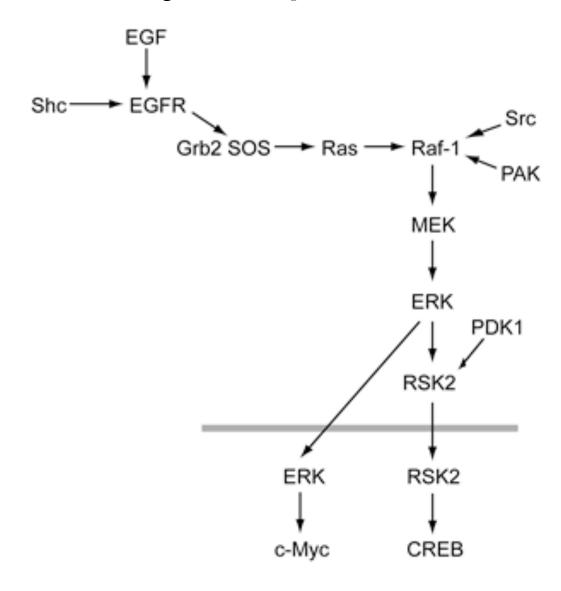


Process Diagram and Relationship Diagram

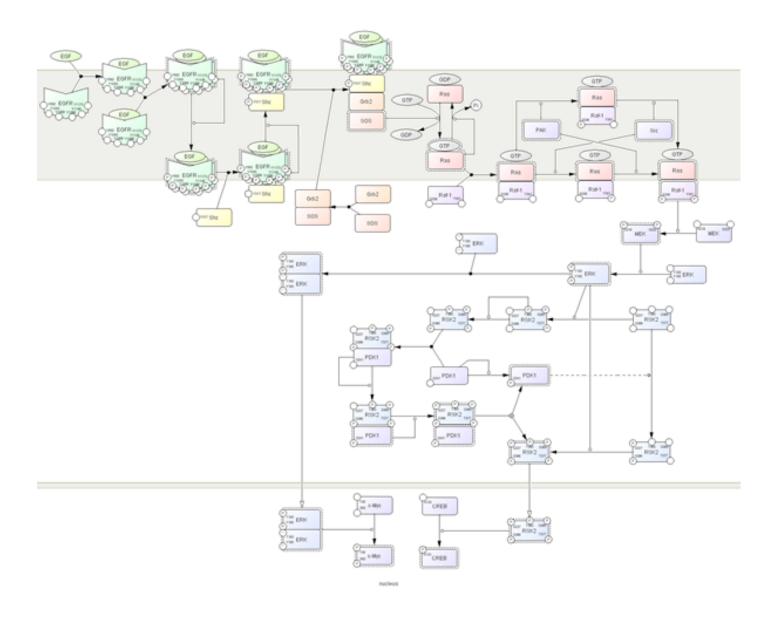
Hiroaki Kitano The Systems Biology Institute

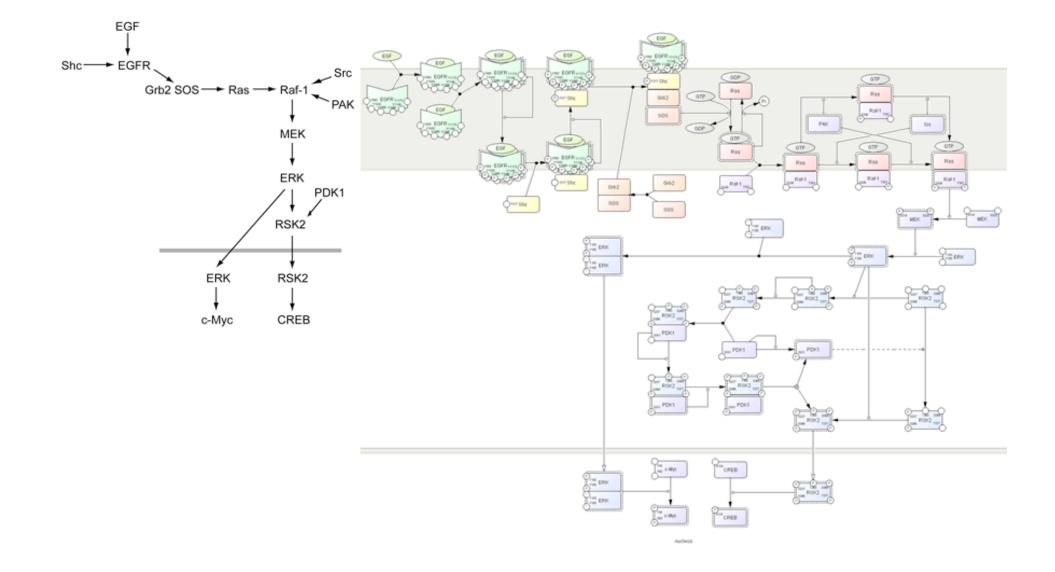
Funded by NEDO International Grant, Genome Network Project of MEXT, ERATO-SORST Program of JST.

Pathway map used now

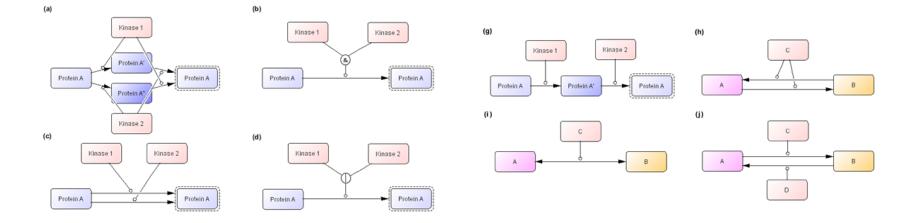


The Process Diagram

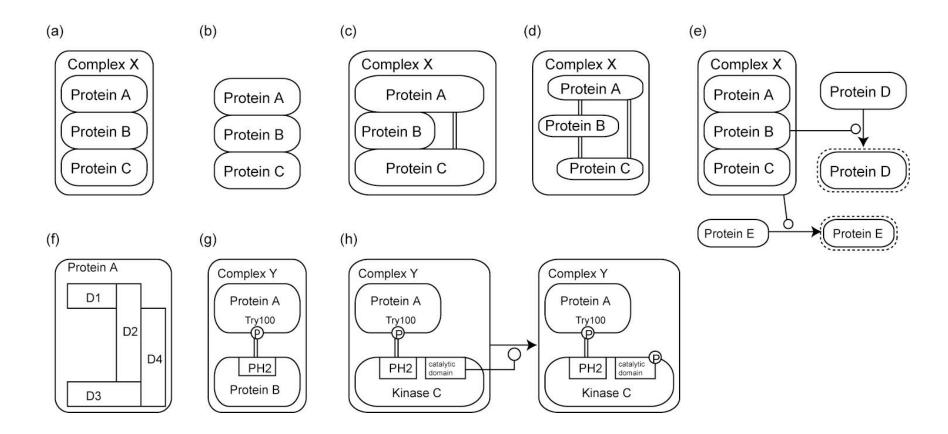




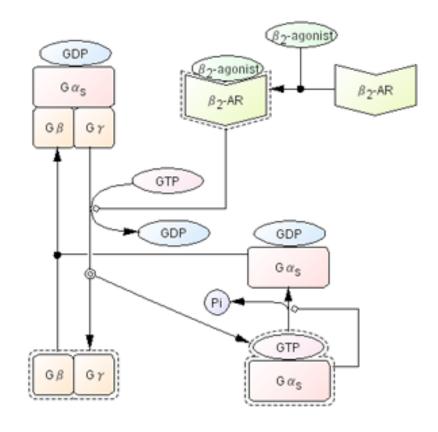
State Node Symbols Arc Symbols **Reduced Notation Symbols** (Transit Node and Edges) Class-I Reduced Notation protein_name Protein State transition Degradation Known transition omitted Receptor receptor name Transcription Unknown transition Ion Channel name Bidirectional transition (Closed) Translation Ion Channel Translocation name (Open) Module Truncated name Association Protein Class-II Reduced Notation (Viewer Only) Gene name Dissociation Activation/ index Inhibition/ RNA name Truncation Modification **Node Structure** Anti-sense name Promote RNA transition Residue (mod)res_pos phosphorylated modification name (Ac) acetylated Ion name Inhibit (b) ubiquitinated transition empty (v_o) methylated Simple name don't care Molecule (on) hydroxylated unknown Add reactant Complex complex name name Unknown State C1 Node Add product Phenotype name Connectivity (binding, etc) AND Homodimer / О Promotor N-mer with protein_name and coding region2 region2 N stacked structure gene_name symbols for gene OR exon1)-[exon2 Active exon structure protein name for RNA Protein



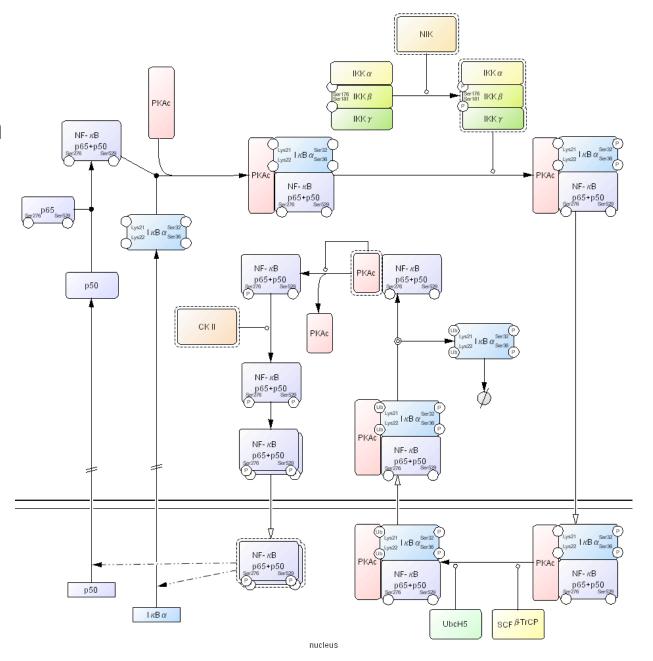
Structure of Complex



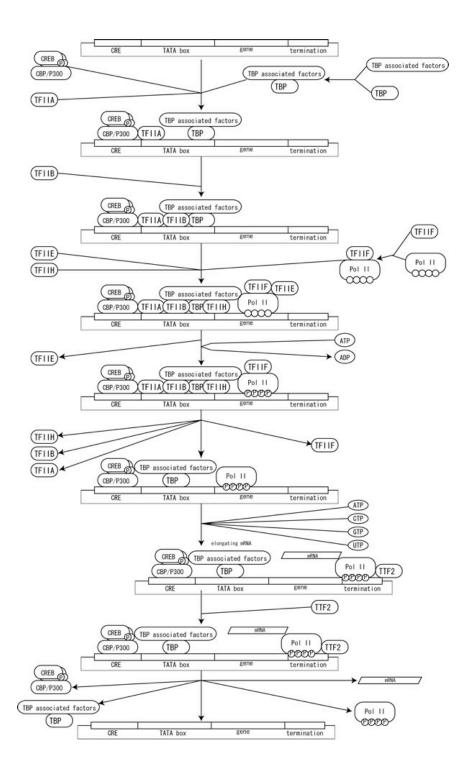
Example of Process Diagram G-protein



Example of Process Diagram NFkB

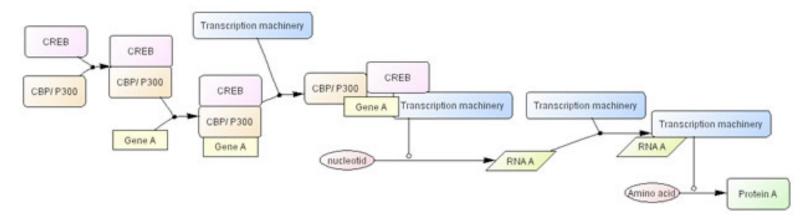


Process Diagram for Transcription

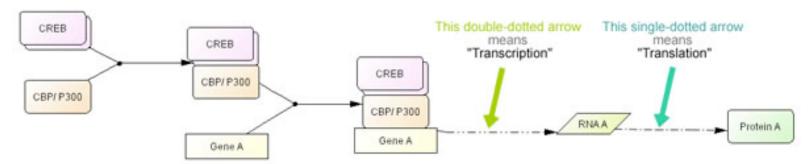


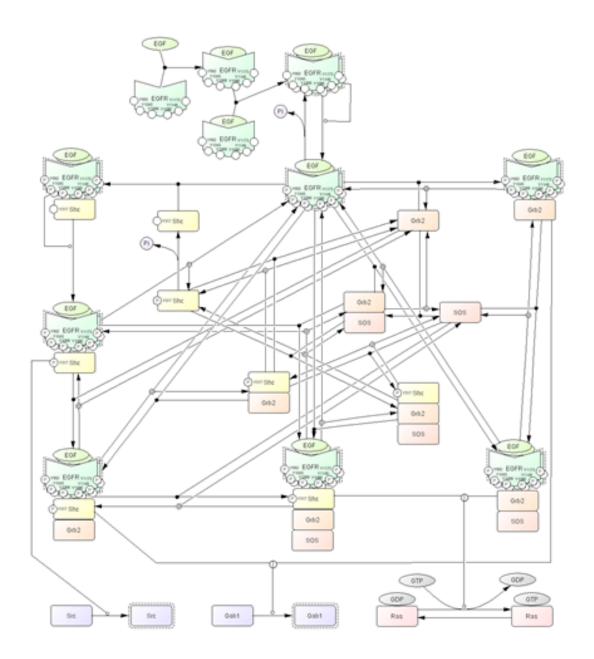
transcription and translation

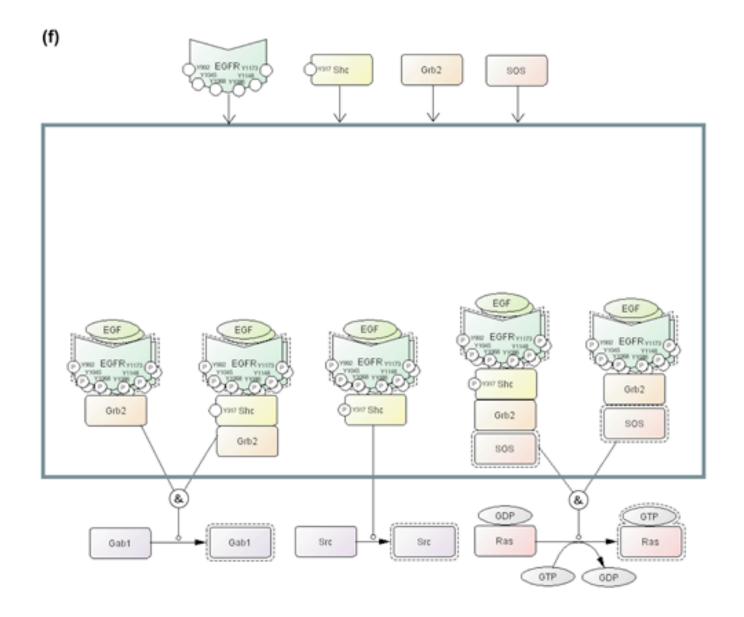
Simplified notation

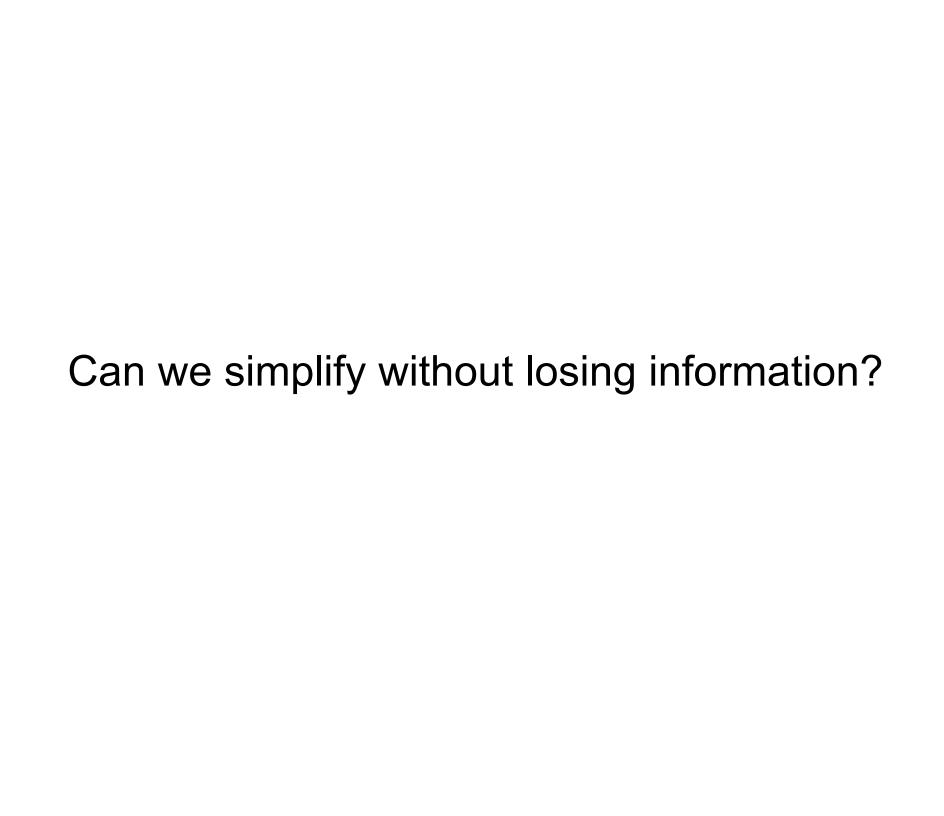


Reduced notation









Syntax for Index on class-II reduced notation

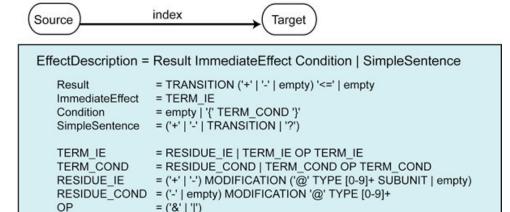
Syntax for index on class-II reduced notation

MODIFICATION

TRANSITION

SUBUNIT NAME = [a-zA-Z0-9]+

TYPE SUBUNIT

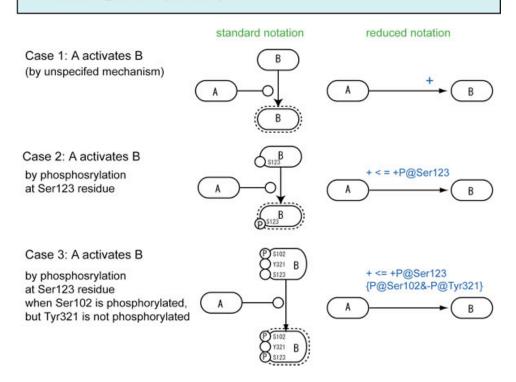


= (P | Me | Ac | Ub | Hy) | (P | M | A | U | H)

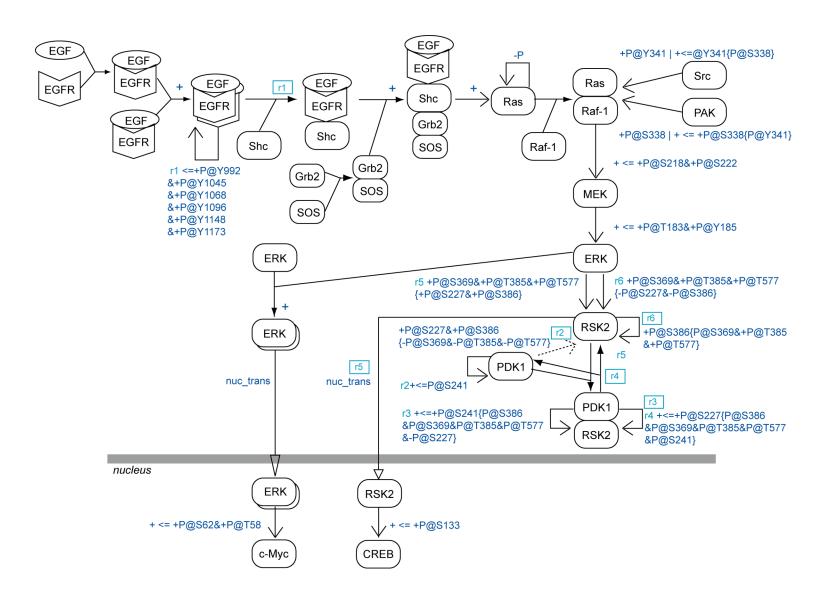
= (Tyr | Ser | Thr) | (Y | S | T)

= empty | '/' SUBUNIT NAME

= [a-zA-Z]+[0-9]*



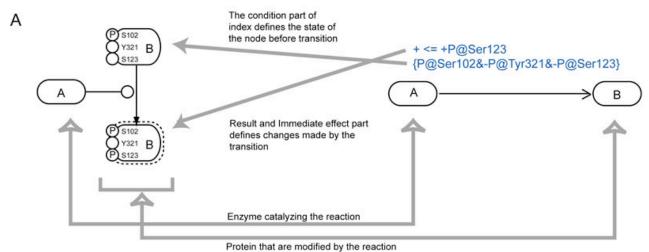
Reduced Notation

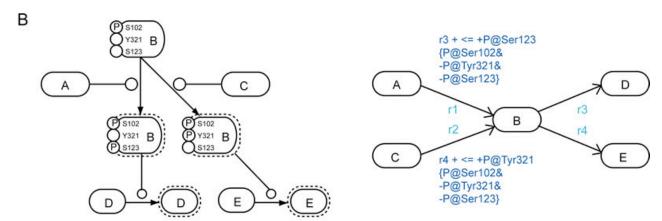


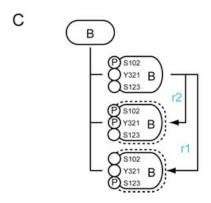
STANDARD NOTATION

REDUCED NOTATION

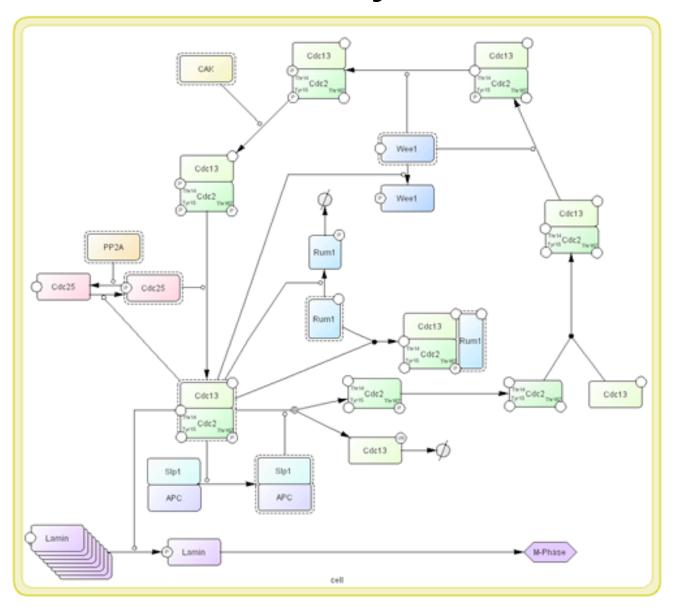
Standard Notation vs Reduced Notation

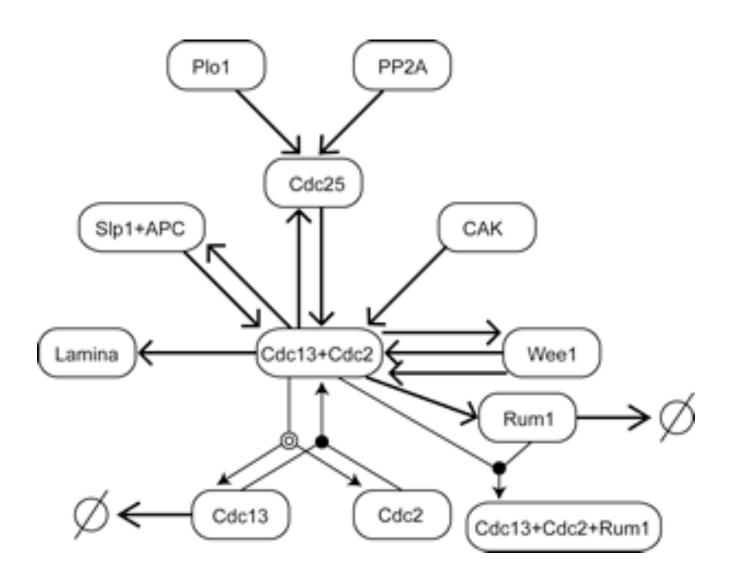




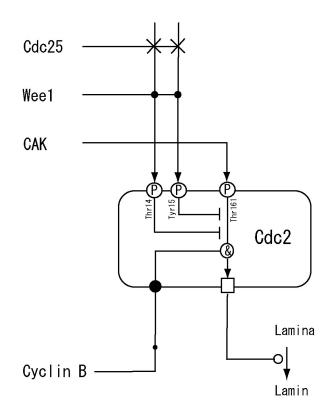


MPF cycle



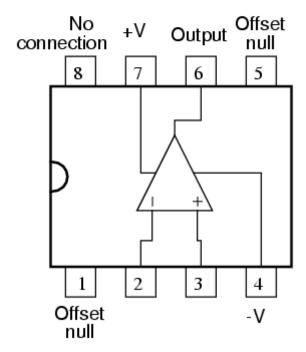


Relationship View

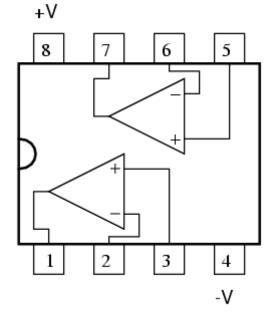


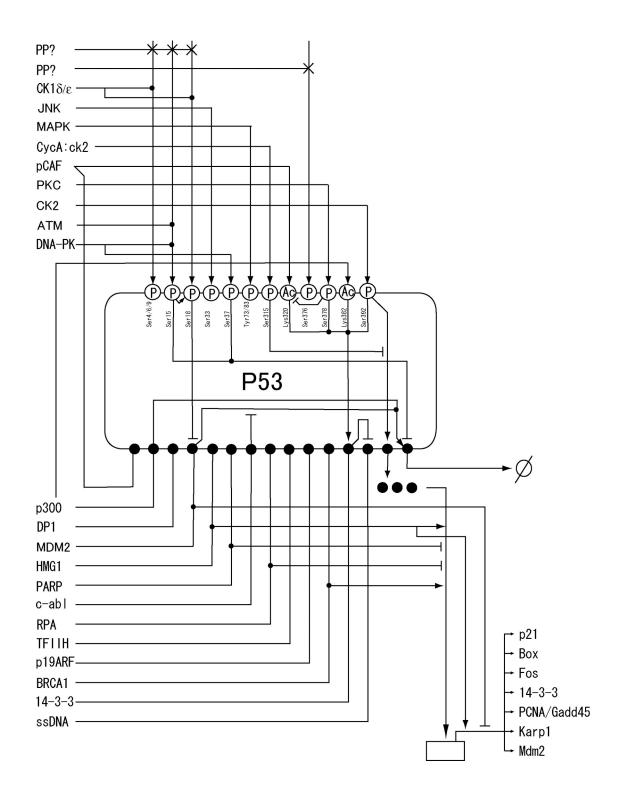
LSI diagram

Typical 8-pin "DIP" op-amp integrated circuit

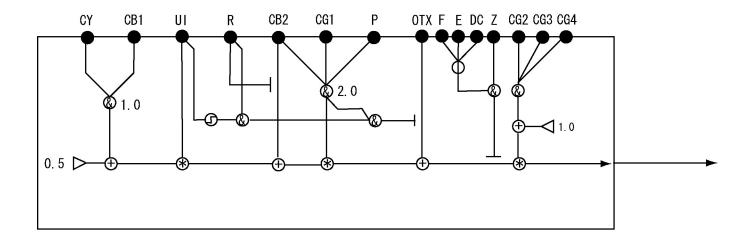


Dual op-amp in 8-pin DIP

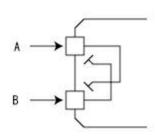




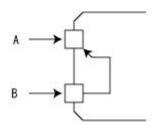
endo16



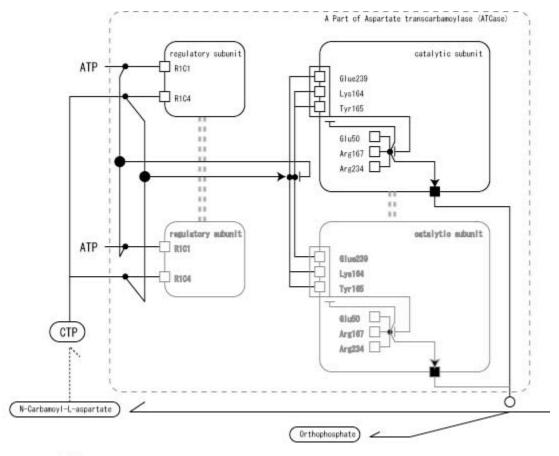
Allosteric Reaction



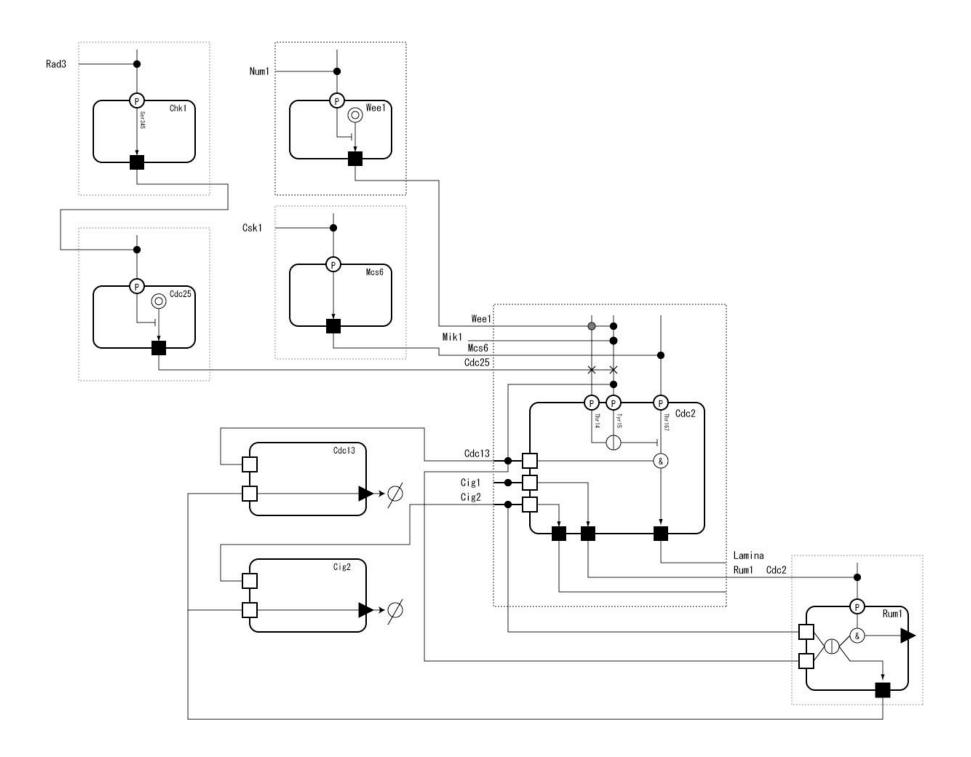
(A) Inhibitory Allosteric Reaction



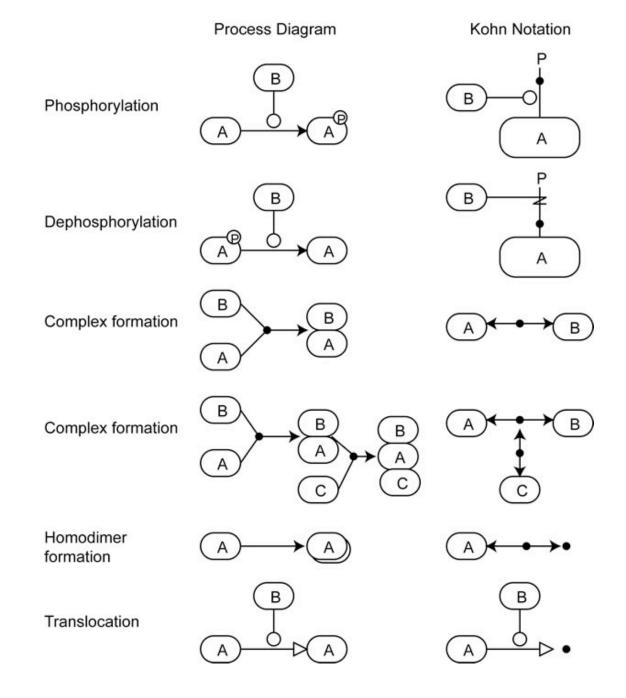
(B) Cooperative Allosteric Reaction



(C) A Part of Allosteric Reactions in aspartate transcarbamoylase



Process Diagram vs Kohn Notation



Summary

- Process diagram (state-transition) + entityrelationship diagram
- Reduced notation can be "information/activation flow diagram"
- Not on PPI, etc.
- Compatibility need to be ensured.

Motivation

- Graphical diagram is an essential aspects of systems science
 - Electronics industry could not have prospered without solid circuit diagram notation
- Graphical diagram in biology is very informal
 - Lack information contents
 - Ambiguous or even misleading
 - Not grounded on mathematical basis
 - Hampers large-scale efforts
- Systems Biology Graphical Notation (SBGN: http://www.sbgn.org/) as the standard graphical notation

SBGN features

- Well defined graphical notation
- Consistent with SBML and other standards
- Model-View Approach
 - Process Diagram View
 - One state = One Node
 - State Transition Diagram
 - Relationship Diagram View (similar to Kohn Map)
 - One Species = One Node
 - Entity-Relationship Diagram