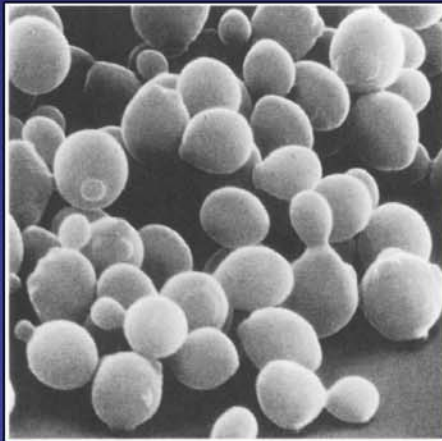




IGM  
UMR CNRS U-PSUD

# Stress-induced oscillatory nucleocytoplasmic behavior of the transcription factor Msn2 in yeast



Michel Jacquet

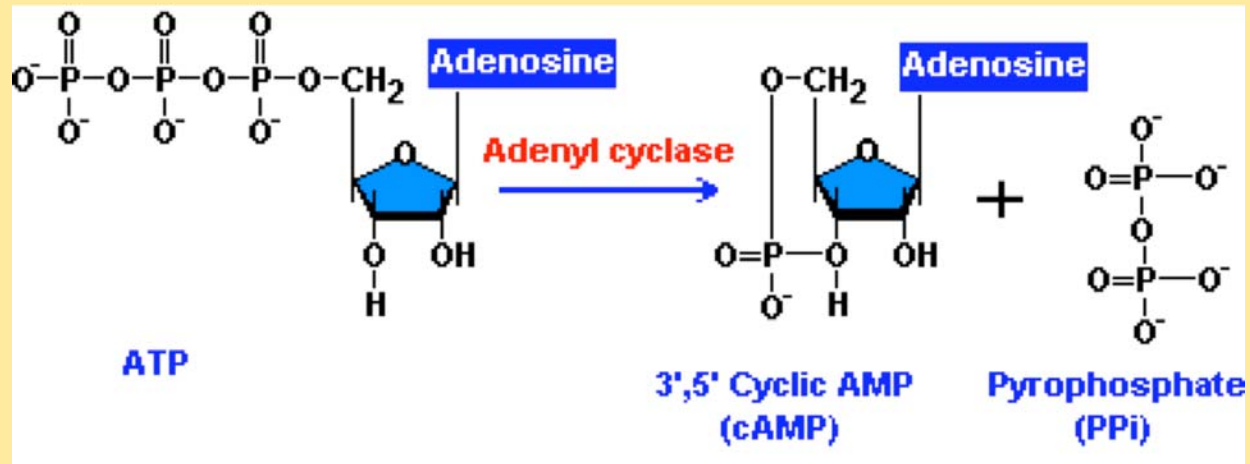
Georges Renault  
Cecilia Garmendia-Torres

Albert Goldbeter

# cAMP a signaling molecule (Sutherland 1957)

Formation of a Cyclic Adenine Ribonucleotide by Tissue Particles (Rall, T. W., and Sutherland, E. W. (1958) *J. Biol. Chem.* 232, 1065)

Fractionation and Characterization of a Cyclic Adenine Ribonucleotide Formed by Tissue Particles (Sutherland, E. W., and Rall, T. W. (1958) *J. Biol. Chem.* 232, 1077)



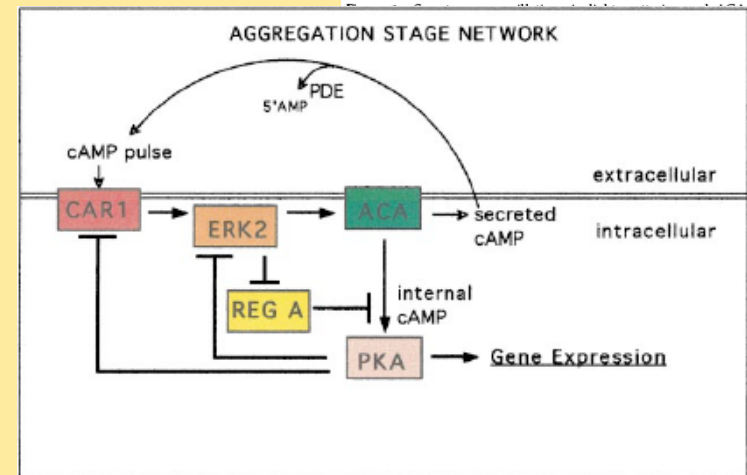
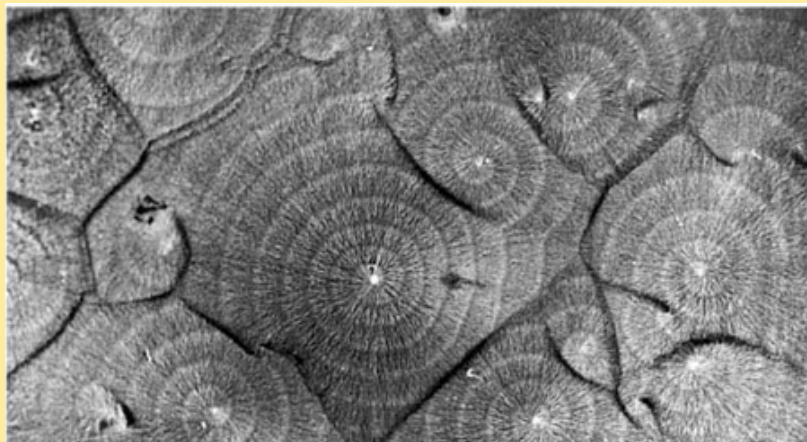
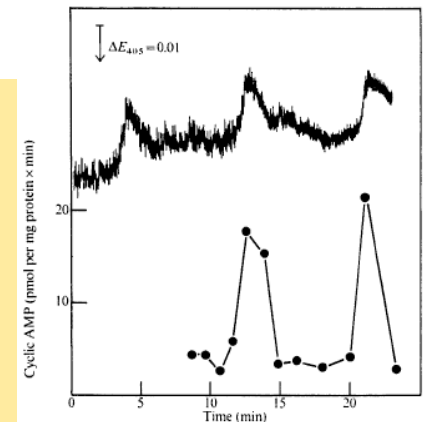
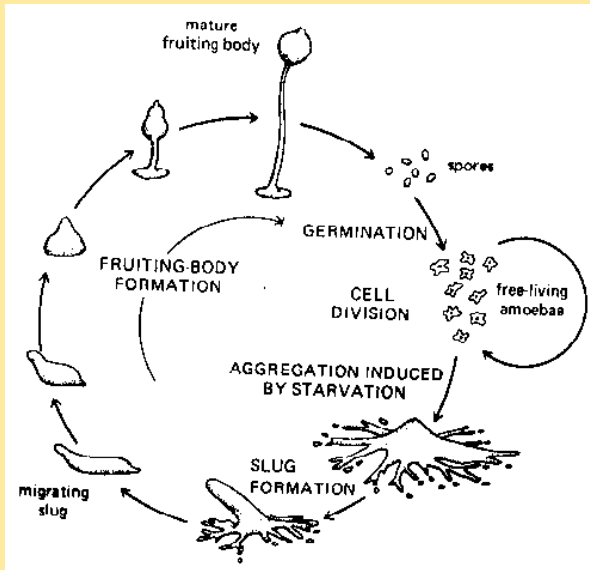
The step sensitive to catabolite repression and its reversal by 3'-5' cyclic AMP during induced synthesis of  $\beta$ -galactosidase in *E. coli*; **Biochemical and Biophysical Research Communications**, Volume 36, Issue 1, 7 July 1969, Pages 84-92. Michel Jacquet and Adam Kepes

# cAMP oscillations in *Dictyostelium discoideum*

Molecular Biology of the Cell  
Vol. 9, 3521-3532, December 1998

## A Molecular Network That Produces Spontaneous Oscillations in Excitable Cells of *Dictyostelium*

Michael T. Laub and William F. Loomis\*



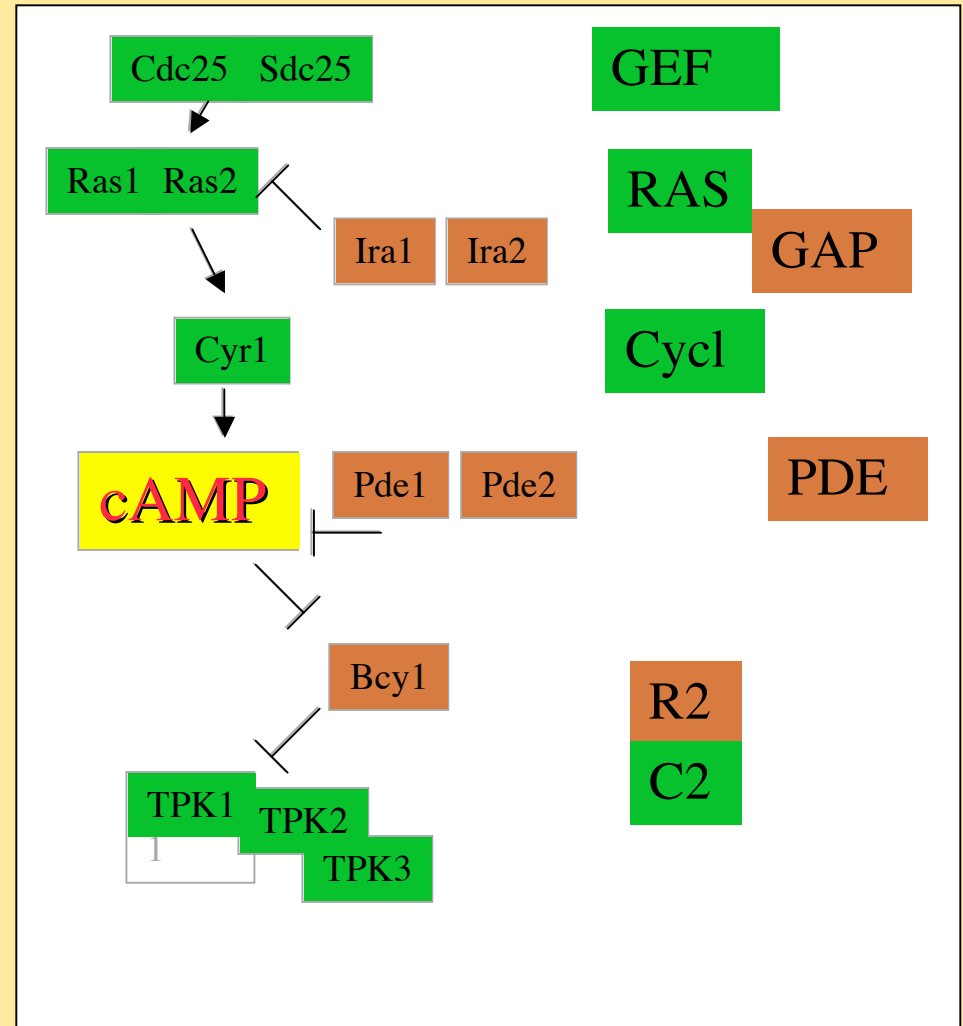
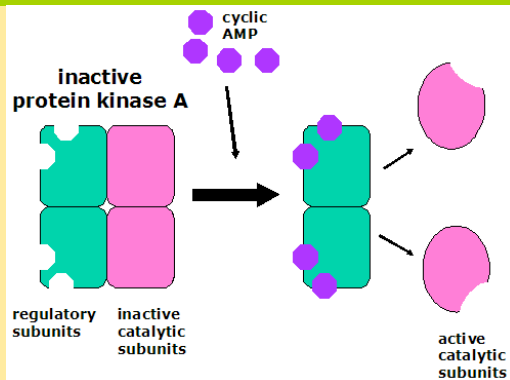
# cAMP in yeast

Classical genetic (BC) 75..

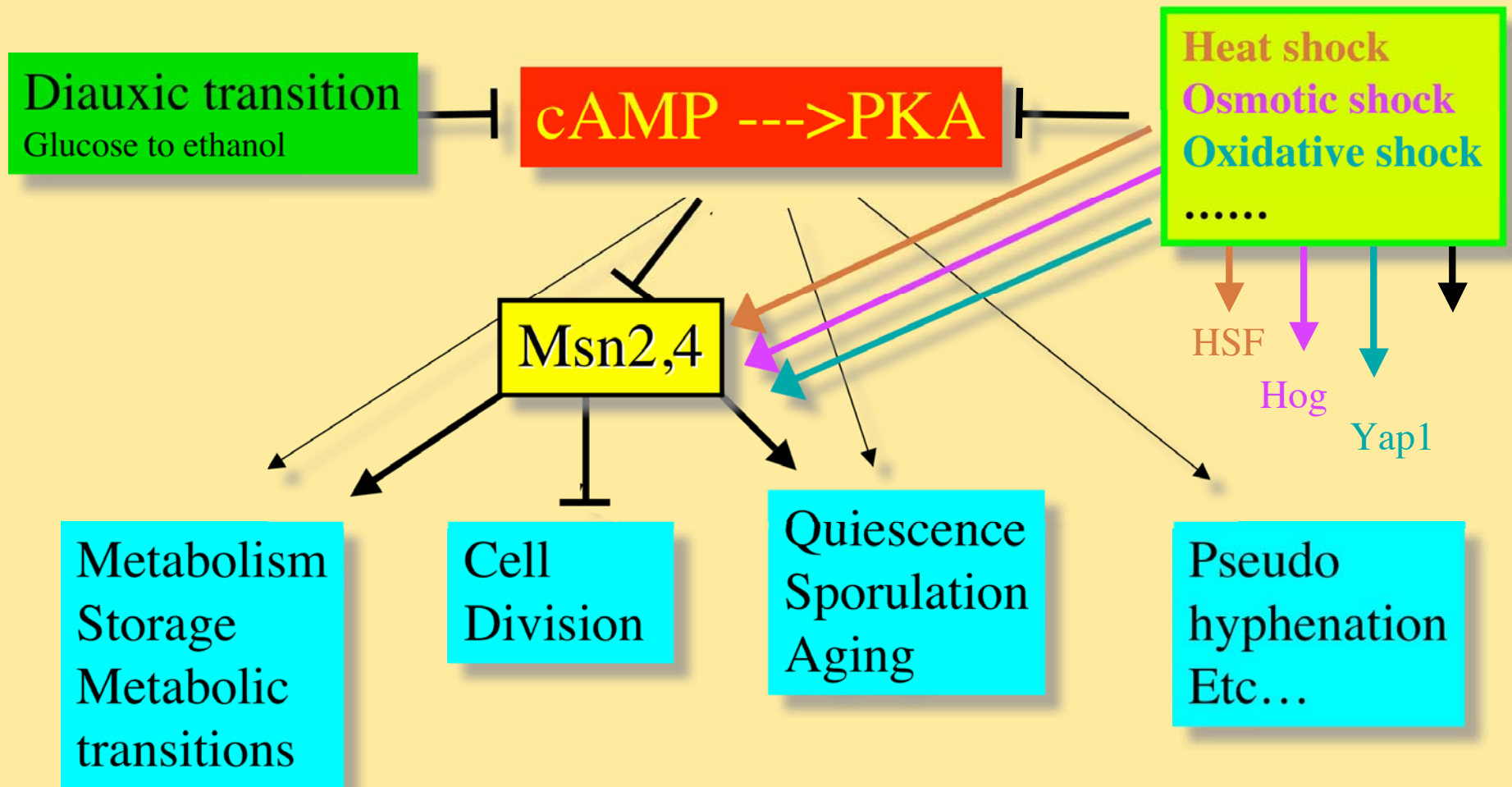
*cdc25, cdc35* (Hartwell, Hilger),  
*cyr1* (Matsumoto et al.; 1982)  
*bcy1* (Matsumoto et al.; 1982)

Mol. cloning and sequencing (..80-90)

*CYR1/CDC35* (Masson 1984, Wigler 1985)  
*RAS1, RAS2* (...Wigler 1984)  
*CDC25, SDC25* (...Jacquet 1986)  
*BCY1* (...Wigler 1987)  
*TPK1, TPK2, TPK3* (...Wigler 1987)  
*PDE1, PDE2* (...Wigler 1987)  
*IRA1, IRA2* (Matsumoto 1990)



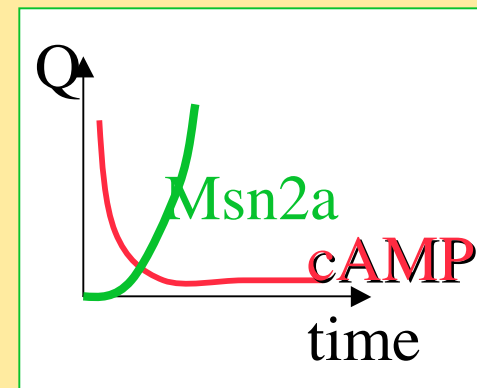
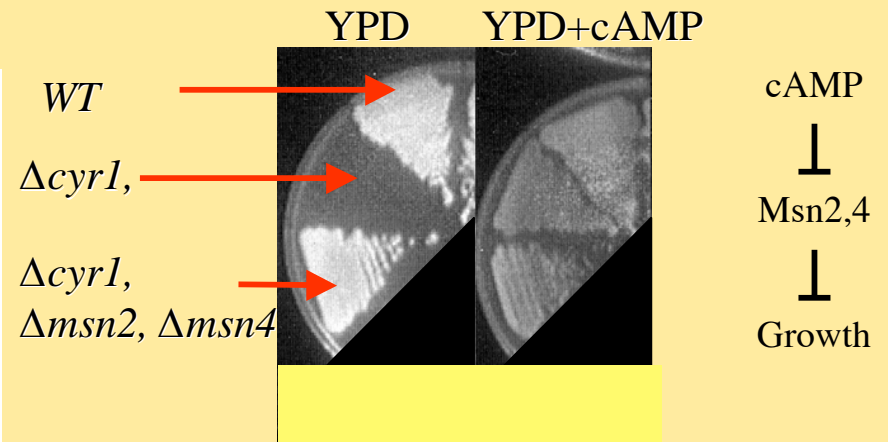
# What is the role of the cAMP-PKA system in yeast ?



# Msn2 and Msn4 are targets of cAMP

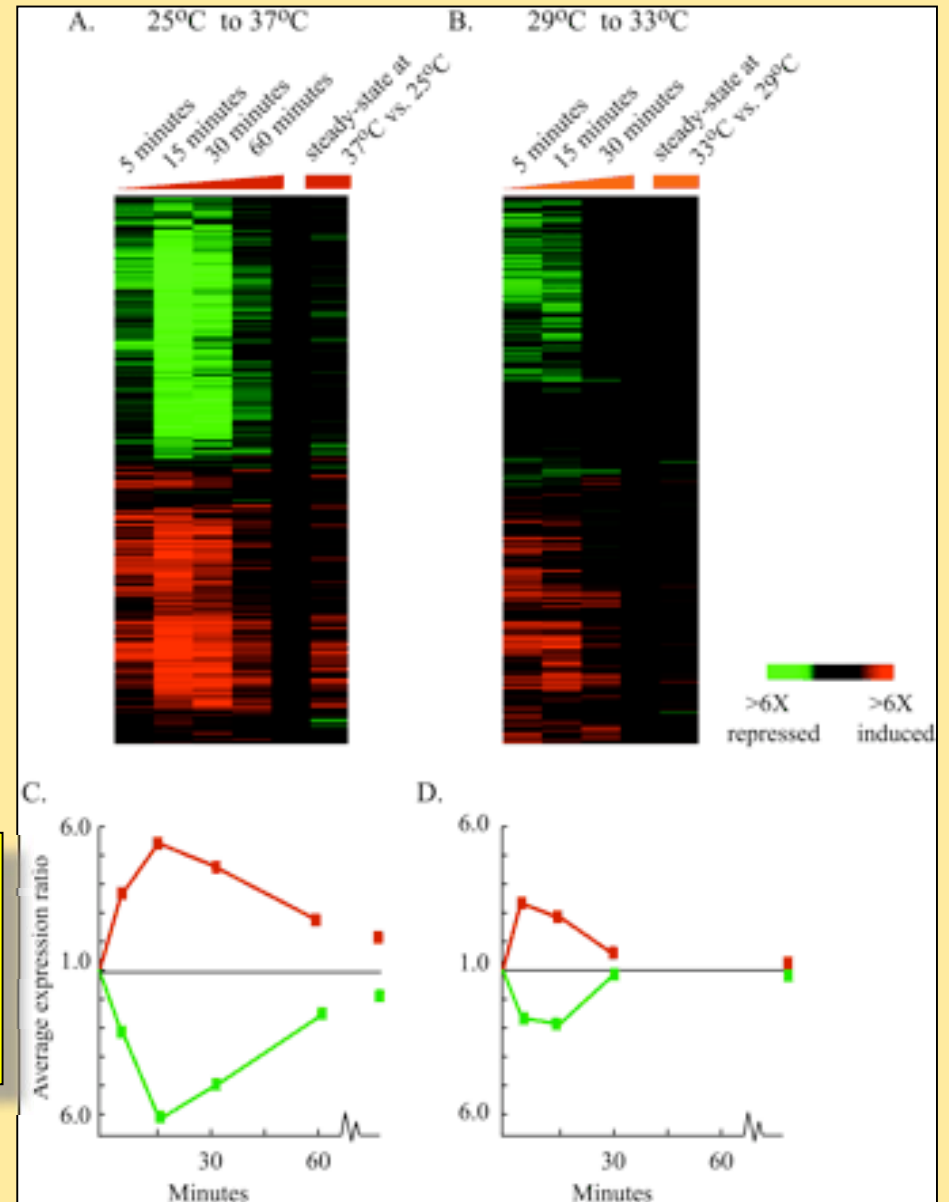
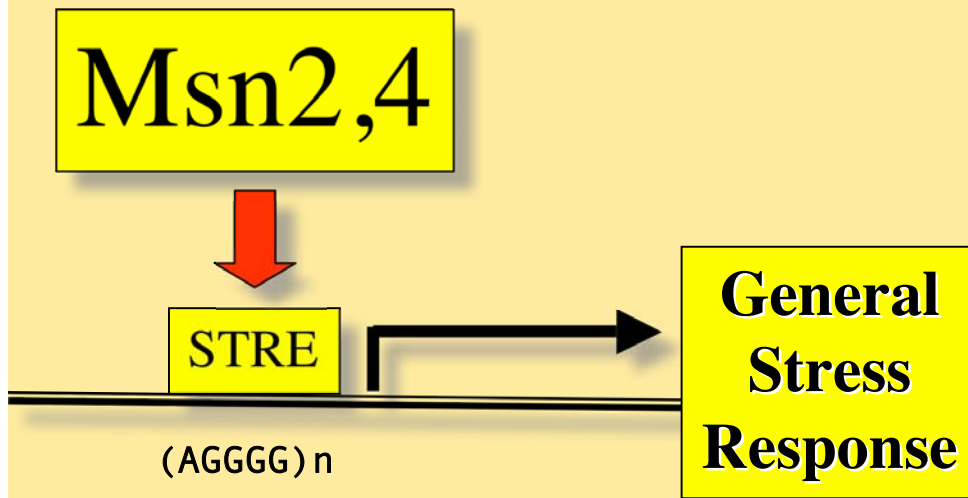
- **Msn2 and Msn4**

- Suppressor of growth defect of  $\Delta\text{cyr1}$
- Mediates diauxic transition when cAMP is low
- Activated upon heat shock (low cAMP)
- Activated upon oxidative shock (low cAMP)
- ...Osmotic shock
- ...weak acid
- ...





# Msn2 and Msn4 activate the “STRE” régulon



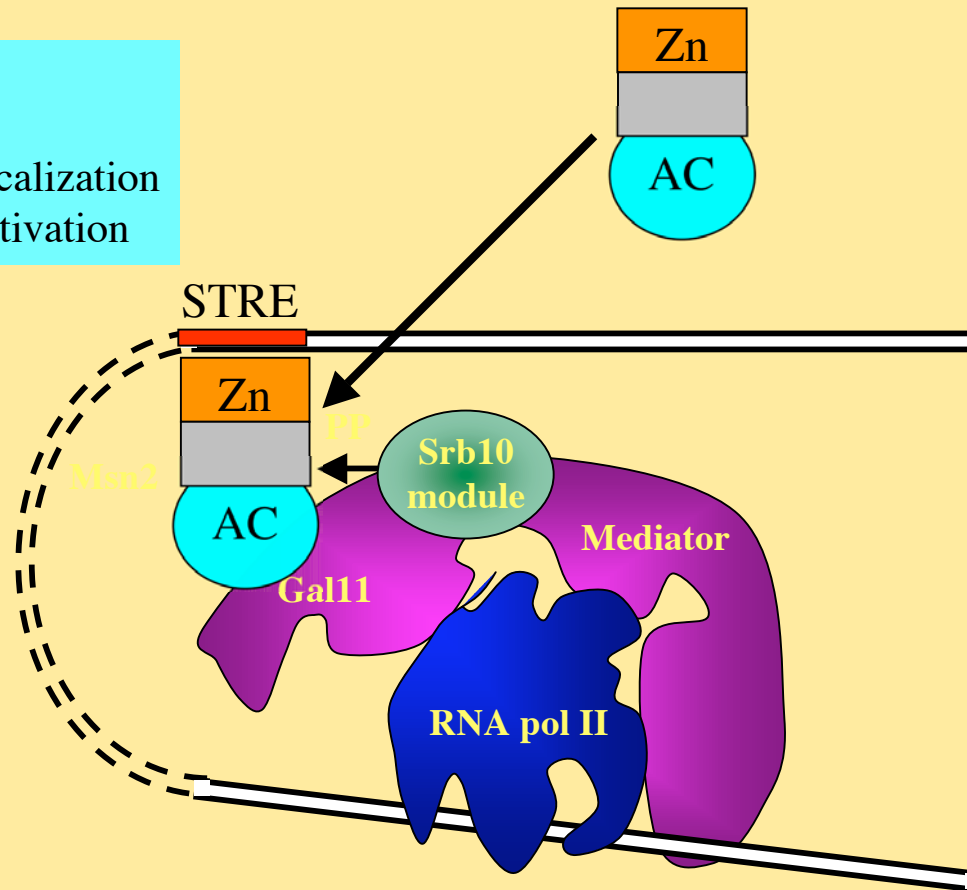
# Functional anatomy of Msn2

## Msn2



Activation domain  
Stress response:  
- Stress dependent localization  
- Stress dependent activation

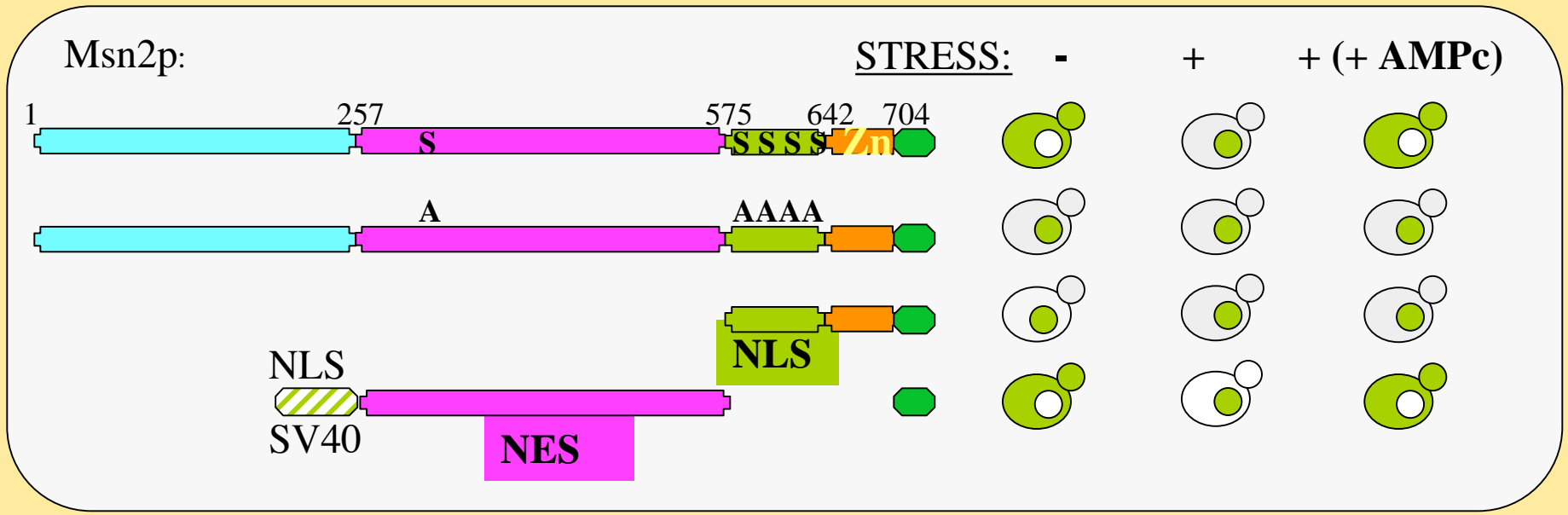
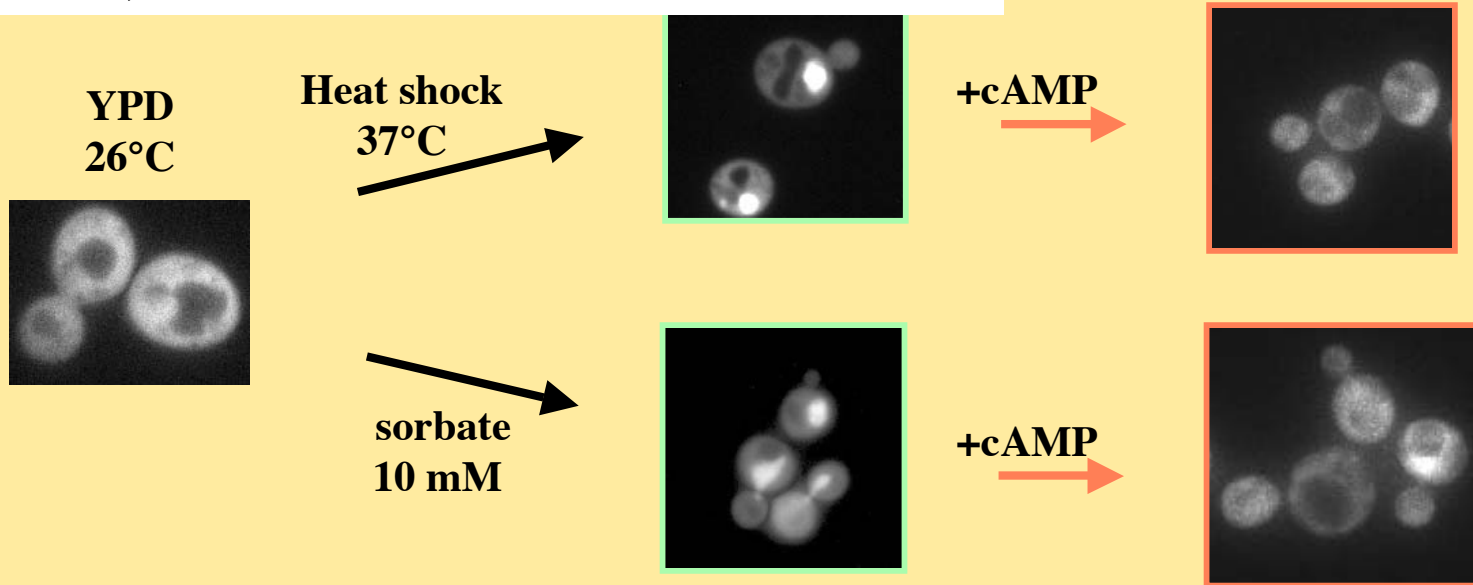
DNA binding  
Zn





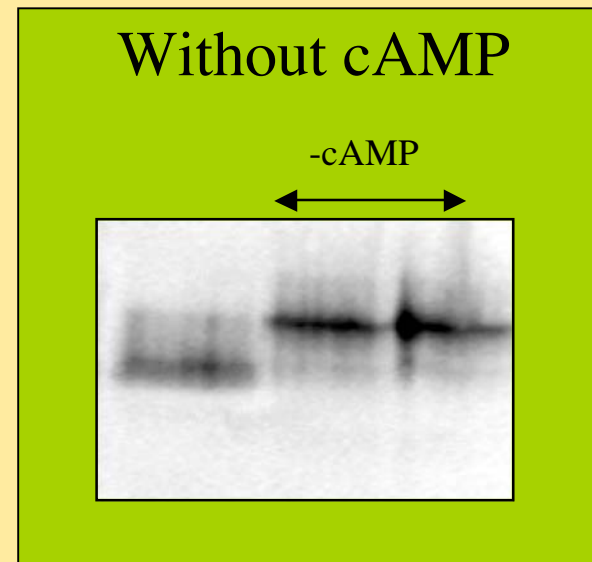
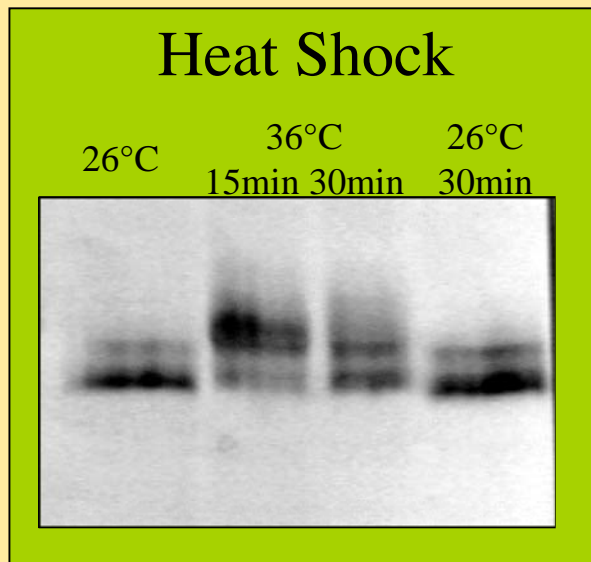
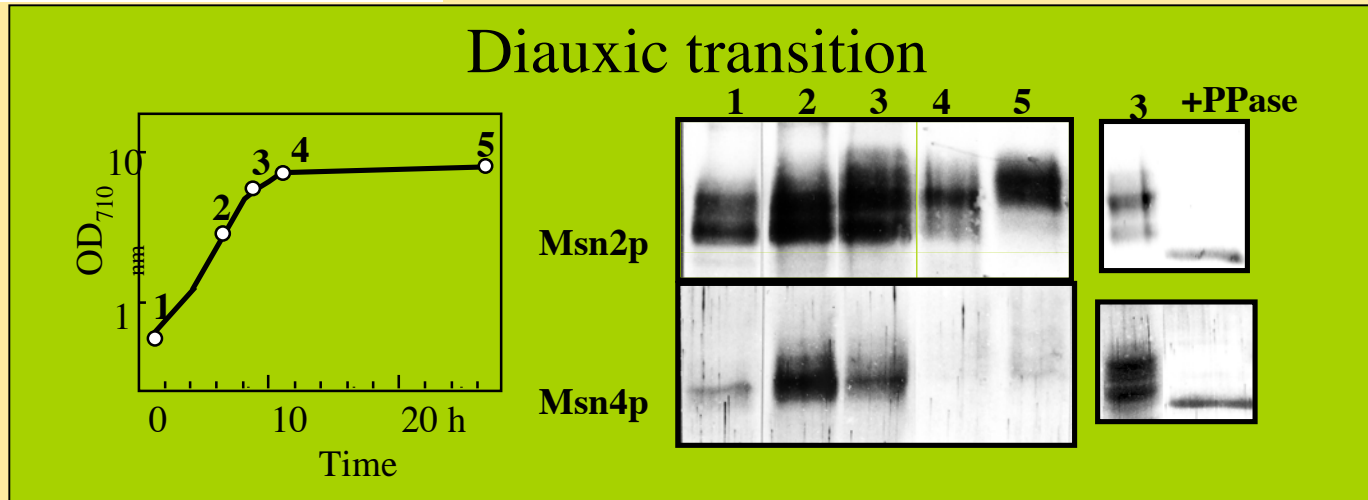
# Nucleocytoplasmic localization of Msn2

Gorner *et al*, Genes Dev. 1998 12: 586-97.1998



# Msn2 is hyperphosphorylated when activated

Garreau et al Microbiology. 2000 146 2113-20.



# The search for the hyperphosphorylating kinase (S. Lallet and H. Garreau)

Lallet et al Mol Microbiol. 2006 Oct;62(2):438-52.

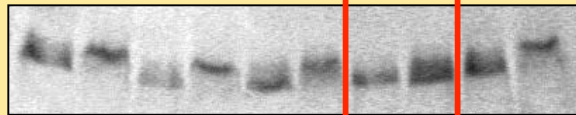
Using 120 mutants for protein kinase

The only two mutant strains

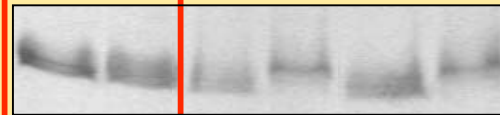
*srb10/ssn3*

*ste11*

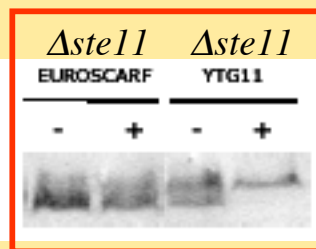
Δ *ctk2* *iks1* *pho85* *srb10* wt



Δ *ste11* *ctk1* *ctk3*

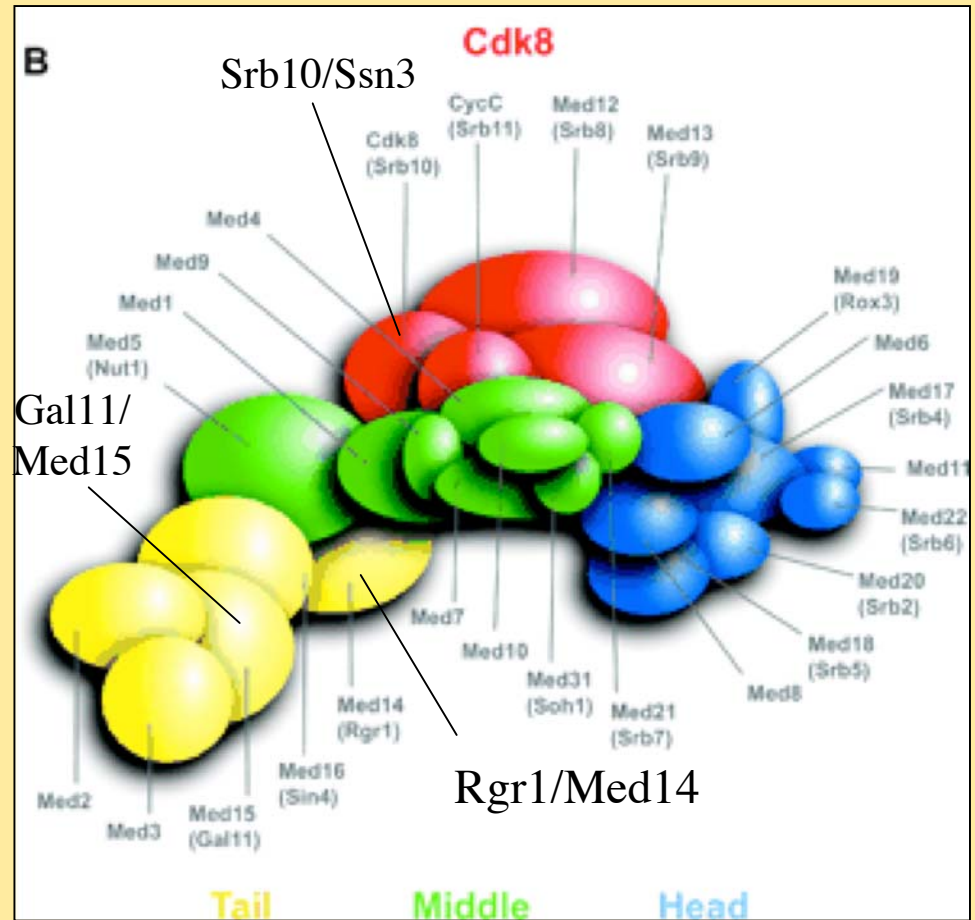
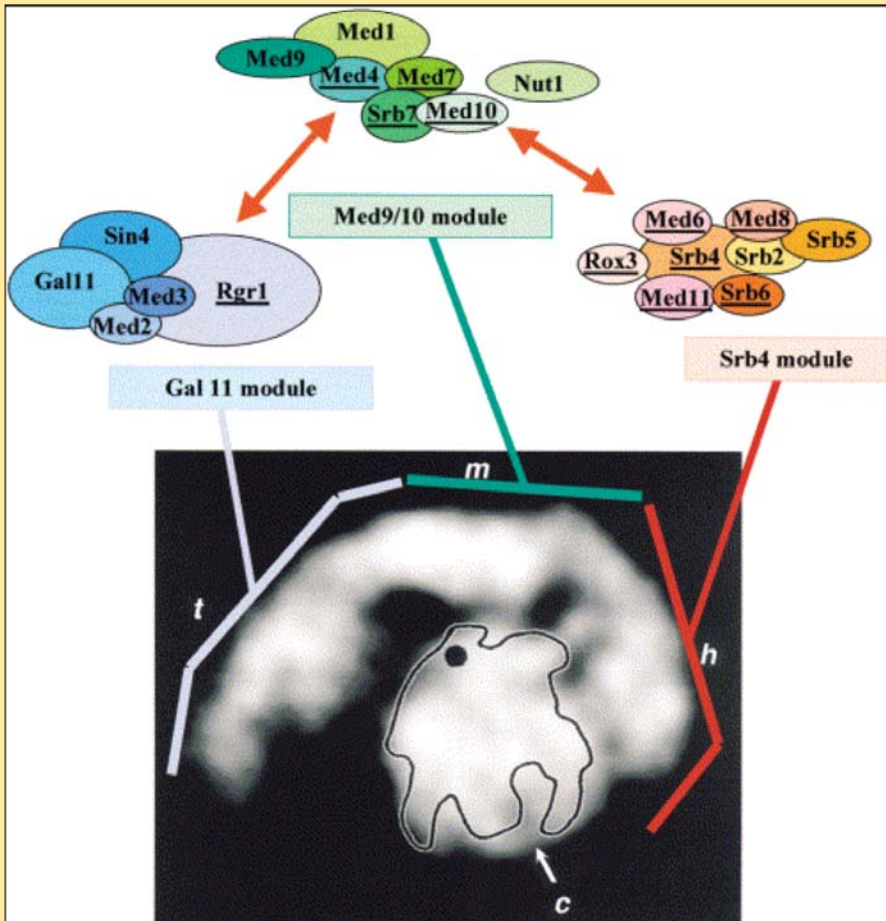


choc thermique



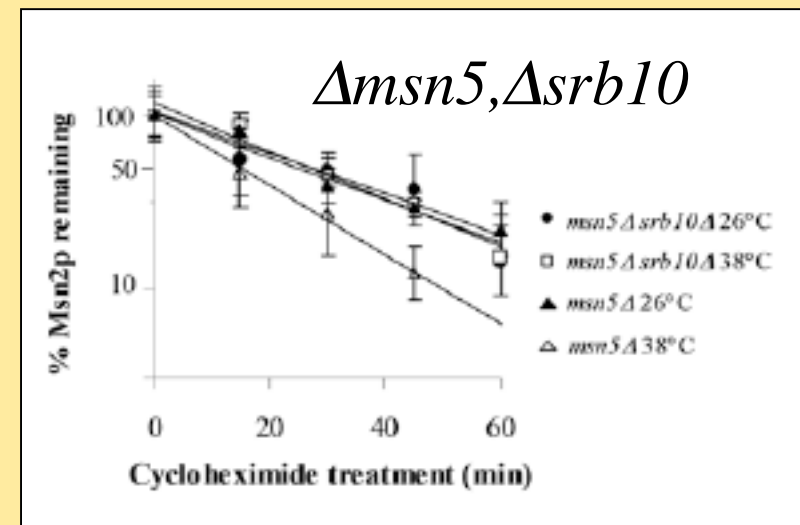
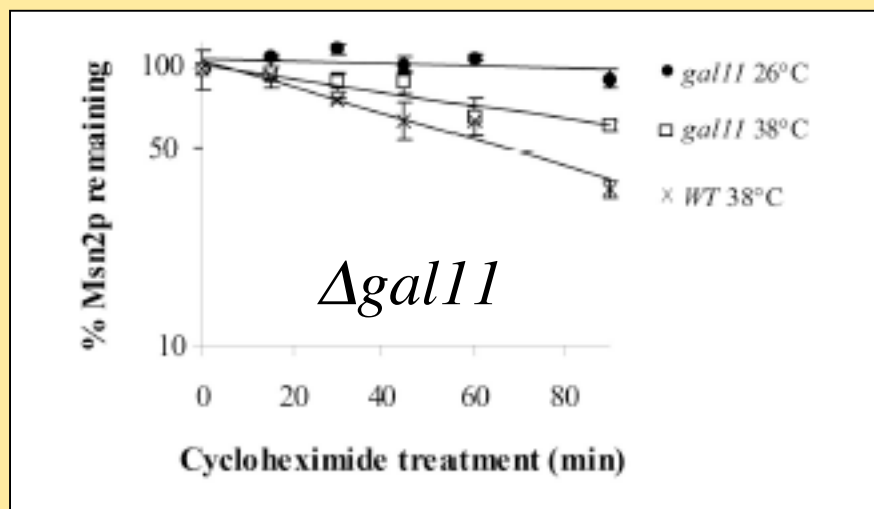
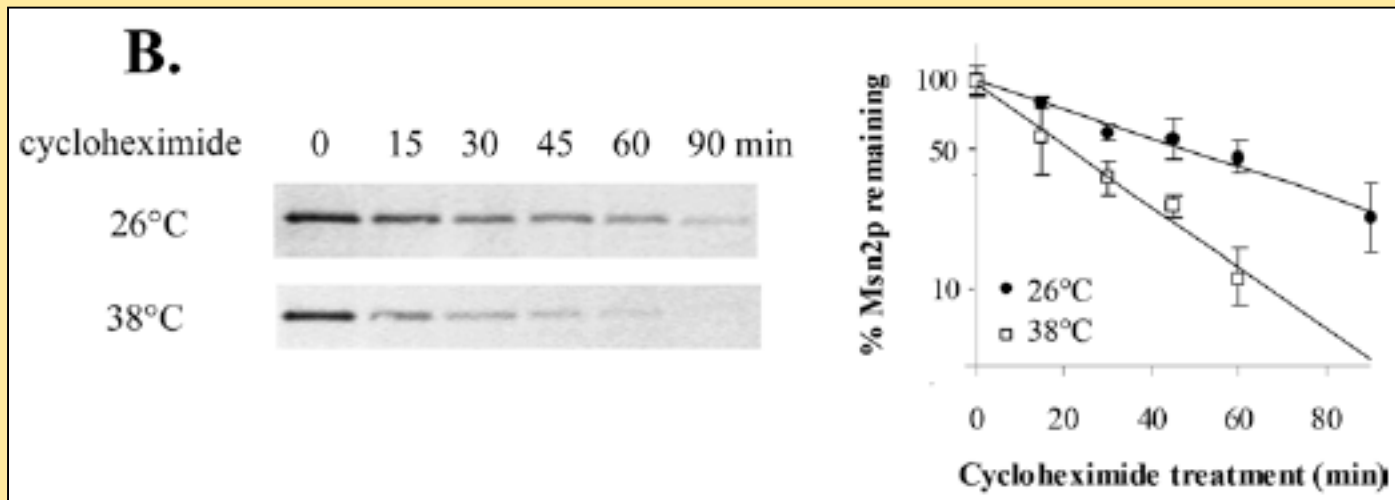
~~*Ste11*~~ = X = ? *Gal11*

# The mediator (R. Kornberg)

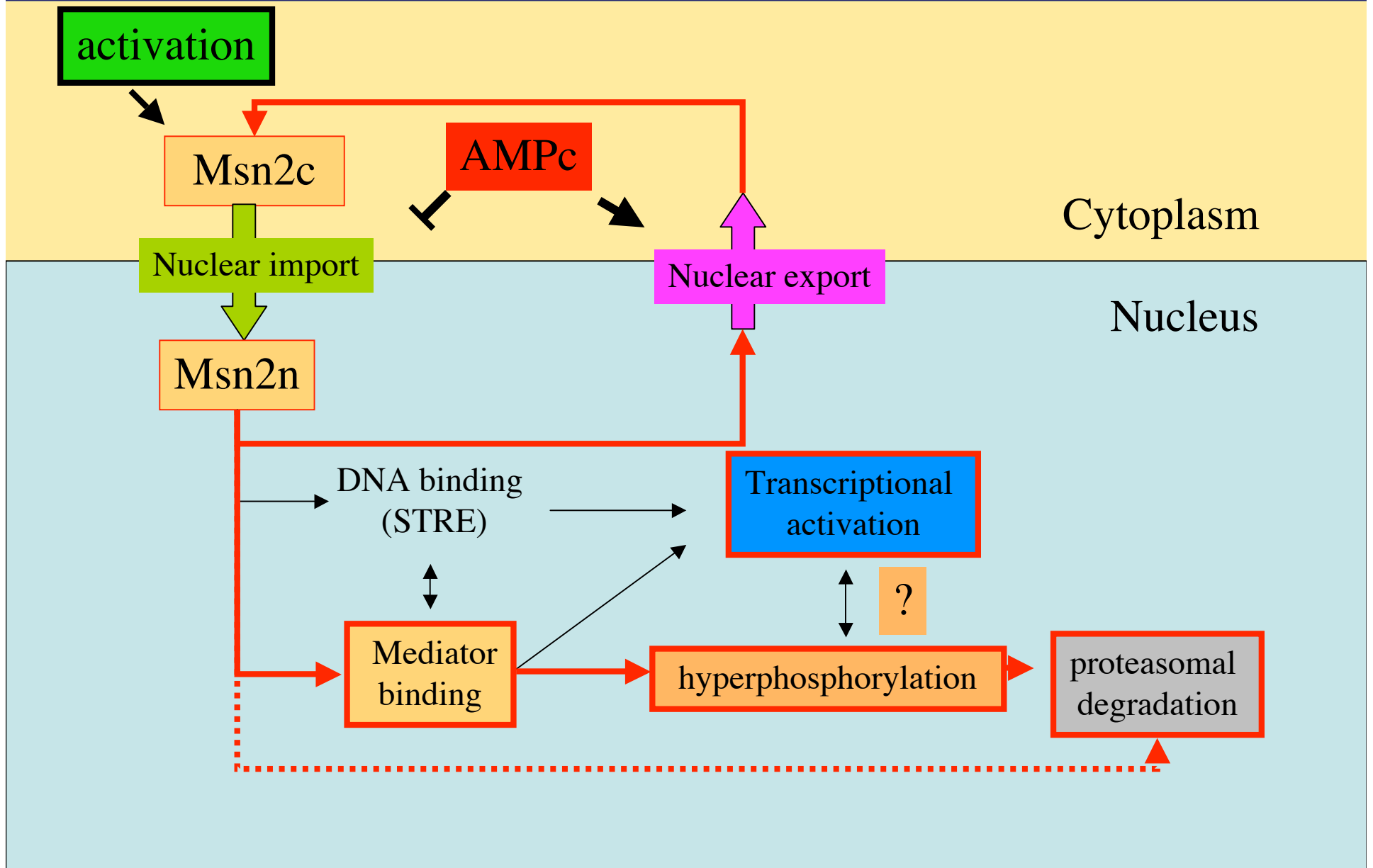


# Degradation of Msn2 occurs upon activation in the nucleus and depends upon Srb10 and Gal11/med15

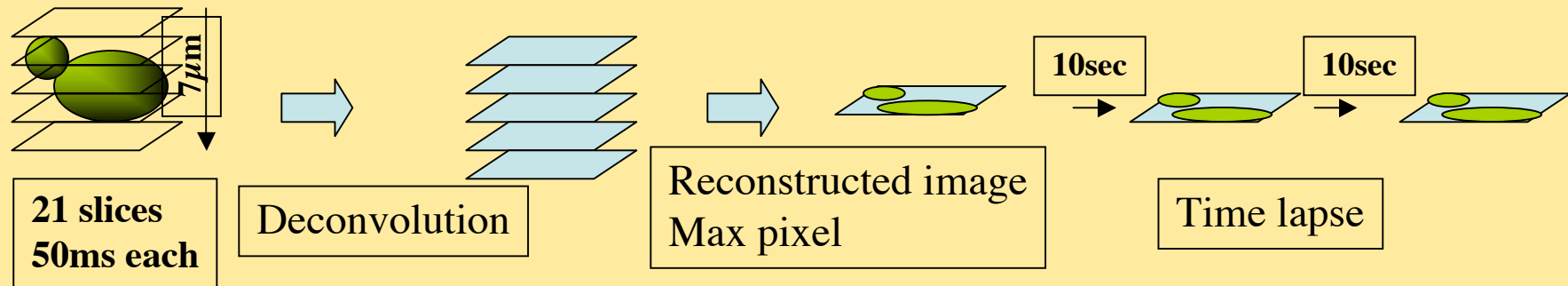
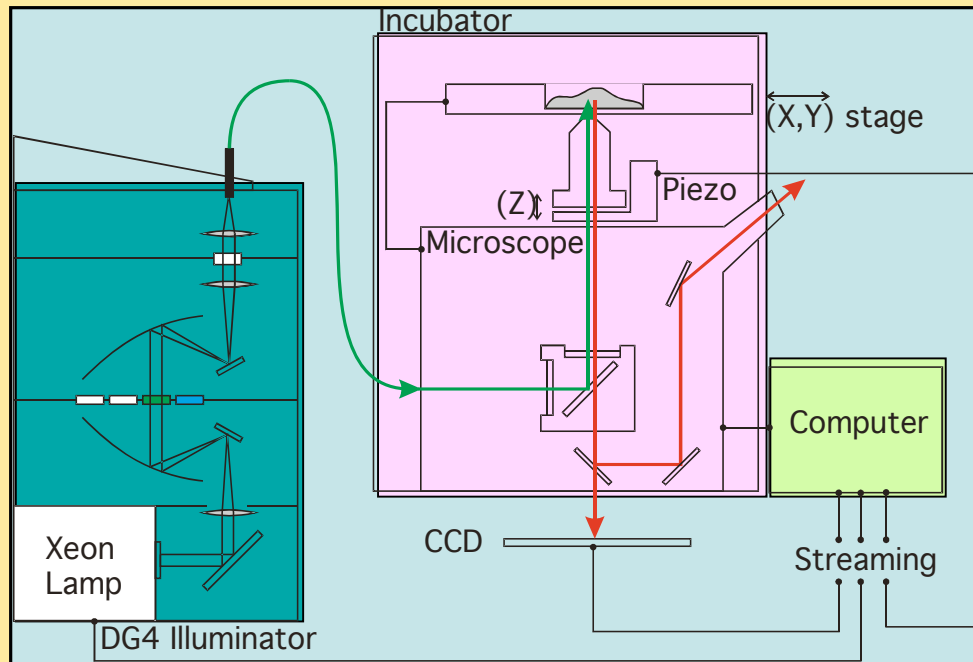
Lallet Mol Genet Genomics. 2004 Oct;272(3):353-62.



# The life of Msn2

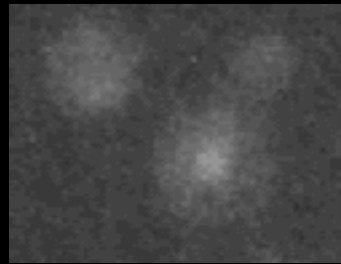


# 3D Ultra-fast video microscope (Jan De Mey)

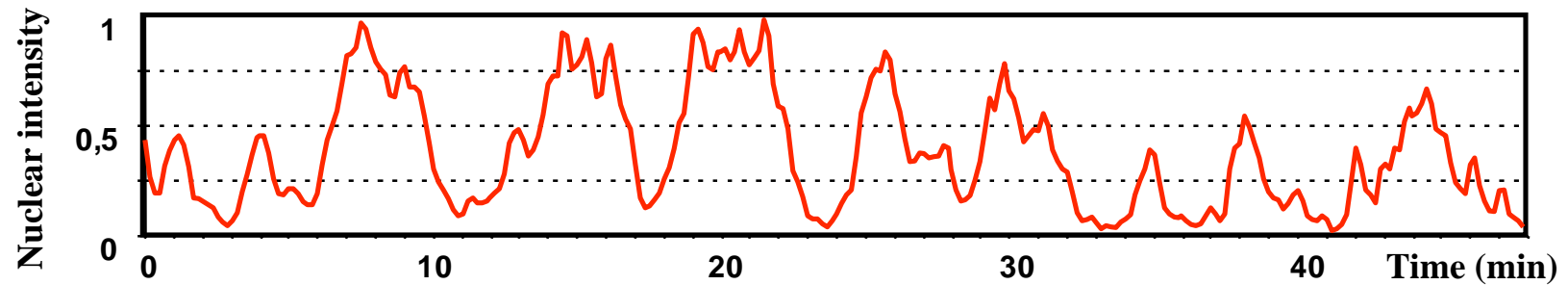




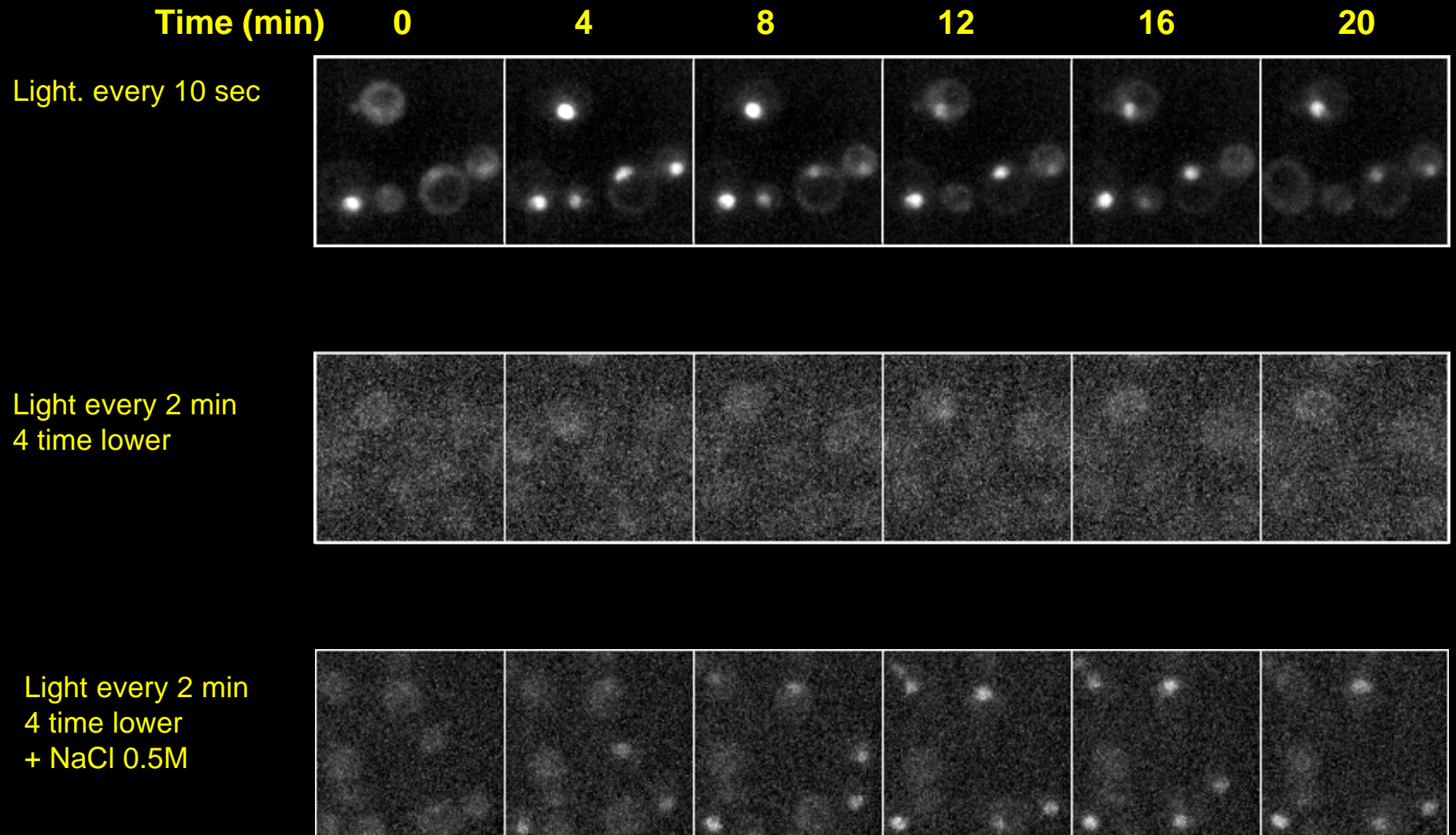
# Kinetics of nucleocytoplasmic localization



Msn2-GFP in WT strain  
48 min

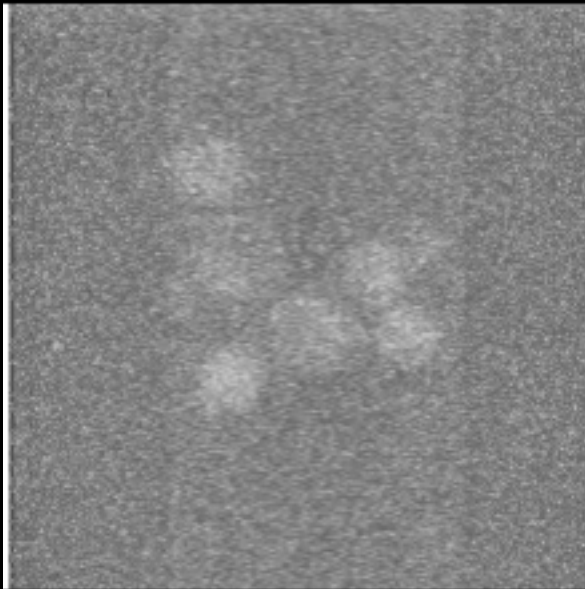


# Is the light a stress for the cell ?



## Is Protein synthesis required ?

Periodic nucleocytoplasmic shuttling of transcriptional activators generally involves feedback loop with delay produced by transcription-translation of an inhibitory product

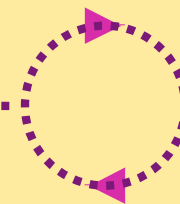
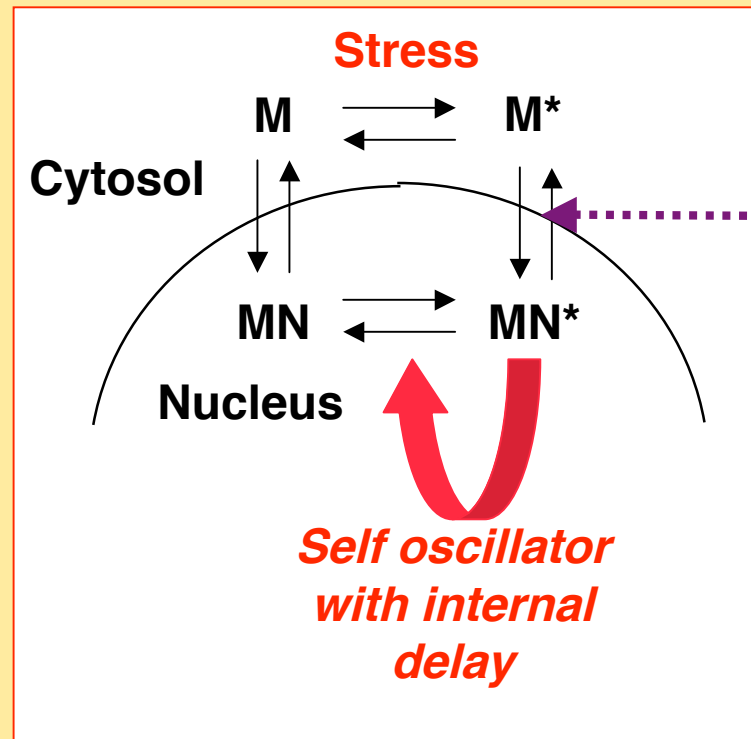


Control



Cycloheximide  
400 $\mu$ g/ml

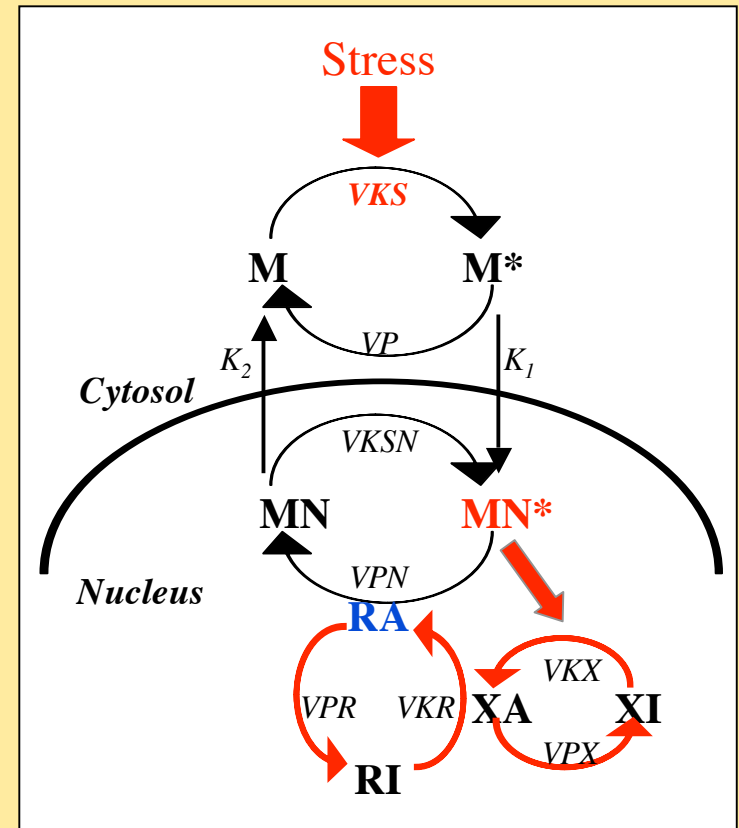
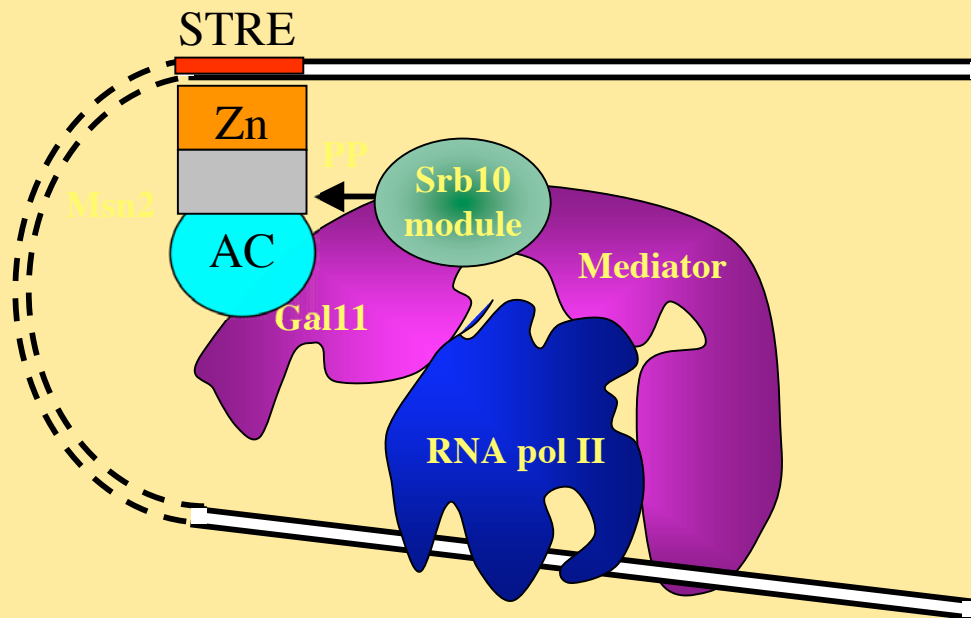
# How to generate an oscillatory behavior ?



*External oscillator*

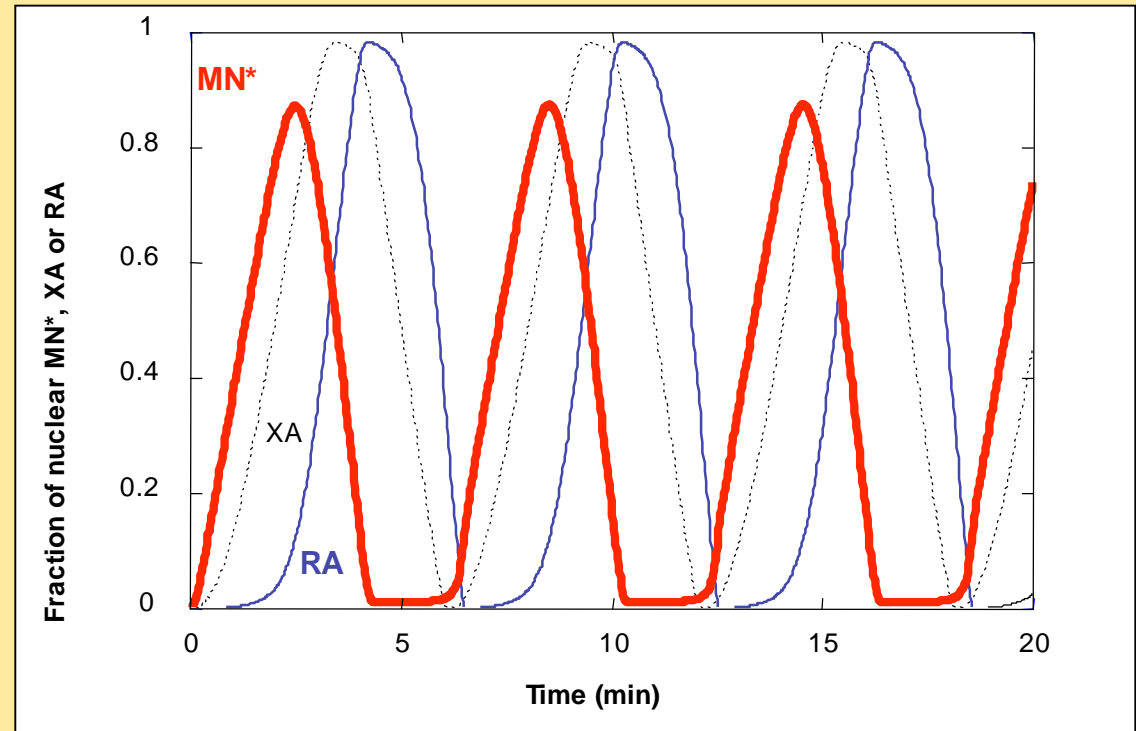
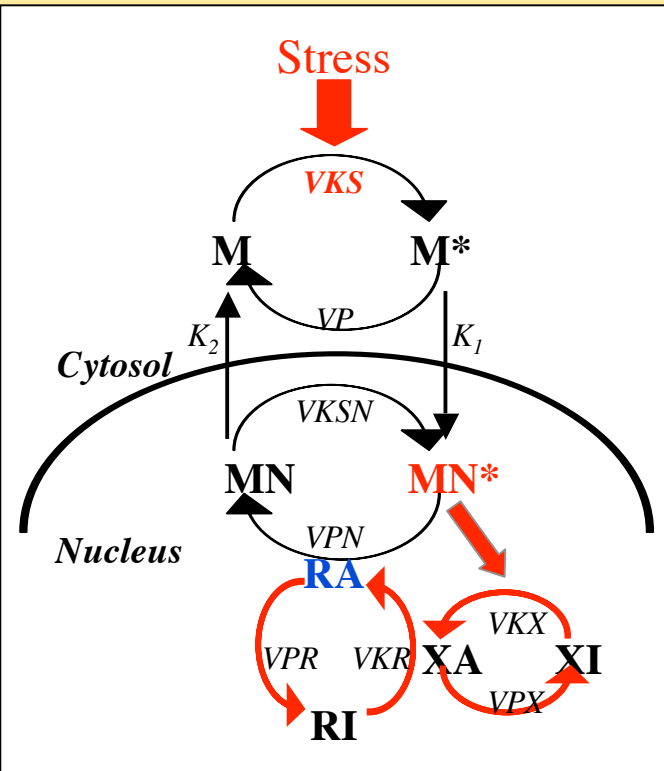


# Some phosphorylation-dephosphorylation process at the transcriptional preinitiation complex



Jacquet M, Renault G, Lallet S, De Mey J, Goldbeter A.  
 J Cell Biol. 2003 161(3):497-505.

# Simulation

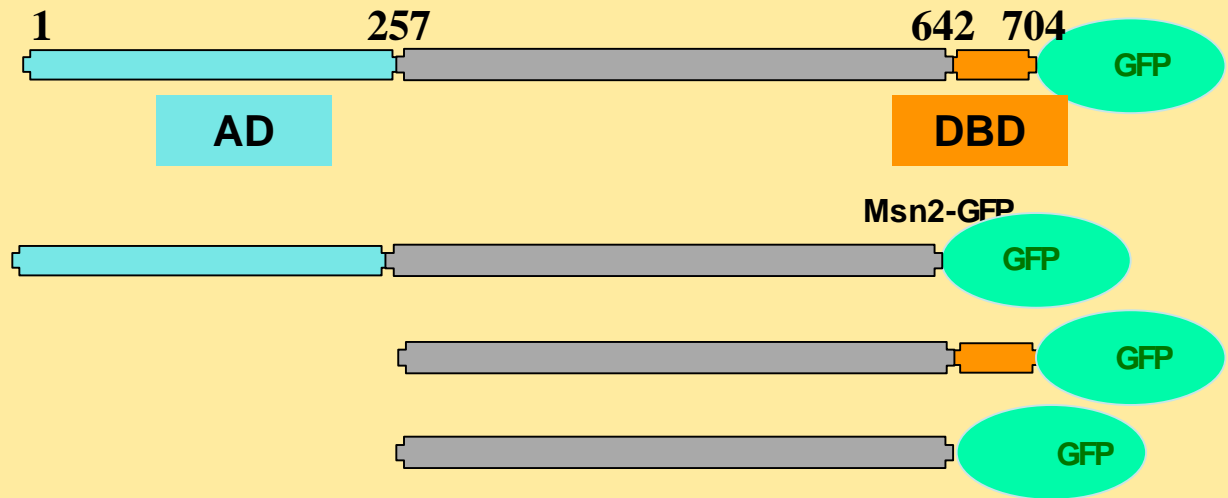
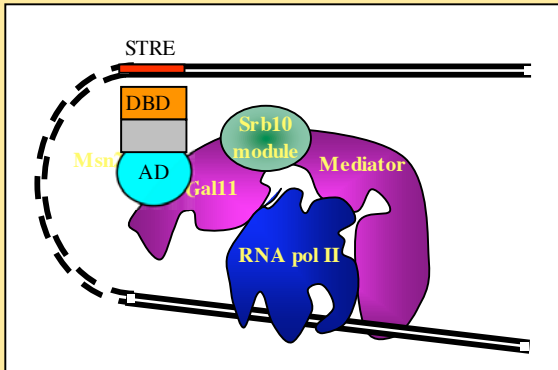


$$\begin{aligned} \frac{dM}{dt} &= -V_1 + V_2 + k_2.MN & V_1 &= V_{KS} \left( \frac{M}{K_1 + M} \right) & V_5 &= V_{KX} \left( \frac{MN^*}{K_{a2} + MN^*} \right) \left( \frac{1-XA}{K_5 + 1-XA} \right) \\ \frac{dM^*}{dt} &= V_1 - V_2 - k_1.M^* & V_2 &= V_P \left( \frac{M^*}{K_2 + M^*} \right) & V_6 &= V_{PX} \left( \frac{XA}{K_6 + XA} \right) \\ \frac{dMN^*}{dt} &= k_1.M^* + V_3 - V_4 & V_3 &= V_{KSN} \left( \frac{MN}{K_3 + MN} \right) & V_7 &= V_{KR} \cdot XA \left( \frac{1-RA}{K_7 + 1-RA} \right) \\ \frac{dMN}{dt} &= V_4 - V_3 - k_2.MN & V_4 &= V_{PN} \left( \frac{RA}{K_{a1} + RA} \right) \left( \frac{MN^*}{K_4 + MN^*} \right) & V_8 &= V_{PR} \left( \frac{RA}{K_8 + RA} \right) \\ \frac{dXA}{dt} &= V_5 - V_6 \\ \frac{dRA}{dt} &= V_7 - V_8 \end{aligned}$$

6 variables,  
10 equations

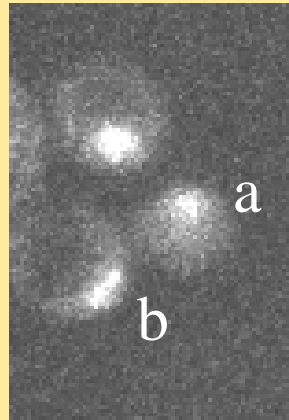
Jacquet M, Renault G, Lallet S, De Mey J, Goldbeter A.  
J Cell Biol. 2003 161(3):497-505.

# Domains of MSN2 dispensables for oscillations

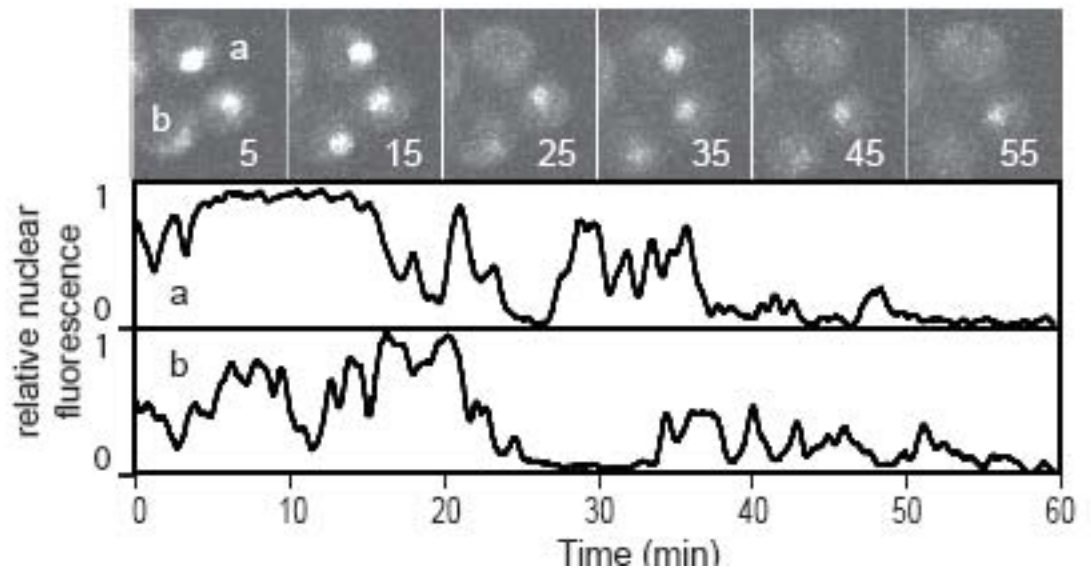


Cecilia  
Garmendia-  
Torres

$\Delta AD, \Delta DBD$  1h

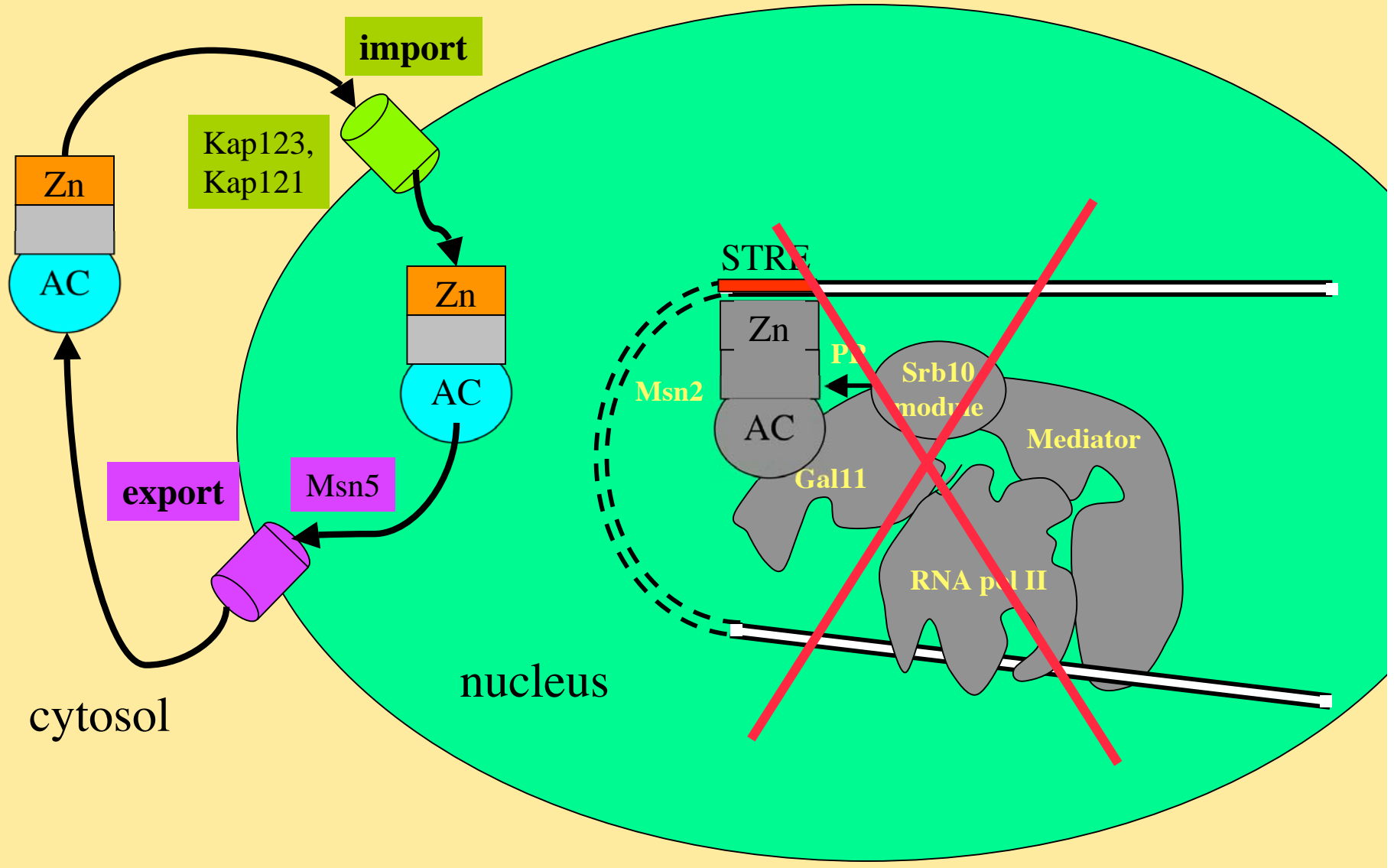


D

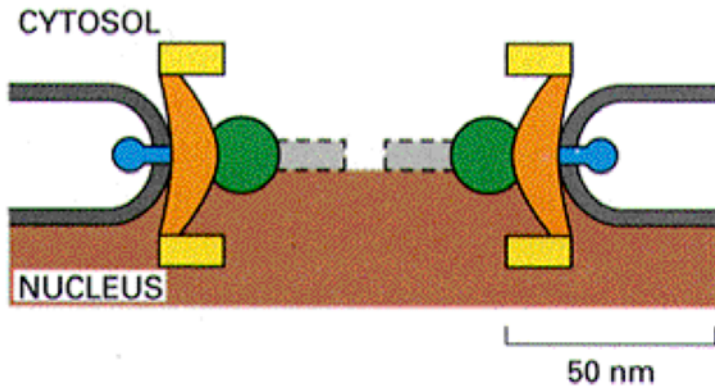




# Interaction with the preinitiation complex of transcription is not essential for the oscillatory behavior



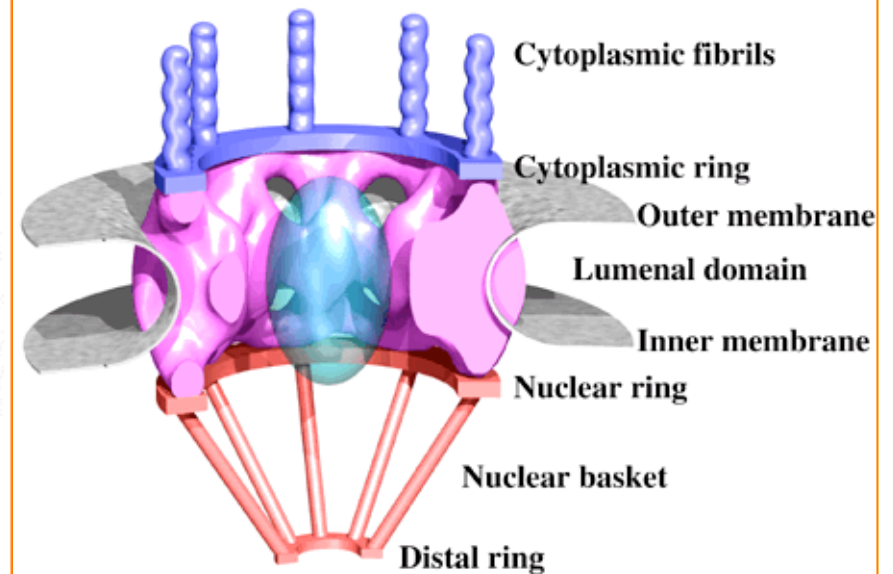
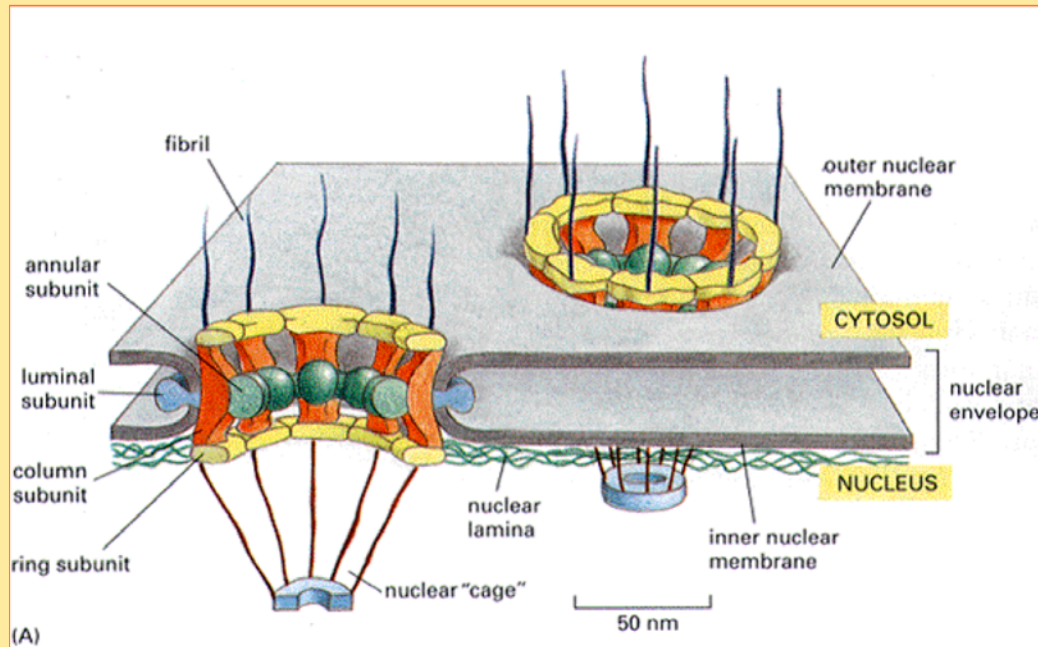
# Nuclear pore



size of proteins  
that enter nucleus  
by free diffusion

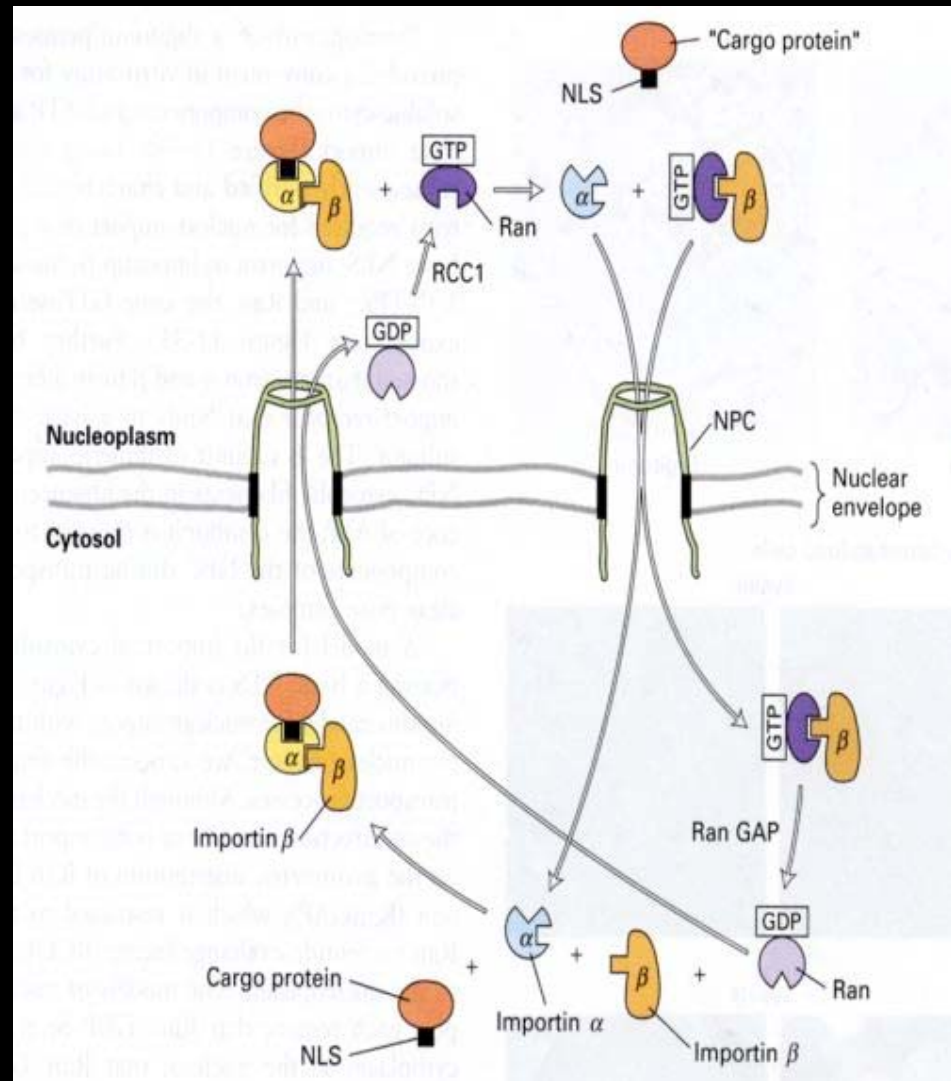


size of proteins  
that enter nucleus  
by active transport



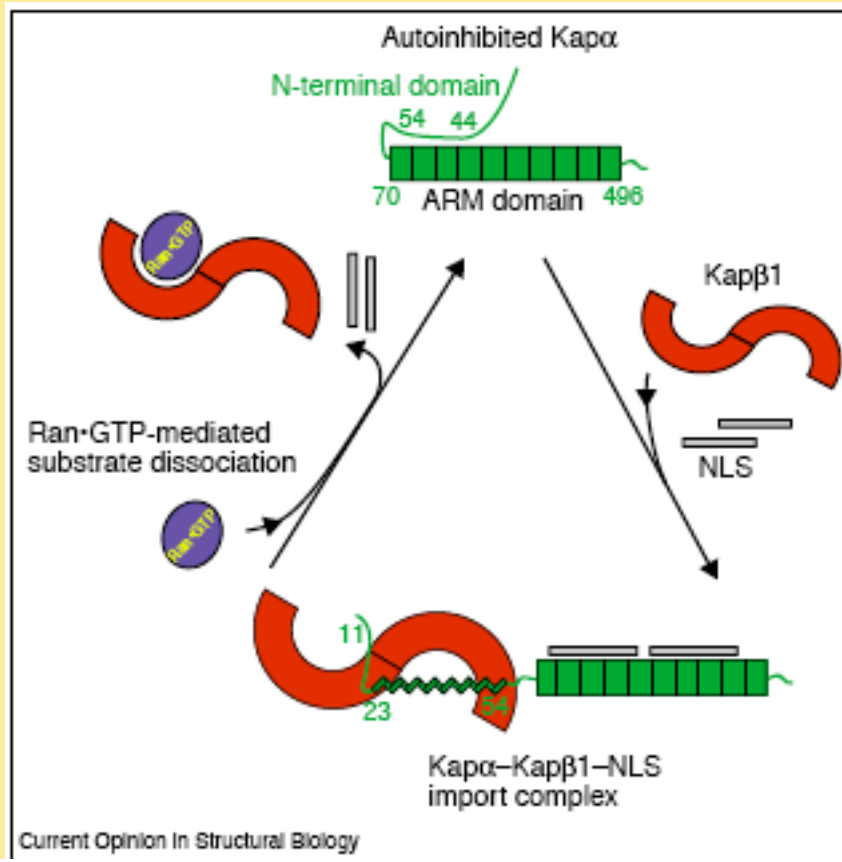
# Nuclear Import Mechanisms

- Proteins to be exported into nucleus have **Nuclear Localization Signals (NLS's)** that enable nuclear import.
- **NLS's** bind to **importin  $\alpha$**  subunit of an importin  $\alpha$ - $\beta$  complex.
- Transport through the NPC is mediated by interaction of degenerative sequences in the NPC proteins with the **importin  $\beta$**  subunit.
- Key to function and regulation are **RAN GTP** [high in nucleus by **RCC1** (Ran nucleotide exchange factor)] & **RAN GDP** [high in cytoplasm by **RAN GAP** (RAN GTP activating protein)].
- The asymmetric distribution of **RCC1** in the nucleus and **RAN GAP** in the cytoplasm drives the nuclear import process.



# Karyopherins and nuclear import

Yuh Min Chook\* and Günter Blobel†

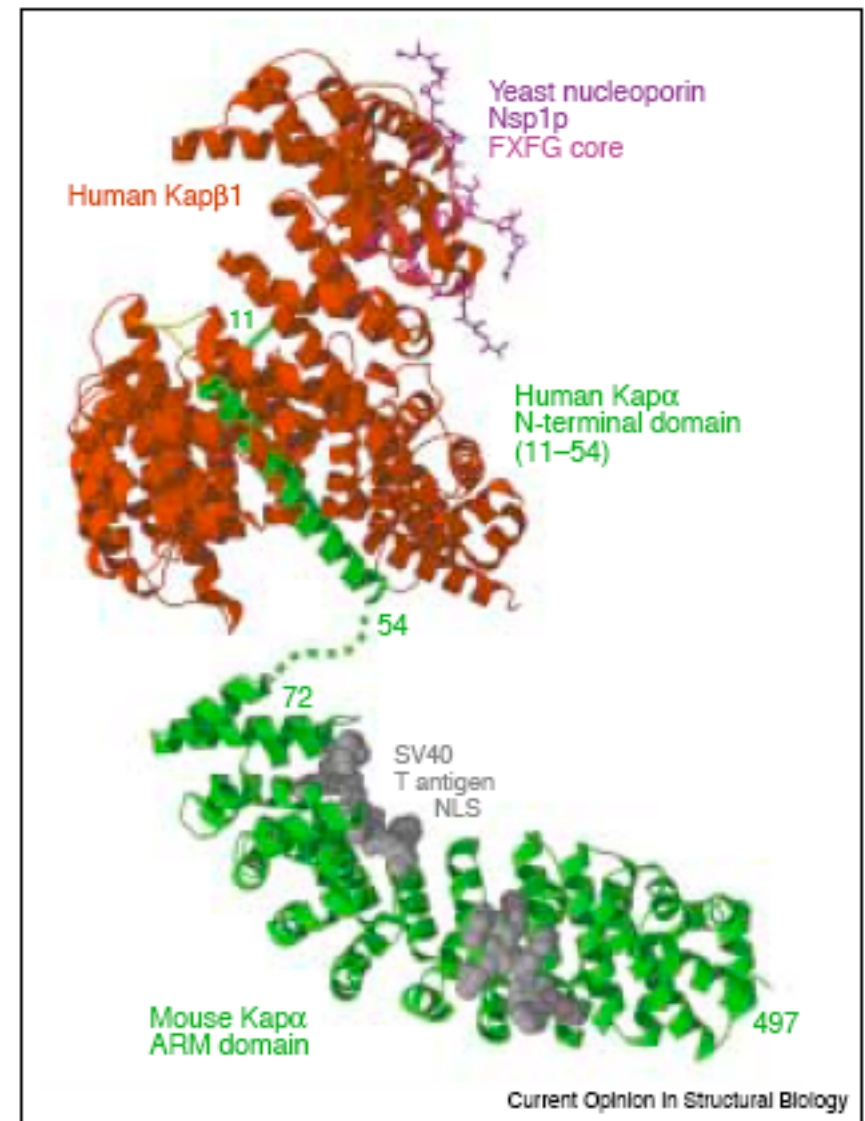


Current Opinion In Structural Biology

Current Opinion in Structural Biology 2001, 11:703-715

0959-440X/01/\$ – see front matter

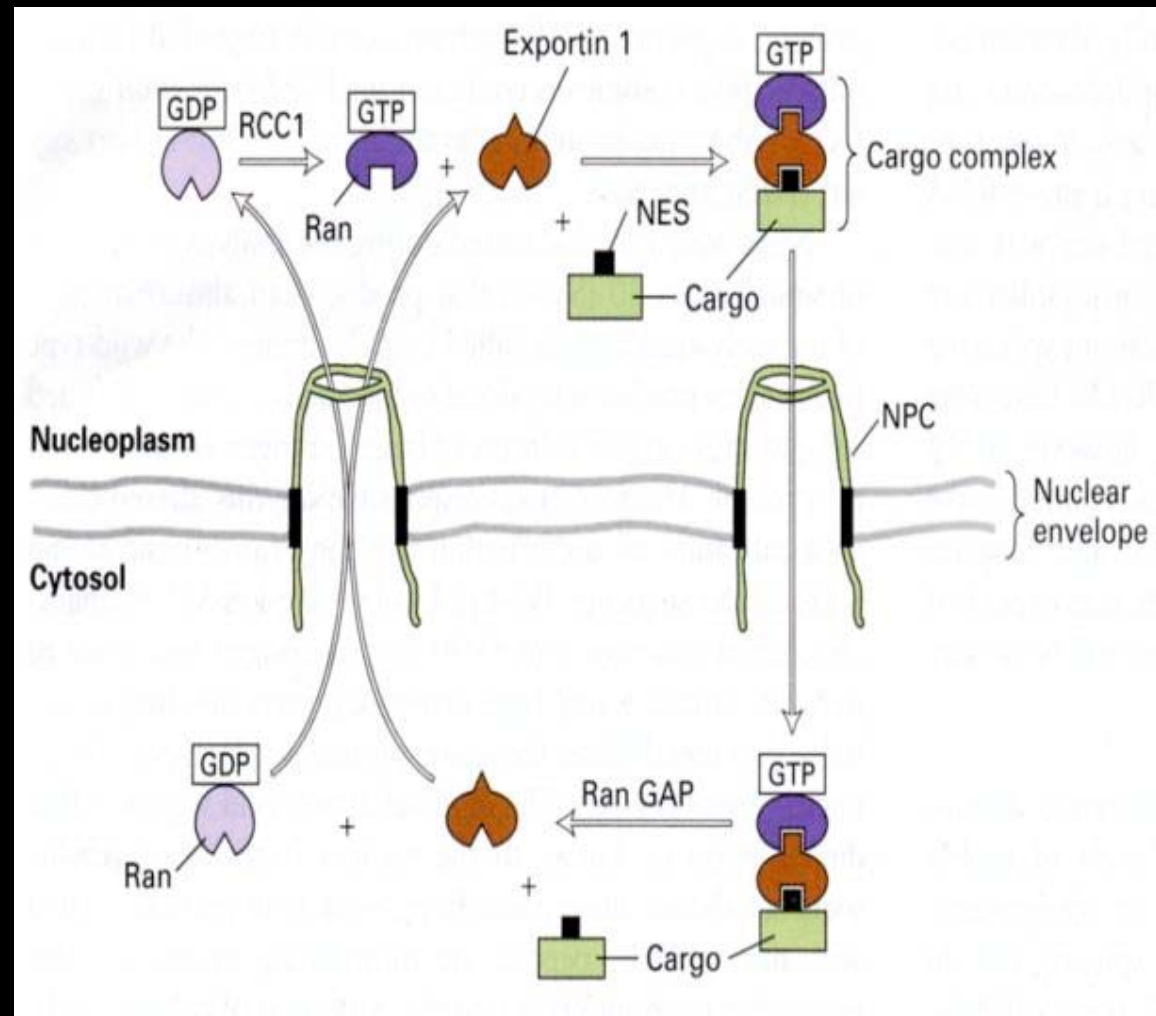
© 2001 Elsevier Science Ltd. All rights reserved.



Current Opinion In Structural Biology

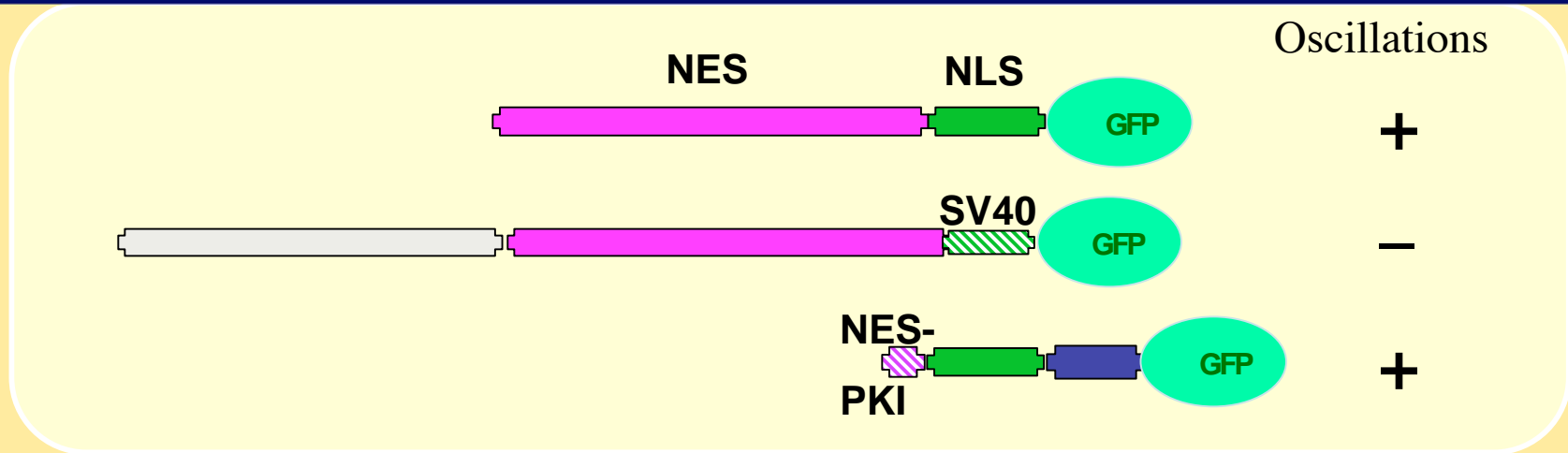
# NUCLEAR EXPORT

- The exporting proteins have special sequences called **Nuclear Export Signals (NES's)** that mediate export through binding to a class of proteins that function in export called *exportins*.
- Exportins are typically monomeric and function in a reverse manner to importin under the control of RAN.
- Thus the cargo complex requires **RAN-GTP** which is found only in the nucleus.
- Disassociation of the 'cargo' from the exportin requires **RAN-GDP** which occurs only in the cytoplasm.

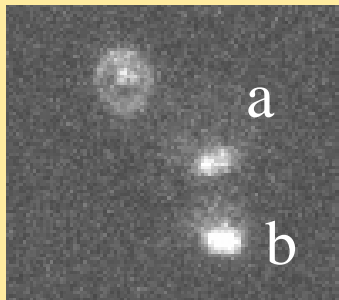




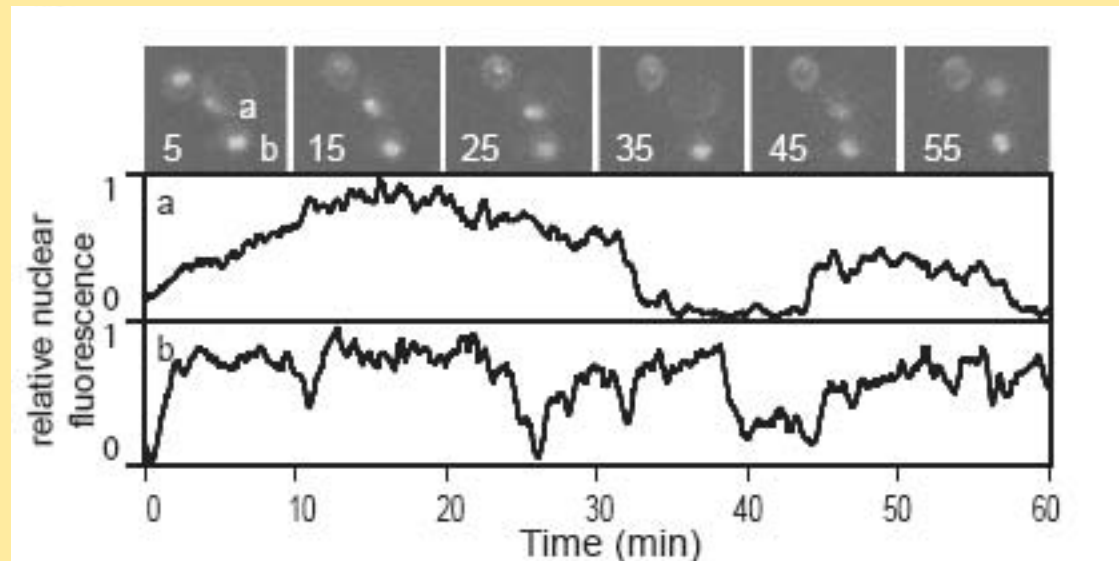
# Swapping NLS and NES



NLS-Msn2, NES-PKI



1h



The NLS region is sufficient for the oscillatory behavior

# The NLS domain of Msn2

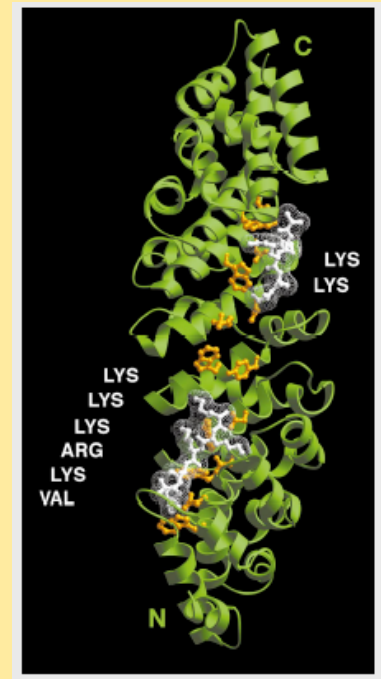
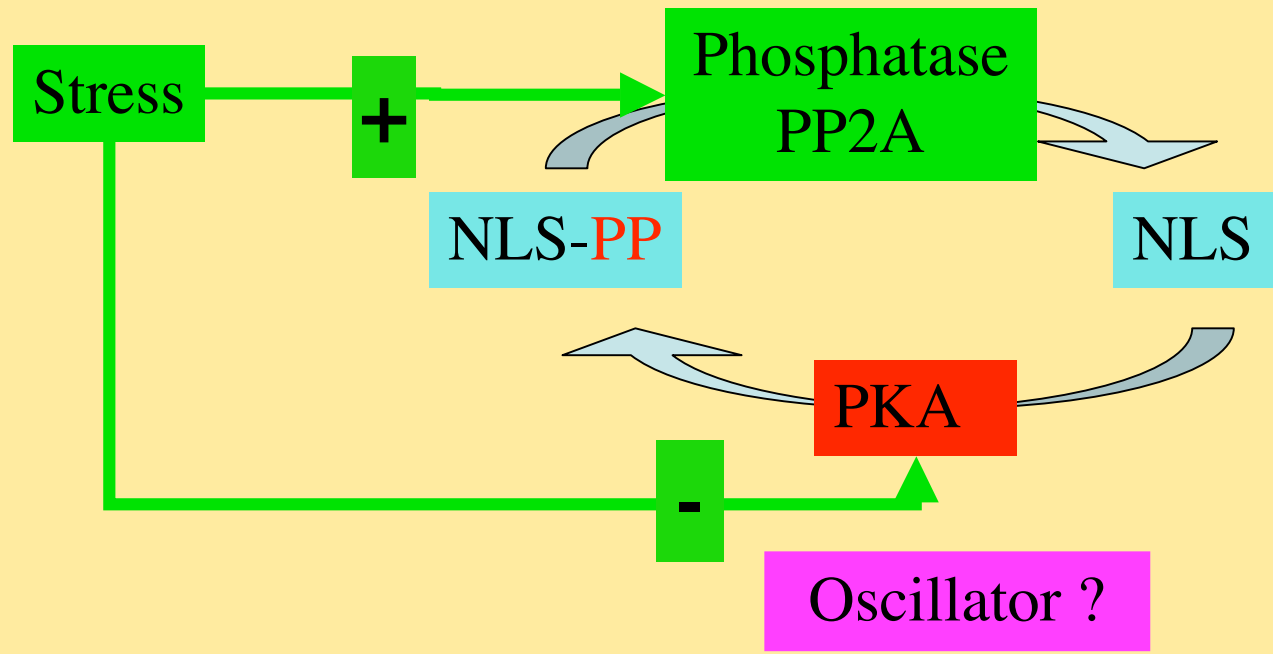
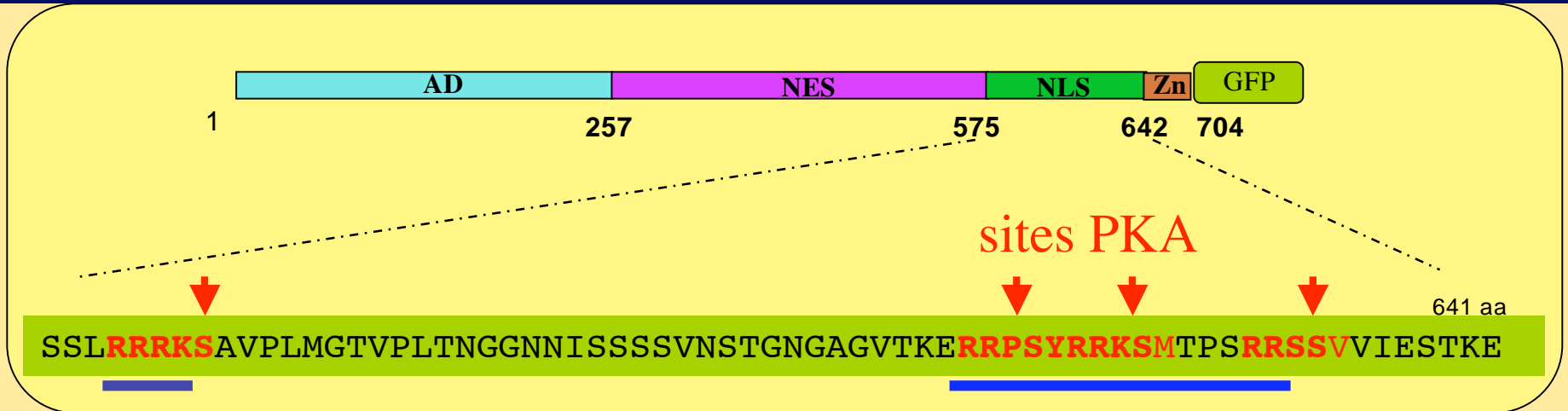
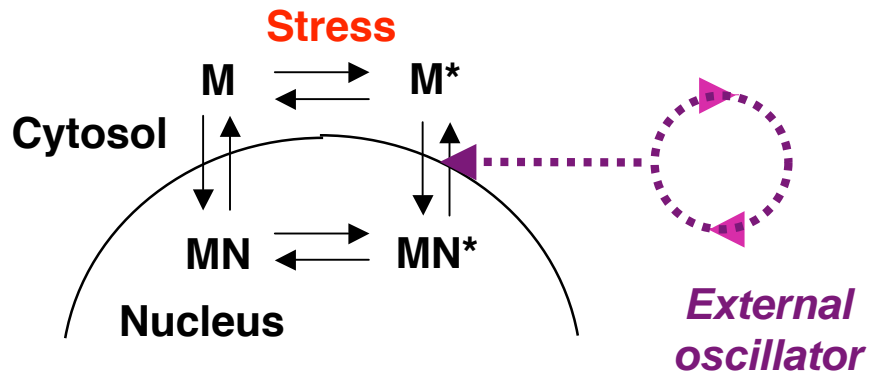


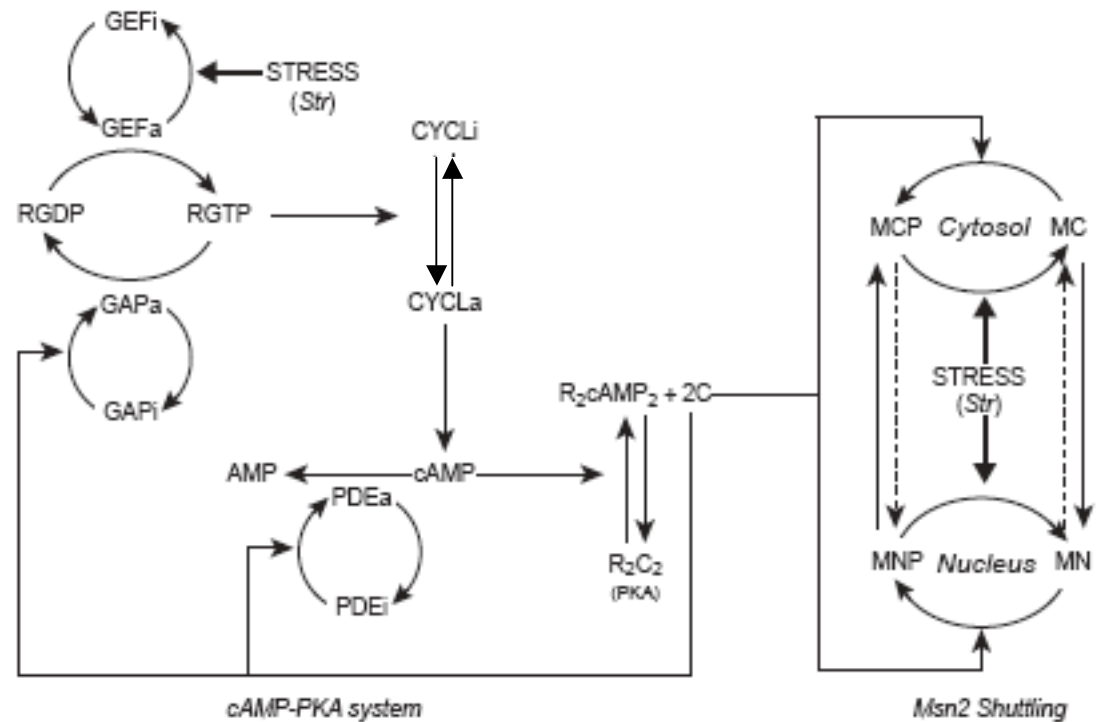
FIGURE 5  
Yeast (*Saccharomyces cerevisiae*) karyopherin- $\alpha$ .  
Image kindly provided by Elena Conti,  
Heidelberg, Germany.



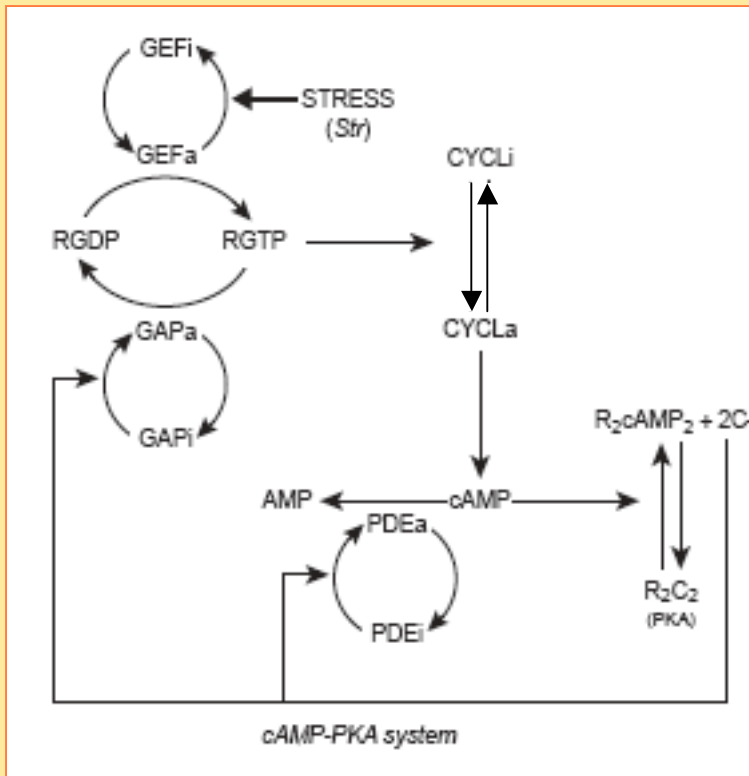
# The new model



Curr Biol. 2007 Jun 19; 17(12):1044-9.  
 Nucleocytoplasmic Oscillations of the Yeast  
 Transcription Factor Msn2: Evidence for Periodic PKA  
 Activation.  
 Garmendia-Torres C, Goldbeter A, Jacquet M.



# Negative feedback upon cAMP accumulation



| Strain          | TPK1 | TPK2 | TPK3 | BCY1 | cAMP level (pmole/mg prot) |
|-----------------|------|------|------|------|----------------------------|
| S7-1A           | +    | -    | -    | +    | 2,5                        |
| S13-58A         | +    | -    | -    | -    | 0,5                        |
| S18-3B          | W1   | -    | -    | +    | 1500                       |
| RS13-58A1       | W1   | -    | -    | -    | 570                        |
| S7-1B           | -    | +    | -    | +    | 3,7                        |
| S13-7C          | -    | +    | -    | -    | 0,3                        |
| S13-7C          | -    | W1   | -    | +    | 3400                       |
| S15-5BRS13-7C-1 | -    | W1   | -    | -    | 3400                       |

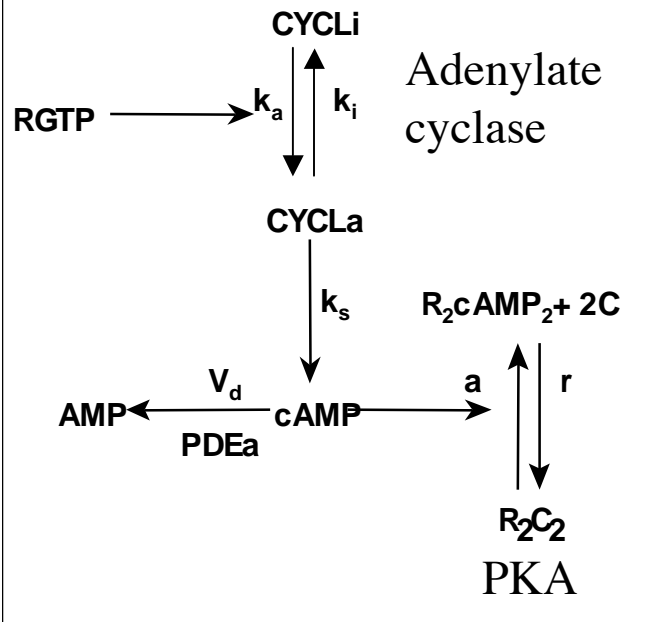
| Strain    | Genotype |      |      |      | cAMP level (pmole/mg prot) |      |      |
|-----------|----------|------|------|------|----------------------------|------|------|
|           | RAS1     | RAS2 | PDE1 | PDE2 | Exp1                       | Exp2 | Exp3 |
| SP1       | +        | G    | +    | +    | 1,7                        | 1,6  | 1,8  |
| TK161-R2V | +        | V    | +    | +    | 2,7                        | ND   | 3,5  |
| DJ23-3C   | +        | G    | -    | -    | 3,6                        | ND   | ND   |
| DJ31-4D   | +        | V    | -    | -    | 2300                       | 450  | 3000 |
| DJ31-6A   | +        | V    | -    | -    | ND                         | 3500 | ND   |

Rigorous feedback control of cAMP levels in *Saccharomyces cerevisiae*.

[Nikawa J](#), [Cameron S](#), [Toda T](#), [Ferguson KM](#), [Wigler M](#).

[Genes Dev.](#) 1987 Nov;1(9):931-7

# cAMP variations and PKA activation



## Equations

$$\frac{dCYCLa}{dt} = k_a(RGTP)(RAS_t)(1 - CYCLa) - k_iCYCLa$$

$$\frac{dcAMP}{dt} = k_s(CYCLa)(CYCL_t) - k_d(PDE_t) \frac{cAMP}{K_{md} + cAMP} - 2V_{PKA_t}PKA_t$$

$$\frac{dR_2C_2}{dt} = -a(R_2C_2)(cAMP)^2 + rC^2(R_2cAMP_2)(PKA_t)^2$$

$$R_2cAMP_2 = 1 - R_2C_2, C = 2(1 - R_2C_2)$$

## Parameters

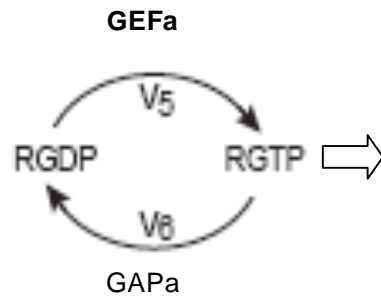
| Kinetic steps                   | Parameters       | Values                                       |
|---------------------------------|------------------|--|
| Activation of adenylate cyclase | CYCLt (Cyr1)     | 0.7 $\mu$ M                                  |
|                                 | $k_a$            | 0.01 $\mu$ M <sup>-1</sup> min <sup>-1</sup> |
|                                 | $k_i$            | 1 min <sup>-1</sup>                          |
| Production of cAMP              | $k_s$            | 4 min <sup>-1</sup>                          |
| Activation of phosphodiesterase | PDEt             | 0.5 $\mu$ M                                  |
|                                 | $k_{c7}$         | 3.333 min <sup>-1</sup>                      |
|                                 | $V_{Max8}$       | 1.5 $\mu$ M min <sup>-1</sup>                |
|                                 | $K_7$            | 0.01   |
|                                 | $K_8$            | 0.01   |
| Degradation of cAMP             | $k_d$            | 100 min <sup>-1</sup>                        |
|                                 | $K_{md}$         | 20 $\mu$ M                                   |
| Activation of PKA               | PKAt (Bcyl, Tpk) | 0.3 $\mu$ M                                  |
|                                 | $a$              | 1 $\mu$ M <sup>-2</sup> min <sup>-1</sup>    |
|                                 | $r$              | 1 min <sup>-1</sup>                          |

## Simplifications

Only one type Ras protein

Only one type Phosphodiesterase protein

# The ras module



## Equations

$$\frac{dRGTP}{dt} = V_{M5}^{GEFa} \frac{(1 - RGTP)}{K_5 + (1 - RGTP)} - V_{M6}^{GAPa} \frac{RGTP}{K_6 + RGTP}$$

$$V_5 = k_{gef} \text{GEFt/RASt}, V_6 = k_{gap} \text{GAPt/RASt}$$

## Parameters

| Ghaemmaghami, <i>et al.</i> ,<br><i>Nature</i> 425, 737-741 (2003) | N per cell   | Cellular concentration<br>(30fl) | Cortical concentration<br>(X 250) |
|--|--------------|----------------------------------|-----------------------------------|
| GEF = Cdc25  | 320          | 16 nM                            | 4 μM                              |
| GAP = Ira1 + Ira2  | nd           |                                  | 1.5 μM                            |
| RAS = Ras1 + Ras2  | 2000 + 20000 | 1.1 μM                           | 250 μM                            |

|                                  |   |
|----------------------------------|---|
| Kd(R <sub>GDP</sub> ) = 0.16 μM; | Kcat <sub>CDC25</sub> = 240 min <sup>-1</sup> |
| Kd(R <sub>GTP</sub> ) = 0.25 μM; | Kcat <sub>GAP</sub> = 600 min <sup>-1</sup>   |

## Ultrasensitivity:

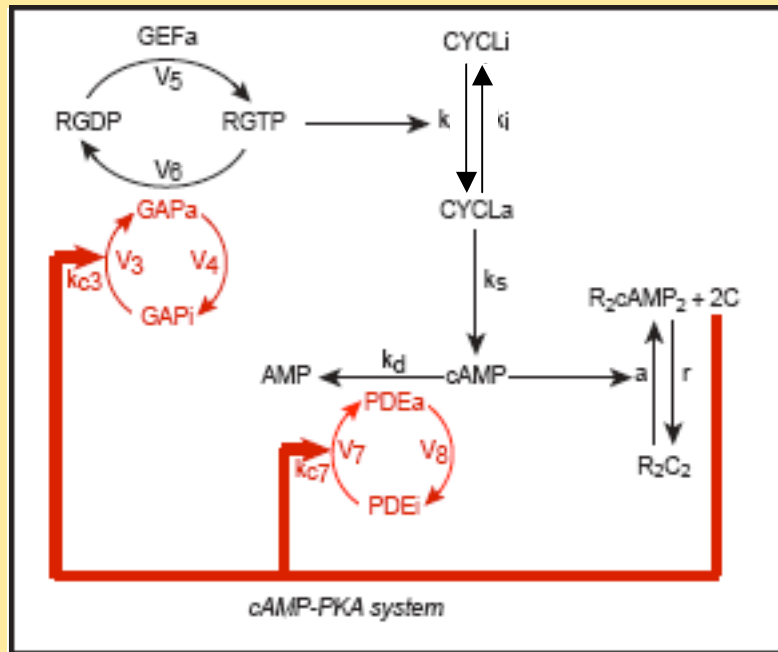
$$[RAS] > [GEF] \text{ et } [GAP]$$

$$250 > 4 ; 1.5$$

$$[RAS] \gg K_d(R_{GDP}) \text{ et } K_d(R_{GTP})$$

$$250 \gg 0.16 ; 0.25$$

# Modeling the negative feedback loop



$$\frac{dGAPa}{dt} = V_{M3} C \frac{(1 - GAPa)}{K_3 + (1 - GAPa)} - V_{M4} \frac{GAPa}{K_4 + GAPa}$$

$$\frac{dPDEa}{dt} = V_{M7} C \frac{(1 - PDEa)}{K_7 + (1 - PDEa)} - V_{M8} \frac{PDEa}{K_8 + PDEa}$$

$$V_3 = k_{c3} PKAt / GAPt, V_4 = V_{max4} / GAPt$$

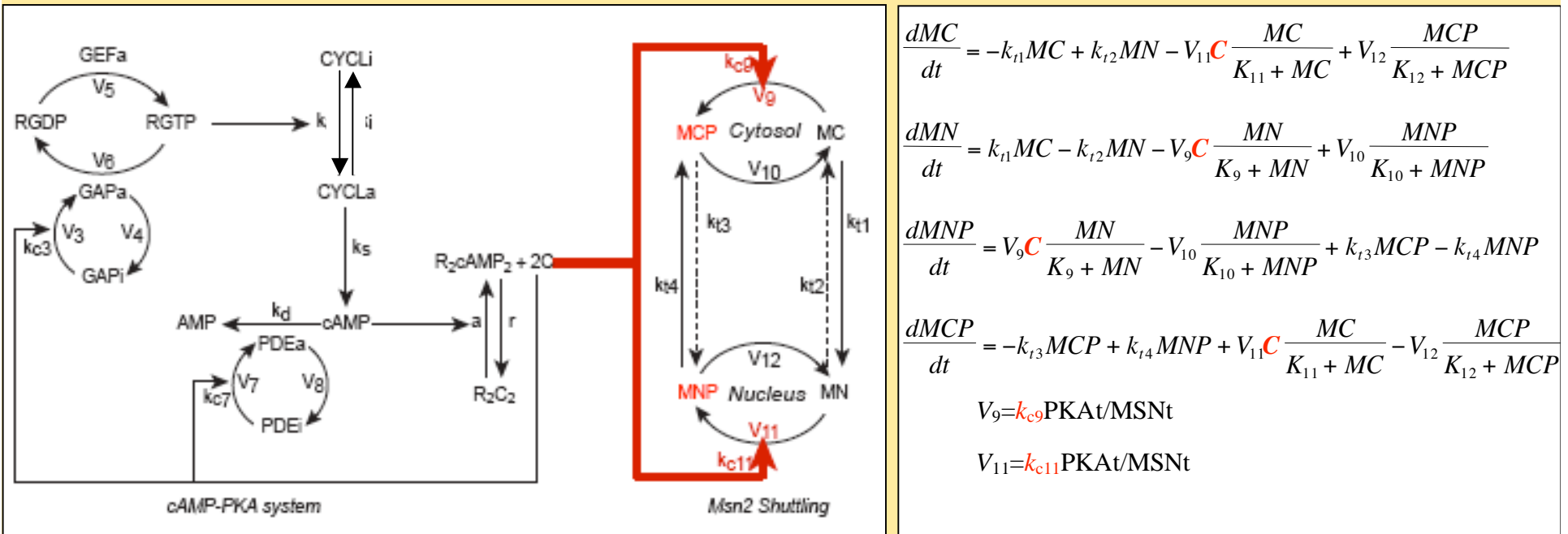
$$V_7 = k_{c7} PKAt / PDEt, V_8 = V_{max8} / PDEt$$

## Assumption

Two different targets PDE and GAP

Similar effect of PKA on each

# Coupling Msn2 to the cAMP-PKA pathway



$$\frac{dMC}{dt} = -k_{i1}MC + k_{i2}MN - V_{11}C \frac{MC}{K_{11} + MC} + V_{12} \frac{MCP}{K_{12} + MCP}$$

$$\frac{dMN}{dt} = k_{i1}MC - k_{i2}MN - V_9C \frac{MN}{K_9 + MN} + V_{10} \frac{MNP}{K_{10} + MNP}$$

$$\frac{dMNP}{dt} = V_9C \frac{MN}{K_9 + MN} - V_{10} \frac{MNP}{K_{10} + MNP} + k_{t3}MCP - k_{t4}MNP$$

$$\frac{dMCP}{dt} = -k_{t3}MCP + k_{t4}MNP + V_{11}C \frac{MC}{K_{11} + MC} - V_{12} \frac{MCP}{K_{12} + MCP}$$

$V_9 = k_{c9}PKA_t/MSN_t$   
 $V_{11} = k_{c11}PKA_t/MSN_t$

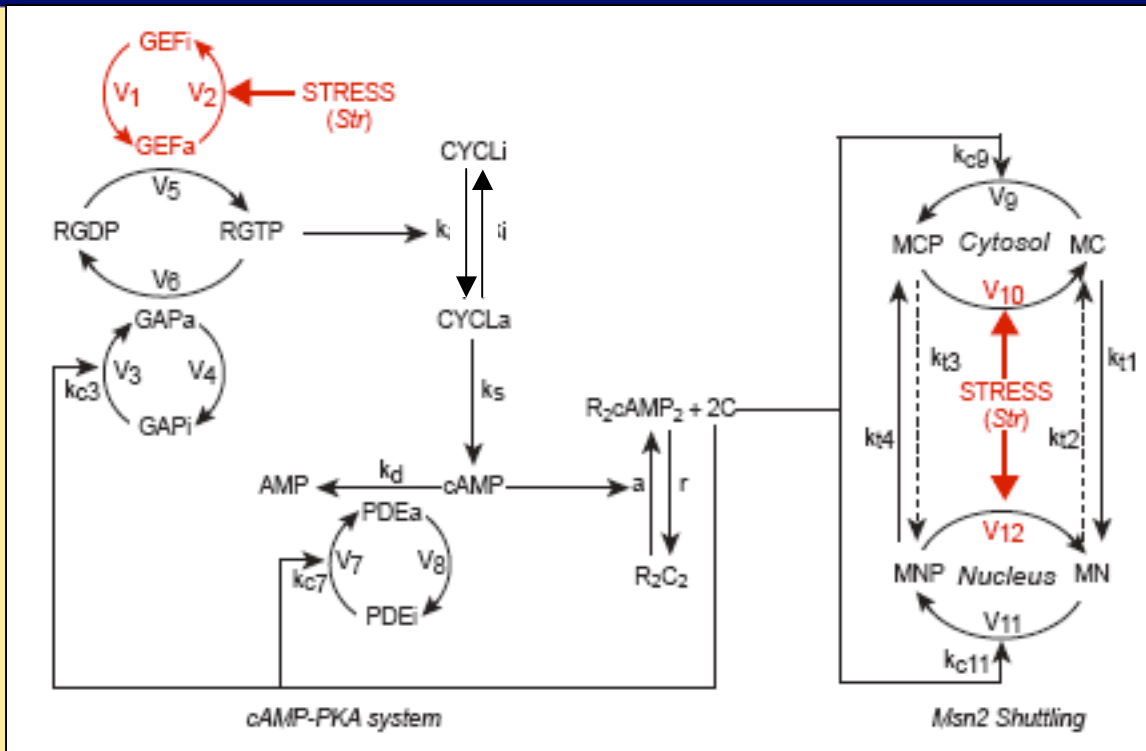
## Simplified assumptions

Only one phosphorylation dephosphorylation event

Same concentration of PKA and Phosphatase in cytosol and nucleus

Direct effect of stress upon the phosphatase in and out the nucleus

# Applying stress



$$\frac{dGEFa}{dt} = V_{M1} \frac{(1 - GEFa)}{K_1 + (1 - GEFa)} - V_{M2} \frac{GEFa}{K_2 + GEFa}$$

$$V_{M1} = \text{Str} V_{\max1}/GEFt, \quad V_{M2} = V_{\max2}/GEFt$$

$$V_{10} = \text{Str} V_{\max10}/MSNt$$

$$V_{12} = \text{Str} V_{\max12}/MSNt$$

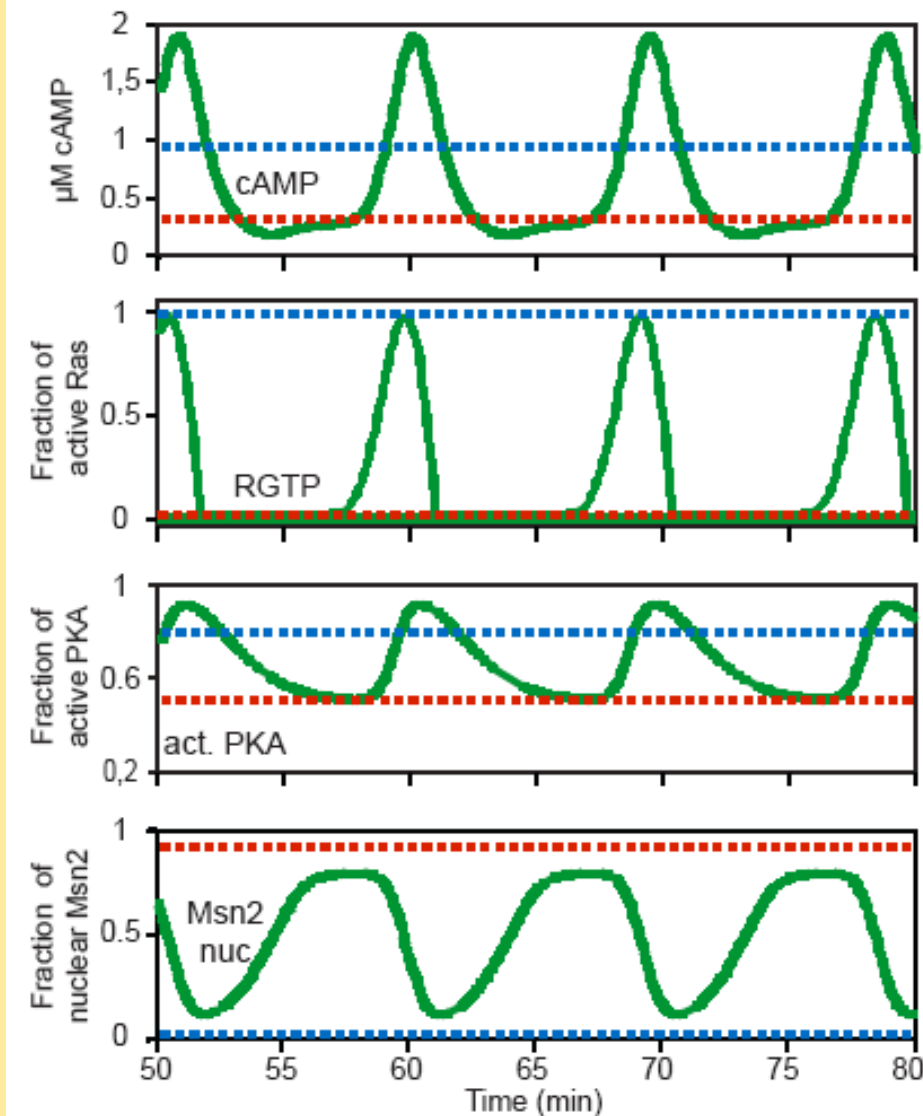
## Simplified assumptions

Stress reduces GEF activity (Wang et al. Microbiology. 2004 150: 3383-91.)

Stress is acting on the dephosphorylation step of Msn2 (PKA independent)



# Linear and oscillatory behaviors as a function of stress



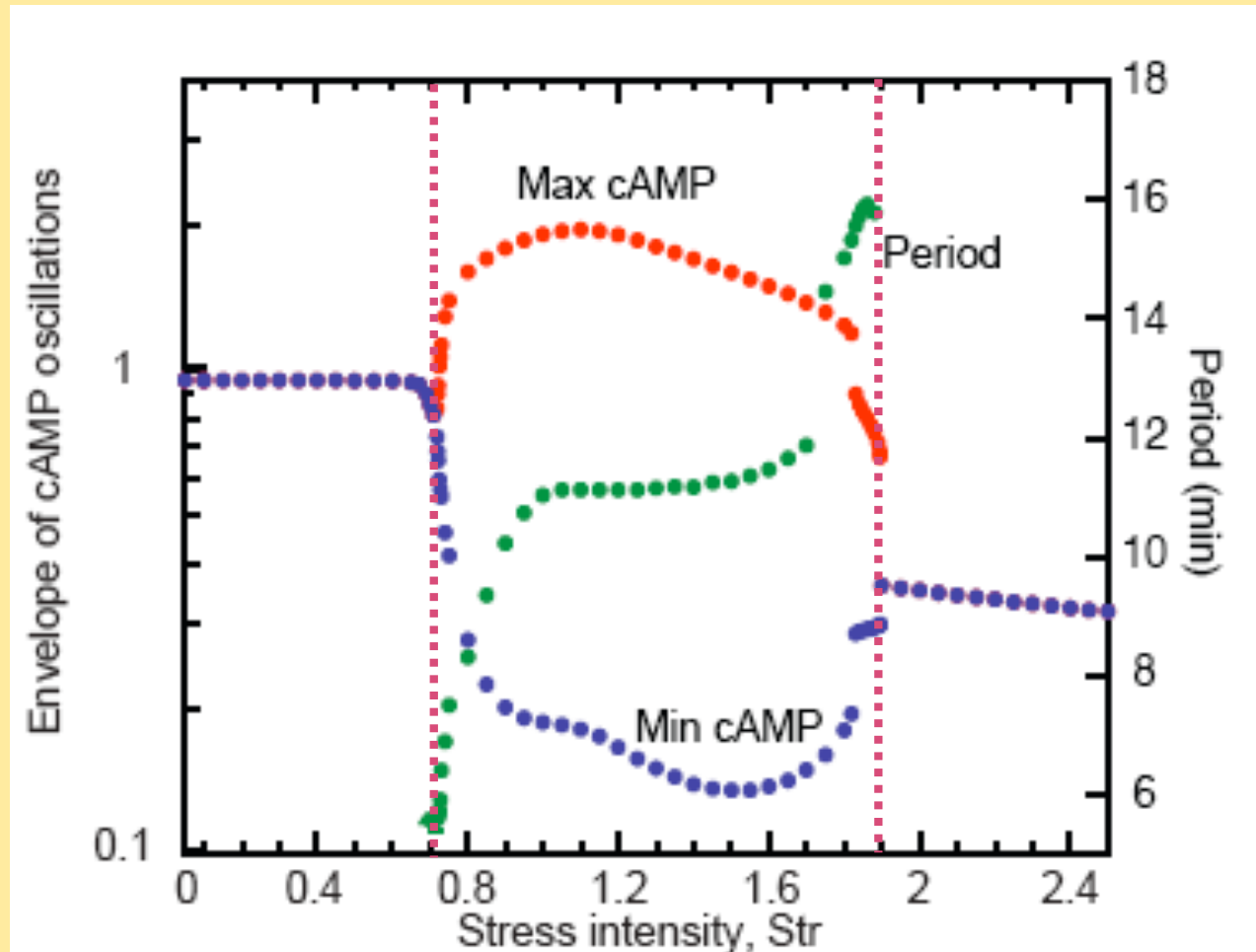
STR=0.5

STR=1

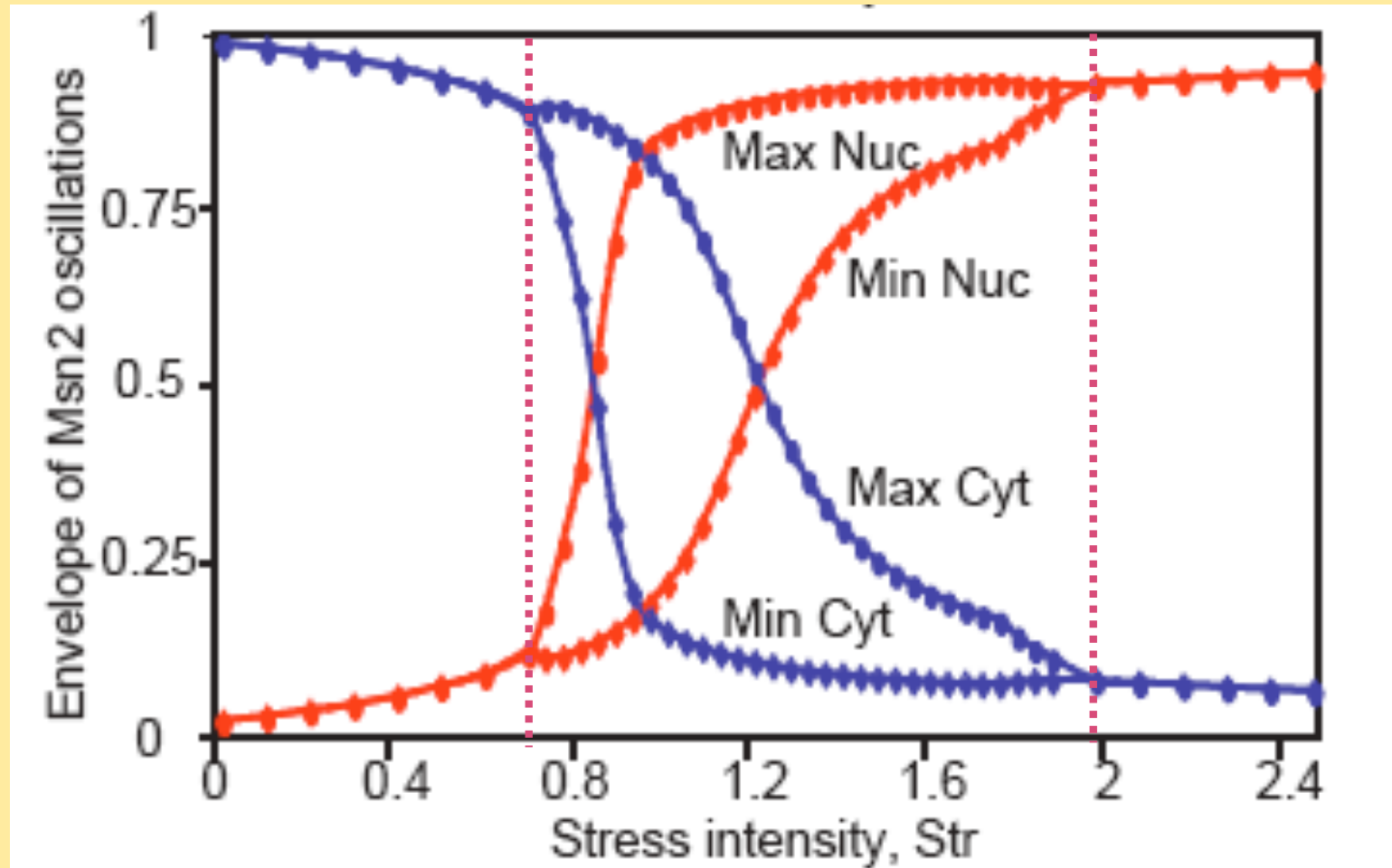
STR=2.5

Berkeley  
madonna

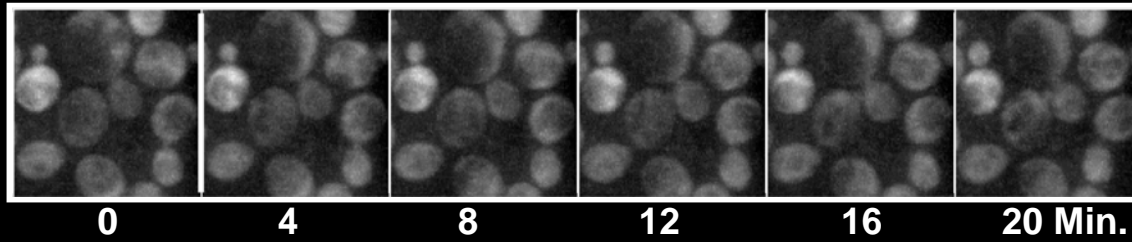
# Envelope of cAMP oscillations



# Envelope of nucleocytoplasmic oscillations of Msn2

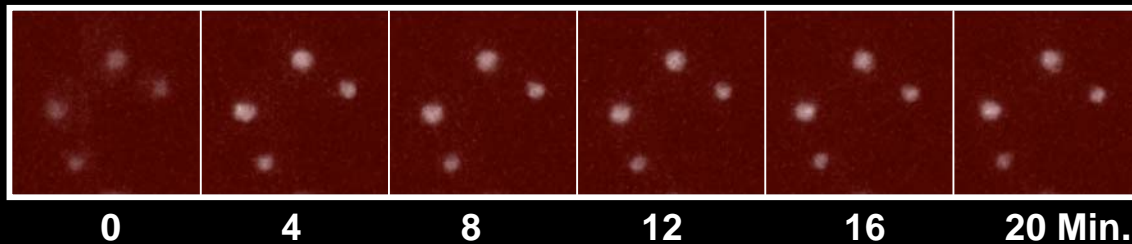


# Role of the cAMP-PKA system



*pde2*

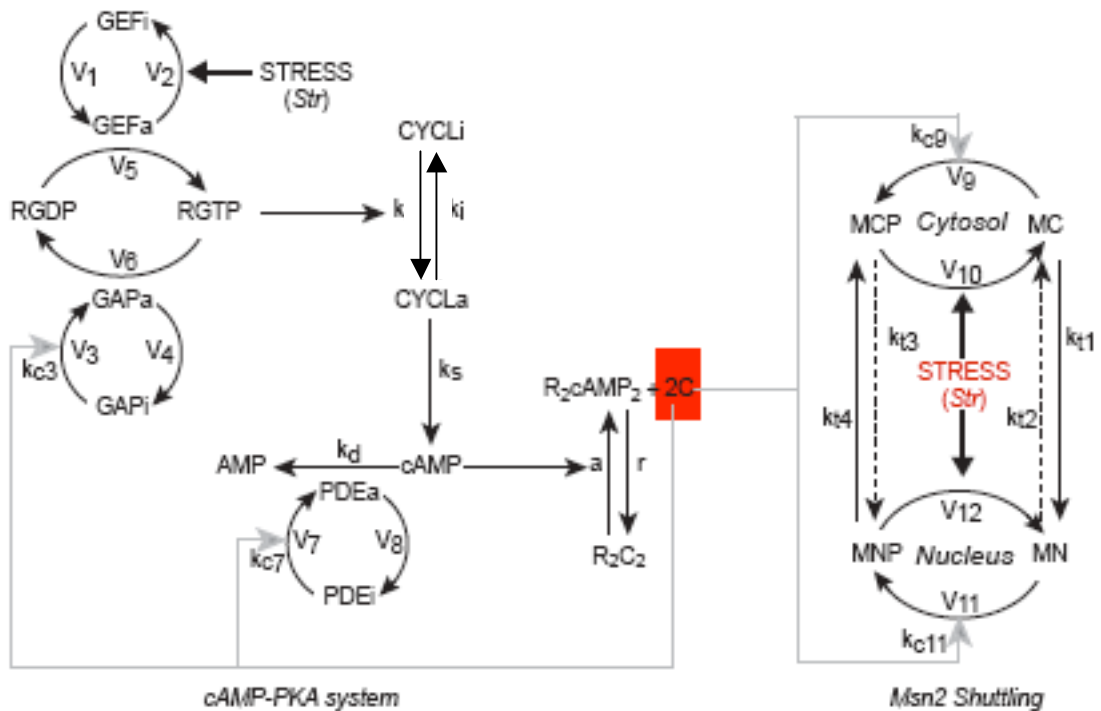
High cAMP



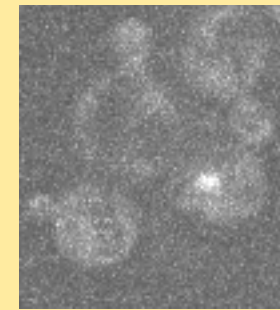
*yak1* $\Delta$ ,  
*tpk1* $\Delta$ ,  
*tpk2* $\Delta$ ,  
*tpk3* $\Delta$

No PKA

# Suppressing the negative feedback loop prevents oscillation but not the stress response

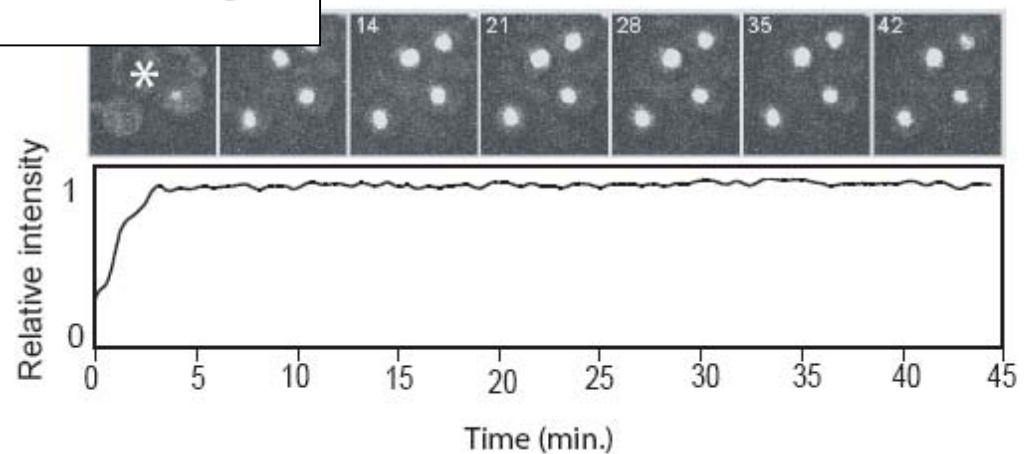


*tpk2<sup>w</sup>*

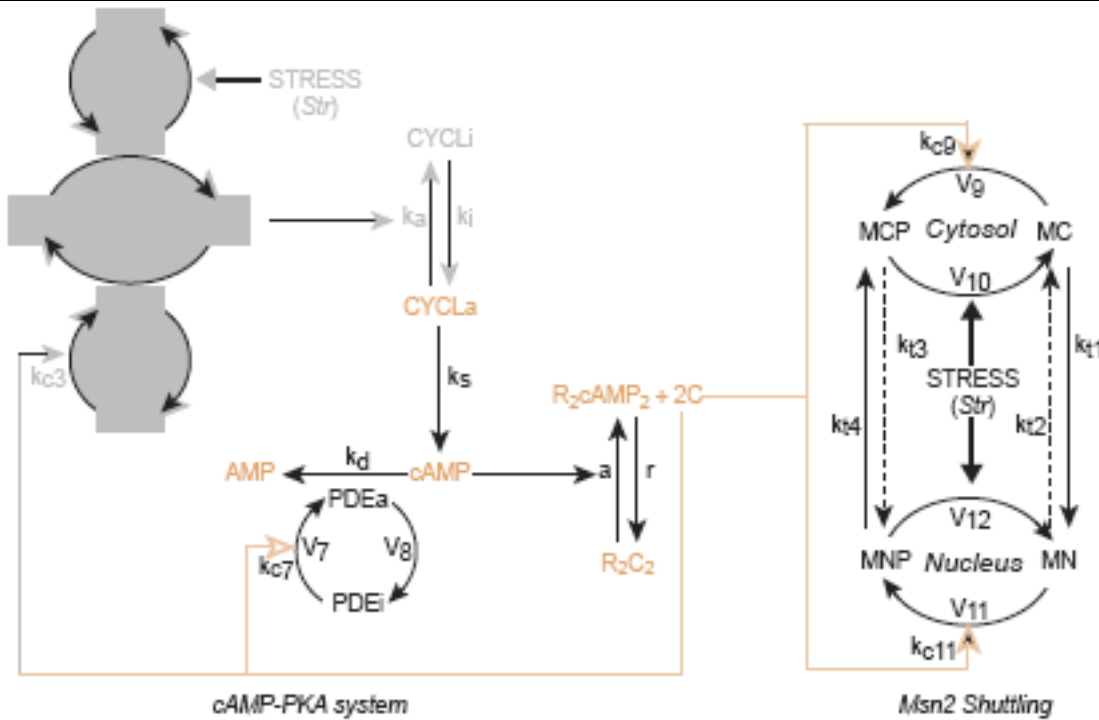


45 min

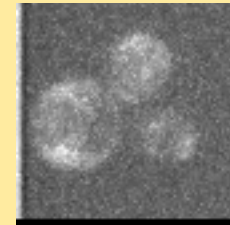
0 osc/ 67 Cell  
7 experiments



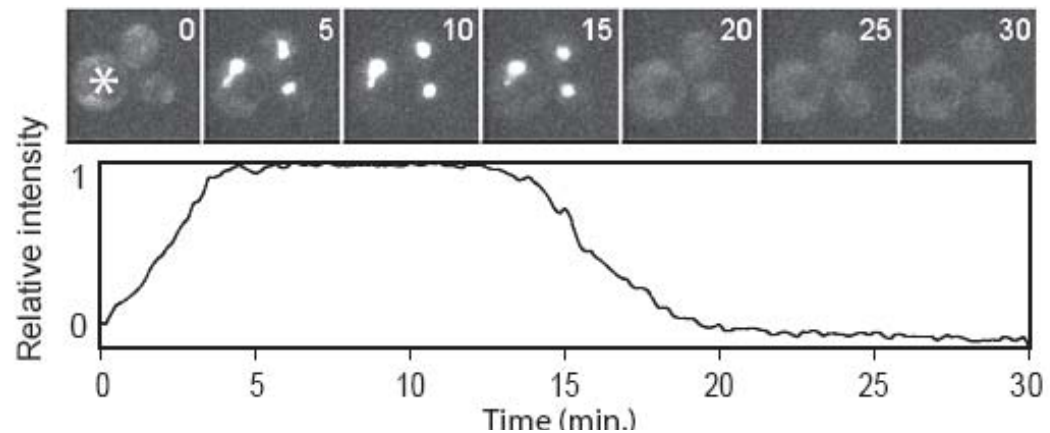
# Alteration of the feedback prevents oscillation but the shuttling is conserved



F1D:  
 $\Delta ras1 \Delta ras2 CYR1m$   
 45min



0 osc / 71 cell  
 20 exp.



## Domain of oscillation: Range of variation of the components

| Component | Value in the model ( $\mu\text{M}$ ) | Minimal value ( $\mu\text{M}$ ) | Maximal value ( $\mu\text{M}$ ) | Ratio  |
|-----------|--------------------------------------|---------------------------------|---------------------------------|--------|
| GEFt      | 4.0                                  | 0.41                            | 7.14                            | 17.5   |
| RASt      | 250.0                                | 2.10                            | 1429                            | 680.00 |
| GAPt      | 1.5                                  | 0.85                            | 20.19                           | 23.75  |
| CYCLt     | 0.7                                  | 0.02                            | 4.93                            | 246.50 |
| PDEt      | 0.5                                  | 0.23                            | 18.30                           | 79.50  |
| PKAt      | 0.3                                  | 0.19                            | 2.38                            | 12.50  |

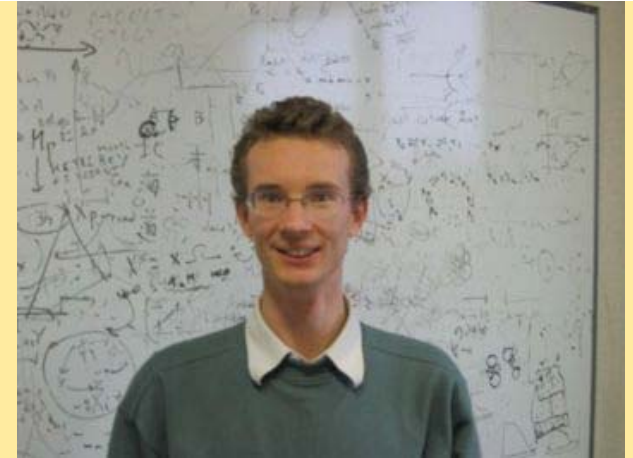


## Domain of oscillation: range of variation of the parameters

| Parameter                                    | Basal value considered in the model | Minimal value | Maximal value | range  |
|--|-------------------------------------|---------------|---------------|--------|
| $r$ ( $\mu\text{M}^{-2} \text{min}^{-1}$ )   | 1                                   | 0.092         | >3000         | >30000 |
| $a$ ( $\mu\text{M}^{-2} \text{min}^{-1}$ )   | 1                                   | < 0.001       | 10.7          | >10700 |
| $K_8$  | 0.01                                | < 0.006       | > 100         | >10000 |
| $K_5$  | 0.001                               | < 0.001       | 8.5           | >8500  |
| $k_{c7}$ ( $\text{min}^{-1}$ )               | 3.333                               | 2.763         | > 3000        | >1000  |
| $K_{\text{md}}$                              | 20                                  | 0.11          | 42.6          | 387    |
| $k_i$ ( $\text{min}^{-1}$ )                  | 1                                   | 0.4           | 123           | 307    |
| $k_s$ ( $\text{min}^{-1}$ )                  | 4                                   | 0.11          | 28.17         | 256    |
| $K_7$  | 0.01                                | < 0.001       | 0.21          | >210   |
| $K_1$  | 0.05                                | 0.006         | 0.945         | 157.5  |
| $K_2$  | 0.05                                | 0.003         | 0.417         | 139    |
| $K_3$  | 0.01                                | < 0.001       | 0.125         | >125   |
| $k_d$ ( $\text{min}^{-1}$ )                  | 100                                 | 47.4          | >3000         | >70    |
| $K_4$  | 0.01                                | < 0.001       | 0.062         | >62    |
| $k_a$ ( $\mu\text{M}^{-1} \text{min}^{-1}$ ) | 0.01                                | < 0.001       | 0.025         | >25    |
| $K_6$  | 0.001                               | < 0.0001      | 0.0023        | >23    |
| $k_{\text{GEF}}$ ( $\text{min}^{-1}$ )       | 240                                 | 25            | 427           | 17     |
| $k_{\text{GAP}}$ ( $\text{min}^{-1}$ )       | 600                                 | 337           | >3000         | >10    |
| $k_c$ ( $\text{min}^{-1}$ )                  | 3.5                                 | 2.75          | 4.05          | 1.4    |

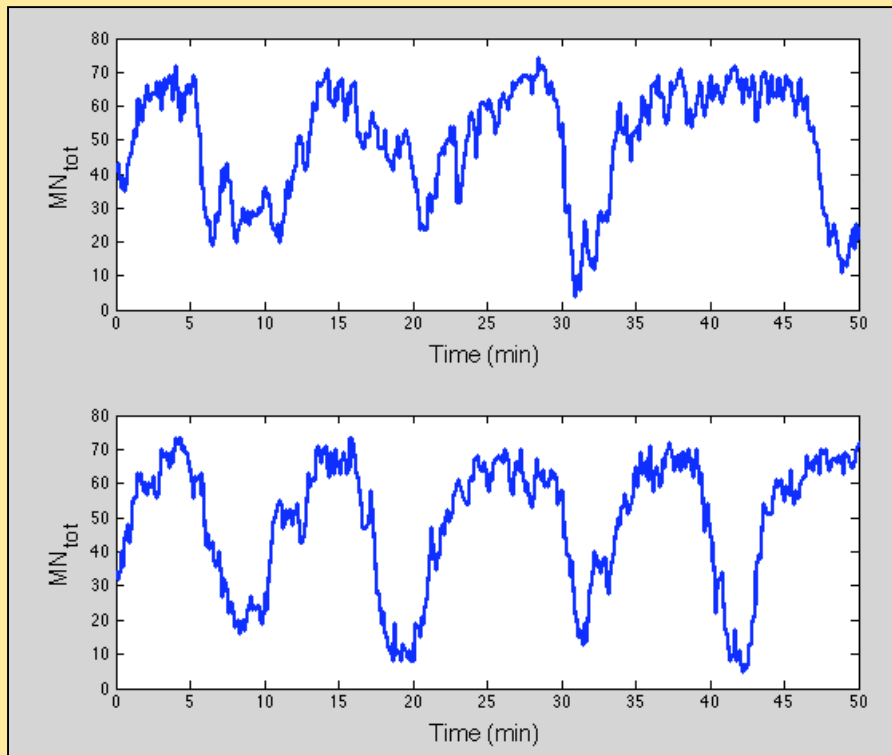
# Stochastic simulation at KITP

## Didier Gonze



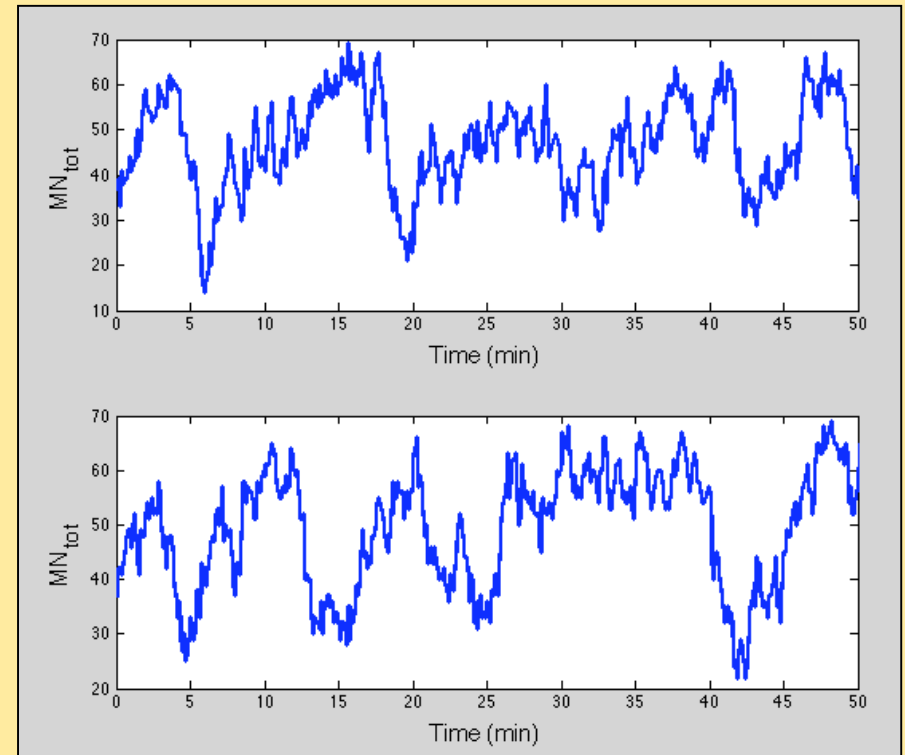
$$\Omega = 75$$

$$K_9=K_{10}=K_{11}=K_{12} = 0.005$$



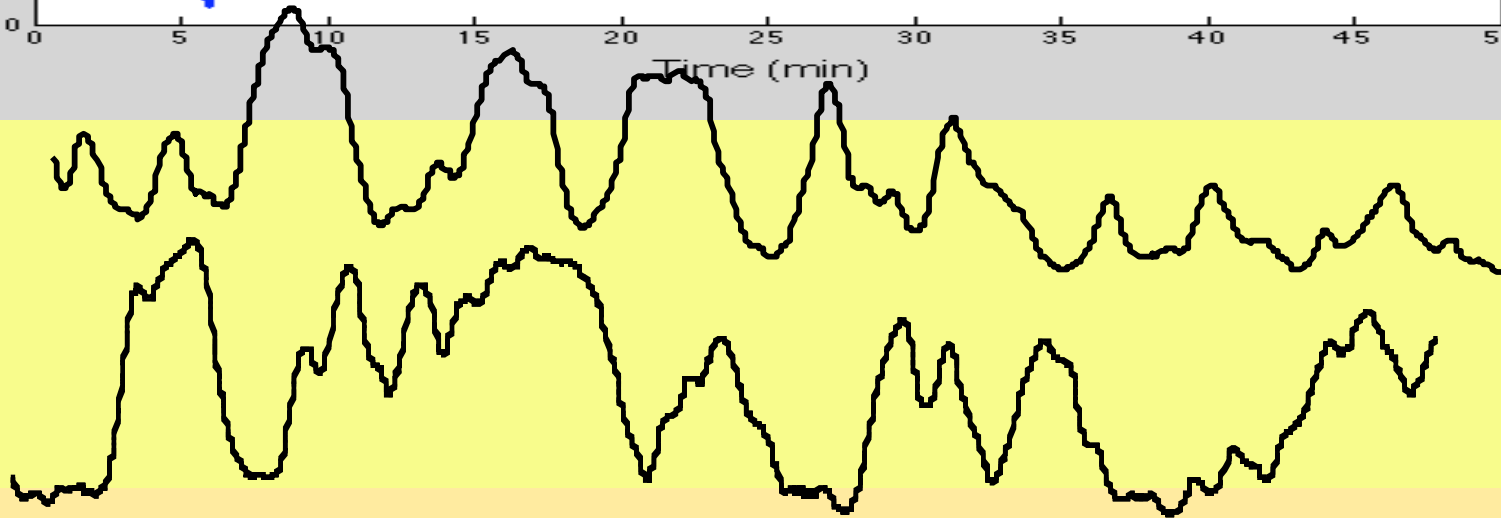
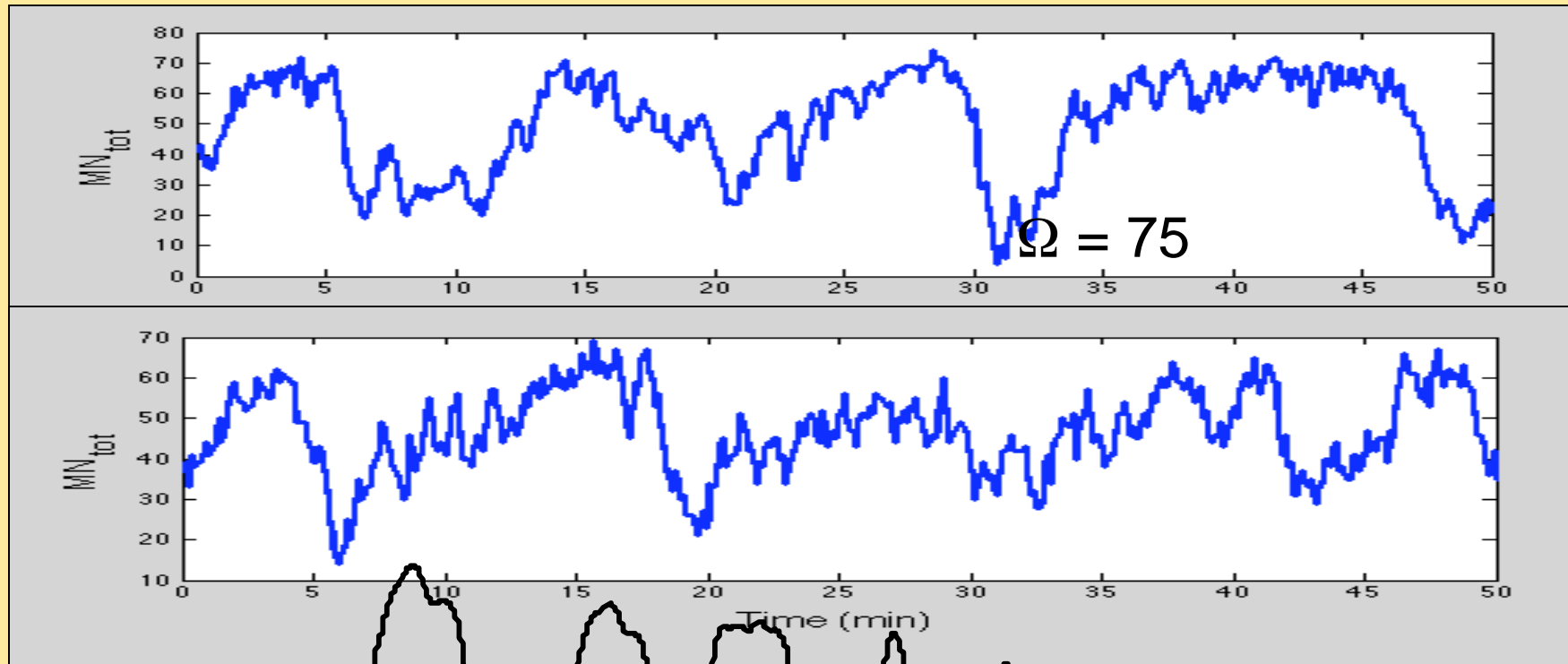
$$\Omega = 75$$

$$K_9=K_{10}=K_{11}=K_{12} = 0.025$$

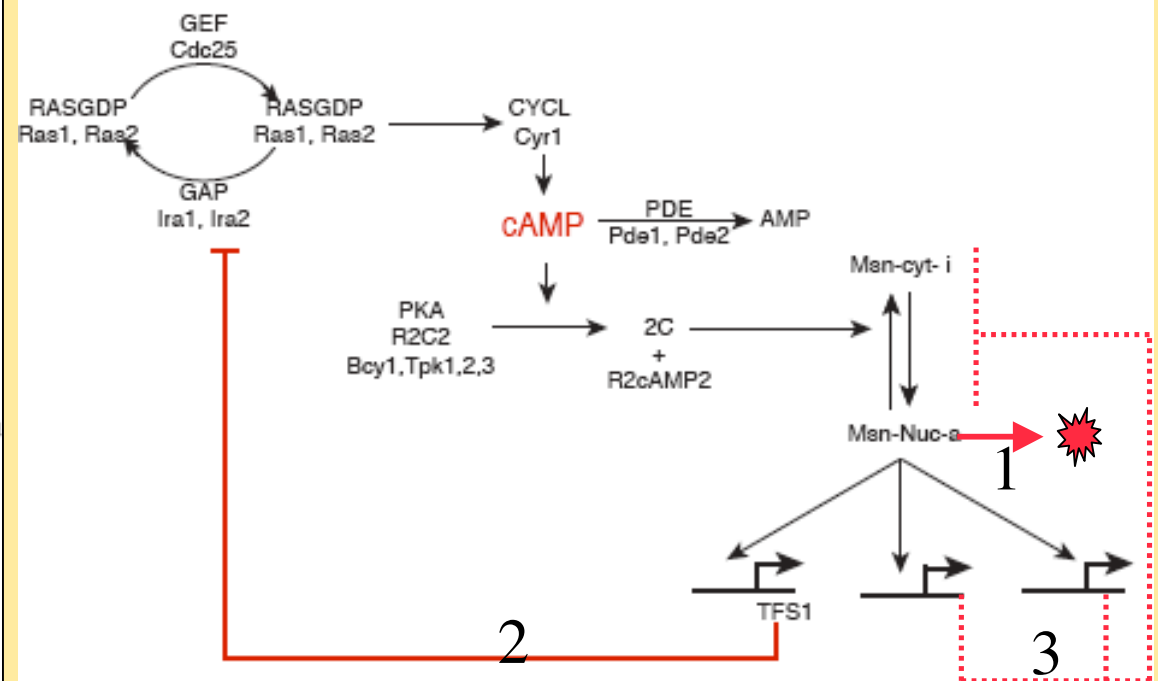
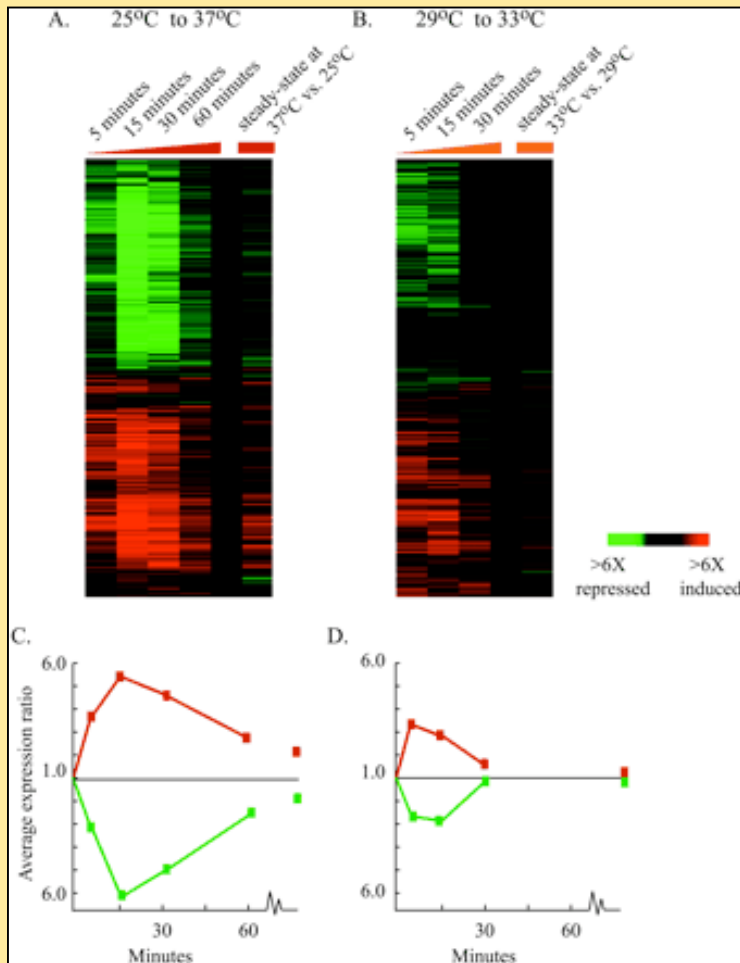


# Stochastic simulation at KITP

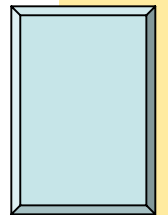
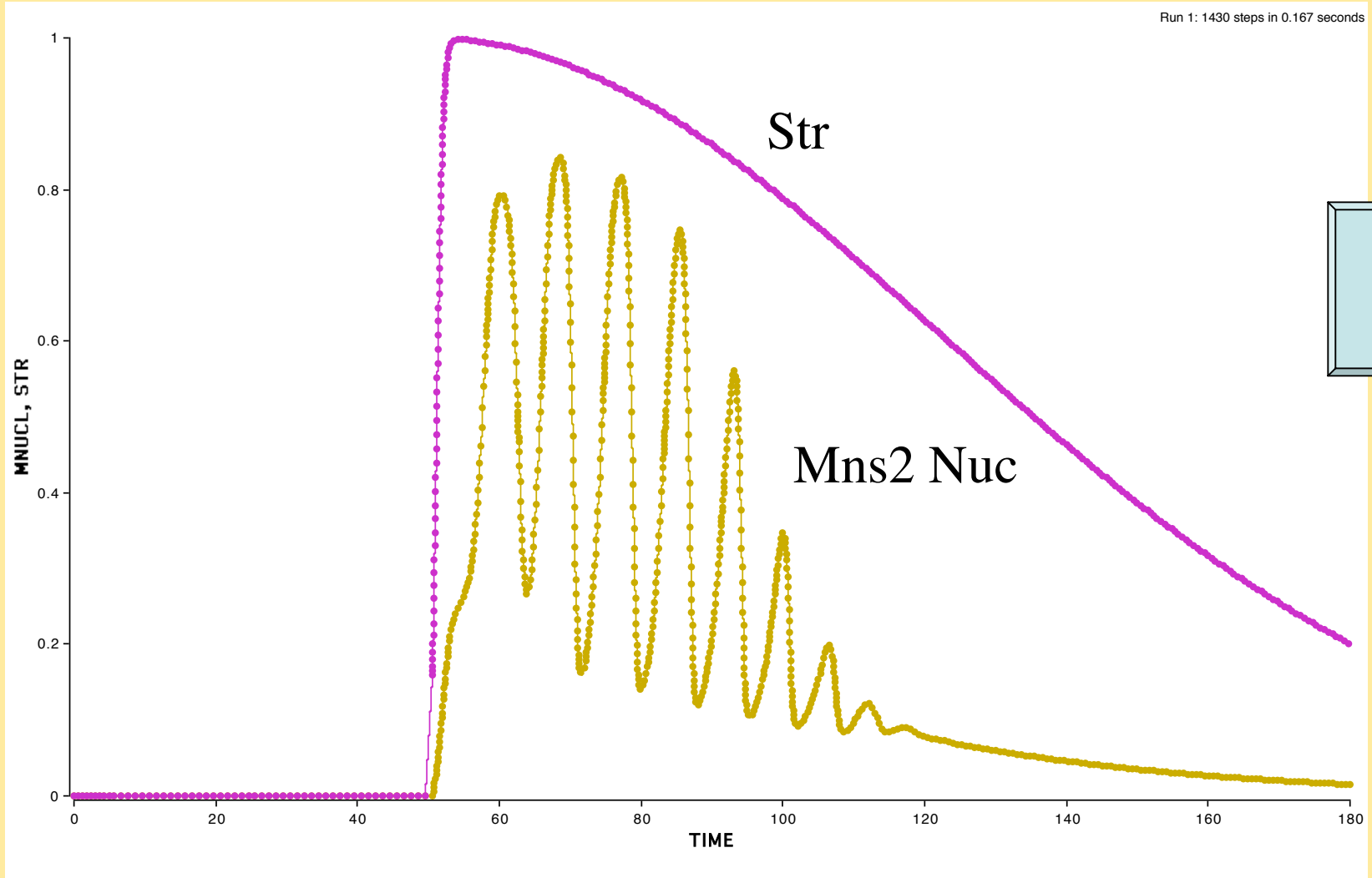
## Didier Gonze



# The stress response is transient



# Simulations with transient stress response



# What would be the interest for the cell to have oscillators ?

Cover the space of targets of Msn2 (N#<nSTRE)

Other cAMP-PKA controlled pathways

cAMP-PKA a clutch for different cellular programs  
Disengage the clutch twice for reducing gear

Msn2 the neutral position before new program

## Conclusions

Evidence for the existence of oscillatory nucleocytoplasmic shuttling of transcription factors independent of transcription

Another example of the complex behavior of the cAMP-PKA system

The emergence of additional oscillatory systems in living cells



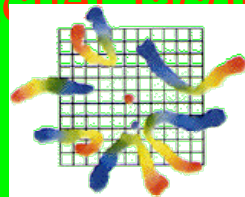
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Marcotte

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*Université libre de Bruxelles*

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