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# Covering a Broad Dynamic Range: Information Processing at the Erythropoietin Receptor

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Cell surface receptors convert extracellular cues into receptor activation, thereby triggering intracellular signaling networks and controlling cellular decisions. A major unresolved issue is the identification of receptor properties that critically determine processing of ligand-encoded information. We show by mathematical modeling of quantitative data and experimental validation that rapid ligand depletion and replenishment of the cell surface receptor are characteristic features of the erythropoietin (Epo) receptor (EpoR). The amount of Epo-EpoR complexes and EpoR activation integrated over time corresponds linearly to ligand input; this process is carried out over a broad range of ligand concentrations. This relation depends solely on EpoR turnover independent of ligand binding, which suggests an essential role of large intracellular receptor pools. These receptor properties enable the system to cope with basal and acute demand in the hematopoietic system.

Cells respond to alterations in their environment that are frequently encoded by changes in the concentration of extracellular ligands. These changes are perceived by cell surface receptors, and the high frequency with which receptors are mutated in diseases and their accessibility to drugs make them key targets for therapeutic interventions. The dynamics of receptor activation are critically determined by the capacity to capture and sequester ligand through endocytosis (1). Ligand-encoded information could be processed in a saturation-like or linear mode for increasing ligand concentrations (Fig. 1A). Receptor proper-

ties enabling cells to cope with ligand concentrations that vary over a broad range remained to be identified.

A prime example for a receptor that encounters an extreme range of ligand concentrations is the erythropoietin receptor (EpoR). The EpoR ensures continuous renewal of short-lived erythrocytes (2) and enhanced expansion of erythroid progenitors upon demands such as blood loss. Plasma concentrations of erythropoietin (Epo) can differ ~1000-fold between basal and acute conditions (3). Only a small proportion of EpoR is present on the cell surface; the majority resides in intracellular pools (4). Ligand binding triggers

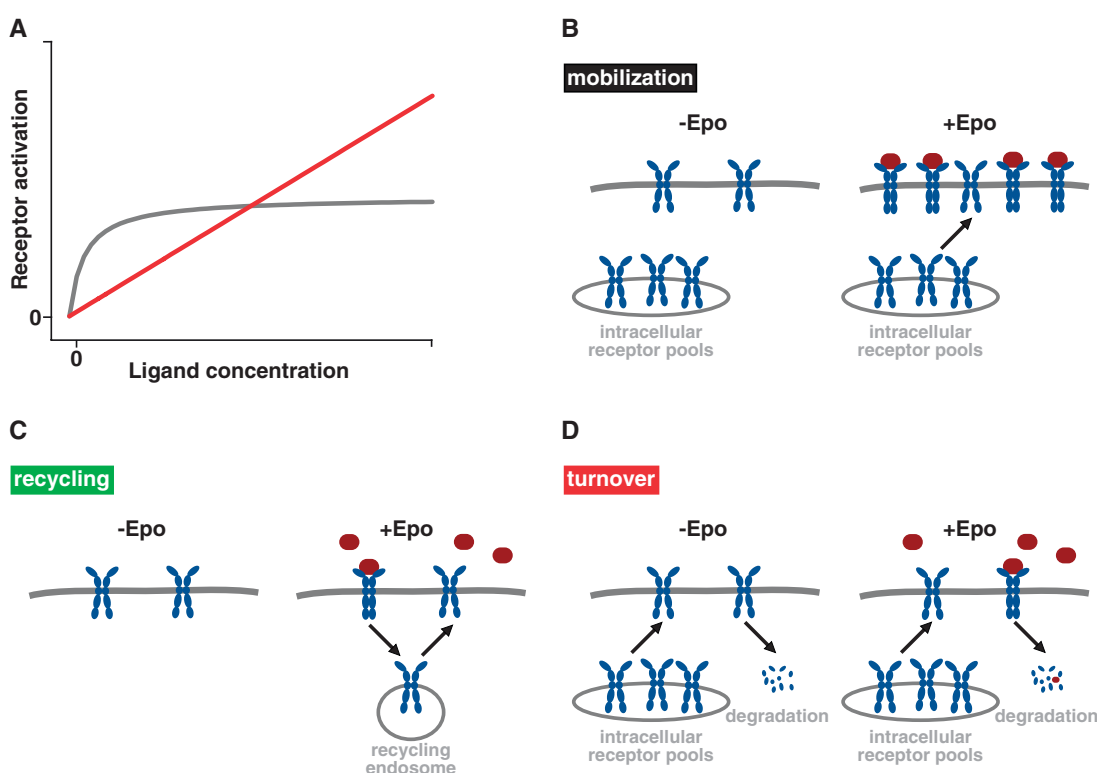
phosphorylation of the cytoplasmic EpoR domain by Janus kinase 2 (JAK2) (5). Ligand-induced endocytosis of EpoR has been proposed to terminate signaling by removing receptors from the cell surface (6). Additionally, the EpoR is subjected to ligand-independent endocytosis (7) [supporting online material (SOM) text]. The specific impact of EpoR transport to the plasma membrane and EpoR endocytosis on processing of ligand-encoded information have remained ill-defined.

Linear detection of ligand over a broad range of concentrations could be facilitated by the following properties reported for other receptors (Fig. 1, B to D, and SOM text): (i) mobilization, defined as ligand-induced additional transport of newly synthesized receptor from intracellular pools to the plasma membrane (8); (ii) recycling, consisting of ligand-induced receptor endocytosis and subsequent transport back to the plasma membrane (9); and (iii) turnover, comprising ligand-independent transport of newly synthesized receptor to the plasma membrane and removal from the plasma membrane by ligand-

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**Fig. 1.** Strategies of information processing through cell surface receptors for a broad range of ligand concentrations. (A) Representation of two modes for information processing. (B to D) Hypothetical mechanisms for linear information processing through the EpoR: mobilization, recycling, and turnover (see text).



independent receptor endocytosis and subsequent degradation (10). A further potential strategy to cope with particularly high ligand concentrations is expression of large amounts of receptor on the plasma membrane (11). However, the abundance of EpoR on the cell surface is rather low (12) (fig. S1 and SOM text).

Receptor mobilization, recycling, and turnover are highly dynamic and intertwined processes that are difficult to disentangle experimentally. To address these nonlinear processes, we developed dynamic mathematical models for ligand-receptor interaction and trafficking kinetics and fitted them to quantitative experimental data (13).

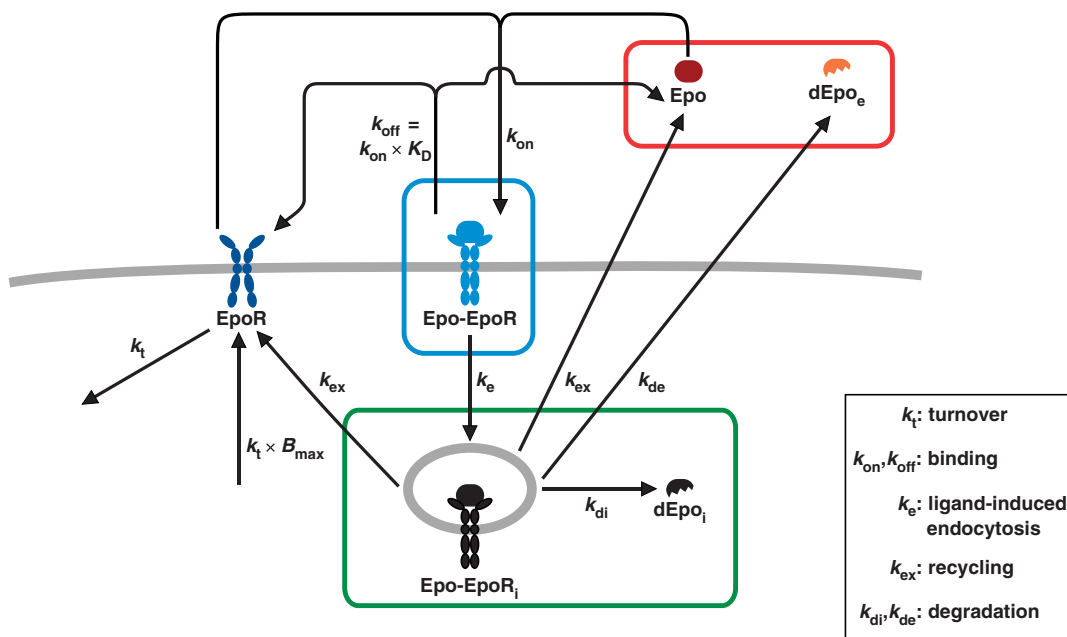
The core model included parameters for EpoR recycling and turnover (Fig. 2A) and was compared with an extended model encompassing receptor mobilization (core model +  $k_{\text{mob}}$ ) (fig. S5A). Briefly, unoccupied cell surface EpoR is subjected to turnover with transport of newly synthesized receptor to the plasma membrane ( $k_i \times B_{\text{max}}$ )—where  $B_{\text{max}}$  is the maximal binding capacity of the total cell surface receptor population—and ligand-independent endocytosis ( $k_t$ ). Epo binds to cell surface receptor with the association rate  $k_{\text{on}}$  and dissociates with the rate  $k_{\text{off}}$ . The definition of the parameter  $k_{\text{off}}$  is based on the dissociation constant  $K_D$  ( $k_{\text{off}} \times K_D$ ). Epo-EpoR complexes

are subjected to endocytosis ( $k_e$ ). These complexes dissociate, and EpoR and Epo recycle back to the plasma membrane ( $k_{\text{ex}}$ ) or undergo degradation. Degraded Epo is retained in intracellular compartments ( $k_{\text{di}}$ ) or released to the extracellular space in an inactive state ( $k_{\text{de}}$ ), unable to bind to EpoR. In our extended model, we additionally integrated EpoR mobilization as a single parameter  $k_{\text{mob}}$  to summarize its overall effect, including a chaperone action mediated by the protein kinase JAK2 (14) (fig. S2A).

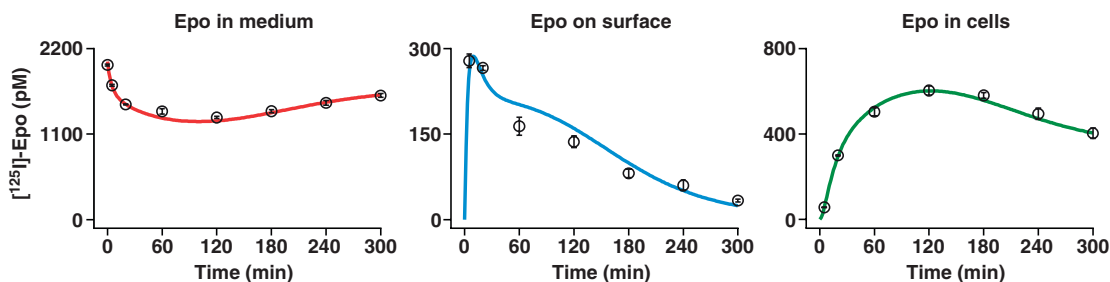
We calibrated the mathematical model on the basis of experimental data from BaF3-EpoR cells, a murine proB cell line that exogenously

**Fig. 2.** Dynamic modeling of the EpoR system. (A) Graphical representation of the mathematical core model. Colored boxes indicate the experimentally accessible quantities “Epo in medium” (Epo + dEpo<sub>e</sub>, red), “Epo on surface” (Epo-EpoR, blue), and “Epo in cells” (Epo-EpoR<sub>i</sub> + dEpo<sub>i</sub>, green). Biological processes described by individual reaction rates are given in the inset. (B) Global parameter estimation was performed simultaneously for the core model and the auxiliary model (fig. S4). Experimental data for the core model are represented with standard deviations ( $n = 3$ ), and trajectories of the best fit are shown. (C) Trajectories for the predicted behavior of experimentally unobserved dynamic variables of the core model.

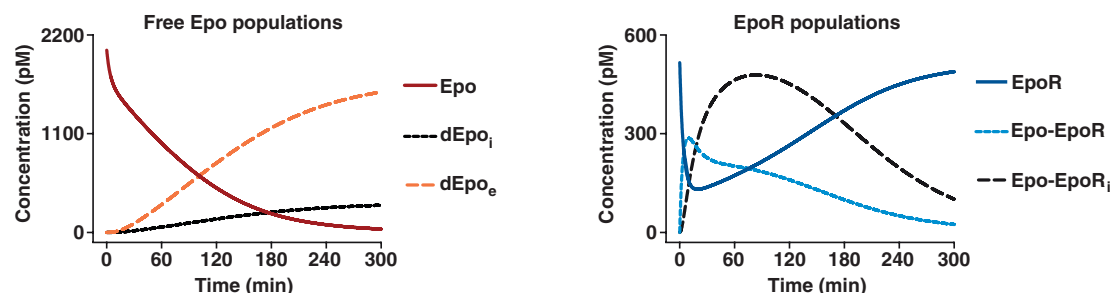
**A Mathematical core model**



**B Model calibration**



**C Dynamic model predictions**



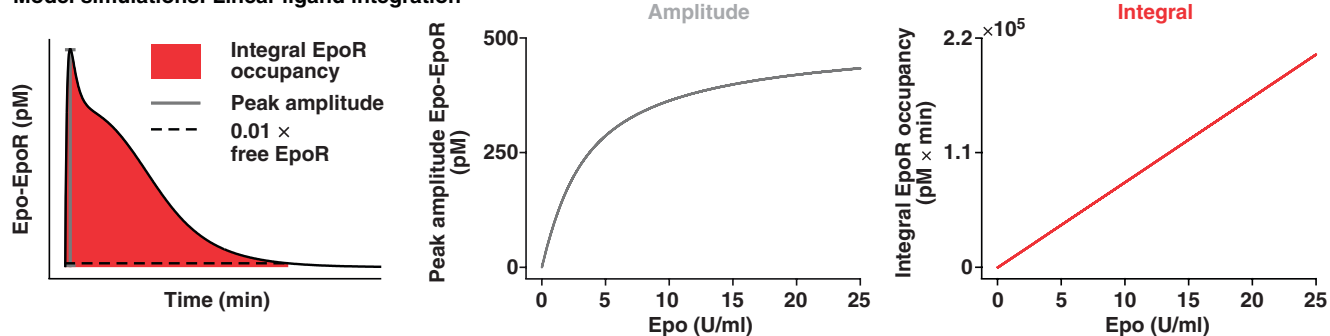


by to cope with both basal and acute demand-driven ligand concentrations. Epo has been widely applied to treat anemia (19), and current research focuses on engineering more efficient erythropoiesis-

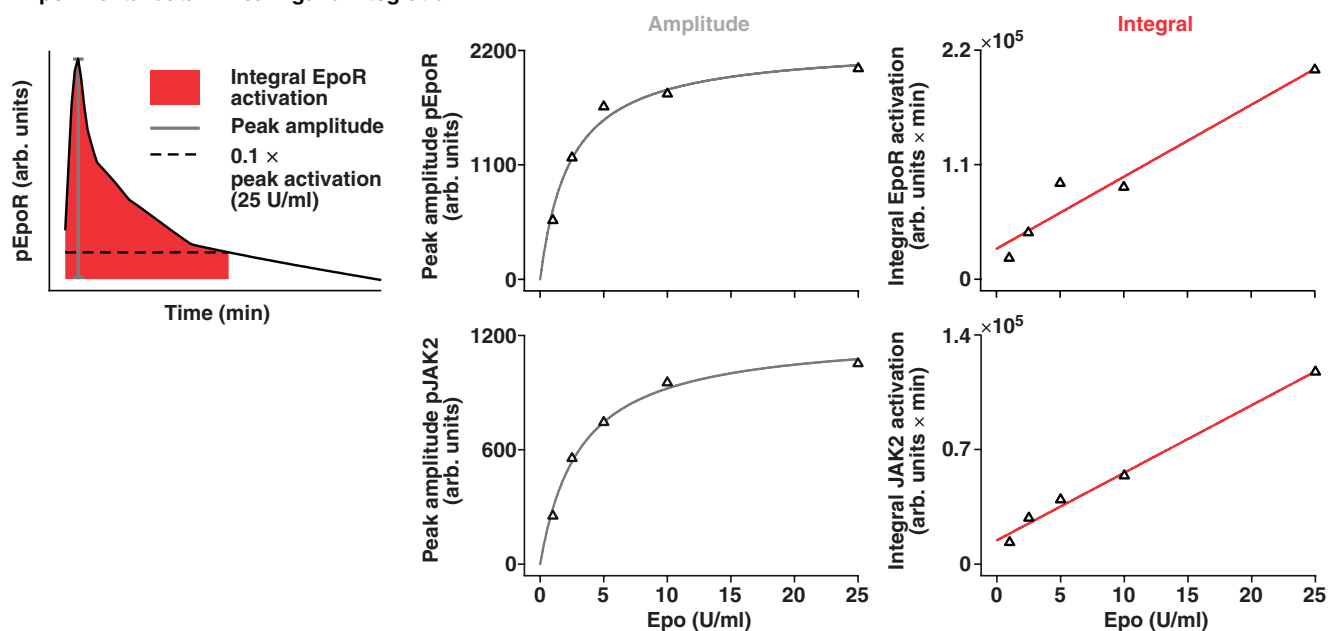
stimulating agents (20). Model simulations for various ligand-binding rates point to a parameter region that displays a trade-off between bio-availability and bioactivity of Epo derivatives (figs.

S14 to S16 and SOM text). Thus, the combination of mathematical modeling and quantitative biochemical analysis enables a more rational development of therapeutic agents.

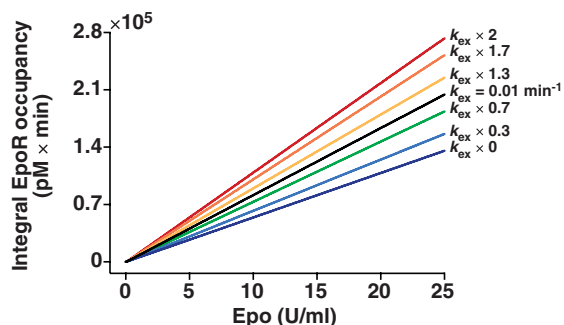
### A Model simulations: Linear ligand integration



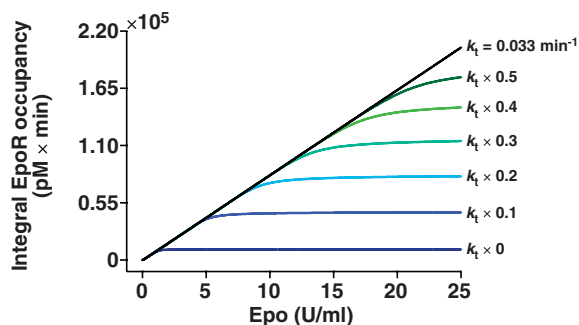
### B Experimental data: Linear ligand integration



### C Model simulations: Dependence on $k_{ex}$



### D Model simulations: Dependence on $k_t$



**Fig. 4.** Linear conversion of Epo concentrations into integral receptor occupancy depends on EpoR turnover. **(A)** Simulations for peak amplitude of Epo-EpoR complexes at the plasma membrane (middle) and integral EpoR occupancy defined as the amount of cell surface Epo-EpoR complexes integrated over time relative to their dependence on Epo (right). Graphical representations are shown for peak amplitude and integral EpoR occupancy (left). **(B)** Experimental data (triangles) were acquired by quantitative immunoblot analysis of EpoR and JAK2 activation in BaF3-EpoR cells (figs.

S10 and S11). A Michaelis-Menten-like saturation and a linear function were fitted to the data for peak amplitude (middle) and integral EpoR and JAK2 activation, defined as the amount of phosphorylated protein integrated over time (right), respectively. Graphical representations are shown for peak amplitude and integral EpoR activation (left). **(C and D)** Simulations for integral EpoR occupancy for various parameter values around the estimated rates of **(C)** recycling  $k_{ex}$  or **(D)** turnover  $k_t$ . Details for calculating the integral are provided in the SOM text. pEpoR and pJAK2, phosphorylated proteins.

## References and Notes

1. H. Shankaran, H. Resat, H. S. Wiley, *PLOS Comput. Biol.* **3**, e101 (2007).
2. H. Wu, X. Liu, R. Jaenisch, H. F. Lodish, *Cell* **83**, 59 (1995).
3. W. Jelkmann, *Intern. Med.* **43**, 649 (2004).
4. A. Yoshimura, A. D. D'Andrea, H. F. Lodish, *Proc. Natl. Acad. Sci. U.S.A.* **87**, 4139 (1990).
5. T. D. Richmond, M. Chohan, D. L. Barber, *Trends Cell Biol.* **15**, 146 (2005).
6. P. Walrafen *et al.*, *Blood* **105**, 600 (2005).
7. D. L. Beckman, L. L. Lin, M. E. Quinones, G. D. Longmore, *Blood* **94**, 2667 (1999).
8. K. S. Price *et al.*, *Am. J. Respir. Cell Mol. Biol.* **28**, 420 (2003).
9. Z. Bajzer, A. C. Myers, S. Vuk-Pavlović, *J. Biol. Chem.* **264**, 13623 (1989).
10. S. Belouzard, D. Delcroix, Y. Rouillé, *J. Biol. Chem.* **279**, 28499 (2004).
11. G. Carpenter, S. Cohen, *Annu. Rev. Biochem.* **48**, 193 (1979).
12. H. Youssoufian, G. Longmore, D. Neumann, A. Yoshimura, H. F. Lodish, *Blood* **81**, 2223 (1993).
13. Materials and methods are available as supporting material on *Science Online*.
14. L. J. Huang, S. N. Constantinescu, H. F. Lodish, *Mol. Cell* **8**, 1327 (2001).
15. T. Maiwald, J. Timmer, *Bioinformatics* **24**, 2037 (2008).
16. A. Raue *et al.*, *Bioinformatics* **25**, 1923 (2009).
17. H. Resat, J. A. Ewald, D. A. Dixon, H. S. Wiley, *Biophys. J.* **85**, 730 (2003).
18. H. S. Wiley *et al.*, *J. Biol. Chem.* **266**, 11083 (1991).
19. W. Jelkmann, *Eur. J. Haematol.* **78**, 183 (2007).
20. I. C. Macdougall, K. U. Eckardt, *Lancet* **368**, 947 (2006).
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## Supporting Online Material

[www.sciencemag.org/cgi/content/full/science.1184913/DC1](http://www.sciencemag.org/cgi/content/full/science.1184913/DC1)

Materials and Methods

SOM Text

Figs. S1 to S16

References

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