

Systems Biology of the Epo-Receptor

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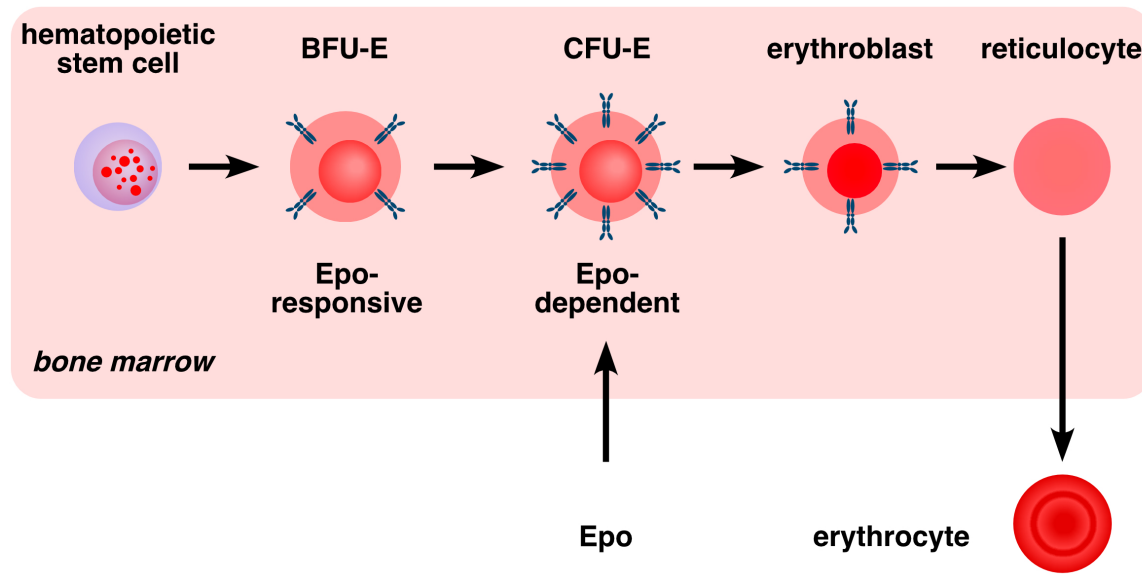
Outline

- **Systems Biology**
- **A dynamical model for the Epo receptor**
- **Validating the model**
- **Infering systems' properties**
- **Understand what is known**

Outline

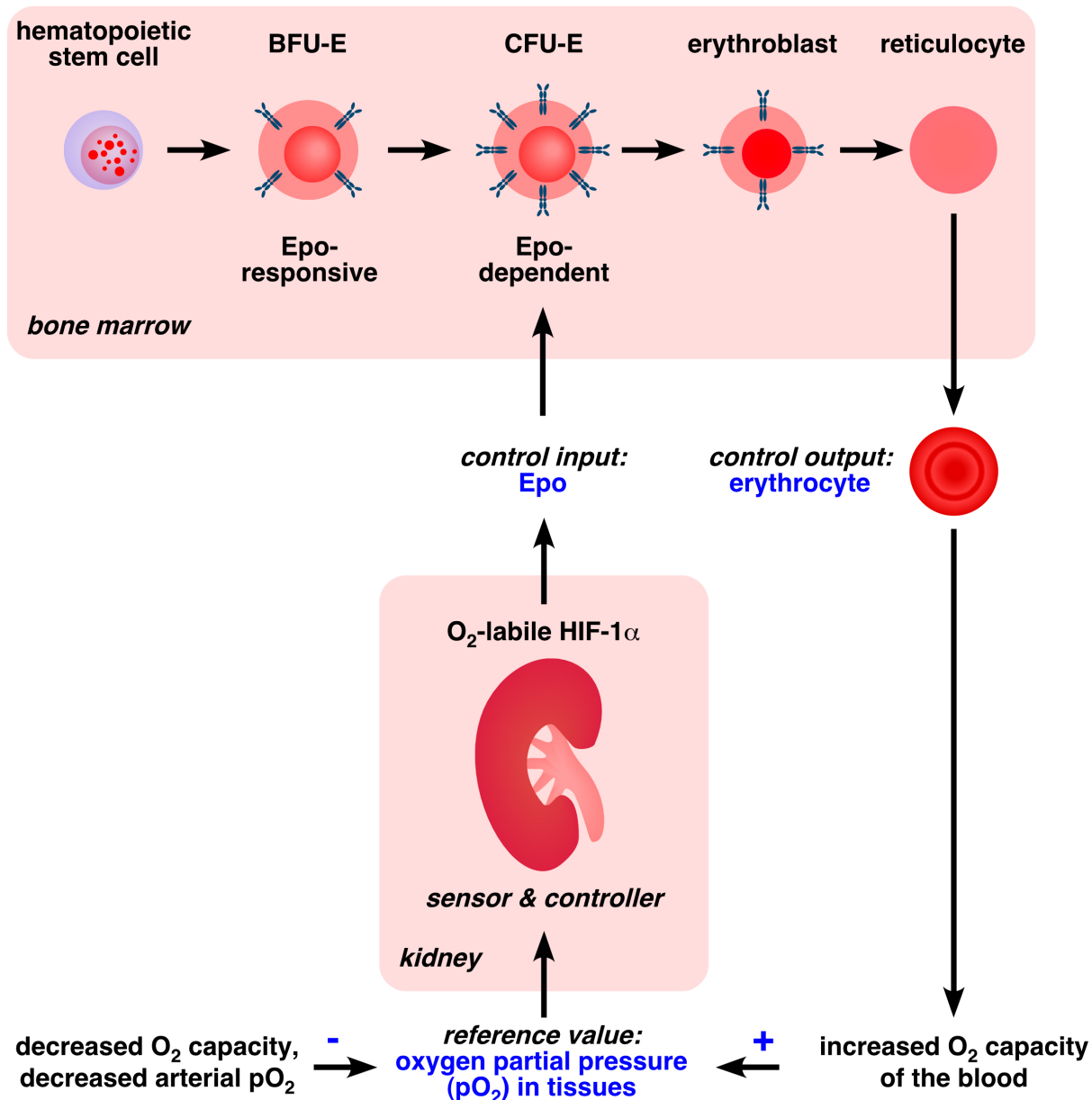
- ~~Systems Biology~~
- A dynamical model for the Epo receptor
- Validating the model
- Inferring systems' properties
- Understand what is known
- Latest results

Erythropoiesis - A Closed-Loop Control System



- **Epo**: key regulator of erythropoiesis

Erythropoiesis - A Closed-Loop Control System



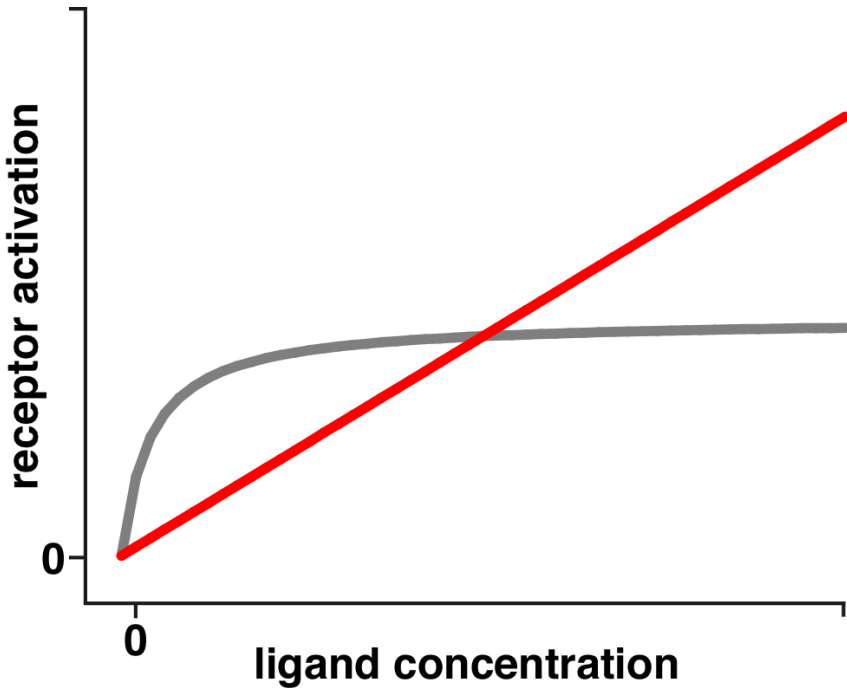
- **Epo**: key regulator of erythropoiesis

- **feedback via red blood cell mass**: establishing a closed-loop control circuit

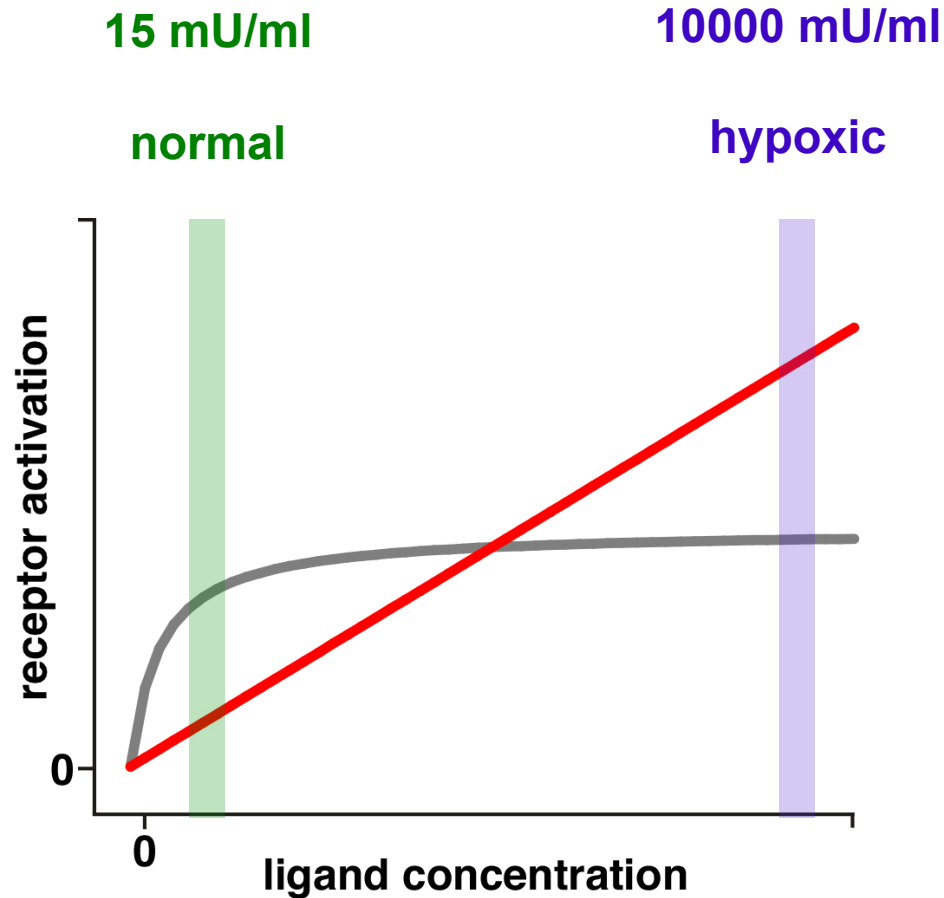
- **normal conditions**: low levels of plasma Epo
15 mU/ml

- **hypoxic conditions**: increased Epo levels
up to 10000 mU/ml

Erythropoiesis - Coping with Different Ligand Concentrations



Erythropoiesis - Coping with Different Ligand Concentrations

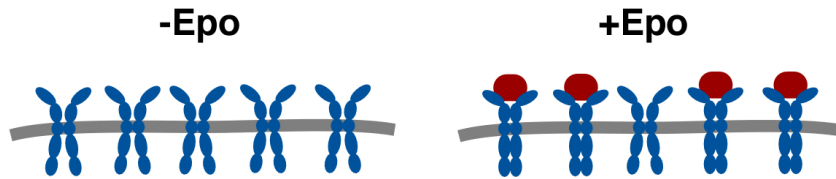


→ How is ligand-encoded information processed by the EpoR?

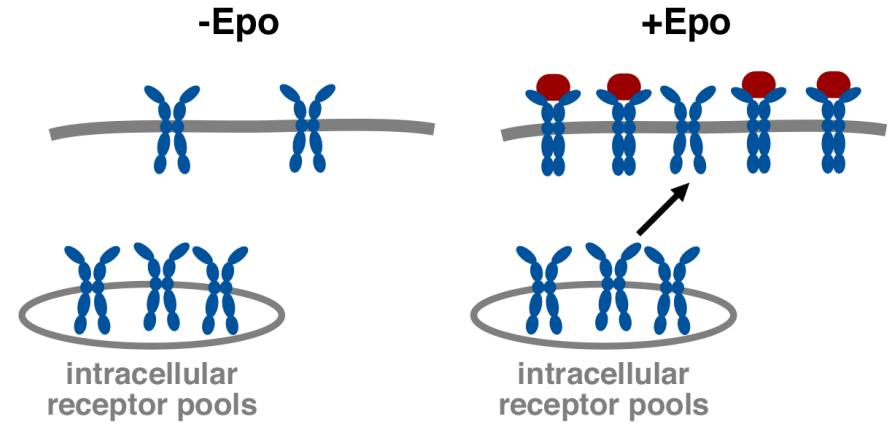
→ Which dynamic properties of the EpoR facilitate information processing over a broad ligand range?

Strategies for Processing Ligand-Encoded Information

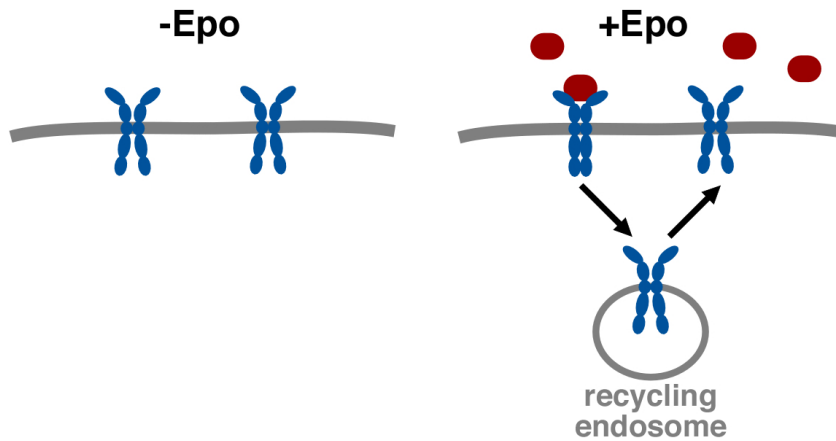
abundance



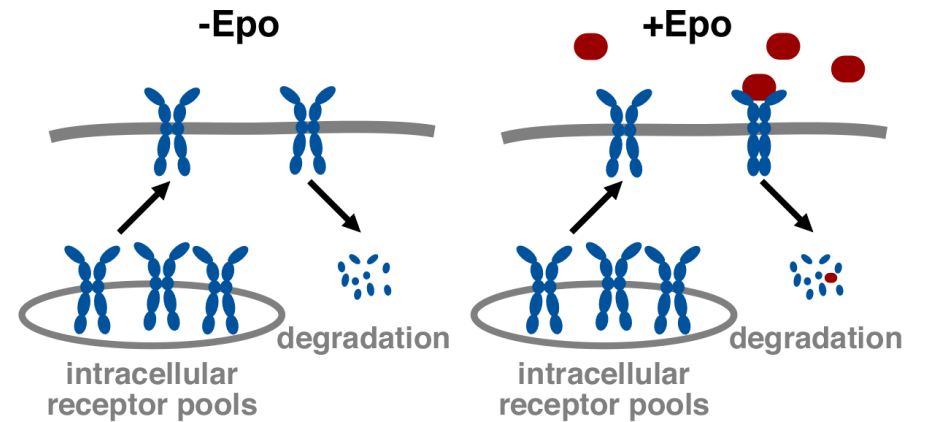
mobilization



recycling

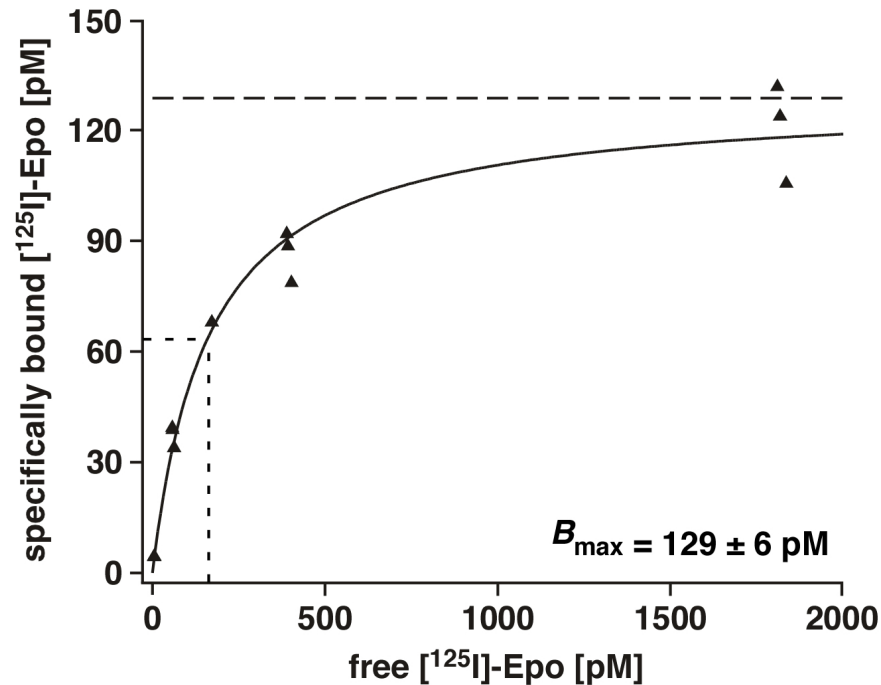
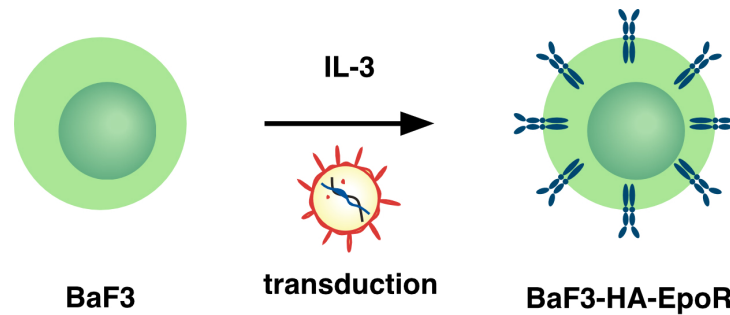


turnover



Low EpoR Abundance on the Plasma Membrane

lymphoid murine
BaF3-EpoR cell line



→ Epo binding sites:

- BaF3-EpoR:

appr. 7800

- primary erythroid progenitor cells:

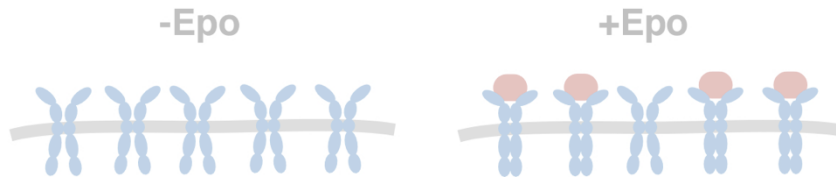
up to 1000

- EGFR: up to 100000 receptors

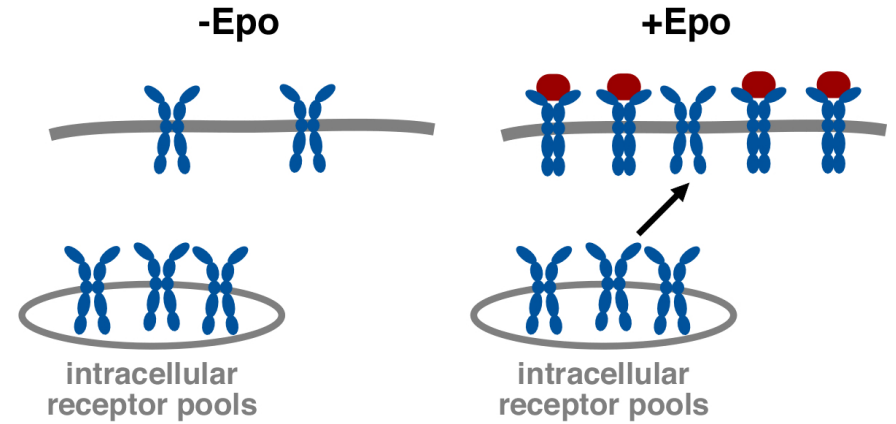
→ EpoR abundance excluded as a strategy to cope with large ligand concentrations

Strategies for Processing Ligand-Encoded Information

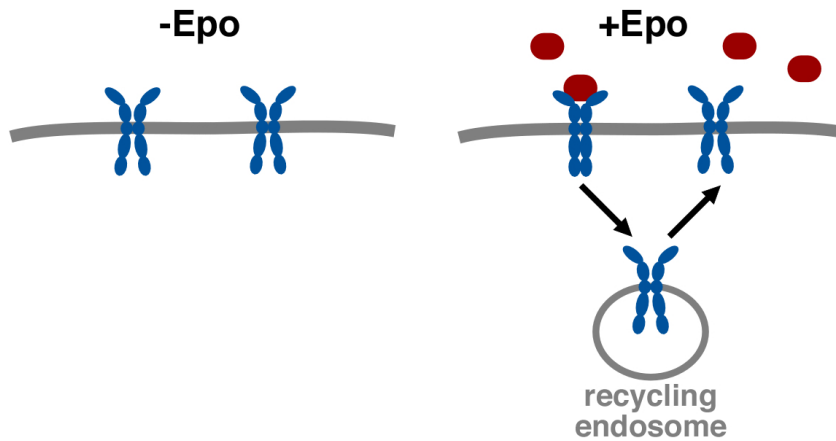
abundance



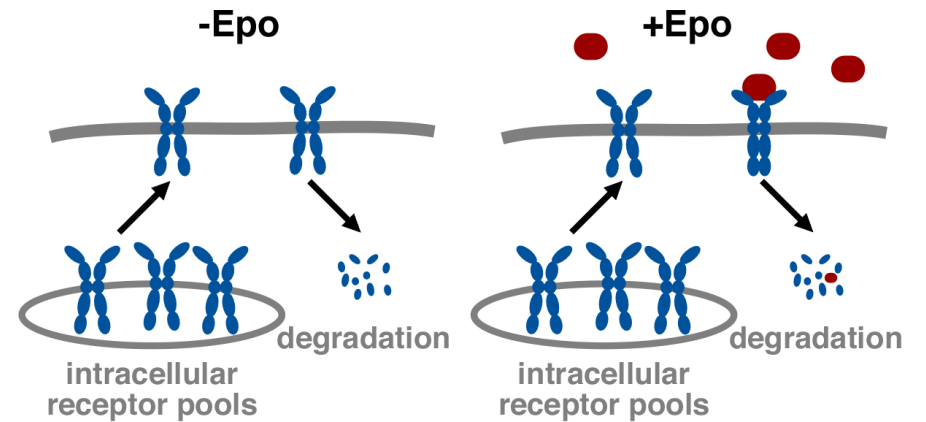
mobilization



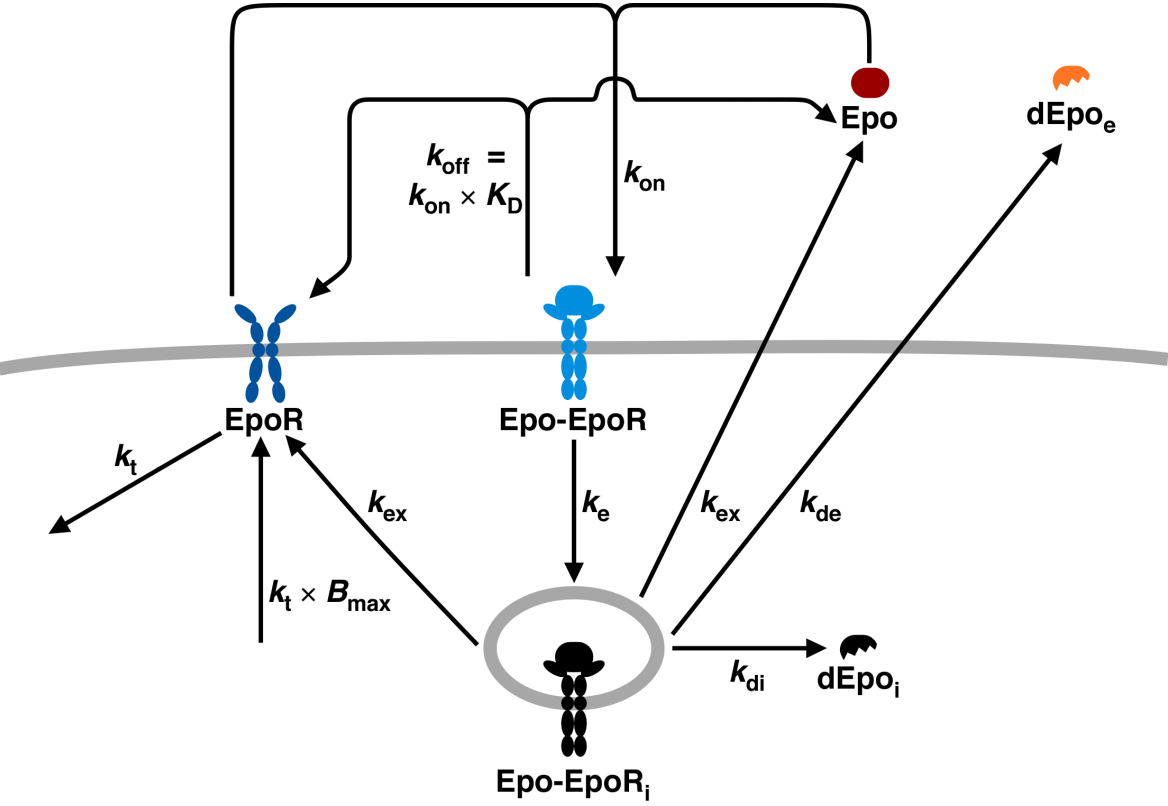
recycling



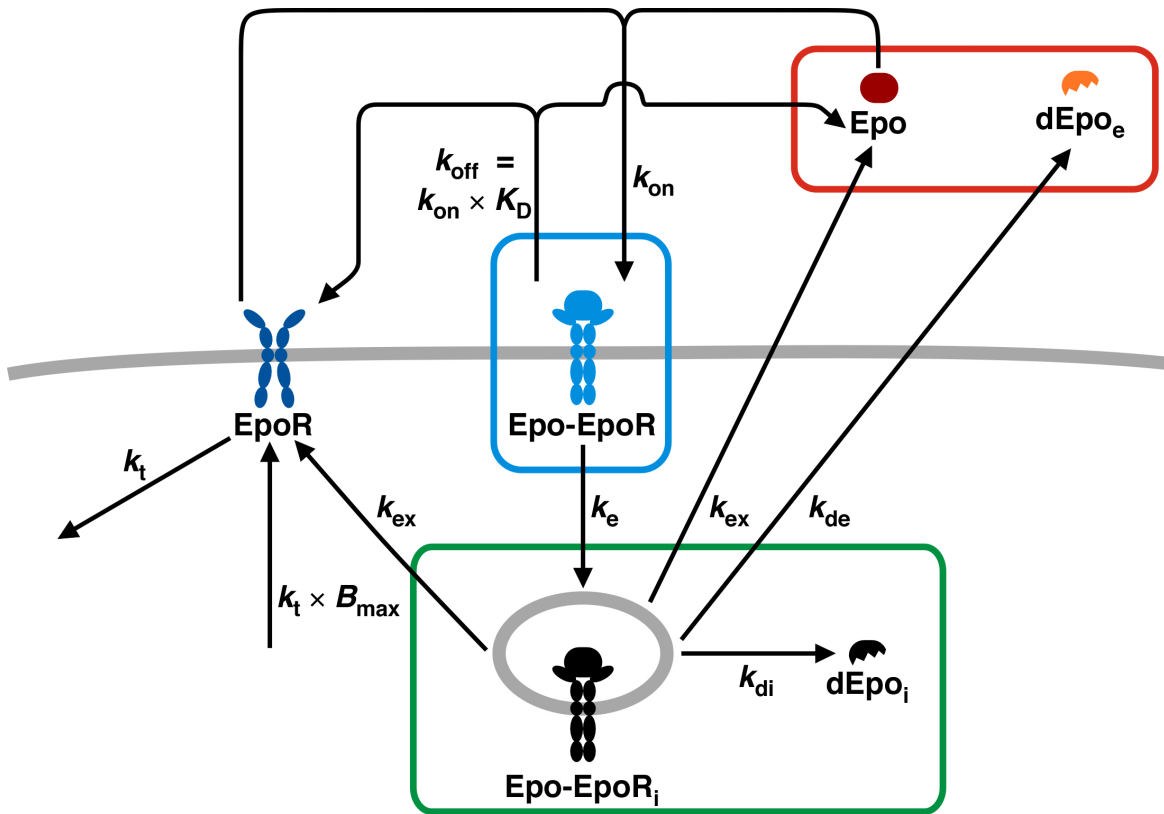
turnover



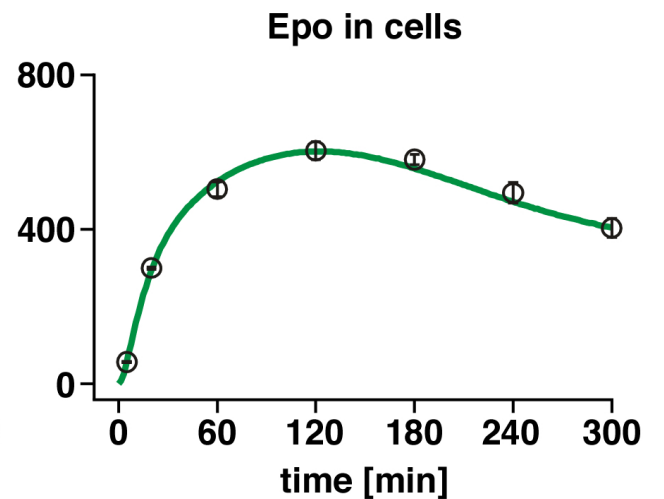
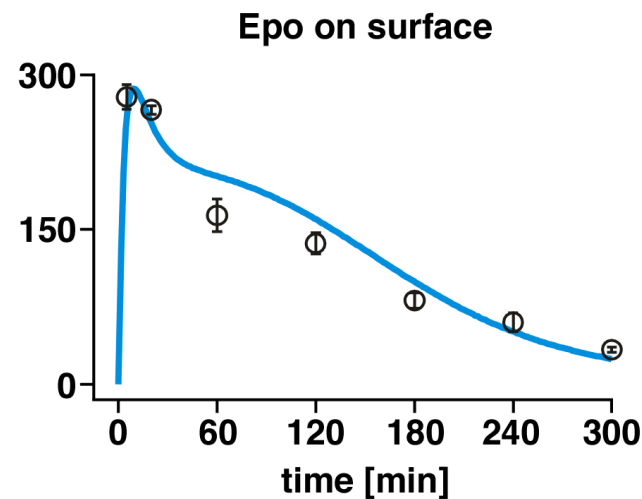
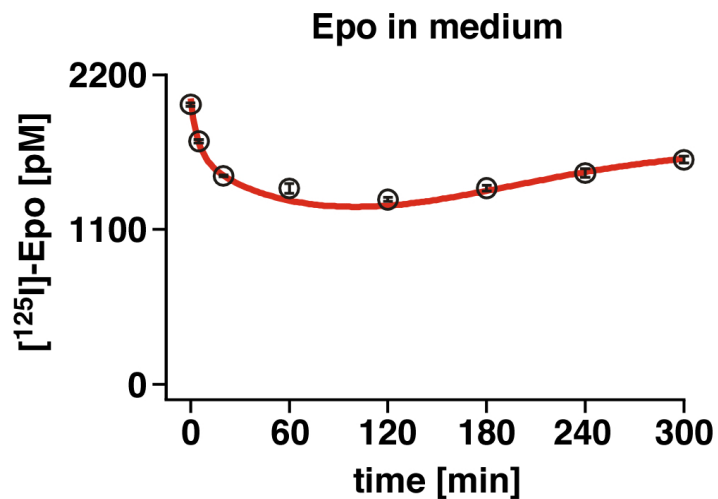
Mathematical Model for Epo-EpoR Interaction and Trafficking Kinetics



Mathematical Model for Epo-EpoR Interaction and Trafficking Kinetics

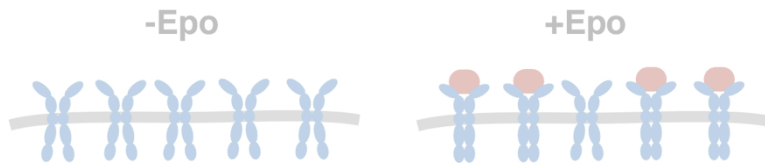


- all parameters identifiable with small confidence intervals
- allowing for accurate predictions
- extended model: EpoR mobilization excluded as a major strategy

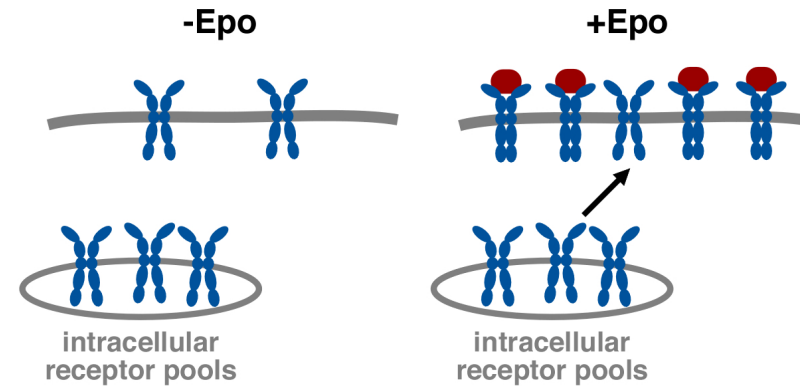


Strategies for Processing Ligand-Encoded Information

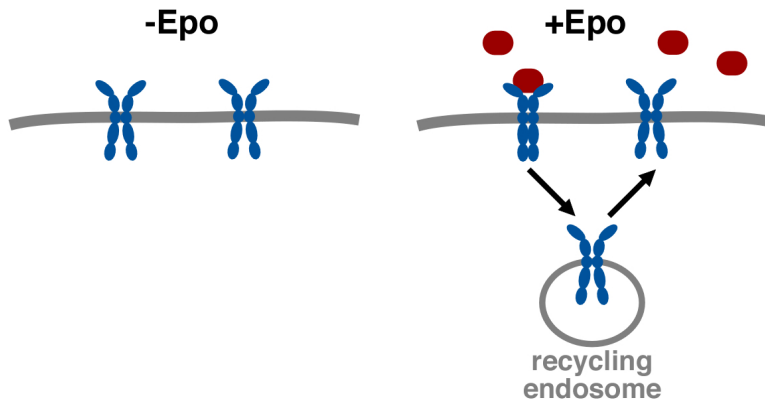
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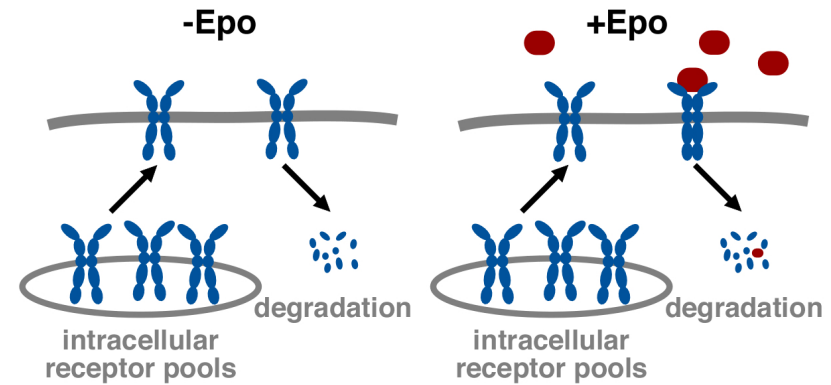
mobilization



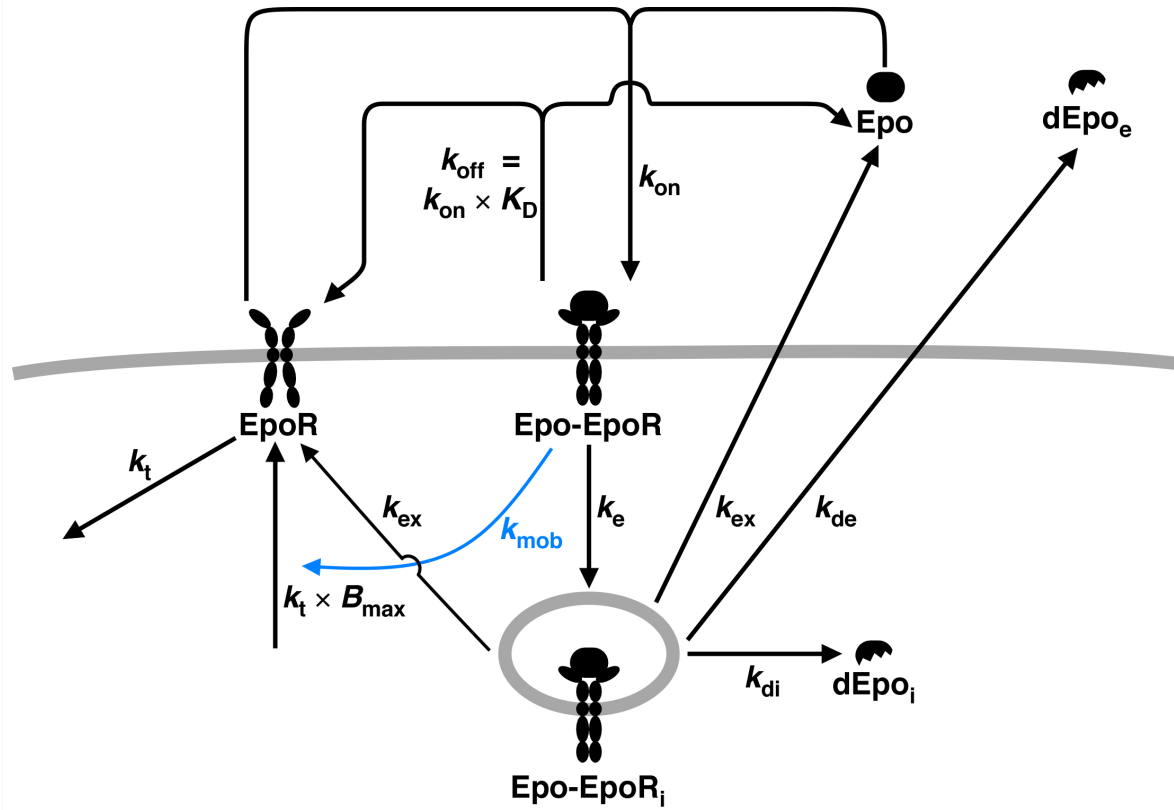
recycling



turnover



Analysis of Model Including EpoR Mobilization



Model Topology – Core Model / Core Model + k_{mob}

‘Core model’ / ‘Core model + k_{mob} ’

Ordinary differential equations (‘core model’)

$$\begin{aligned} \text{EpoR} & \quad \dot{x}_1 = k_t \cdot B_{\max} - k_t \cdot x_1 - k_{on} \cdot x_1 \cdot x_2 + k_{off} \cdot x_3 + k_{ex} \cdot x_4 \\ \text{Epo} & \quad \dot{x}_2 = -k_{on} \cdot x_1 \cdot x_2 + k_{off} \cdot x_3 + k_{ex} \cdot x_4 \\ \text{Epo-EpoR} & \quad \dot{x}_3 = k_{on} \cdot x_1 \cdot x_2 - k_{off} \cdot x_3 - k_e \cdot x_3 \\ \text{Epo-EpoR}_i & \quad \dot{x}_4 = k_e \cdot x_3 - k_{ex} \cdot x_4 - k_{di} \cdot x_4 - k_{de} \cdot x_4 \\ \text{dEpo}_i & \quad \dot{x}_5 = k_{di} \cdot x_4 \\ \text{dEpo}_e & \quad \dot{x}_6 = k_{de} \cdot x_4 \end{aligned}$$

Ordinary differential equations (‘core model + k_{mob} ’)

$$\begin{aligned} \text{EpoR} & \quad \dot{x}_1 = k_t \cdot B_{\max} + k_{mob} \cdot x_3 - k_t \cdot x_1 - k_{on} \cdot x_1 \cdot x_2 + k_{off} \cdot x_3 + k_{ex} \cdot x_4 \\ \text{Epo} & \quad \dot{x}_2 = -k_{on} \cdot x_1 \cdot x_2 + k_{off} \cdot x_3 + k_{ex} \cdot x_4 \\ \text{Epo-EpoR} & \quad \dot{x}_3 = k_{on} \cdot x_1 \cdot x_2 - k_{off} \cdot x_3 - k_e \cdot x_3 \\ \text{Epo-EpoR}_i & \quad \dot{x}_4 = k_e \cdot x_3 - k_{ex} \cdot x_4 - k_{di} \cdot x_4 - k_{de} \cdot x_4 \\ \text{dEpo}_i & \quad \dot{x}_5 = k_{di} \cdot x_4 \\ \text{dEpo}_e & \quad \dot{x}_6 = k_{de} \cdot x_4 \end{aligned}$$

Assignment rules

$$k_{off} \quad k_{off} = k_{on} \cdot K_D$$

Nonzero initial values

$$\begin{aligned} \text{EpoR} & \quad x_1 = B_{\max} \quad (t=0) \\ \text{Epo} & \quad x_2 \quad (t=0) \end{aligned}$$

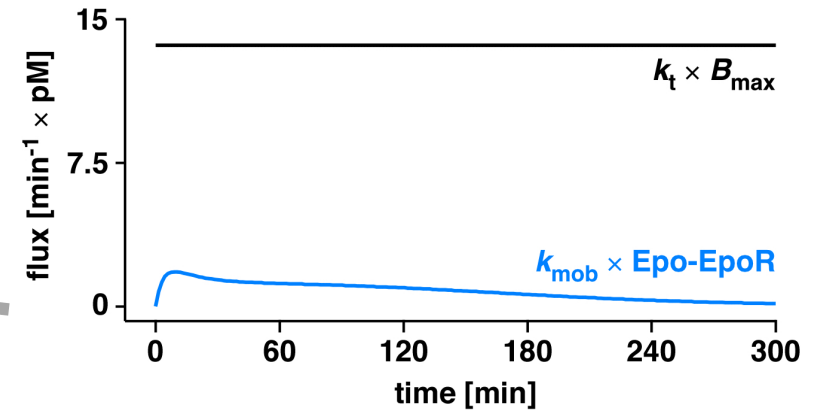
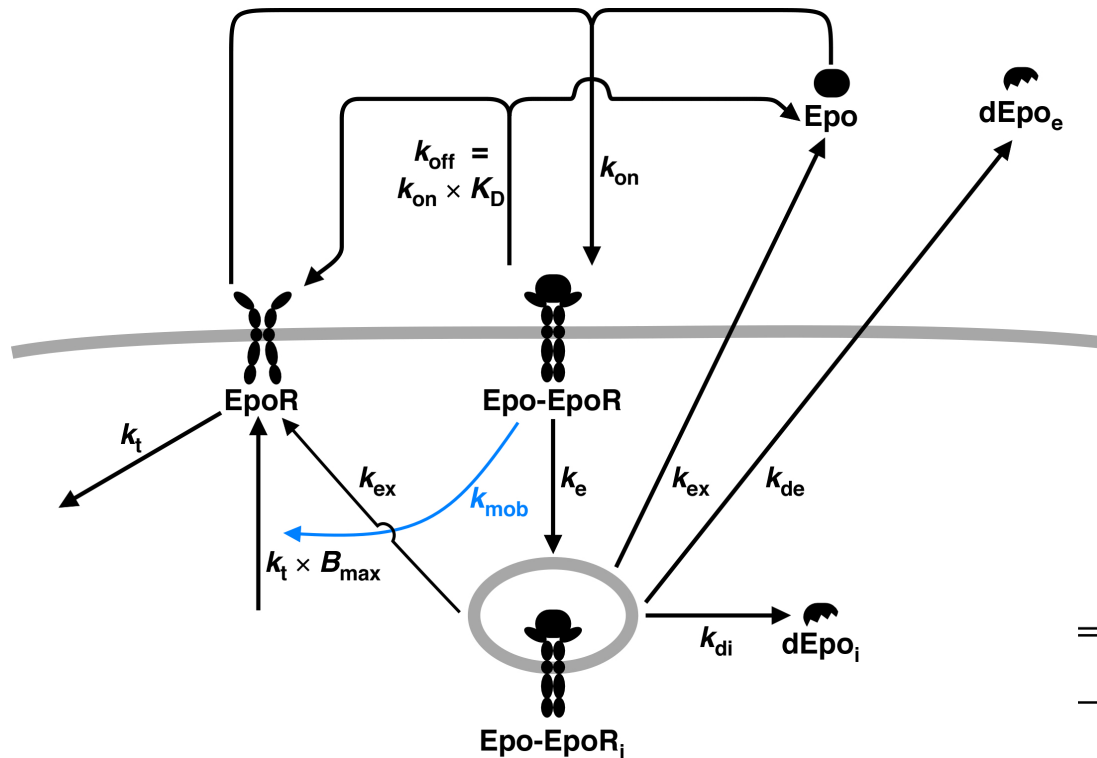
Observables

$$\begin{aligned} \text{Epo in medium} & \quad y_1 = x_2 + x_6 \quad (\text{Epo} + \text{dEpo}_e) \\ \text{Epo on surface} & \quad y_2 = x_3 \quad (\text{Epo-EpoR}) \\ \text{Epo in cells} & \quad y_3 = x_4 + x_5 \quad (\text{Epo-EpoR}_i + \text{dEpo}_i) \end{aligned}$$

Parameters

k_t	ligand-independent EpoR endocytosis
k_{mob}	ligand-induced EpoR mobilization
k_{on}	association of Epo and EpoR
k_{off}	dissociation of Epo and EpoR
K_D	dissociation constant for Epo-EpoR
k_e	ligand-induced EpoR endocytosis
k_{ex}	recycling of Epo and EpoR
k_{di}	degradation of ligand-EpoR complexes, remaining intracellular
k_{de}	degradation of ligand-EpoR complexes, secreted extracellular

Analysis of Model Including EpoR Mobilization

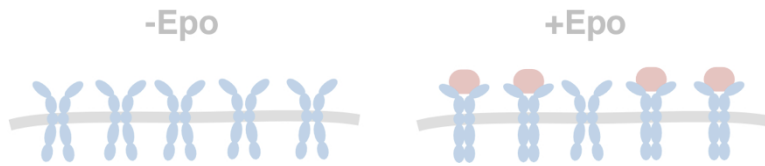


	# of parameters	$p(\text{LRT})$	AIC	BIC
'Core model'	10		172.2	186.9
'Core model + k_{mob} '	11	0.4178	173.6	189.7

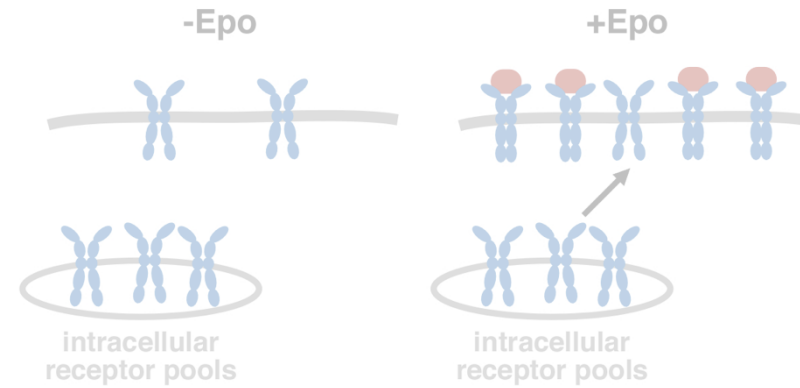
→ EpoR mobilization excluded as a major strategy to cope with large ligand concentrations

Strategies for Processing Ligand-Encoded Information

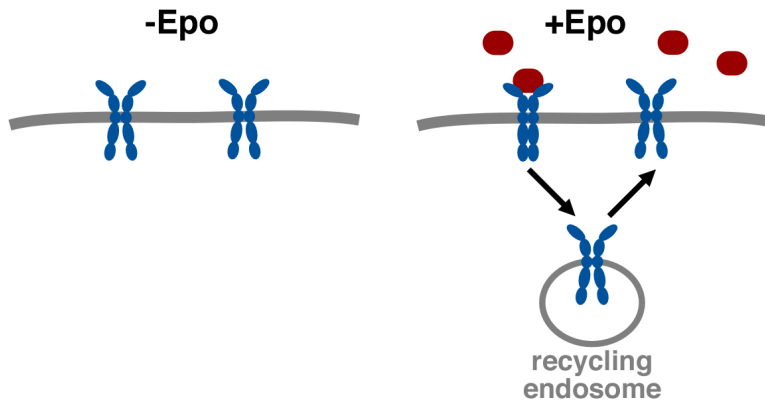
abundance



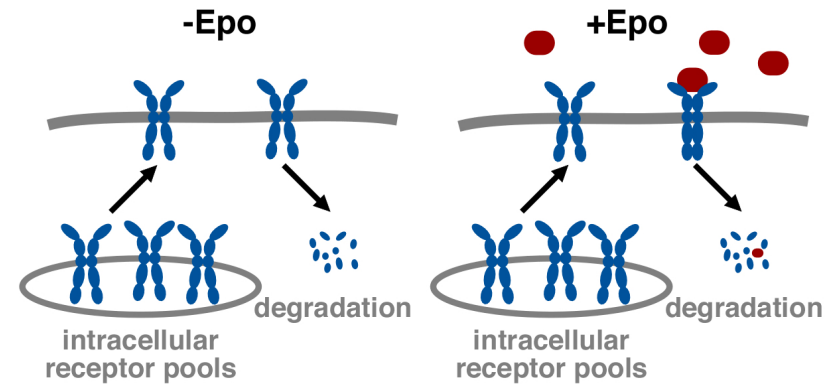
mobilization



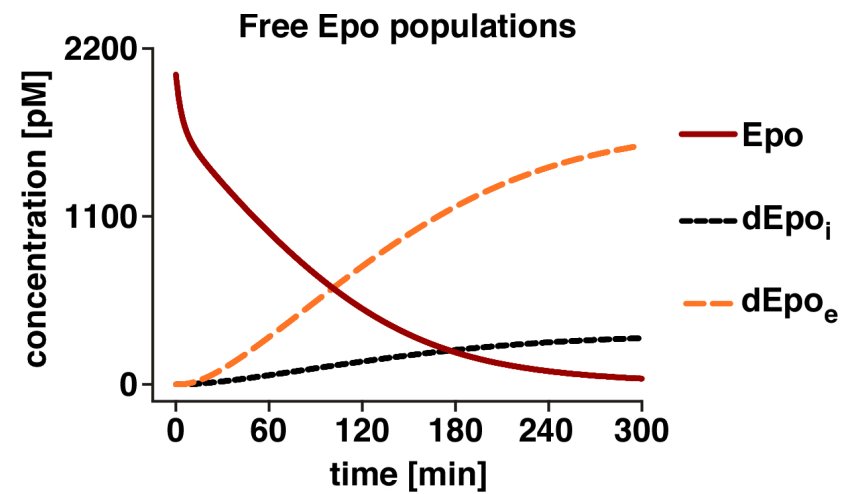
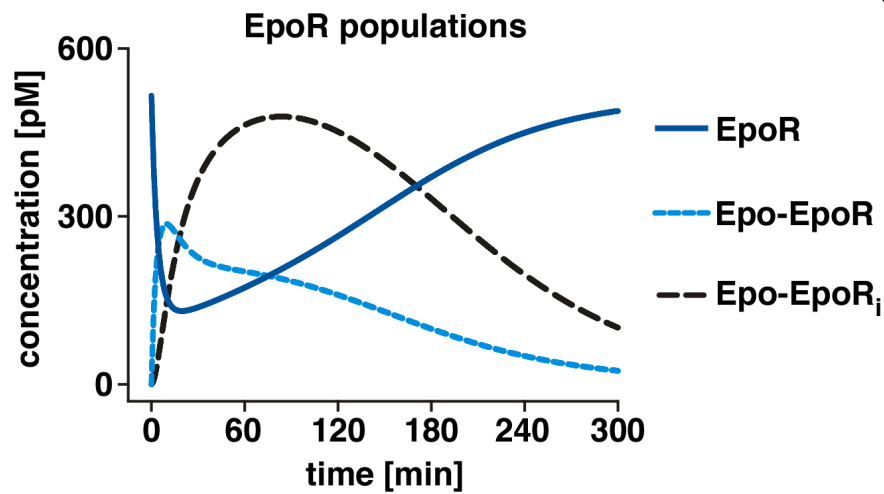
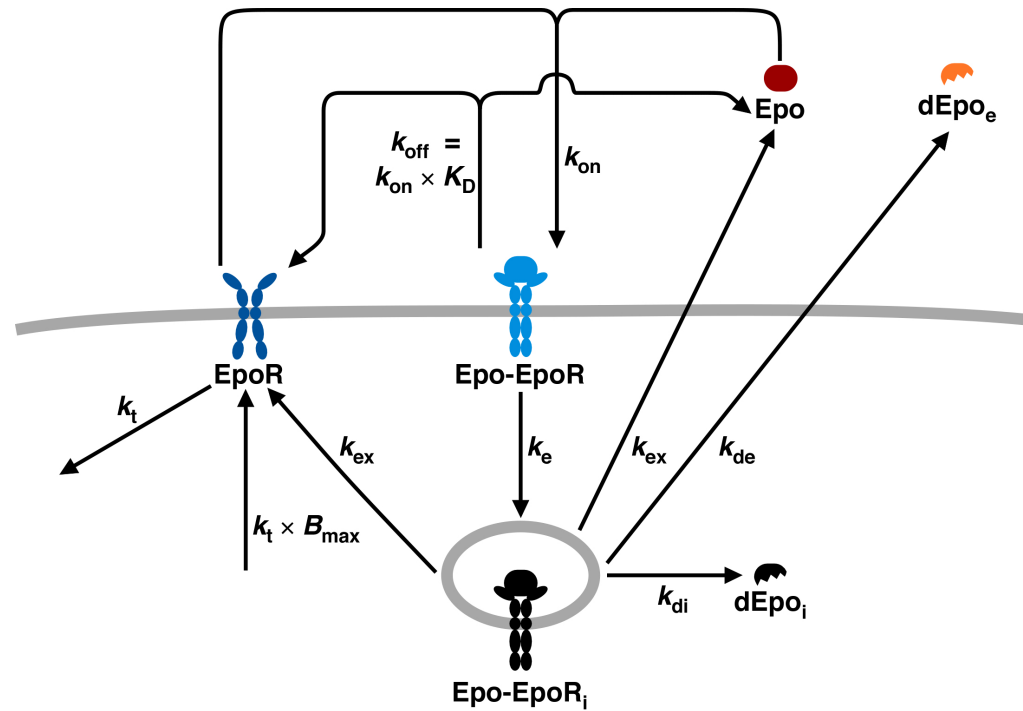
recycling



turnover



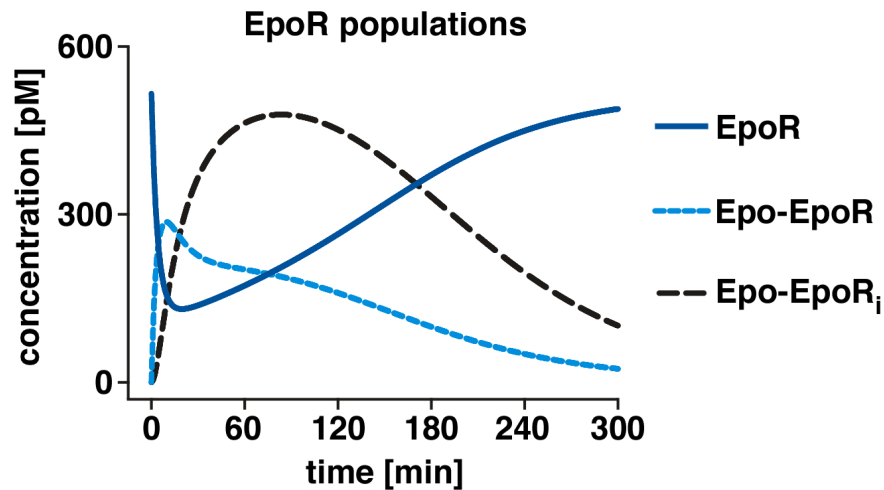
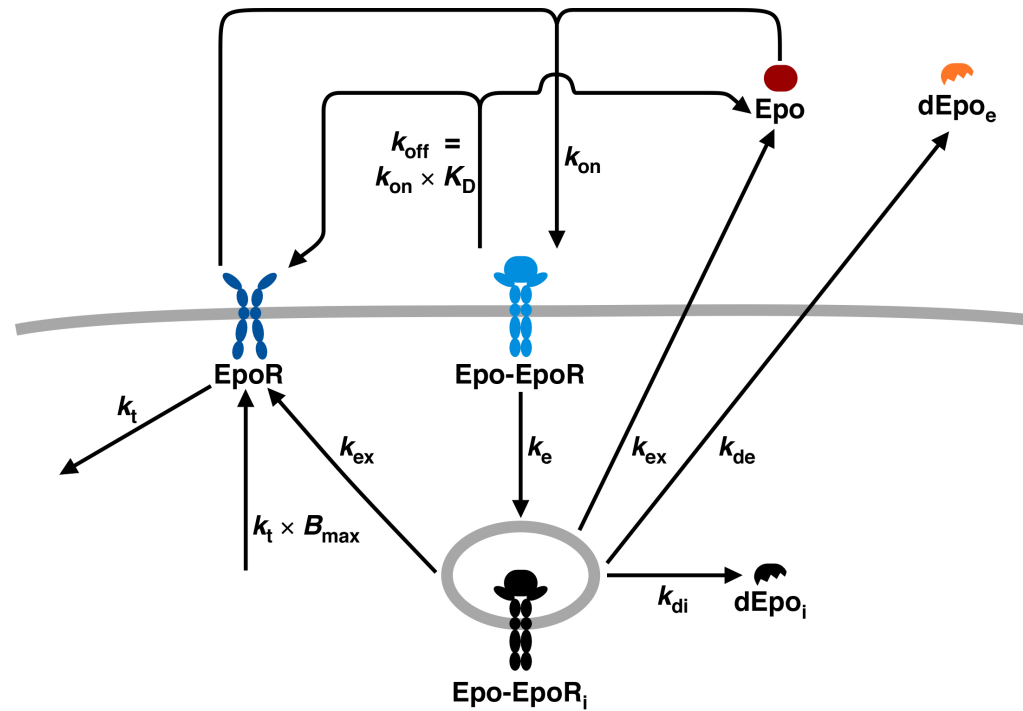
Key Properties of the EpoR System



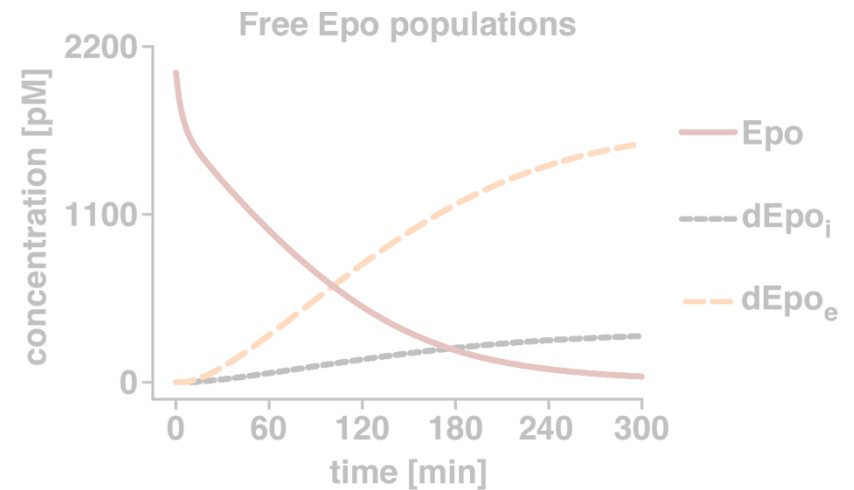
→ fast recovery of cell surface EpoR

→ rapid depletion of intact Epo

EpoR Recovery at the Cell Surface - Model Validation

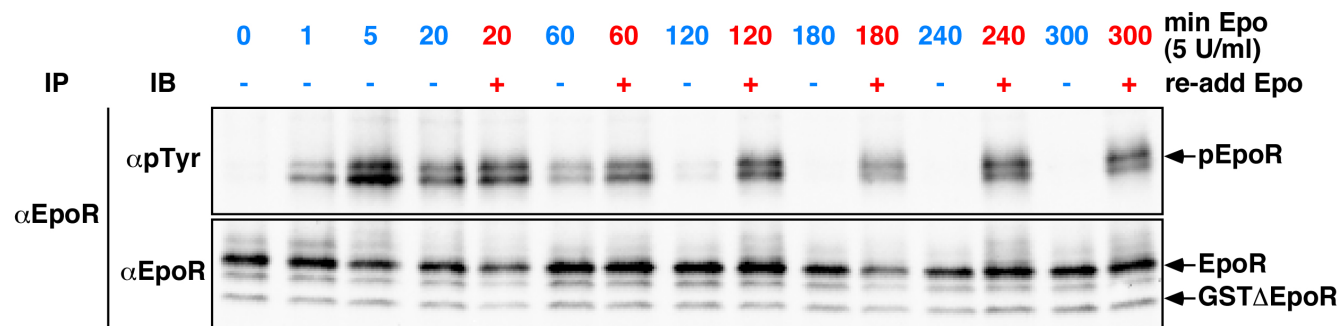
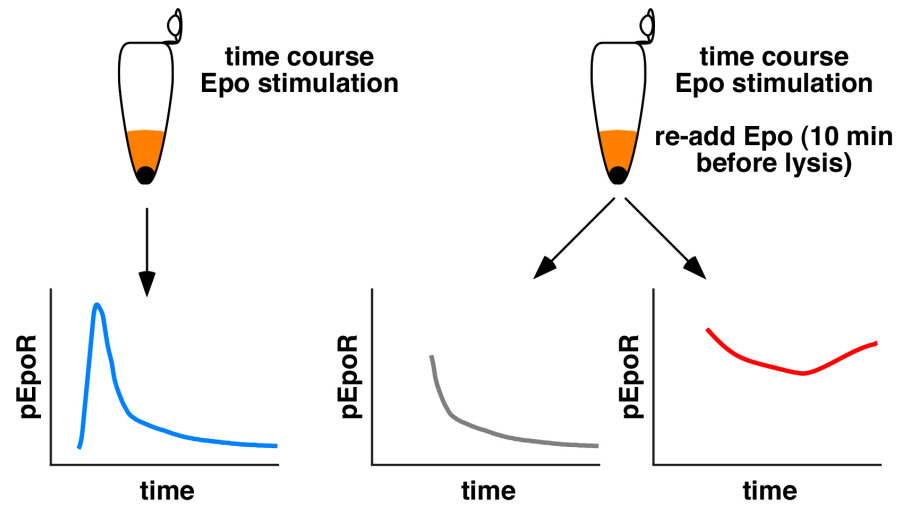


→ fast recovery of cell surface EpoR



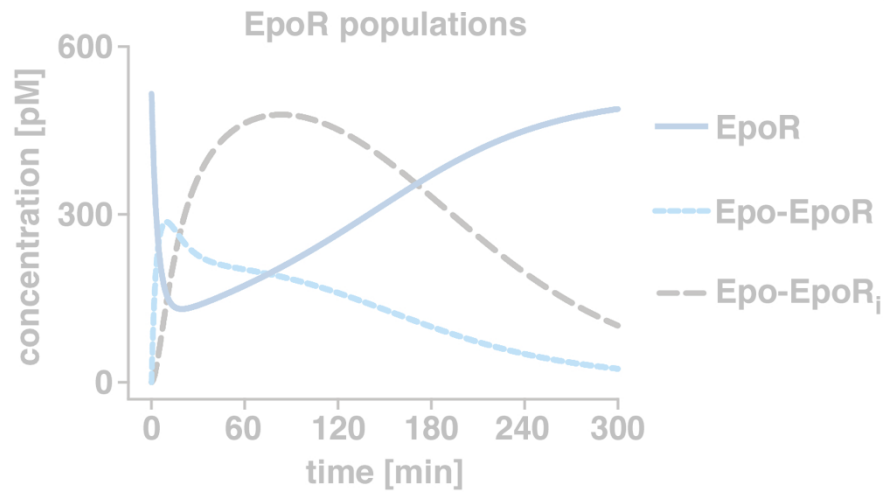
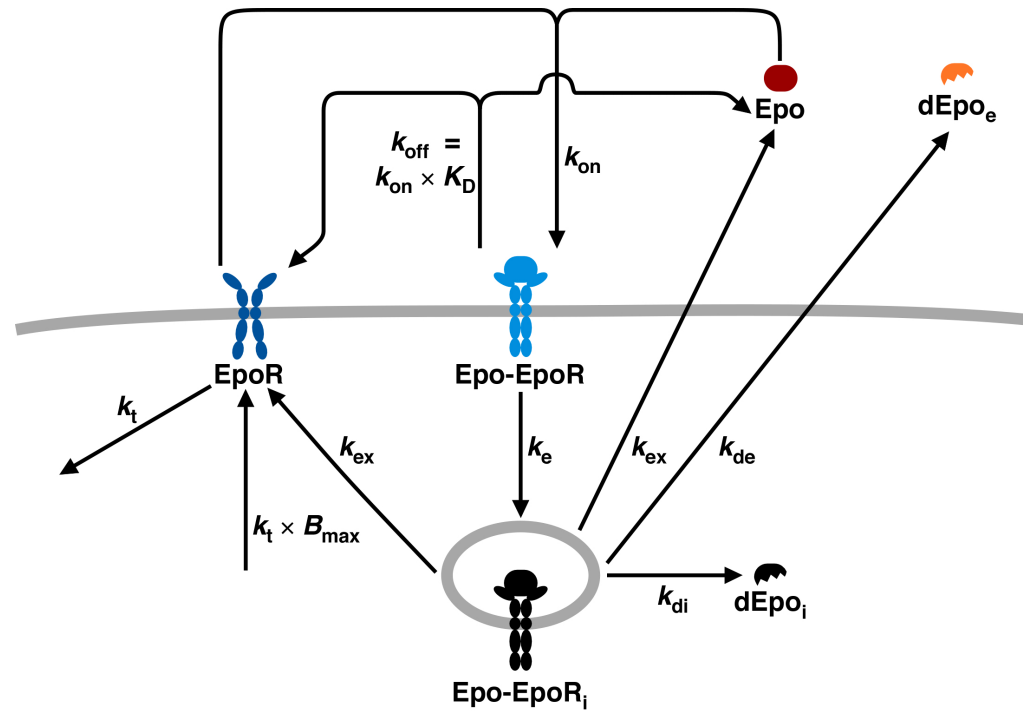
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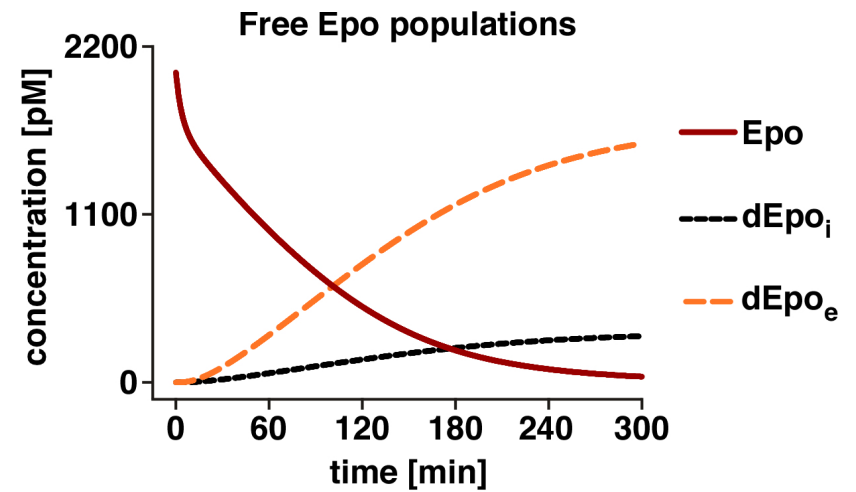


→ recovery of EpoR, cells remain ligand-responsive

Epo Depletion - Model Validation

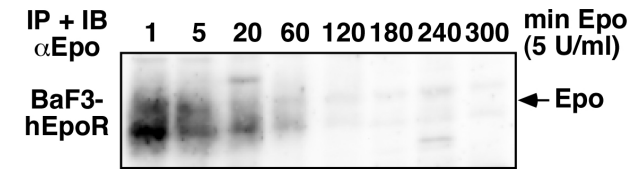
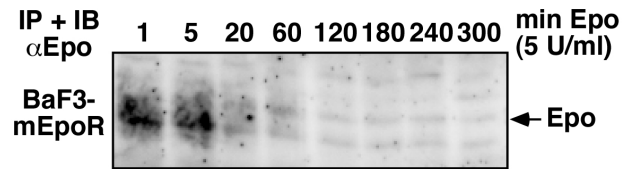


→ fast recovery of cell surface EpoR

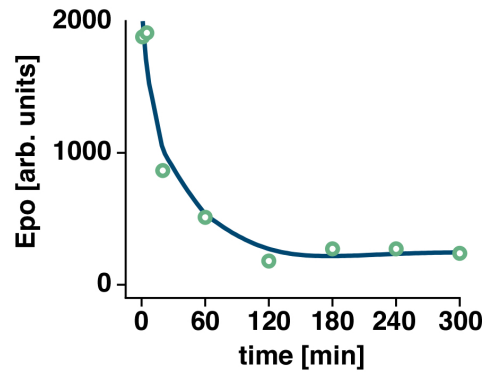
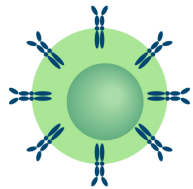


→ rapid depletion of intact Epo

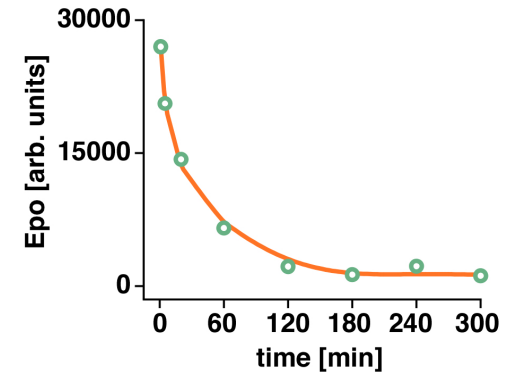
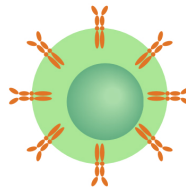
Epo Depletion - Model Validation by Direct Measurements



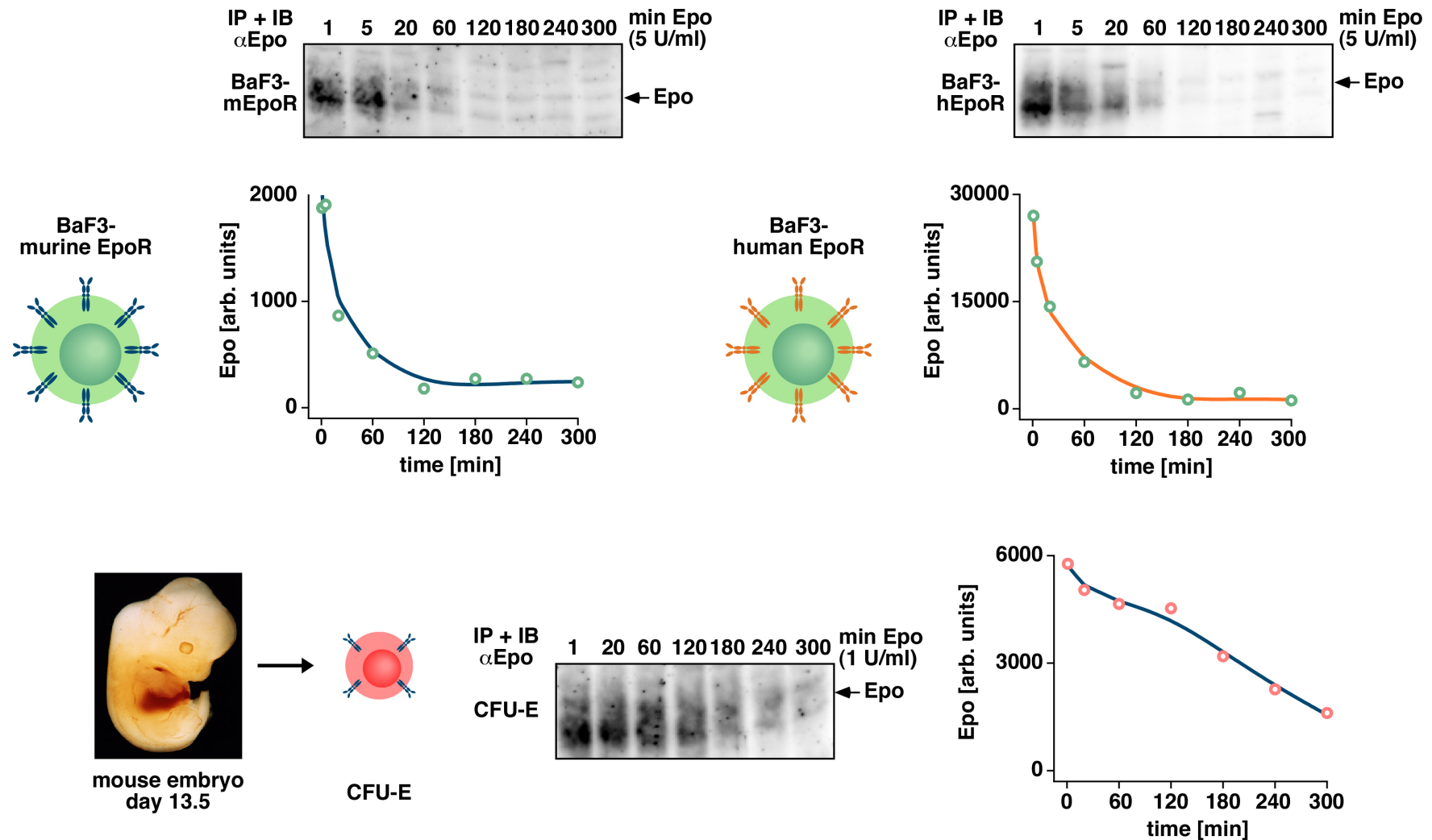
BaF3-
murine EpoR



BaF3-
human EpoR



Epo Depletion - Model Validation by Direct Measurements

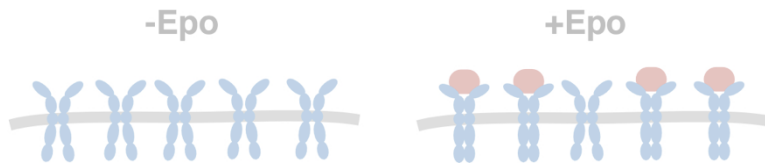


→ ligand depletion in both murine and human system

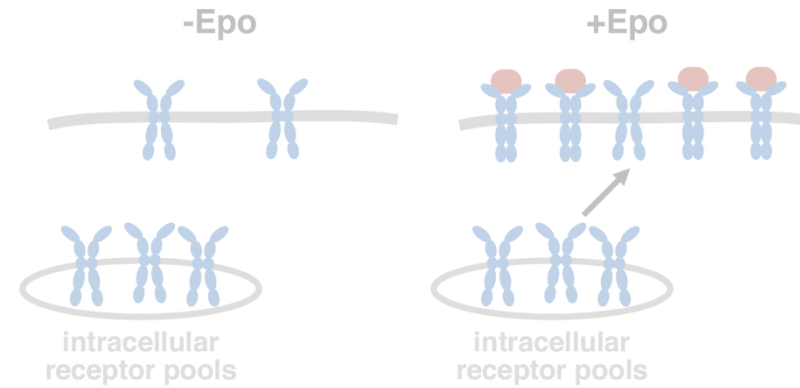
→ regulation of signal initiation by EpoR endocytosis through ligand depletion

Strategies for Processing Ligand-Encoded Information

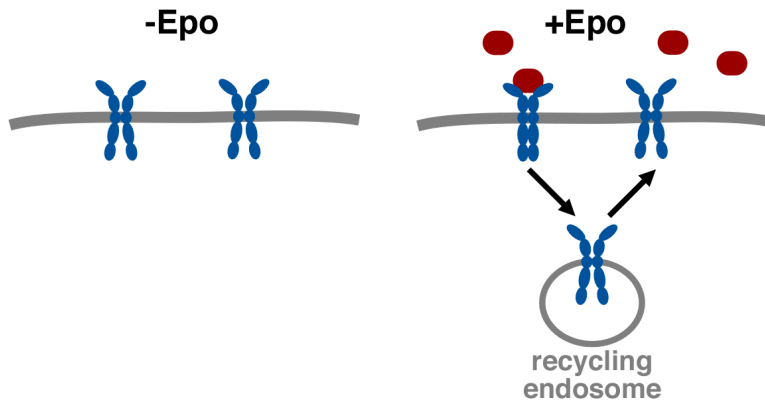
abundance



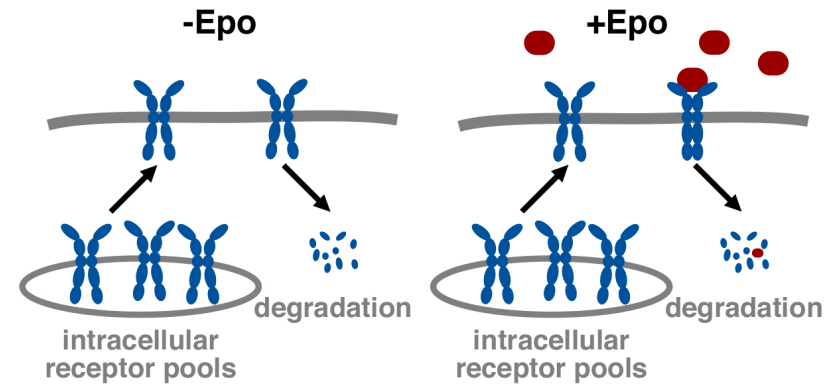
mobilization



recycling

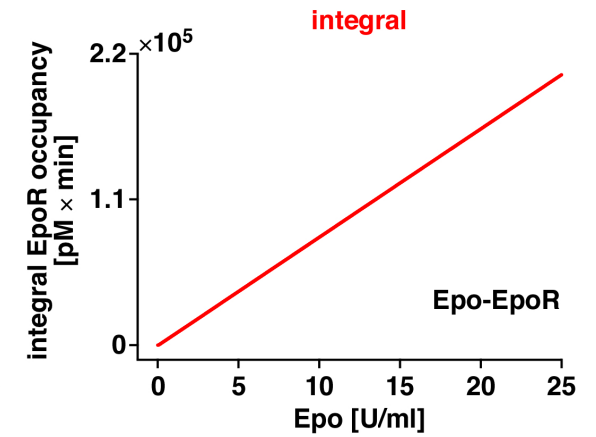
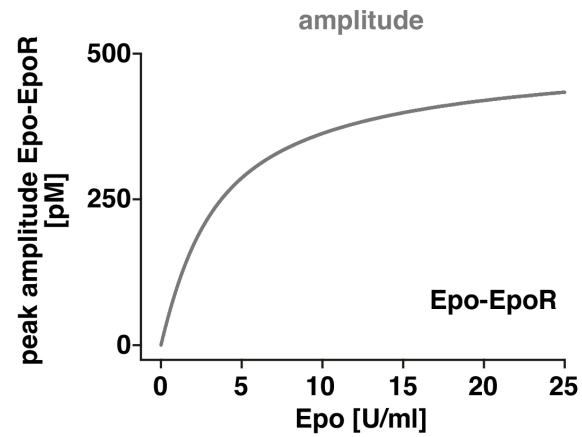
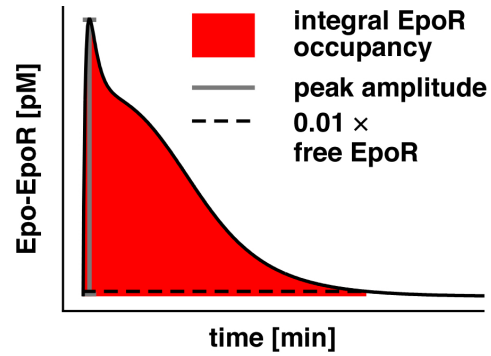


turnover



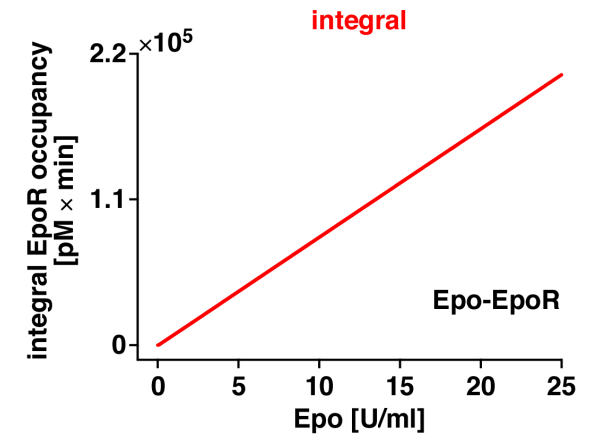
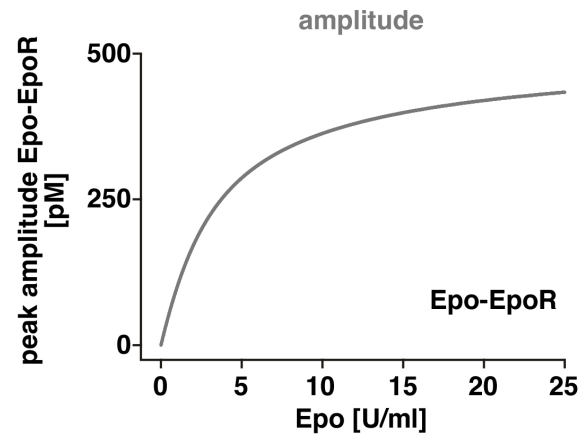
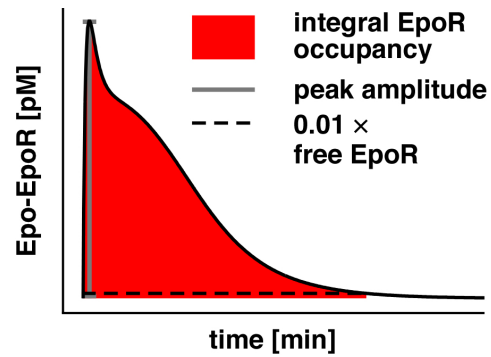
Linear EpoR Signaling for a Broad Range of Epo Levels

model simulations

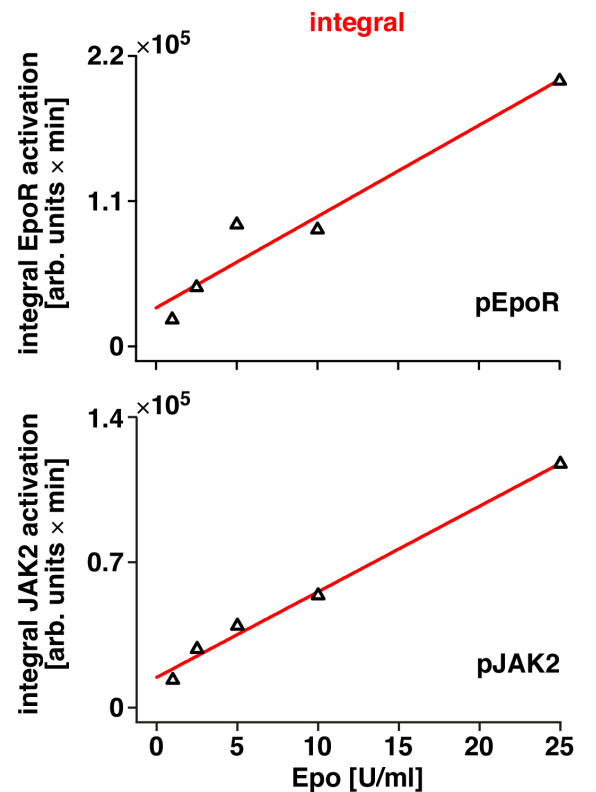
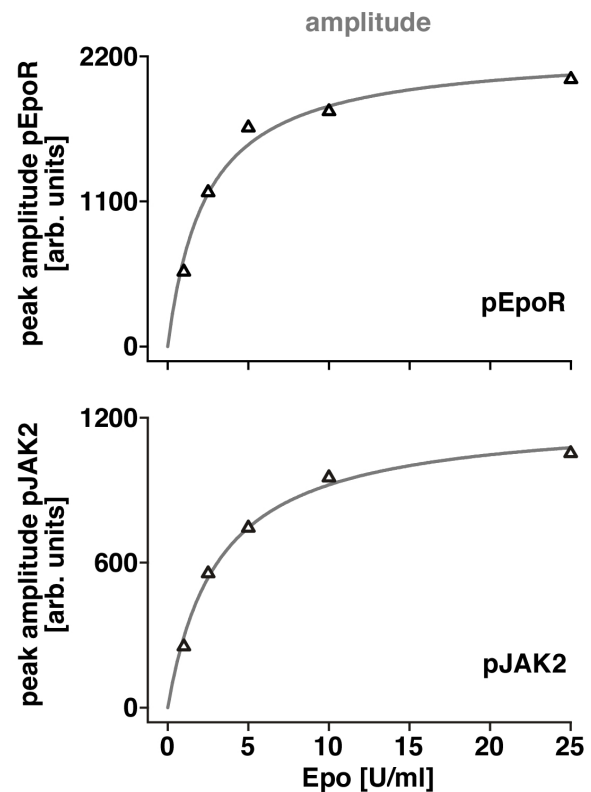
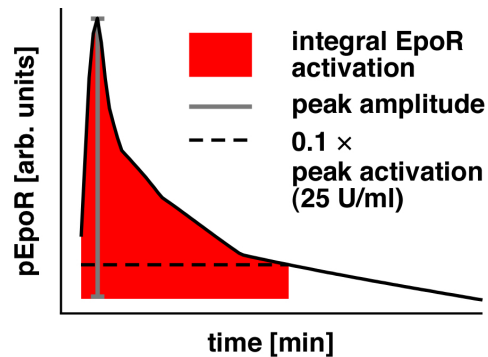


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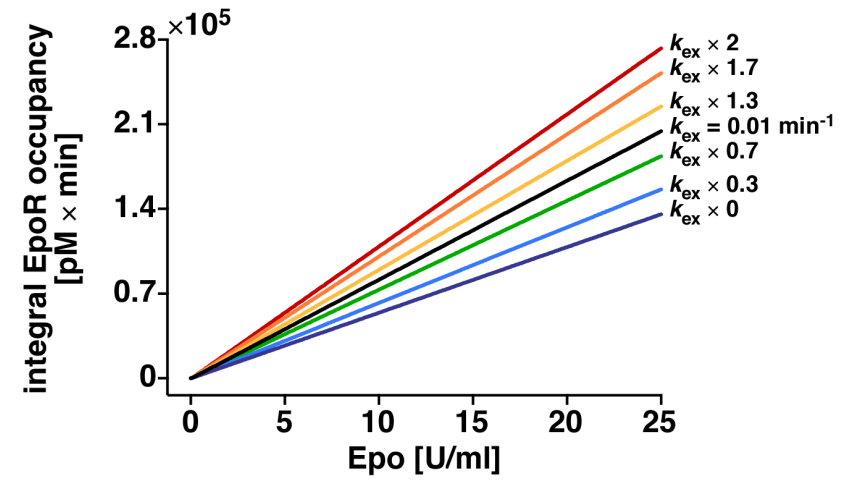
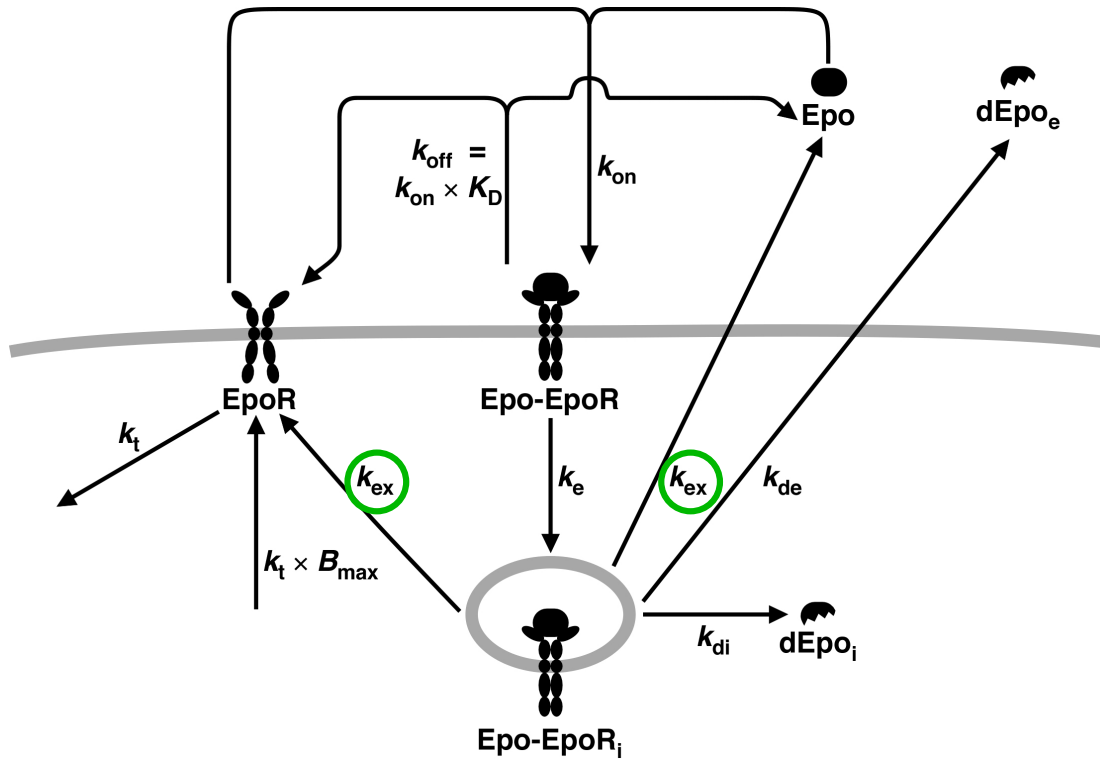


experiments

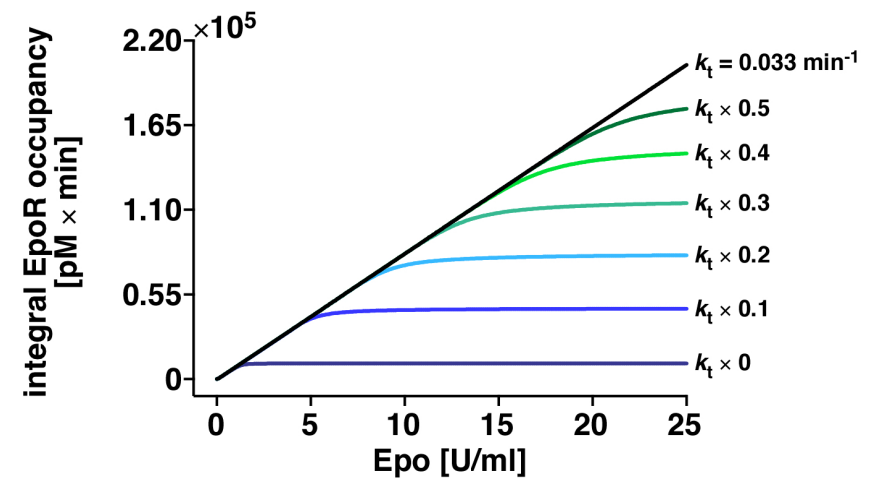
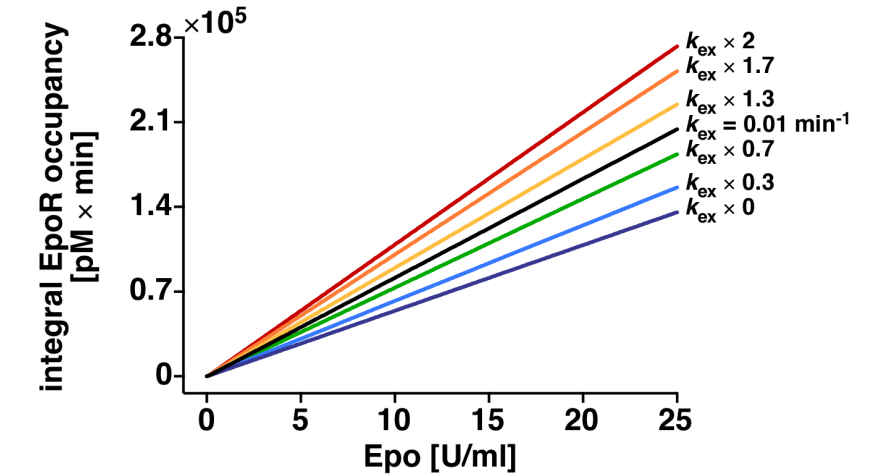
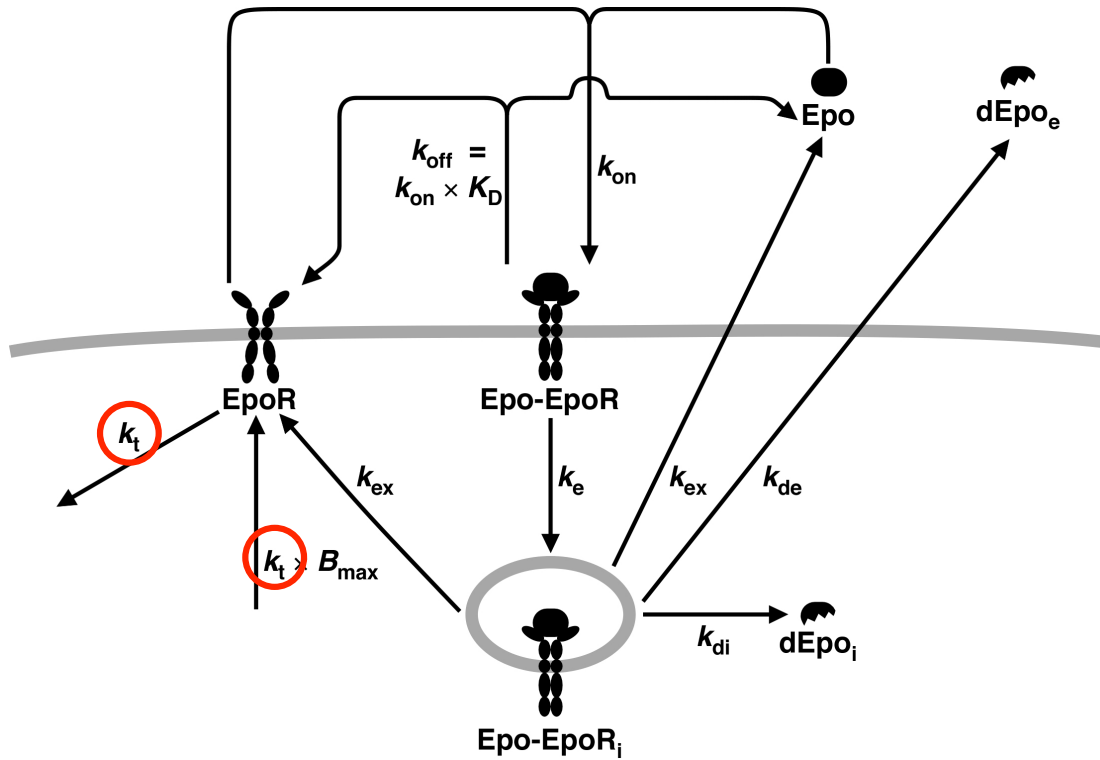


→ linear relation of Epo input and integral EpoR activation

Dependency of Linear Relation

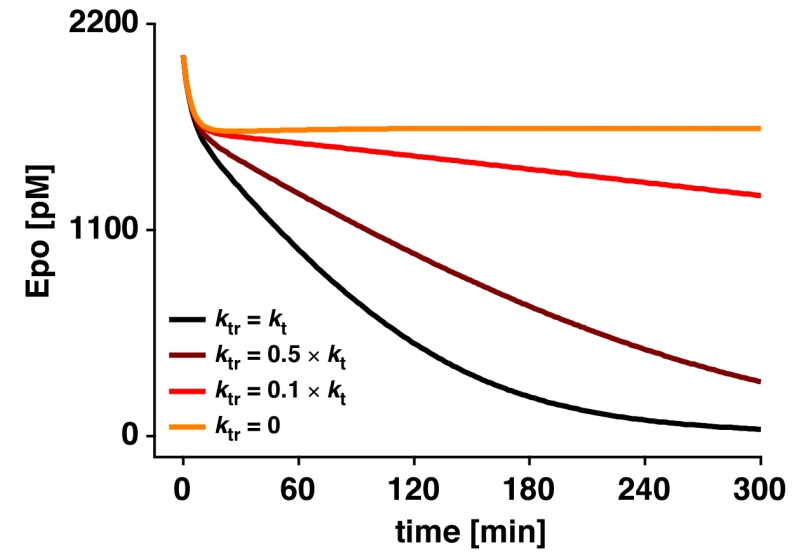
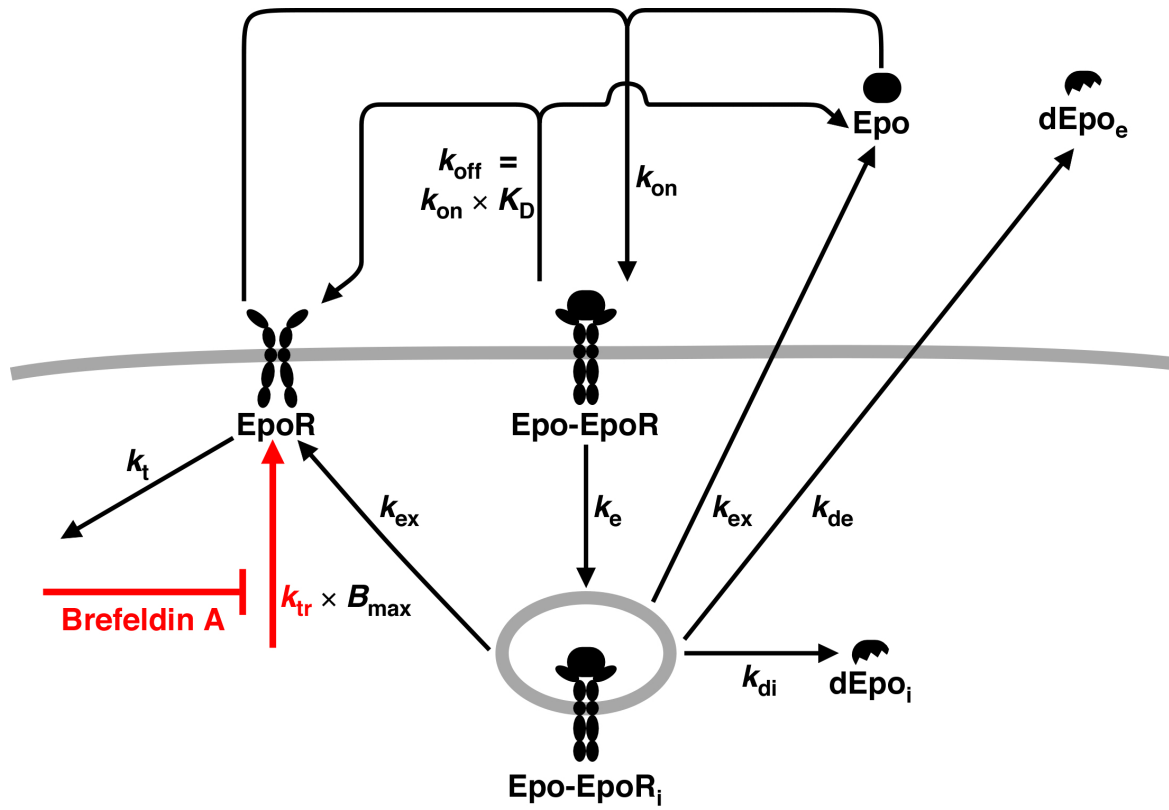


Dependency of Linear Relation on EpoR Turnover

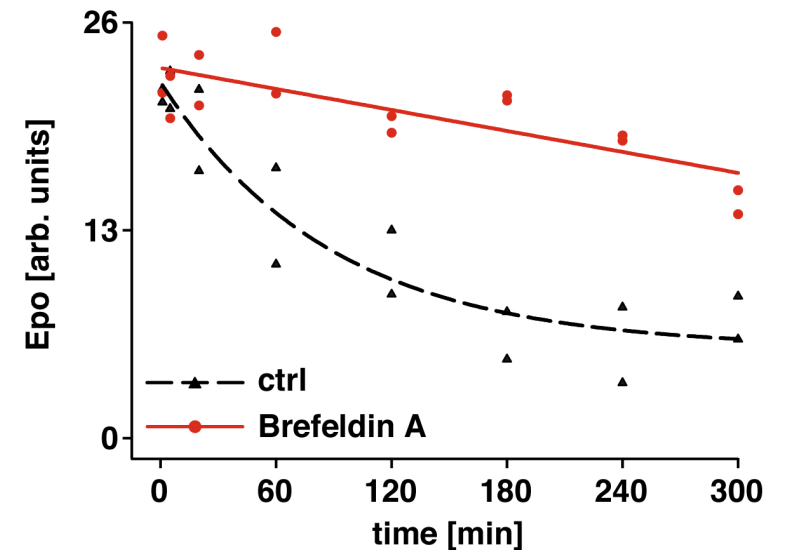
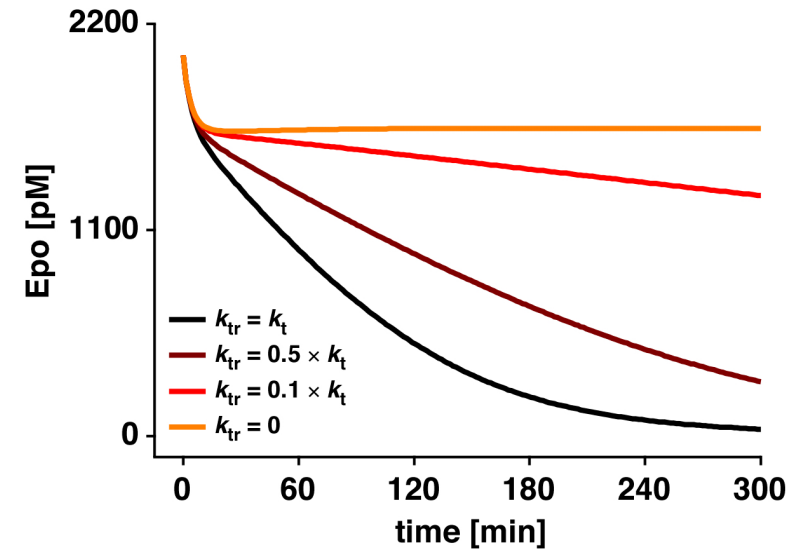
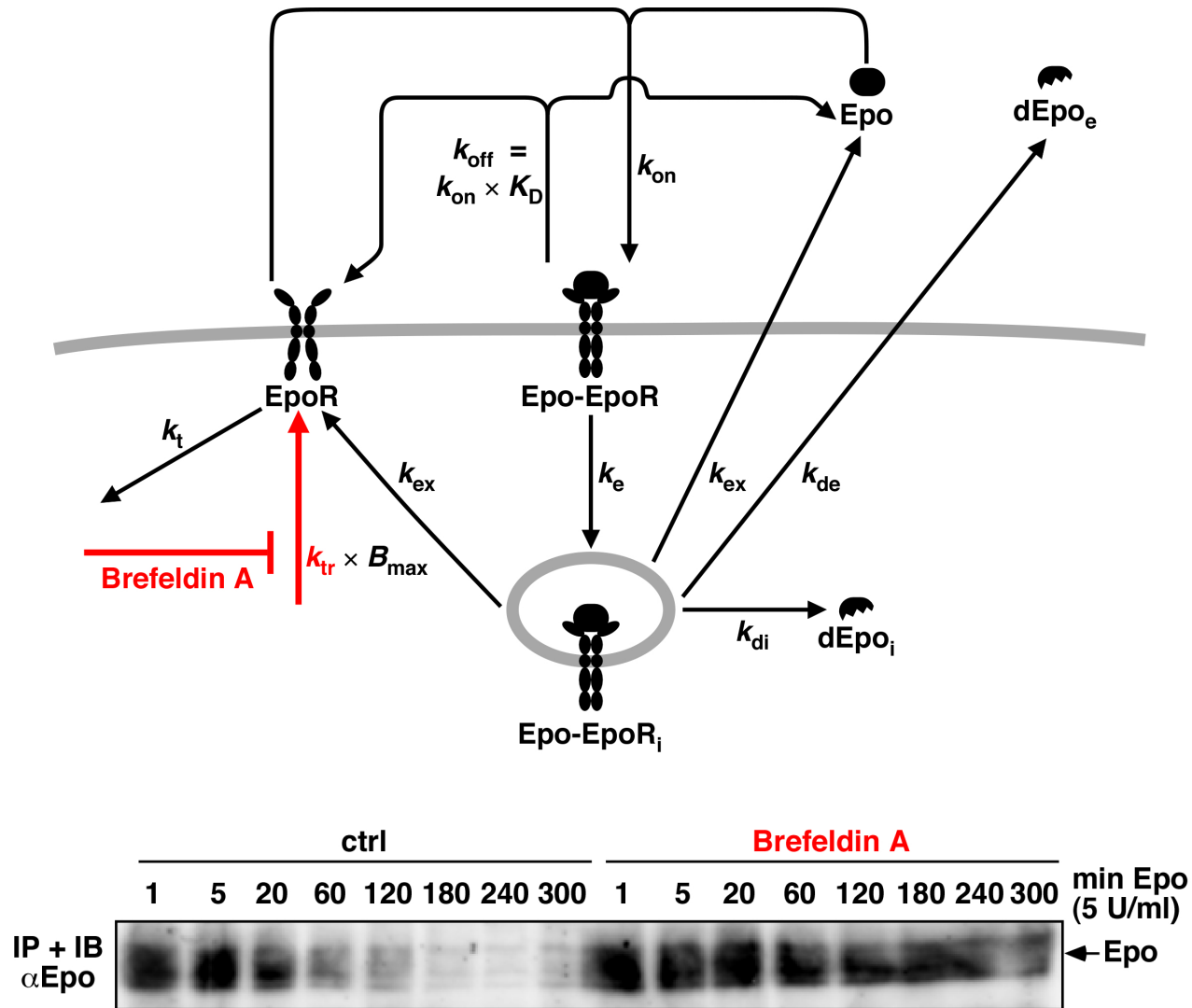


→ constitutive EpoR turnover: linear signal integrator

Contribution of Intracellular EpoR Pools



Contribution of Intracellular EpoR Pools

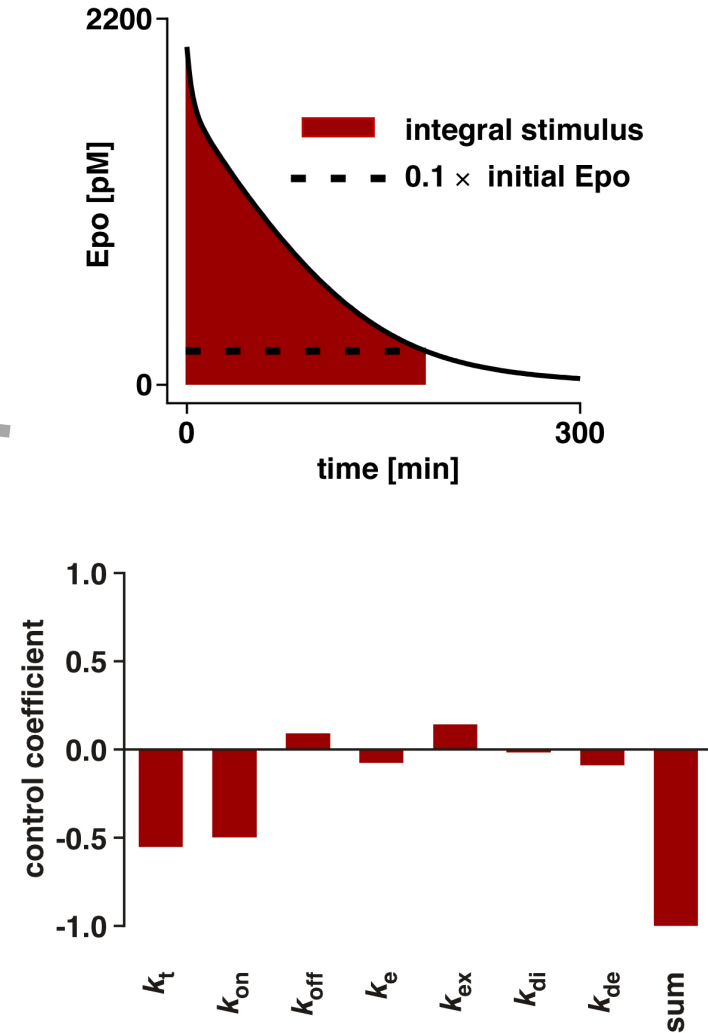
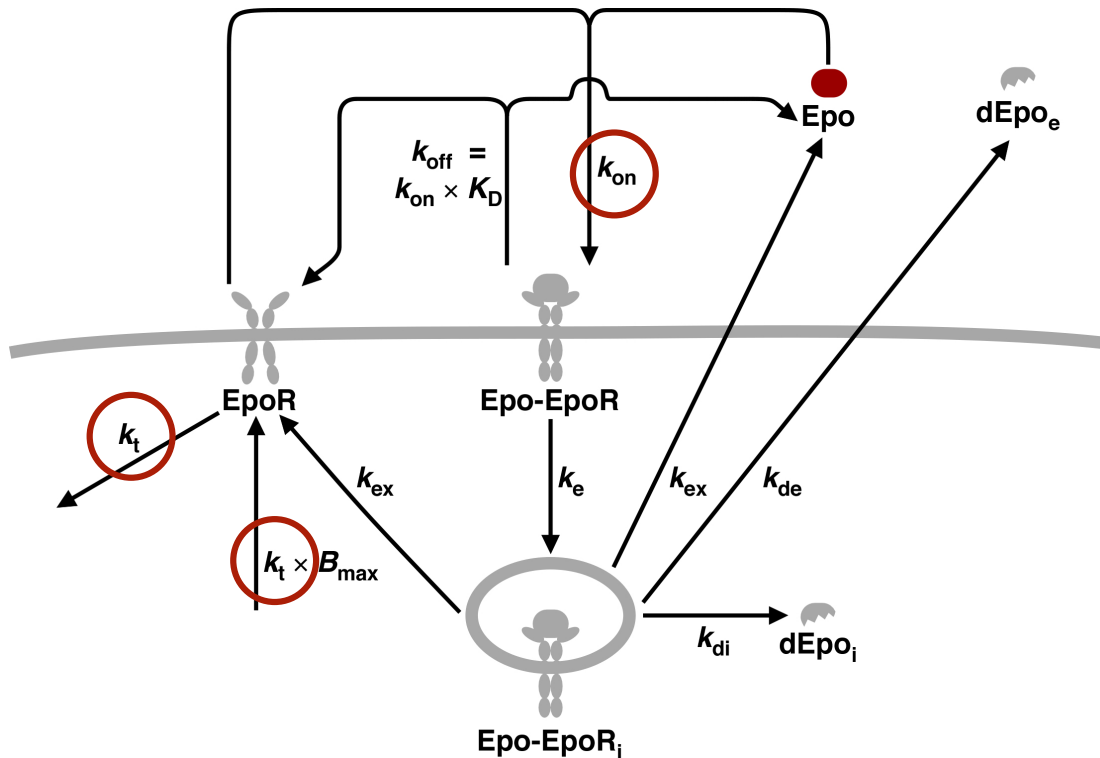


→ EpoR transport as a prerequisite for sampling and integrating ligand

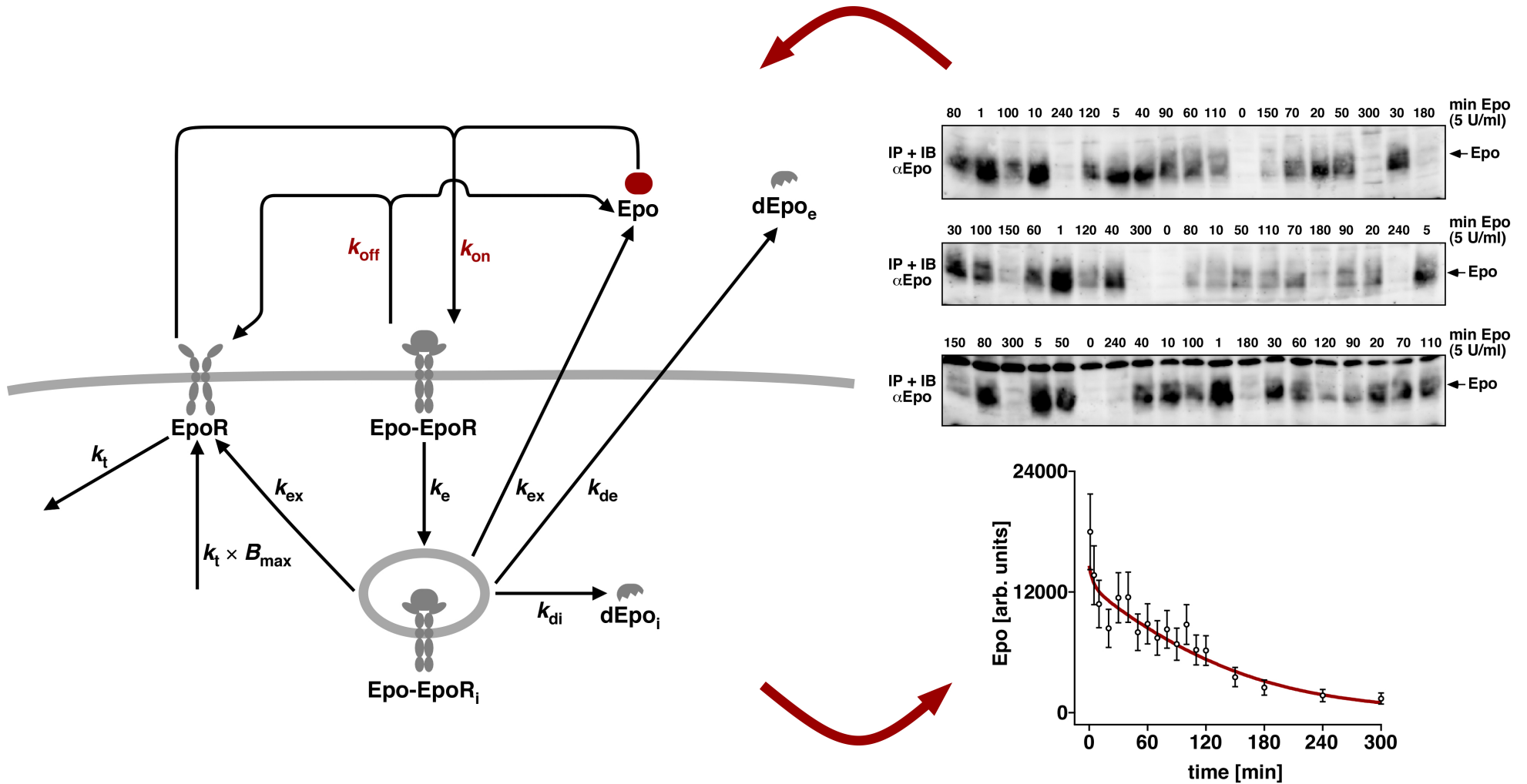
→ critical role of large pools of newly synthesized EpoR in ER and Golgi

Differential Ligand Binding Properties of Epo Derivatives

→ sensitivity analysis: k_{on} essential ligand binding property for Epo depletion

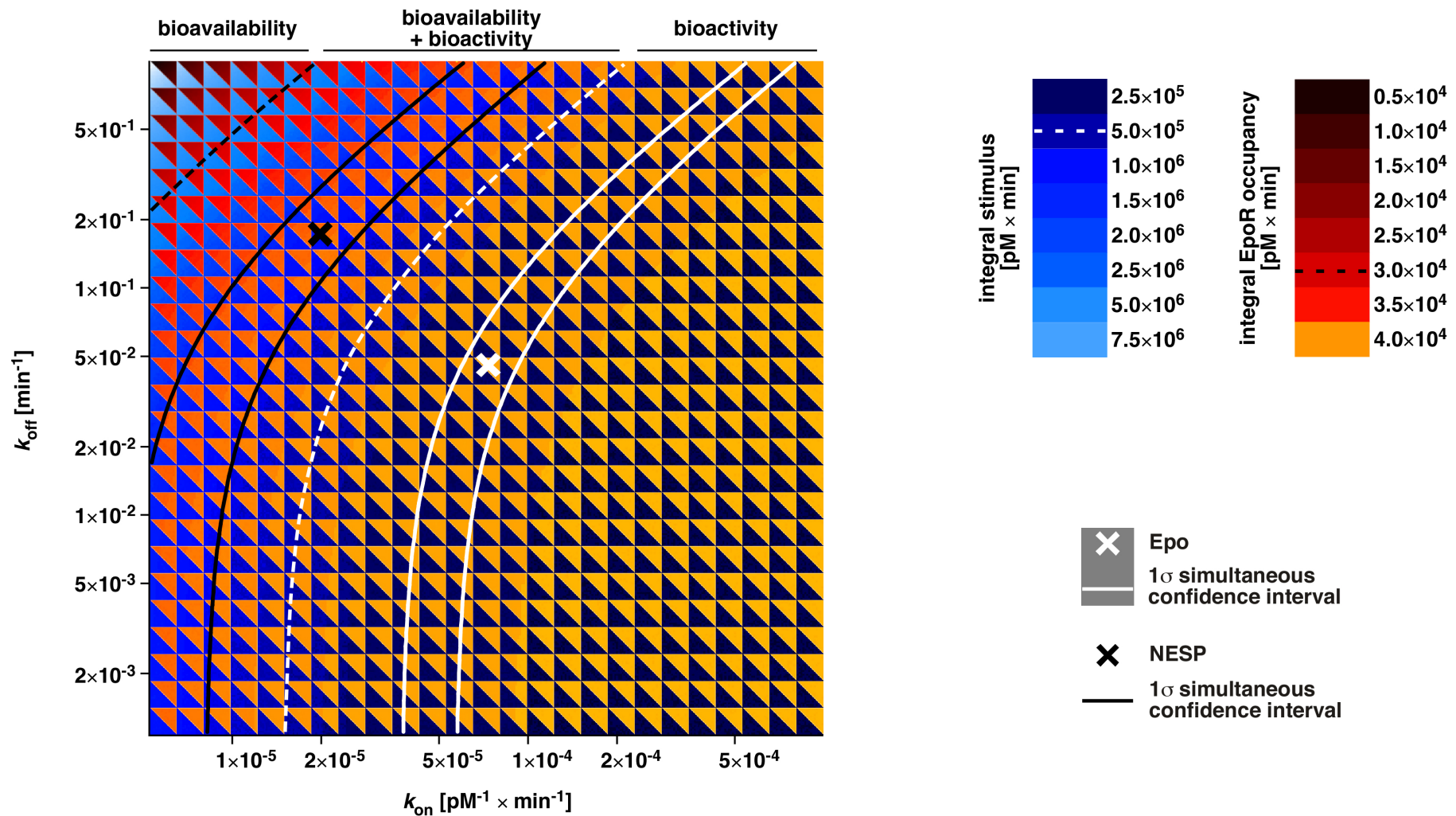


Simulation of Bioactivity and Bioavailability of Epo Derivatives



- simulate system dynamics for different k_{on}/k_{off} rate couples
- calibrated model employed to estimate k_{on} and k_{off} parameter values by using immunoblot data for Epo and NESP

Simulation of Bioactivity and Bioavailability of Epo Derivatives



- estimation of bioactivity and bioavailability of Epo derivatives via ligand binding kinetics
- rapid application, circumvents radioactivity or animal experiments

Generalisation of the Model

- Different cell types: CFU-E, m/hBaF3, H838
- Different ligands: Epo α , Epo β , NESP, CERA

$$\dot{x} = f(x, p), \quad x(0) = x_o$$

Different cell types, three possibilities:

- different x_o : different expression levels
- different p : different reaction rates
- different $f(\cdot)$: different topology

Generalisation of the Model

Ansatz: Fit all data by one model, individual parameters for

- **number of receptors**
- **ligand-receptor affinities**

Amount of data: 600 from 22 experimental conditions

Result: It works !

Generalisation of the Model

Number of receptors

CFU-E: 1463 ± 156

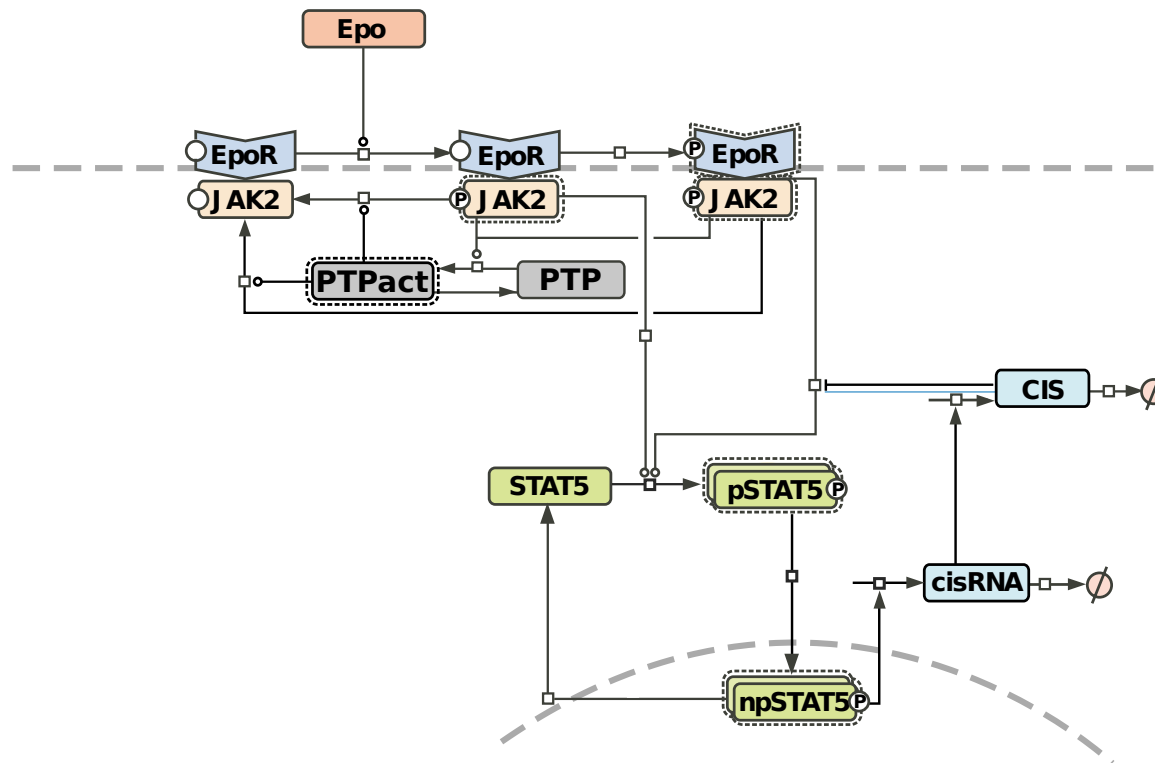
BaF3: 10293 ± 485

H838: 458 ± 46

- **# receptors CFU-E & BaF3 agree with experiments**
- **# receptors for H838 not determinable by experiments**

Looking Downstream

Combine receptor model with STAT5 signaling model

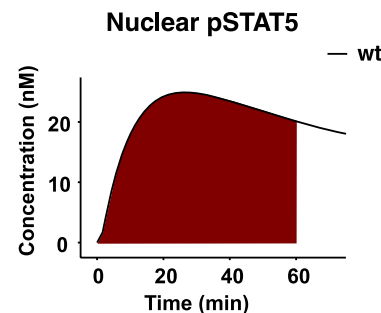


Epo and Cancer

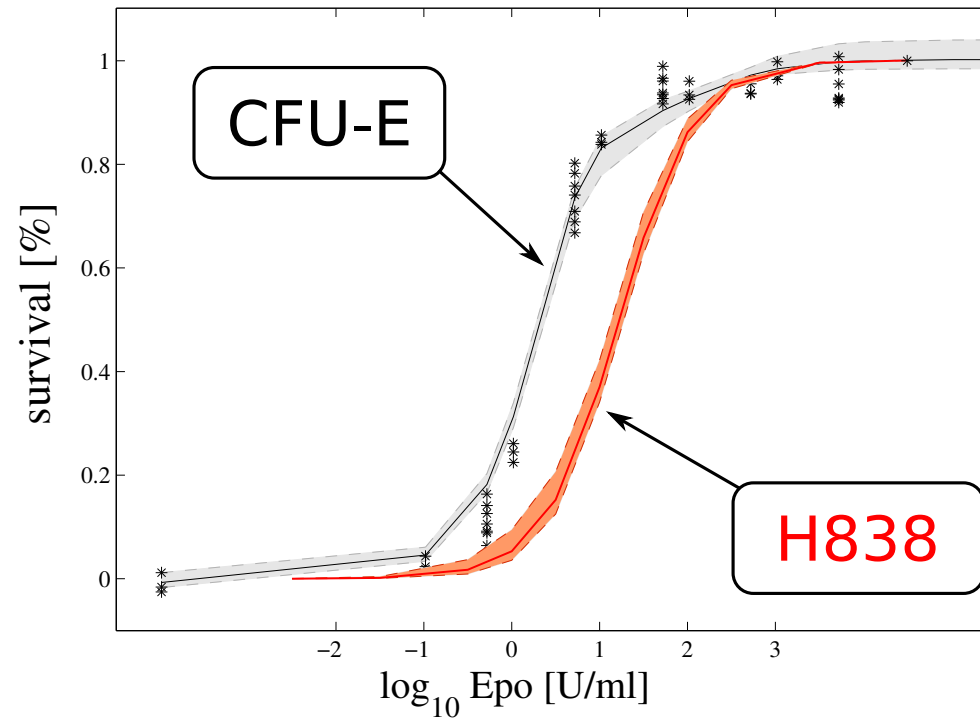
- Epo often applied during chemotherapy to fight anemia
- But, Epo-receptors also expressed on tumor cells

Question: Is there a difference in dosing effects ?

Integral nuclear pSTAT5 determines cell survival



Dosing Effects

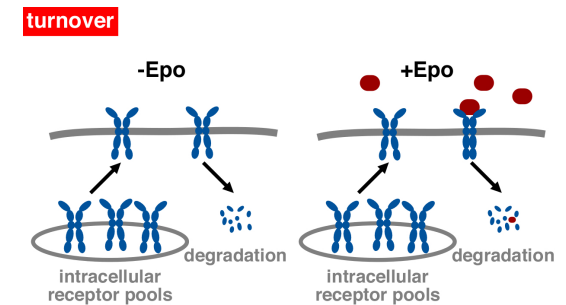
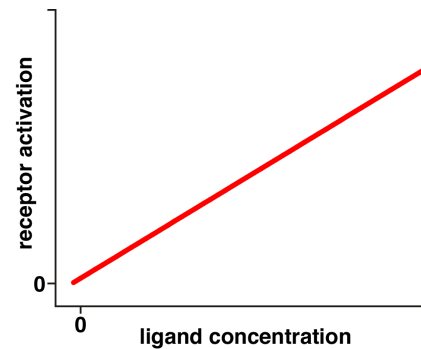


Suggests: There is a range of differential effects

Summary

Information processing through EpoR:

- rapid Epo depletion
- fast recovery of cell surface EpoR
- linear relation of Epo levels and integral EpoR activation over a broad range of ligand concentrations
- accurate translation of ligand input into erythrocyte production

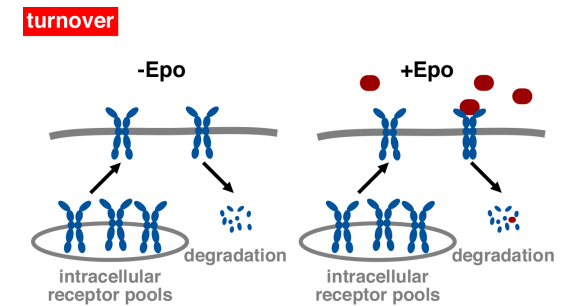
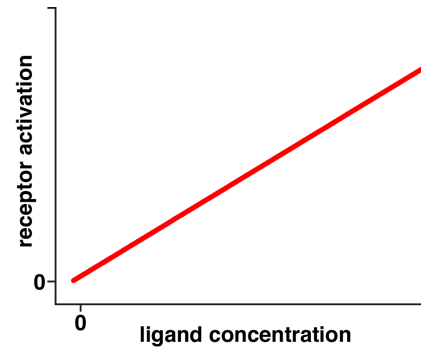


V. Becker, M. Schilling, J. Bachmann, U. Baumann, A. Raue, T. Maiwald, J. Timmer, and U. Klingmüller (2010). *Science* 328(5984):1404-1408.

Summary

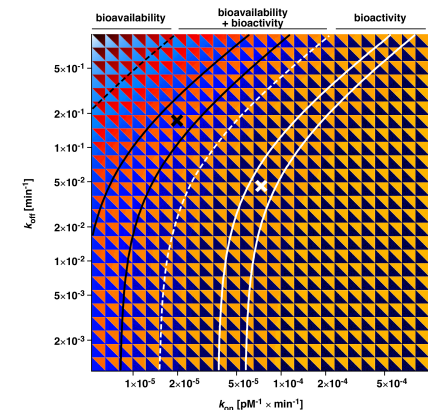
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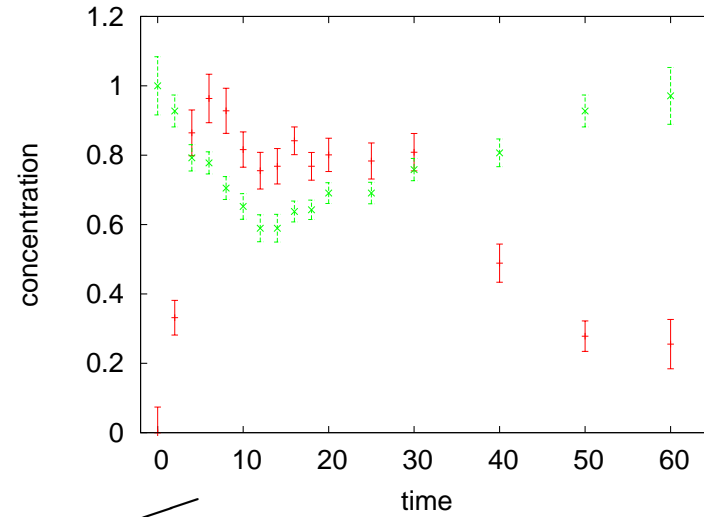
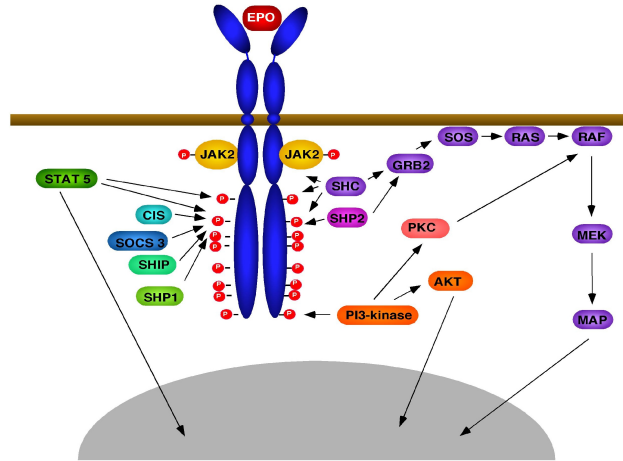
Rational design of therapeutics and cancer treatment strategies:

- estimation of k_{on} and k_{off} rates
- identification of risks in Epo treatment of lung cancer patients



V. Becker, M. Schilling, J. Bachmann, U. Baumann, A. Raue, T. Maiwald, J. Timmer, and U. Klingmüller (2010). *Science* 328(5984):1404-1408.

Signal transduction through the Erythropoietin receptor (EpoR)



$$\dot{\vec{x}} = \vec{f}(\vec{x}, \vec{p})$$

In silico biology
 Test the prior knowledge
 Understanding systems' properties
 Identification of potential drug targets

Acknowledgements

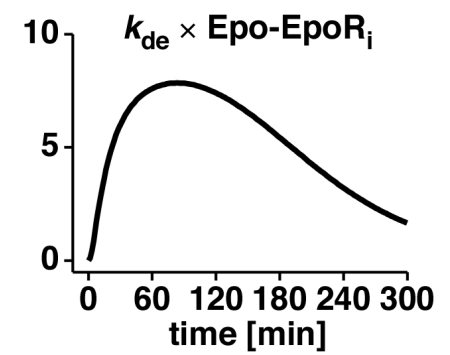
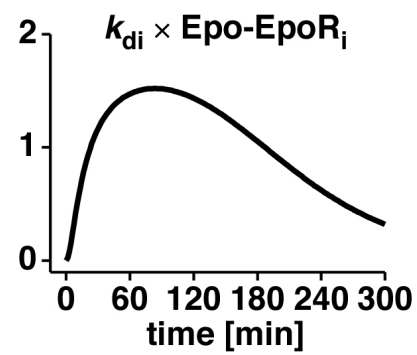
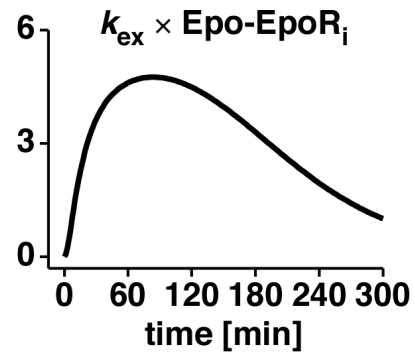
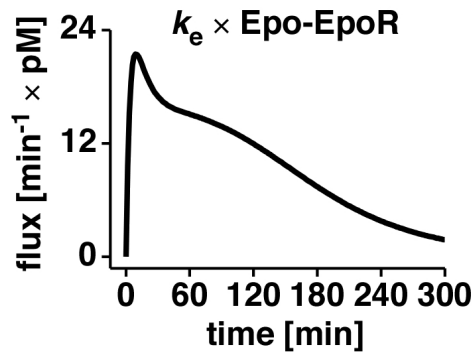
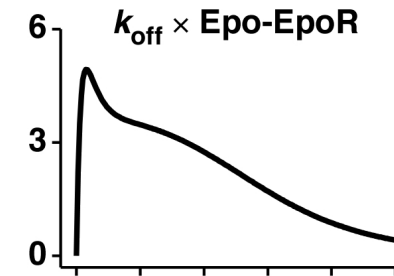
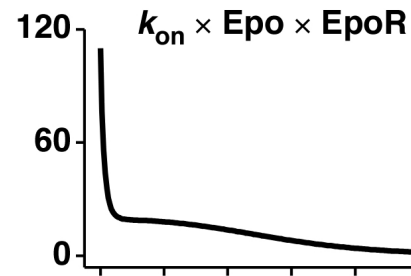
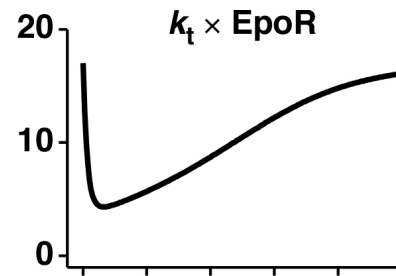
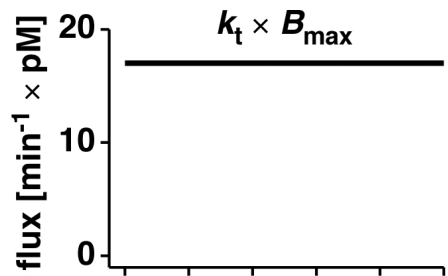
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Flux Analysis Core Model

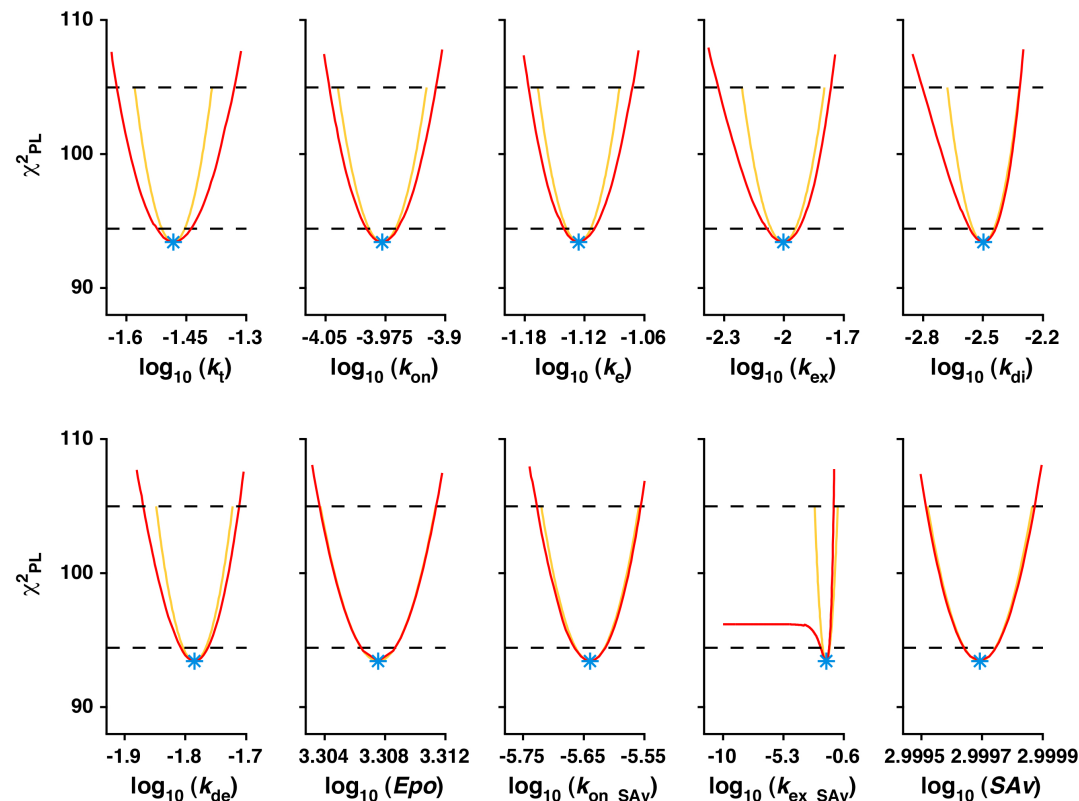


Identifiability Analysis by Profile Likelihood Exploit

$$\chi_{PL}^2(\theta_i) = \min_{\theta_{j \neq i}} [\chi^2(\theta)]$$

$$\left\{ \theta \mid \chi^2(\theta) - \chi^2(\hat{\theta}) < \Delta_\alpha \right\} \quad \text{with} \quad \Delta_\alpha = \chi^2(\alpha, df)$$

Raue et al. (2009), Bioinformatics



parameter	best fit
k_t [min ⁻¹]	0.03294 (+ 0.00356 / - 0.00293) (+ 10.81% / - 8.89%)
k_{on} [pM ⁻¹ × min ⁻¹]	0.10496×10^{-3} (+ 4.72×10^{-6} / - 4.68×10^{-6}) (+ 4.50% / - 4.46%)
k_{off} [min ⁻¹]	0.01721 (+ 0.00077 / - 0.00077) (+ 4.47% / - 4.47%)
k_e [min ⁻¹]	0.07483 (+ 0.00277 / - 0.00248) (+ 3.70% / - 3.31%)
k_{ex} [min ⁻¹]	0.00994 (+ 0.00195 / - 0.00169) (+ 19.62% / - 17.00%)
k_{di} [min ⁻¹]	0.003179 (+ 0.000475 / - 0.000461) (+ 14.94% / - 14.50%)
k_{de} [min ⁻¹]	0.01640 (+ 0.00086 / - 0.00083) (+ 5.24% / - 5.06%)
Epo [pM]	2030.19 (+ 5.22 / - 5.21) (+ 0.26% / - 0.26%)
k_{on_SAV} [pM ⁻¹ × min ⁻¹]	2.294×10^{-6} (+ 1.36×10^{-7} / - 1.32×10^{-7}) (+ 5.93% / - 5.75%)
k_{off_SAV} [min ⁻¹]	0.006799 (+ 0.000403 / - 0.000391) (+ 5.93% / - 5.75%)
k_{ex_SAV} [min ⁻¹]	0.0110 (+ 0.0076 / - 0.0069) (+ 69.09% / - 62.73%)
SAV [pM]	999.293 (+ 0.120 / - 0.120) (+ 0.01% / - 0.01%)

→ good model accuracy:

- all parameters identifiable with small confidence intervals

→ allowing for accurate predictions