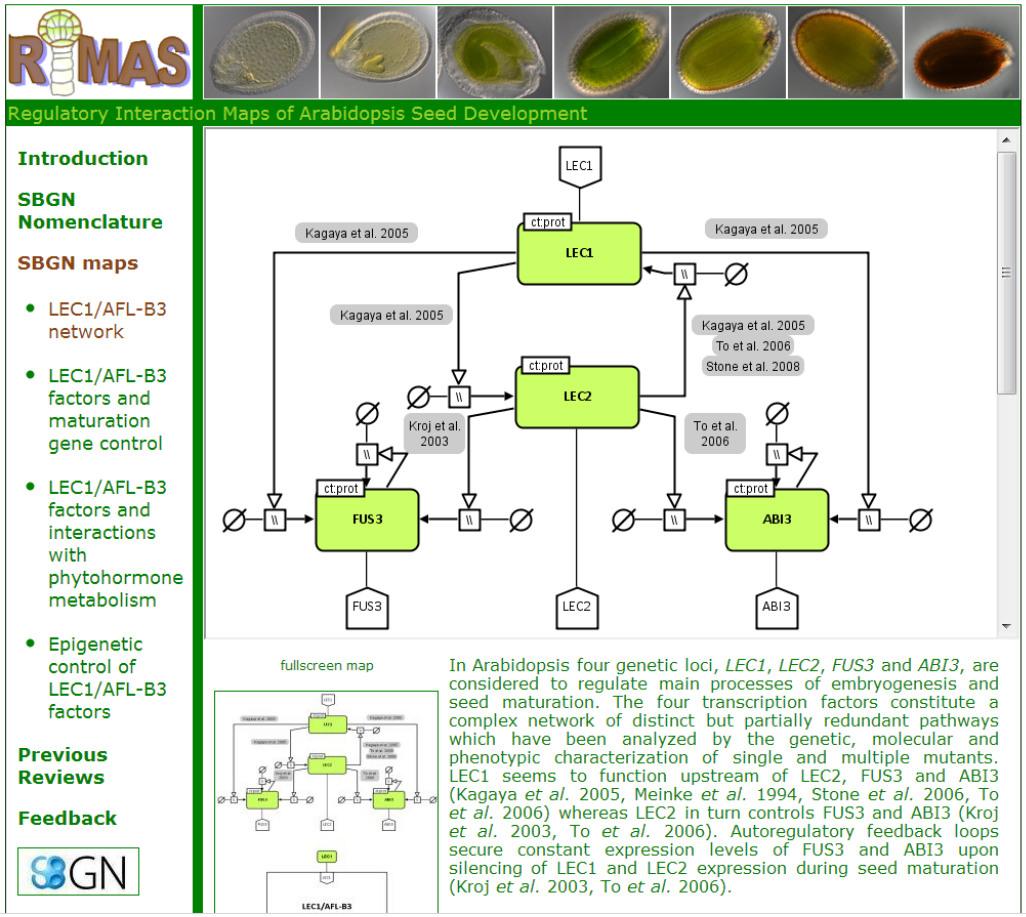
SBGN from a user‘s perspective

Astrid Junker IPK Gatersleben
30.04.2013

- I started in 2009 > regulatory maps of Arabidopsis seed development



Junker A., Hartmann A., Schreiber F. and Bäumlein H., (2010) An engineer's view on regulation of seed development. *Trends in Plant Science*, 15(6):303-307.

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NATURE PROTOCOLS | PROTOCOL

Creating interactive, web-based and data-enriched maps with the Systems Biology Graphical Notation

Astrid Junker, Hendrik Rohn, Tobias Czauderna, Christian Klukas, Anja Hartmann & Falk Schreiber

Affiliations | Contributions | Corresponding author

Nature Protocols **7**, 579–593 (2012) | doi:10.1038/nprot.2012.002

Published online 01 March 2012

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Abstract

Abstract • Author information • Supplementary information

The Systems Biology Graphical Notation (SBGN) is an emerging standard for the uniform representation of biological processes and networks. By using examples from gene regulation and metabolism, this protocol shows the construction of SBGN maps by either manual drawing or automatic translation using the tool SBGN-ED. In addition, it discusses the enrichment of SBGN maps with different kinds of -omics data to bring numerical data into the context of these networks in order to facilitate the interpretation of experimental data. Finally, the export of such maps to public websites, including clickable images, supports the communication of results within the scientific community. With regard to the described functionalities, other tools partially overlap with SBGN-ED.

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Published online 2011 November 15. doi: 10.1093/nar/gkr1004

PMCID: PMC3245004

MetaCrop 2.0: managing and exploring information about crop plant metabolism

Falk Schreiber,[1,2,*] Christian Colmsee,[1] Tobias Czauderna,[1] Eva Grafahrend-Belau,[1] Anja Hartmann,[1] Astrid Junker,[1] Björn H. Junker,[1] Matthias Klapperstück,[1] Uwe Scholz,[1] and Stephan Weise[1]

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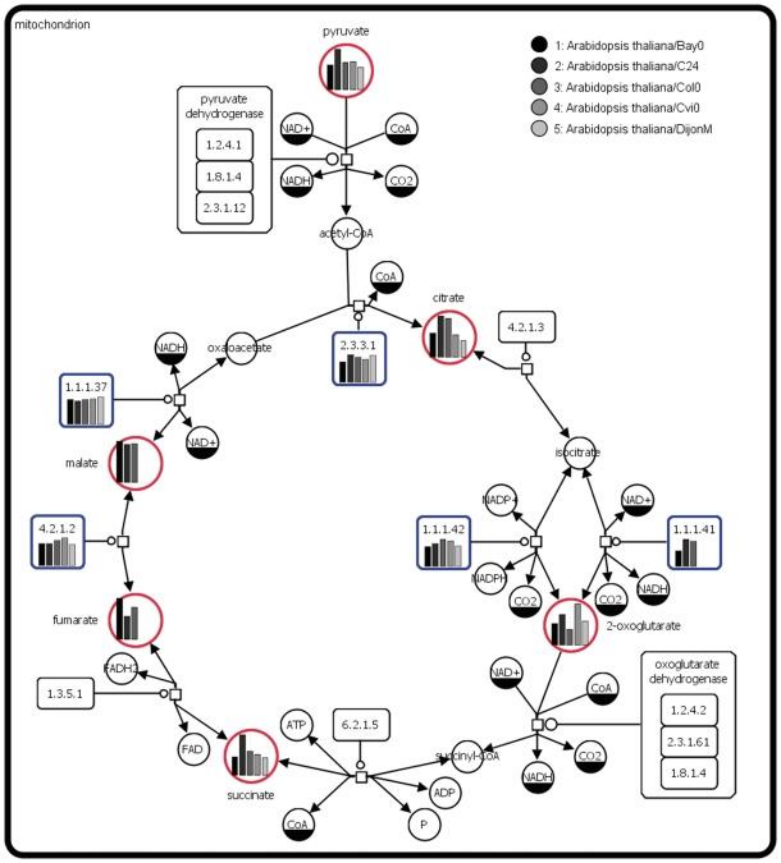
ally curated repository of high-quality data about plant metabolism, providing
ail from overview maps of primary metabolism to kinetic data of enzymes. It
about seven major crop plants with high agronomical importance and two model
ntended to support research aimed at the improvement of crops for both nutrition
can be accessed via web, web services and an add-on to the Vanted software. Here,
vel developments of the MetaCrop system and the extended database content.
ilable in version 2.0 at http://metacrop.ipk-gatersleben.de.



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METHODS ARTICLE » This article is part of a Research Topic

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Front. Plant Sci., 15 November 2012 | doi: 10.3389/fpls.2012.00252

Visual analysis of transcriptome data in the context of anatomical structures and biological networks

Astrid Junker[1†], Hendrik Rohn[1*†] and Falk Schreiber[1,2,3]

[1] Leibniz Institute of Plant Genetics and Crop Plant Research Gatersleben, Gatersleben, Germany

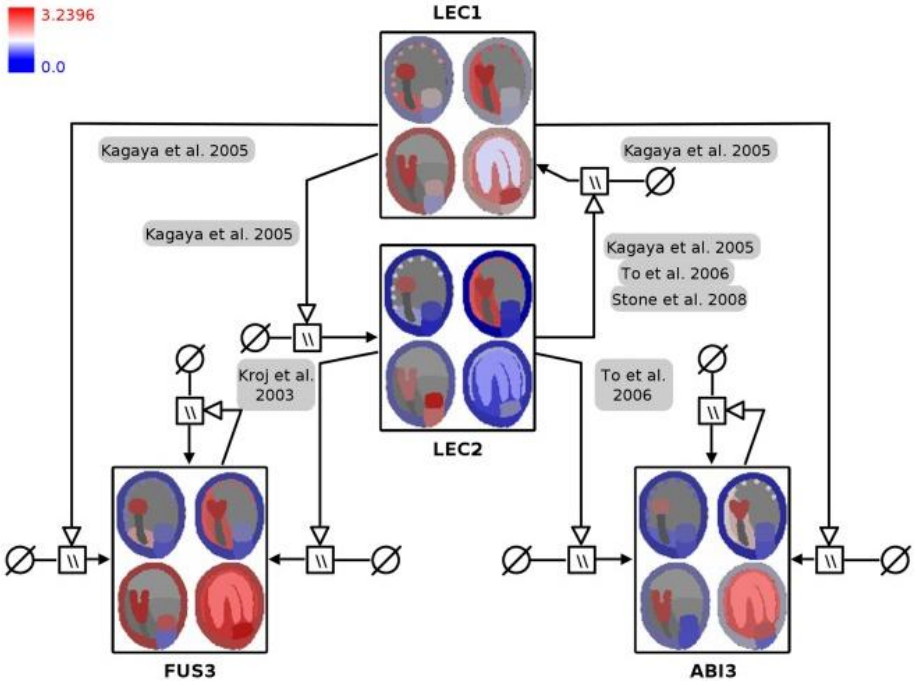
[2] Institute of Computer Science, Martin Luther University Halle-Wittenberg, Halle, Germany

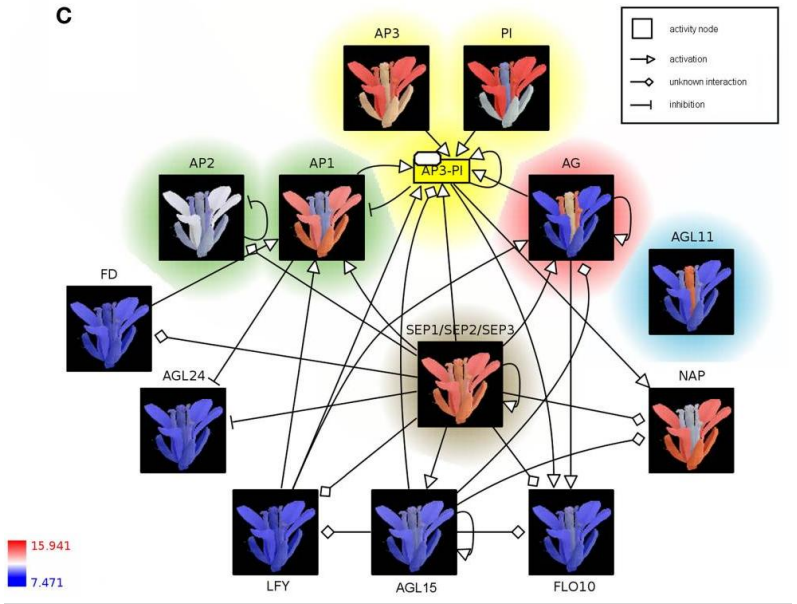
[3] Clayton School of Information Technology, Monash University, Clayton, VIC, Australia

The complexity and temporal as well as spatial resolution of transcriptome datasets is constantly increasing due to extensive technological developments. Here we present methods for advanced visualization and intuitive exploration of transcriptomics data as necessary prerequisites in order to facilitate the gain of biological knowledge. Color-coding of structural images based on the expression level enables a fast visual data analysis in the background of the examined biological system. The network-based exploration of these visualizations allows for comparative analysis of genes with specific transcript patterns and supports the extraction of functional relationships even from large datasets. In order to illustrate the presented methods, the tool HIVE was applied for visualization and exploration of database-retrieved expression data for master regulators of *Arabidopsis thaliana* flower and seed development in the context of corresponding tissue-specific regulatory networks.

Keywords: omics data visualization, expression atlas, data integration, color-coding, biological network, systems biology graphical notation, visual analytics

Citation: Junker A, Rohn H and Schreiber F (2012) Visual analysis of transcriptome data in the context of anatomical structures and biological networks. *Front. Plant Sci.* 3:252. doi: 10.3389/fpls.2012.00252



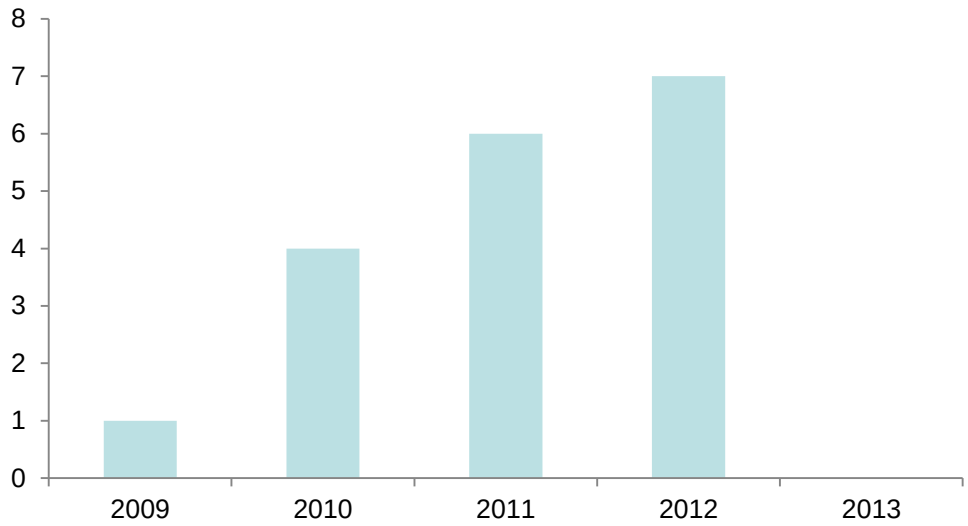


Literature survey

- Citations for Le Novère et al. 2009 (Nat Biotech)
- PubMed > 90 citations
- Google Scholar > 240 citations

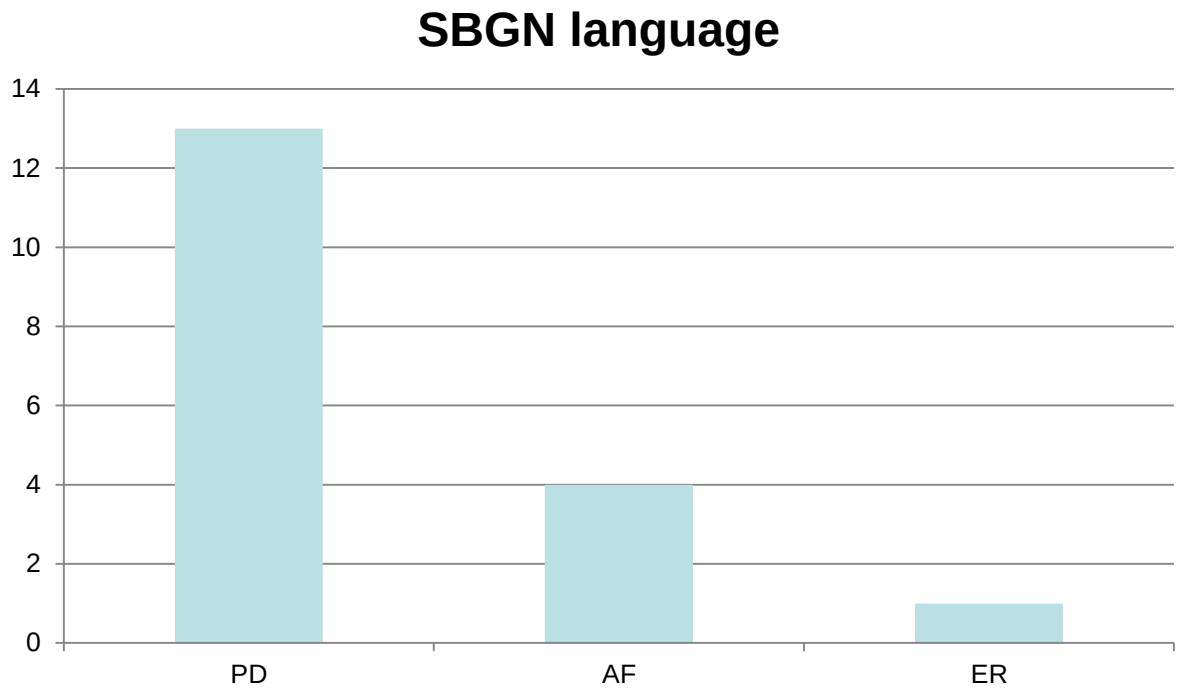
Literature survey

- 17 biological papers citing and using SBGN (no reviews, no tools)

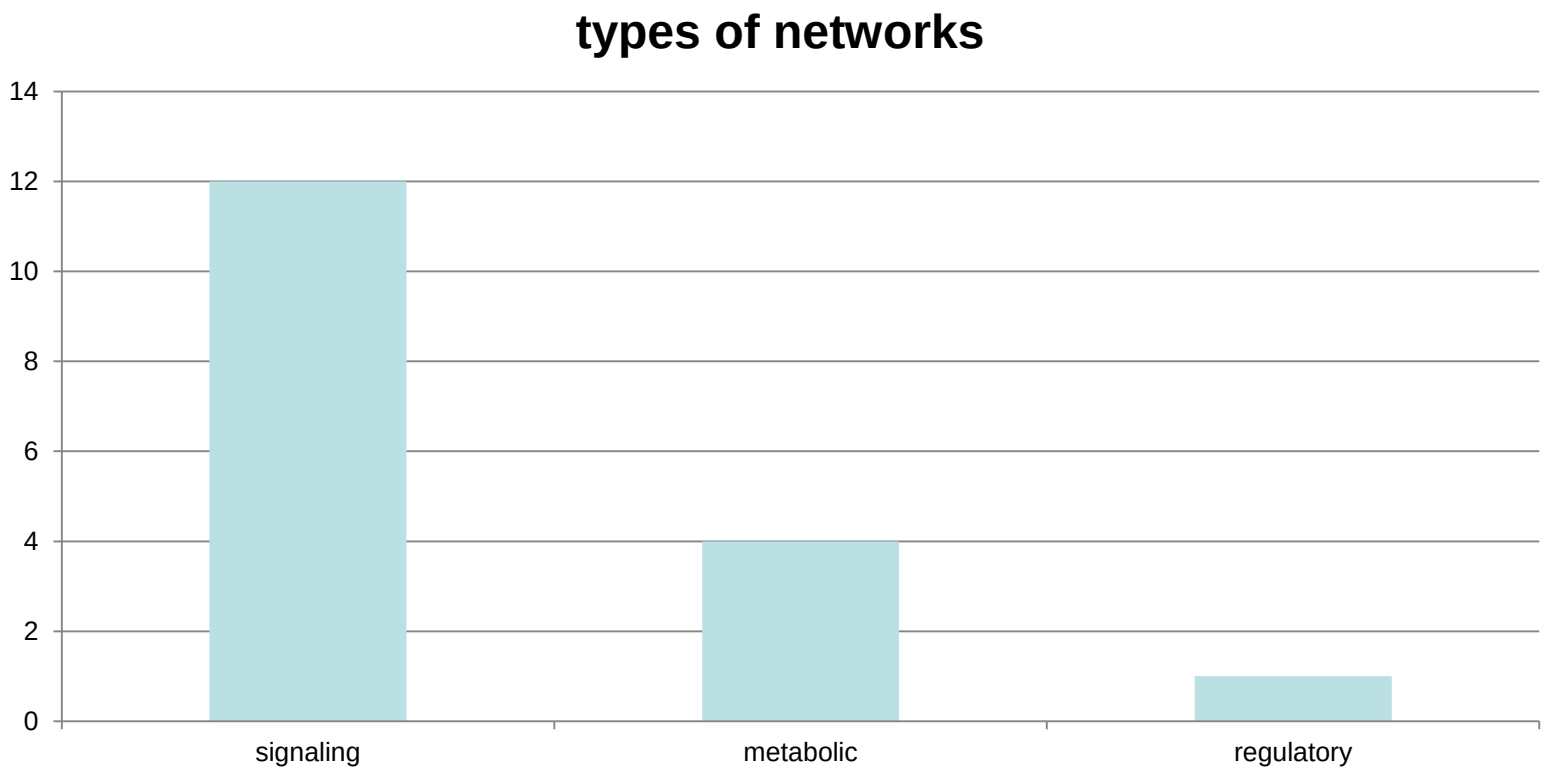


Which language of SBGN?

- Biologists mostly use PD or AF



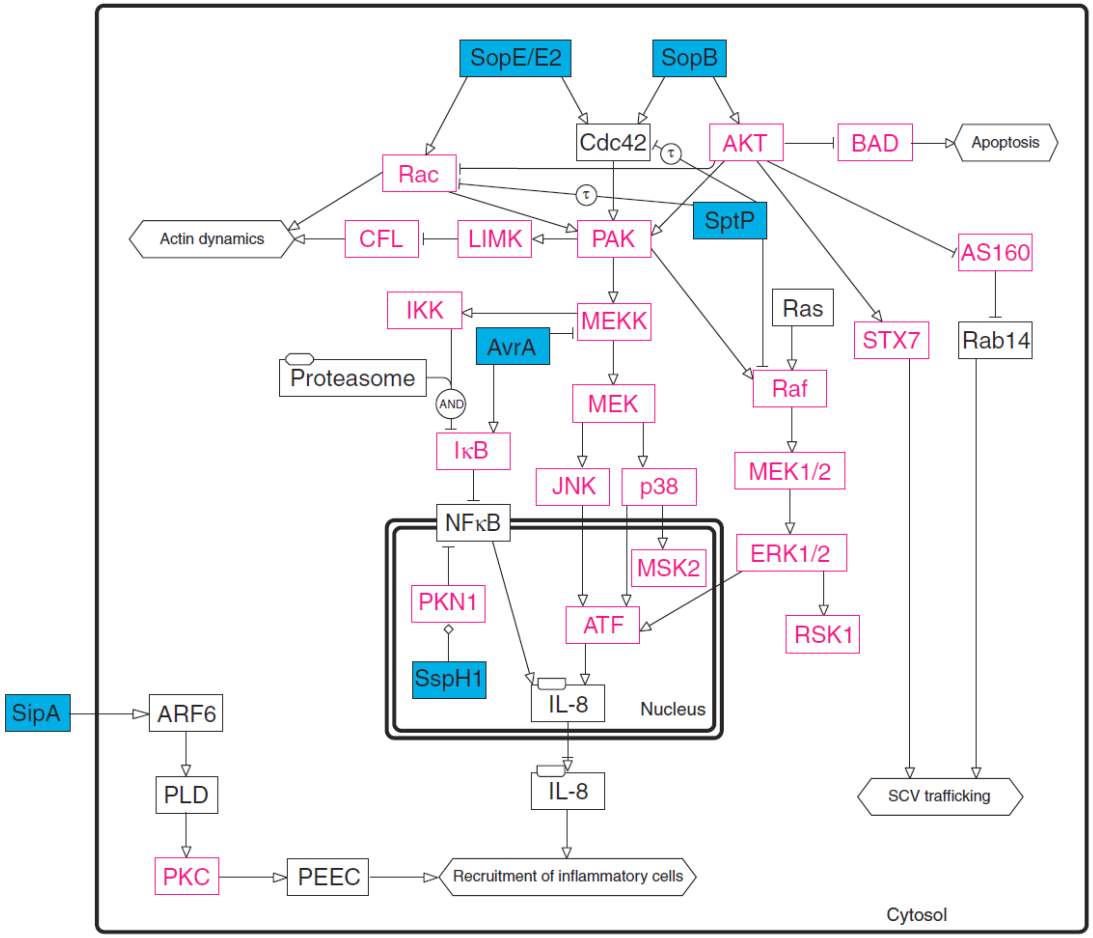
Which type of networks?



` **Phosphoproteomic Analysis of Salmonella-Infected Cells Identifies Key Kinase Regulators and SopB-Dependent Host Phosphorylation Events**

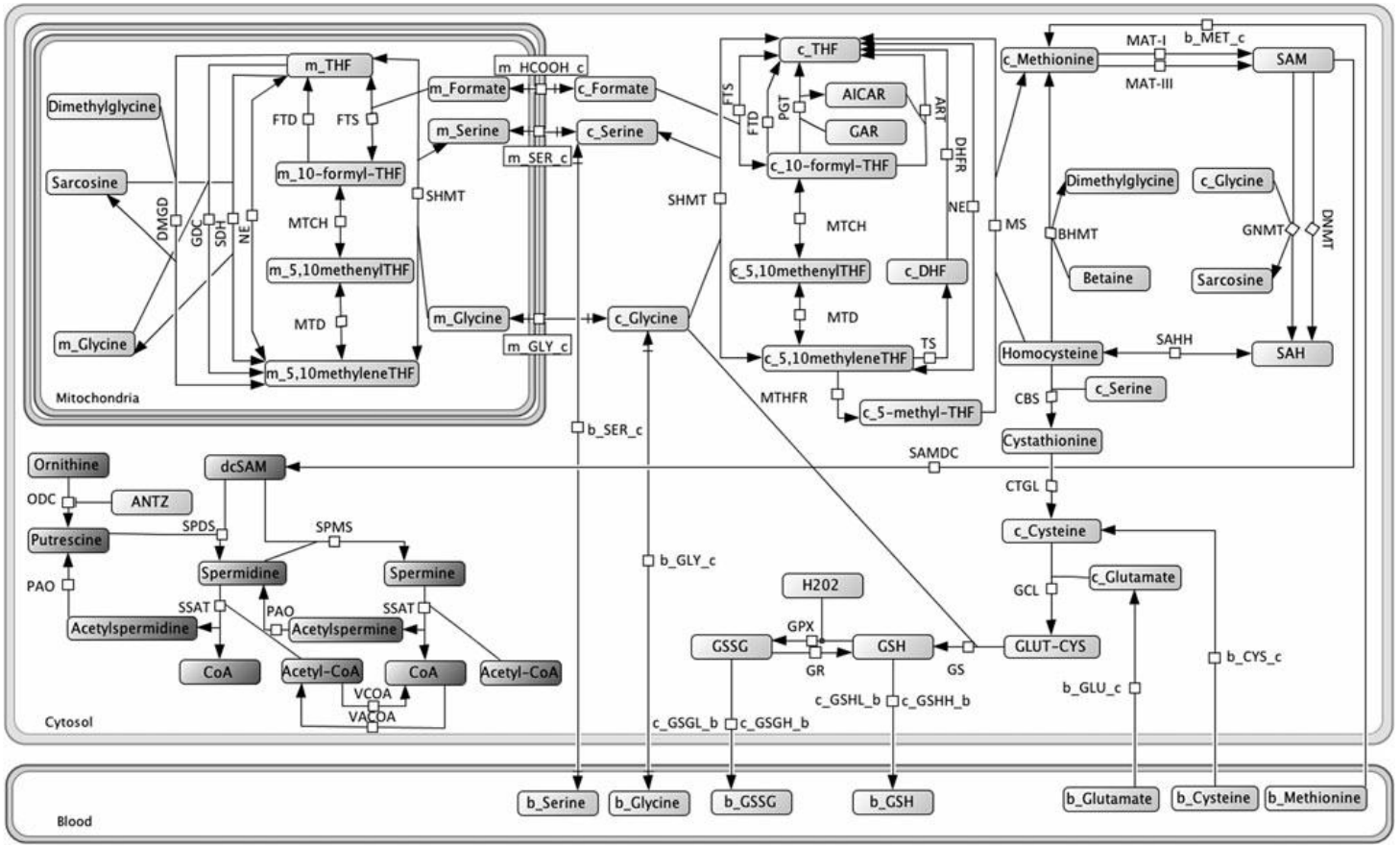
Lindsay D. Rogers, Nat F. Brown, Yuan Fang, Steven Pelech and Leonard J. Foster (20 September 2011)

Science Signaling **4** (191), rs9. [DOI: 10.1126/scisignal.2001668]



A combined model of hepatic polyamine and sulfur amino acid metabolism to analyze S-adenosyl methionine availability

Armando Reyes-Palomares · Raúl Montañez · Francisca Sánchez-Jiménez · Miguel Ángel Medina



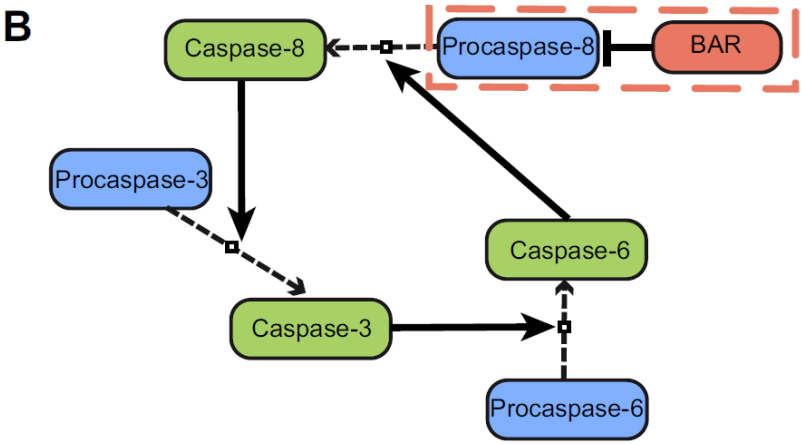
The Caspase-8 Dimerization/Dissociation Balance Is a Highly Potent Regulator of Caspase-8, -3, -6 Signaling*[S]

Received for publication, February 12, 2010, and in revised form, July 20, 2010 Published, JBC Papers in Press, August 11, 2010, DOI 10.1074/jbc.M110.113860

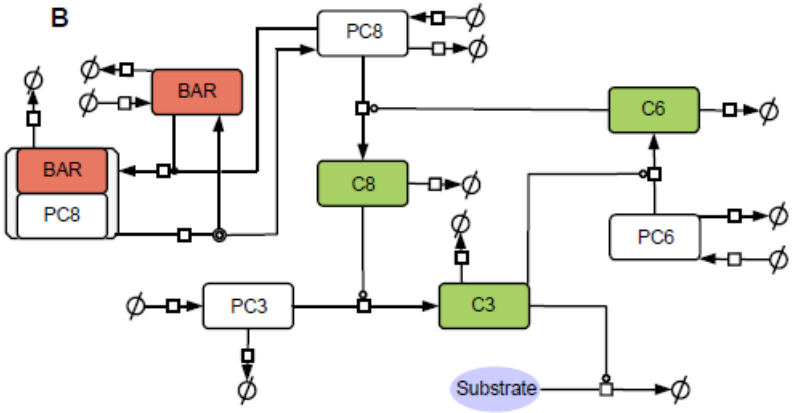
Maximilian L. Würstle[‡§], **Maike A. Laussmann**[‡§], **and Markus Rehm**[‡§1]

From the [‡]*Department of Physiology and Medical Physics, and the* [§]*Systems Biology Group, Royal College of Surgeons in Ireland, Dublin 2, Ireland*

Figure in the paper



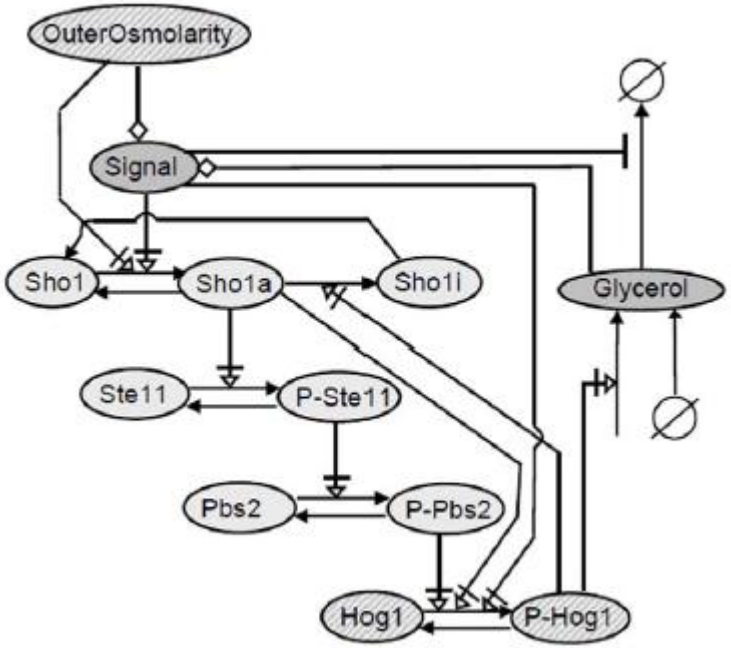
Suppl. Figure



Automated Ensemble Modeling with *modelMaGe*: Analyzing Feedback Mechanisms in the Sho1 Branch of the HOG Pathway

Jörg Schaber[1,2]*, Max Flöttmann[2], Jian Li[2], Carl-Fredrik Tiger[3], Stefan Hohmann[3], Edda Klipp[2]

1 Institute for Experimental Internal Medicine, Medical Faculty, Otto von Guericke University, Magdeburg, Germany, **2** Theoretical Biophysics, Department of Biology, Humboldt University, Berlin, Germany, **3** Department of Cell and Molecular Biology, University of Gothenburg, Göteborg, Sweden

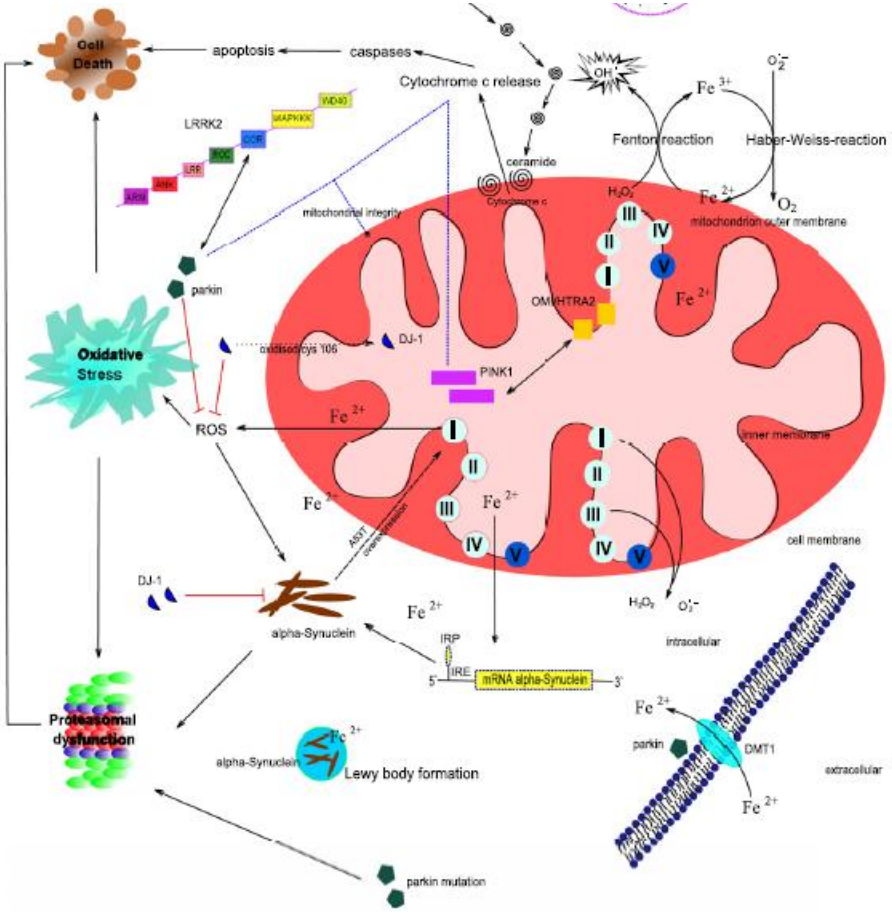


SBGN?

Genetics and iron in the systems biology of Parkinson's disease and some related disorders

Claudia Funke [a], Susanne A. Schneider [b,c], Daniela Berg [a,d,*], Douglas B. Kell [e,*]

[a] *Department of Neurodegeneration, Hertie Institute for Clinical Brain Research, University of Tübingen, Otfried-Müller-Strasse 27, 72076 Tübingen, Germany*
[b] *Department of Neurology, University Kiel, Arnold Heller Str. 3, 24105 Kiel, Germany*
[c] *Department of Clinical Neuroscience, Imperial College London, Charing Cross Campus, London, UK*
[d] *DZNE, German Center of Neurodegenerative Diseases, Tübingen, Germany*
[e] *School of Chemistry and Manchester Institute of Biotechnology, The University of Manchester, 131 Princess St., Manchester M1 7DN, UK*



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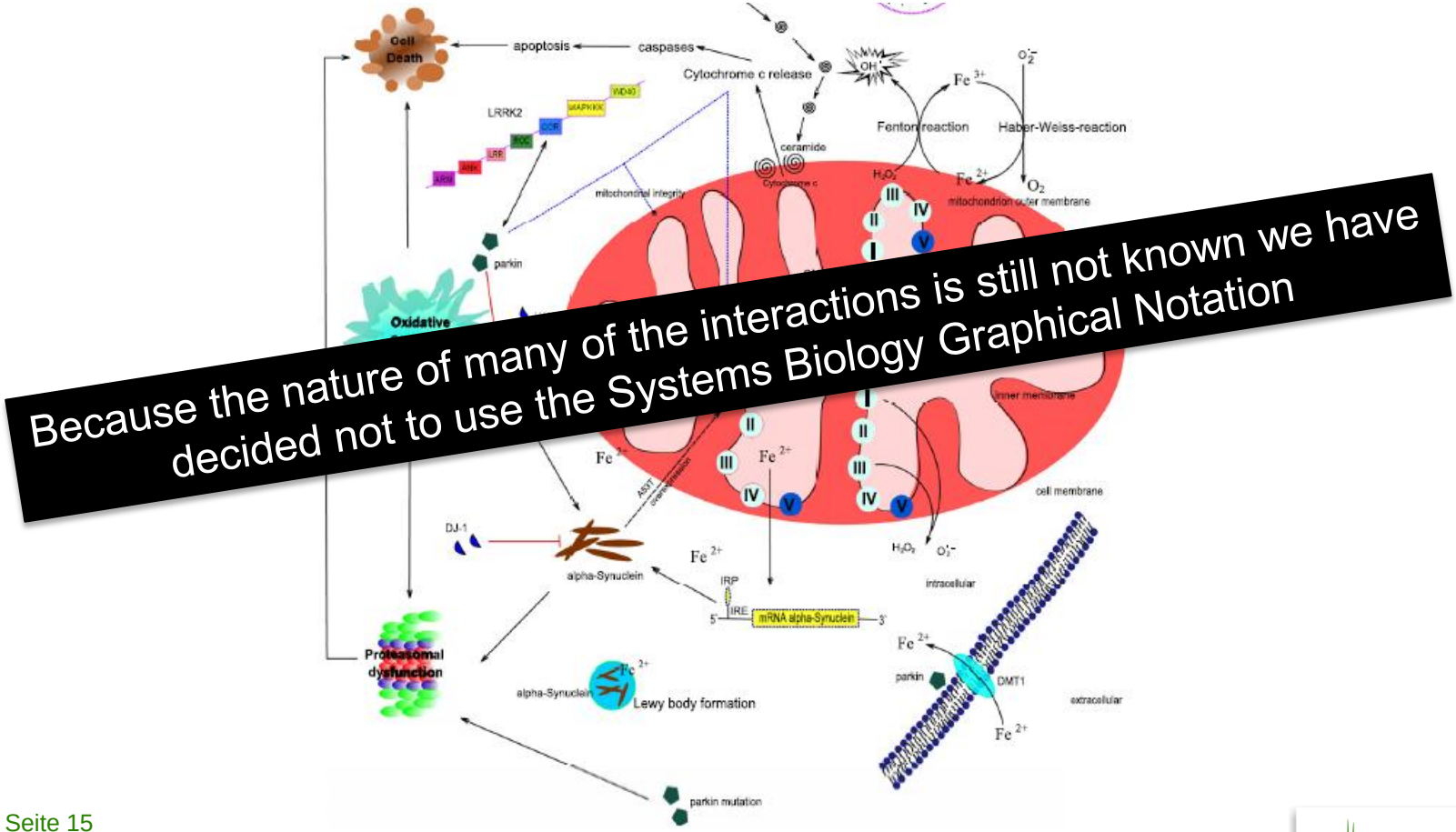
[b] Department of Neurology, University Kiel, Arnold Heller Str. 3, 24105 Kiel, Germany
[c] Department of Clinical Neuroscience, Imperial College London, Charing Cross Campus, London, UK
[d] DZNE, German Center of Neurodegenerative Diseases, Tübingen, Germany
[e] School of Chemistry and Manchester Institute of Biotechnology, The University of Manchester, 131 Princess St., Manchester M1 7DN, UK

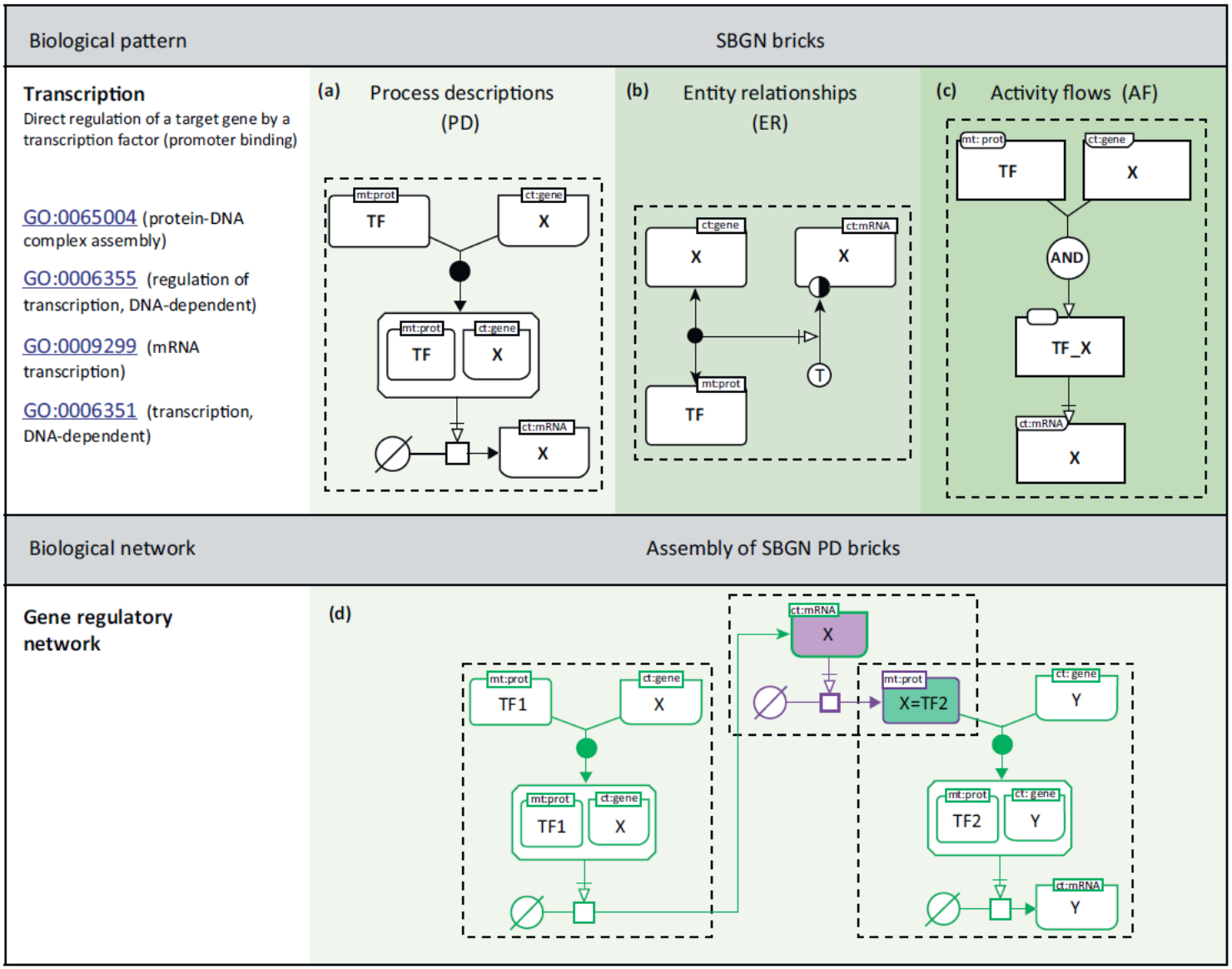


Because the nature of many of the interactions is still not known we have decided not to use the Systems Biology Graphical Notation

The question is: WHY?

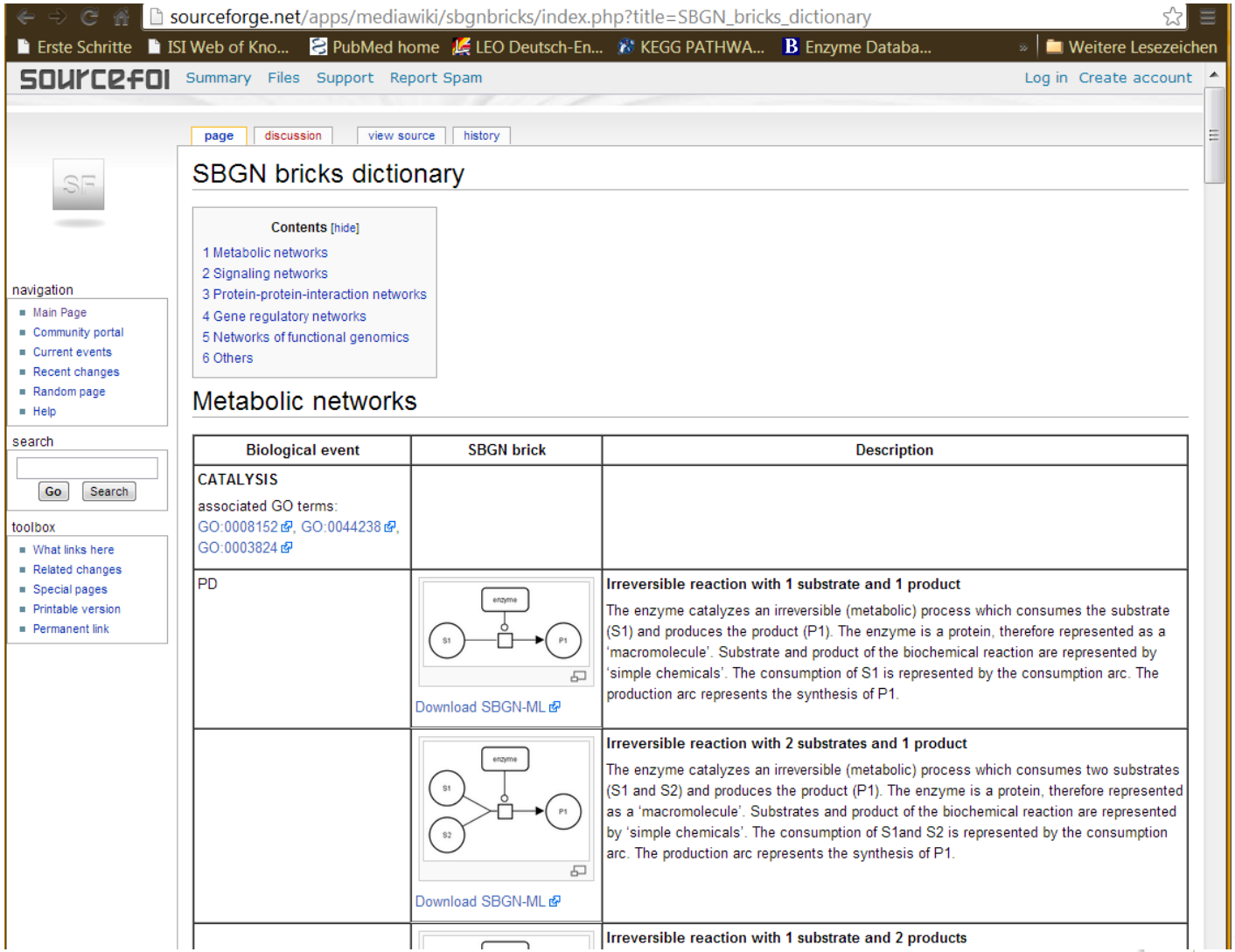
- Threshold is very high > reading and understanding specs requires a lot of efforts
- Cost-benefit ratio

- More pressure/request by publishers
- Ways to facilitate the application of SBGN

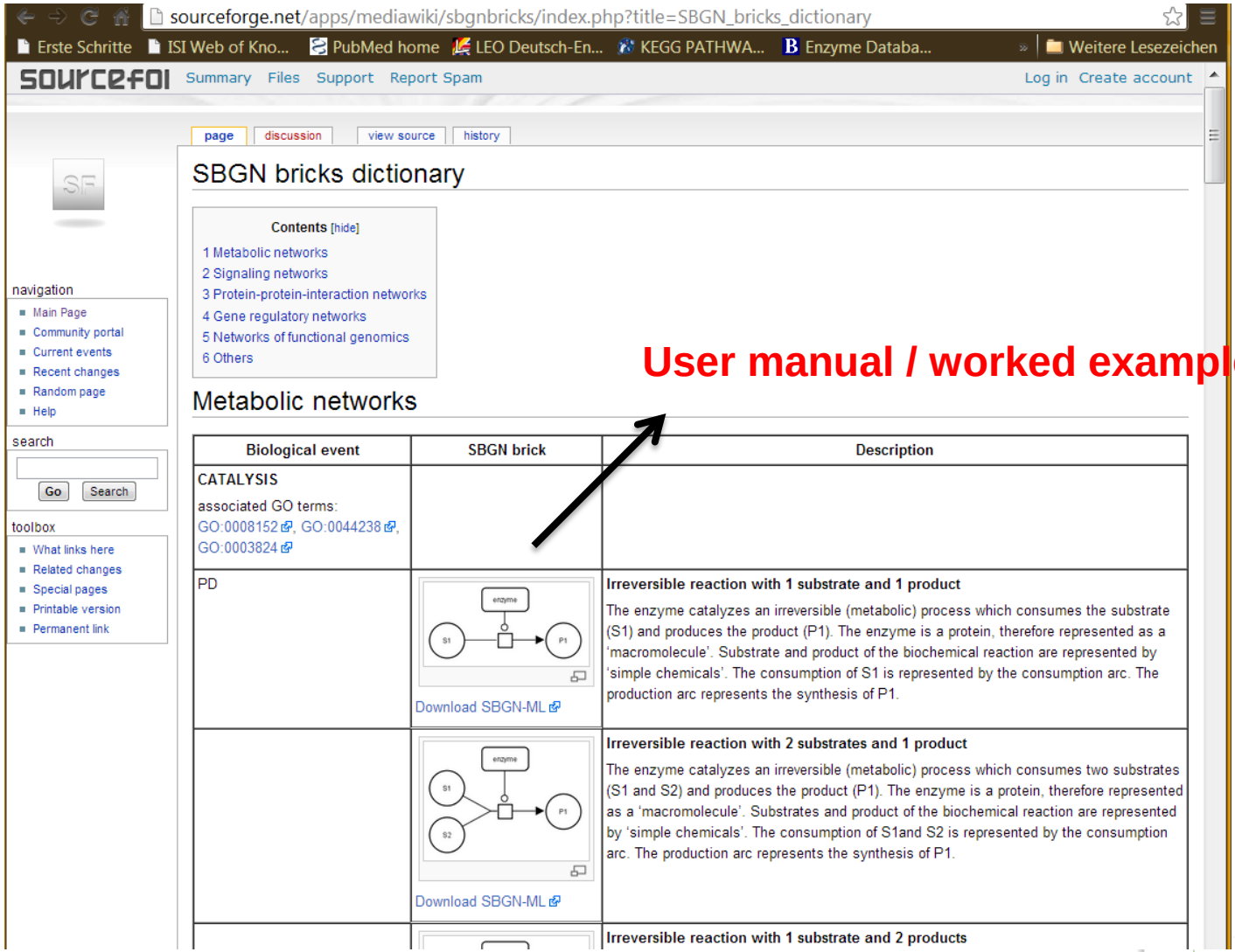


TRENDS in Biotechnology

SBGN bricks


sourceforge.net/apps/mediawiki/sbgnbricks/index.php?title=SBGN_bricks_dictionary
Erste Schritte
ISI Web of Kno...
PubMed home
LEO Deutsch-En...
KEGG PATHWA...
Enzyme Databa...
Weitere Lesezeichen
sourceforge
Summary
Files
Support
Report Spam
Log in
Create account
page
discussion
view source
history
navigation
Main Page
Community portal
Current events
Recent changes
Random page
Help
search
Go
Search
toolbox
What links here
Related changes
Special pages
Printable version
Permanent link
SBGN bricks dictionary
Contents [hide]
1 Metabolic networks
2 Signaling networks
3 Protein-protein-interaction networks
4 Gene regulatory networks
5 Networks of functional genomics
6 Others
Metabolic networks
Biological event
SBGN brick
Description
CATALYSIS
associated GO terms:
GO:0008152, GO:0044238, GO:0003824
PD
enzyme
S1
P1
Download SBGN-ML
Irreversible reaction with 1 substrate and 1 product
The enzyme catalyzes an irreversible (metabolic) process which consumes the substrate (S1) and produces the product (P1). The enzyme is a protein, therefore represented as a 'macromolecule'. Substrate and product of the biochemical reaction are represented by 'simple chemicals'. The consumption of S1 is represented by the consumption arc. The production arc represents the synthesis of P1.
enzyme
S1
S2
P1
Download SBGN-ML
Irreversible reaction with 2 substrates and 1 product
The enzyme catalyzes an irreversible (metabolic) process which consumes two substrates (S1 and S2) and produces the product (P1). The enzyme is a protein, therefore represented as a 'macromolecule'. Substrates and product of the biochemical reaction are represented by 'simple chemicals'. The consumption of S1and S2 is represented by the consumption arc. The production arc represents the synthesis of P1.
Irreversible reaction with 1 substrate and 2 products

SBGN bricks



User manual / worked examples

SBGN bricks

sourceforge.net/apps/mediawiki/sbgnbricks/index.php?title=SBGN_bricks_dictionary
Erste Schritte
ISI Web of Kno...
PubMed home
LEO Deutsch-En...
KEGG PATHWA...
Enzyme Databa...
Weitere Lesezeichen
sourceforge
Summary
Files
Support
Report Spam
Log in
Create account
page
discussion
view source
history
SBGN bricks dictionary
Contents [hide]
1 Metabolic networks
2 Signaling networks
3 Protein-protein-interaction networks
4 Gene regulatory networks
5 Networks of functional genomics
6 Others
navigation
Main Page
Community portal
Current events
Recent changes
Random page
Help
search
Go
Search
toolbox
What links here
Related changes
Special pages
Printable version
Permanent link
Metabolic networks
Biological event
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Description
CATALYSIS
Associated GO terms:
GO:0008152, GO:0044238, GO:0003824
PD
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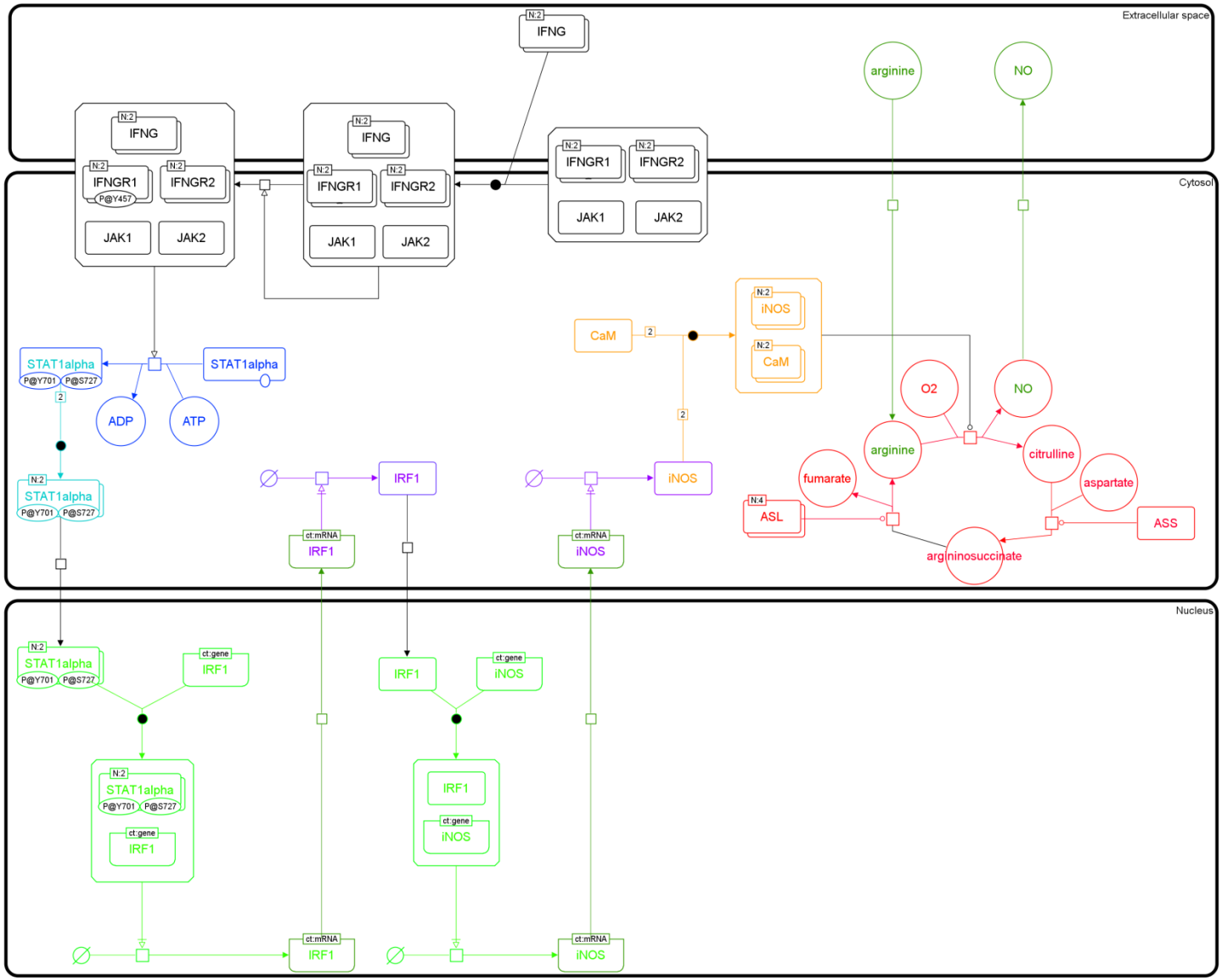
Irreversible reaction with 1 substrate and 2 products


Extracellular space
IFNG
arginine
NO
IFNGR1
IFNGR2
JAK1
JAK2
P@Y457
Cytosol
STAT1alpha
P@Y701
P@S727
ADP
ATP
CaM
iNOS
O2
fumarate
citrulline
aspartate
ASL
ASS
argininosuccinate
IRF1
ct:mRNA
ct:gene
Nucleus

Looking into the future

- Survey > ask people who used SBGN

➢ What was the motivation?

➢ How much time needed for learning SBGN?

➢ Which tools?