SBML Model Report

Model name: "Becker2010_EpoR_AuxiliaryModel"



May 6, 2016

1 General Overview

This is a document in SBML Level 2 Version 4 format. This model was created by the following three authors: Vijayalakshmi Chelliah¹, Marcel Schilling² and Verena Becker³ at May 26th 2010 at 4:11 p. m. and last time modified at January 31st 2012 at 1:51 p. m. Table 1 gives an overview of the quantities of all components of this model.

Table 1: Number of components in this model, which are described in the following sections.

Element	Quantity	Element	Quantity
compartment types	0	compartments	3
species types	0	species	6
events	0	constraints	0
reactions	8	function definitions	0
global parameters	9	unit definitions	5
rules	2	initial assignments	0

Model Notes

This is the auxiliary model described in the article:

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

¹EMBL-EBI, viji@ebi.ac.uk

²German Cancer Research Center, m.schilling@dkfz.de

 $^{^3}$ Department of Systems Biology, Harvard Medical School, Boston, USA, verena_becker@hms.harvard.edu

Verena Becker, Marcel Schilling, Julie Bachmann, Ute Baumann, Andreas Raue, Thomas Maiwald, Jens Timmer and Ursula Klingmller; <u>Science</u> Published Online May 20, 2010; DOI: 10.1126/science.1184913 PMID: 20488988

Abstract:

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 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, covering a broad range of ligand concentrations. This relation solely depends on EpoR turnover independent of ligand binding, suggesting 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.

SBML model exported from PottersWheel.

```
% PottersWheel model definition file
function m = BeckerSchilling2010_EpoR_AuxiliaryMode()
              = pwGetEmptyModel();
%% Meta information
m.ID
              = 'BeckerSchilling2010_EpoR_AuxiliaryMode';
              = 'BeckerSchilling2010_EpoR_AuxiliaryModel';
m.description = 'BeckerSchilling2010_EpoR_AuxiliaryModel';
m.authors
              = {'Verena Becker',' Marcel Schilling'};
m.dates
              = {'2010'};
              = 'PW-2-0-42';
m.type
%% X: Dynamic variables
% m = pwAddX(m, ID, startValue, type, minValue, maxValue, unit, compartment, name, descri
m = pwAddX(m, 'EpoR'
                                 76, 'fix'
                                                 0, 10000,
                                                              [], 'cell', []
                                                                               , []
                                                                                     , []
                           999.293, 'global', 900, 1100,
                                                              [], 'cell', []
m = pwAddX(m, 'SAv'
                                                                               , []
                                                                                     , []
                                  0, 'fix'
m = pwAddX(m, 'SAv_EpoR'
                                                              [], 'cell', []
                                                 0, 10000,
                                                                               , []
                                                                                      m = pwAddX(m, 'SAv_EpoRi',
                                  0, 'fix'
                                                              [], 'cell', []
                                                                                     , []
                                                 0, 10000,
                                                                               , []
                                  0, 'fix'
                                                 0, 10000,
                                                              [], 'cell', []
m = pwAddX(m, 'dSAvi')
                                                                               , []
                                                                                     , []
m = pwAddX(m, 'dSAve')
                                  0, 'fix'
                                                 0, 10000,
                                                              [], 'cell', []
                                                                               , []
                                                                                     , []
%% R: Reactions
% m = pwAddR(m, reactants, products, modifiers, type, options, rateSignature, parameters
```

```
m = pwAddR(m, {
                                          }, { }, 'C' , [] , 'k1*k2', {'kt', 'Bmax_SAv']
                          }, {'EpoR'
m = pwAddR(m, {'EpoR'
                         }, {
                                          }, { }, 'MA', [] , []
                                                                    , {'kt'
m = pwAddR(m, {'SAv', 'EpoR'}, {'SAv_EpoR'
                                          }, { }, 'MA', [] , []
                                                                     , {'kon_SAv'
m = pwAddR(m, {'SAv_EpoR' }, {'SAv', 'EpoR'}, { }, 'MA', [] , []
                                                                     , {'koff_SAv'
                         }, {'SAv_EpoRi' }, { }, 'MA', [] , []
m = pwAddR(m, {'SAv_EpoR'
                                                                     , {'kt'
m = pwAddR(m, {'SAv_EpoRi'}, {'SAv'
                                         }, { }, 'MA', [] , []
                                                                   , {'kex_SAv'
m = pwAddR(m, {'SAv_EpoRi' }, {'dSAvi'
                                         }, { }, 'MA', [] , []
                                                                    , {'kdi'
m = pwAddR(m, {'SAv_EpoRi' }, {'dSAve'
                                          }, { }, 'MA', [] , []
                                                                     , {'kde'
%% C: Compartments
% m = pwAddC(m, ID, size, outside, spatialDimensions, name, unit, constant)
m = pwAddC(m, 'cell', 1);
%% K: Dynamical parameters
% m = pwAddK(m, ID, value, type, minValue, maxValue, unit, name, description)
m = pwAddK(m, 'kt')
                                     , 'global', 1e-007, 1000);
                       , 0.0329366
m = pwAddK(m, 'Bmax_SAv', 76
                                     , 'fix' , 61
                                                    , 91 );
m = pwAddK(m, 'kon_SAv' , 2.29402e-006, 'global', 1e-007, 1000);
m = pwAddK(m, 'koff_SAv', 0.00679946 , 'global', 1e-007, 1000);
m = pwAddK(m, 'kex_SAv', 0.01101)
                                 , 'global', 1e-007, 1000);
m = pwAddK(m, 'kdi' , 0.00317871 , 'global', 1e-007, 1000);
m = pwAddK(m, 'kde'
                      , 0.0164042 , 'global', 1e-007, 1000);
%% Default sampling time points
m.t = 0:3:99;
%% Y: Observables
% m = pwAddY(m, rhs, ID, scalingParameter, errorModel, noiseType, unit, name, description
m = pwAddY(m, 'SAv + dSAve'
                              , 'SAv_extracellular_obs');
                                , 'SAv_cellsurface_obs' );
m = pwAddY(m, 'SAv_EpoR'
m = pwAddY(m, 'SAv_EpoRi + dSAvi', 'SAv_intracellular_obs');
```

%% S: Scaling parameters

```
% m = pwAddS(m, ID, value, type, minValue, maxValue, unit, name, description)
m = pwAddS(m, 'scale_SAv_extracellular_obs', 1, 'fix', 0, 100);
m = pwAddS(m, 'scale_SAv_cellsurface_obs', 1, 'fix', 0, 100);
m = pwAddS(m, 'scale_SAv_intracellular_obs', 1, 'fix', 0, 100);
%% Designer properties (do not modify)
m.designerPropsM = [1 1 1 0 0 0 400 250 600 400 1 1 1 0 0 0 0];
```

This model originates from BioModels Database: A Database of Annotated Published Models. It is copyright (c) 2005-2010 The BioModels.net Team.

For more information see the terms of use.

To cite BioModels Database, please use: Li C, Donizelli M, Rodriguez N, Dharuri H, Endler L, Chelliah V, Li L, He E, Henry A, Stefan MI, Snoep JL, Hucka M, Le Novre N, Laibe C (2010) BioModels Database: An enhanced, curated and annotated resource for published quantitative kinetic models. BMC Syst Biol., 4:92.

2 Unit Definitions

This is an overview of eight unit definitions of which three are predefined by SBML and not mentioned in the model.

2.1 Unit time

Name minute

Definition 60 s

2.2 Unit substance

Name picomole

Definition 10^{-12} mol

2.3 Unit per_minute

Definition $(60 \text{ s})^{-1}$

2.4 Unit pM

Definition $10^{-12} \text{ mol} \cdot 1^{-1}$

2.5 Unit per_minute_per_pM

Definition $(60 \text{ s})^{-1} \cdot (10^{-12} \text{ mol})^{-1} \cdot 1$

2.6 Unit volume

Notes Litre is the predefined SBML unit for volume.

Definition 1

2.7 Unit area

Notes Square metre is the predefined SBML unit for area since SBML Level 2 Version 1.

Definition m²

2.8 Unit length

Notes Metre is the predefined SBML unit for length since SBML Level 2 Version 1.

Definition m

3 Compartments

This model contains three compartments.

Table 2: Properties of all compartments.

Id	Name	SBO	Spatial Dimensions	Size	Unit	Constant	Outside
medium	medium	0000290	3	1	litre		
cellsurface	cellsurface	0000290	3	1	litre	$\overline{\mathbf{Z}}$	
cell	cell	0000290	3	1	litre	$ \overline{\mathbf{Z}} $	

3.1 Compartment medium

This is a three dimensional compartment with a constant size of one litre.

Name medium

SBO:0000290 physical compartment

3.2 Compartment cellsurface

This is a three dimensional compartment with a constant size of one litre.

Name cellsurface

SBO:0000290 physical compartment

3.3 Compartment cell

This is a three dimensional compartment with a constant size of one litre.

Name cell

SBO:0000290 physical compartment

4 Species

This model contains six species. Section 8 provides further details and the derived rates of change of each species.

Table 3: Properties of each species.

Id	Name	Compartment	Derived Unit	Constant	Boundary Condi-
					tion
EpoR	EpoR	cellsurface	$10^{-12} \text{mol} \cdot 1^{-1}$		
SAv	SAv	medium	$10^{-12} \text{ mol} \cdot 1^{-1}$	\Box	
SAv_EpoR	SAv_EpoR	cellsurface	$10^{-12} \text{ mol} \cdot 1^{-1}$		
SAv_EpoRi	SAv_EpoRi	cell	$10^{-12} \text{ mol} \cdot 1^{-1}$		
dSAvi	dSAvi	cell	$10^{-12} \operatorname{mol} \cdot 1^{-1}$	\Box	
dSAve	dSAve	medium	$10^{-12} \text{mol} \cdot l^{-1}$		

5 Parameters

This model contains nine global parameters.

Table 4: Properties of each parameter.

		1	1		
Id	Name	SBO	Value	Unit	Constant
kt		0000256	0.033	$(60 \text{ s})^{-1}$	
${\tt Bmax_SAv}$		0000256	76.000	$10^{-12} \text{ mol} \cdot 1^{-1}$	$ \overline{\mathbf{Z}} $
kon_SAv		0000341	$2.29402 \cdot 10^{-6}$	$(60 \text{ s})^{-1}$	
				$(10^{-12} \text{ mol})^{-1} \cdot 1$	
koff_SAv		0000338	0.007	$(60 \text{ s})^{-1}$	
kex_SAv		0000256	0.011	$(60 \text{ s})^{-1}$	$\overline{\mathbf{Z}}$
kdi		0000356	0.003	$(60 \text{ s})^{-1}$	
kde		0000356	0.016	$(60 \mathrm{s})^{-1}$	$ \overline{\mathbf{Z}} $
SAv_medium	SAv_medium		0.000	•	
${\tt SAv_cells}$	SAv_cells		0.000		

6 Rules

This is an overview of two rules.

6.1 Rule SAv_medium

Rule SAv_medium is an assignment rule for parameter SAv_medium :

$$SAv_medium = [SAv] + [dSAve]$$
 (1)

Derived unit $10^{-12} \text{ mol} \cdot l^{-1}$

6.2 Rule SAv_cells

Rule SAv_cells is an assignment rule for parameter SAv_cells:

$$SAv_cells = [SAv_EpoRi] + [dSAvi]$$
 (2)

Derived unit $10^{-12} \text{ mol} \cdot l^{-1}$

7 Reactions

This model contains eight reactions. All reactions are listed in the following table and are subsequently described in detail. If a reaction is affected by a modifier, the identifier of this species is written above the reaction arrow.

Table 5: Overview of all reactions

N⁰	Id	Name	Reaction Equation	SBO
1	reaction_1		$\emptyset \longrightarrow \text{EpoR}$	0000176
2	$reaction_2$		$EpoR \longrightarrow \emptyset$	0000179
3	$reaction_3$		$SAv + EpoR \longrightarrow SAv_EpoR$	0000177
4	${\tt reaction_4}$		$SAv_EpoR \longrightarrow SAv + EpoR$	0000180
5	$reaction_5$		SAv_EpoR SAv_EpoRi	0000185
6	${\tt reaction_6}$		SAv_EpoRi SAv	0000180
7	$reaction_7$		SAv_EpoRi dSAvi	0000179
8	reaction_8		$SAv_EpoRi \longrightarrow dSAve$	0000179

7.1 Reaction reaction_1

This is an irreversible reaction of no reactant forming one product.

SBO:0000176 biochemical reaction

Reaction equation

$$\emptyset \longrightarrow \text{EpoR}$$
 (3)

Product

Table 6: Properties of each product.

Id	Name	SBO
EpoR	EpoR	

Kinetic Law

Derived unit $(60 \text{ s})^{-1} \cdot 10^{-12} \text{ mol}$

$$v_1 = kt \cdot Bmax_SAv \cdot vol (cell)$$
 (4)

7.2 Reaction reaction_2

This is an irreversible reaction of one reactant forming no product.

SBO:0000179 degradation

Reaction equation

$$EpoR \longrightarrow \emptyset \tag{5}$$

Reactant

Table 7: Properties of each reactant.

Id	Name	SBO
EpoR	EpoR	

Kinetic Law

Derived unit $(60 \text{ s})^{-1} \cdot 10^{-12} \text{ mol}$

$$v_2 = kt \cdot [EpoR] \cdot vol(cell) \tag{6}$$

7.3 Reaction reaction_3

This is an irreversible reaction of two reactants forming one product.

SBO:0000177 non-covalent binding

Reaction equation

$$SAv + EpoR \longrightarrow SAv \cdot EpoR \tag{7}$$

Reactants

Table 8: Properties of each reactant.

Id	Name	SBO
SAv	SAv	
EpoR	EpoR	

Product

Table 9: Properties of each product.

1		1
Id	Name	SBO
SAv_EpoR	SAv_EpoR	

Kinetic Law

Derived unit $(60 \text{ s})^{-1} \cdot 10^{-12} \text{ mol}$

$$v_3 = \text{kon_SAv} \cdot [\text{SAv}] \cdot [\text{EpoR}] \cdot \text{vol} (\text{cell})$$
 (8)

7.4 Reaction reaction_4

This is an irreversible reaction of one reactant forming two products.

SBO:0000180 dissociation

Reaction equation

$$SAv_EpoR \longrightarrow SAv + EpoR \tag{9}$$

Reactant

Table 10: Properties of each reactant.

Id	Name	SBO
SAv_EpoR	SAv_EpoR	

Products

Table 11: Properties of each product.

Id	Name	SBO
SAv	SAv	
EpoR	EpoR	

Kinetic Law

Derived unit $(60 \text{ s})^{-1} \cdot 10^{-12} \text{ mol}$

$$v_4 = \text{koff_SAv} \cdot [\text{SAv_EpoR}] \cdot \text{vol}(\text{cell})$$
 (10)

7.5 Reaction reaction_5

This is an irreversible reaction of one reactant forming one product.

SBO:0000185 transport reaction

Reaction equation

$$SAv_EpoR \longrightarrow SAv_EpoRi \tag{11}$$

Reactant

Table 12: Properties of each reactant.

Id	Name	SBO
SAv_EpoR	SAv_EpoR	

Product

Table 13: Properties of each product.

Id	Name	SBO
SAv_EpoRi	SAv_EpoRi	

Id	Name	SBO

Kinetic Law

Derived unit $(60 \text{ s})^{-1} \cdot 10^{-12} \text{ mol}$

$$v_5 = \text{kt} \cdot [\text{SAv_EpoR}] \cdot \text{vol} (\text{cell})$$
 (12)

7.6 Reaction reaction_6

This is an irreversible reaction of one reactant forming one product.

SBO:0000180 dissociation

Reaction equation

$$SAv_EpoRi \longrightarrow SAv \tag{13}$$

Reactant

Table 14: Properties of each reactant.

Id	Name	SBO
SAv_EpoRi	SAv_EpoRi	

Product

Table 15: Properties of each product.

Id	Name	SBO
SAv	SAv	

Kinetic Law

Derived unit $(60 \text{ s})^{-1} \cdot 10^{-12} \text{ mol}$

$$v_6 = \text{kex_SAv} \cdot [\text{SAv_EpoRi}] \cdot \text{vol} (\text{cell})$$
 (14)

7.7 Reaction reaction_7

This is an irreversible reaction of one reactant forming one product.

SBO:0000179 degradation

Reaction equation

$$SAv_EpoRi \longrightarrow dSAvi$$
 (15)

Reactant

Table 16: Properties of each reactant.

Id	Name	SBO
SAv_EpoRi	SAv_EpoRi	

Product

Table 17: Properties of each product.

Id	Name	SBO
dSAvi	dSAvi	

Kinetic Law

Derived unit $(60 \text{ s})^{-1} \cdot 10^{-12} \text{ mol}$

$$v_7 = \text{kdi} \cdot [\text{SAv_EpoRi}] \cdot \text{vol}(\text{cell})$$
 (16)

7.8 Reaction reaction_8

This is an irreversible reaction of one reactant forming one product.

SBO:0000179 degradation

Reaction equation

$$SAv_EpoRi \longrightarrow dSAve \tag{17}$$

Reactant

Table 18: Properties of each reactant.

Id	Name	SBO
SAv_EpoRi	SAv_EpoRi	

Product

Table 19: Properties of each product.

Id	Name	SBO
dSAve	dSAve	

Kinetic Law

Derived unit $(60 \text{ s})^{-1} \cdot 10^{-12} \text{ mol}$

$$v_8 = \text{kde} \cdot [\text{SAv_EpoRi}] \cdot \text{vol}(\text{cell})$$
 (18)

8 Derived Rate Equations

When interpreted as an ordinary differential equation framework, this model implies the following set of equations for the rates of change of each species.

8.1 Species EpoR

Name EpoR

SBO:0000244 receptor

Initial concentration $76 \ 10^{-12} \ mol \cdot l^{-1}$

This species takes part in four reactions (as a reactant in reaction_2, reaction_3 and as a product in reaction_1, reaction_4).

$$\frac{d}{dt}EpoR = v_1 + v_4 - v_2 - v_3 \tag{19}$$

8.2 Species SAv

Name SAv

SBO:0000280 ligand

Initial concentration $999.293 \ 10^{-12} \ mol \cdot l^{-1}$

This species takes part in three reactions (as a reactant in reaction_3 and as a product in reaction_4, reaction_6).

$$\frac{\mathrm{d}}{\mathrm{d}t}\mathrm{SAv} = v_4 + v_6 - v_3 \tag{20}$$

8.3 Species SAv_EpoR

Name SAv_EpoR

SBO:0000297 protein complex

Initial concentration $0.10^{-12} \text{ mol} \cdot l^{-1}$

This species takes part in three reactions (as a reactant in reaction_4, reaction_5 and as a product in reaction_3).

$$\frac{\mathrm{d}}{\mathrm{d}t}\mathrm{SAv}\underline{\mathrm{EpoR}} = v_3 - v_4 - v_5 \tag{21}$$

8.4 Species SAv_EpoRi

Name SAv_EpoRi

SBO:0000297 protein complex

Initial concentration $0.10^{-12} \text{ mol} \cdot l^{-1}$

This species takes part in four reactions (as a reactant in reaction_6, reaction_7, reaction_8 and as a product in reaction_5).

$$\frac{\mathrm{d}}{\mathrm{d}t}\mathrm{SAv}\underline{\mathrm{EpoRi}} = v_5 - v_6 - v_7 - v_8 \tag{22}$$

8.5 Species dSAvi

Name dSAvi

SBO:0000291 empty set

Initial concentration $0.10^{-12} \text{ mol} \cdot l^{-1}$

This species takes part in one reaction (as a product in reaction_7).

$$\frac{\mathrm{d}}{\mathrm{d}t}\mathrm{d}S\mathrm{Avi} = v_7 \tag{23}$$

8.6 Species dSAve

Name dSAve

SBO:0000291 empty set

Initial concentration $0.10^{-12} \text{ mol} \cdot l^{-1}$

This species takes part in one reaction (as a product in reaction_8).

$$\frac{\mathrm{d}}{\mathrm{d}t}\mathrm{d}\mathrm{SAve} = v_8 \tag{24}$$

A Glossary of Systems Biology Ontology Terms

- **SBO:0000176** biochemical reaction: An event involving one or more chemical entities that modifies the electrochemical structure of at least one of the participants.
- **SBO:0000177 non-covalent binding:** Interaction between several biochemical entities that results in the formation of a non-covalent comple
- SBO:0000179 degradation: Complete disappearance of a physical entity
- **SBO:0000180 dissociation:** Transformation of a non-covalent complex that results in the formation of several independent biochemical entitie
- **SBO:0000185 transport reaction:** Movement of a physical entity without modification of the structure of the entity
- **SBO:0000244 receptor:** Participating entity that binds to a specific physical entity and initiates the response to that physical entity. The original concept of the receptor was introduced independently at the end of the 19th century by John Newport Langley (1852-1925) and Paul Ehrlich (1854-1915). Langley JN.On the reaction of cells and of nerve-endings to certain poisons, chiefly as regards the reaction of striated muscle to nicotine and to curari. J Physiol. 1905 Dec 30;33(4-5):374-413
- **SBO:0000256** biochemical parameter: Parameter that depends on the biochemical properties of a system
- **SBO:0000280 ligand:** In biochemistry, a ligand is an effector, a physical entity that binds to a site on a receptor's surface by intermolecular forces
- **SBO:0000290 physical compartment:** Specific location of space, that can be bounded or not. A physical compartment can have 1, 2 or 3 dimensions
- **SBO:0000291 empty set:** Entity defined by the absence of any actual object. An empty set is often used to represent the source of a creation process or the result of a degradation process.
- **SBO:0000297 protein complex:** Macromolecular complex containing one or more polypeptide chains possibly associated with simple chemicals. CHEBI:3608
- **SBO:0000338 dissociation rate constant:** Rate with which a complex dissociates into its components
- **SBO:0000341** association rate constant: Rate with which components associate into a complex
- **SBO:0000356 decay constant:** Kinetic constant characterising a mono-exponential decay. It is the inverse of the mean lifetime of the continuant being decayed. Its unit is "per tim".

 $\mathfrak{BML2}^{AT}$ EX was developed by Andreas Dräger^a, Hannes Planatscher^a, Dieudonné M Wouamba^a, Adrian Schröder^a, Michael Hucka^b, Lukas Endler^c, Martin Golebiewski^d and Andreas Zell^a. Please see http://www.ra.cs.uni-tuebingen.de/software/SBML2LaTeX for more information.

^aCenter for Bioinformatics Tübingen (ZBIT), Germany

^bCalifornia Institute of Technology, Beckman Institute BNMC, Pasadena, United States

 $^{{}^}c \hbox{European Bioinformatics Institute, Wellcome Trust Genome Campus, Hinxton, United Kingdom}$

^dEML Research gGmbH, Heidelberg, Germany