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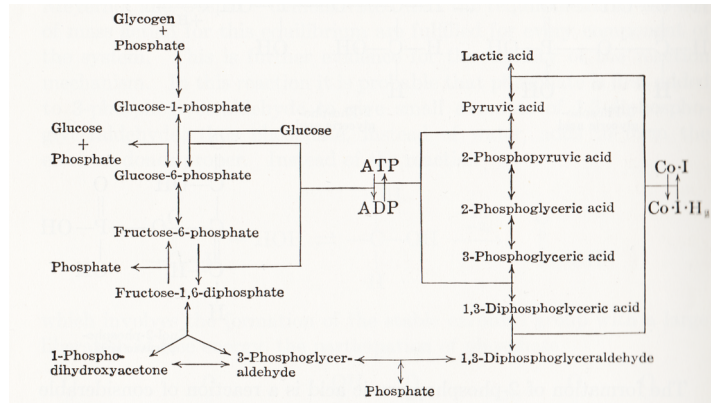


Building the biological Babylon Tower with standard representations of pathways

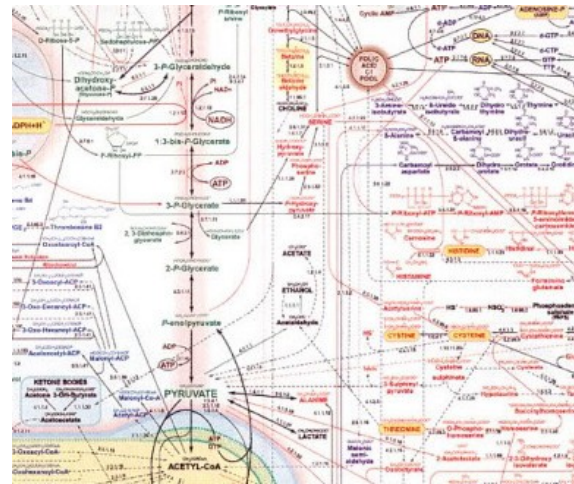


Biochemical pathways are old ...

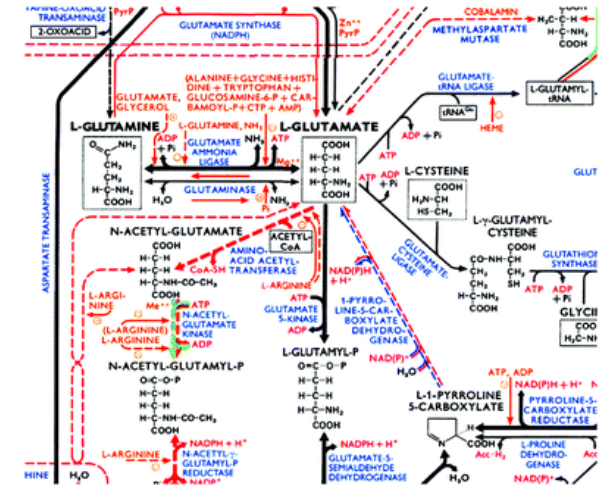
Gortner (1949)



Nicholson (1970)



Michal (1984)

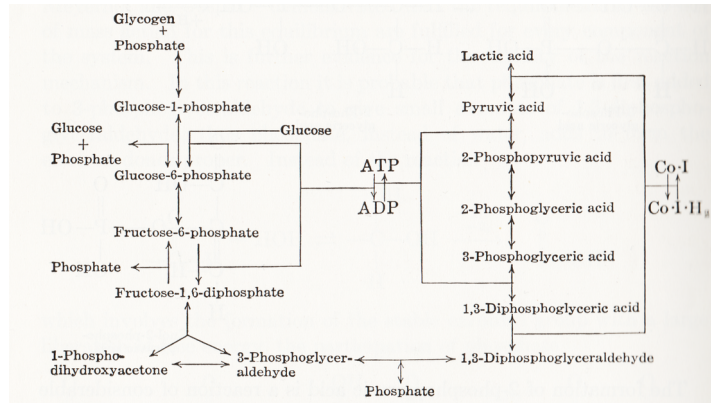


“Hand drawing” on paper

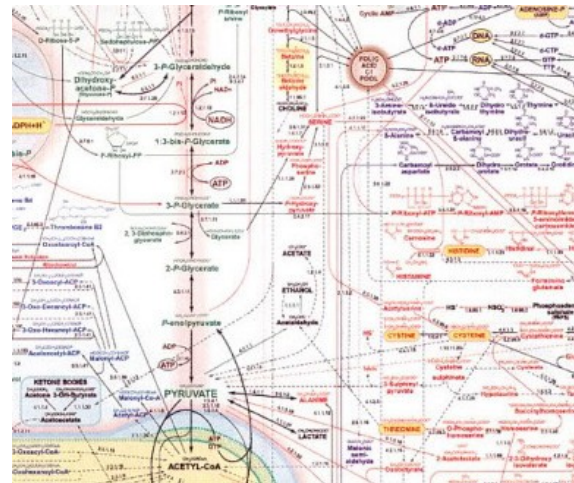
→ no software-based browsing, processing and analysis

Biochemical pathways are old ... or not so much

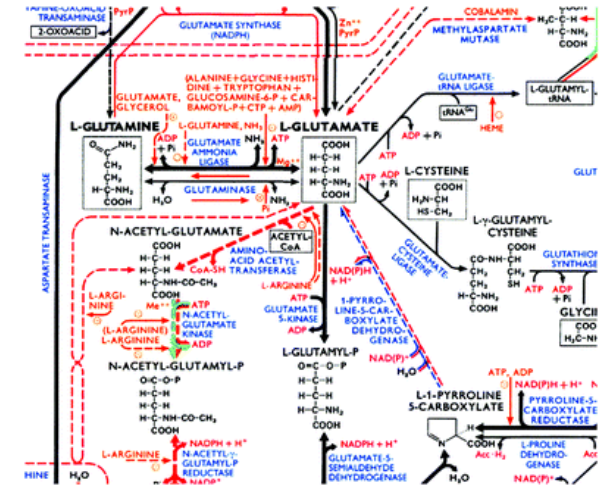
Gortner (1949)



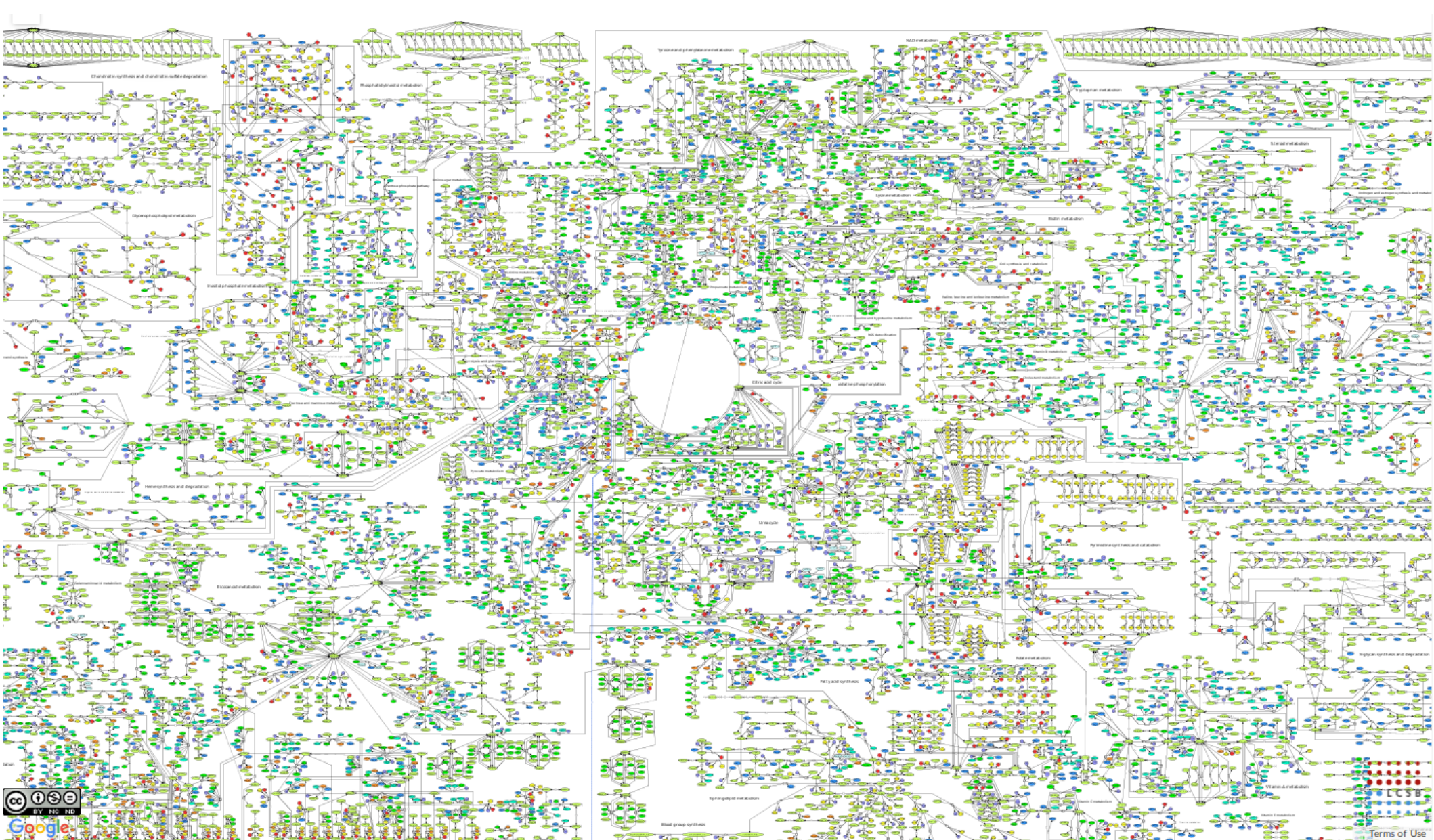
Nicholson (1970)



Michal (1984)



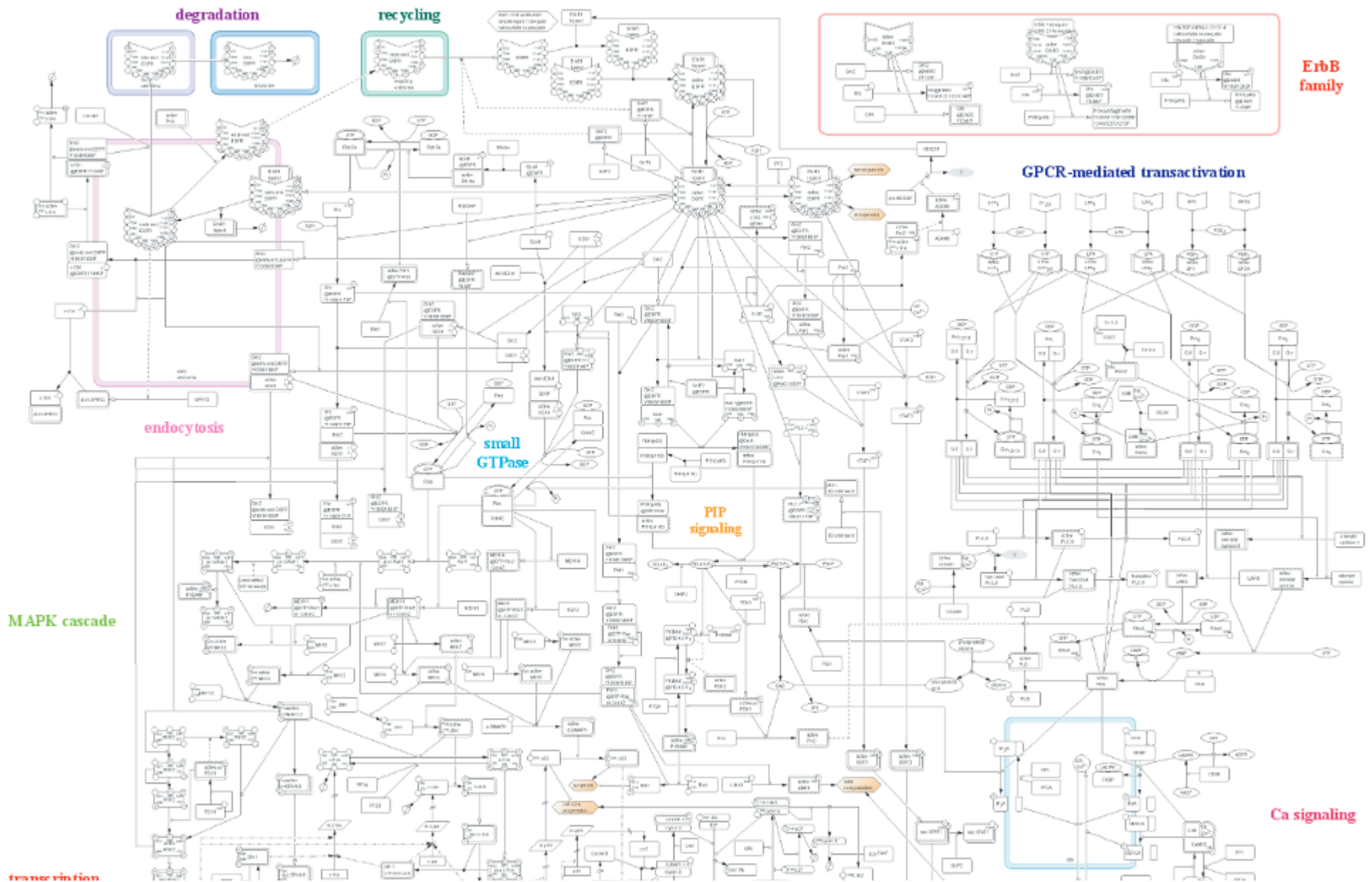
- 1990s: high-throughput data generation → Large amount of knowledge increase in computing power → automatic reconstruction, browsing and analysis
- Databases: EcoCyc (1994), KEGG (1995), Reactome (2000)
- Formats: BioPAX (2000), SBML (2000), PSI-MI (2002)



<http://vmh.uni.lu>

UNDERSTAND

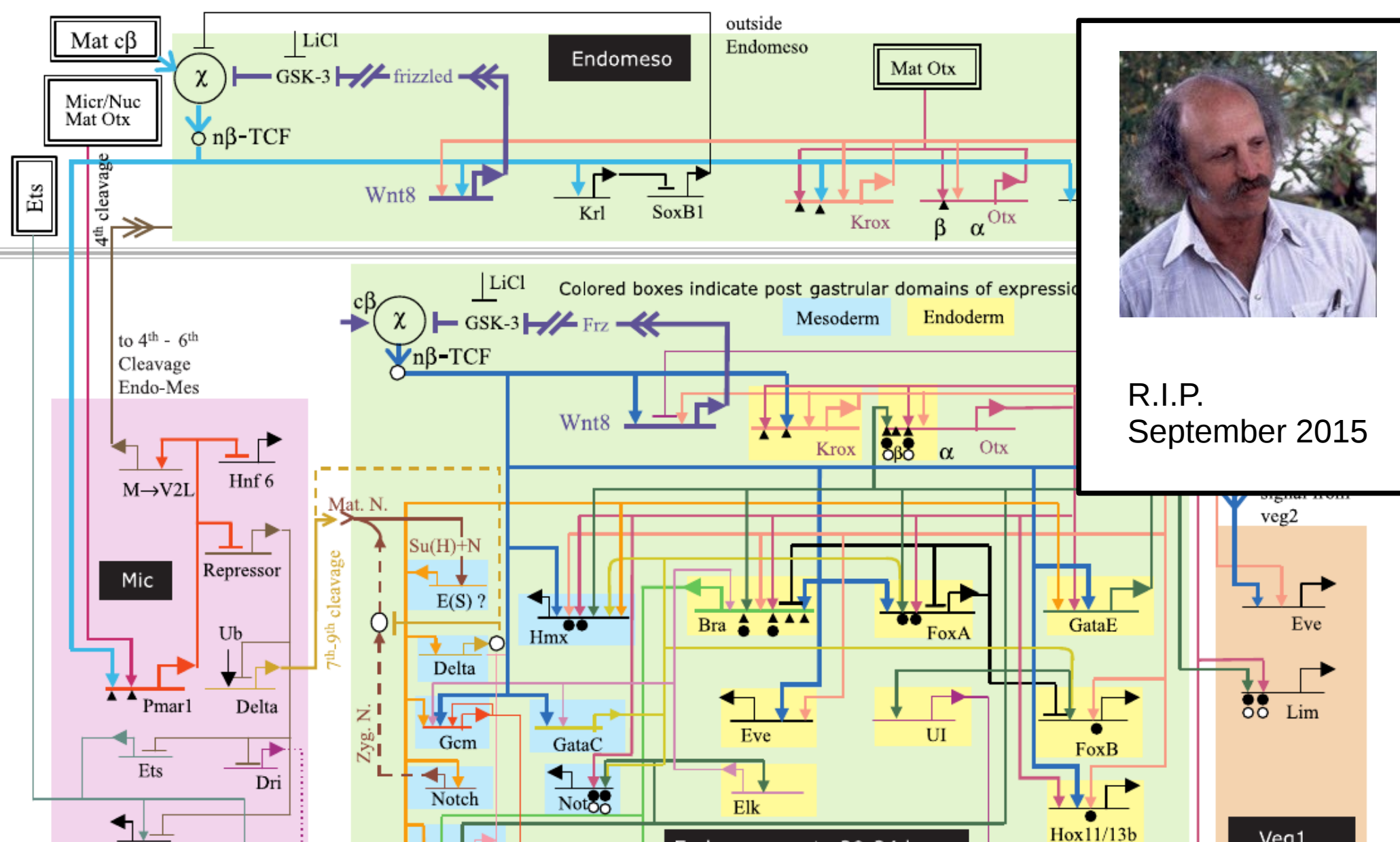
Metabolic networks



Oda K. Mol Syst Biol. 2005;1:2005.0010.

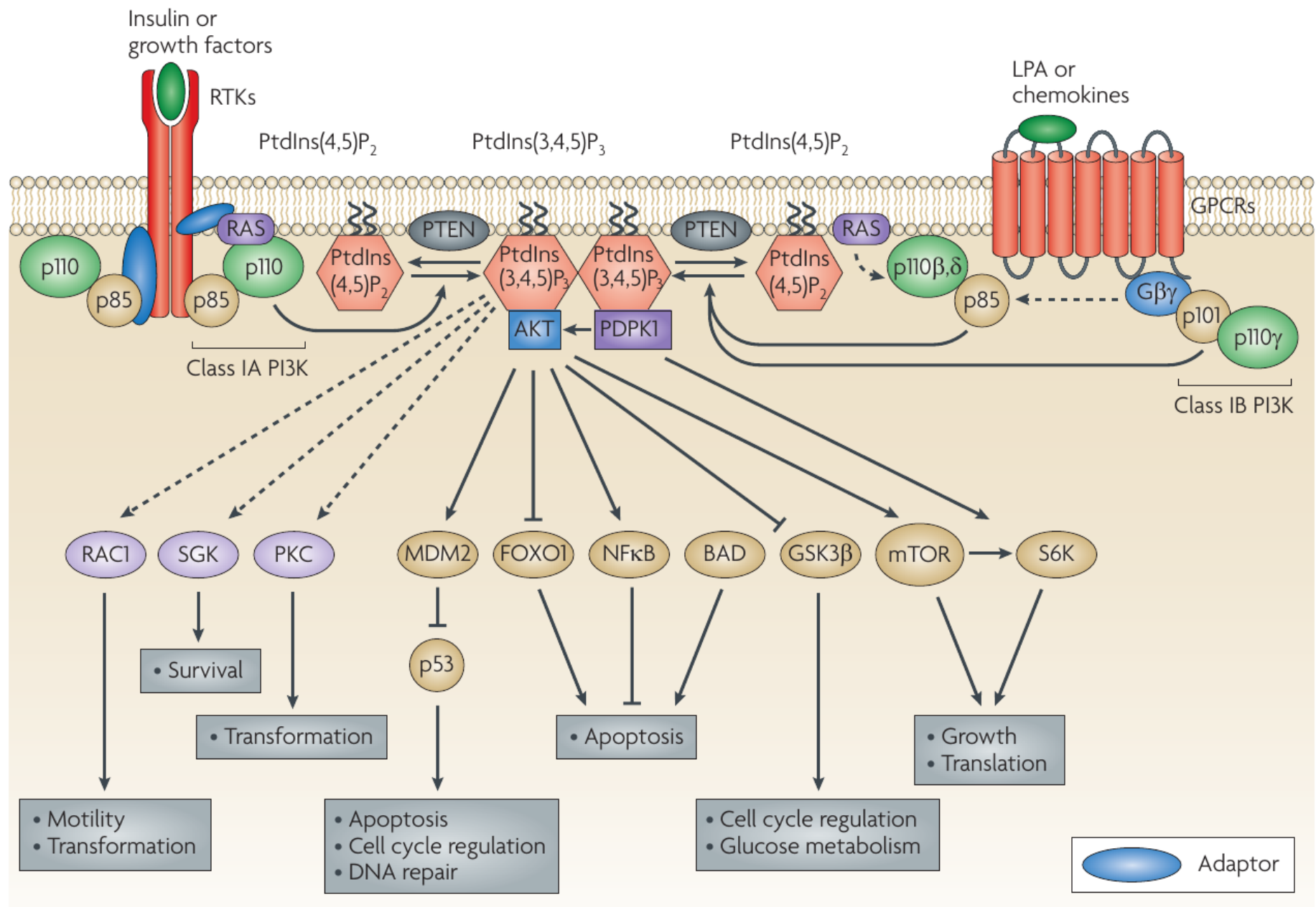
UNDERSTAND

Signalling pathways



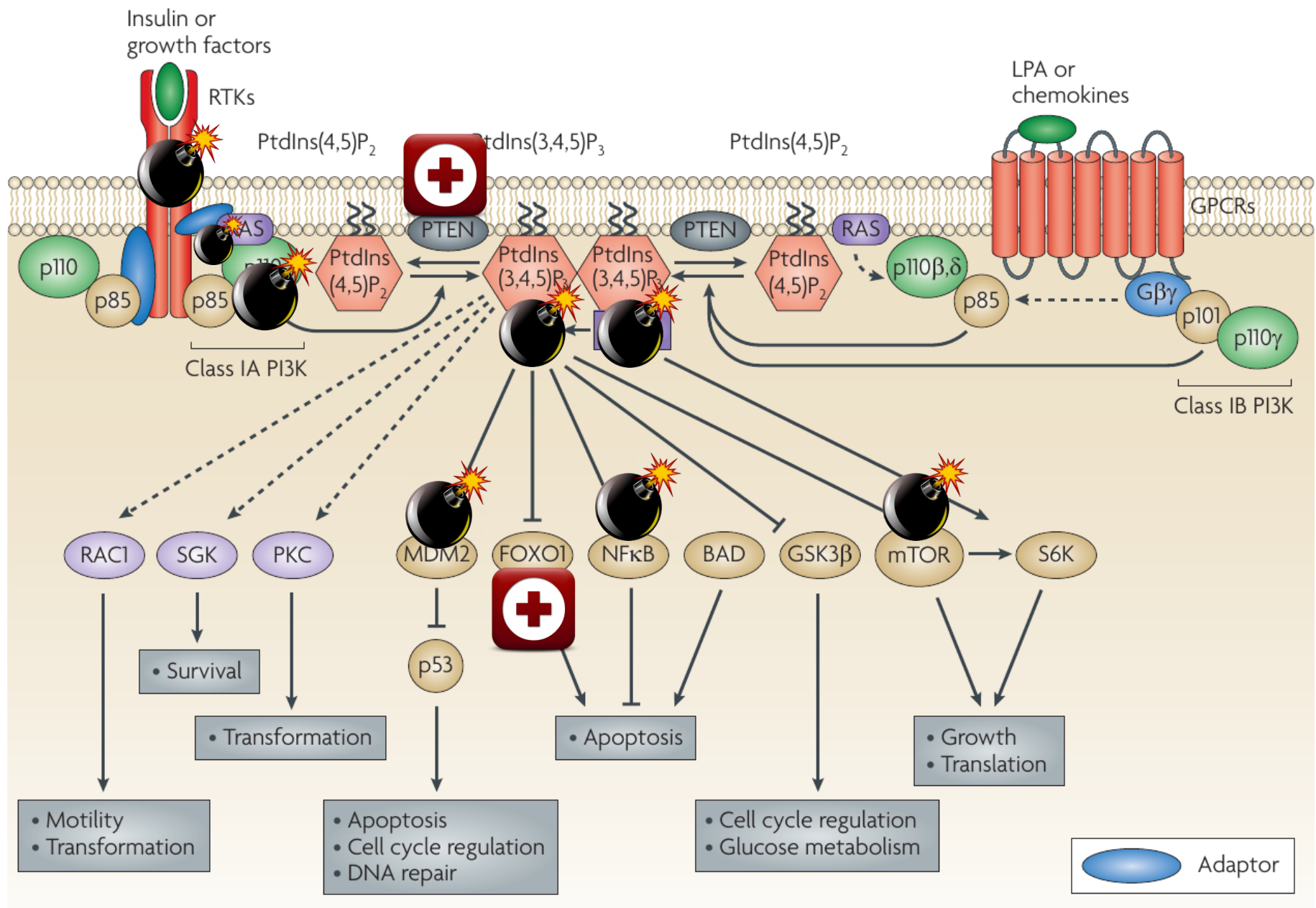
UNDERSTAND

Gene regulatory networks



CURE

Liu et al (2009) *Nat Rev Drug Discov*

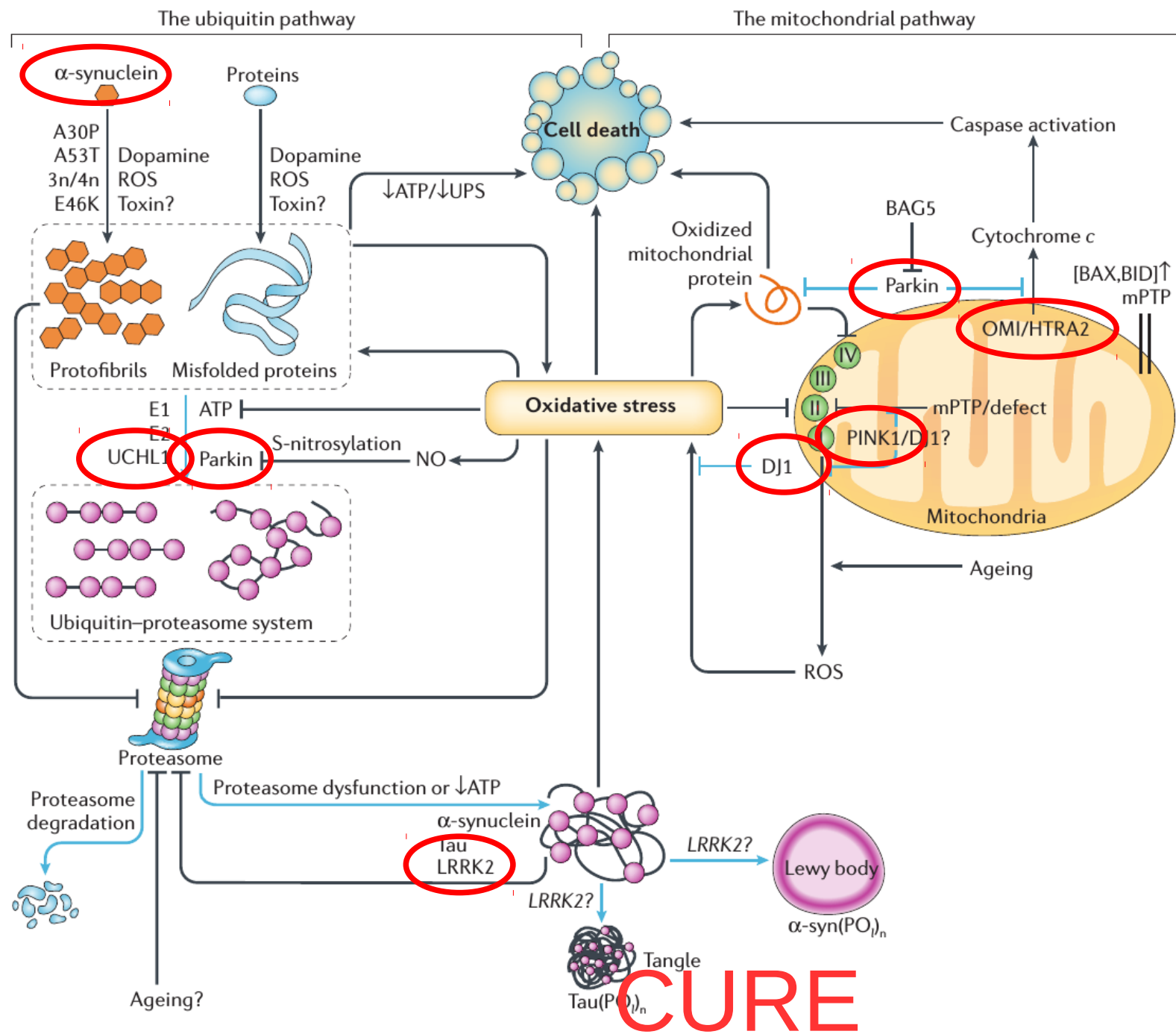


Liu et al (2009) *Nat Rev Drug Discov*

CURE

Breast cancer





Abou-Sleiman et al (2006) Nat Rev Neurosci

CURE

Parkinson's disease

systems medicine disease maps

ABOUT
PROJECTS
GUIDELINES
PUBLISHED MAPS
TOOLS
EVENTS
GET INVOLVED
CONTACT

Welcome to the portal for communication, news, guidelines, and other information about the **Disease Maps Project**, an effort to comprehensively represent disease mechanisms for various diseases.

Upcoming events

The second Disease Maps Community Meeting is scheduled 2-3 October 2017 in Belval, Luxembourg, as a satellite event before the [Impact of Big Data Analytics on Healthcare](#) conference 4-5 October 2017.

What is a disease map?

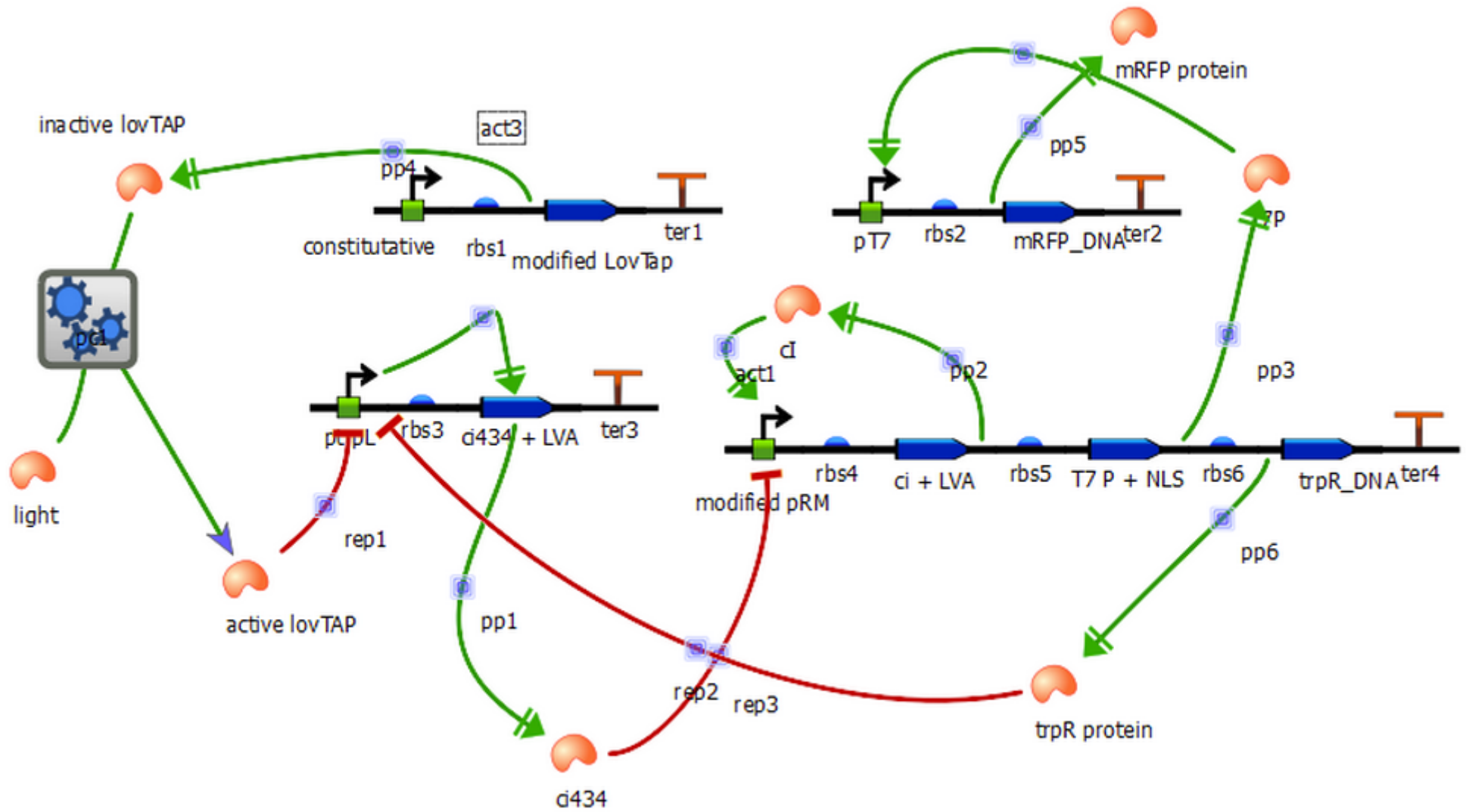
A systems medicine disease map is a high-quality expert-approved representation of disease mechanisms, a conceptual model of a disease. The detailed layer consists of interconnected signalling, metabolic and gene regulatory pathways stored in standard formats such as [SBGN](#), [SBML](#) and [BioPAX](#). The involvement of domain experts (clinicians and biologists) ensures that all the disease hallmarks are covered and relevant knowledge is adequately represented.

What are the disease maps for?

In translational medicine projects disease maps are used for advanced 'omics data interpretation and hypothesis generation, as the basis for mathematical models, for predictive analysis and for building clinical decision support systems (CDSS). The maps can be used for educational purposes as teaching aids.

The community

The Disease Maps Project is designed as a large-scale community effort. It is a network of groups that work together in order to better understand disease mechanisms. We exchange best practices, share information, develop tools to make it easier for all the involved groups to achieve their goals.



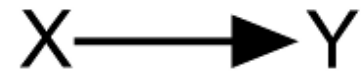
BUILD

Synthetic Biology

Ambiguity of usual representations

$X \longrightarrow Y$

Ambiguity of usual representations



is transformed into

translocates ($X = Y$)

is degraded into

associates into

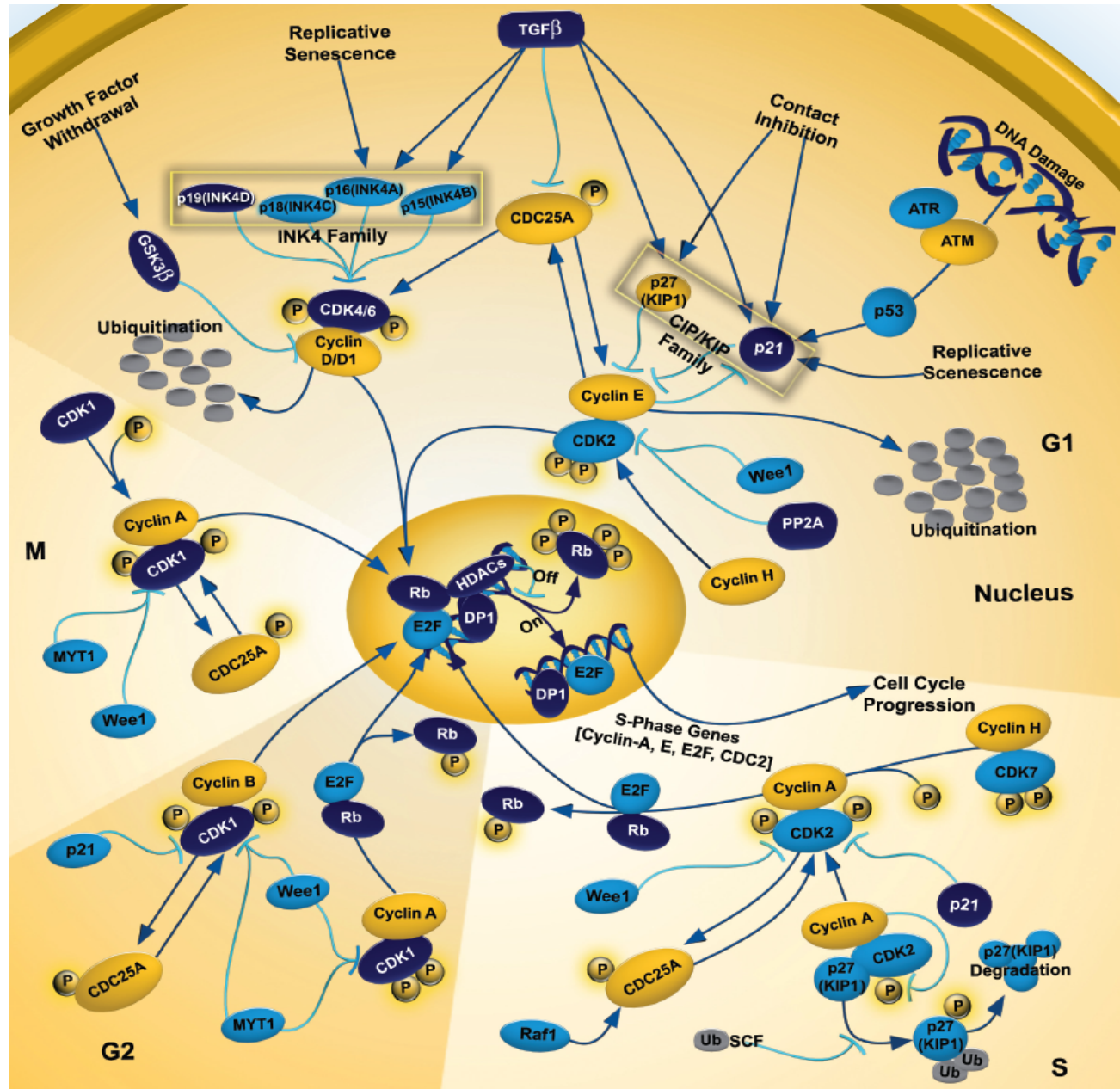
dissociates into

stimulates the activity of

stimulates the expression of

catalyses the formation of

Can-this be understood by biologists?





Replicative Scenescence

...ates?

Reciprocal

Ambiguity of usual representations

X inhibits Y

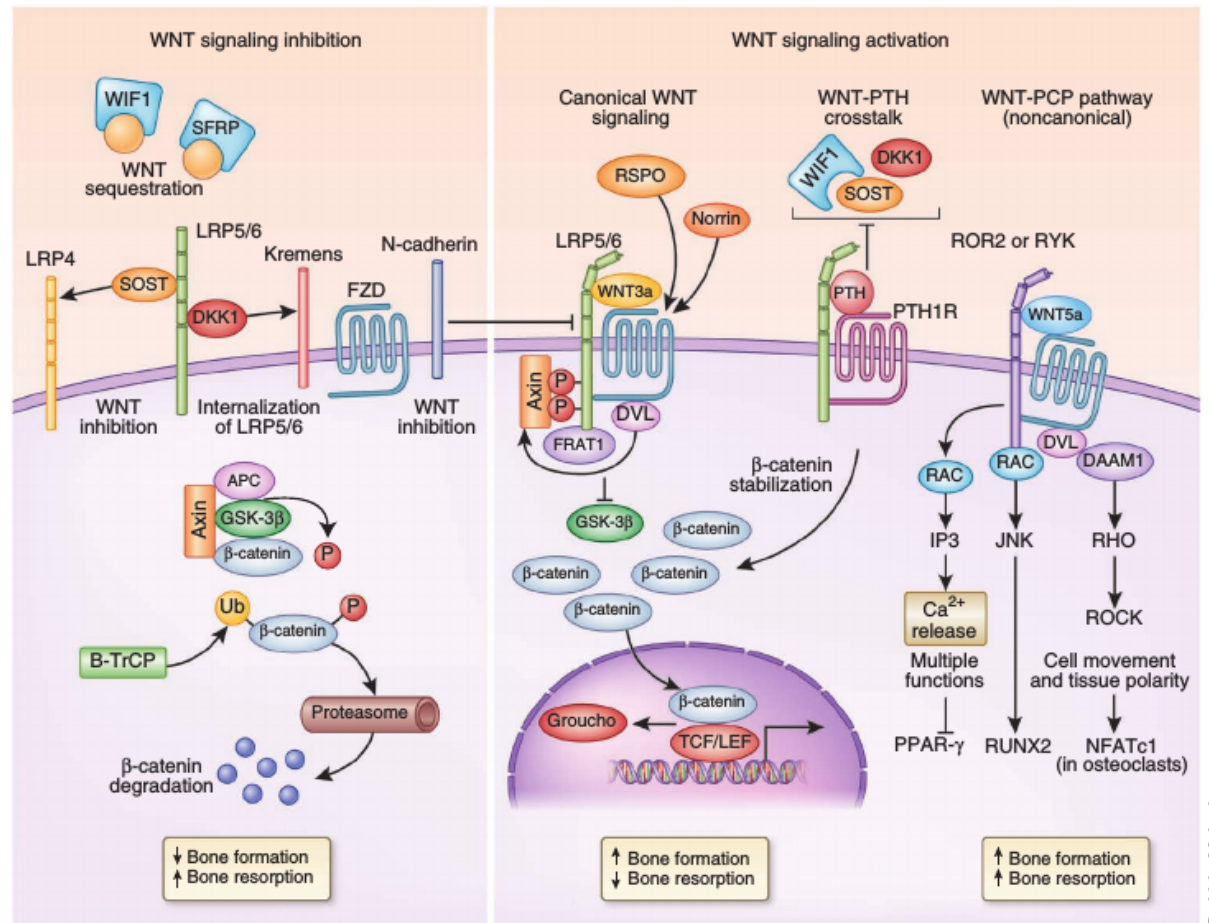
Ambiguity of usual representations

X inhibits Y



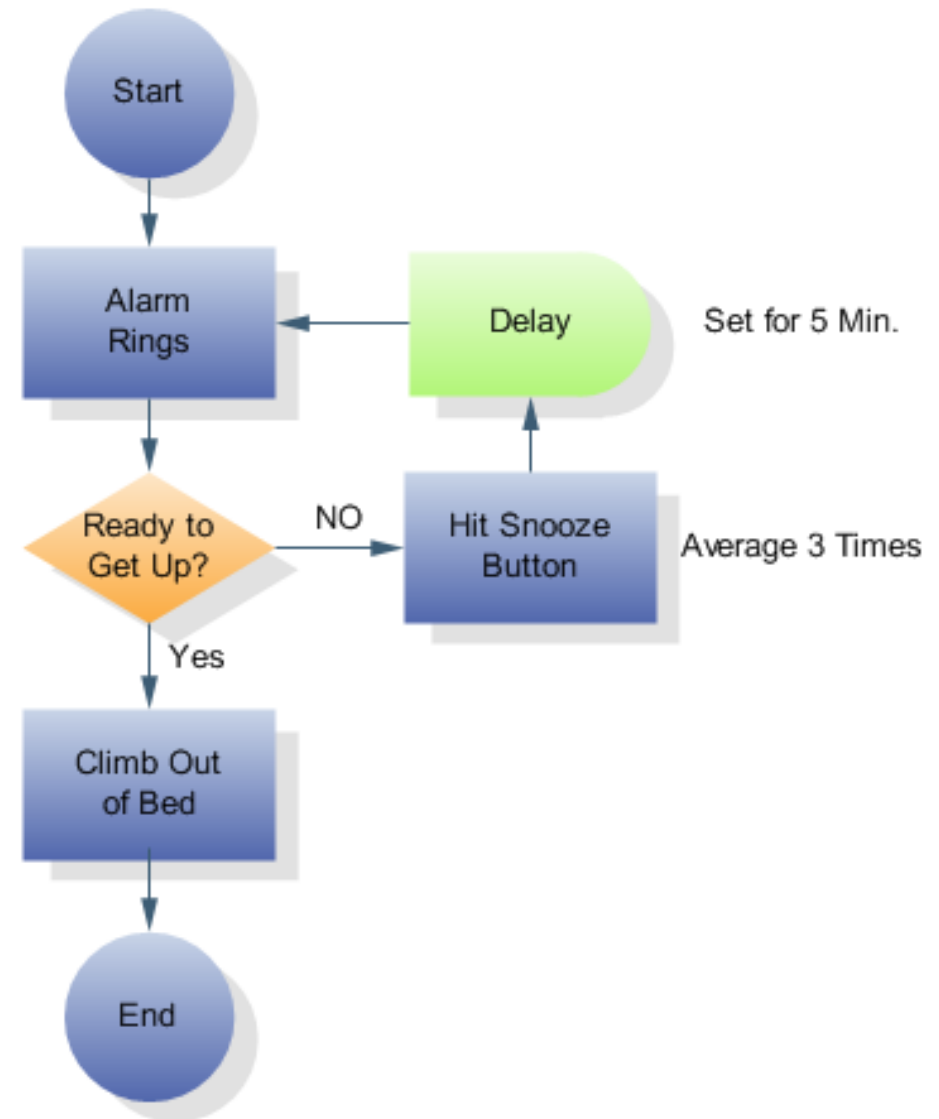
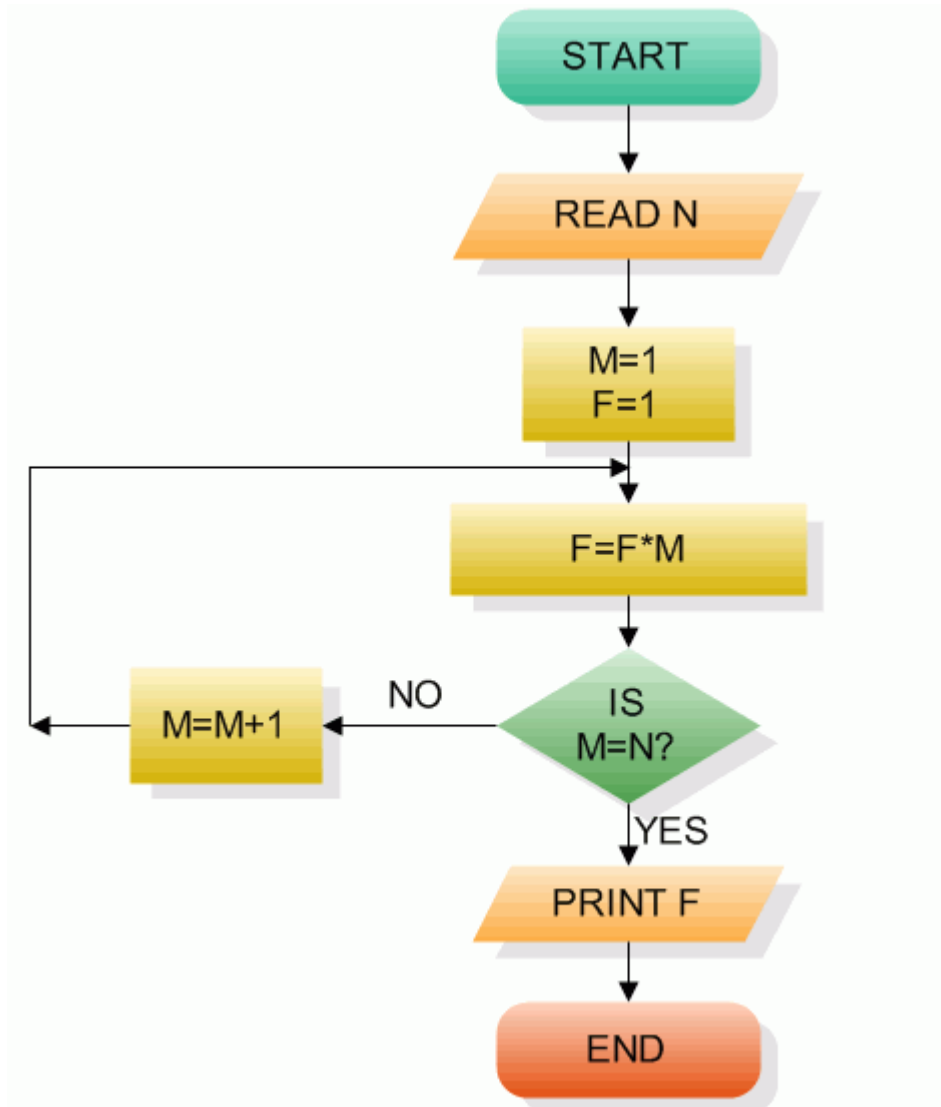
Figure 1 WNT signaling: a simplified view. In the absence of WNT, the amounts of β -catenin are low, except in adherens junctions, because of its constitutive targeting by a multiprotein destruction complex (left). The tumor suppressors axin and adenomatous polyposis (APC) bring β -catenin to GSK-3 β and casein kinase 1 (CK1) (not shown), resulting in its phosphorylation (Ps in circles) at specific serine/threonine residues (left). Phosphorylated β -catenin is then targeted for polyubiquitination (Ub) (predominantly by the E3 ligase B-TrCP) and proteosomal destruction. T cell factor/lymphoid enhancer factor (TCF/LEF) transcription factors are repressed by Groucho in the nucleus. Binding of canonical WNT ligands to a dual receptor complex comprising the WNT co-receptors LRP5 or LRP6 (LRP5/6) and one of the seven transmembrane receptors of the FZD family (right) initiates WNT- β -catenin signaling. Axin moves to the LRP5/6 tail at the membrane through its interaction with dishevelled (DVL, also called DSH), which is recruited by FZD (right). This forms a complex that also includes FRAT1 and GSK-3 β , which prevents phosphorylation of

β -catenin and its proteosomal degradation. β -catenin accumulates in the cytoplasm and translocates into the nucleus, where it associates with members of the TCF/LEF transcription factors while displacing Groucho to control target gene transcription. WNT signaling is modulated not only through fine tuning by a large number of WNT ligands and RSPO proteins and norrin (right) but also by extracellular antagonists such as DKK1, SOST and Wise, which bind LRP5/6 (left). Their antagonism is mediated or enhanced by receptors such as Kremen proteins and LRP4. In addition to sequestering β -catenin, N-cadherin also inhibits WNT- β -catenin signaling by interacting with LRP5 (left to right). In contrast, secreted frizzled-related proteins (SFRPs) and WNT inhibitory factor 1 (WIF1), which have ligand specificity, inhibit WNT signaling by directly sequestering WNT ligands and inhibiting both canonical and noncanonical WNT signaling (left). The PTH1 receptor can also activate the pathway in the absence of WNT ligands by forming a complex with LRP5/6 after PTH binding (right). In the WNT-PCP pathway (right), WNT binding to FZD also recruits DVL, which forms a complex with dishevelled associated activator of morphogenesis 1 (DAAM1) to trigger activation of the small G protein RHO, which in turn activates RHO-associated kinase (ROCK). Alternatively, DVL forms a complex with RAC, resulting in Jun kinase (JNK) activity. The WNT-Ca²⁺ pathway is activated by WNT5a binding to FZD and receptor-tyrosine-kinase-like orphan receptor (ROR). Intracellular calcium concentrations increase after WNT-induced coupled G protein activation of phospholipase C (PLC), resulting in dystroglycan 1 (DAG) and inositol 1,4,5-trisphosphate, type 3 (IP3) generation and cyclic GMP (cGMP)-specific phosphodiesterase (PDE) decreasing the amount of cGMP. NFATc1, nuclear factor of activated T cells, cytoplasmic, calcineurin dependent 1; PPAR- γ , peroxisome proliferator activated receptor- γ .

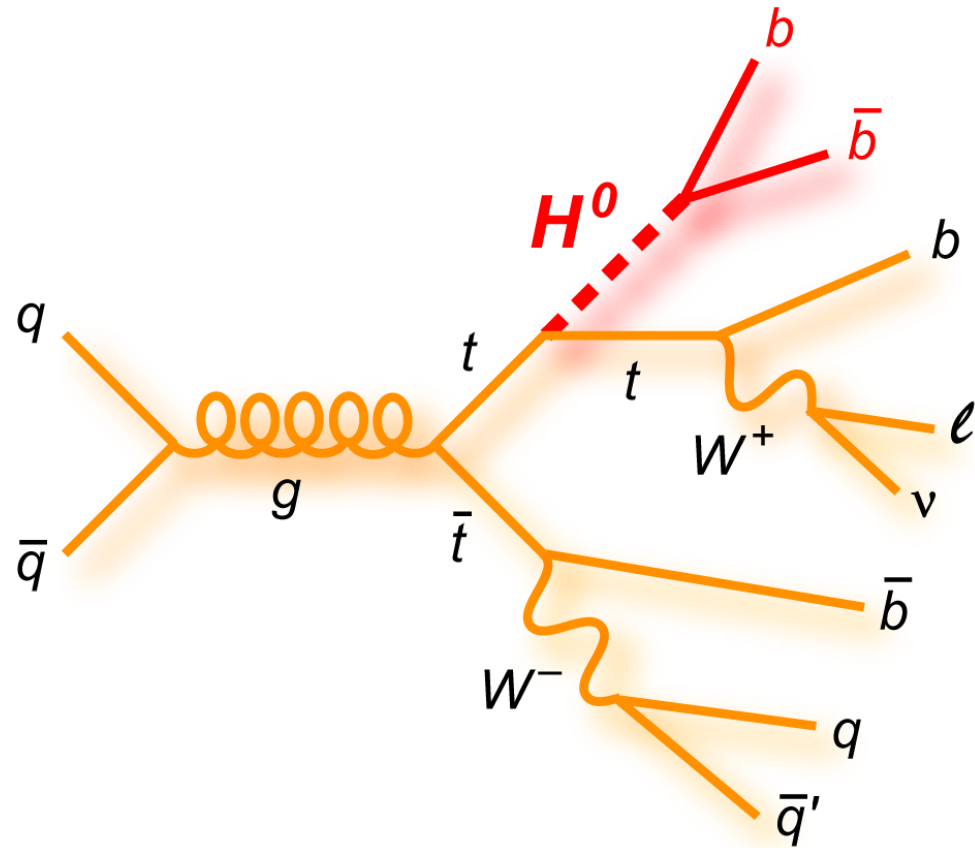


Debbie Maizels

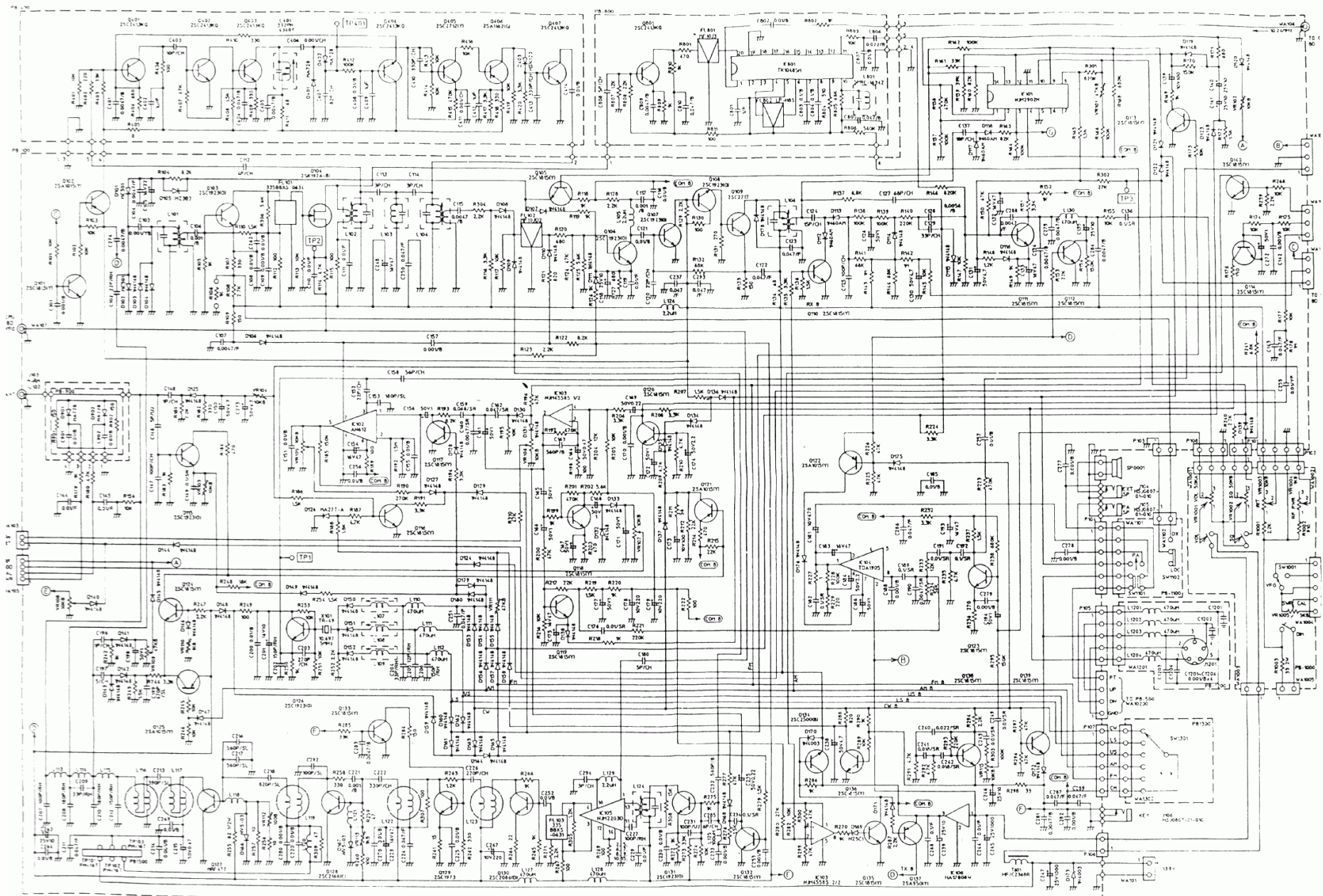
Every computer scientist understands those



Every physicist understands this



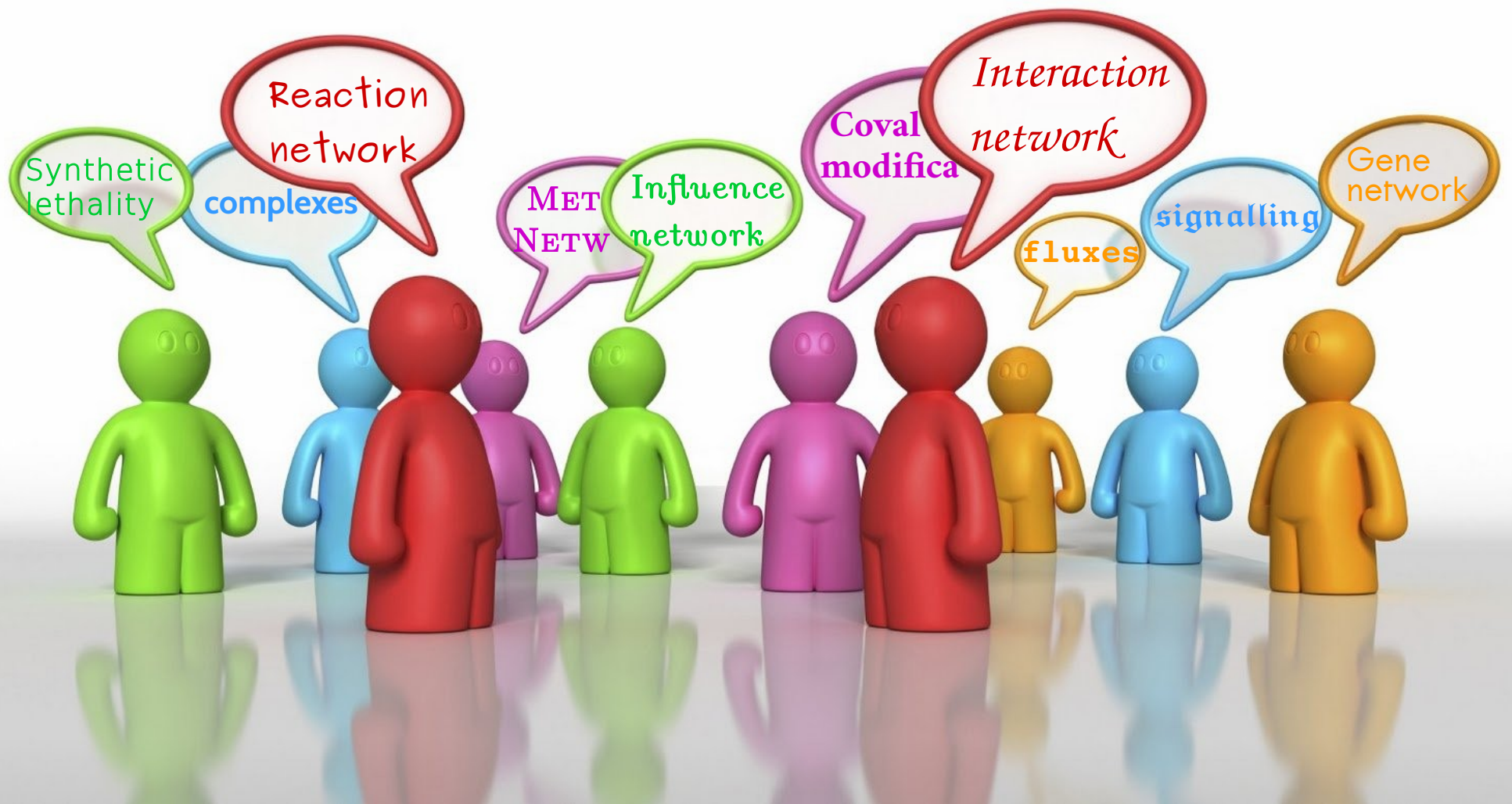
Every engineer understands that



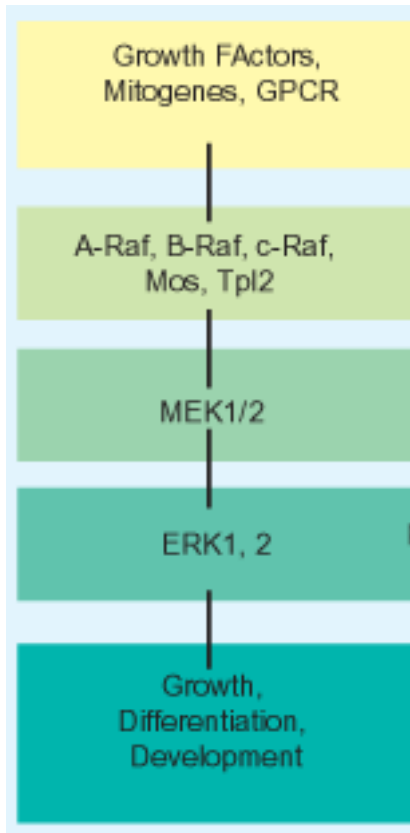
The Systems Biology Graphical Notation

- A tool to graphically describe and unambiguously interpret biochemical and cellular events
- Limited amount of symbols ➡ Smooth learning curve
- Can represent logical or mechanistic models, biochemical pathways, at different levels of granularity
- Detailed technical specification, precise data-models, standard API and growing software support
- Developed over ten years by a diverse community, including biologists, modellers, computer scientists etc.

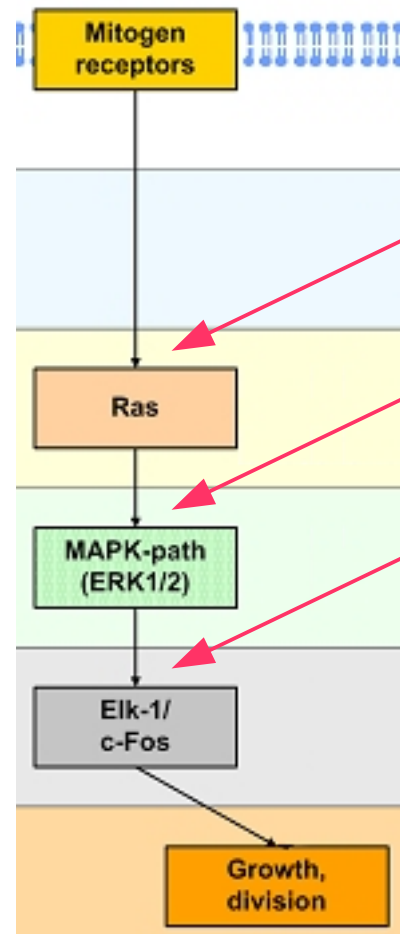
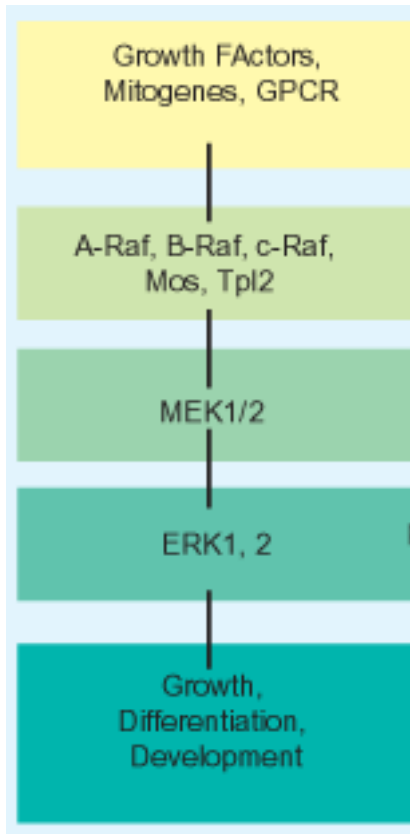




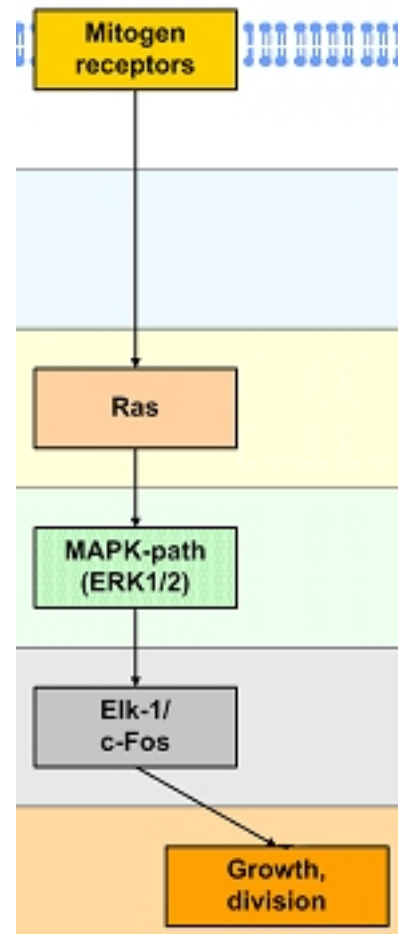
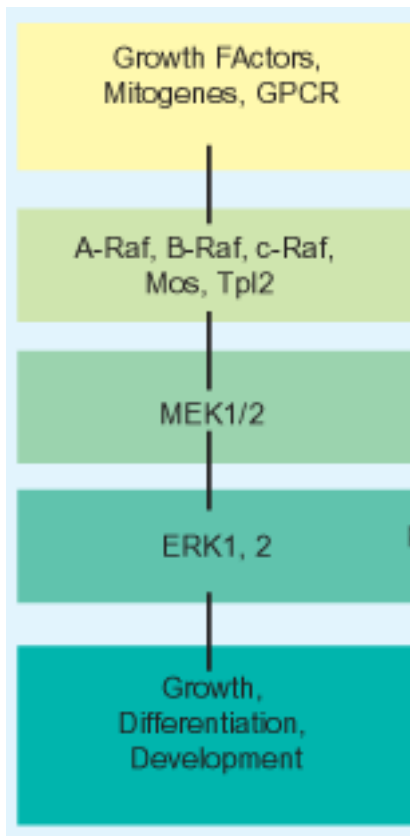
Different granularities of a pathway



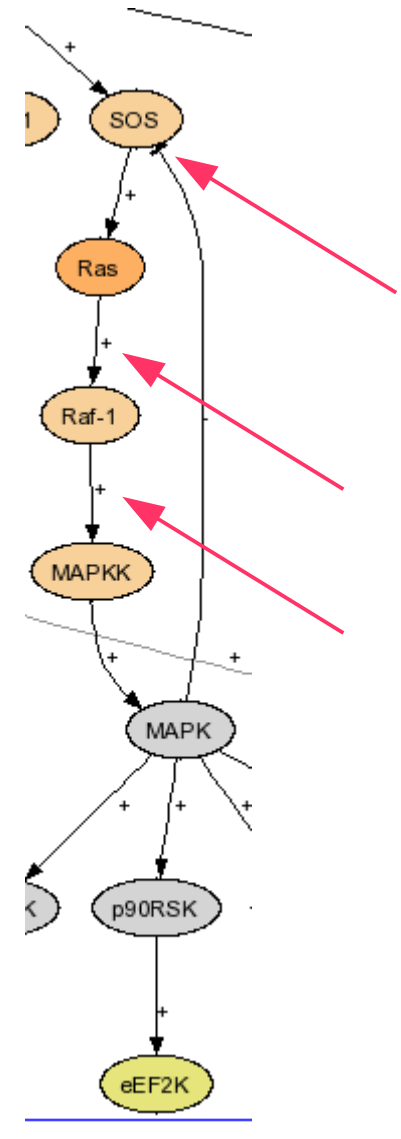
- No temporal sequence
- No directionality
- No biochemical effects
- No mechanistic descriptions

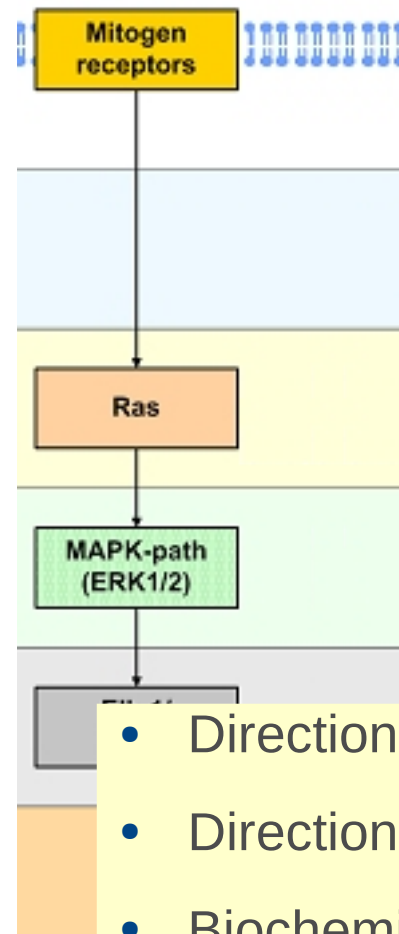
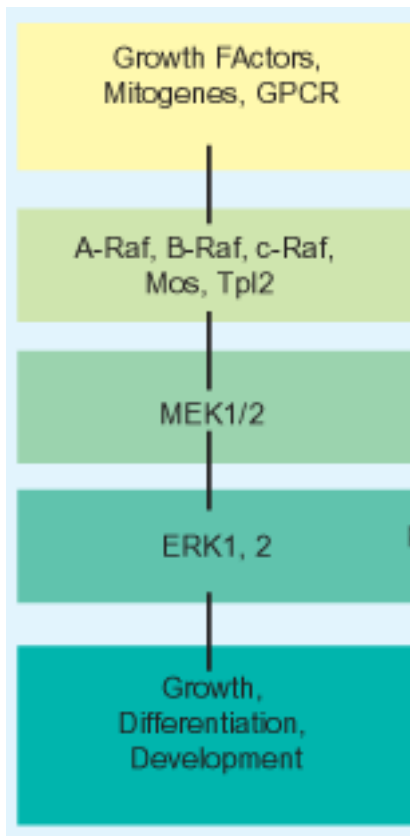


- Directionality of influence

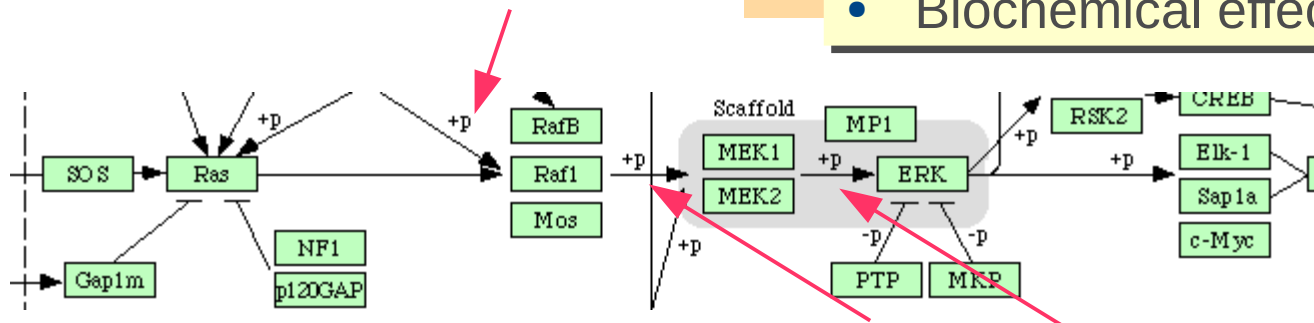
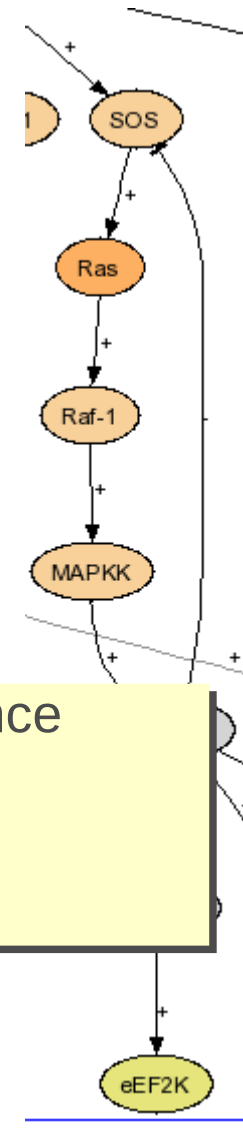


- Directionality of influence
- Directionality of effect



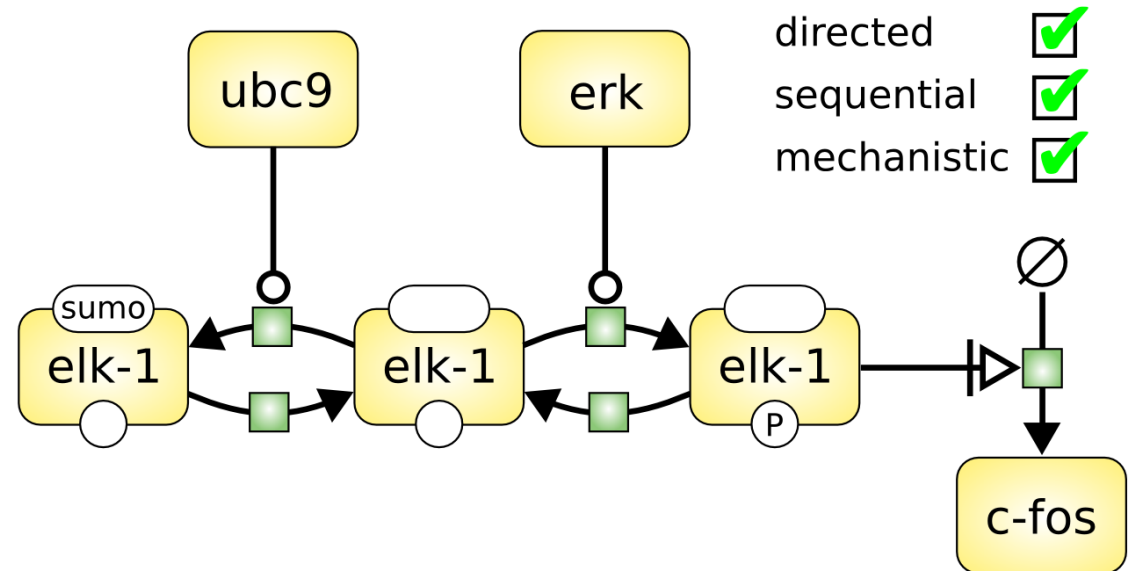


- Directionality of influence
- Directionality of effect
- Biochemical effect

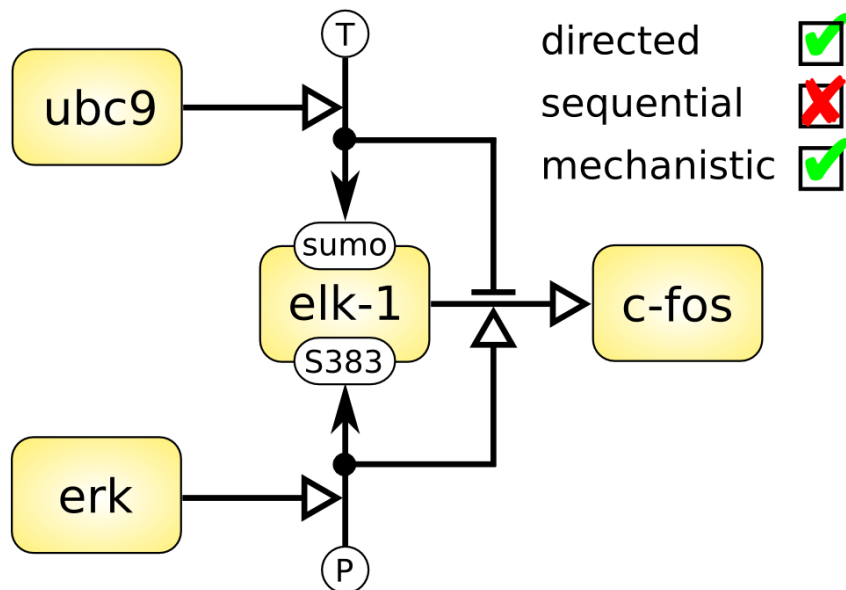


One notation – three languages

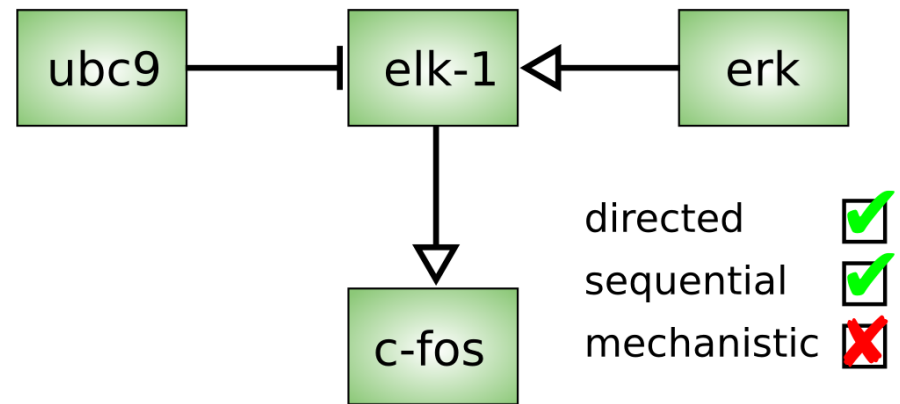
process descriptions



entity relationships

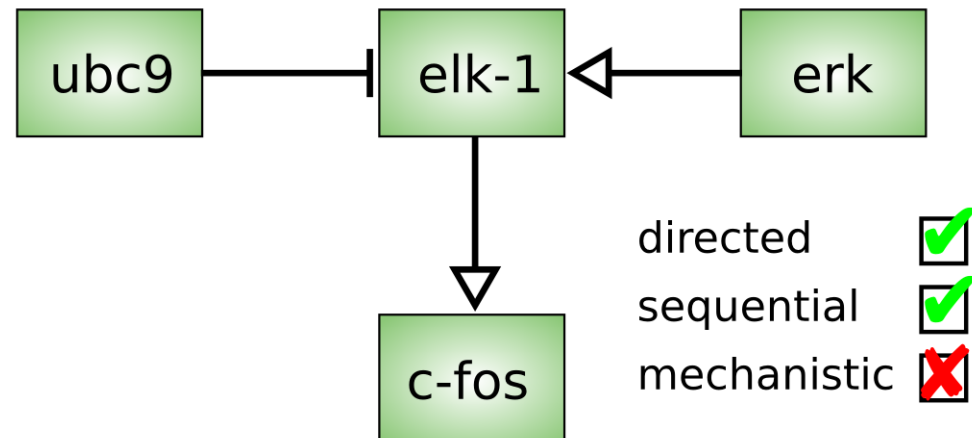


activity flows



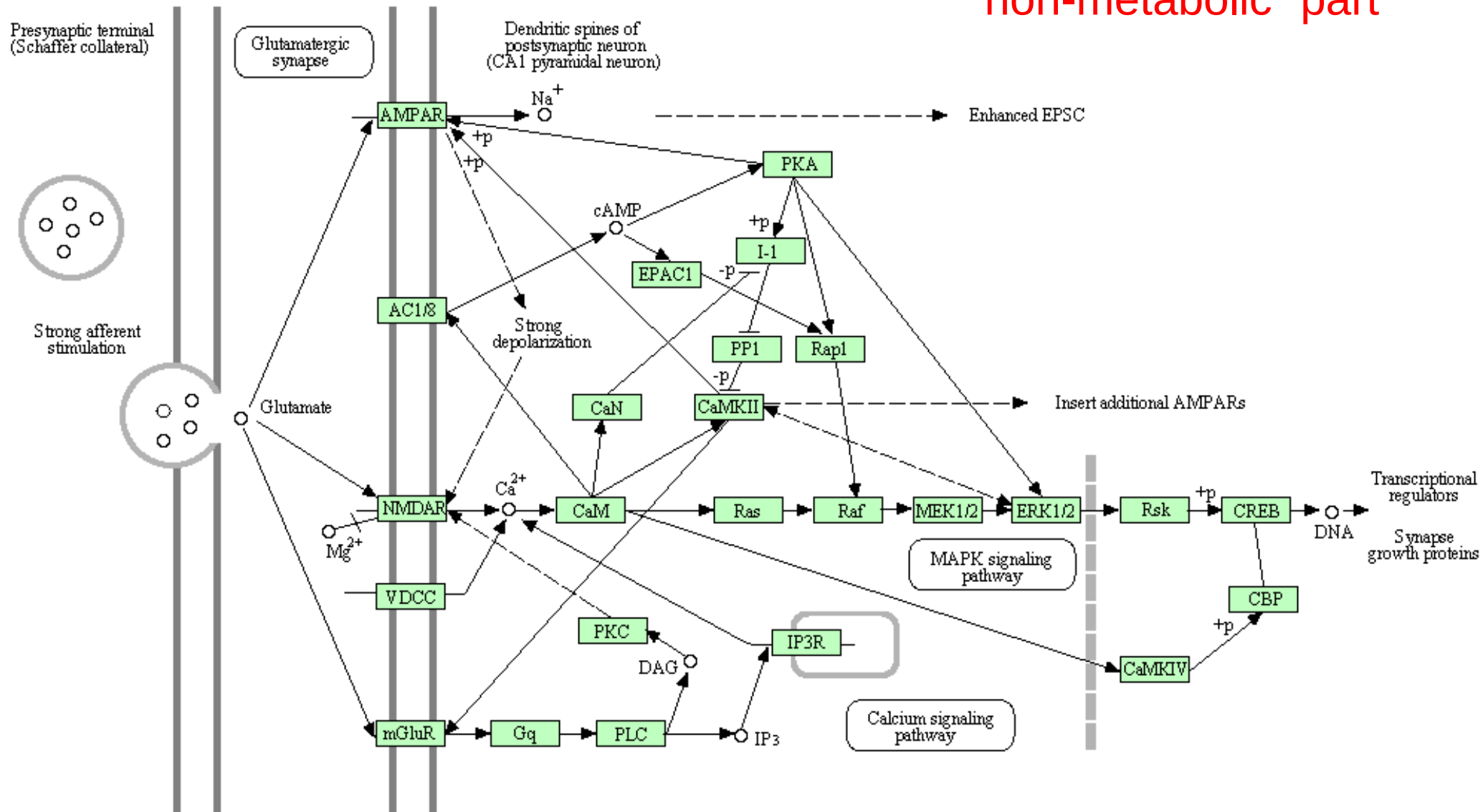
Functional descriptions: the Activity Flows

- Logical modelling
- Signalling pathways, gene regulatory networks



LONG-TERM POTENTIATION

“non-metabolic” part



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Pathway Information

Neuro2A Differentiation by G alpha i/o Pathway

Author(s): [Aul Malayan, et al.](#)

Scope(s): Specific

Organism: vertebrates: mammals: Rodentia: mice

Canonical Pathway(s): [G alpha i Pathway](#)

Tissue/Cell: nervous system: central nervous system: neurons

Citation(s): [Literature](#)

Pathway

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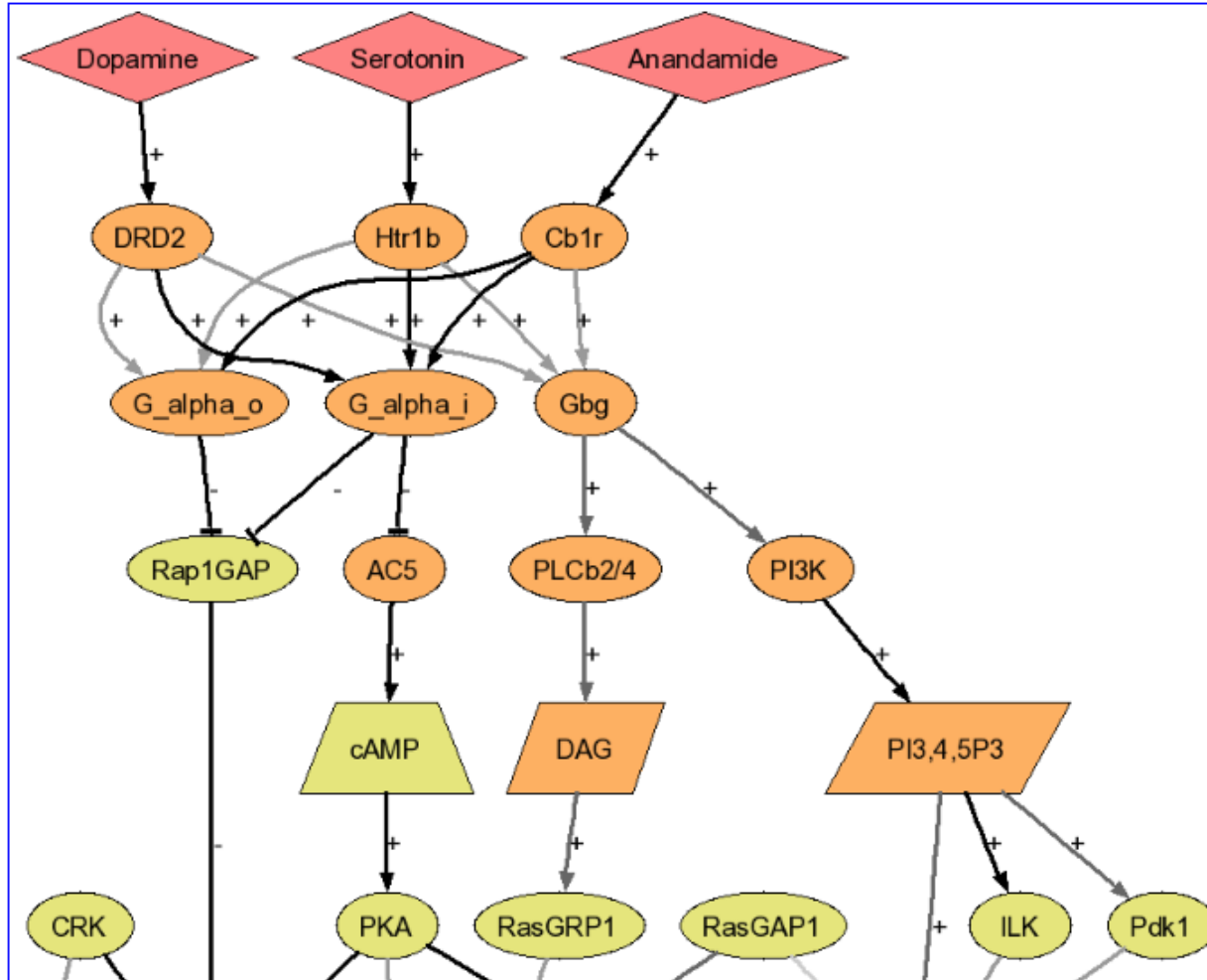
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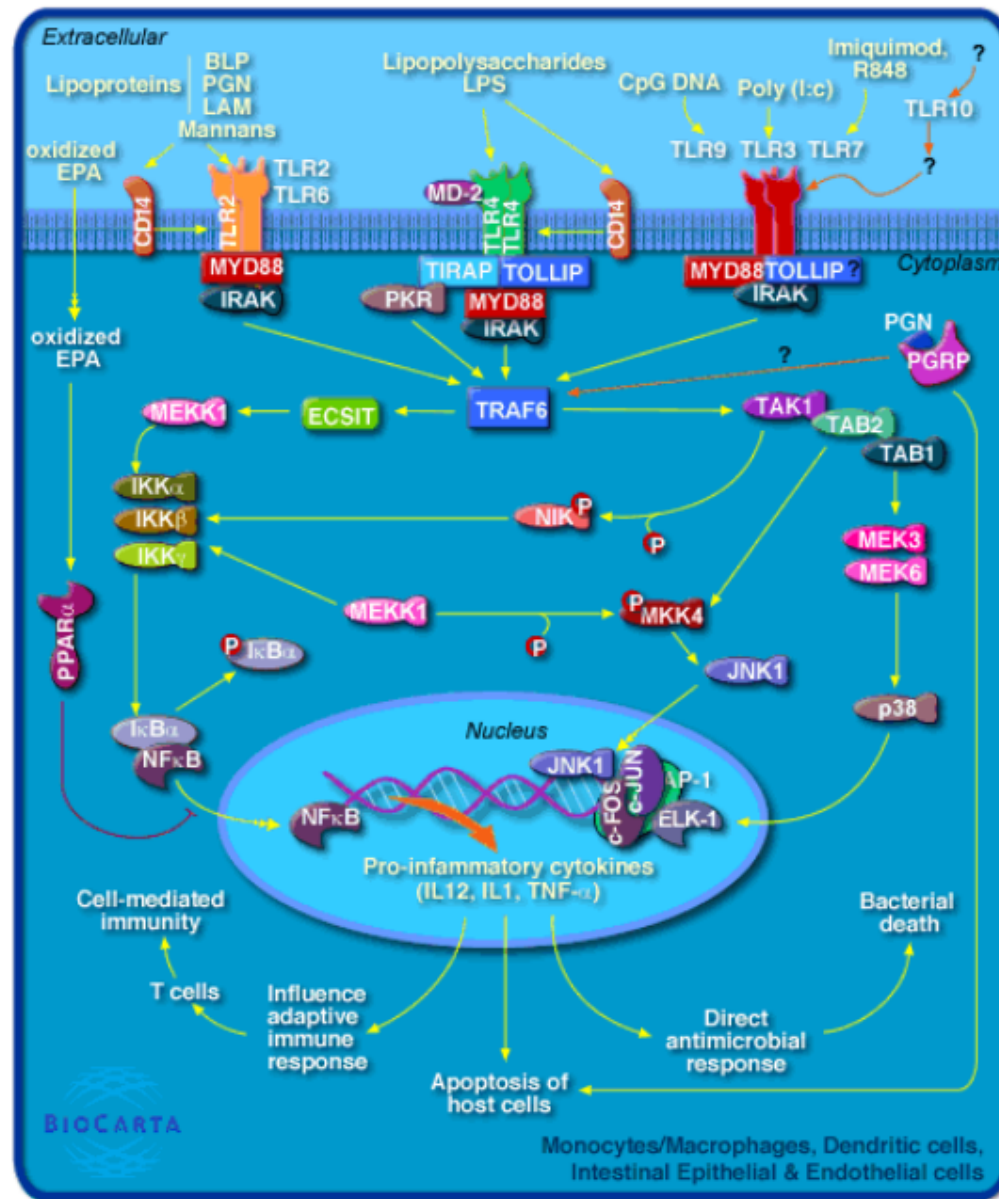
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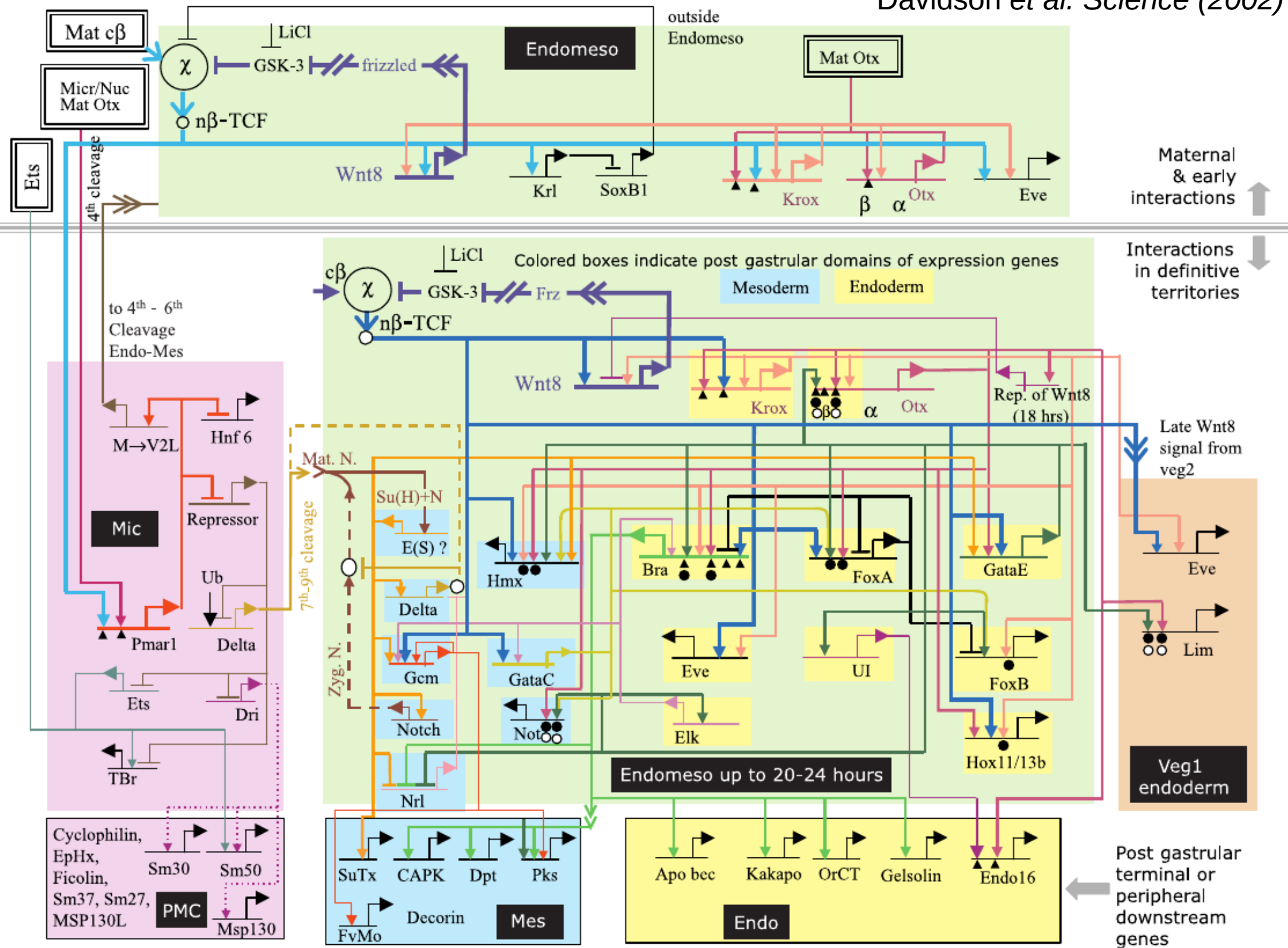
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From the journal Science

ScienceCareers.org

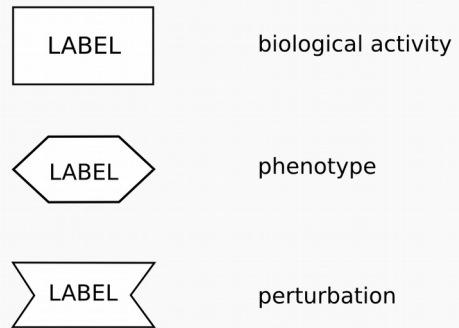
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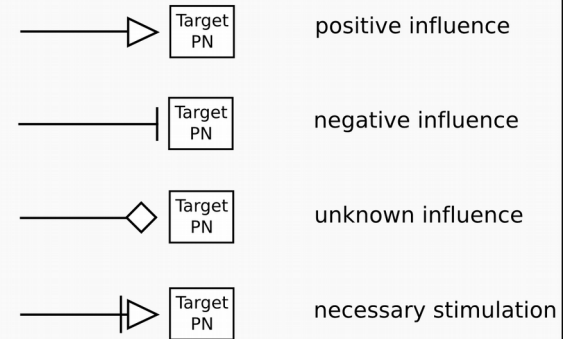


SBGN Activity Flows L1 reference card

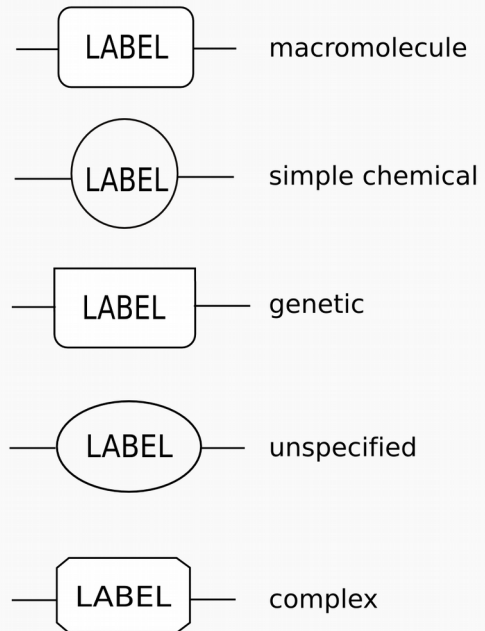
Activity nodes



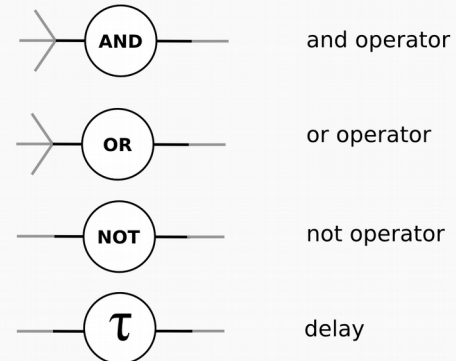
Modulating Arcs



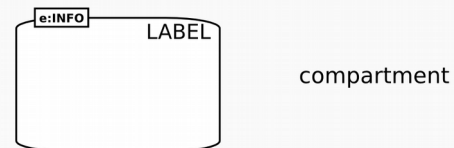
Auxiliary Units



Logical Operators

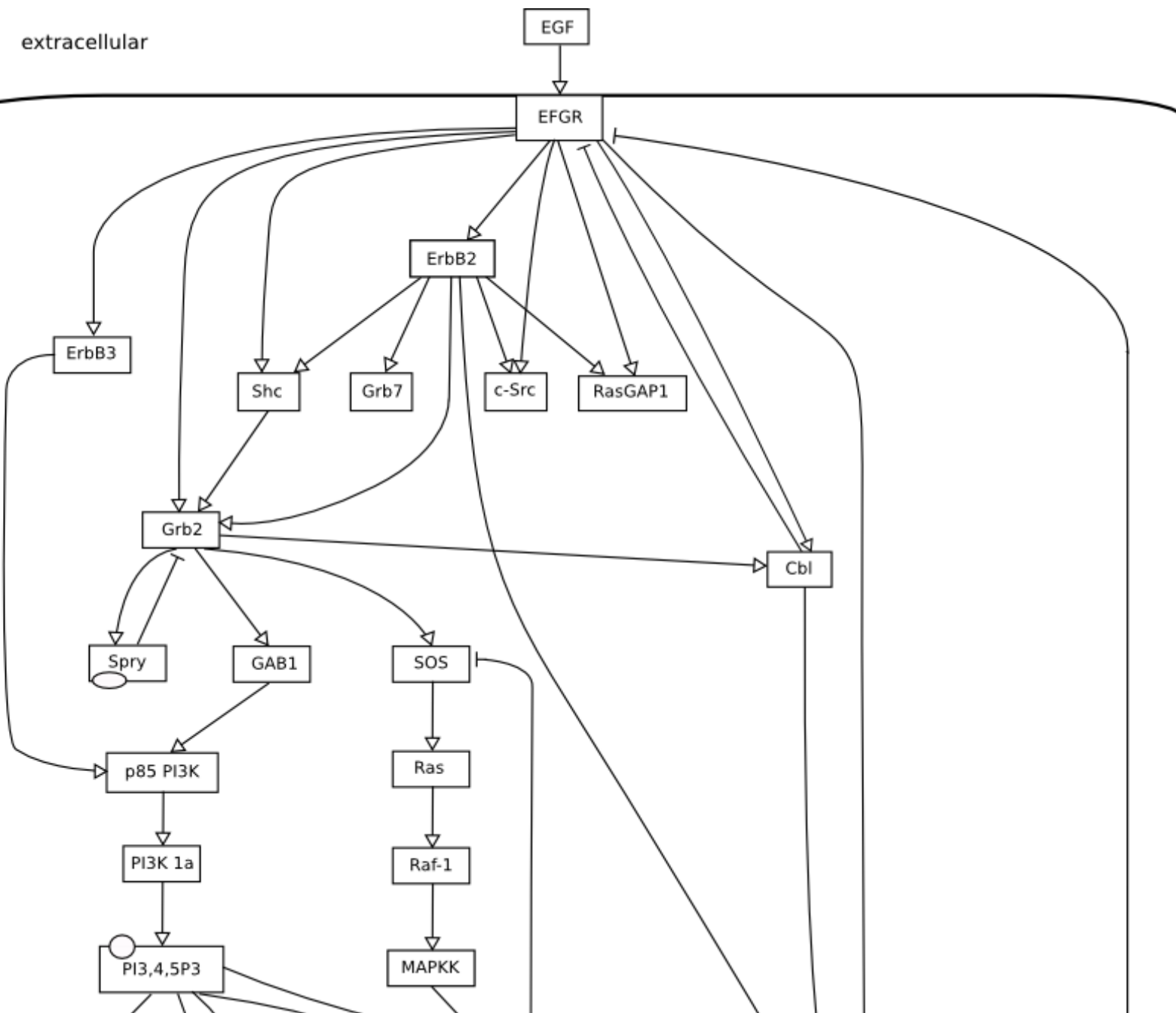


Container Nodes



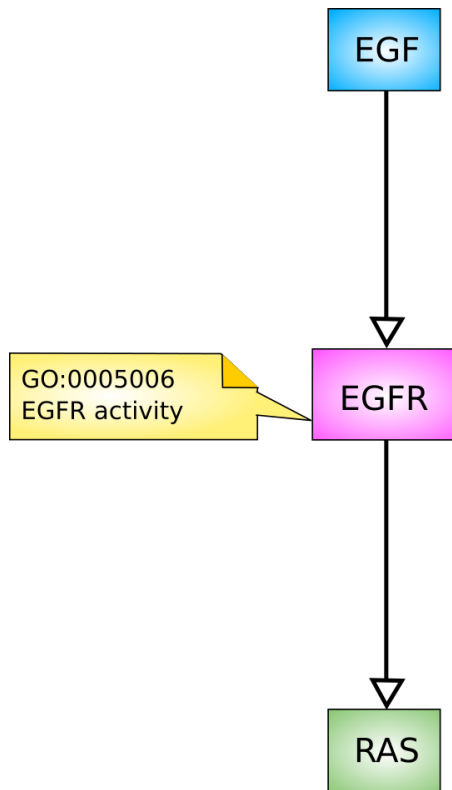
extracellular

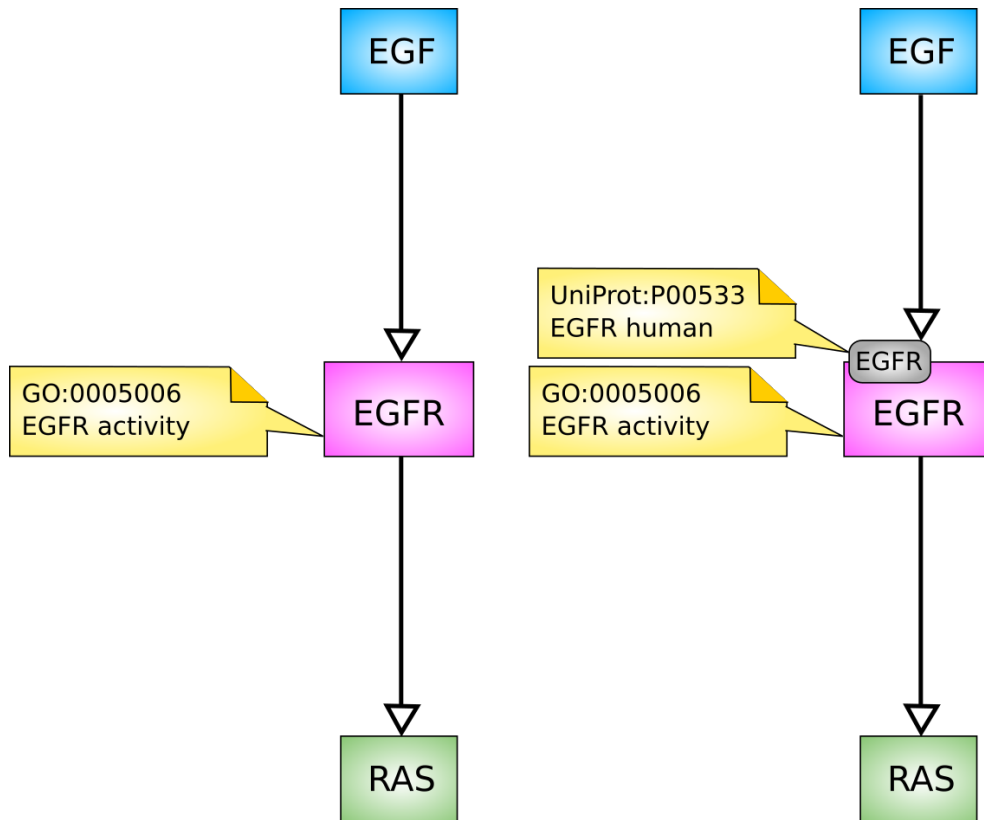
Example of Activity Flow map

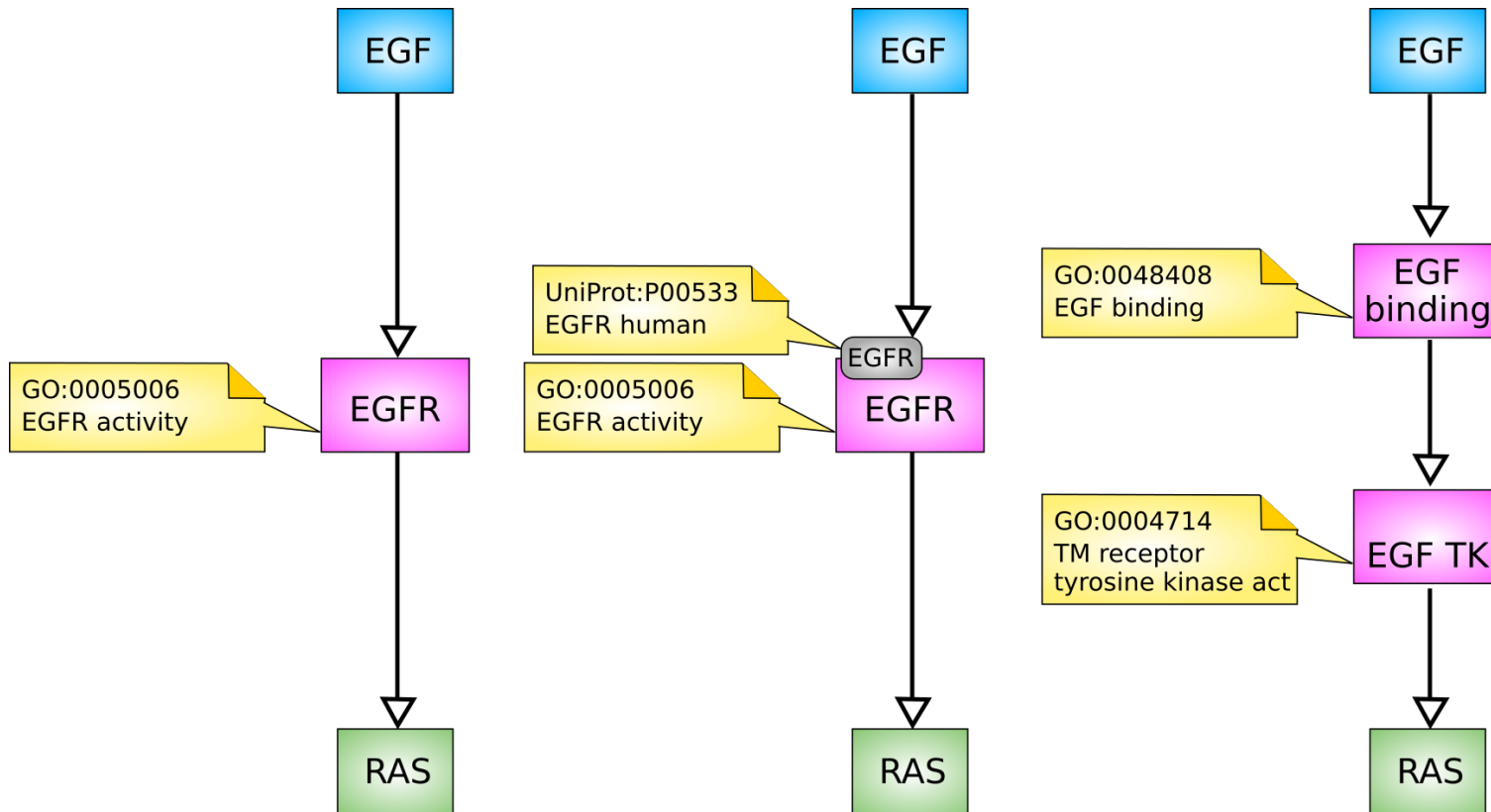


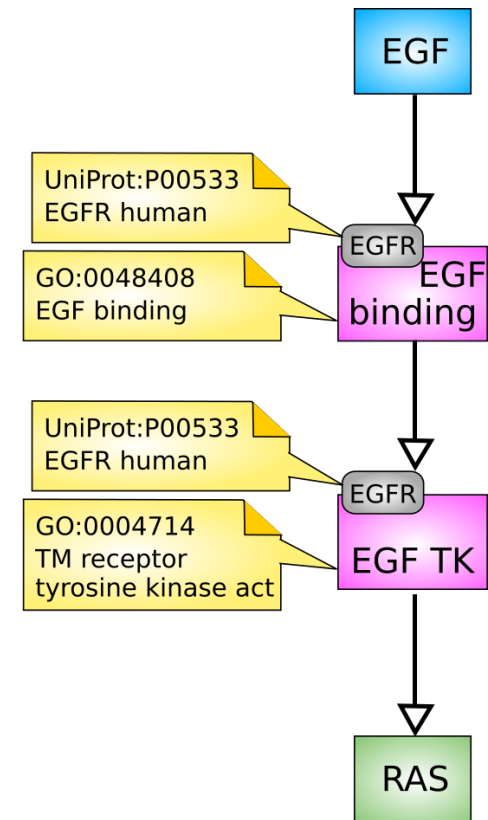
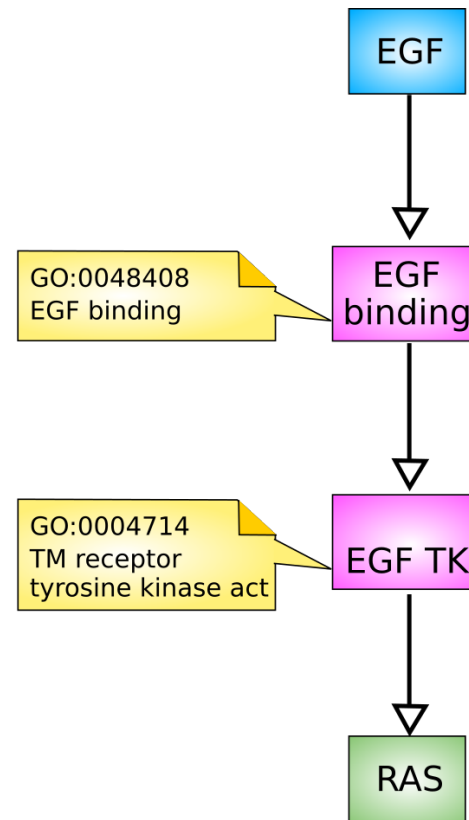
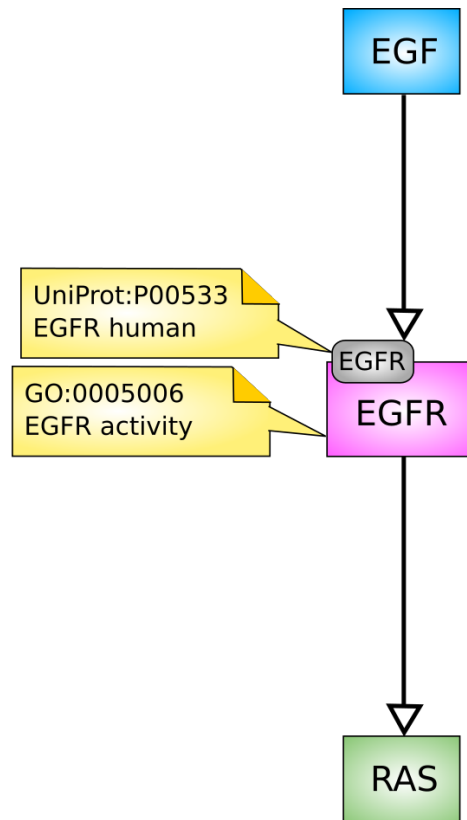
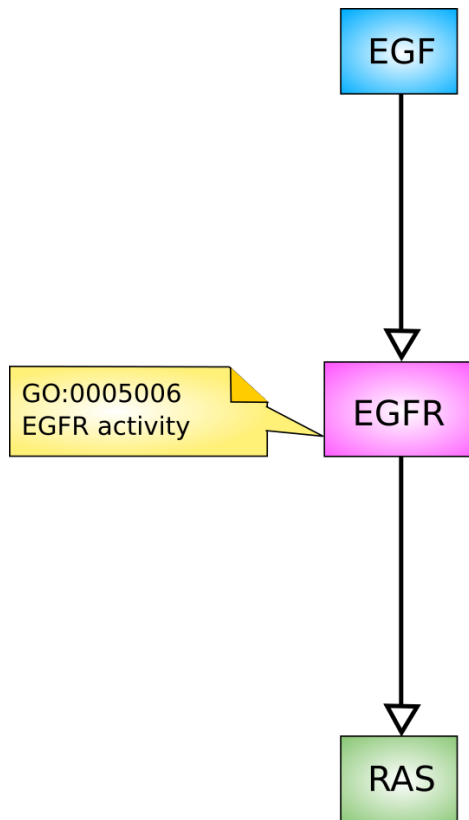
TIMTOWTDI

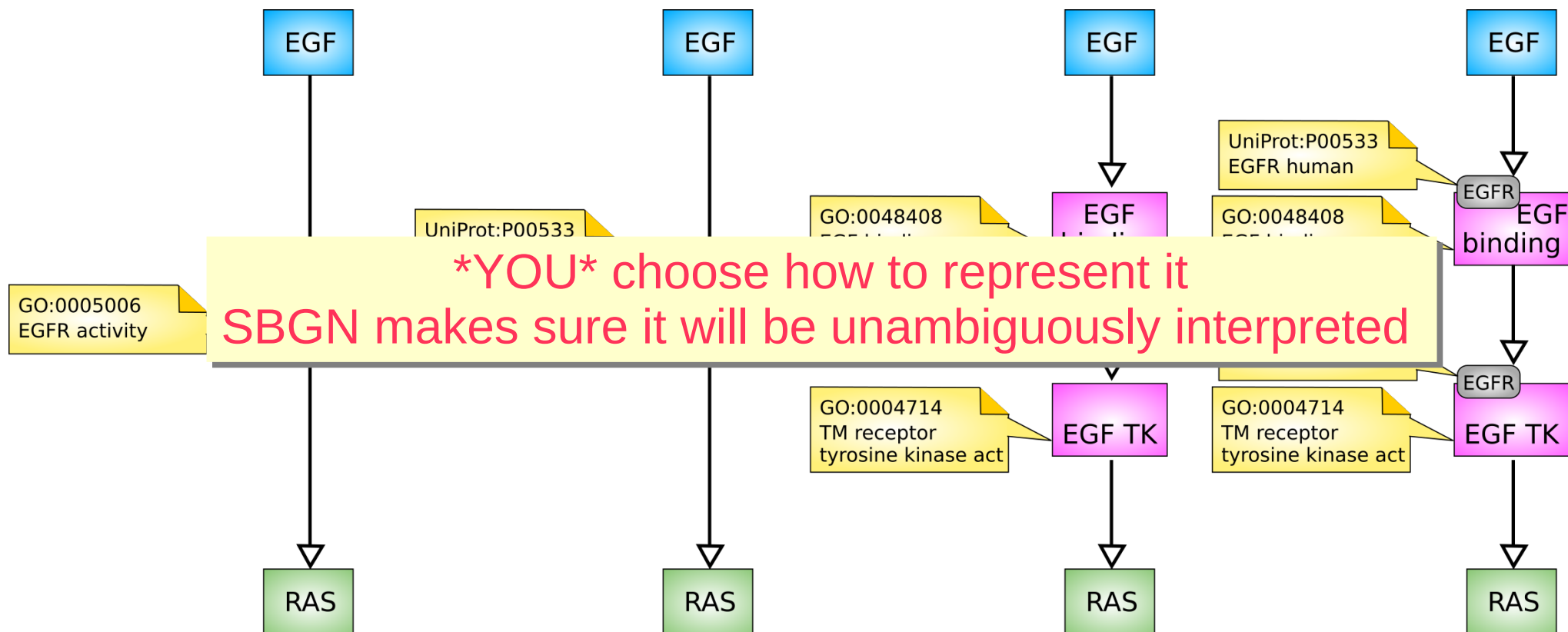
(There Is More Than One Way To Do It)



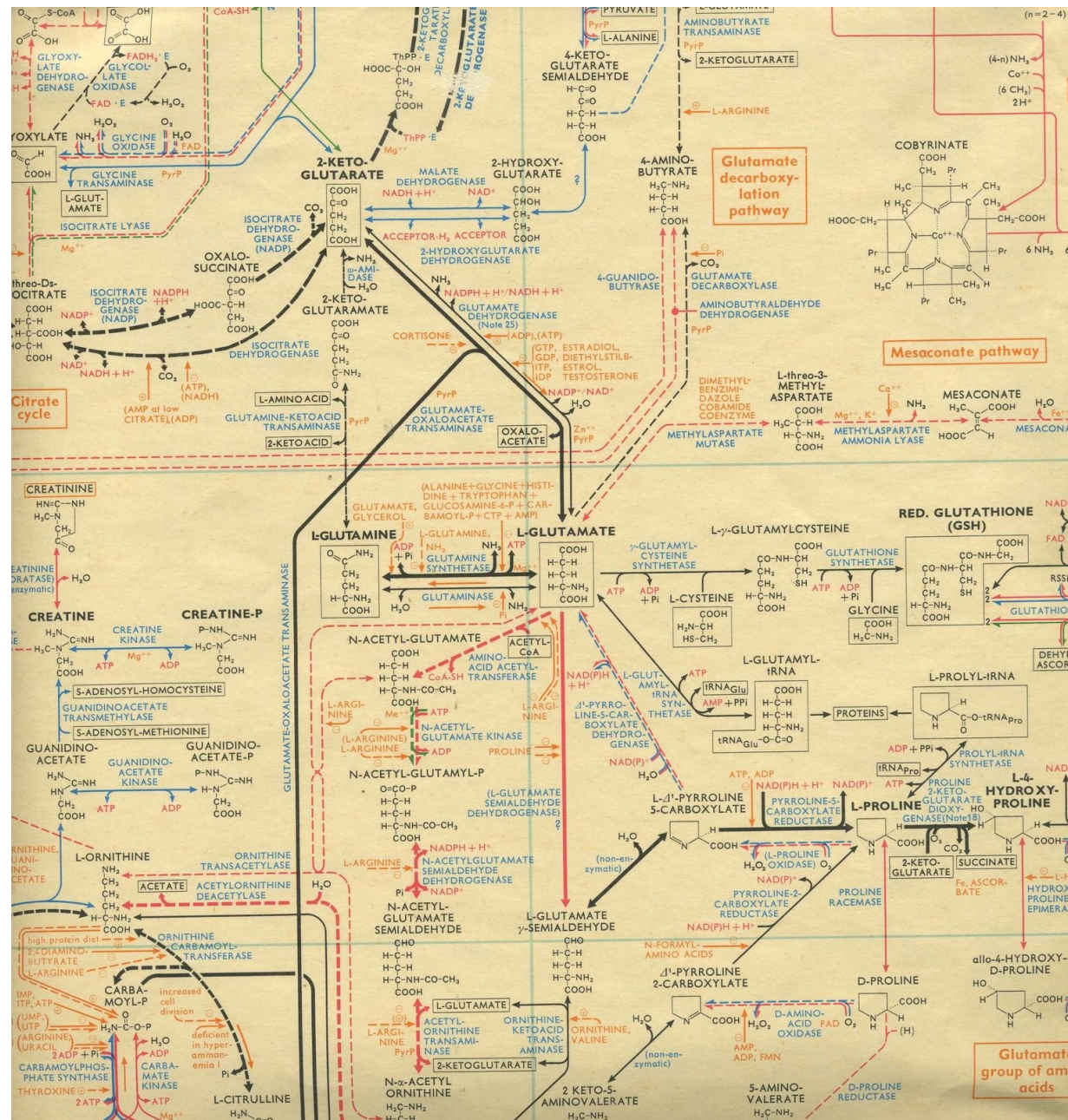




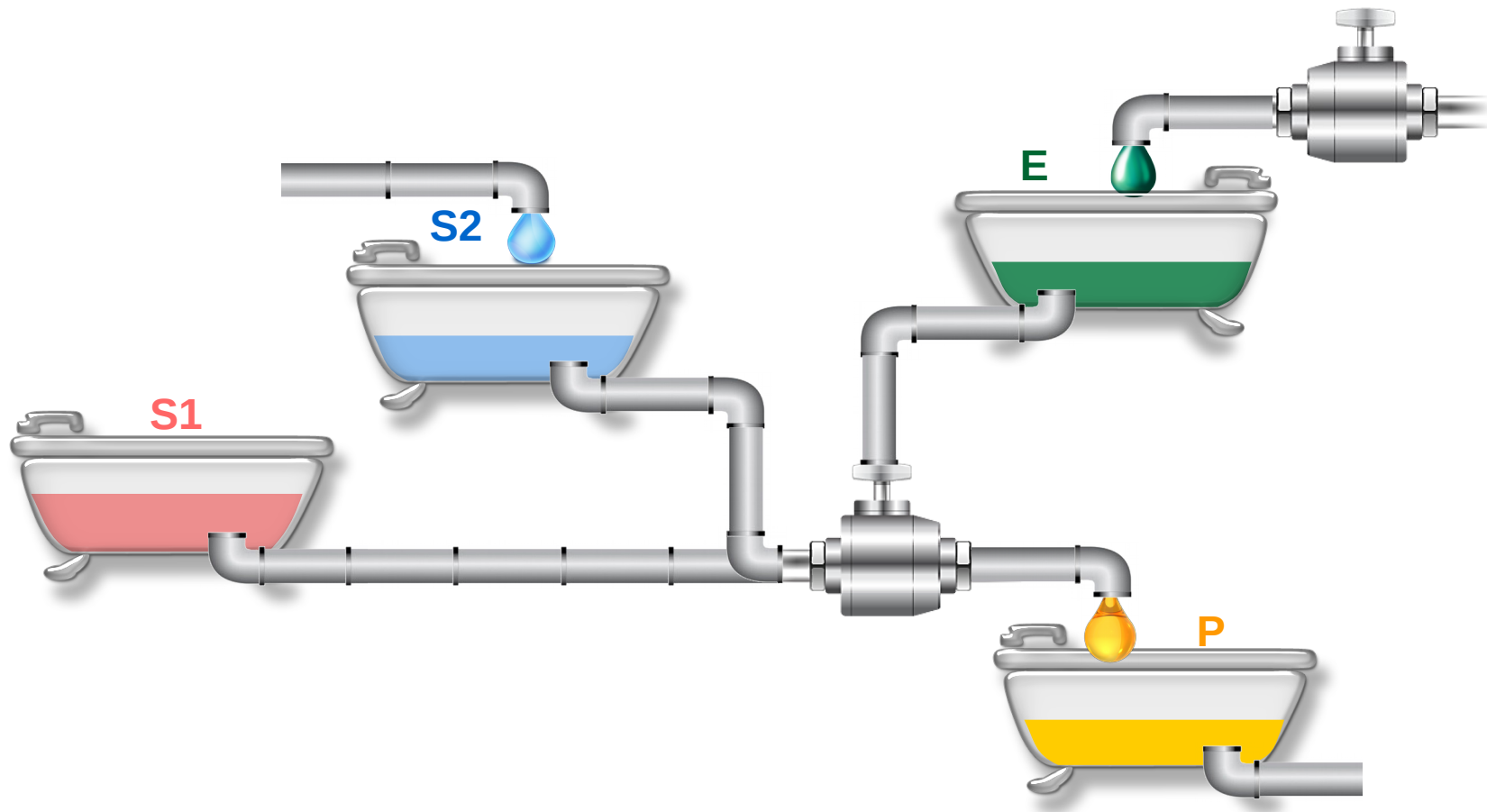




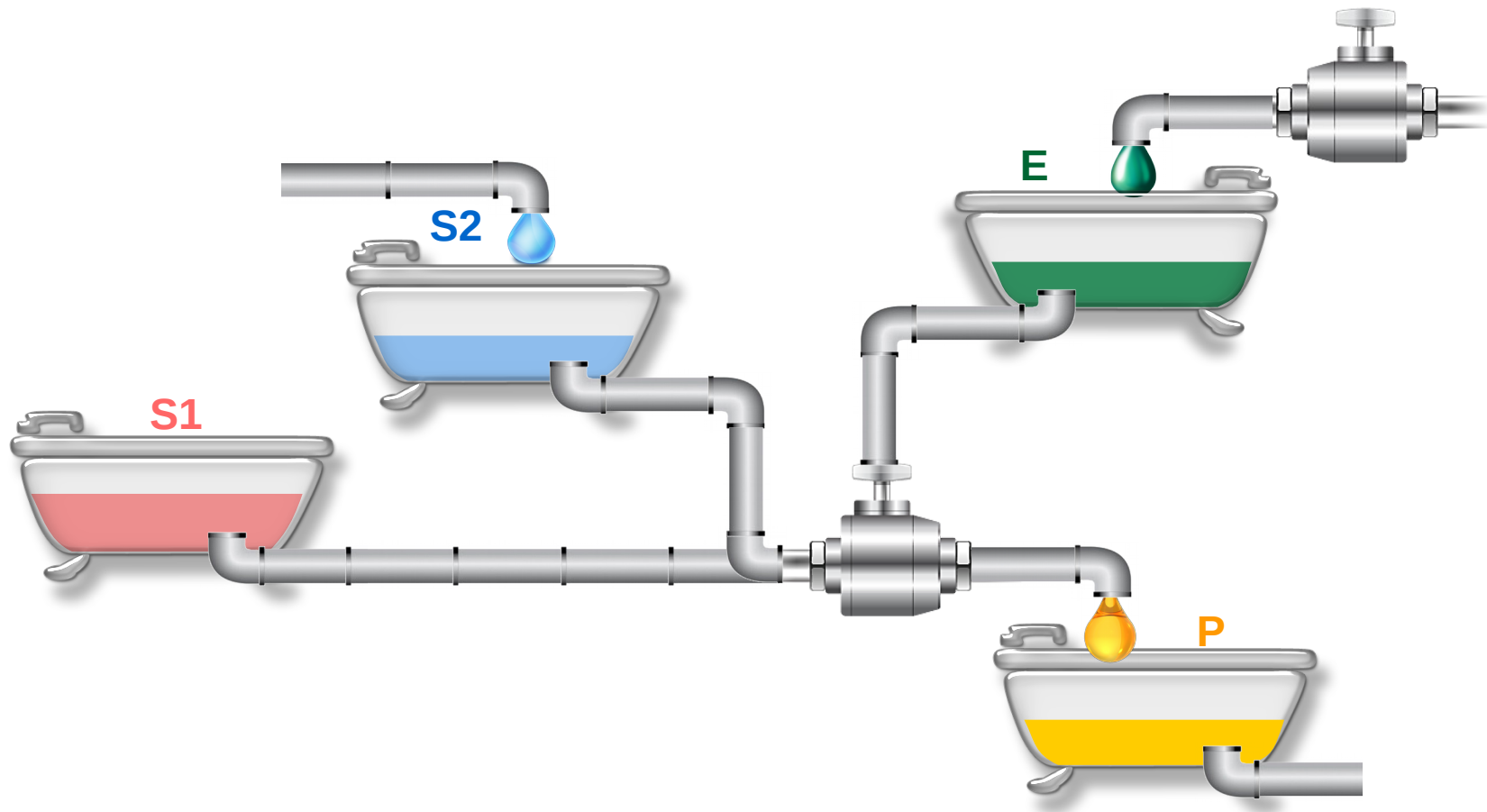
Putting in mechanisms: describing processes



A biochemical reaction is a process



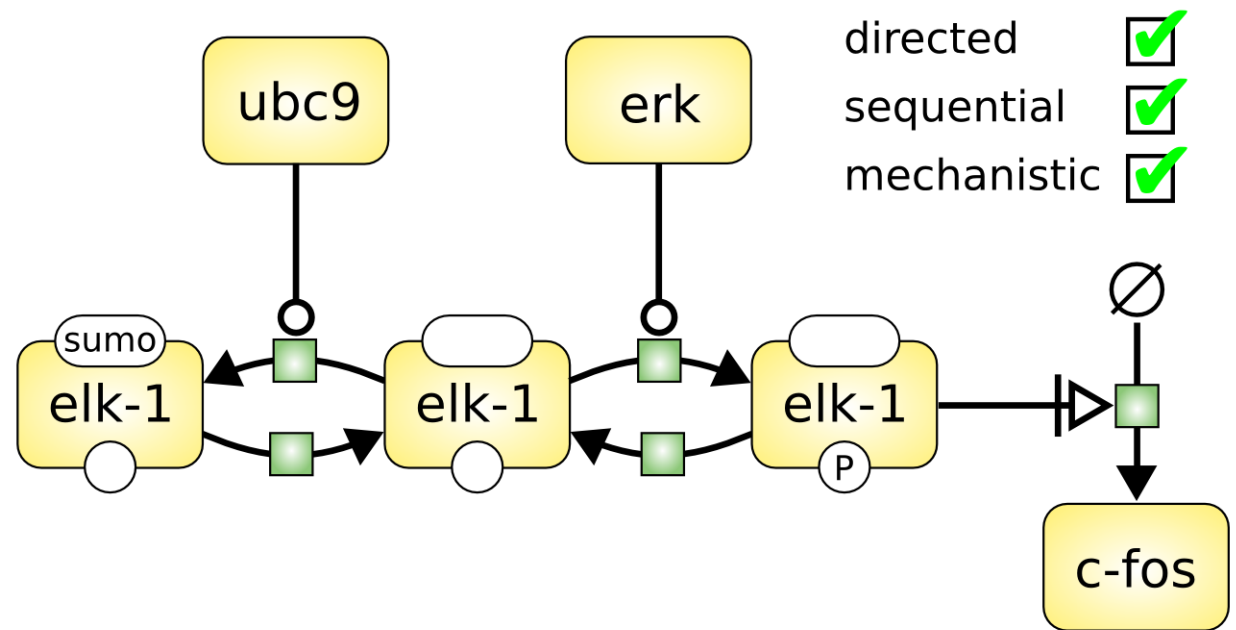
A biochemical reaction is a process



→ Reconstruction of state variable evolution from process descriptions:

- Processes can be combined in ODEs (for deterministic simulations); transformed in propensities (for stochastic simulations)
- Systems can be reconfigured quickly by adding or removing a process

SBGN Process Descriptions



- Process modelling
- Biochemistry, Metabolic networks
- Generally within “**closed world**”
- Subjected to combinatorial explosion

Open world

Anything not explicitly stated is unknown

Failure to observe does not imply non-existence

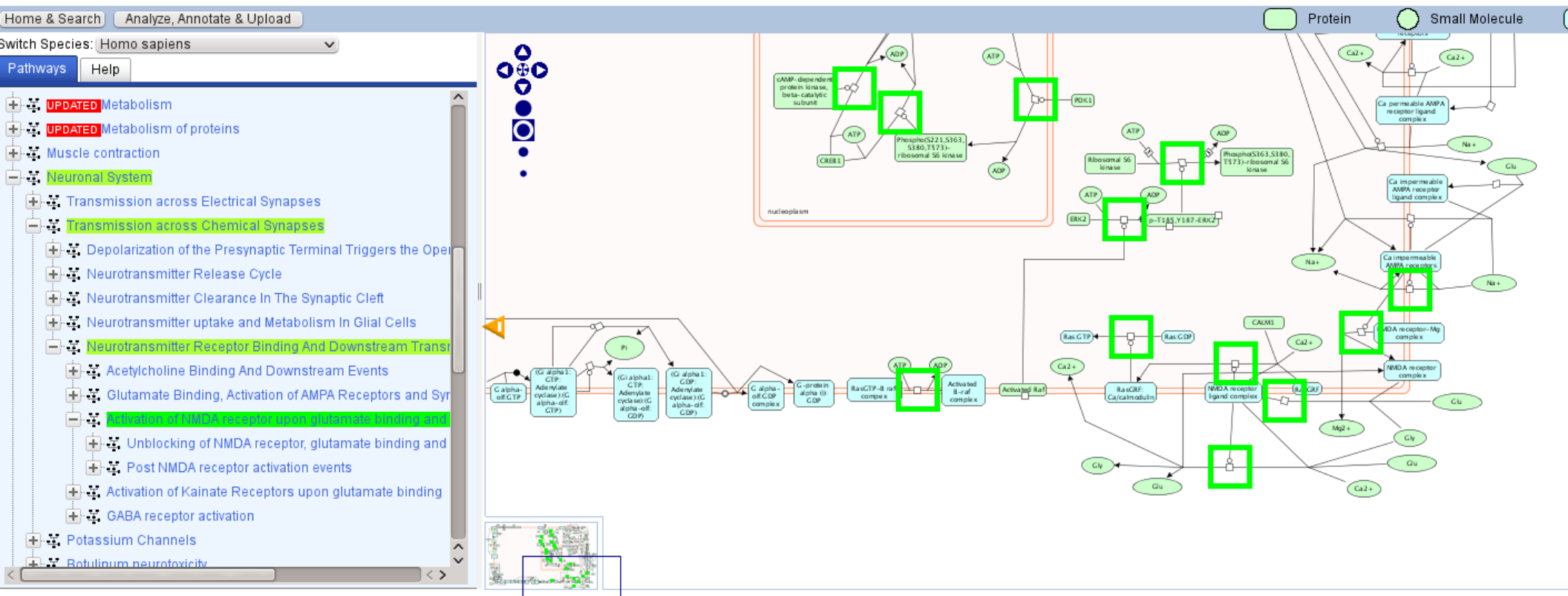
New pieces of knowledge do not affect prior pieces

Closed world

Anything not explicitly stated does not exist

Failure to observe implies non-existence

New pieces of knowledge might change the meaning of prior pieces



Stable identifier	REACT_20563.2
Authored	Mahajan, SS, 2009-10-29
Reviewed	Tukey, D, 2009-11-17

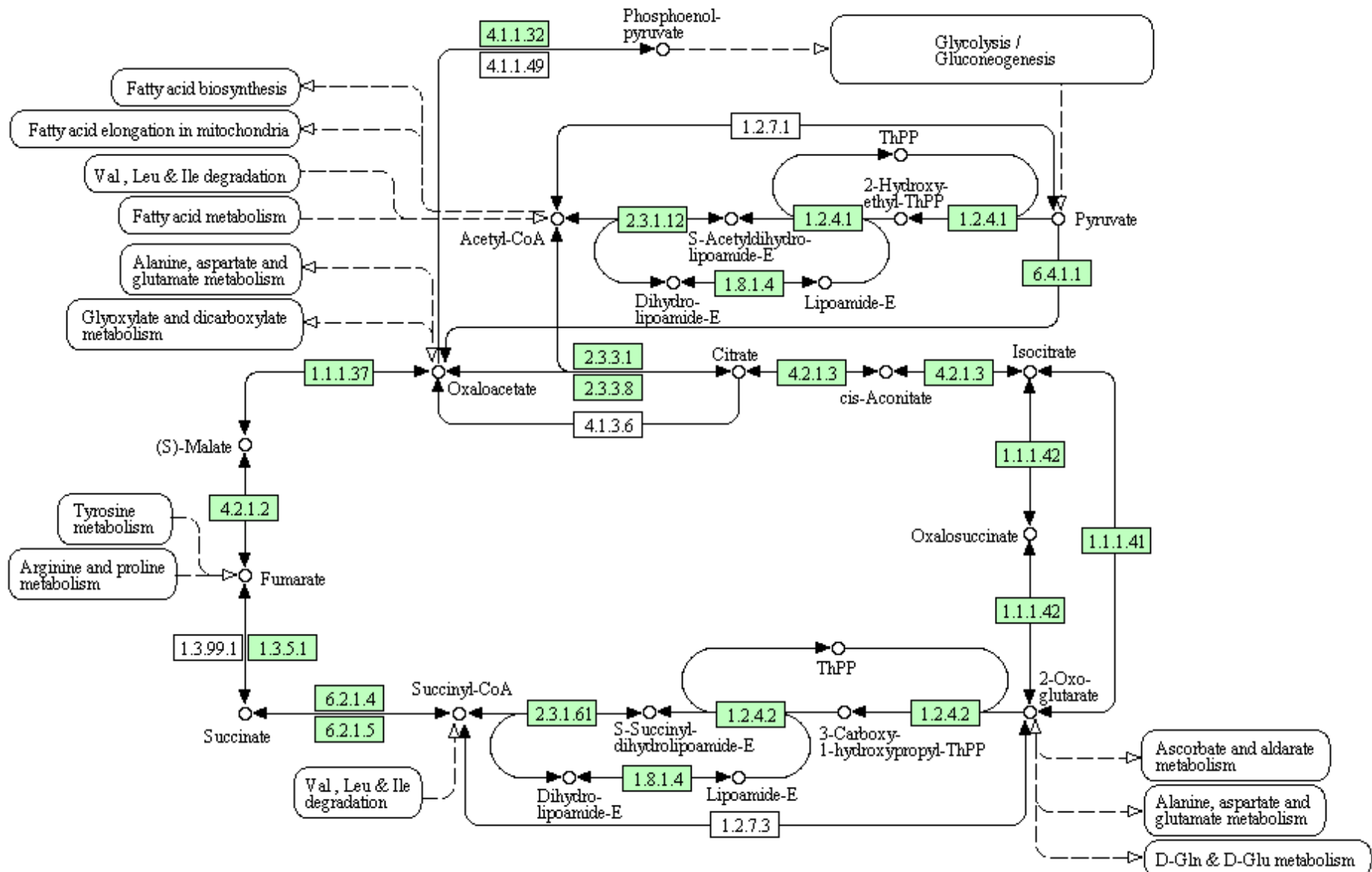
NMDA receptors are a subtype of ionotropic glutamate receptors that are specifically activated by a glutamate agonist N-methyl-D-aspartate (NMDA). Activation of NMDA receptor involves opening of the ion channel that allows the influx of Ca^{2+} . NMDA receptors synaptic strength and are predominantly involved in the synaptic plasticity that pertain to learning and memory. A unique feature of NMDA receptor unlike other glutamate receptors is the requirement of dual activation of the NMDA receptor, which require both glutamate and glycine for activation. At resting membrane potential the NMDA receptors are blocked by Mg^{2+} . The voltage dependent Mg^{2+} block is relieved upon depolarization of the post-synaptic membrane. The ligand dependent activation of the NMDA receptor requires co-activation by glutamate and glycine. NMDA receptors are coincidence detector, and are activated only if there is simultaneous activation of both pre and post-synaptic cell. Upon activation NMDA receptors allow the influx of Ca^{2+} that initiates various molecular signaling cascades that lead to learning and memory.

Organism	Homo sapiens
Cellular compartment	extracellular region GO plasma membrane GO cytoplasm GO nucleoplasm GO

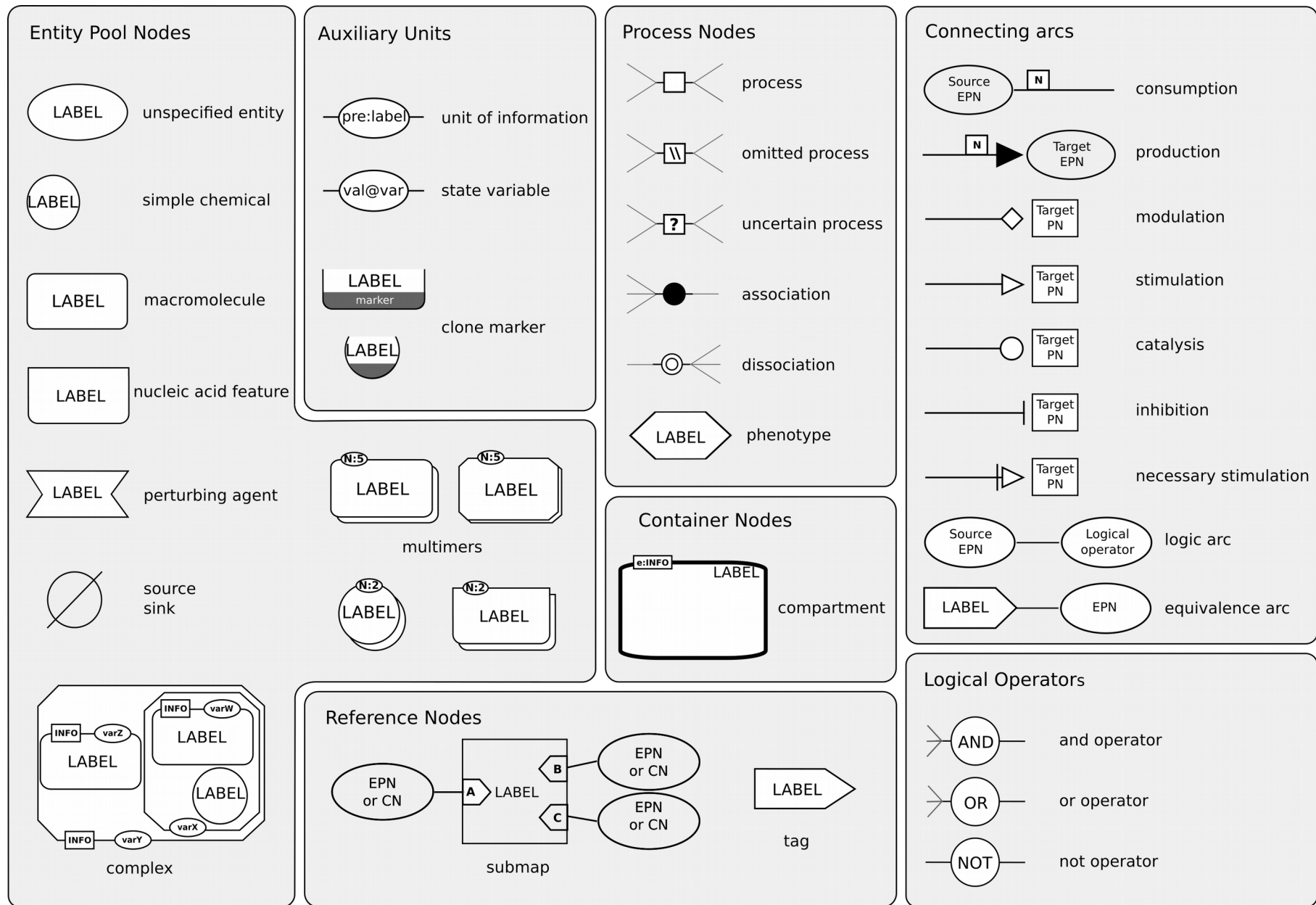
References	Cohen, S, Greenberg, ME <i>Communication between the synapse and the nucleus in neuronal development, plasticity, and disease</i> 2008 Annu Rev Cell Dev Biol PubMed Activation of NMDA receptor upon glutamate binding and postsynaptic events [Dictyostelium discoideum] Activation of NMDA receptor upon glutamate binding and postsynaptic events [Schizosaccharomyces pombe] Activation of NMDA receptor upon glutamate binding and postsynaptic events [Saccharomyces cerevisiae] Activation of NMDA receptor upon glutamate binding and postsynaptic events [Caenorhabditis elegans]
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CITRATE CYCLE (TCA CYCLE)

“metabolic” part

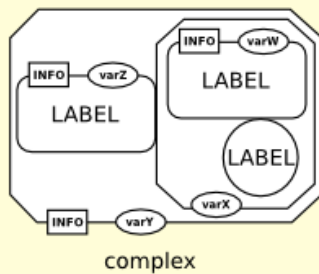
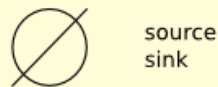
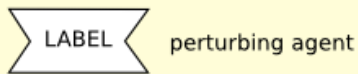
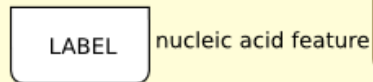
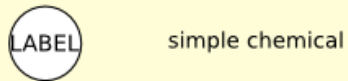
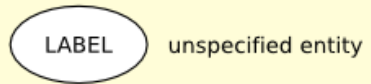


SBGN Process Diagram L1 reference card

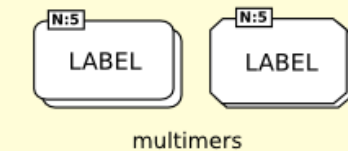
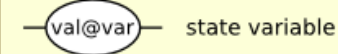
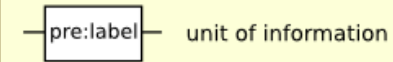


Entity Pool Nodes

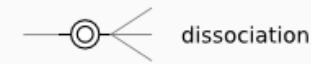
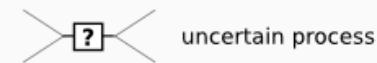
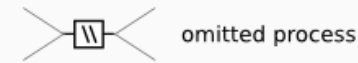
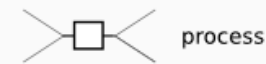
Entity Pool Nodes



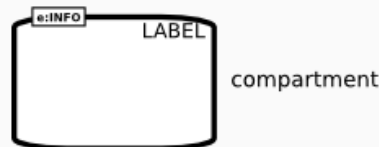
Auxiliary Units



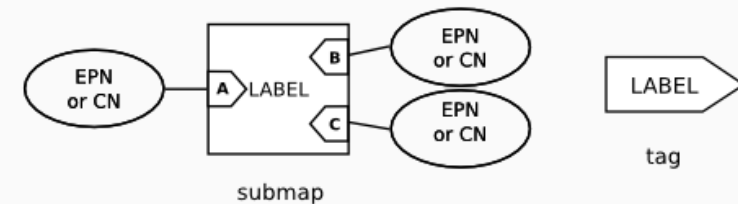
Process Nodes



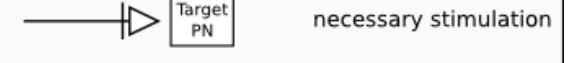
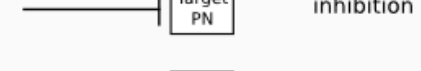
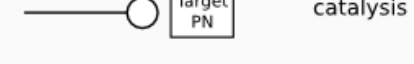
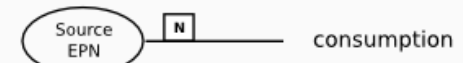
Container Nodes



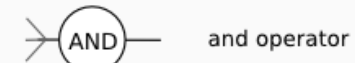
Reference Nodes



Connecting arcs

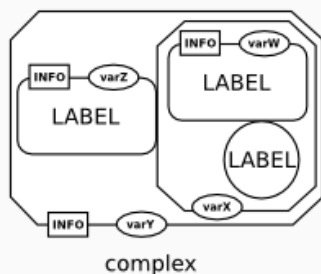
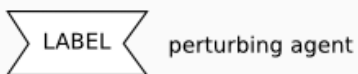
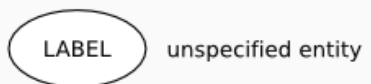


Logical Operators

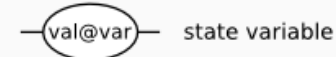
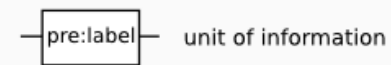


Process Nodes

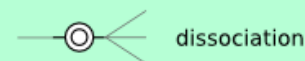
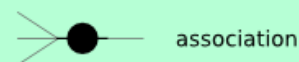
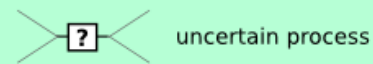
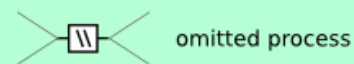
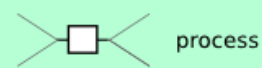
Entity Pool Nodes



Auxiliary Units



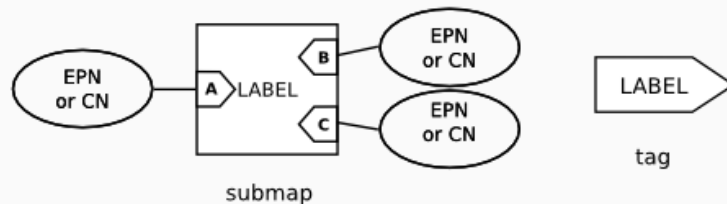
Process Nodes



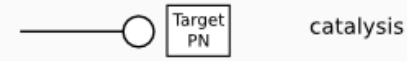
Container Nodes



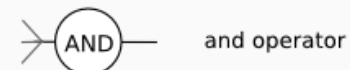
Reference Nodes



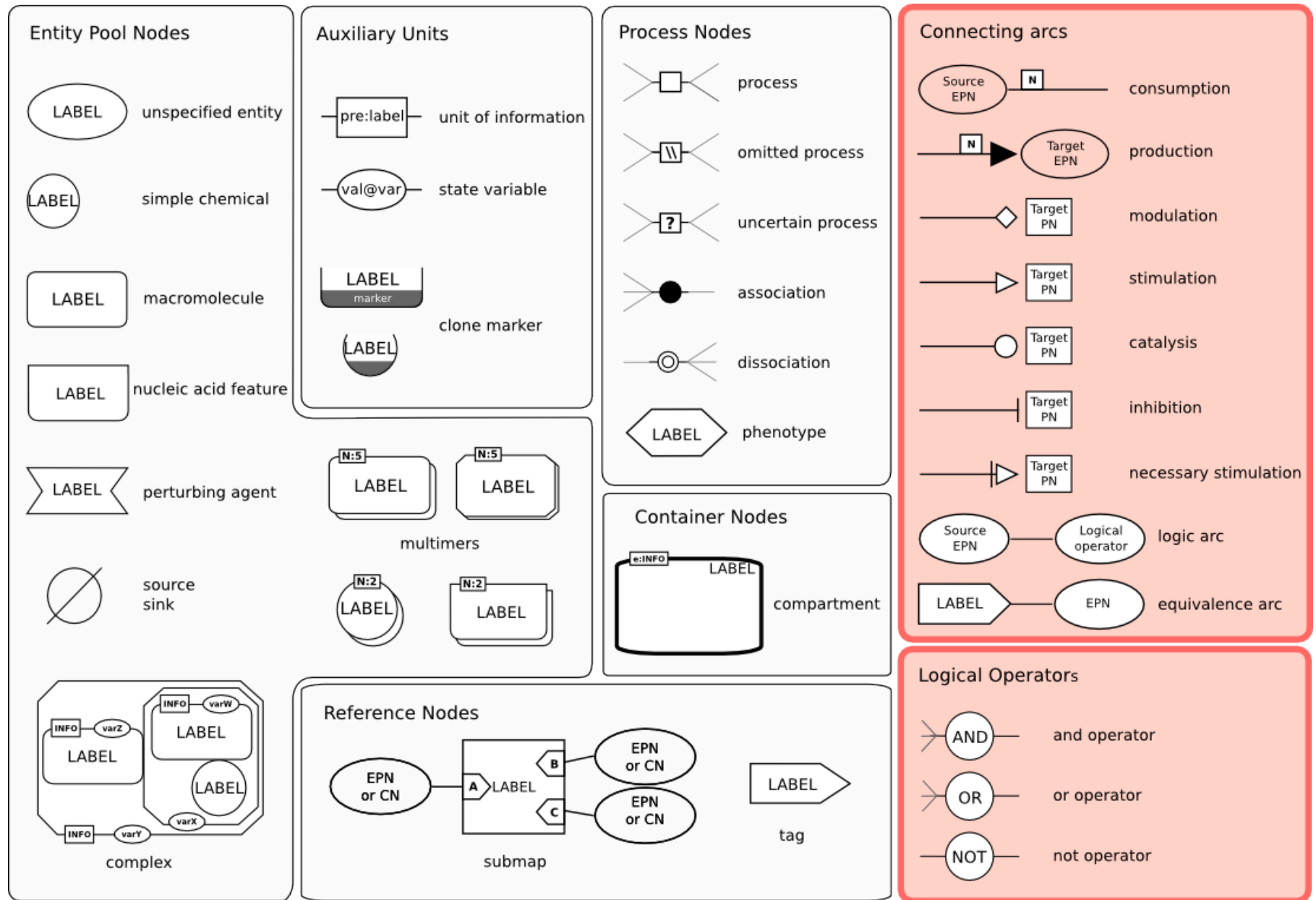
Connecting arcs



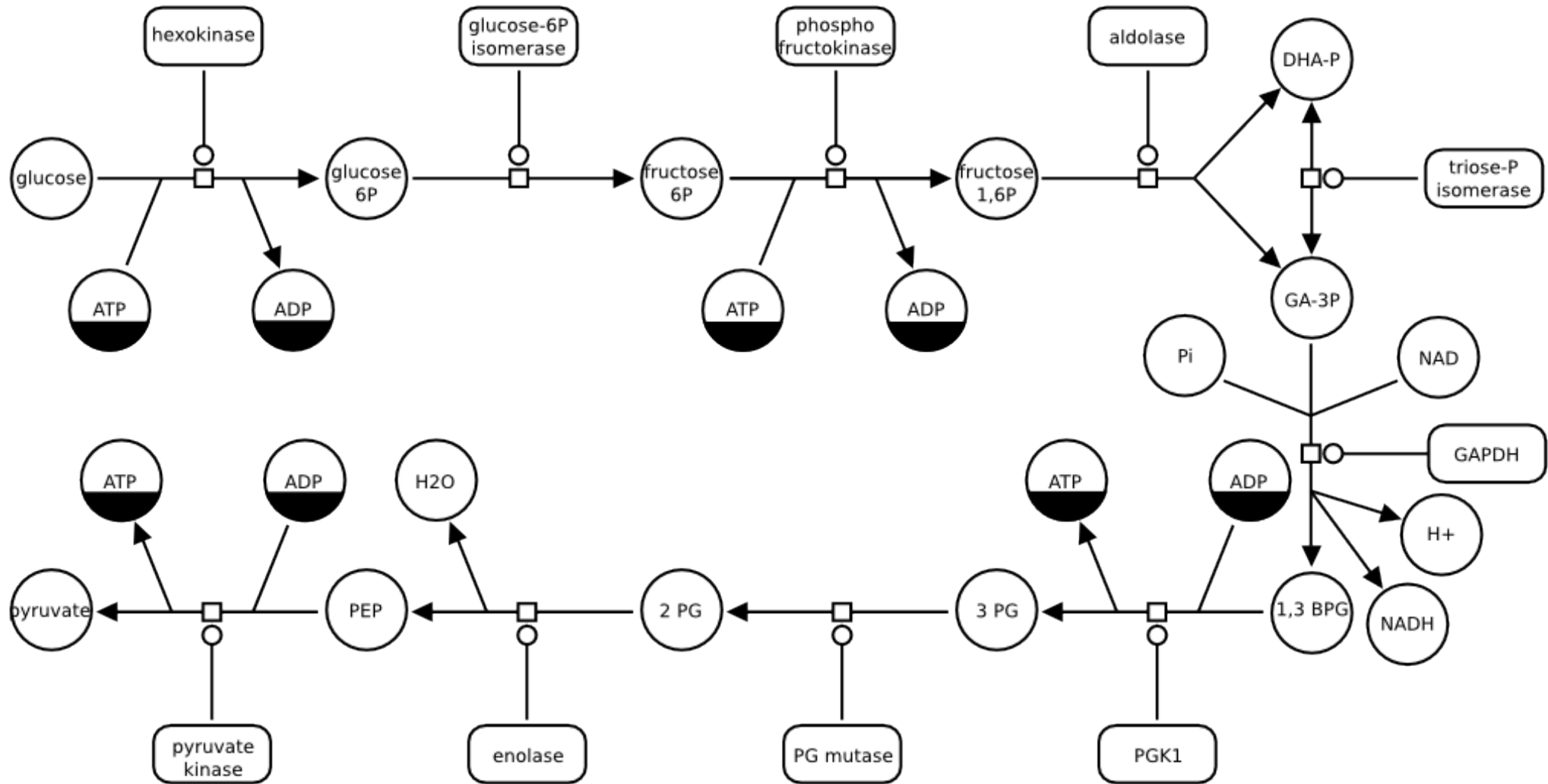
Logical Operators



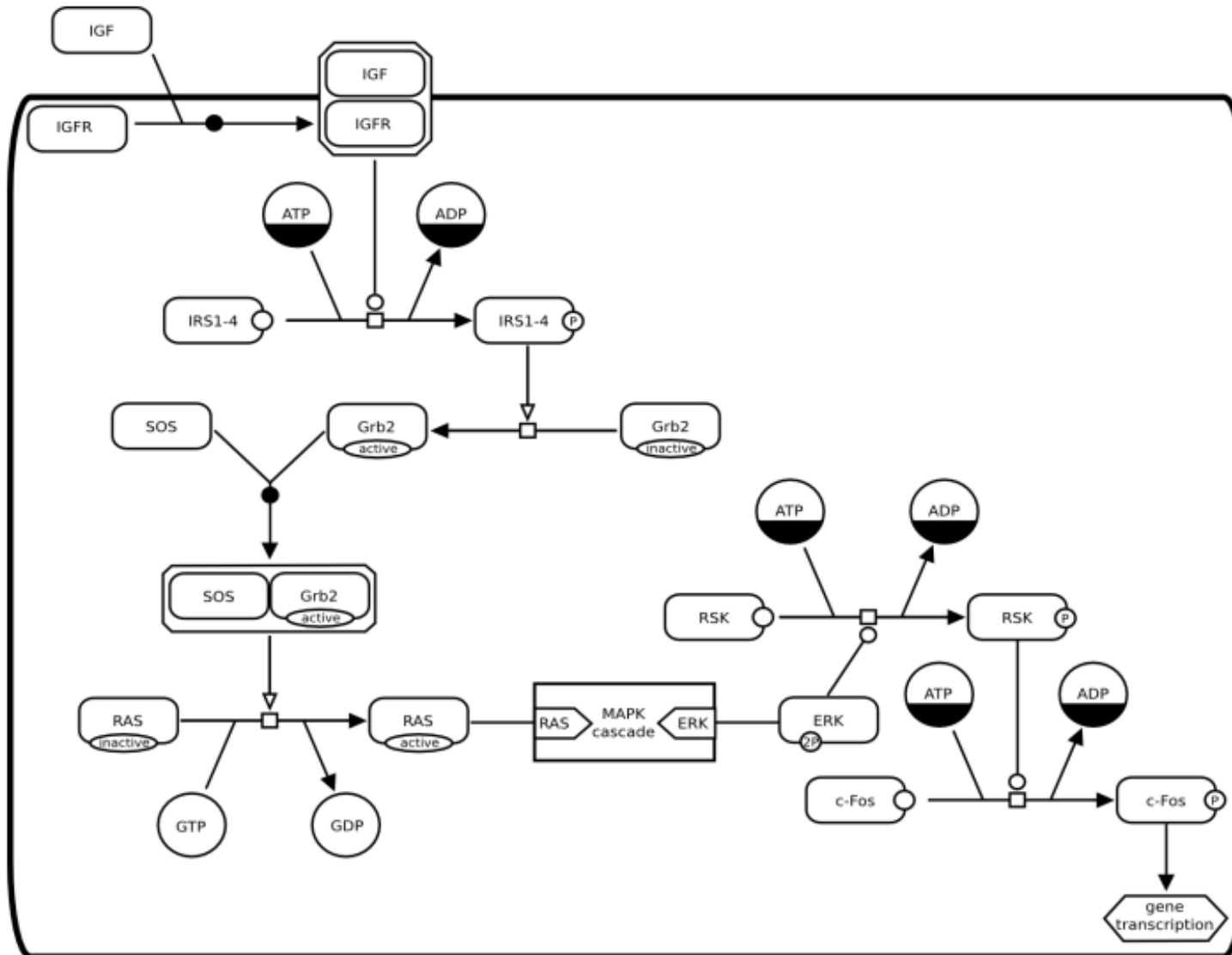
Connecting arcs



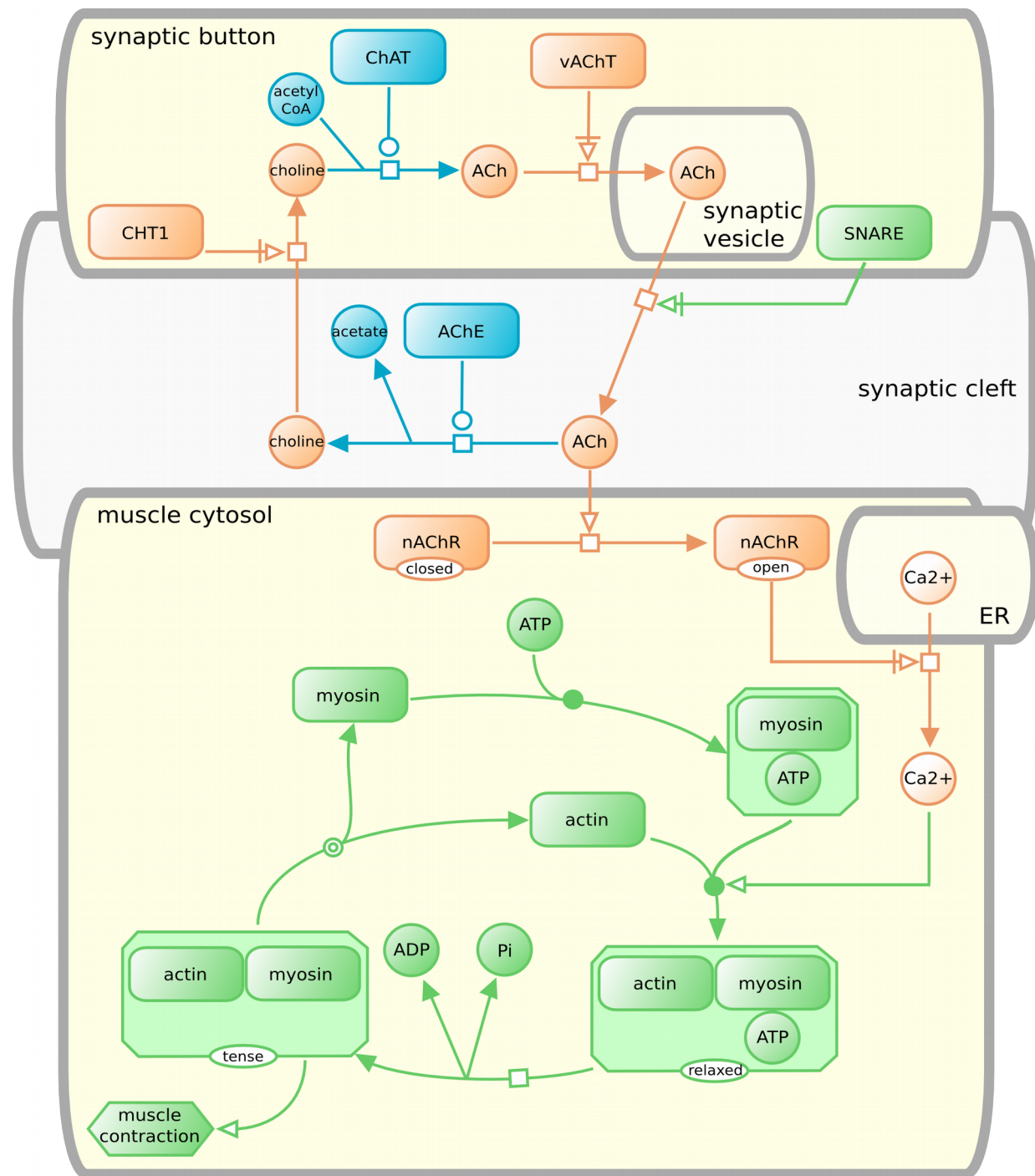
Metabolism in SBGN PD



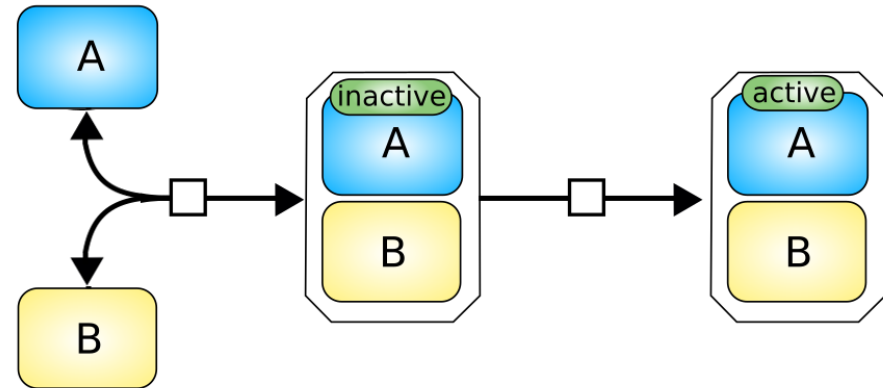
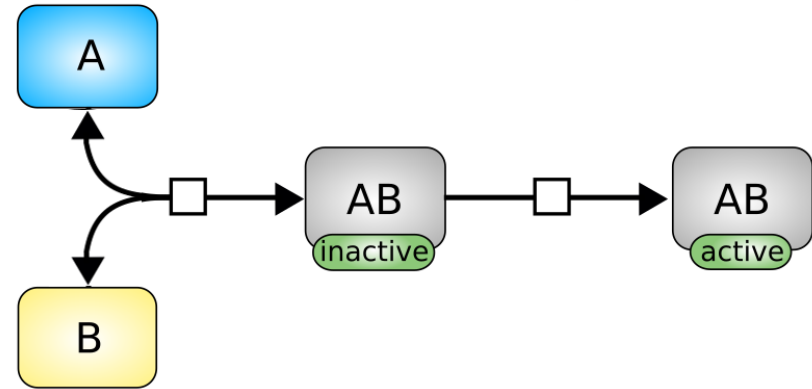
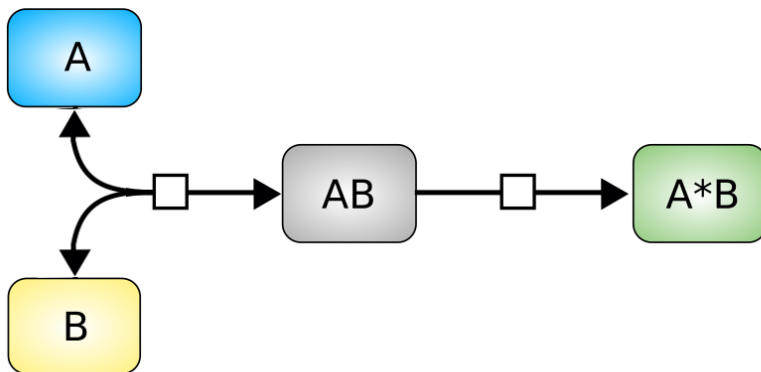
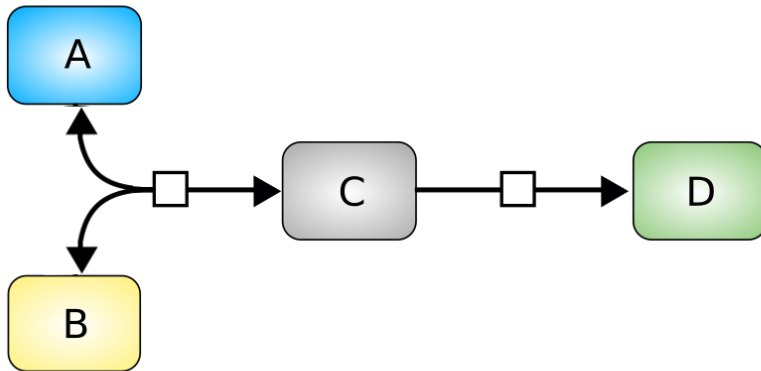
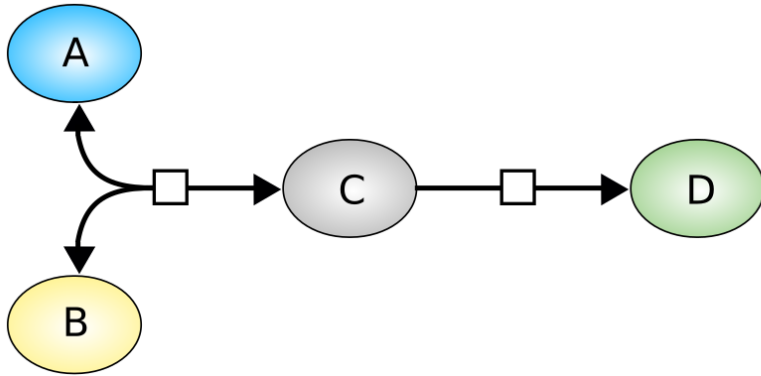
Signalling in SBDG PD



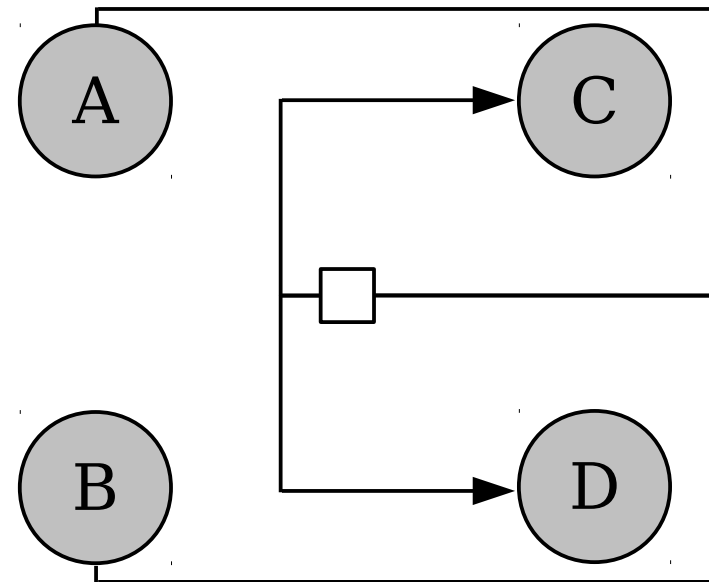
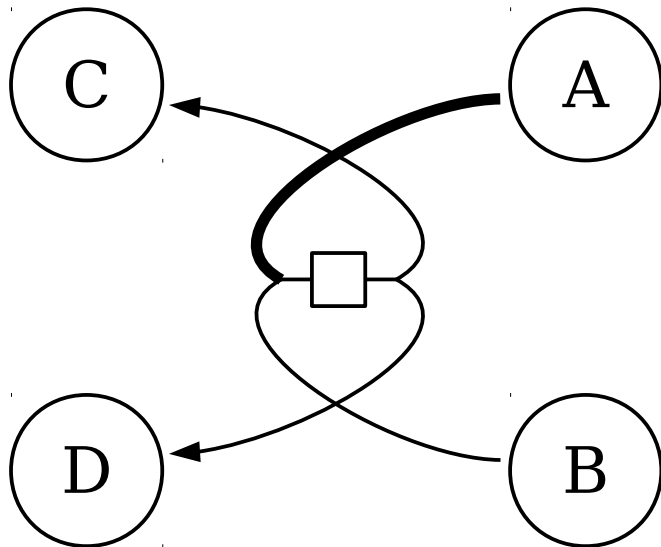
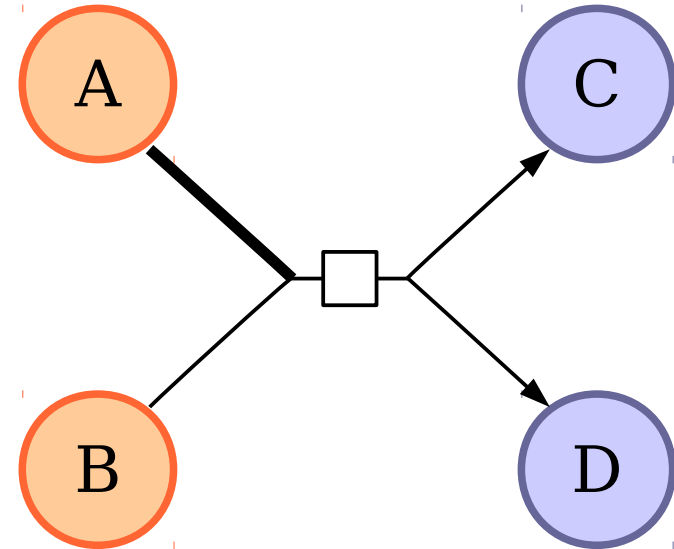
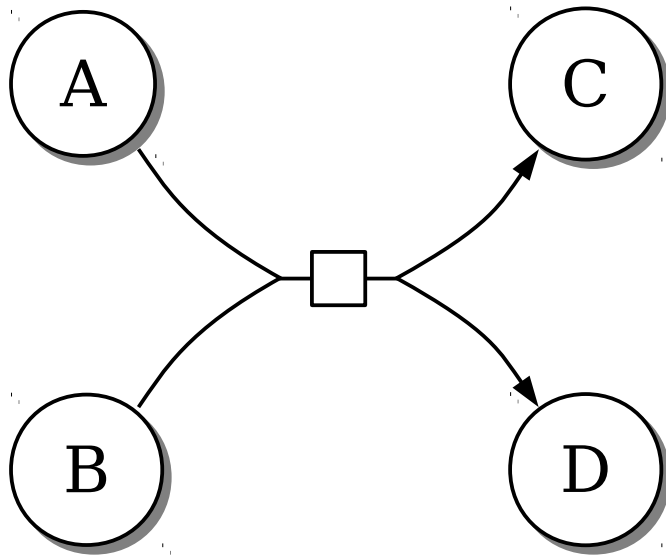
Multicellular processes



Variable granularity

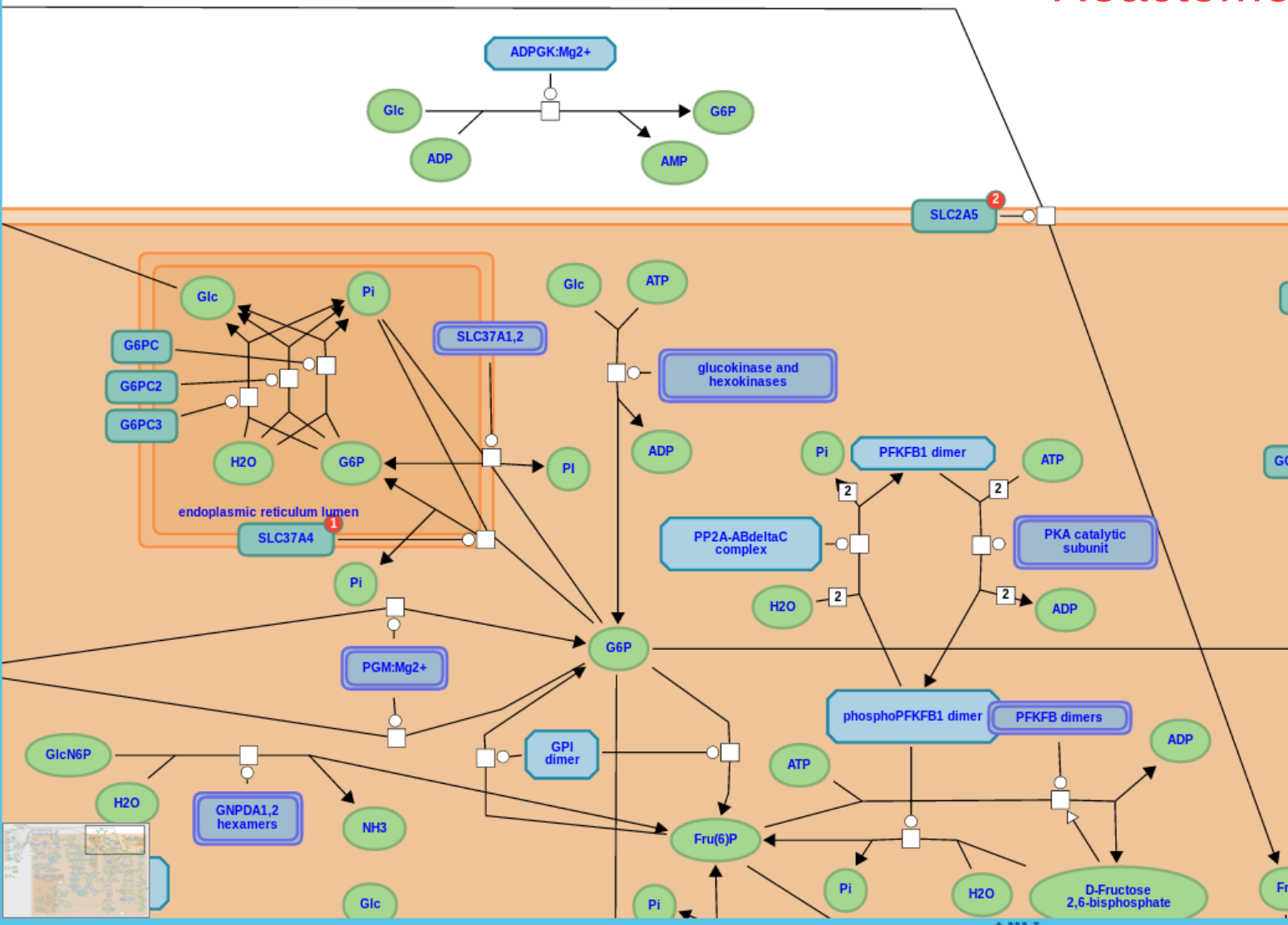


All those diagrams are identical



Event Hierarchy:

- Cell Cycle
- Cell-Cell communication
- Cellular responses to external stimuli
- Chromatin organization
- Circadian Clock
- Developmental Biology
- Digestion and absorption
- Disease
- DNA Repair
- DNA Replication
- Extracellular matrix organization
- Gene expression (Transcription)
- Hemostasis
- Immune System
- Metabolism**
 - Metabolism of carbohydrates**
 - Digestion of dietary carbohydrate
 - CH1A hydrolyses chitin
 - CHIT1 hydrolyses CHIT to 3xADGF
 - Hexose transport
 - Glucose metabolism
 - Glycolysis
 - Gluconeogenesis
 - Exchange of alpha-ketoglutarate
 - Glycogen synthesis
 - Glycogen breakdown (glycog
 - ADPGK:Mg2+ phosphorylates G
 - GNPDA1,2 hexamers deaminat
 - BPGM dimer isomerises 1,3BPC
 - Fructose metabolism
 - Lactose synthesis
 - Galactose catabolism
 - Pentose phosphate pathway (he
 - 5-Phosphoribose 1-diphosphate bi
 - Glycosaminoglycan metabolism
 - Catabolism of glucuronate to xylulc
 - Lysosomal oligosaccharide catabo
 - Inositol phosphate metabolism
 - Metabolism of lipids



Description	Molecules	Structures	Expression	Analysis	Downloads
-------------	-----------	------------	------------	----------	-----------

Metabolism of carbohydrates Species: Homo sapiens

Stable Identifier
[R-HSA-71387.5](#)

Summation

These pathways together are responsible for: 1) the extraction of energy and carbon skeletons for biosyntheses from dietary sugars and related molecules; 2) the short-term storage of glucose from pyruvate during extended fasts.

View computationally predicted event in

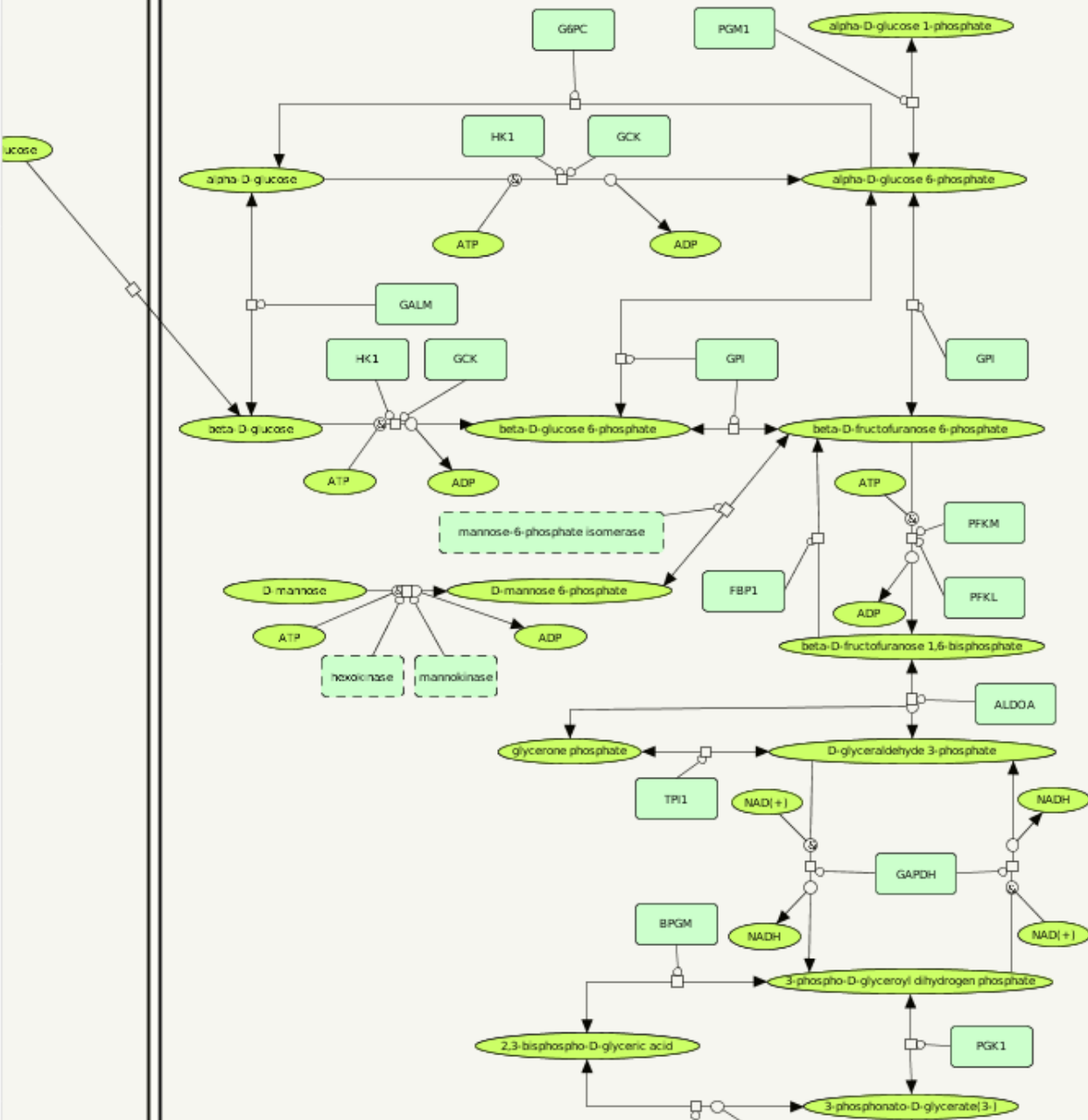
SEARCH:

enter keyword



PERFECT MATCH

Glycolysis



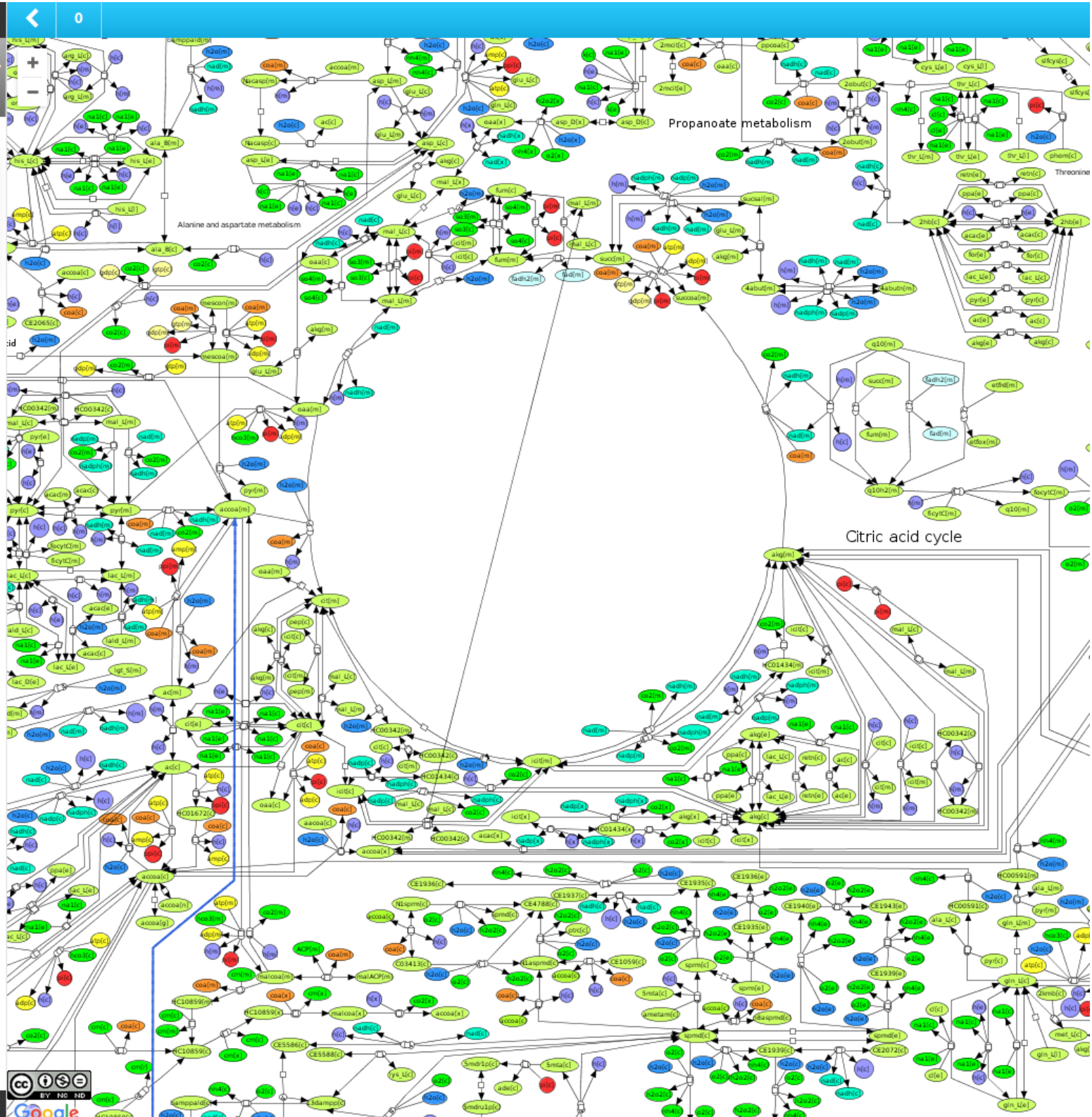
Parkinson's
Disease map

SEARCH:

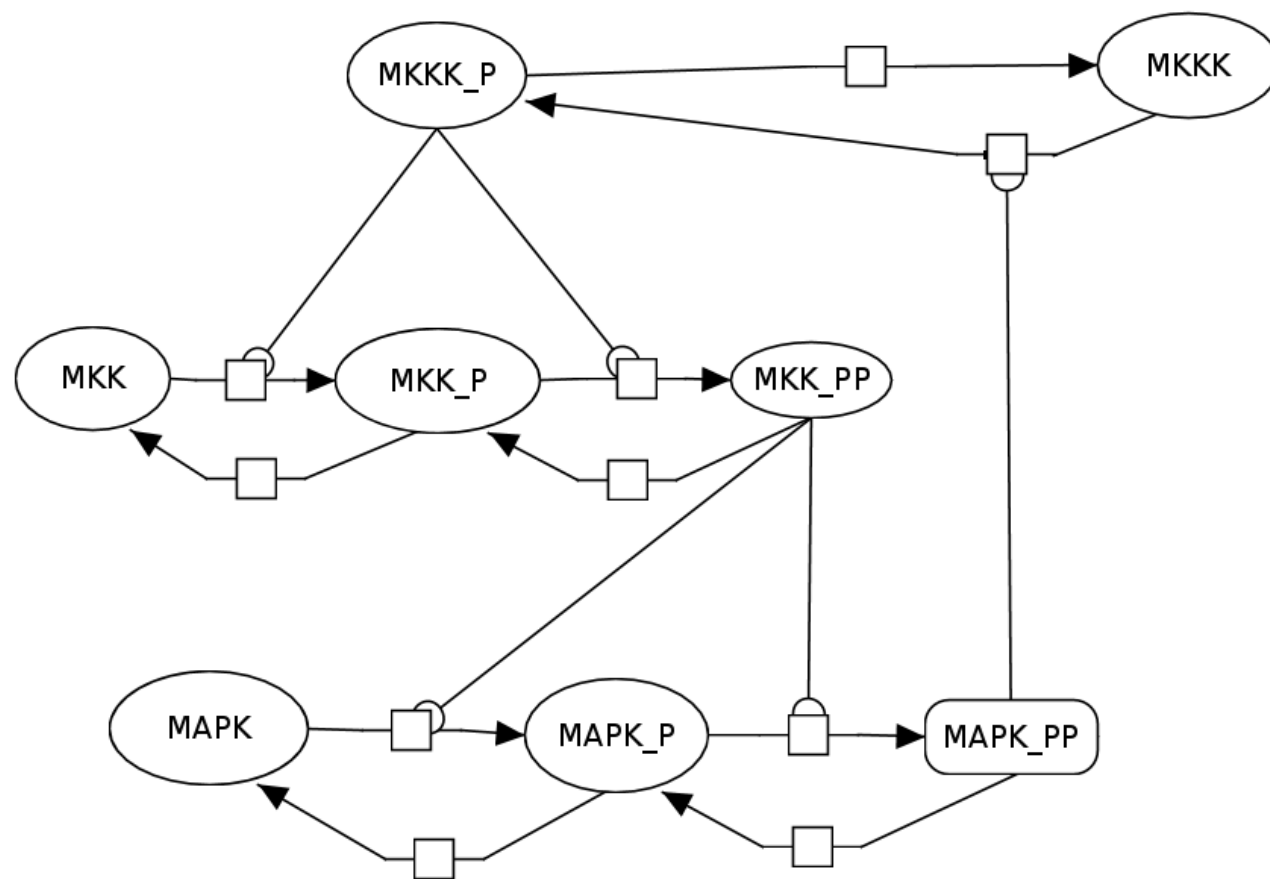
enter keyword



PERFECT MATCH



Recon map



Data Search **SBGN** SBML Legend

Objects Properties Backpage

Language: process description

Entity Pool Nodes

Process Nodes

Arcs

Logical

Containers and annotations

Templates

PathVisio

- ▼ Layer base

The diagram illustrates a signaling pathway for MAPK activation. The nodes and their interactions are as follows:

- MAPK** (top left) is activated by **MAPK-PP** (middle left) via interaction J6.
- MAPK-P** (middle left) is activated by **MAPK-PP** (middle left) via interaction J7.
- MAPK-PP** (middle left) is activated by **MAPKK-PP** (top right) via interaction J8.
- MAPKK-PP** (top right) is activated by **MAPKKK-P** (bottom center) via interaction J9.
- MAPKK-PP** (top right) is activated by **MAPKKK** (bottom left) via interaction J10.
- MAPKK-P** (bottom center) is activated by **MAPKKK** (bottom left) via interaction J1.
- MAPKK-P** (bottom center) is activated by **MAPKKK-P** (bottom center) via interaction J2.
- MAPKK-P** (bottom center) is activated by **MAPKKK** (bottom left) via interaction J3.
- MAPKK-P** (bottom center) is activated by **MAPKKK-P** (bottom center) via interaction J4.
- MAPKK-P** (bottom center) is activated by **MAPKKK** (bottom left) via interaction J5.
- MAPKK-P** (bottom center) is activated by **MAPKKK** (bottom left) via interaction J6.
- MAPKK-P** (bottom center) is activated by **MAPKKK** (bottom left) via interaction J7.
- MAPKK-P** (bottom center) is activated by **MAPKKK** (bottom left) via interaction J8.
- MAPKK-P** (bottom center) is activated by **MAPKKK** (bottom left) via interaction J9.
- MAPKK-P** (bottom center) is activated by **MAPKKK** (bottom left) via interaction J10.

The diagram is enclosed in a yellow rounded rectangle.

Grid Snap OFF

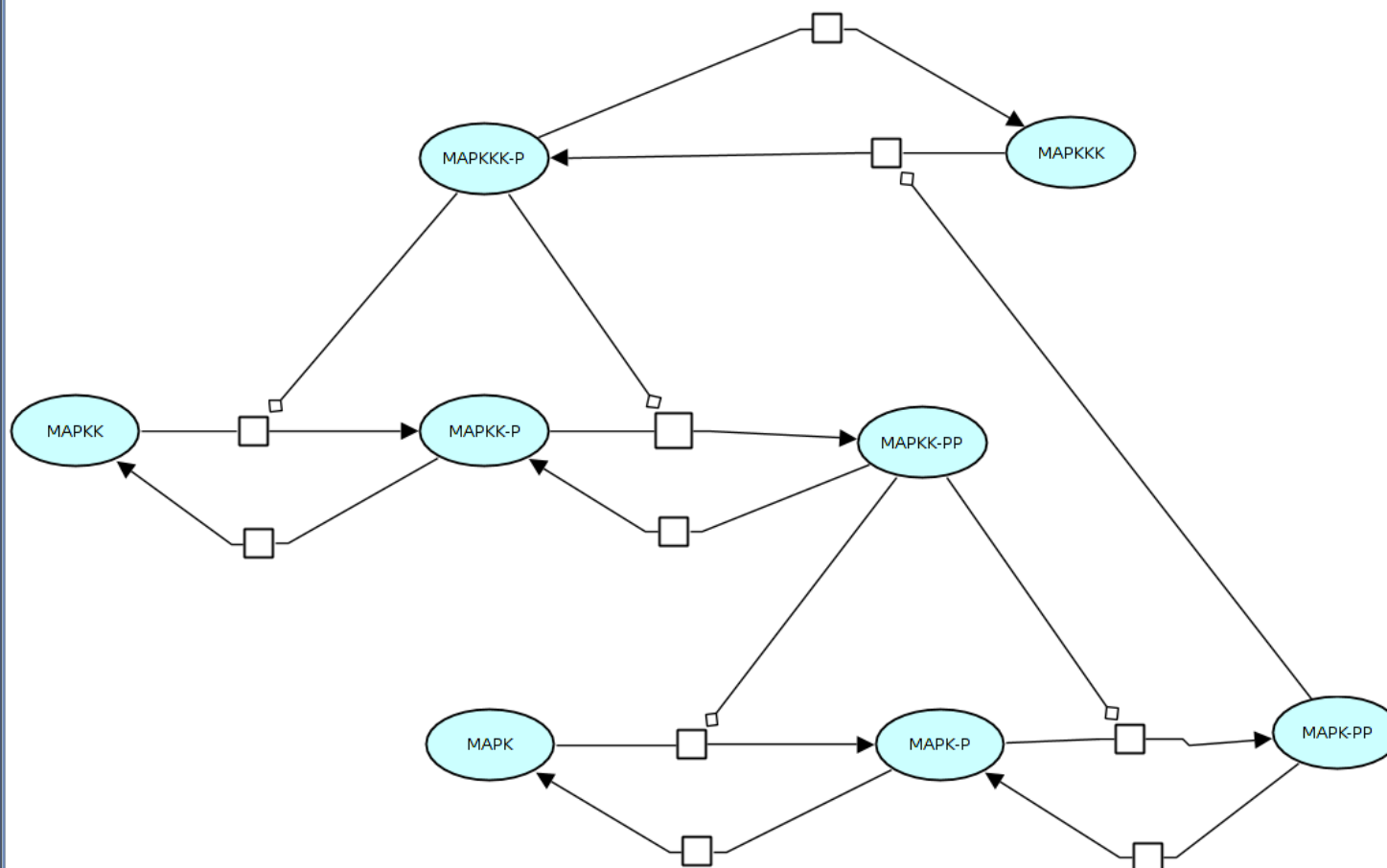
NOTE MIRIAM

Edit Notes

class	id	name	species...	comp...	positi...	included	quan...	initialQuant...	su...	has...	b.c.	c...
PROT...	MK...	MAPKKK		uVol	inside		Conce...	90.0		false	false	fa...
PROT...	MK...	MAPKKK-P		uVol	inside		Conce...	10.0		false	false	fa...
PROT...	MKK	MAPKK		uVol	inside		Conce...	280.0		false	false	fa...
PROT...	MK...	MAPKK-P		uVol	inside		Conce...	10.0		false	false	fa...
PROT...	MK...	MAPKK-PP		uVol	inside		Conce...	10.0		false	false	fa...
PROT...	MK...	MAPKK		uVol	inside		Conce...	280.0		false	false	fa...

CellDesigner

BIOMD0000000010.xml* - view 1



Layout Analysis Attributes
Pathways Experiments SBGN-ED

PD ER AF Bricks Tools Examples

Process Description

Apply Changes Set Type of Map to PD

Clear Glyph Labels Clear Arc Labels

▼ Glyph Label

Entity Pool Nodes

▼ Auxiliary Units

Units of Information

State Variables

Clone Marker ☐ Add

▼ Container Nodes

▼ Reference Nodes

▼ Process Nodes

▼ Connecting Arcs

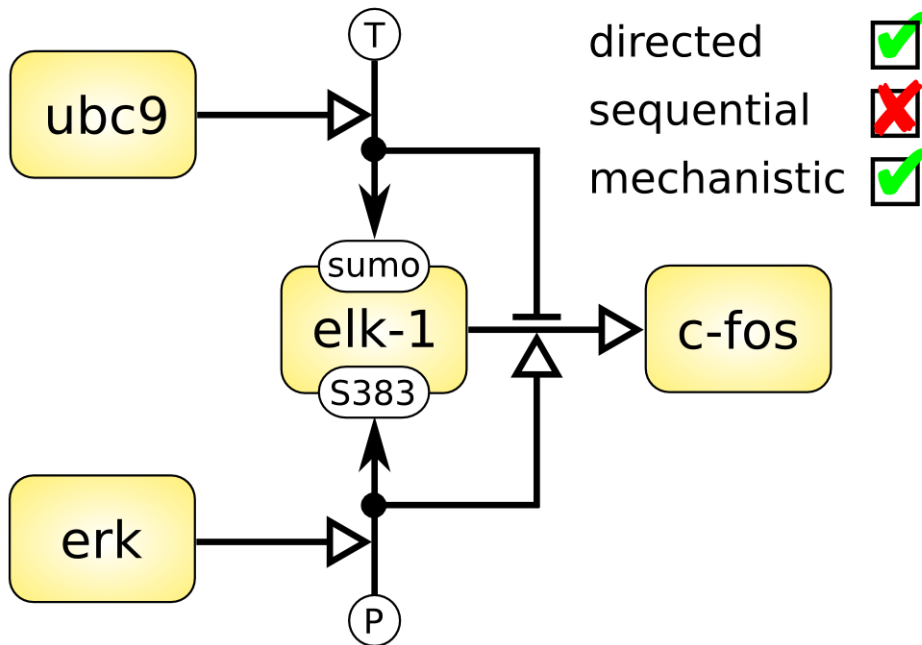


19 nodes 25 edges 345 MB 1 ES

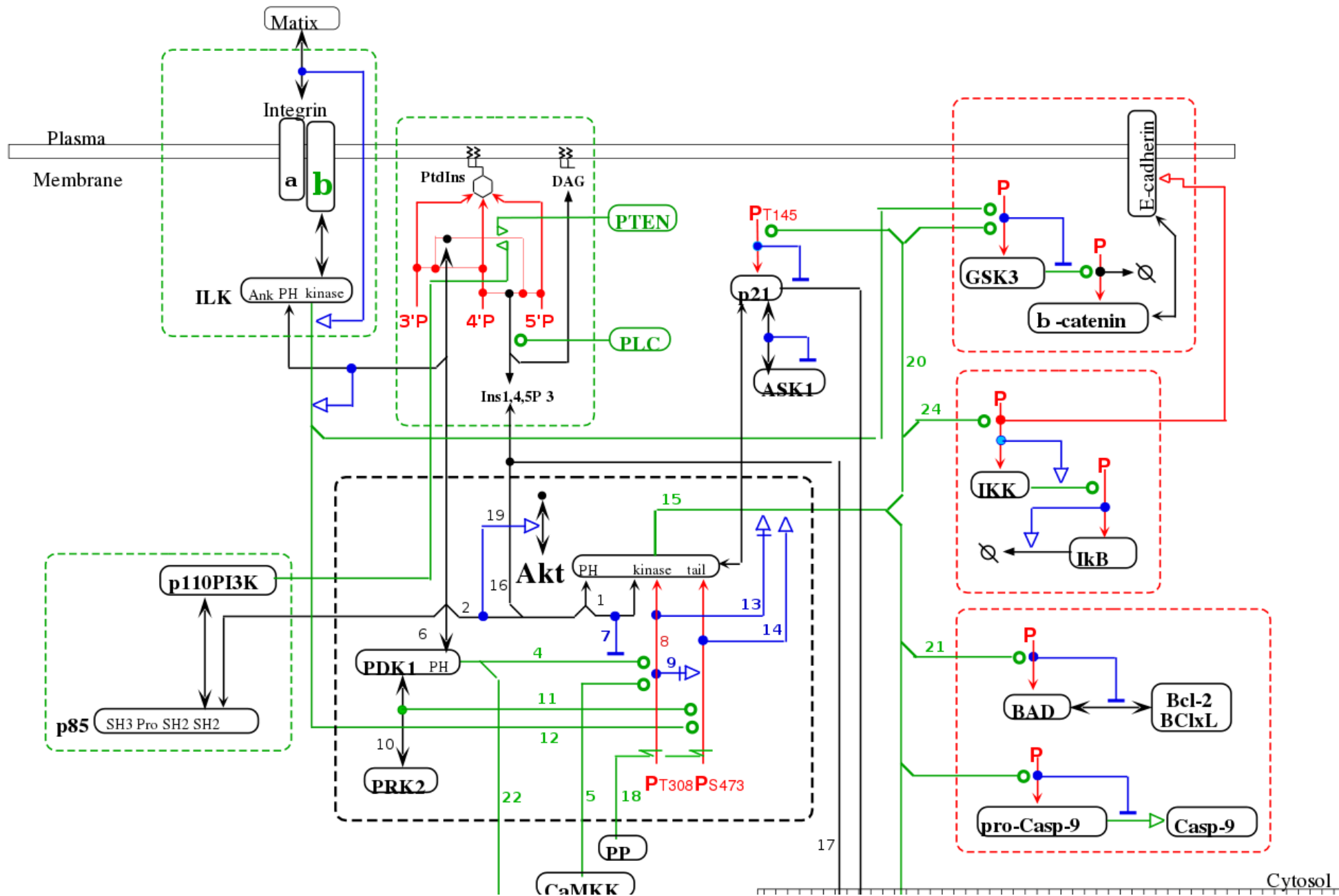
Vanted

Entity Relationships

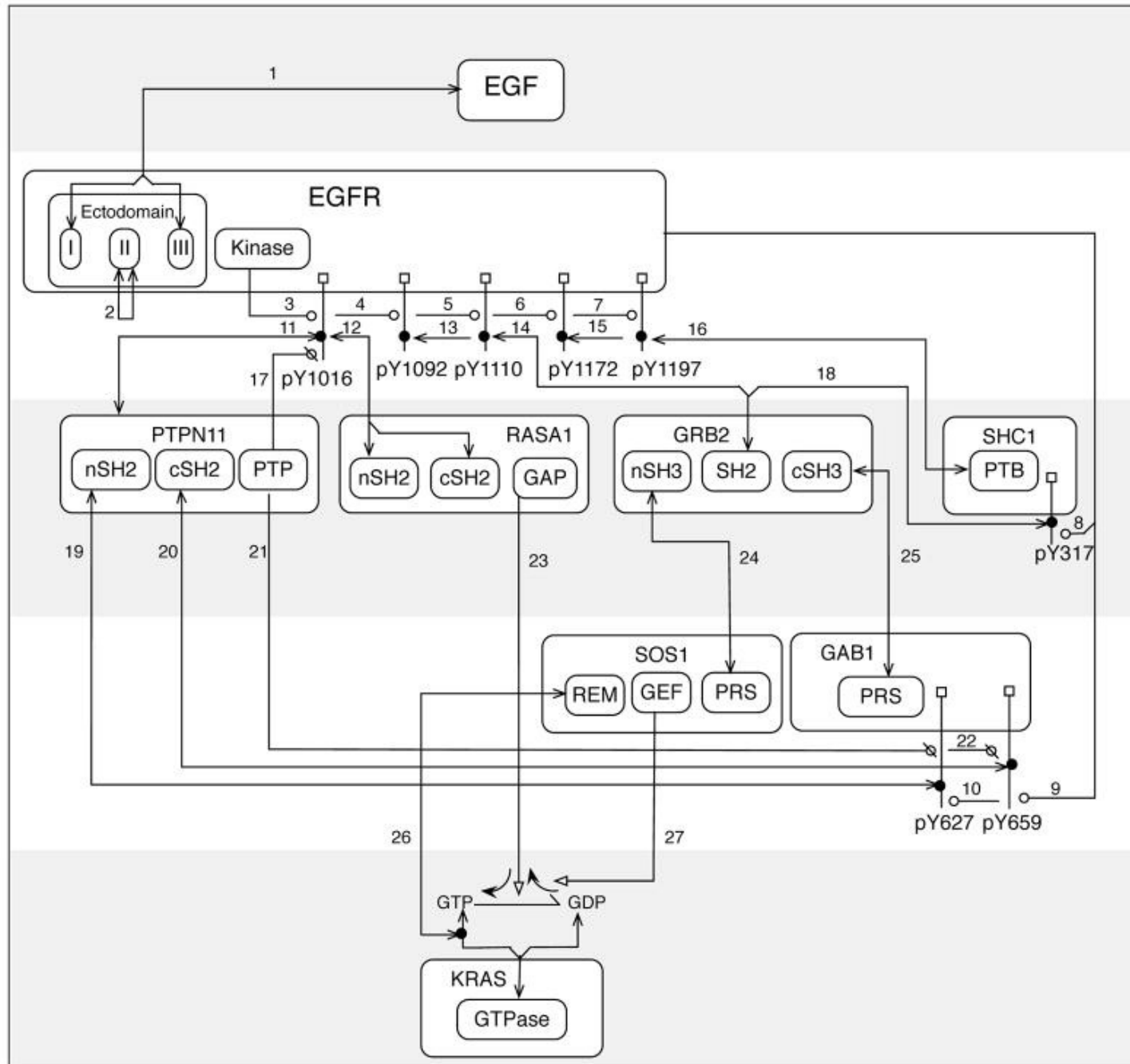
- Rule-based modelling
- Molecular Biology
- “Open world”
- Independent rules: no explosion



Molecular Interaction Maps

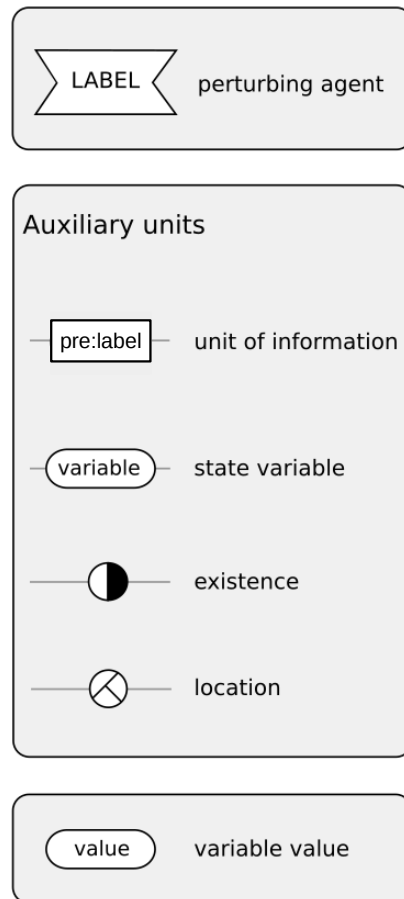
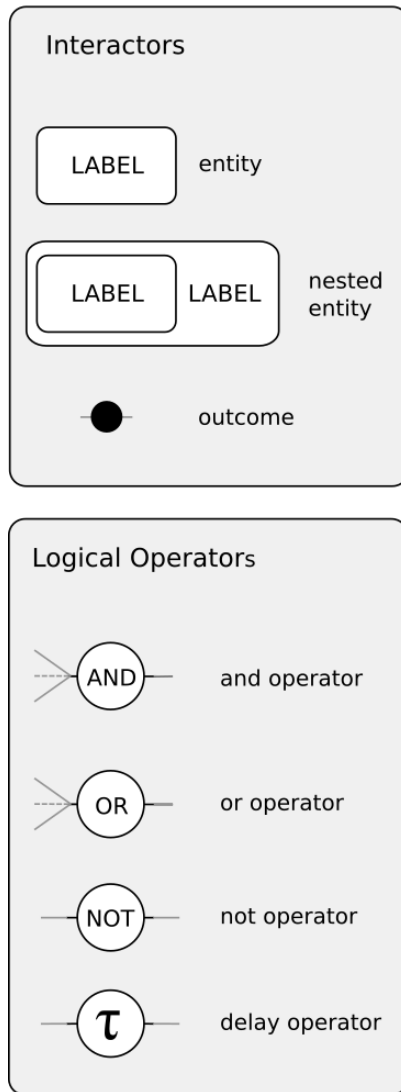


Extended Contact Maps

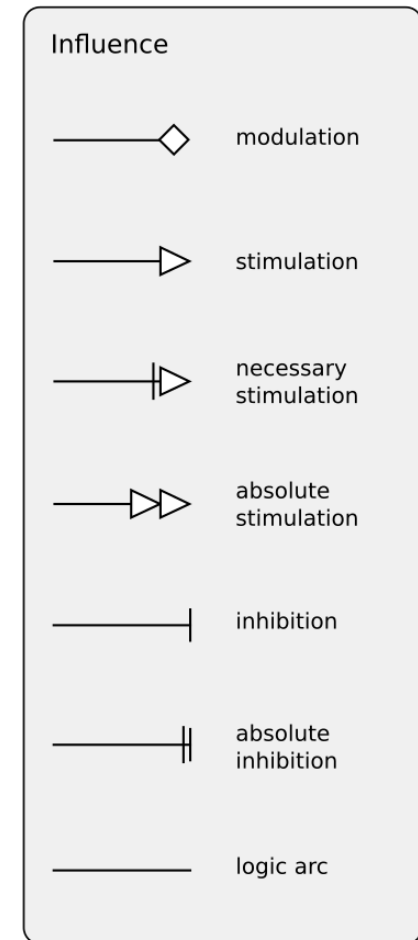
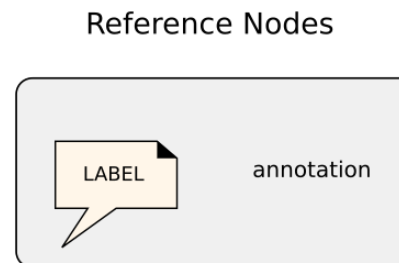
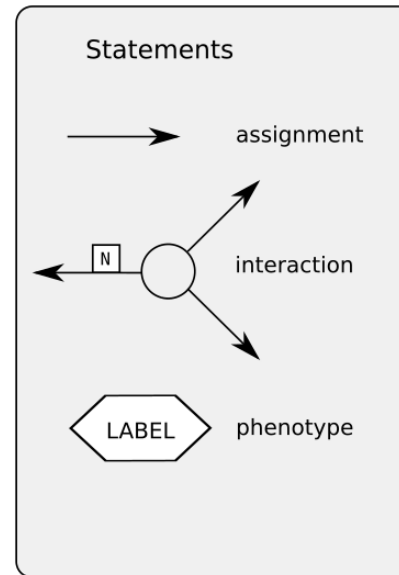


SBGN Entity Relationships L1 reference card

Entity Nodes

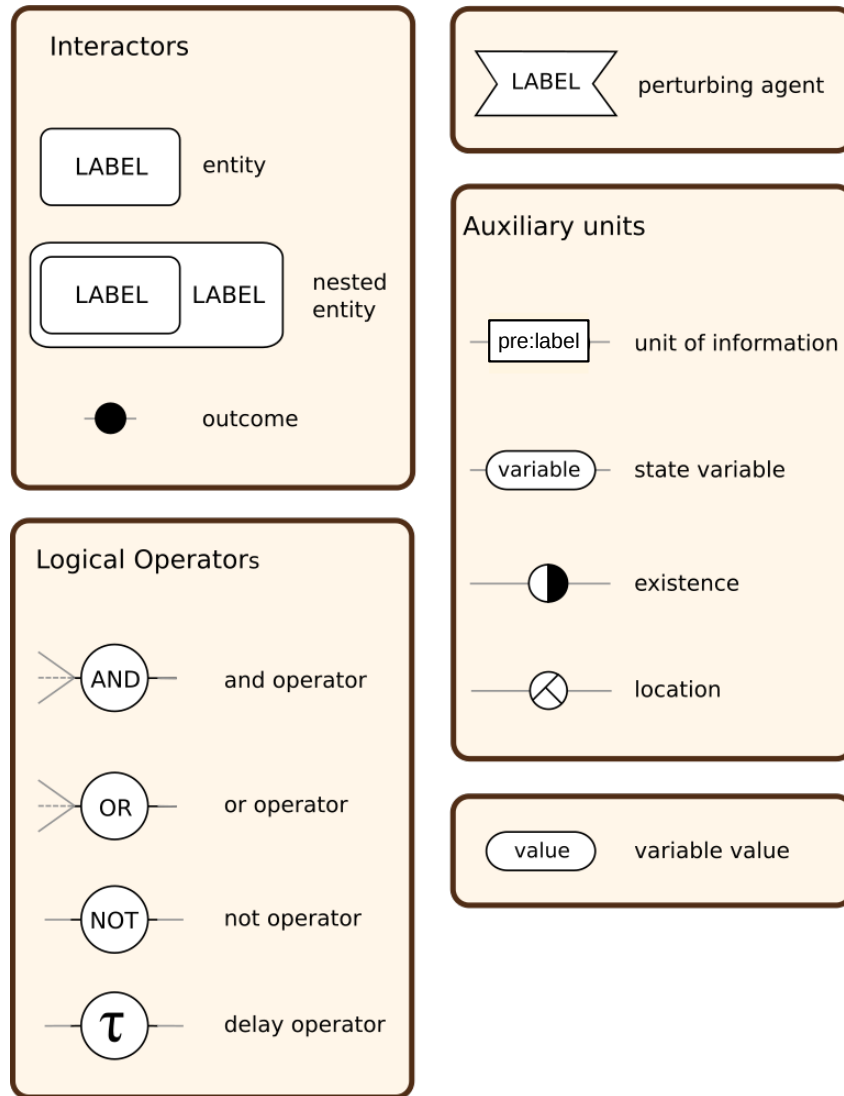


Relationship Nodes

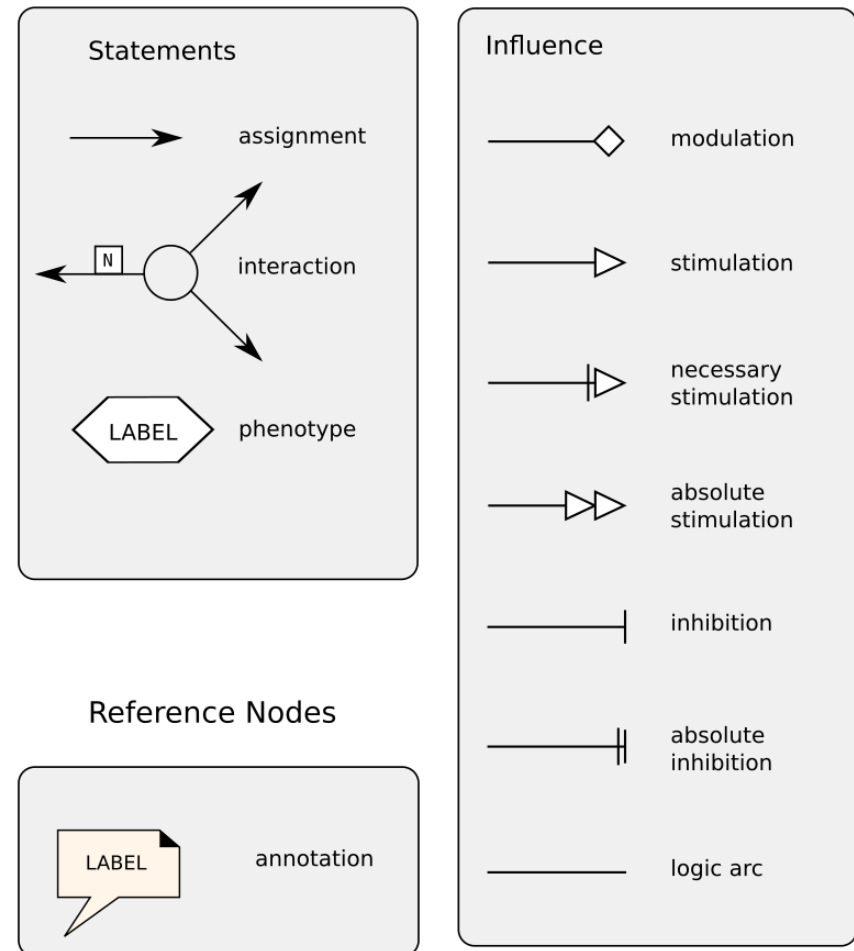


SBGN Entity Relationships L1 reference card

Entity Nodes



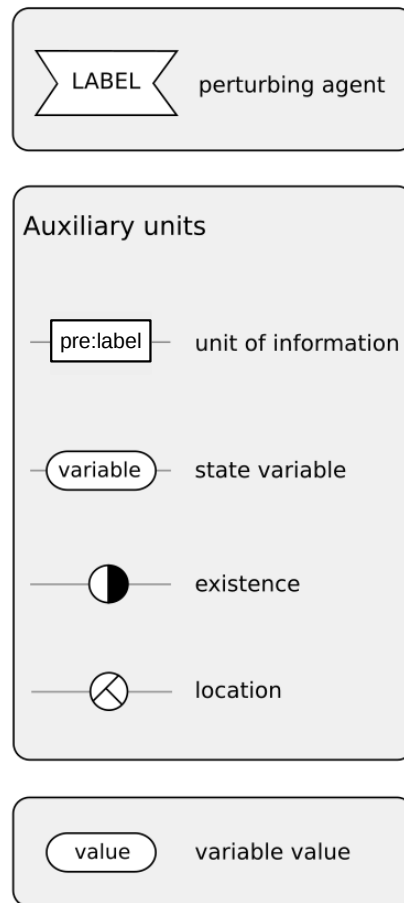
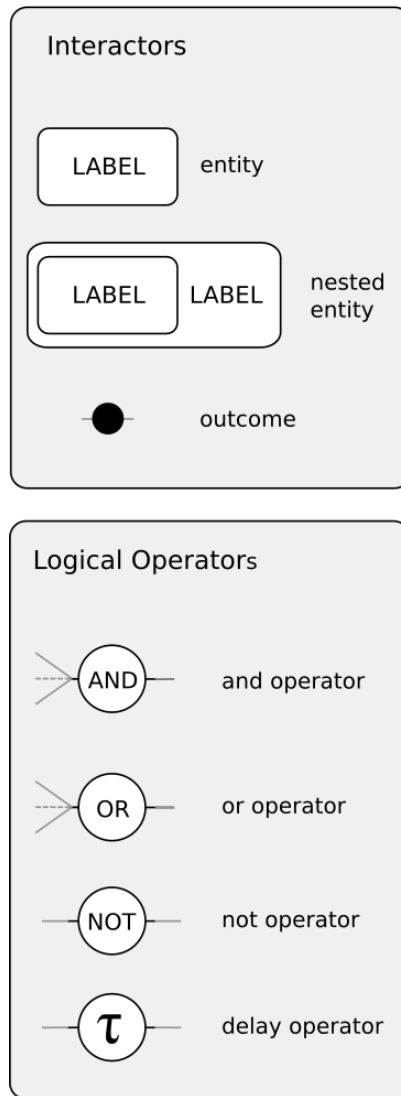
Relationship Nodes



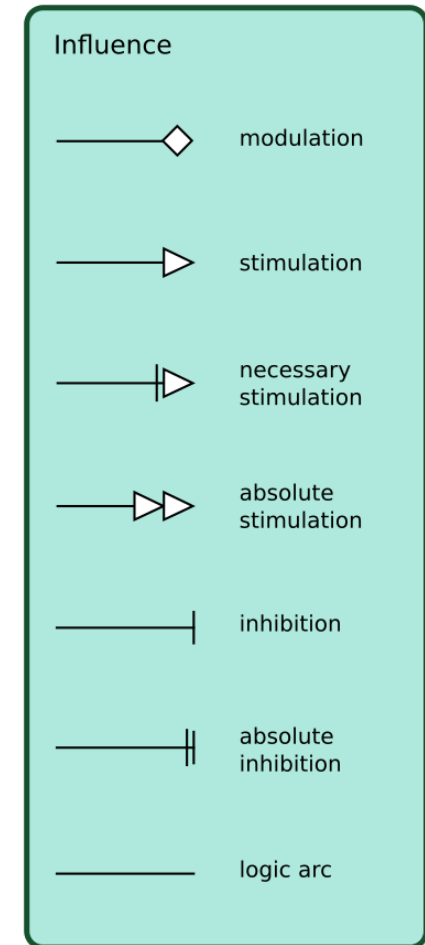
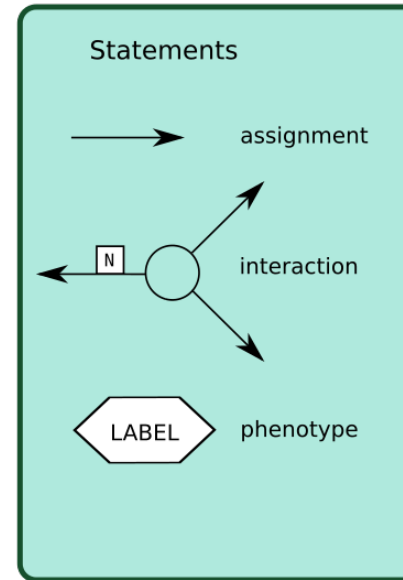
continuants,
things that exists (or not)

SBGN Entity Relationships L1 reference card

Entity Nodes



Relationship Nodes

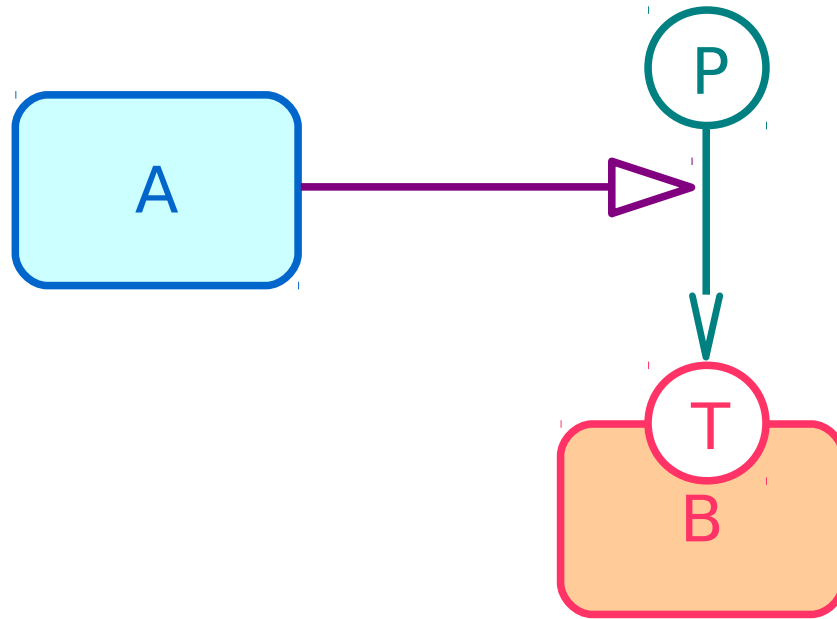


Reference Nodes

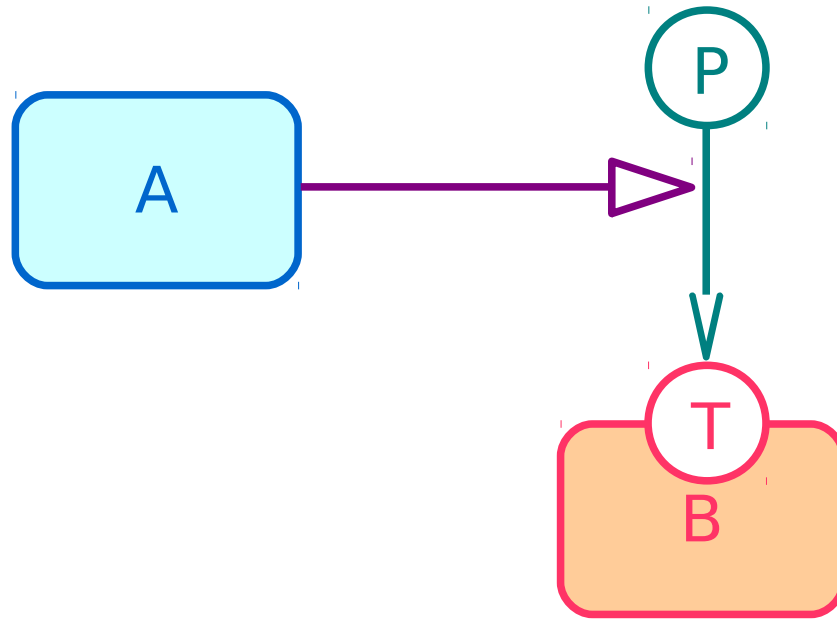


occurrences,
events that may happen (or not)

Entity Relationships can be viewed as rules

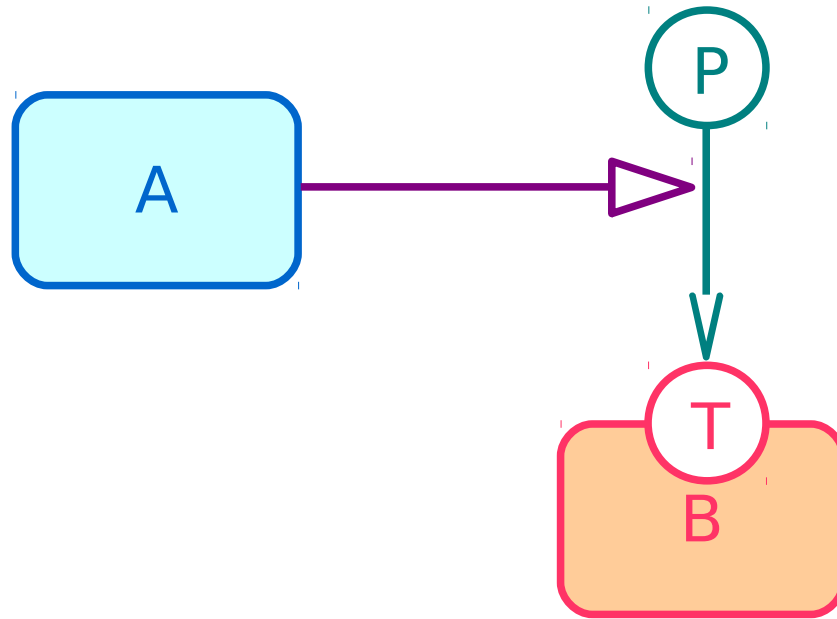


Entity Relationships can be viewed as rules



If **A exists**, the **assignment of the value P** to the **state variable T of B** is **increased**

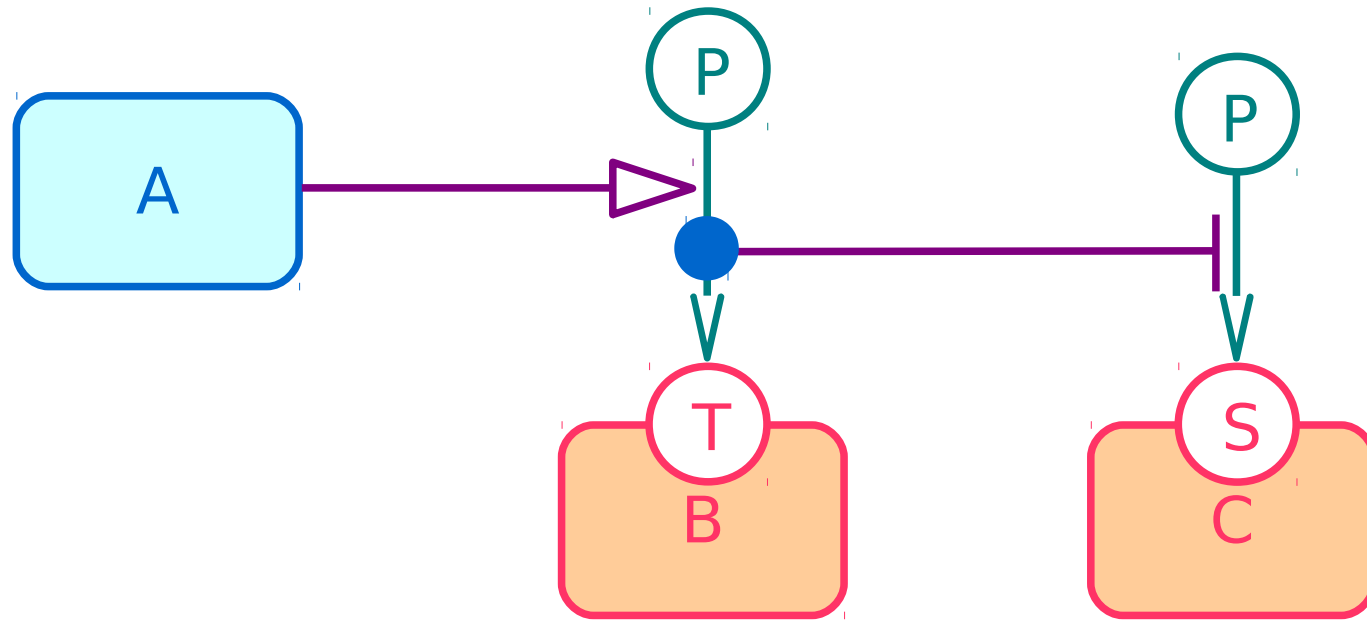
Entity Relationships can be viewed as rules



If **A exists**, the **assignment of the value P** to the **state variable T of B** is **increased**

(**A stimulates** the **phosphorylation** of **B on the threonine**)

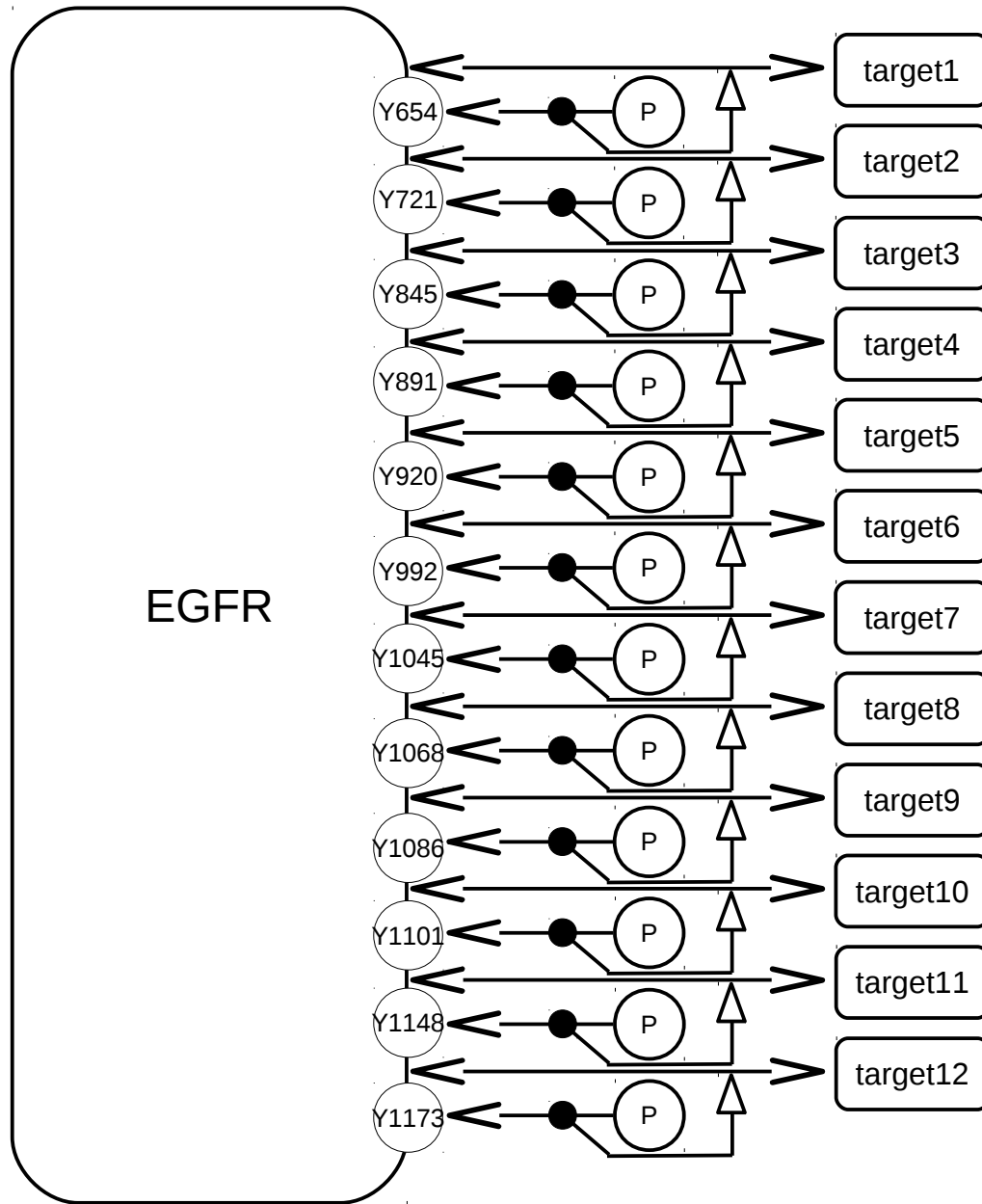
Entity Relationships can be viewed as rules



If **A exists**, the assignment of the value **P** to the **state variable T of B** is increased

If **P** is assigned to the state variable **T of B**, the assignment of the value **P** to the **state variable S of B** is decreased

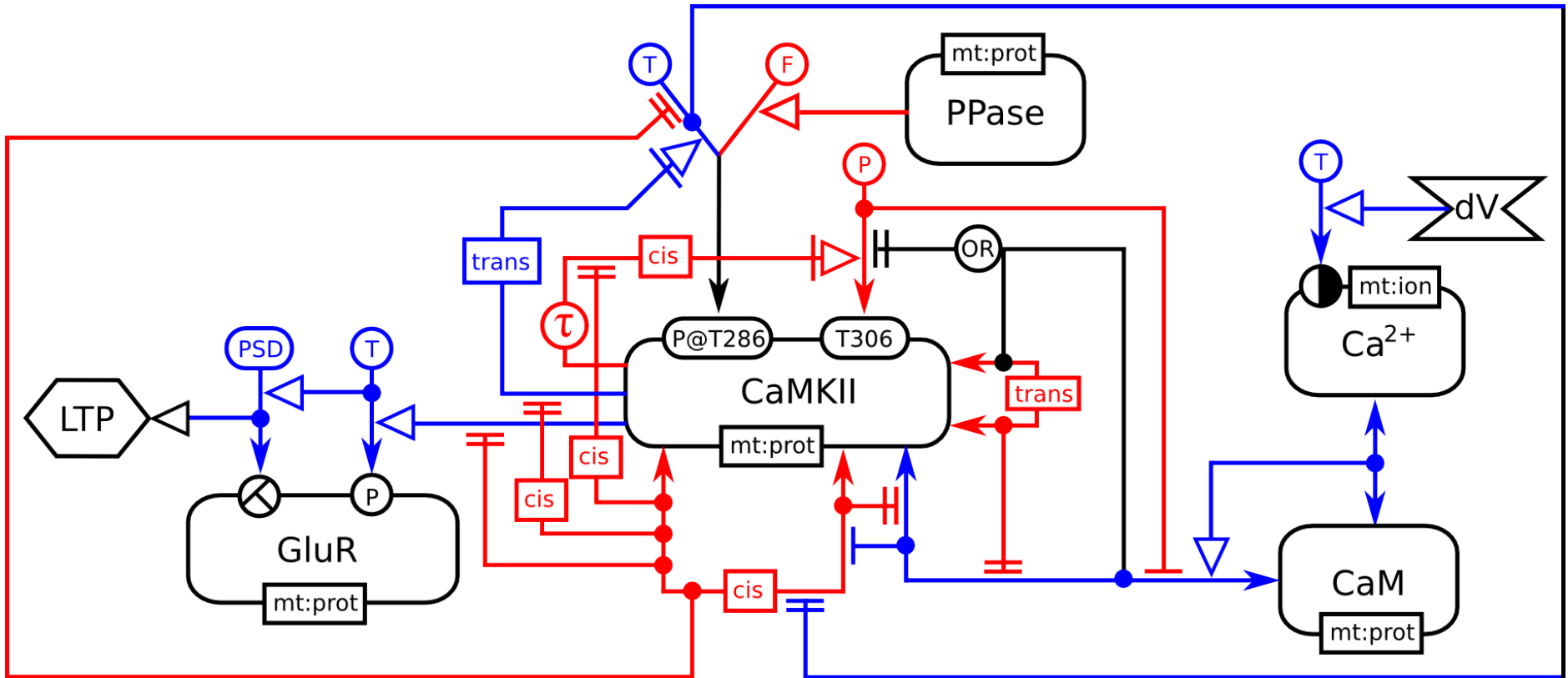
Multistate and combinatorial explosion



Process Descriptions:
“once a state variable value,
always a state variable value”

$2^{12} = 4096$ states
(i.e. EPN glyphs) for EGFR
and 4096 complexes between
EGFR and targets

Regulation of synaptic plasticity by calcium



Systems Biology Graphical Notation: Entity Relationship language Level 1

Version 2.0

Date: August 8, 2015

Editors:

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To discuss any aspect of SBGN, please send your messages to the mailing list sbgn-discuss@caltech.edu. To get subscribed to the mailing list or to contact us directly, please write to sbgn-editors@lists.sourceforge.net. Bug reports and specific comments about the specification should be entered in the issue tracker <http://sourceforge.net/p/sbgn/sbgn-er-11/>.



Systems Biology Graphical Notation: Process Description language Level 1

Version 1.3

14 February, 2010

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Systems Biology Graphical Notation: Activity Flow language Level 1

Version 1.2

Date: July 27, 2015

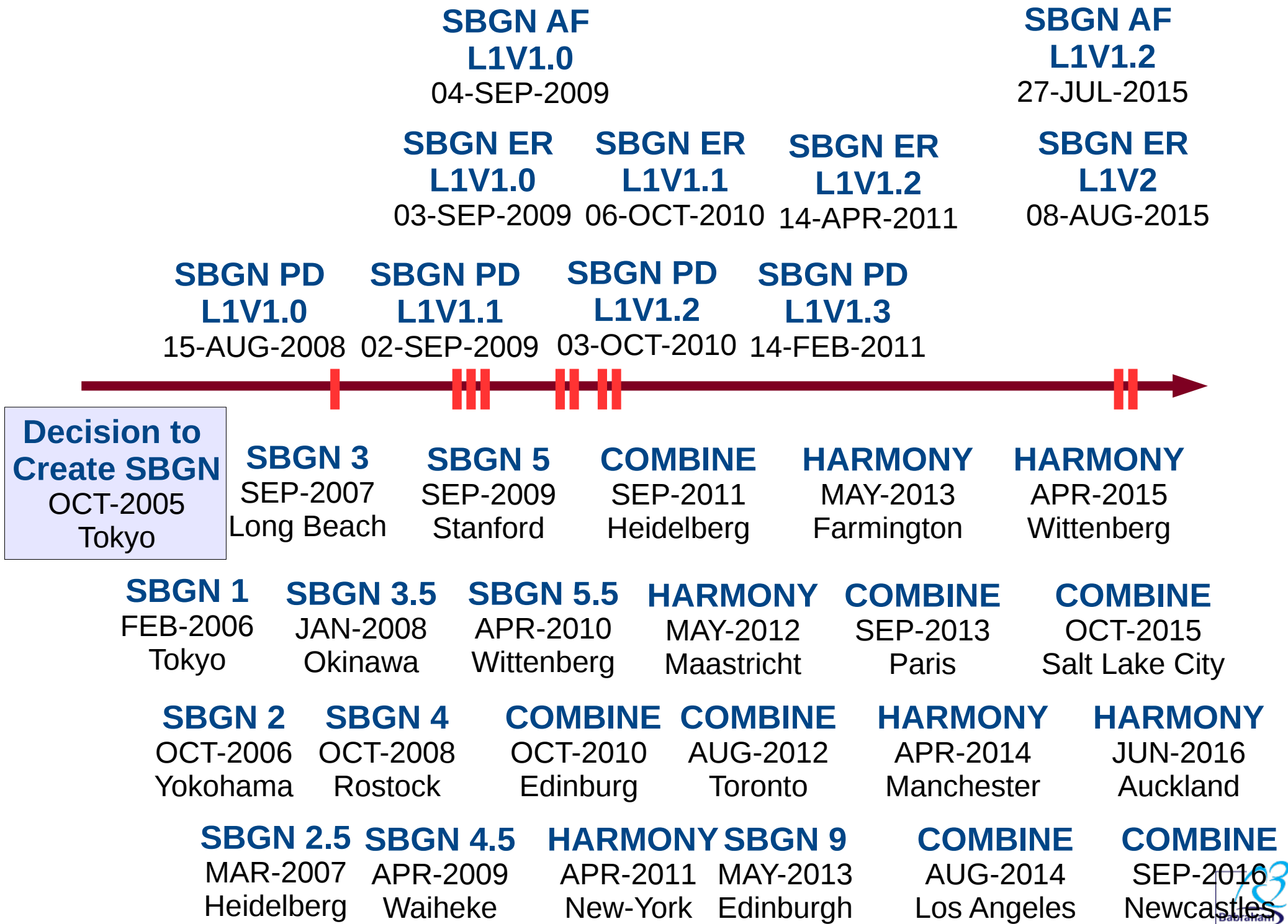
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```

<?xml version="1.0" encoding="UTF-8"?>
<sbgn xmlns="http://sbgn.org/libsbgn/0.3">
  <map version="http://identifiers.org/combine.specifications/
sbgn.pd.level-1.version-1.3" id="map1">
    <bbox x="0" y="0" w="363" h="253"/>
    <glyph class="simple chemical" id="glyph1">
      <label text="Ethanol"/> <!-- fontsize="" etc -->
      <!-- Line breaks are allowed in the text attribute -->
      <bbox x="40" y="120" w="60" h="60"/>
    </glyph>
    <glyph class="simple chemical" id="glyph_ethanal">
      <label text="Ethanal" />
      <bbox x="220" y="110" w="60" h="60"/>
    </glyph>
    <glyph class="macromolecule" id="glyph_adh1">
      <label text="ADH1" />
      <bbox x="106" y="20" w="108" h="60"/>
    </glyph>
    <glyph class="simple chemical" id="glyph_h">
      <label text="H+" />
      <bbox x="220" y="190" w="60" h="60"/>
    </glyph>
    <glyph class="simple chemical" id="glyph_nad">
      <label text="NAD+" />
      <bbox x="40" y="190" w="60" h="60"/>
    </glyph>
    <glyph class="simple chemical" id="glyph_nadh">
      <label text="NADH" />
      <bbox x="300" y="150" w="60" h="60"/>
    </glyph>

    <glyph class="process" orientation="horizontal" id="pn1">
      <bbox x="148" y="168" w="24" h="24"/>
      <port x="136" y="180" id="pn1.1"/>
      <port x="184" y="180" id="pn1.2"/>
    </glyph>

    <arc class="consumption" source="glyph1" target="pn1.1"
id="a01">
      <start x="98" y="160" />
      <end x="136" y="180" />
    </arc>

    <arc class="production" source="pn1.2" target="glyph_nadh"
id="a02">
      <start x="184" y="180" />
      <end x="300" y="180" />
    </arc>

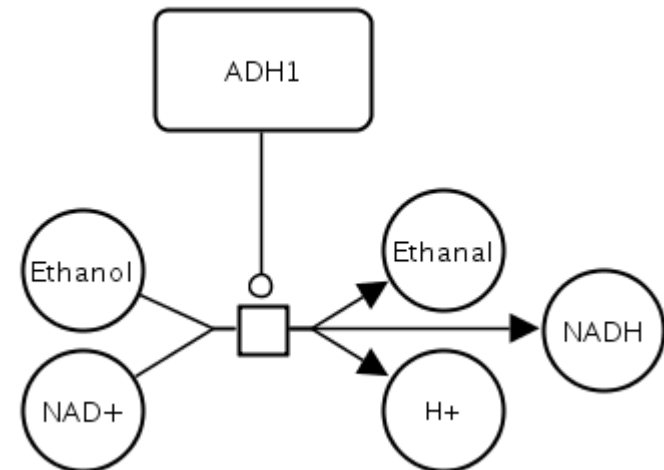
    <arc class="catalysis" source="glyph_adh1" target="pn1"
id="a03">
      <start x="160" y="80" />
      <end x="160" y="168" />
    </arc>

    <arc class="production" source="pn1.2" target="glyph_h"
id="a04">
      <start x="184" y="180" />
      <end x="224" y="202" />
    </arc>

    <arc class="production" source="pn1.2" target="glyph_ethanal"
id="a05">
      <start x="184" y="180" />
      <end x="224" y="154" />

```

SBGN-ML





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LibSBGN

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New Page

Matthias König edited this page on 30 Sep 2016 · 13 revisions

LibSBGN library

► Pages 89

LibSBGN is the library for writing and reading [SBGN-ML](#), a XML-based file format dedicated to the description of SBGN maps.

Source code: <https://github.com/sbgn/libsbgn>

Latest release: <https://github.com/sbgn/libsbgn/releases>

Features

LibSBGN is a library that deals with SBGN maps. It currently supports:

- Reading / writing the [SBGN-ML](#) file format (XML-based format for description of SBGN maps)
- [Validation](#) of semantical and syntactical correctness
- Conversion to other formats such as SBML and BioPAX
- Support for Java and C++

Documentation



Systems Biology Graphical Notation

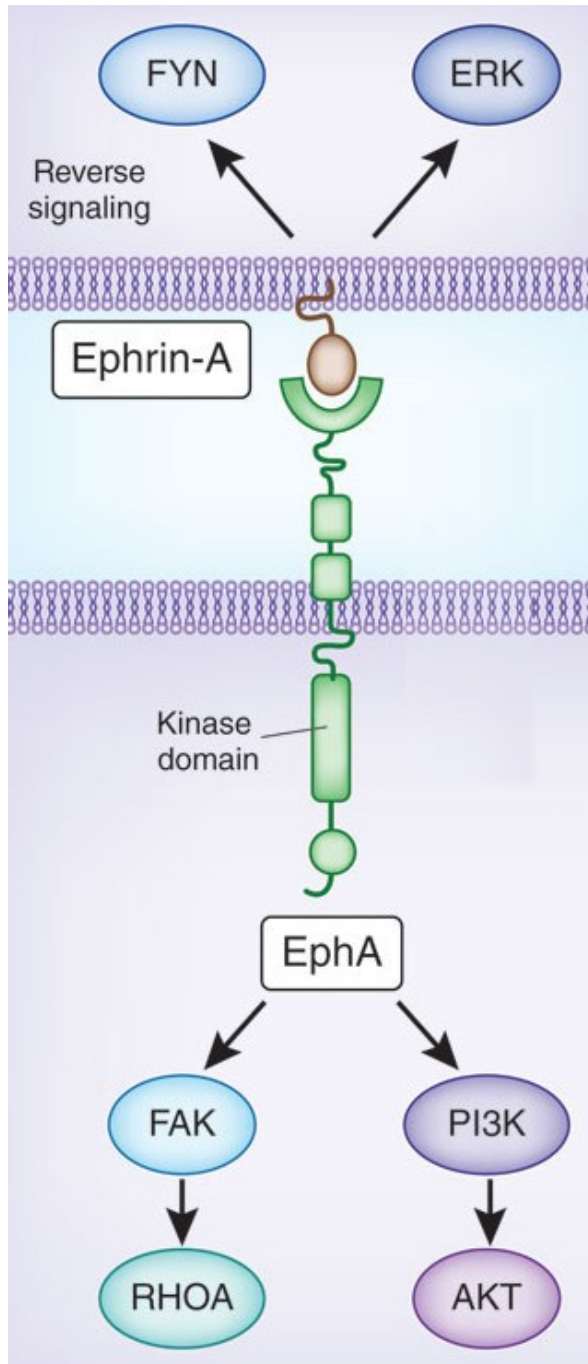
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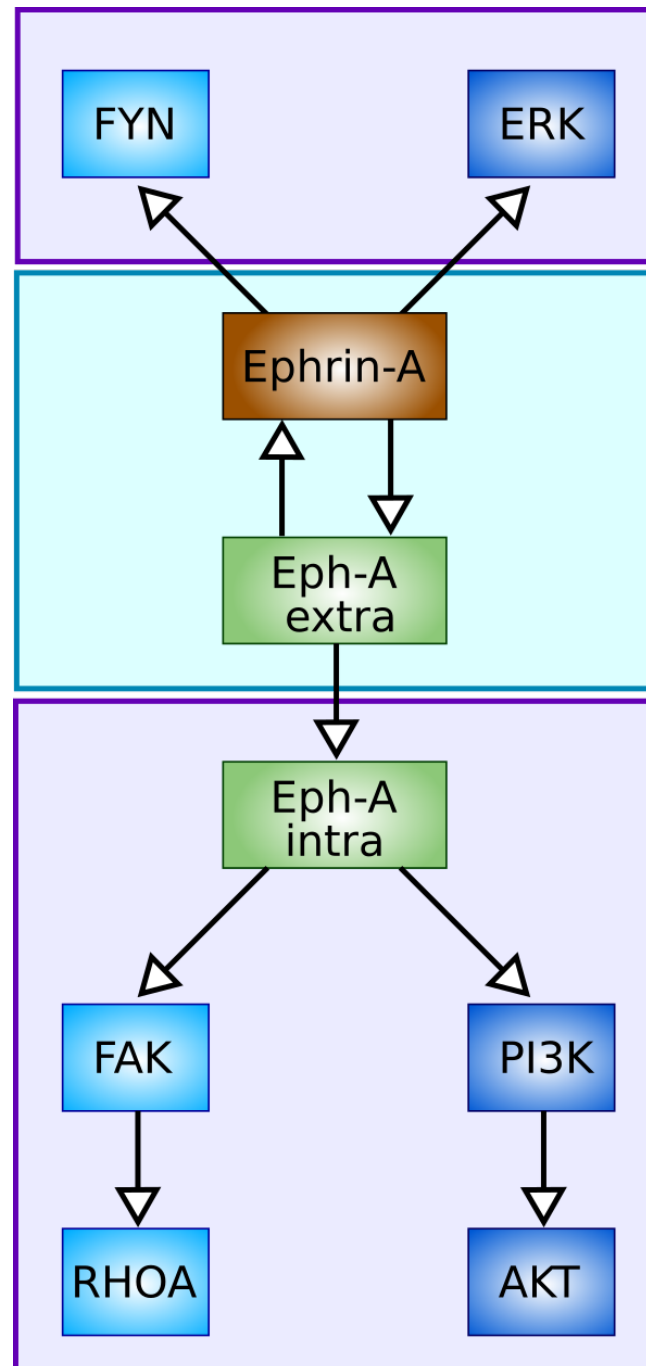
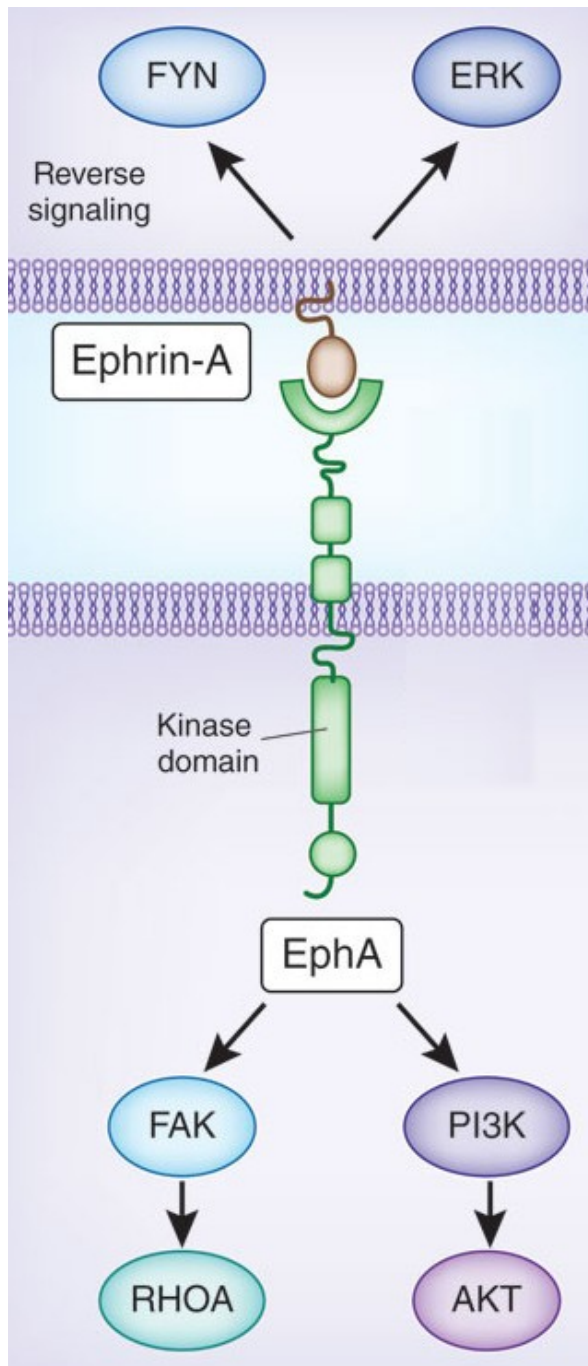
- [Logistics](#)
- [Notes](#)

[Editor Meeting Notes](#)[LibSBGN](#)[Specification Development](#)

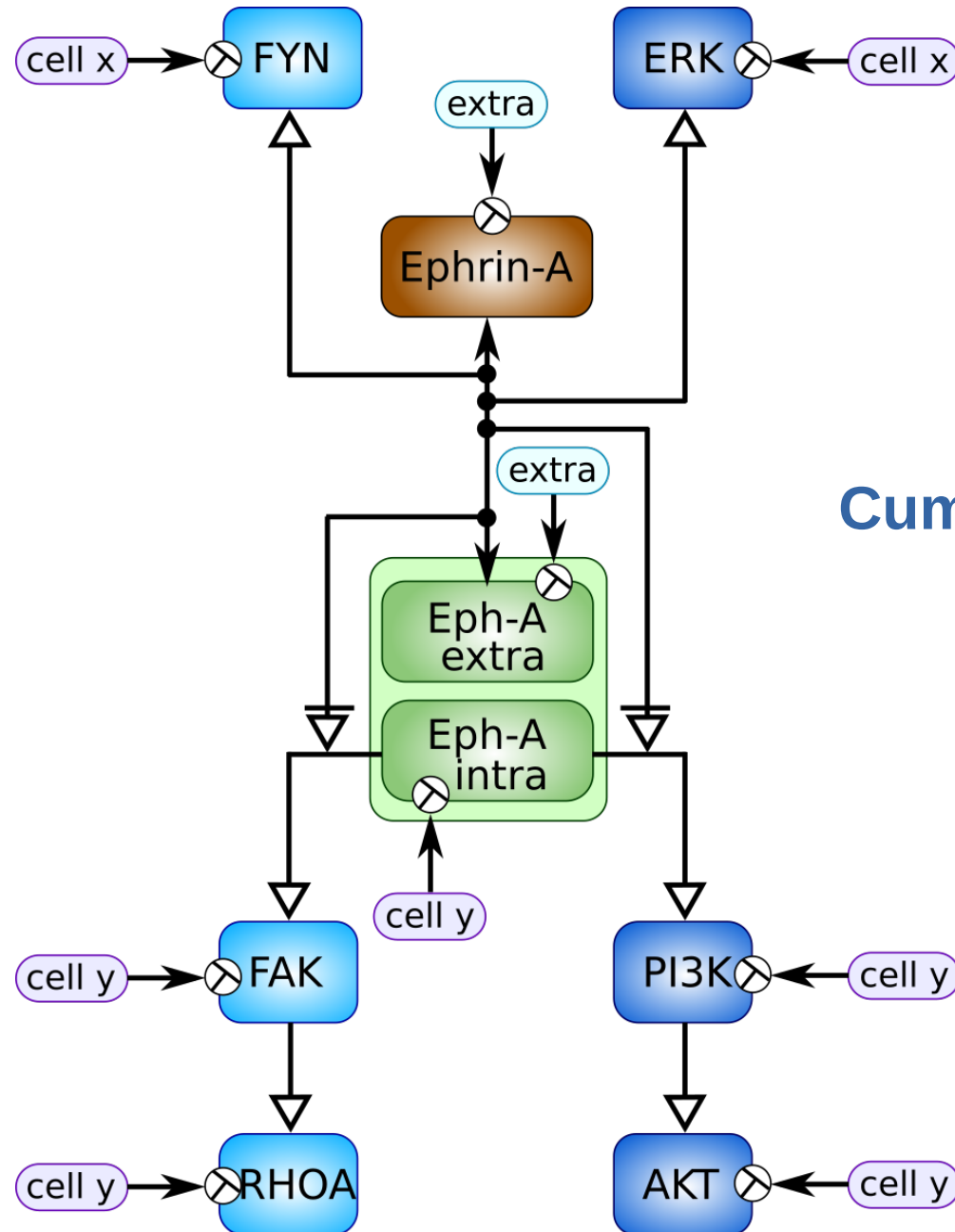
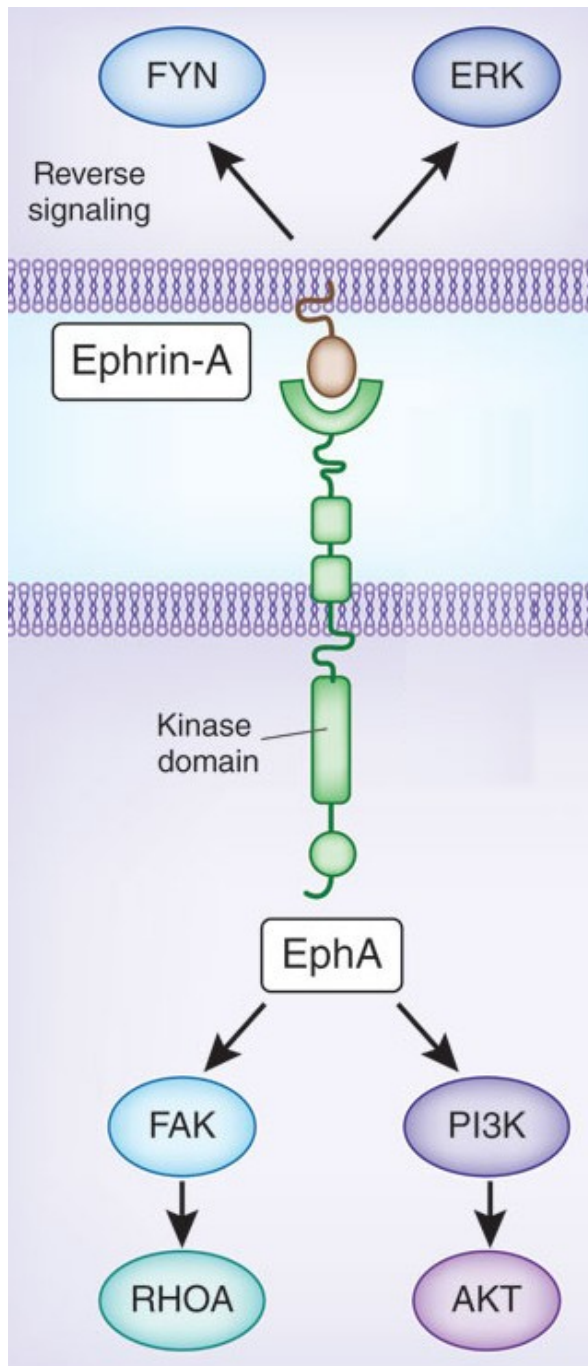
Are we done? Everything is solved, right?

Multi-compartment entities

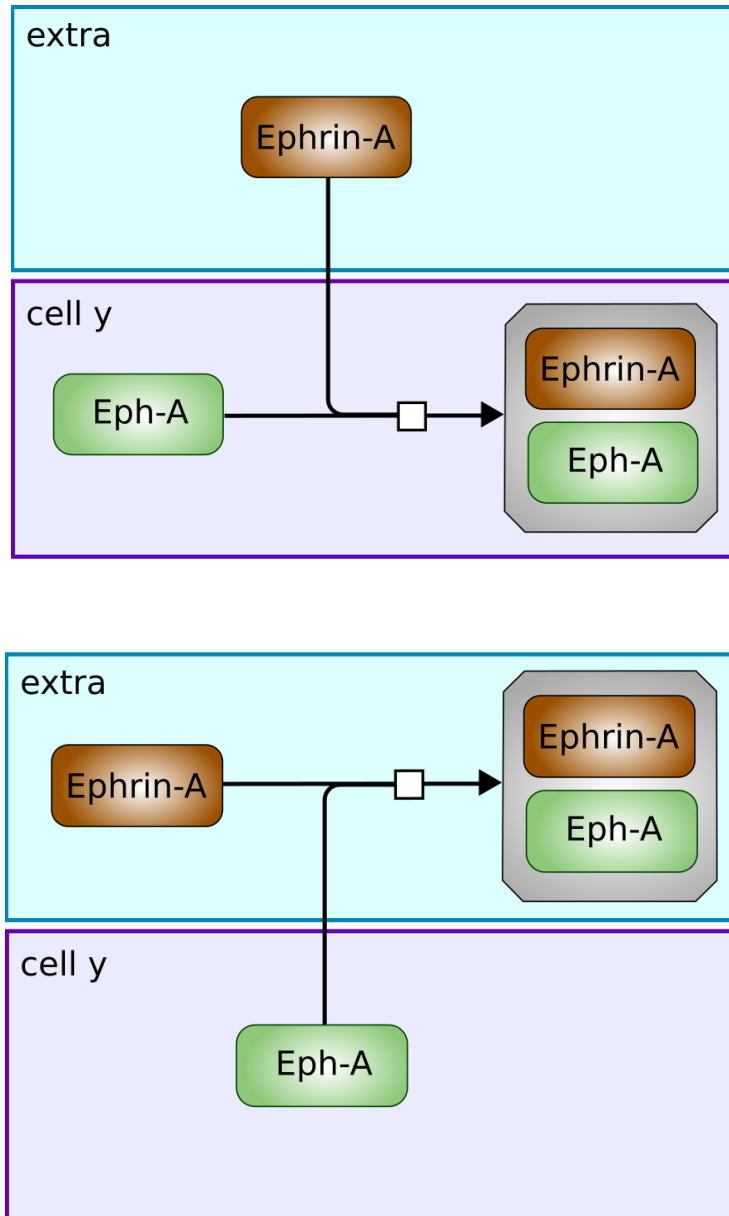
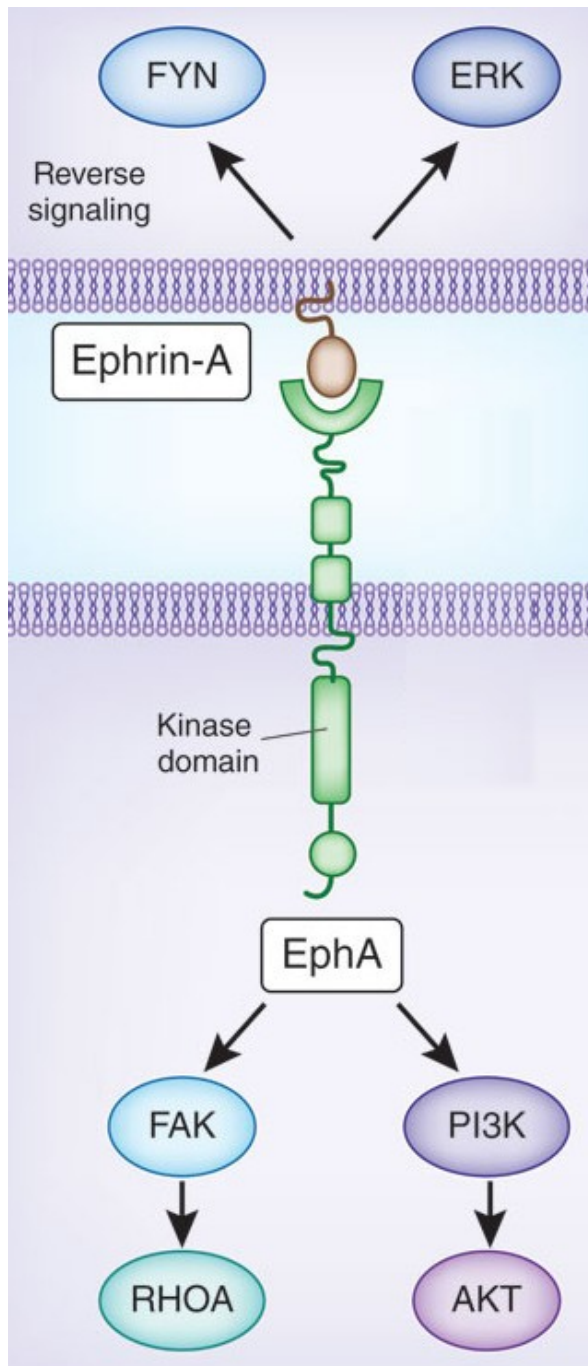




Easy in AF

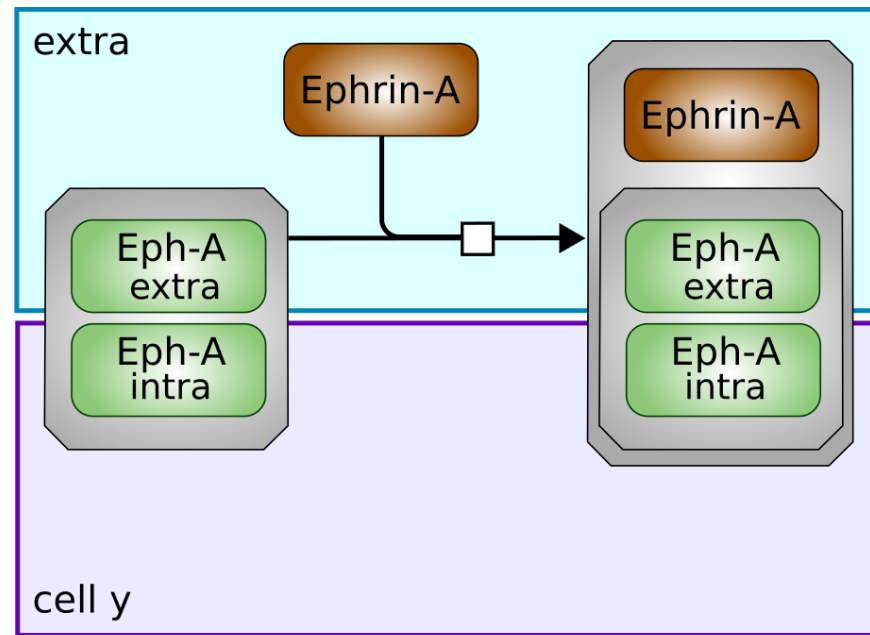
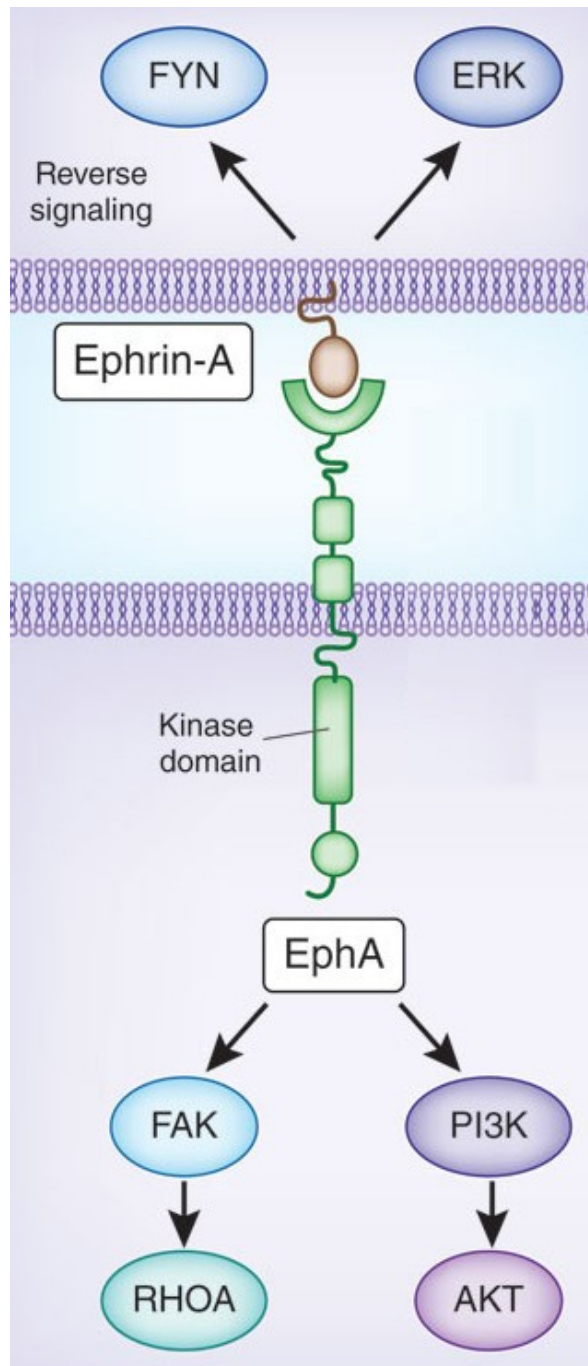


**Cumbersome
in ER**



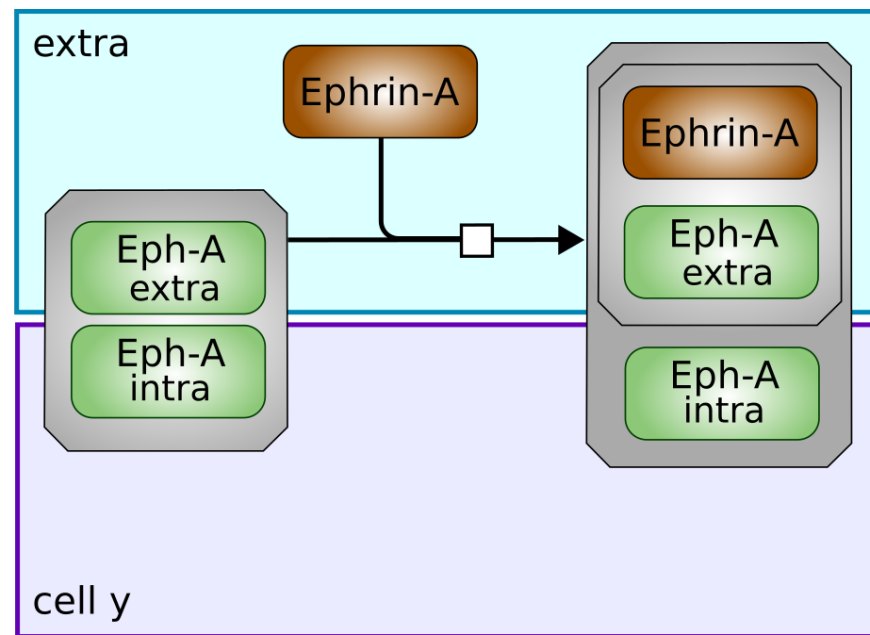
**impossible
In PD**

molecular species
(entity pool nodes)
belong to a single
compartment

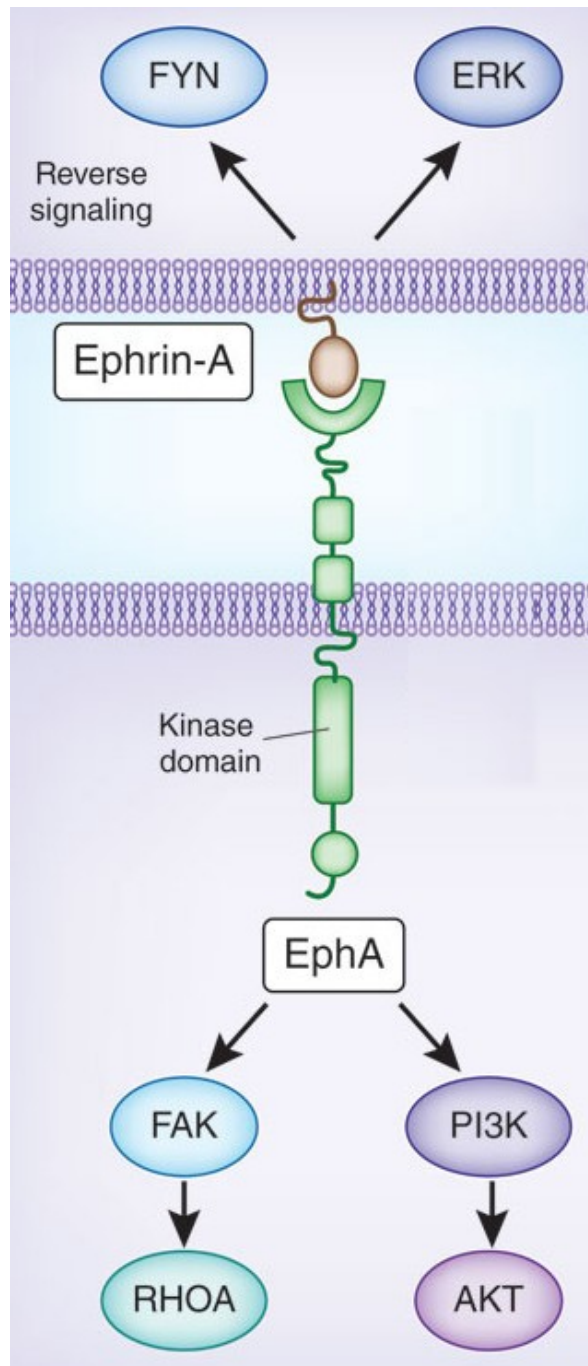


Loose the fact that
Ephrin-A binds to
Extracell part

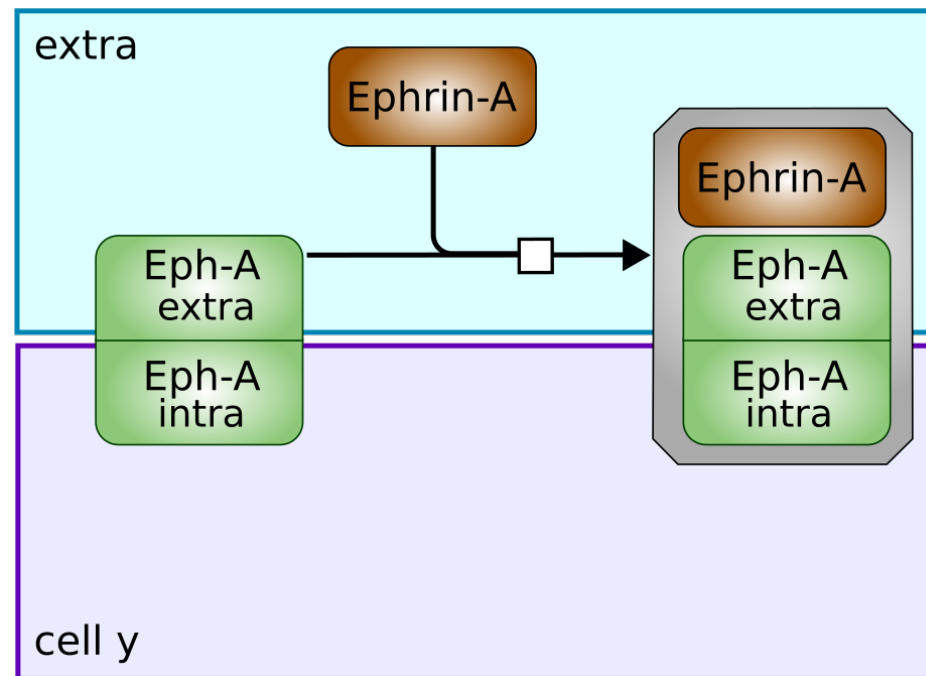
Multi-compartment complexes do not
solve the problem, since they represent
Non-covalent assemblies



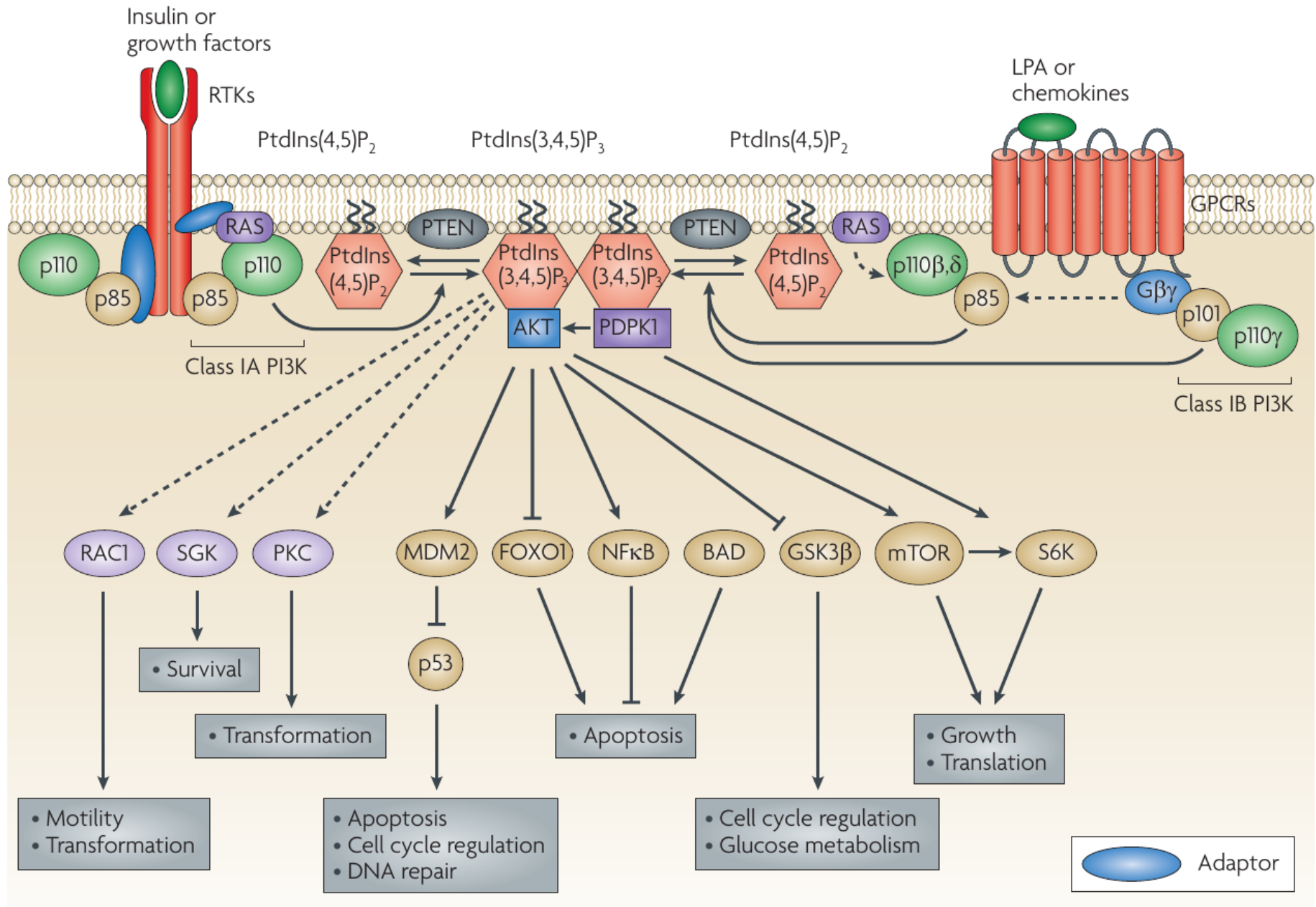
Loose the fact that
Eph-A is a
Multi-domain
molecule



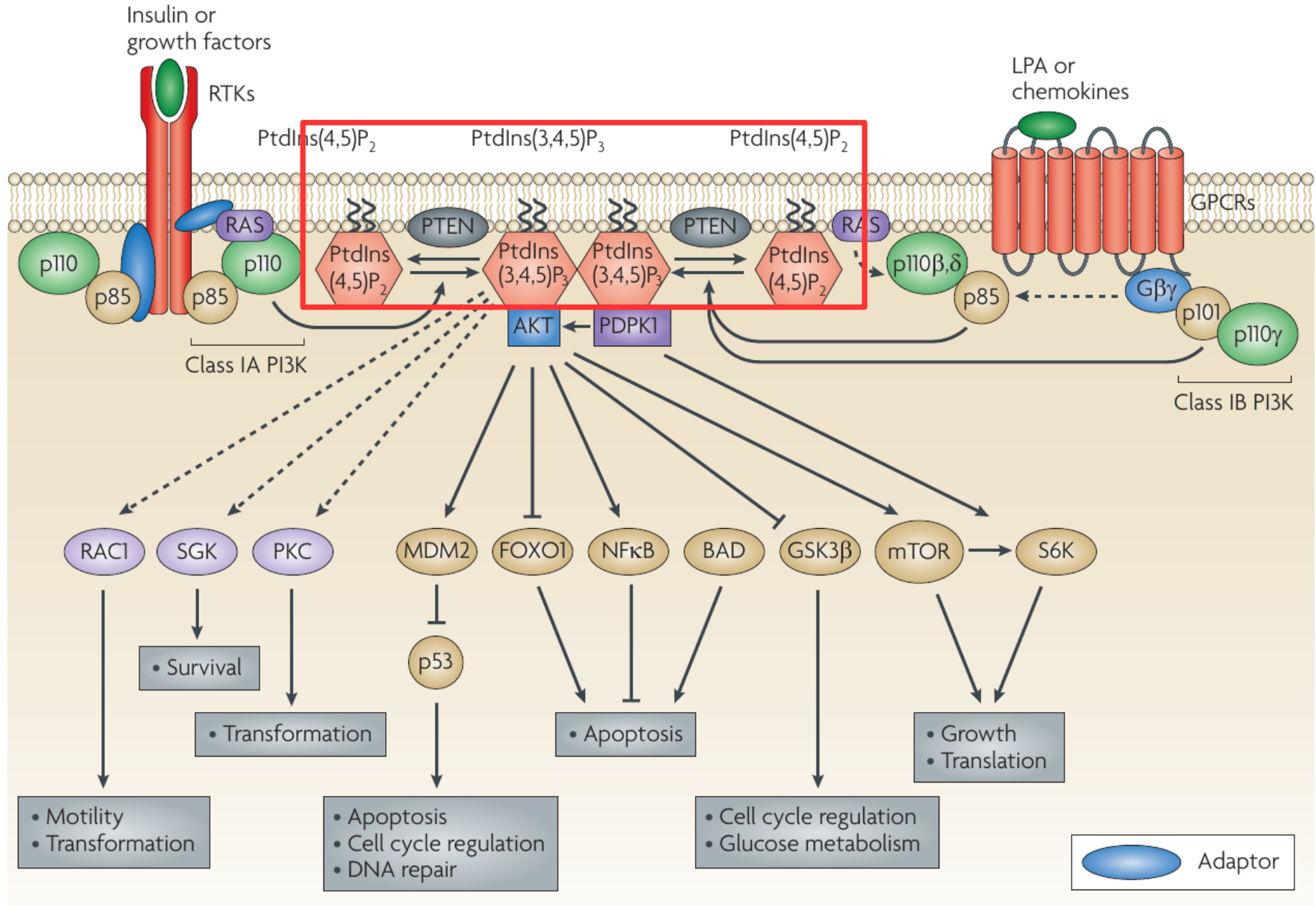
- New glyph: “Domain”; generalisation of the current “Nucleic acid feature”.
- Domains can be associated in multi-domain entities pool nodes, the location being carried by the domains
- Allow complexes to be compartment-less
- Move content of complex from “decorations” to *bona fide* entity pool nodes



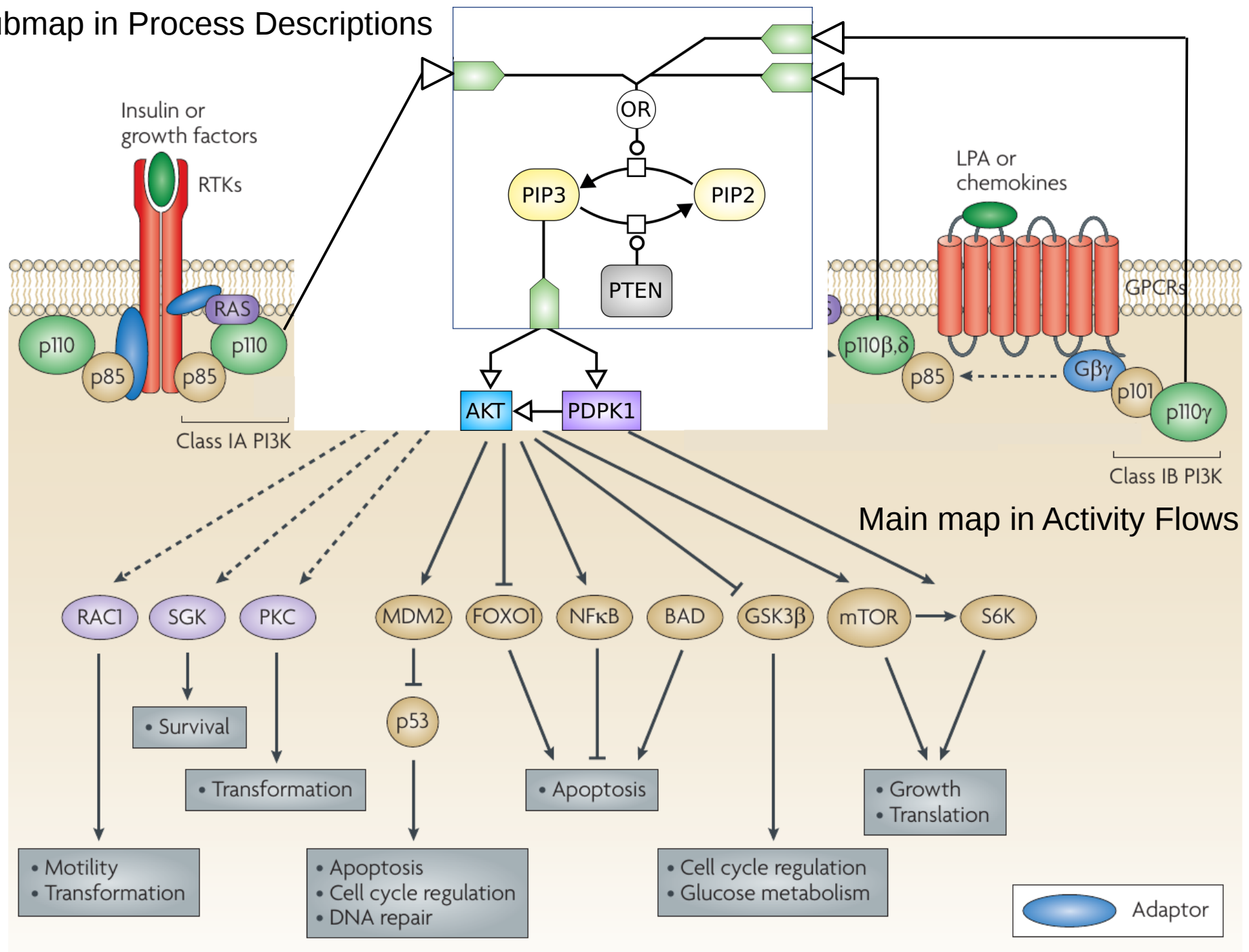
Hybrid maps



Hybrid maps



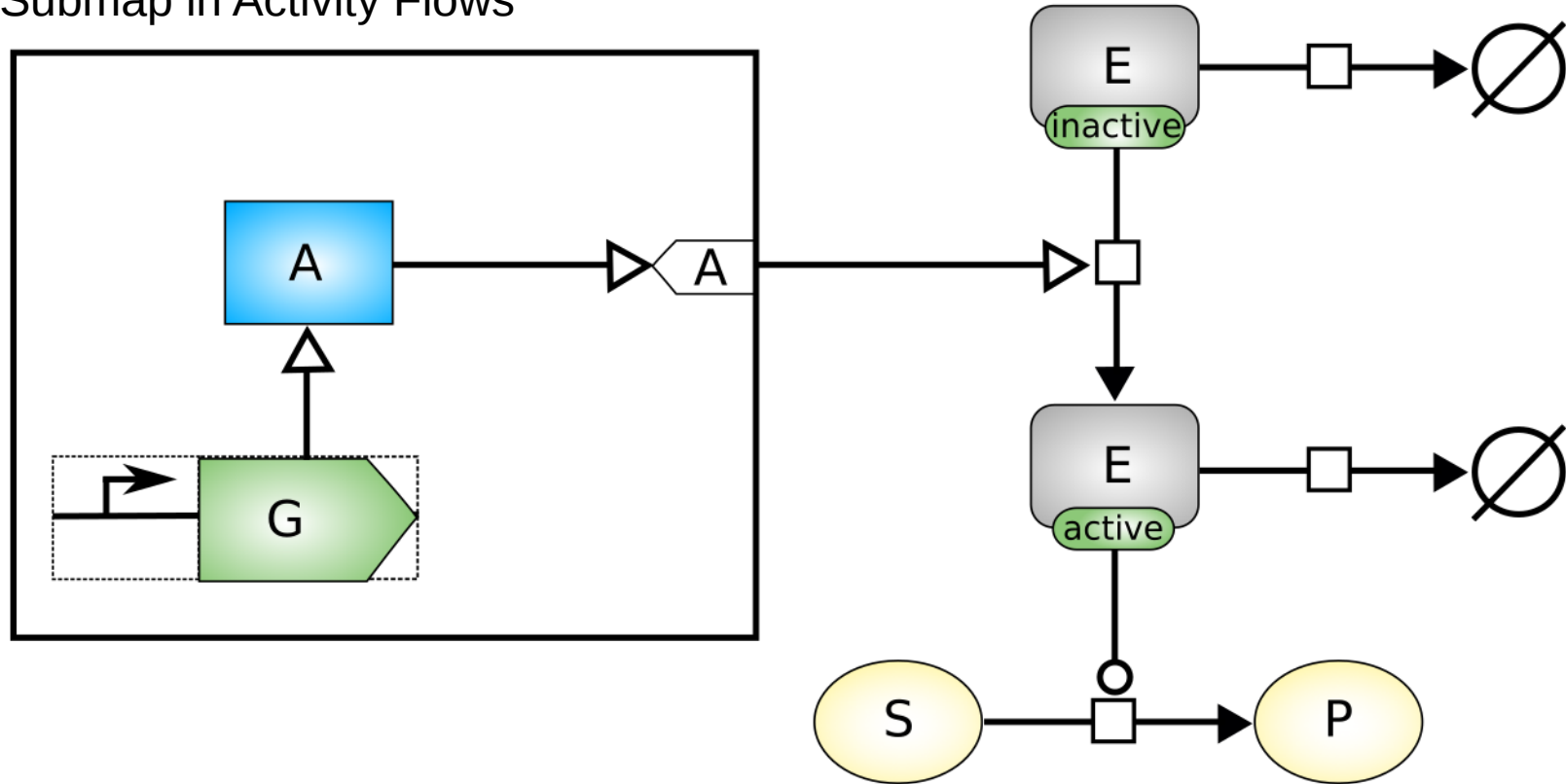
Submap in Process Descriptions



Use Submaps: PD in AF

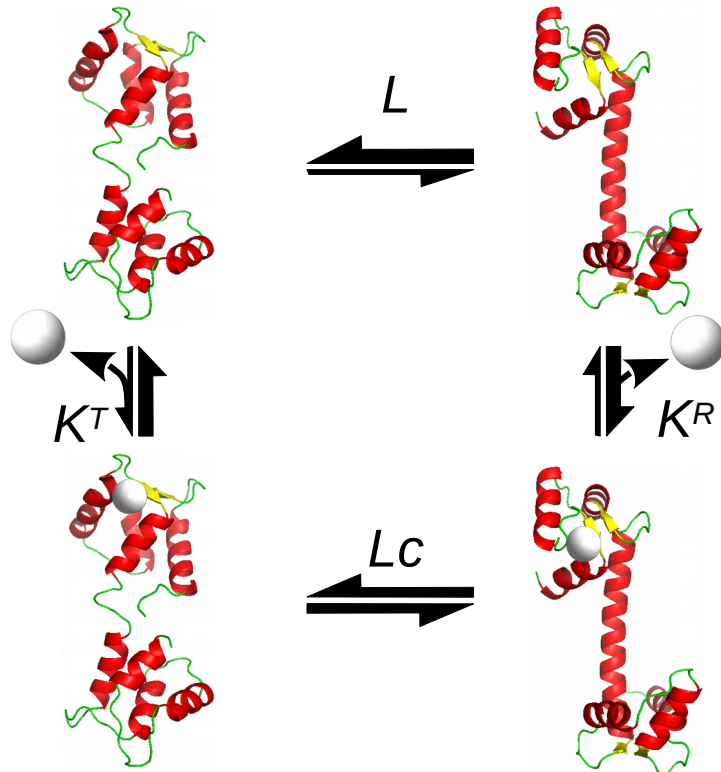
Main map in Process Descriptions

Submap in Activity Flows

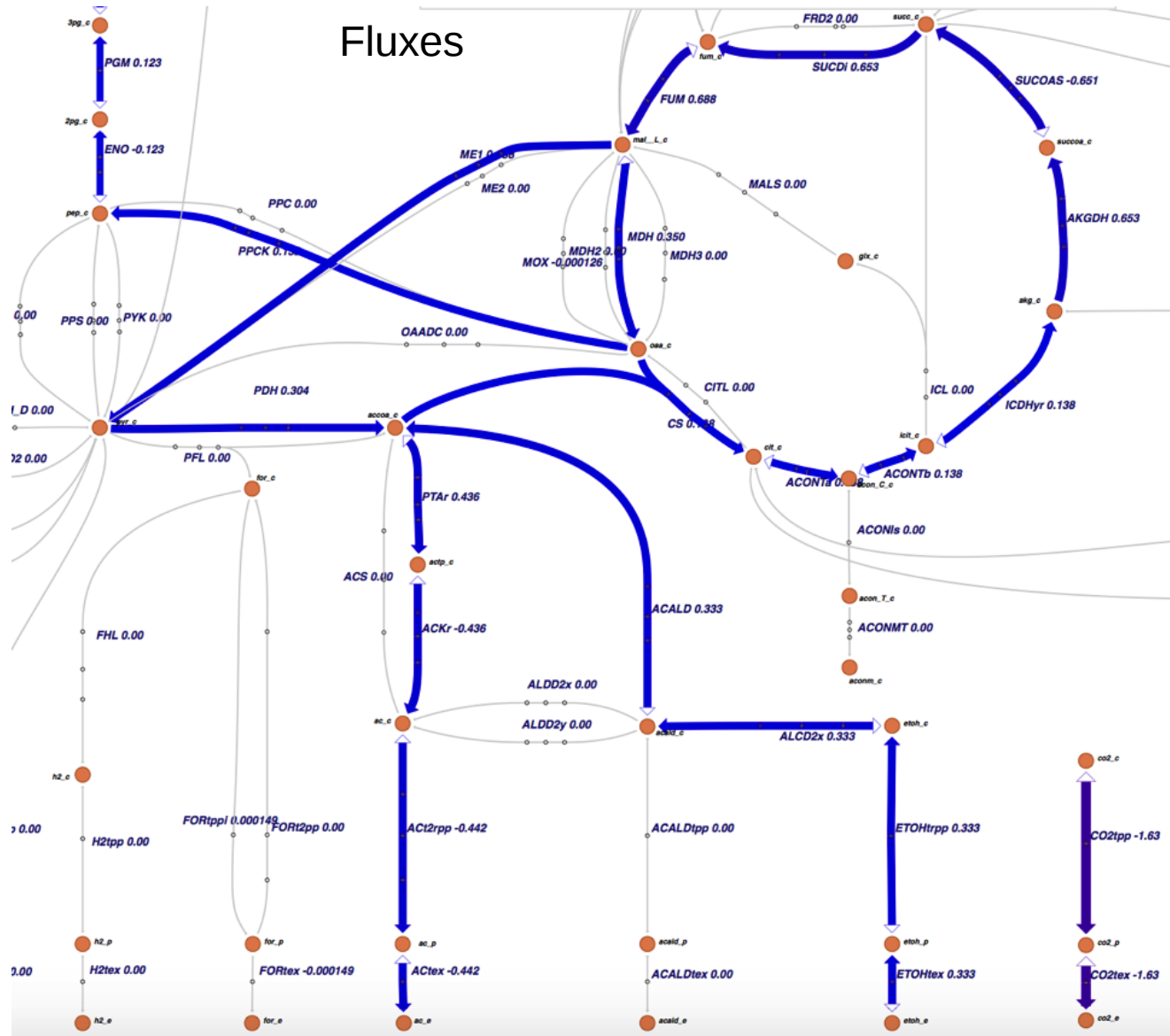


Use Submaps: AF in PD

Allosteric regulations



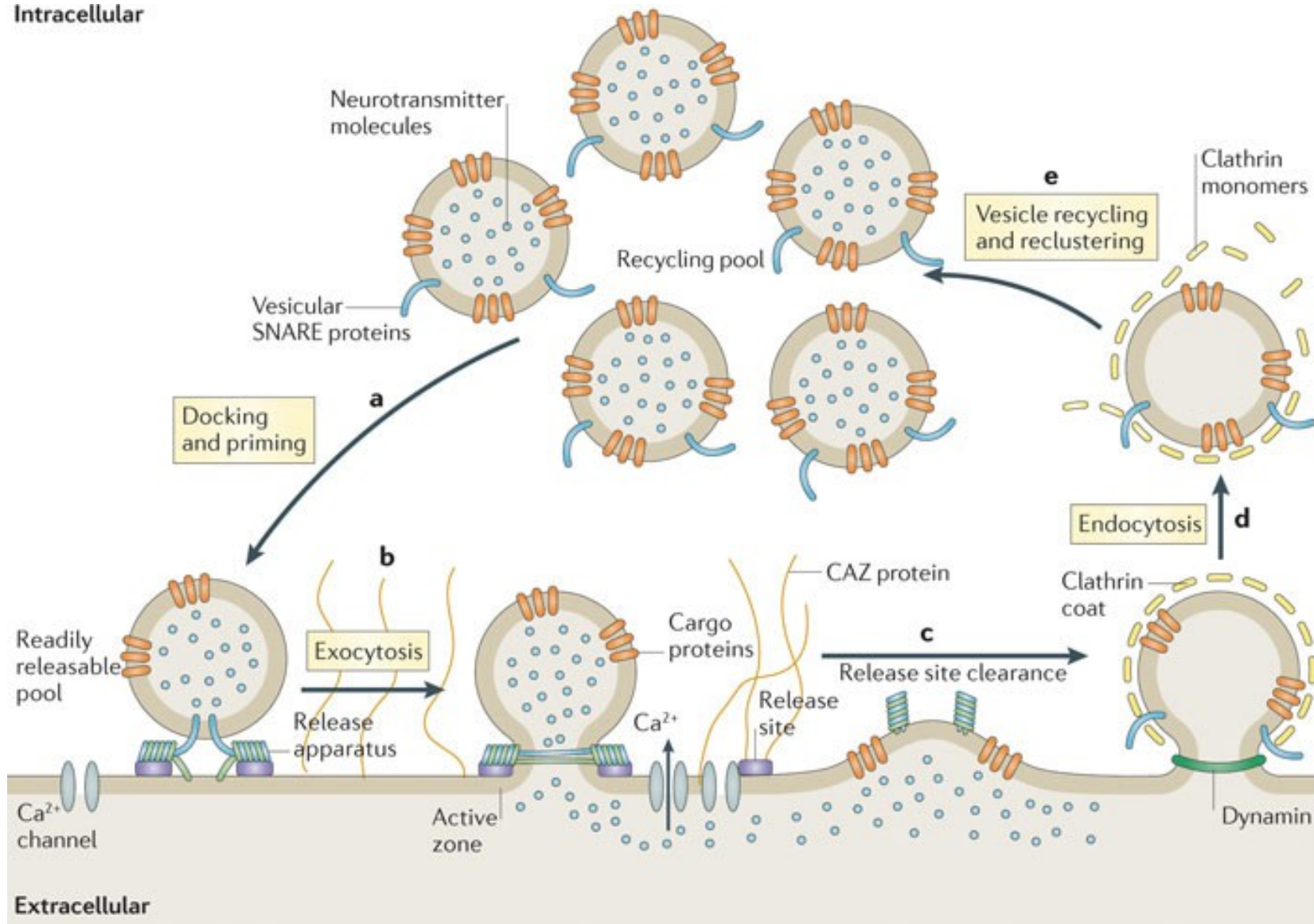
Fluxes



Intensities and amounts

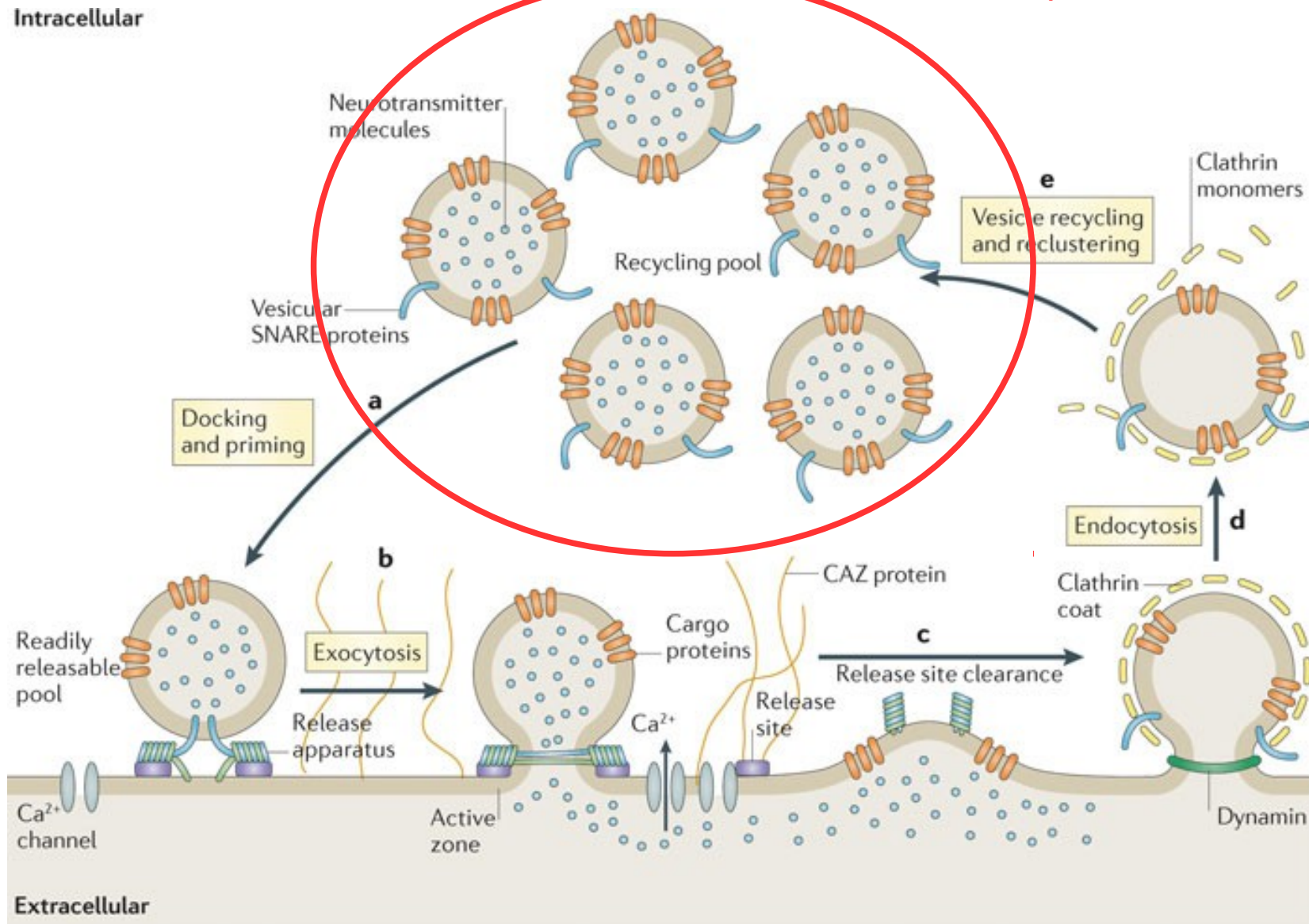
Creation, movement, destruction

Intracellular



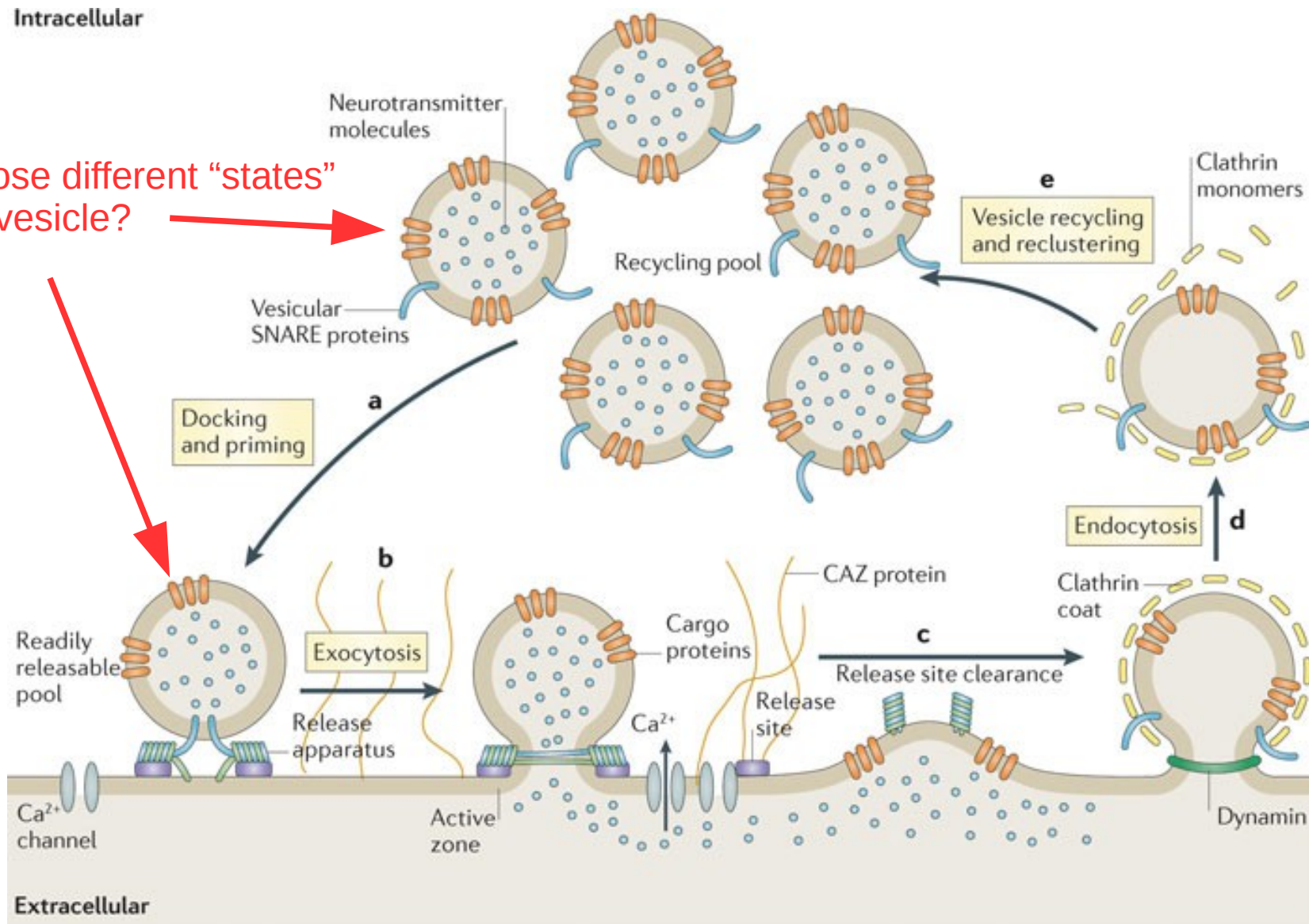
Creation, movement, destruction

Is this a “pool” of identical entities?

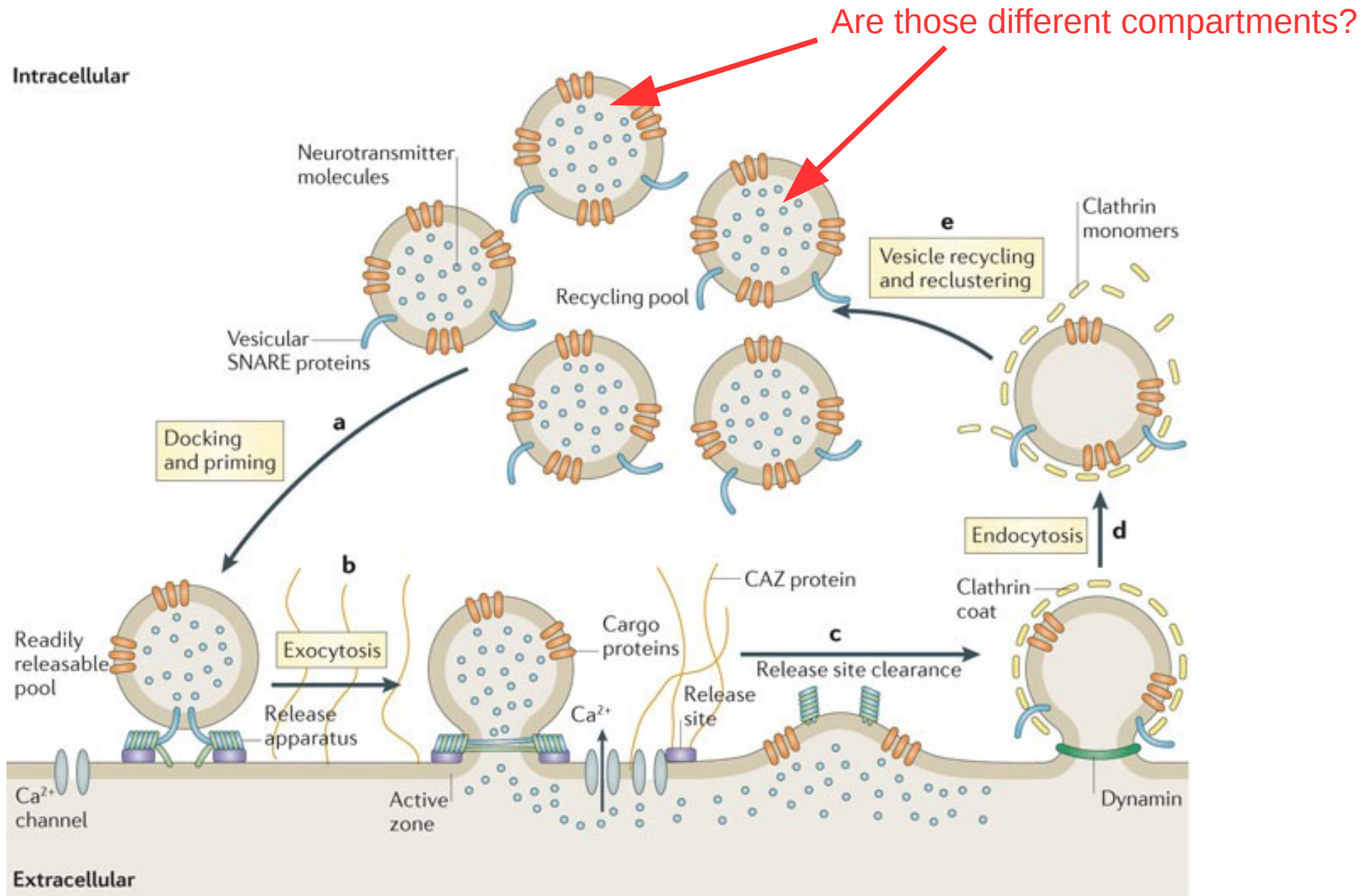


Creation, movement, destruction

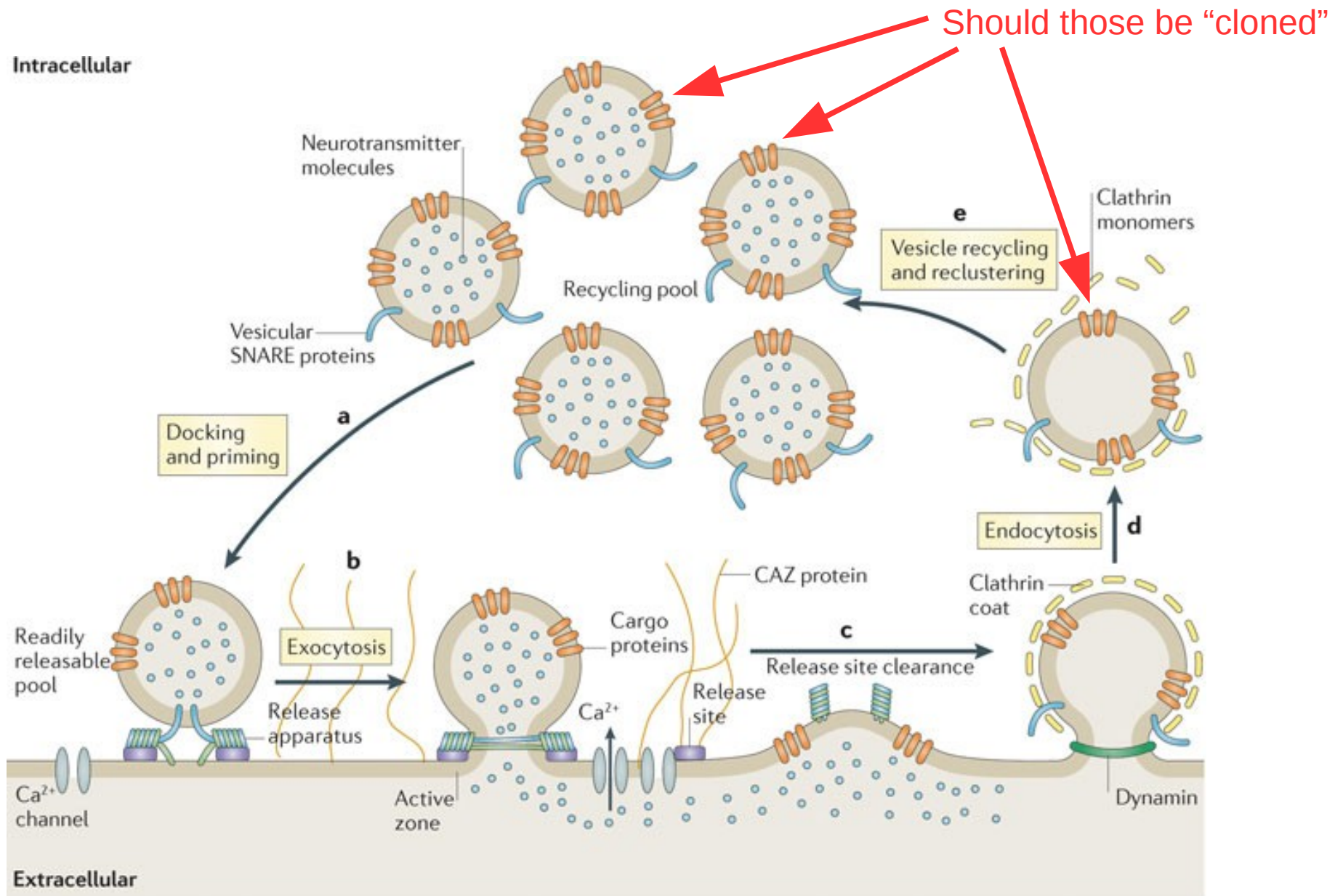
Are those different “states” of the vesicle?



Creation, movement, destruction



Creation, movement, destruction



Temporal order and Dynamics?

Multi-scale?

Topologies?

Data integration?



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Symbol Highlight

Stimulation



Pathway Highlight

This pathway is an SBGN diagram from the following paper published in the July, 2013 issue of the Cell magazine (PubMed ID: [23791384](#)).

Park S., Kukushkin Y., Gupta R., Chen T., Konagai A., Hipp M., Hayer-Hartl M., and Hartl F. (2013) PolyQ Proteins Interfere with Nuclear Degradation of Cytosolic Proteins by Sequestering the Sis1p Chaperone. Cell 154, 134-145.



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