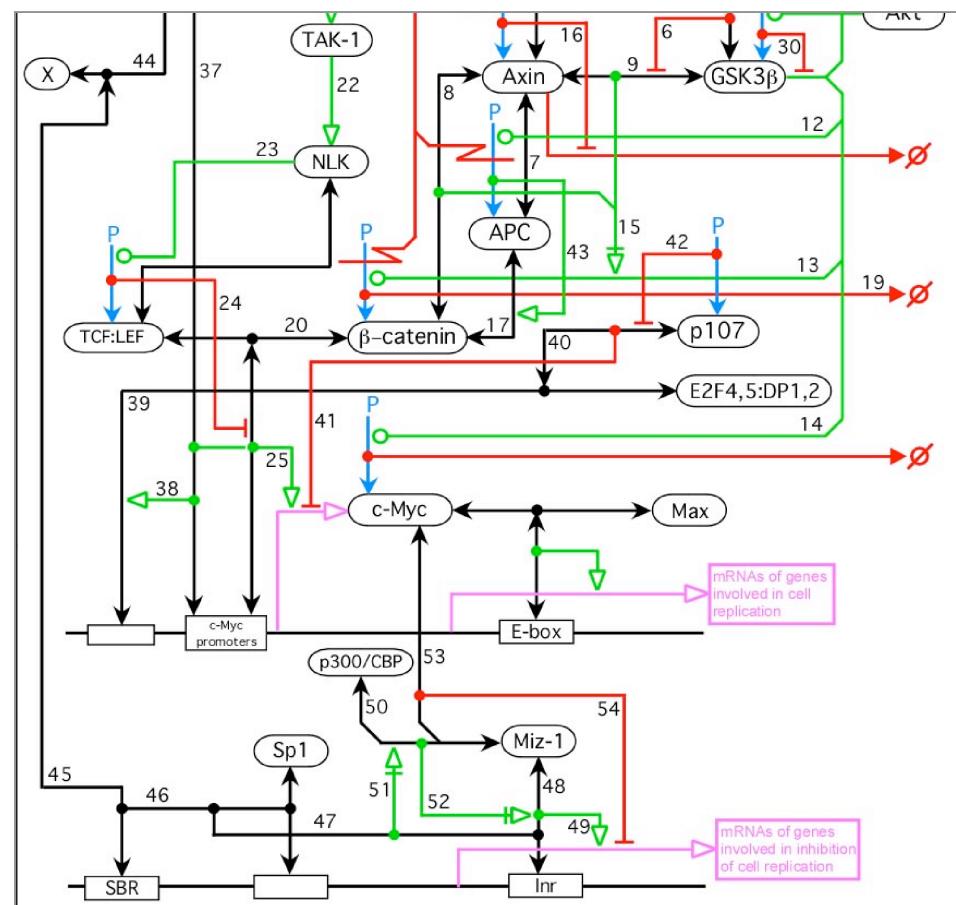


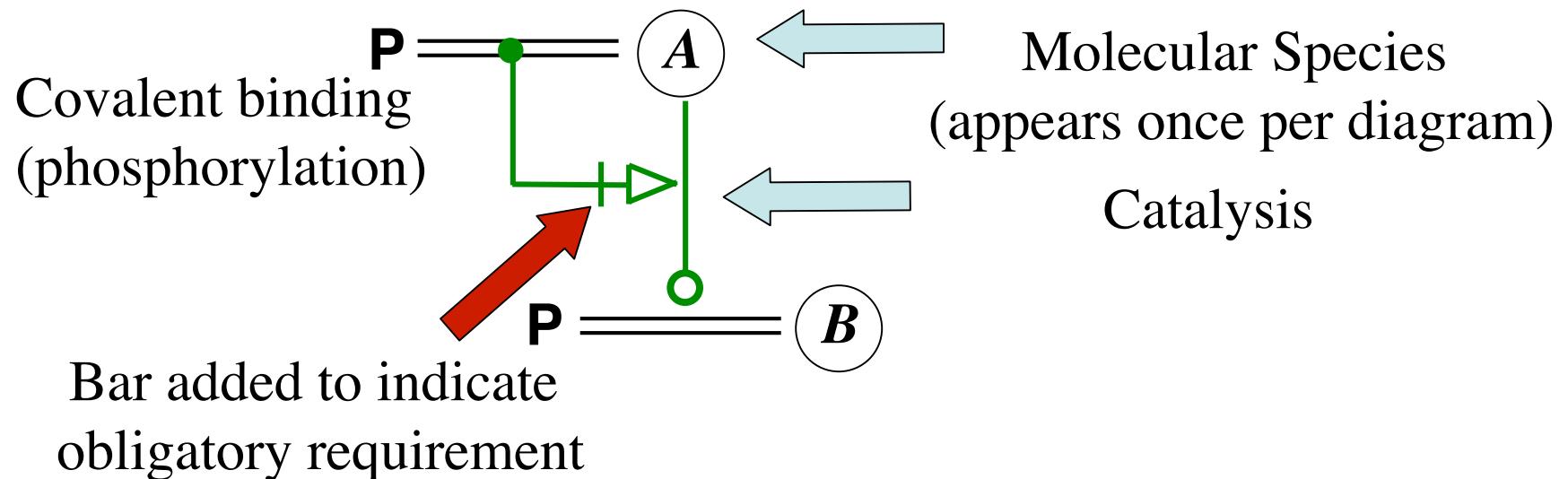
Mirit I. Aladjem
Laboratory of Molecular Pharmacology, NCI

Summary: Molecular Interaction Maps



S. Pasa

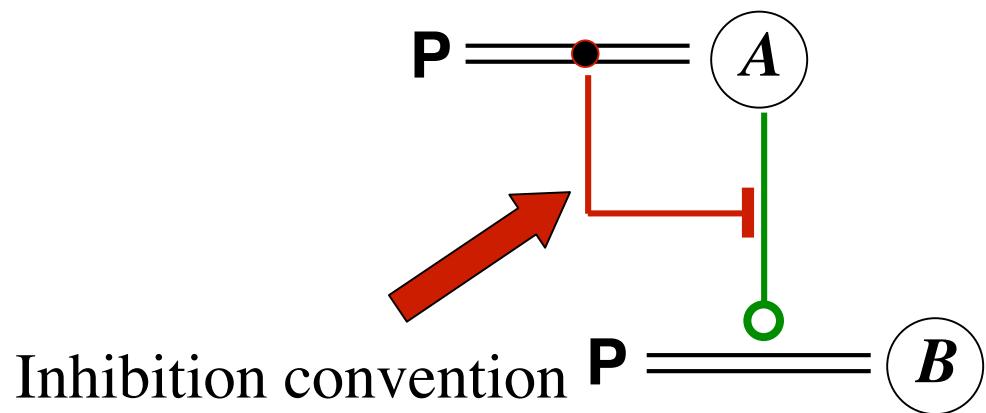
*Molecular Interaction Maps depict
bioregulatory interactions unambiguously in
diagram form using specific lines and nodes.*



Activating phosphorylation:

The phosphorylated form of kinase **A** is the active form, phosphorylates **B**

Molecular Interaction Maps depict bioregulatory interactions unambiguously in diagram form using specific lines and nodes.



Inhibitory phosphorylation:

Phosphorylation of A blocks the kinase activity of A.

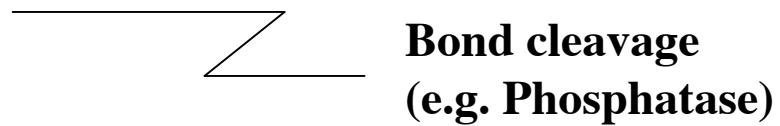
Reactions



Binding (non-covalent)



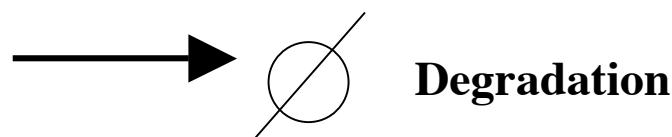
**Covalent Modification
(e.g. phosphorylation)**



**Bond cleavage
(e.g. Phosphatase)**



**Stoichiometric
Conversion (A to B)**



Degradation



Transcription/translation

Contingencies



Catalysis



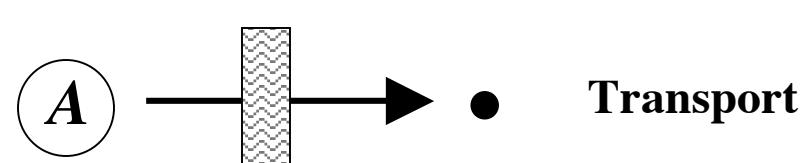
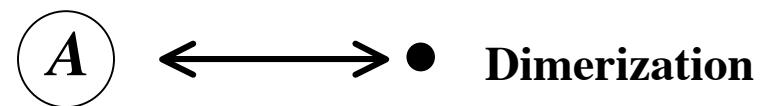
Stimulation



**Stimulation
required**

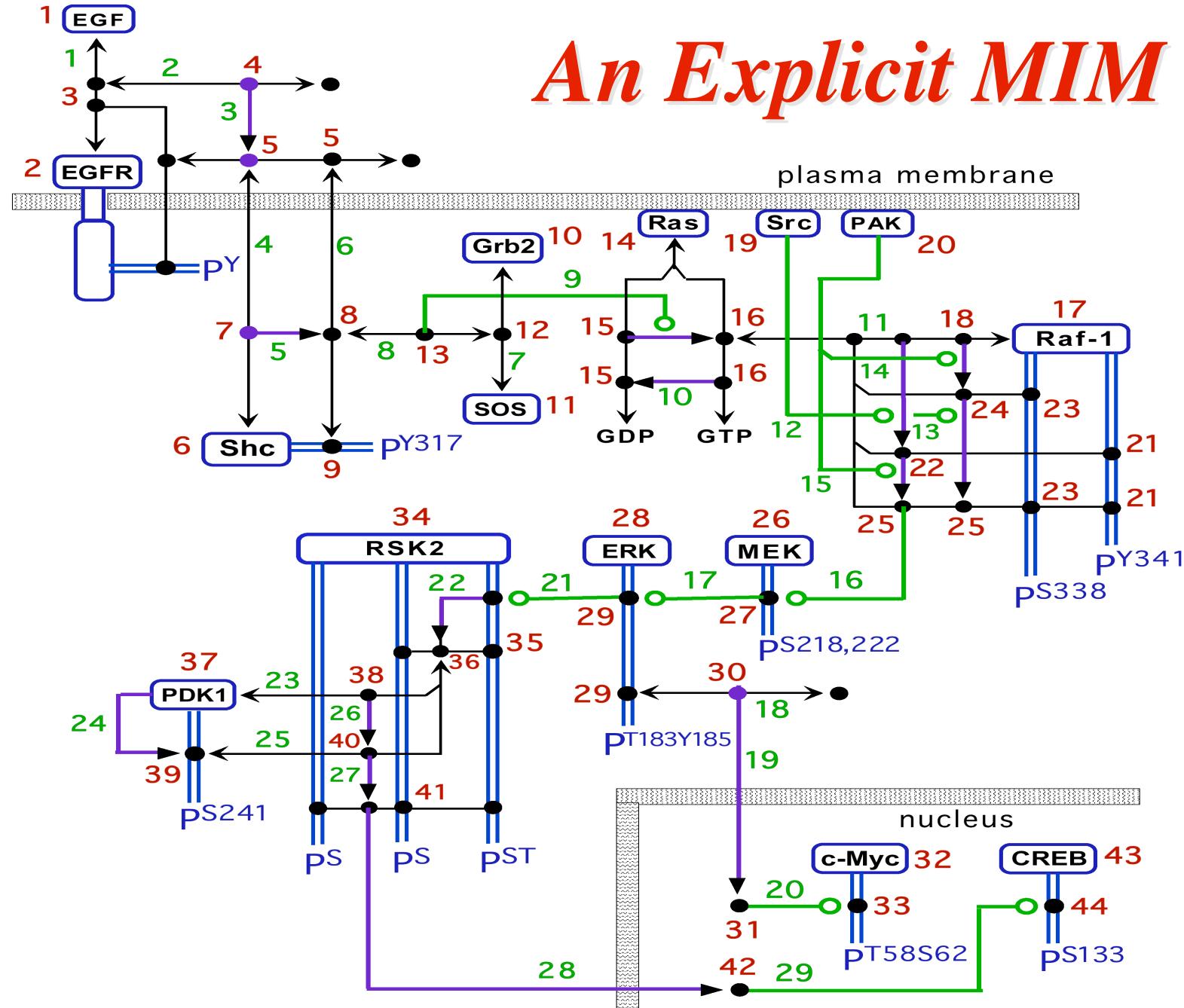


Inhibition



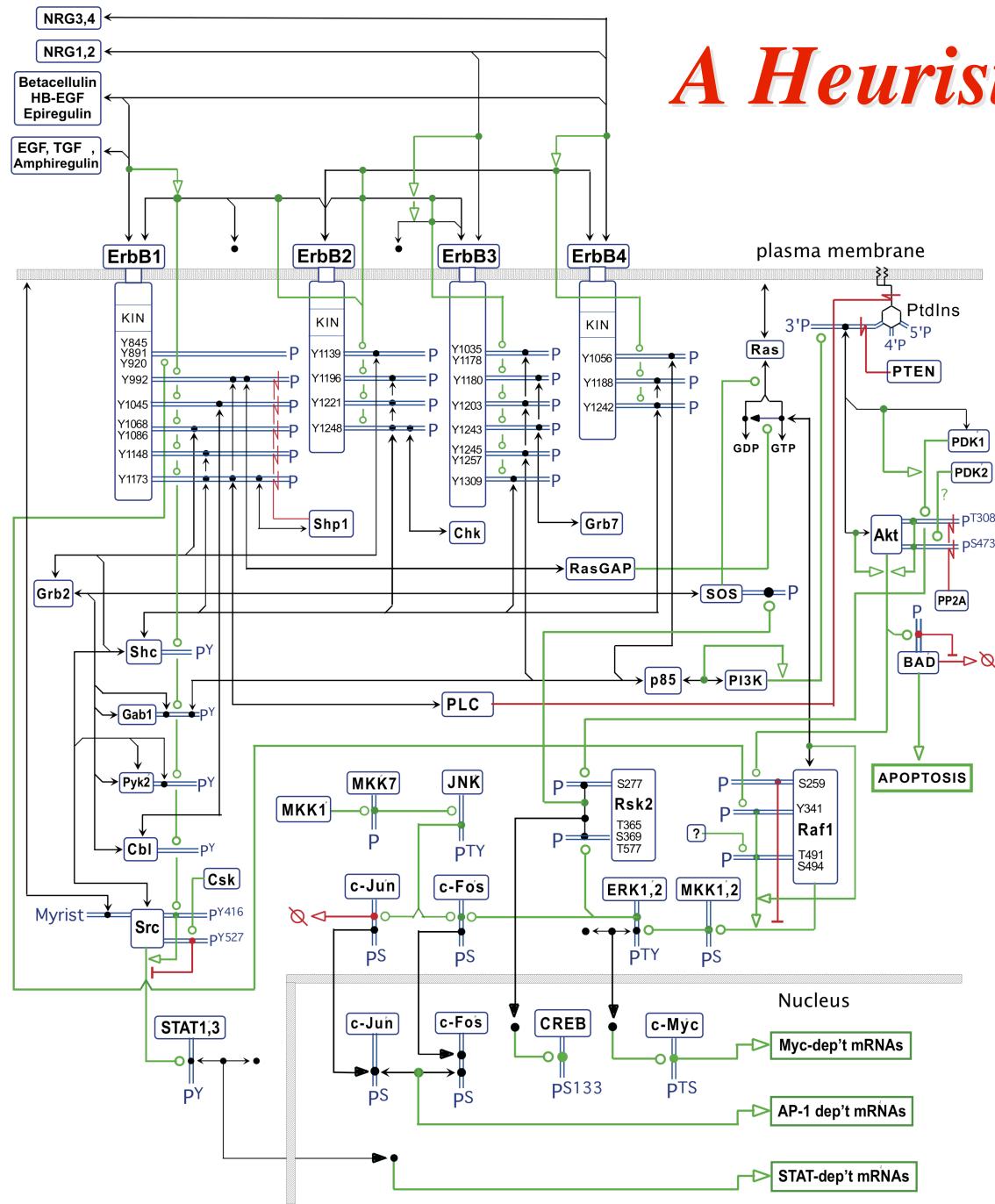
Transport

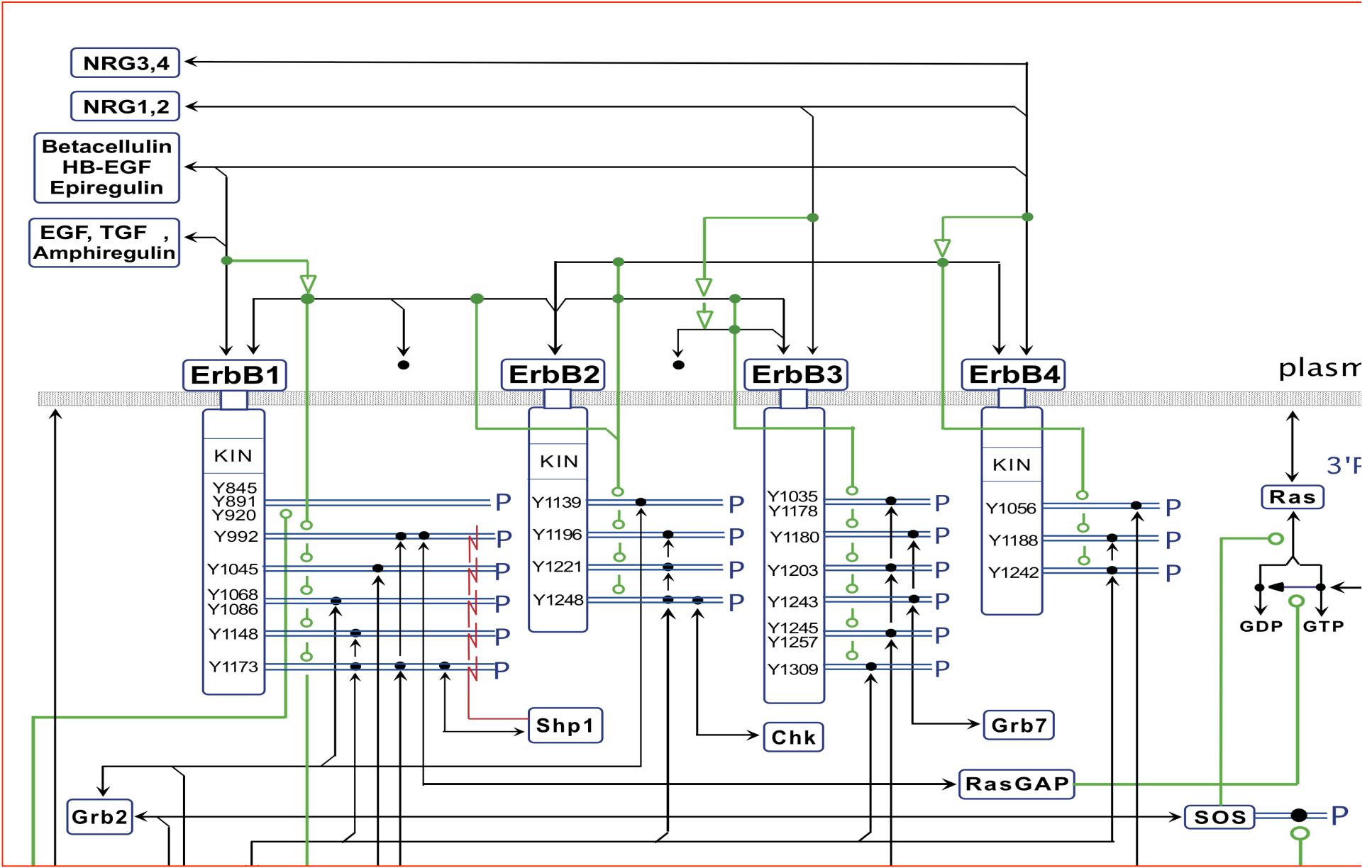
An Explicit MIM



An Explicit MIM Depicts
Molecular Interactions With
Sufficient Detail Required for
Simulation

A Heuristic MIM

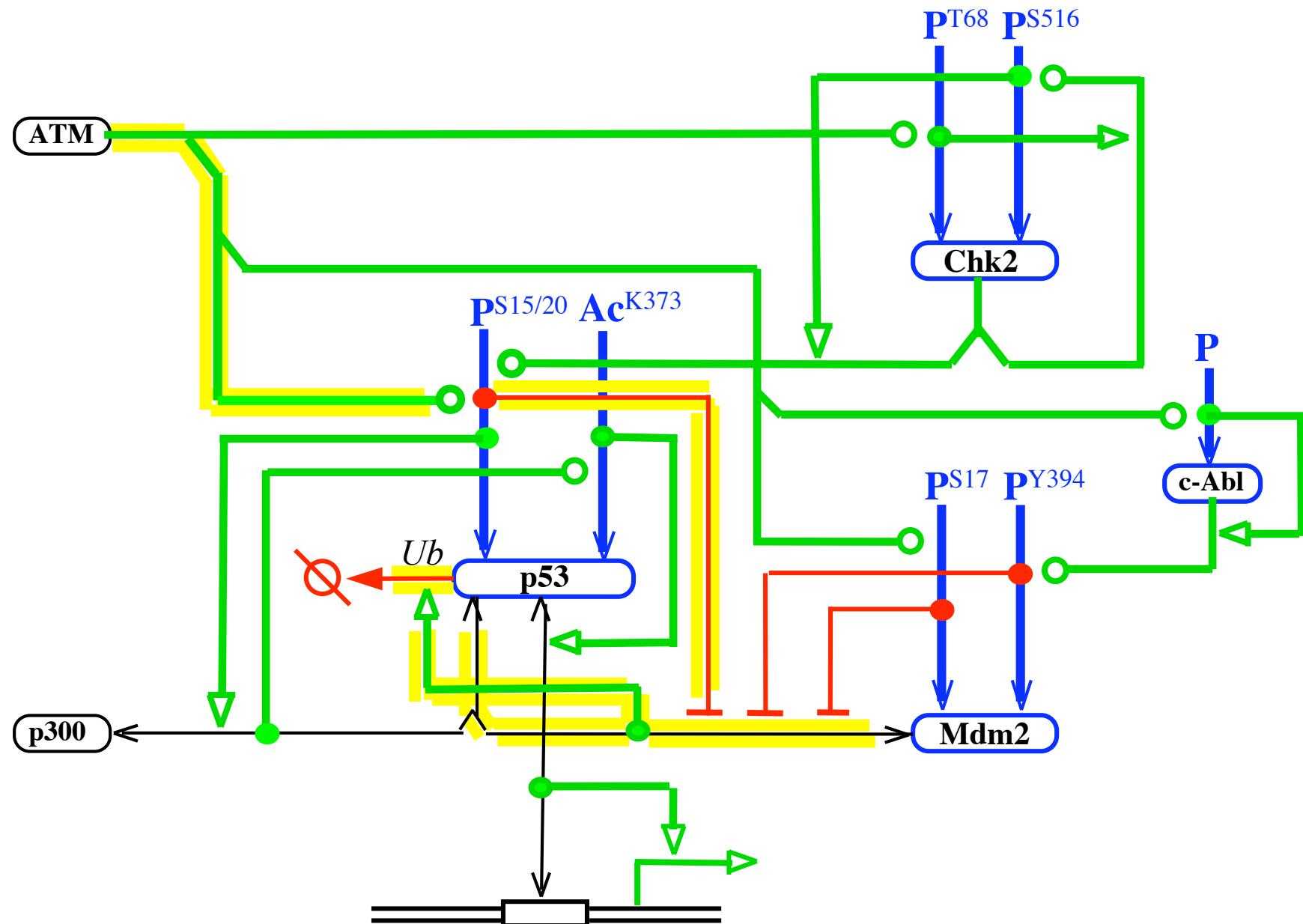




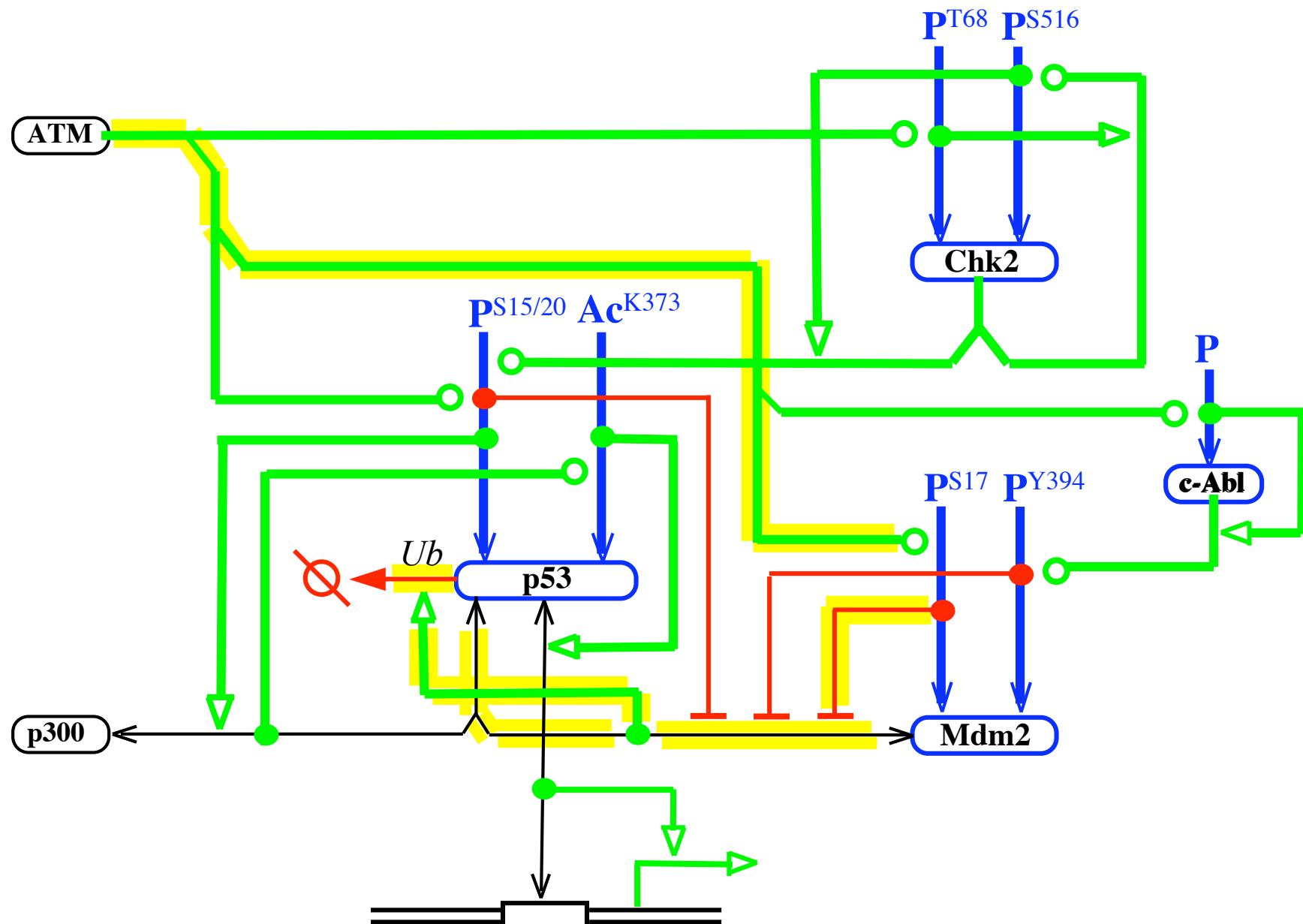
**Heuristic MIMs Concisely Depict
Complex Networks Of Potential
Molecular Interactions.**

**Biological Processes Can Be
Inferred From the Interactions
Described in Heuristic MIMs**

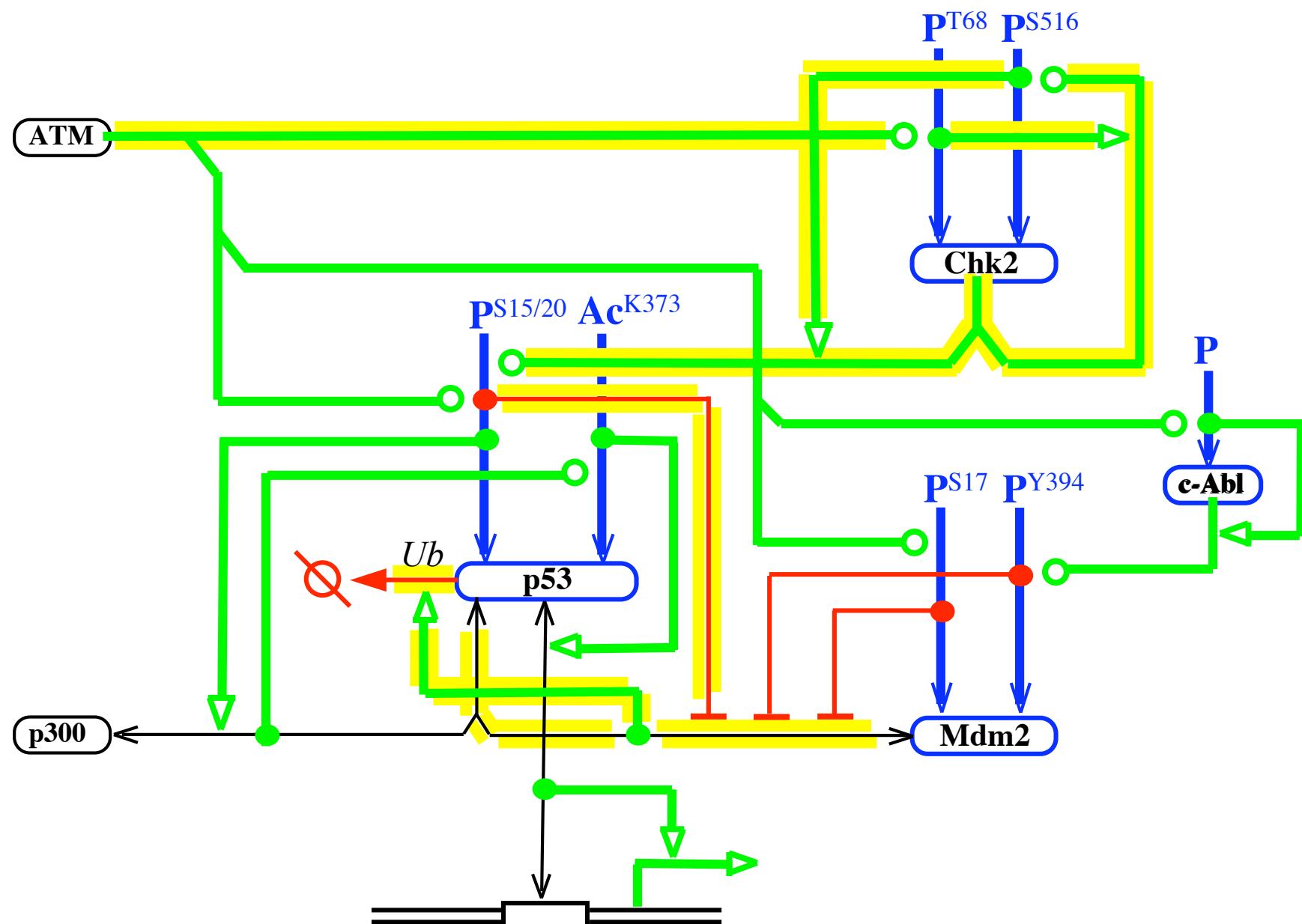
ATM &(S15P) --| p53 :>Mdm2 &(Ub) >% p53 [4+]



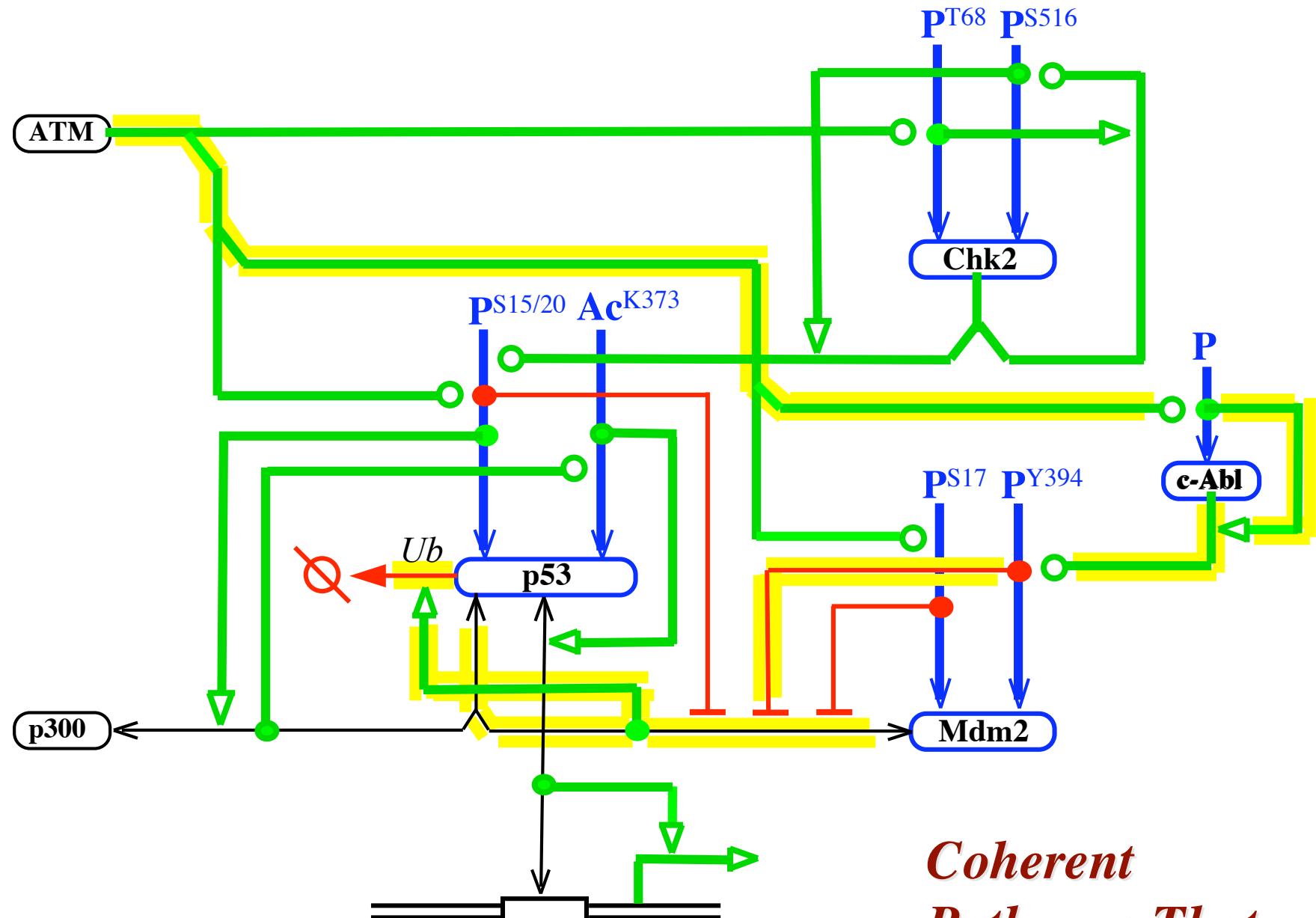
ATM &(S17P) --| Mdm2 :> p53 &(Ub) >% p53 [4+]



ATM &(T68P) >Chk2 &(S516P) >Chk2 &(S20P) --| p53 : >Mdm2 &(Ub) >%p53 [6+]



ATM &(P) > c-Abl &Mdm2(Y394P) --| Mdm2 :> p53 &p53(Ub) >% p53 [5+]



*Coherent
Pathways That*
S 1 11 52

eMIMs Can Provide Links to Annotations, References & Databases

[MIM home](#)

[STKE Paper](#)

[Introduction](#)

[Replication Initiation Maps](#)

- [Complete map](#)
- [Radiation](#)
- [Inhibitors](#)
- [Mitosis](#)

[Map Symbols](#)

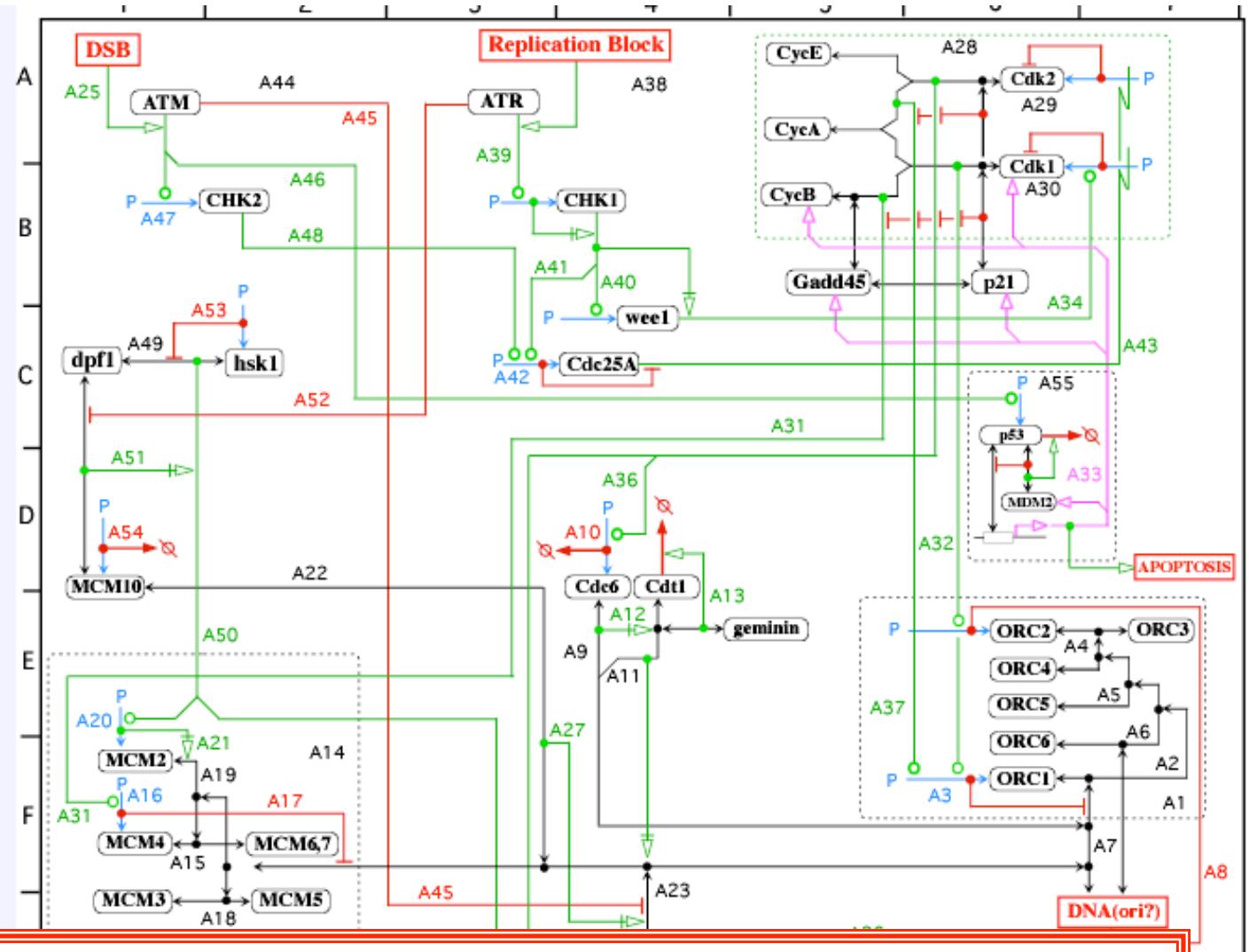
[Map Navigation](#)

[Annotations](#)

[References](#)

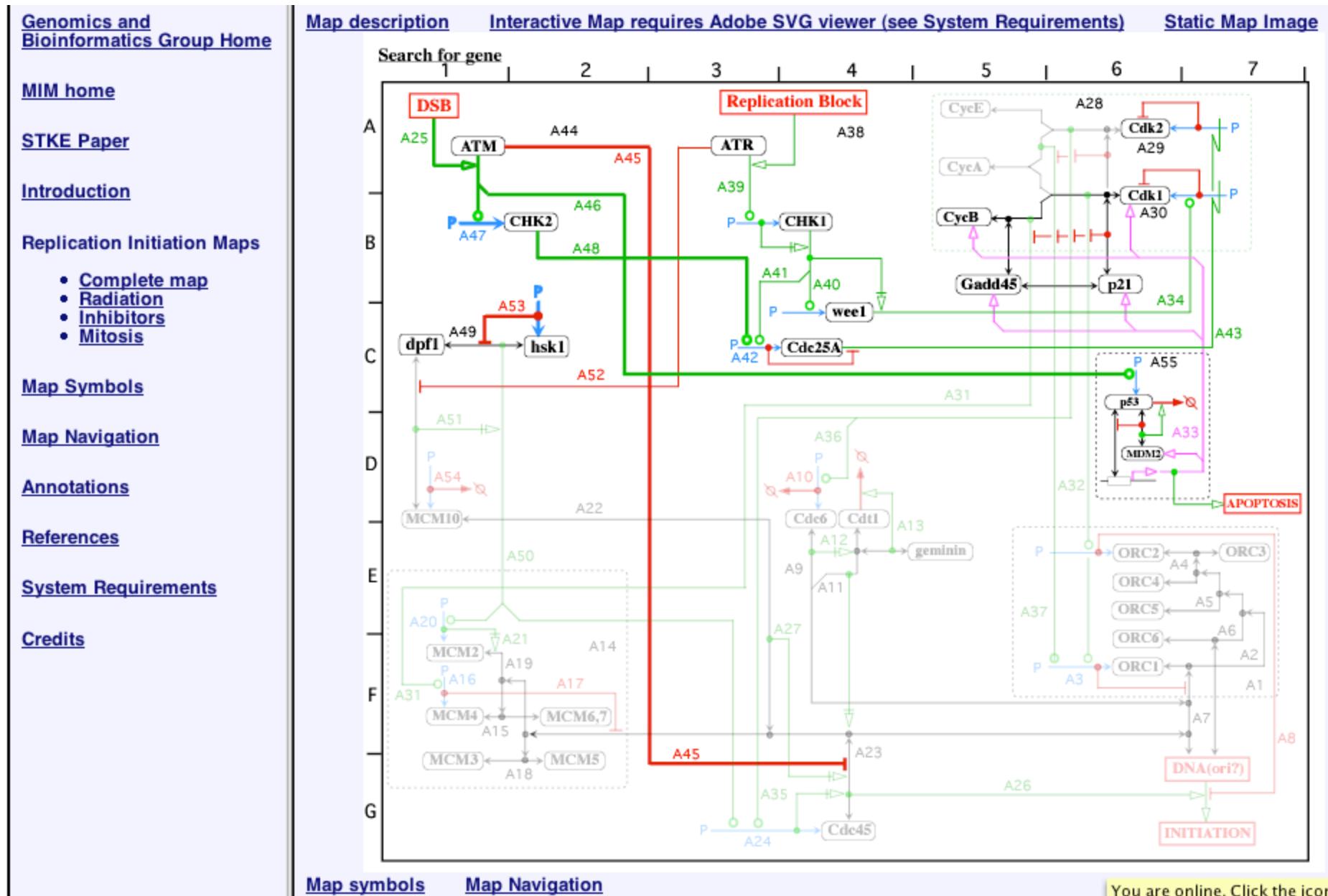
[System Requirements](#)

[Credits](#)



<http://discover.nci.nih.gov>

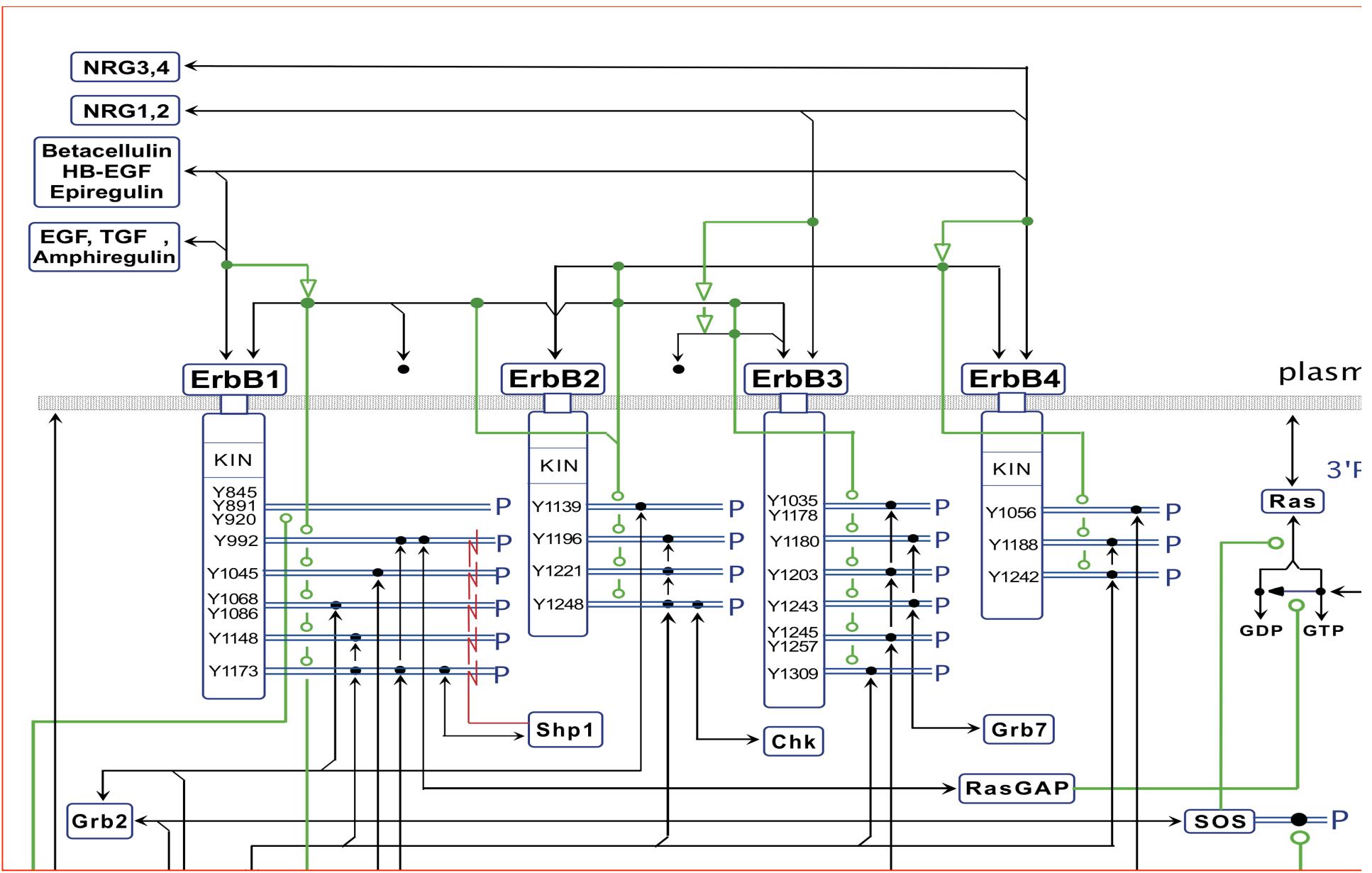
Cellular Response Pathways Depicted in eMIMs



MIMs depict what molecules “see”

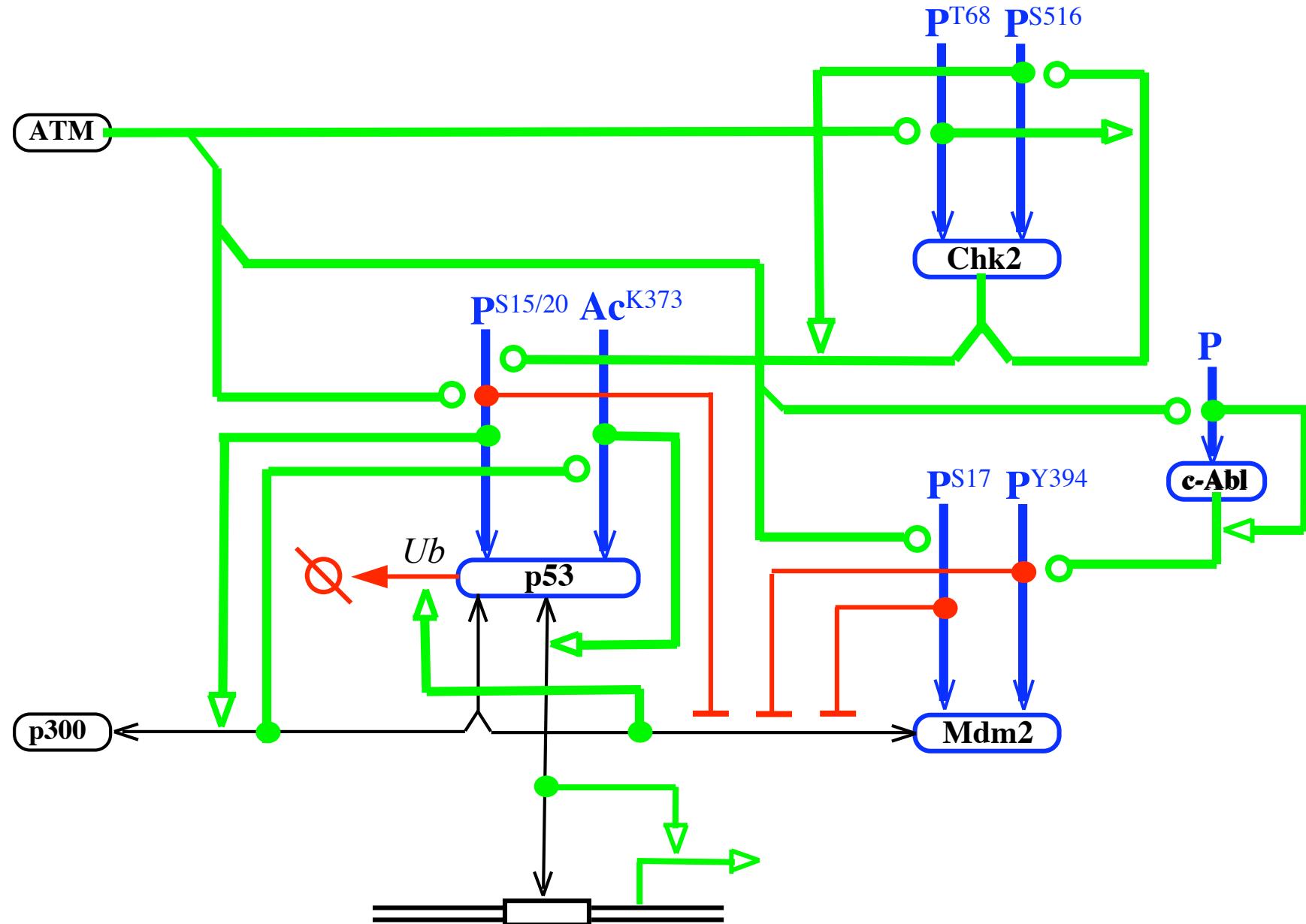
- potential interactions between depicted molecular species.

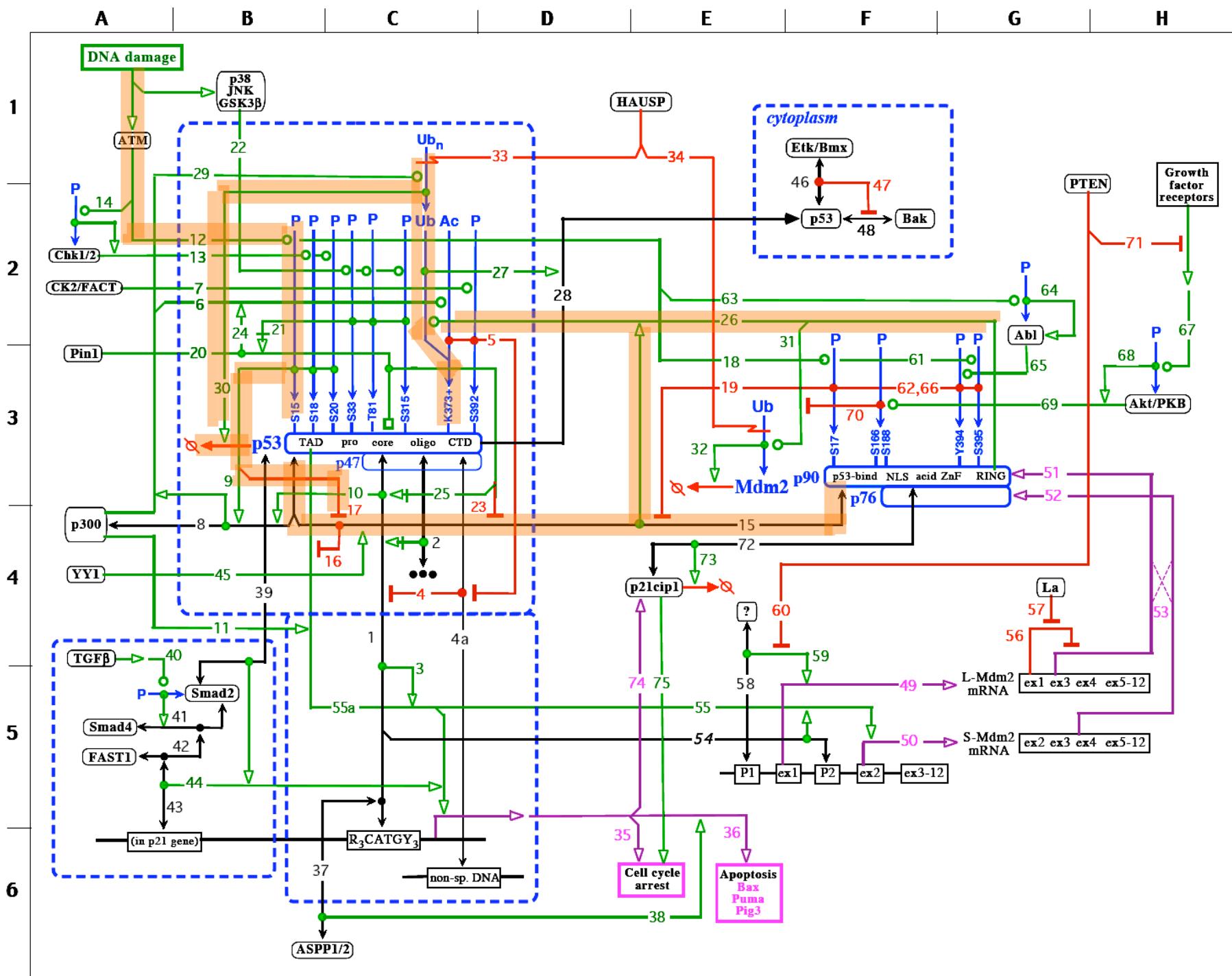
Heuristic MIMs can describe complex networks of potential interactions without encountering “combinatorial explosion”.



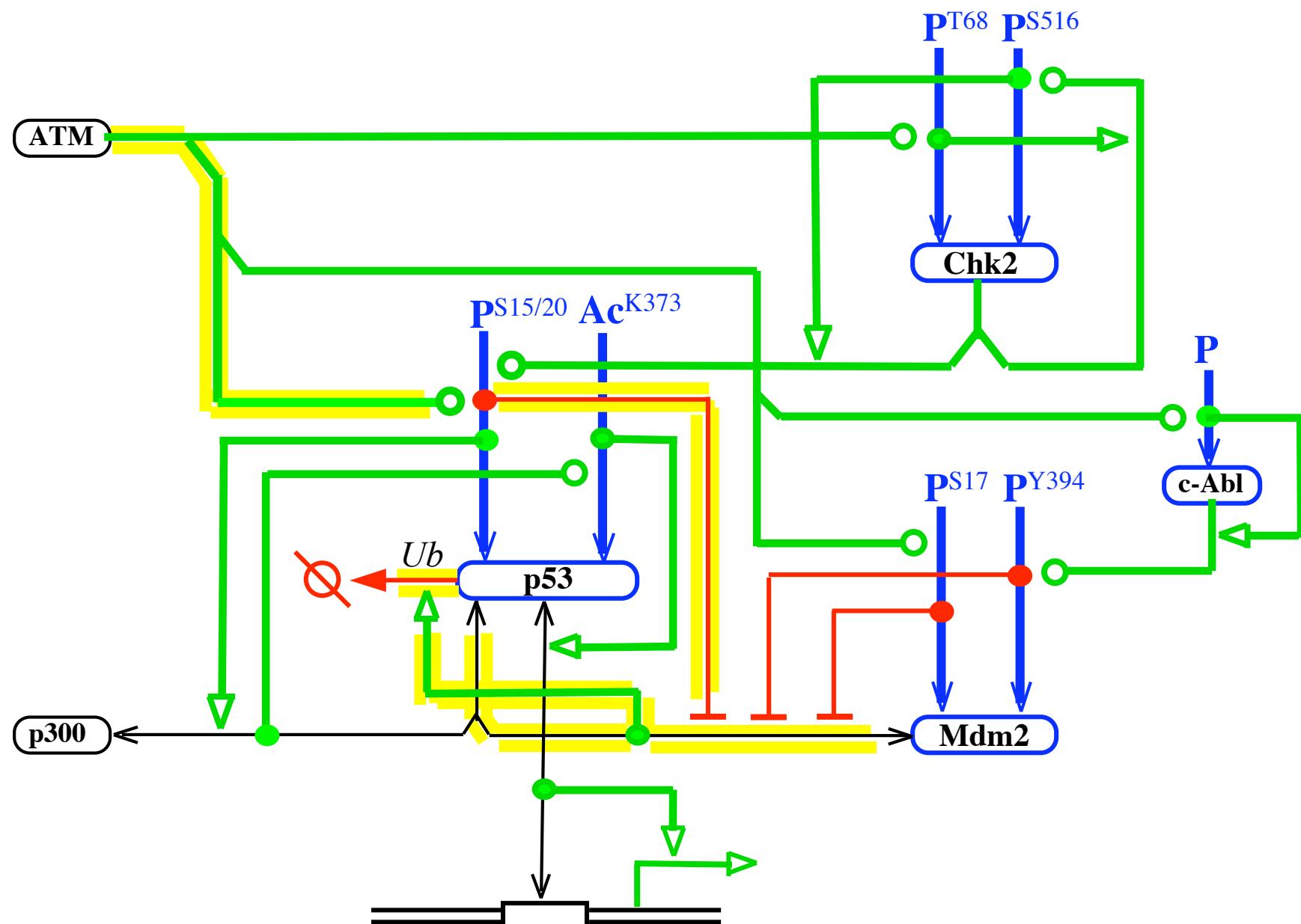
48 Receptor-ligand-dimer combinations; 96+144 phosphorylation states;
 3749 individual reactions in a model for SOS recruitment by EGFR .
 (Blinov et al., 2005)

Addition of a Contingency to a MIM Without Increasing Overall Combinatorial Complexity





ATM &(S15P) --| p53 :>Mdm2 &(Ub) >% p53 [4+]



MIMs address the challenges of depicting complex networks:

MIMs can depict the different types of reactions common in bioregulatory networks, and contingencies affecting such reactions.

MIMs can unambiguously and concisely represent intramolecular interactions.

Explicit MIMs contain sufficient detail to describe models suitable for simulation of biological networks

Heuristic MIMs summarize large sets of data about molecular interactions with different levels of detail; eMIMs can provide links to pertinent external information

MIMs are useful to represent the combinatorial complexity of biological networks.



The MIM Team

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