generate quantitative dynamic models, describing the main functional features of the synaptic networks, 3) iterate on modelling by relating model predictions to synaptic function, and 4) identify vulnerabilities in gene networks that are at the basis of human brain disease and may help design future therapy.
- **Post 1:** to determine, based on experimental and computational information from the consortium, literature and databases, the pre- and post-synaptic “signalosomes”. This will encompass modulations taking place in the different synaptic compartments. Influence networks will then be reconstructed, providing a reference map of the synapse signaling. Logical models will finally be developed for specific modules, identified as relevant for the consortium's aims. Necessitates an understanding of the biology, and in particular of signalling, but also basis of mathematics and computing methods used to reconstruct and analyse pathways.
- **Post 2:** to develop detailed and realistic dynamic models of post-synaptic processes involving protein movements and modifications. In particular we will study the movements and function of glutamate receptors, and the spatio-temporal dynamics of calcium regulated proteins. Multi-agents models and stochastic simulations will be used, among other computational methods. Necessitates an understanding of the biology, and in particular of signalling, but also of mathematics and computing methods used to build and simulate quantitative models.

Joint post-doctoral position EMBL-EBI/Sanger Institute

Inference and representation of post-synaptic protein pathways using proteomics and phenotypic data

SANGER partner: Seth Grant

EBI partners: Nicolas Le Novère and Julio Saez-Rodriguez

3 years, contract extensible 2 years for fellowship applications