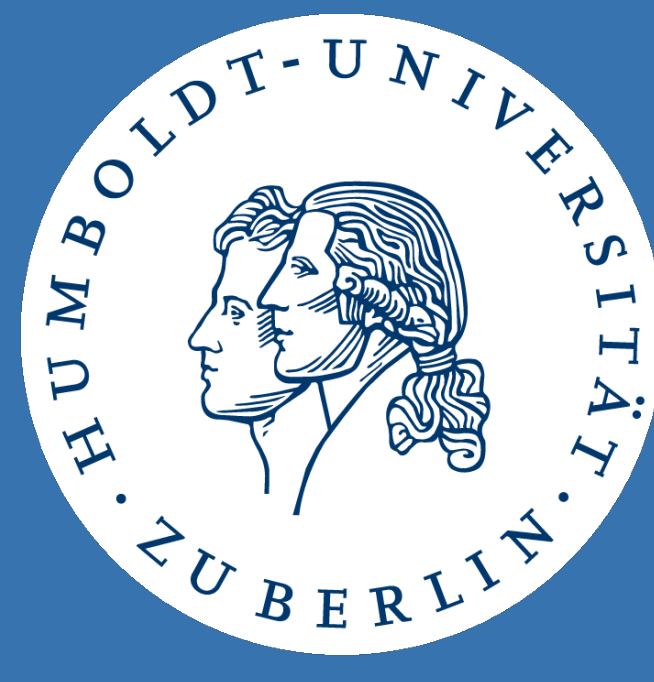
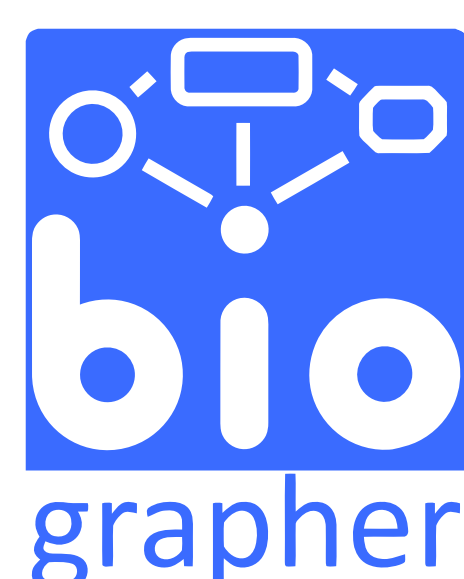




From rxncon to SBGN formats via biographer



The rxncon framework allows the user to annotate biological networks based on **elemental reactions** and **contingencies**. The network definition is unambiguous and at the same granularity as the experimental data. The network can automatically be visualised in different formats and translated into mathematical models.



biographer is a web-based **editor** and **renderer** for **SBGN-PD, -ER, and -AF diagrams**. It features an HTML5 based package (using HTML5, CSS3, JavaScript, and SVG) that can be used on-line and off-line or integrated into existing projects. biographer works with standardised Systems Biology document formats (SBML, SBGN-ML, and JSBGN) and supports touch devices like tablet computers.

Modification

Kinase Domain (KD) of Ste7 phosphorylates Fus3 at residue T180

Ste7_[KD]_P+_Fus3_[(T180)]

Msg5 dephosphorylates Fus3 at residue T180

Msg5_[PD]_P-_Fus3_[(T180)]

The Dbp homologous domain (DH) of Rom2 exchanges GDP with GTP at the guanine nucleotide binding domain (GnP) of Rho1

Rom2_[DH]_GEF_Rho1_[GnP]

Bem2 hydrolyses GTP to GDP at the guanine nucleotide binding domain (GnP) of Rho1

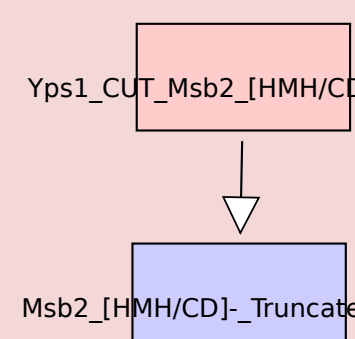
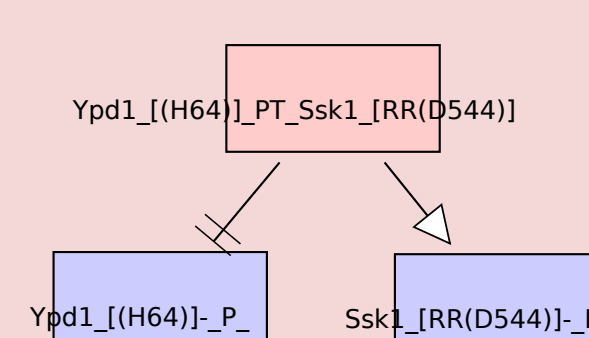
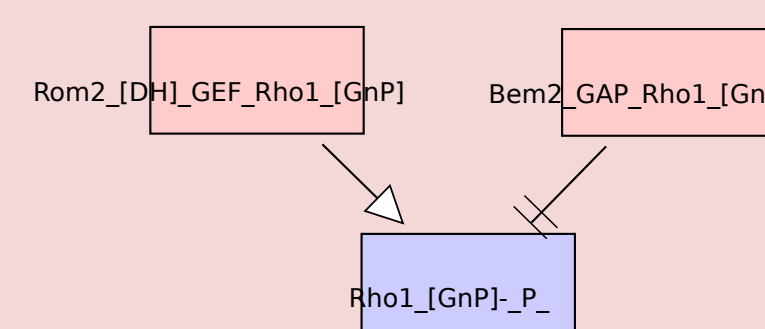
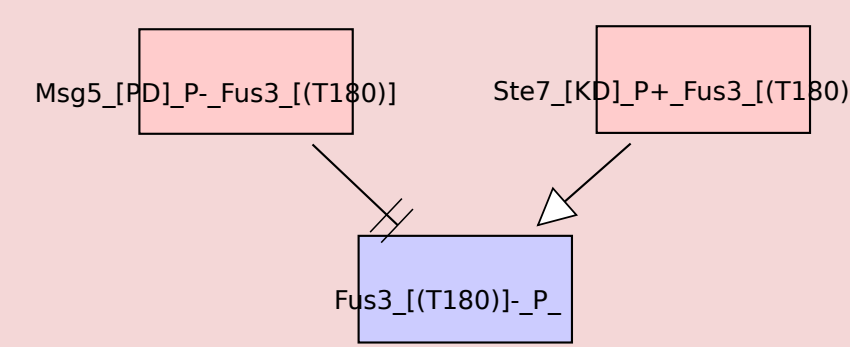
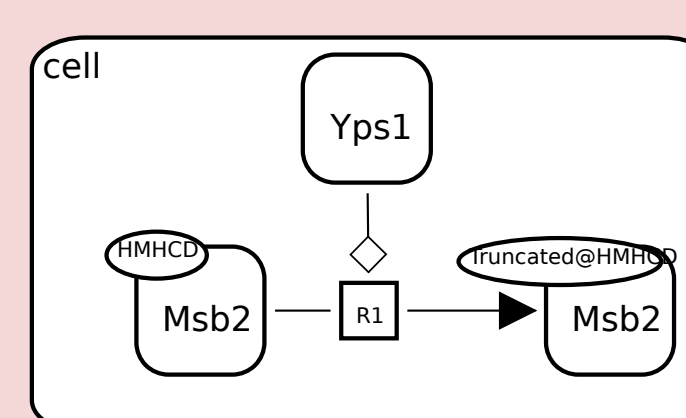
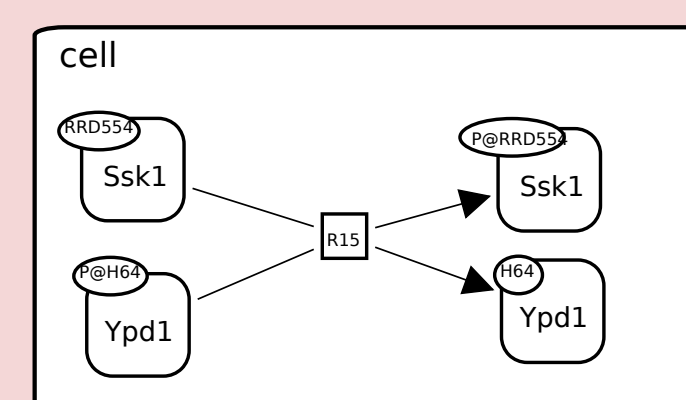
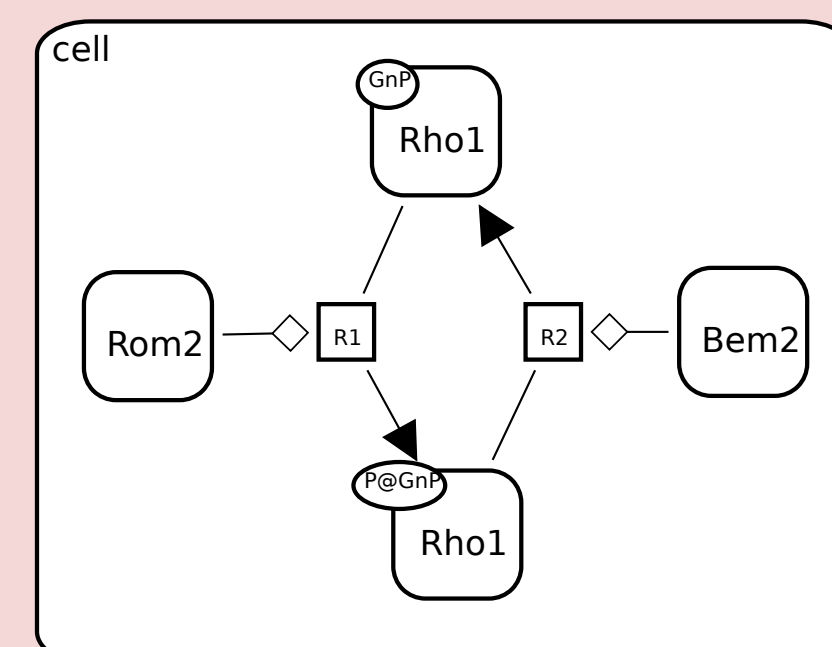
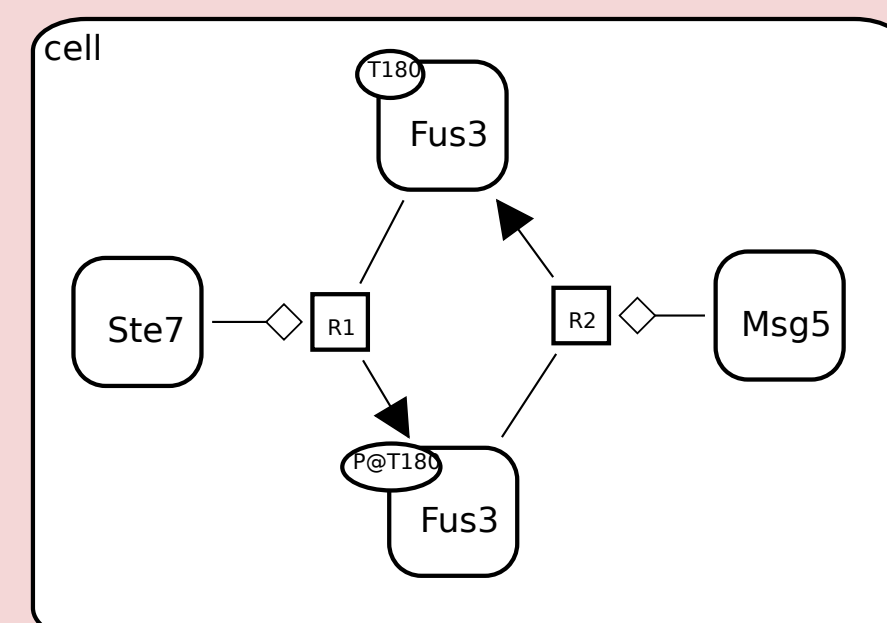
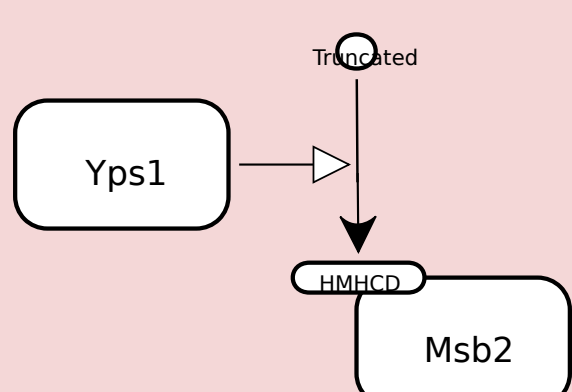
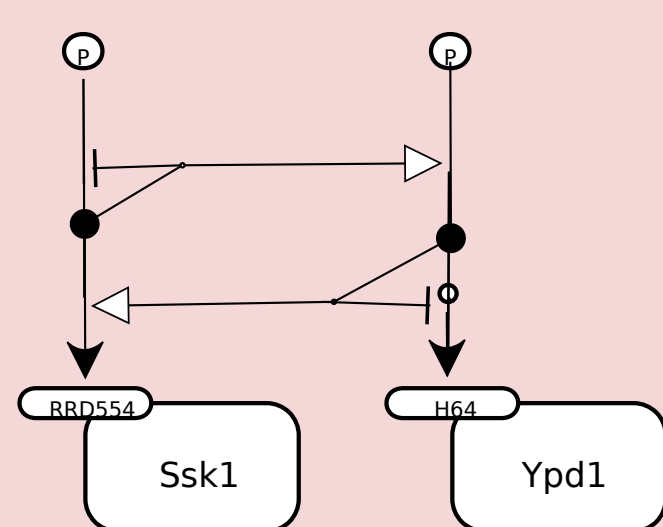
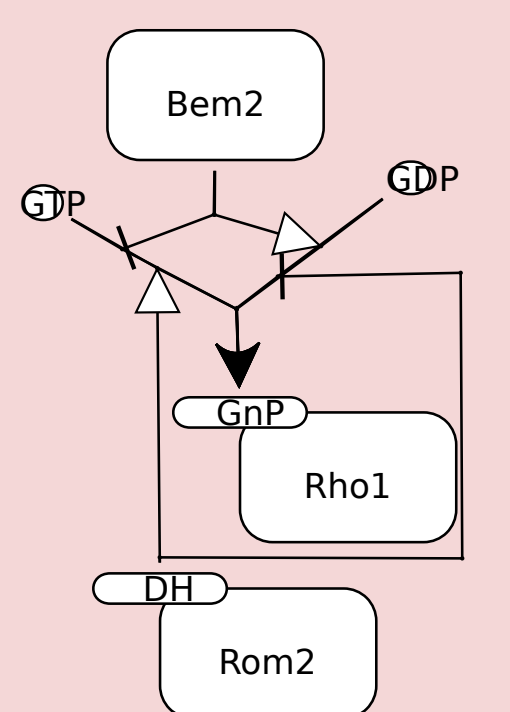
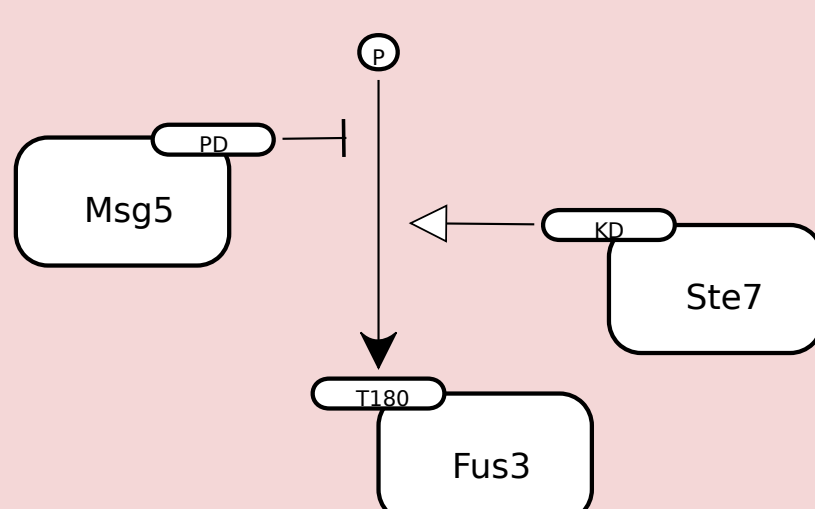
Bem2_GAP_Rho1_[GnP]

Ypd1 transfers a phosphate group from residue H64 to Ssk1, response regulator receiver domain, residue D554*

Ypd1_[(H64)]_PT_Ssk1_[RR(D554)]

Yps1 truncates Msb2 at the cleavage subdomain (CD) of the HMH domain

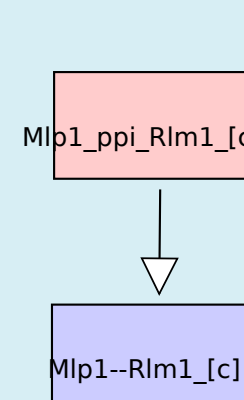
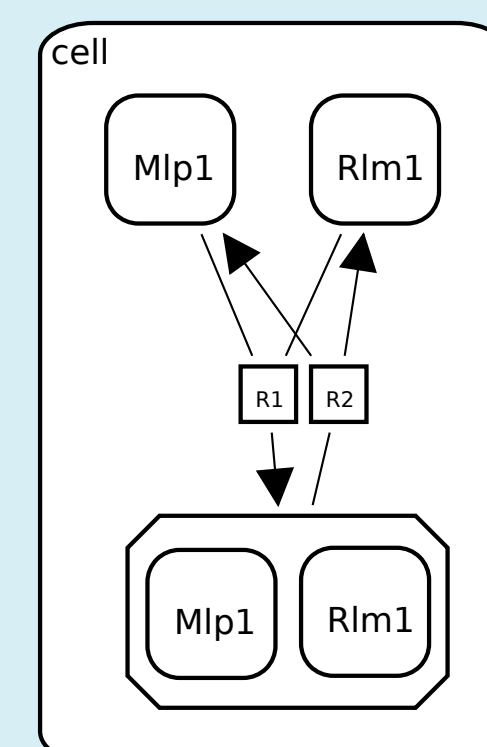
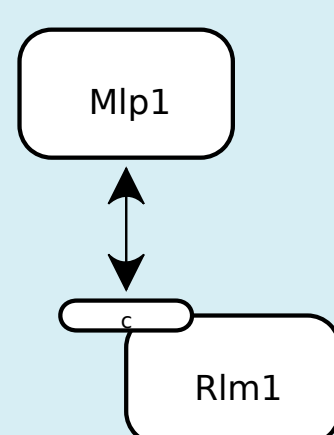
Yps1_CUT_Msb2_[HMH/CD]



Association

Mlp1 undergoes a protein-protein interaction with the c-terminal domain of Rlm1

Mlp1_ppi_Rlm1_[c]



Synthesis/ Degradation

Polymerase II transcribes CLN3

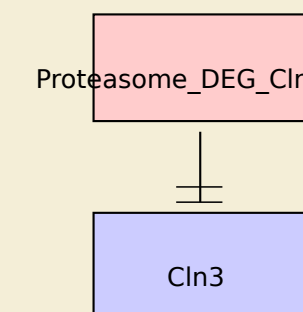
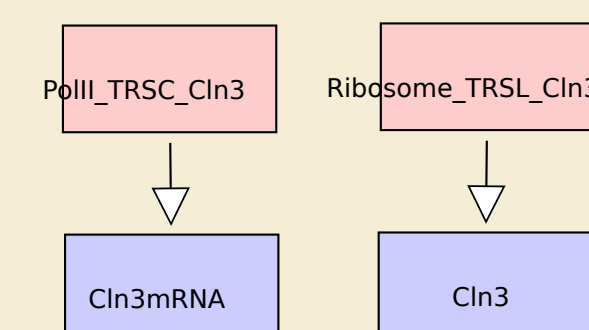
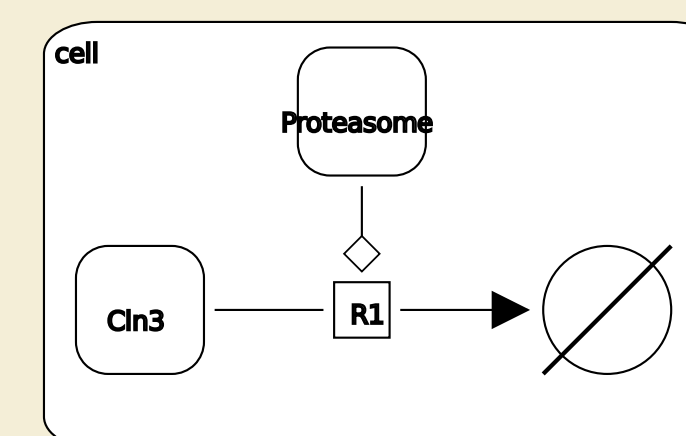
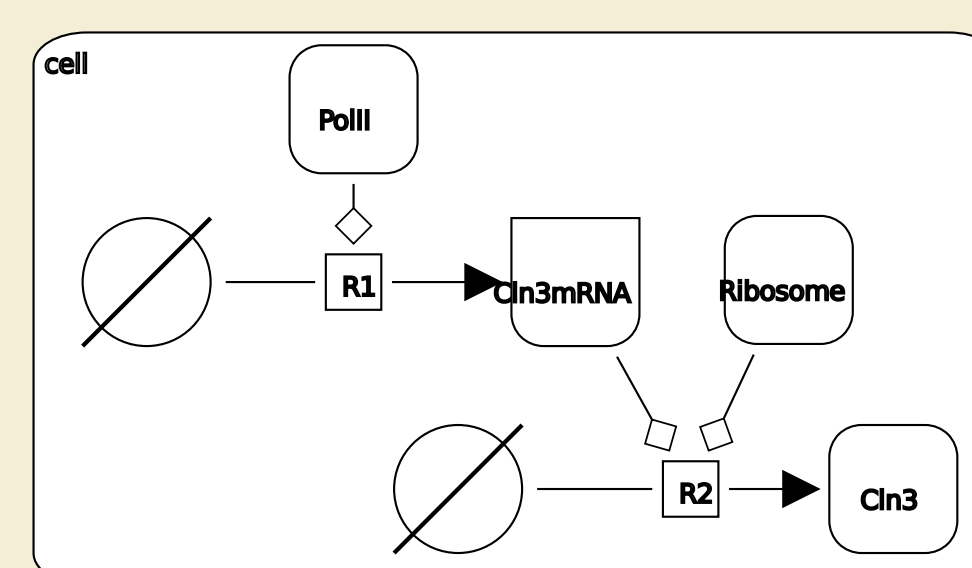
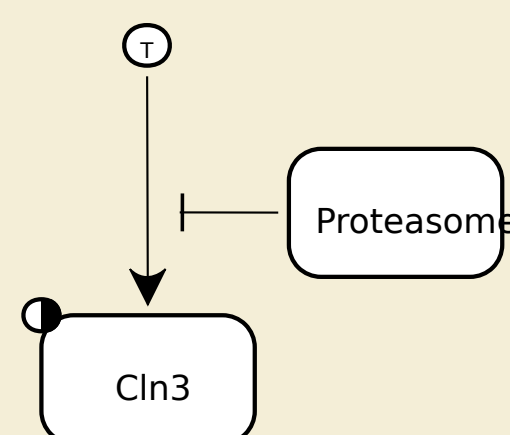
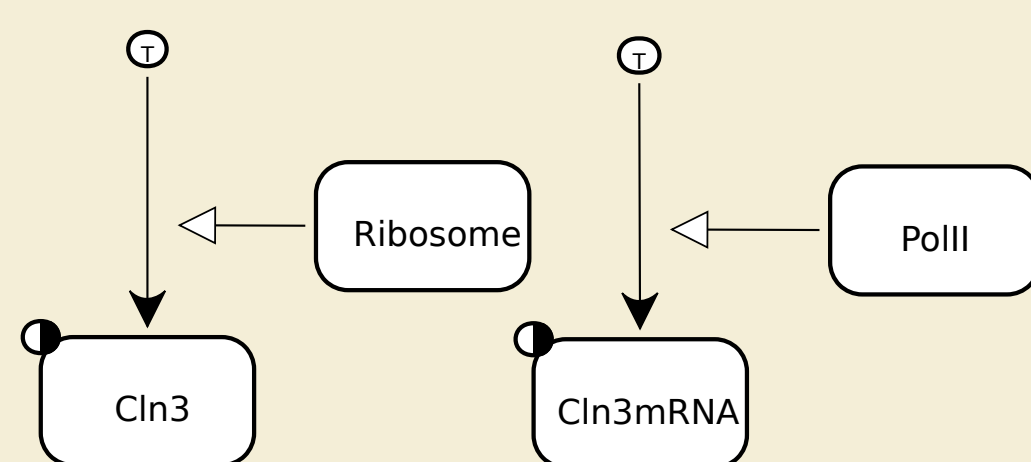
PollII_TRSC_Cln3

Ribosome translates mCLN3

Ribosome_TRSL_Cln3

The proteasome degrades Cln3

Proteasome_DEG_Cln3



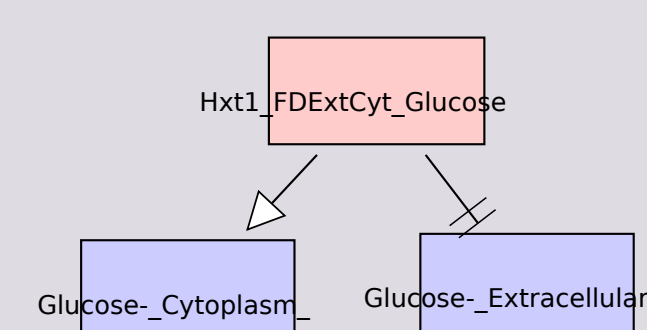
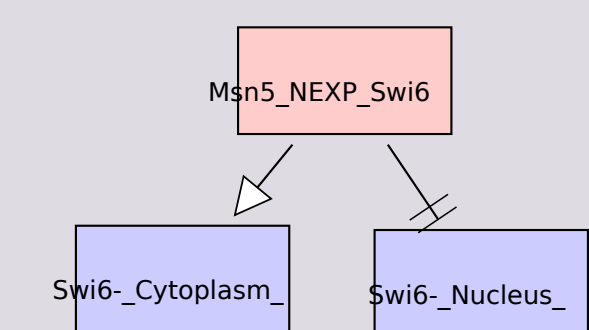
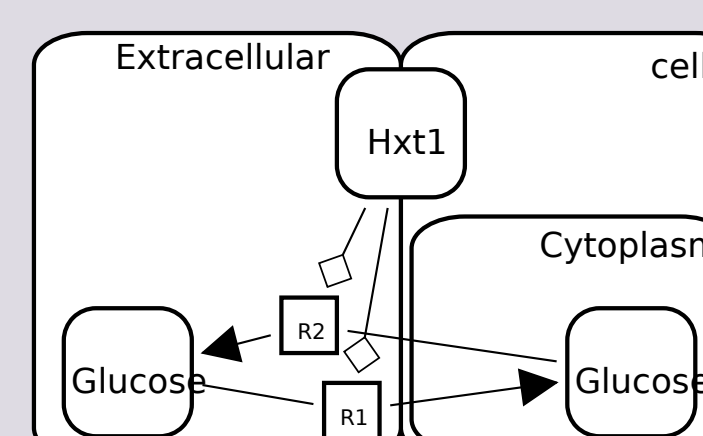
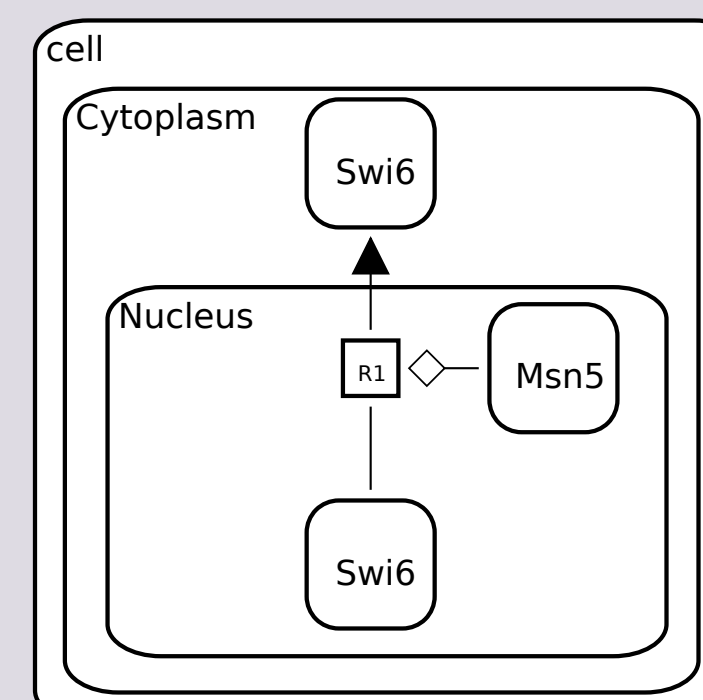
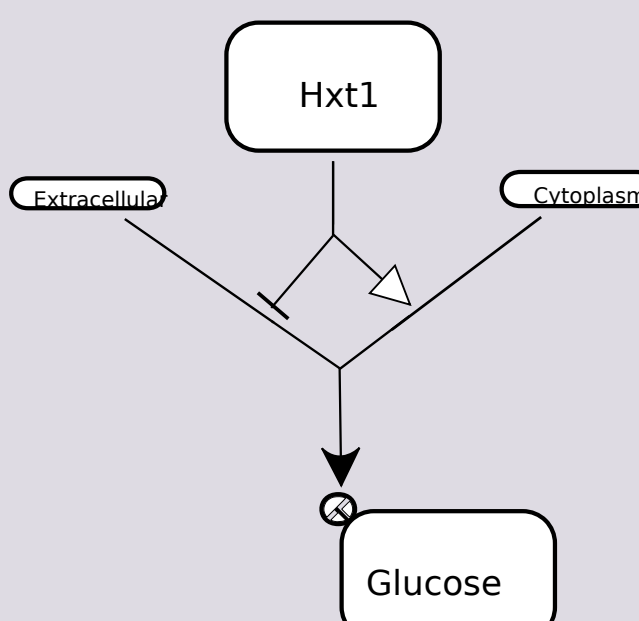
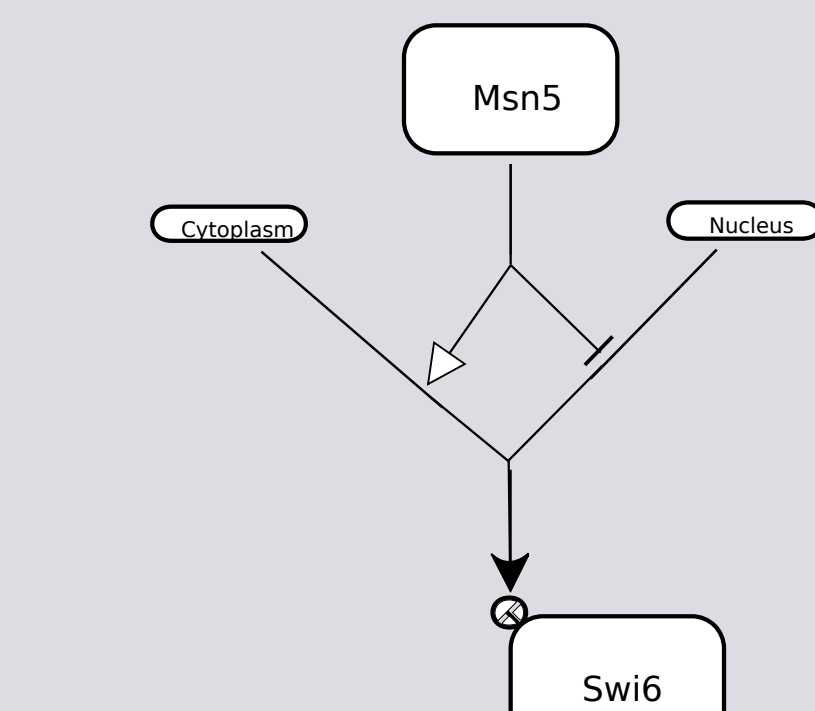
Relocalisation

Msn5 exports Swi6 from the nucleus to the cytosol

Msn5_NEXP_Swi6

Hxt1 facilitates diffusion of glucose from the extracellular matrix into the cytoplasm

Hxt1_FDExtCyt_Glucose



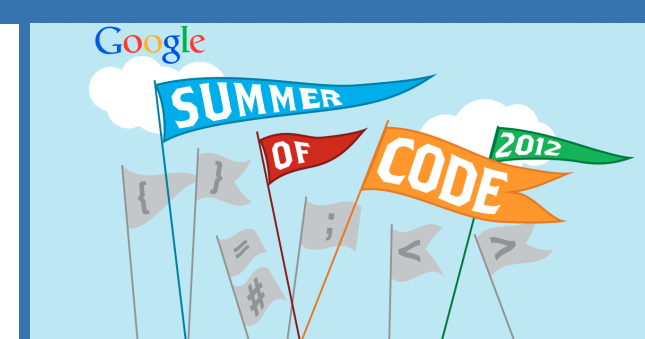
Web

rxncon.org
biographer.biologie.hu-berlin.de

References

biographer: Krause, F. *et al.*: biographer: web based editing and rendering of SBGN compliant biochemical networks. *Bioinformatics* 2013.
rxncon: Tiger, C.-F. *et al.*: A framework for mapping, visualisation and automatic model creation of signal-transduction networks. *Mol Syst Biol.* 2012.
Review: Rother, M. *et al.*: Information content and scalability in signal transduction network reconstruction formats. *Molecular BioSystems* 2013.

Funding



* Accurate implementation requires additional reaction context.

