

Útvonalak és hálózatok

Korcsmáros Tamás

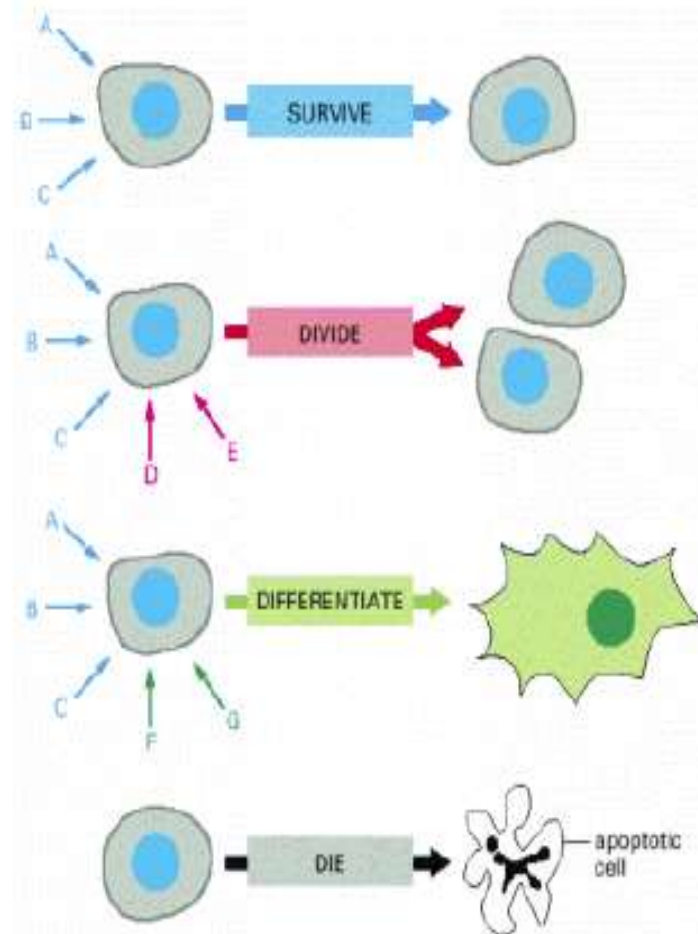
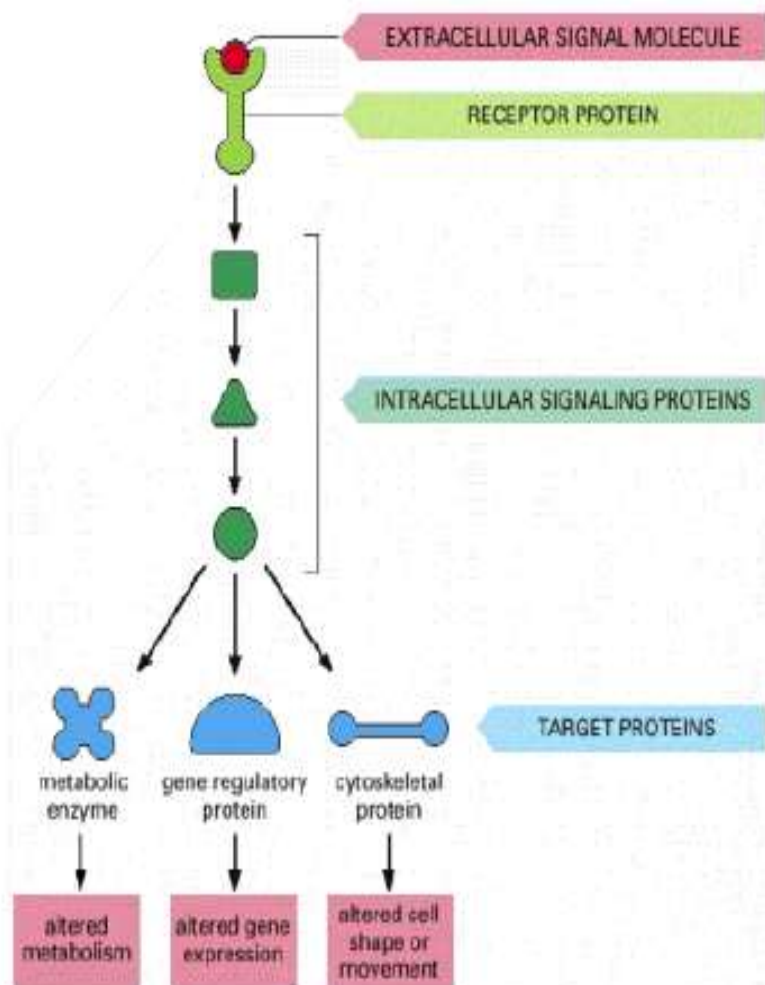
ELTE Genetikai Tanszék
Hálózatbiológiai-csoport



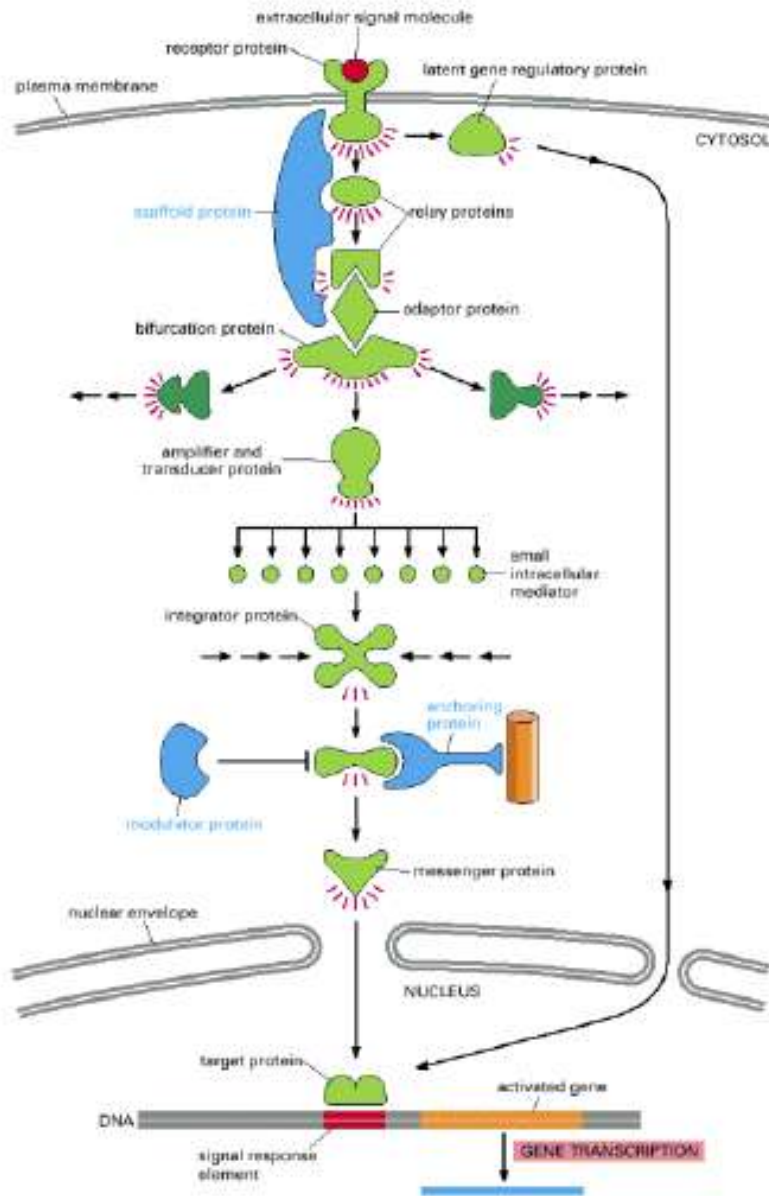
Útvonalak és hálózatok

- Útvonalakról általában
- Jelátviteli és regulációs útvonalak
- Génhálózatok
- Metabolikus útvonalak

Extracelluláris jelek központi szerepe



Sejten belüli szignálfehérjék típusai



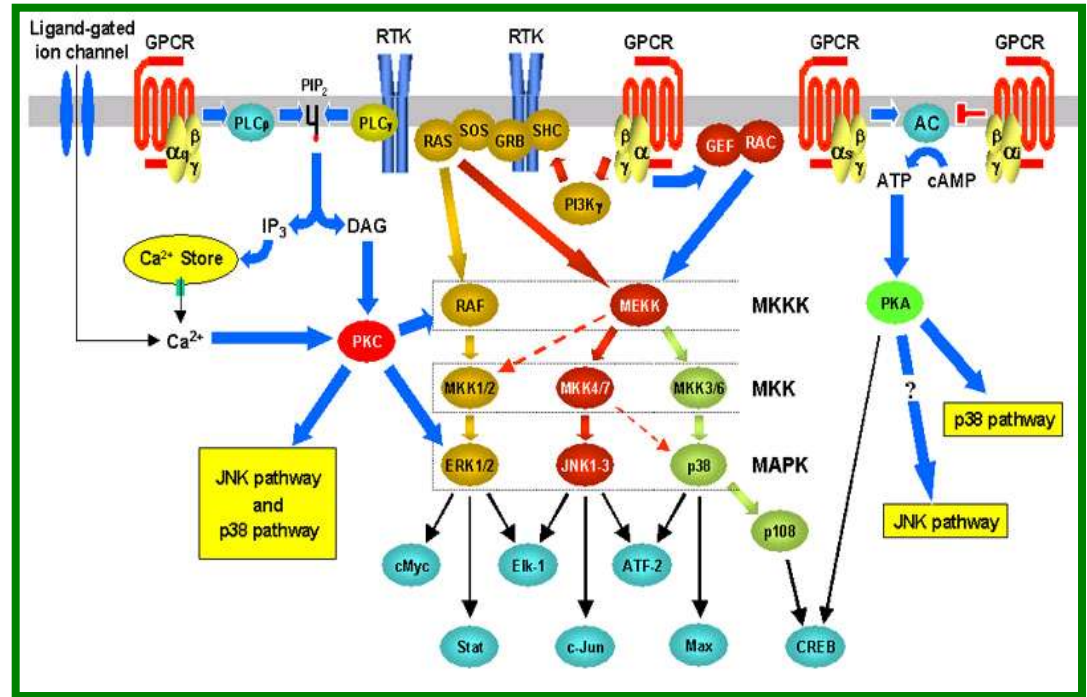
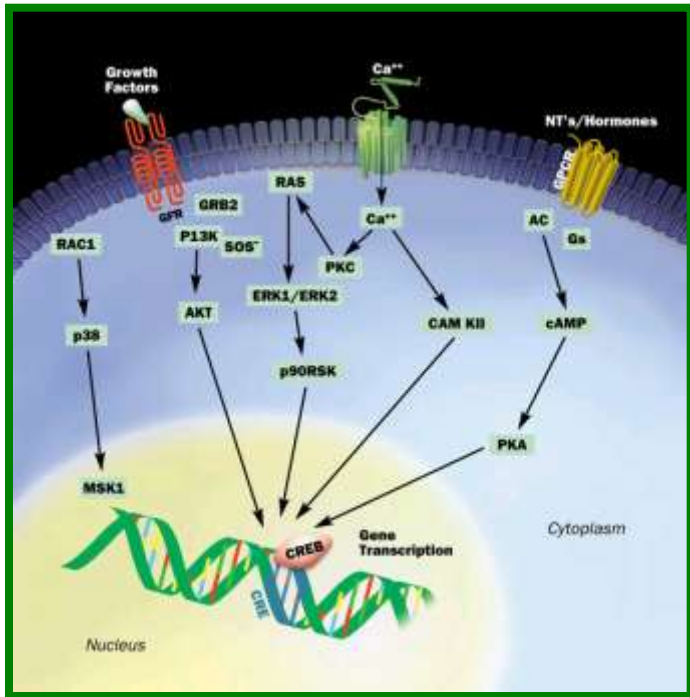
1. Receptorok
2. Relé-fehérjék
3. Adaptorok
4. Villa-fehérjék
5. Erősítők
6. Integrátorok
7. Messenger fehérjék
8. Látens génaktivitás regulátorok

Útvonalak csoportosításának problematikája

- Mi egy útvonal?
- Mi alapján csoportosítják az útvonalakat?
- Mi alapján kéne csoportosítani?
- Léteznek egyáltalán útvonalak?

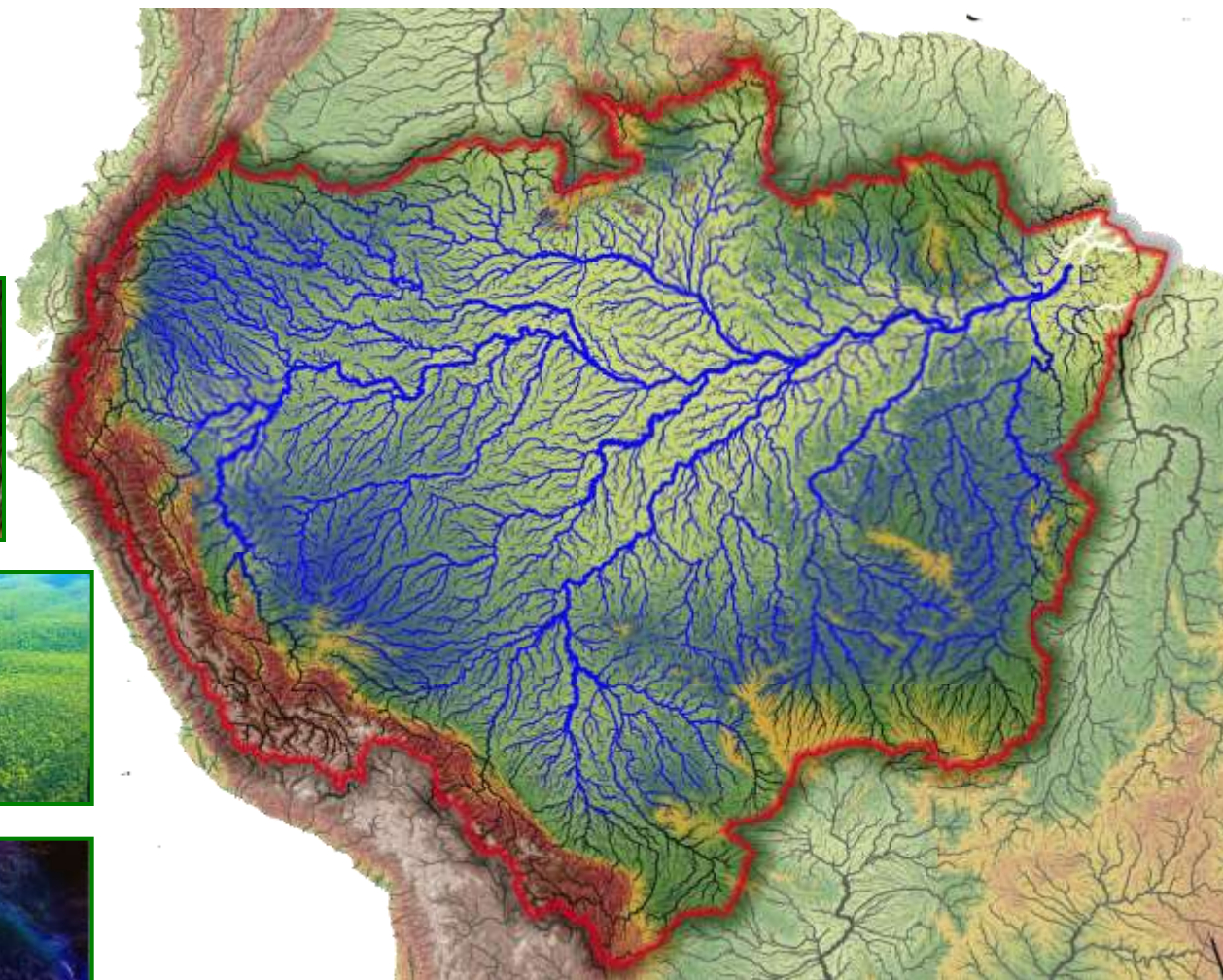
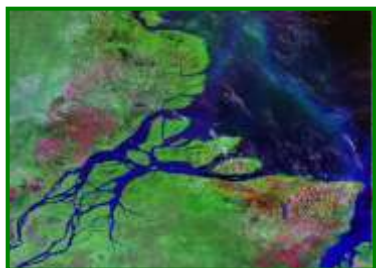
Jelátvitel kutatás

Az önálló útvonalaktól a hálózatokig

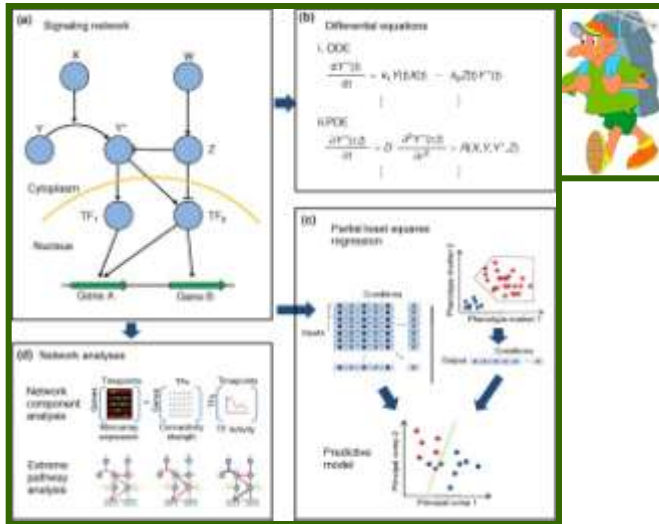


1. Önálló, lineáris útvonalak
2. Egyre több bizonyíték az útvonalak közötti (cross-talk) kapcsolatokra
3. Teljesen összekapcsolt útvonal-rendszer: egységes jelátviteli hálózat

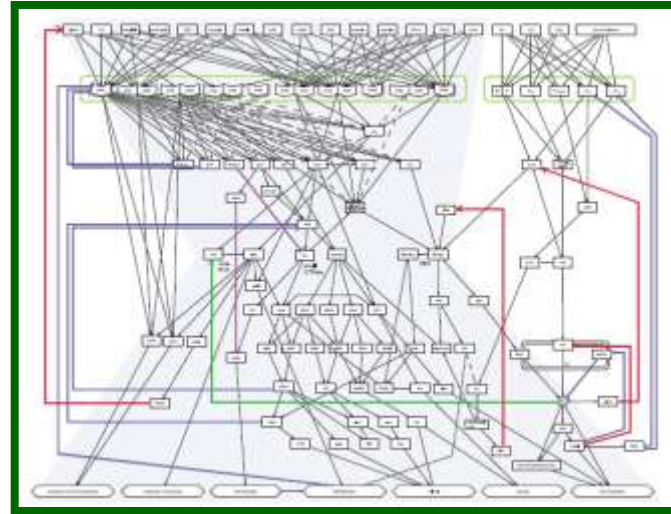
Útvonal-hálózatok felfedezésének megközelítései és módszerei



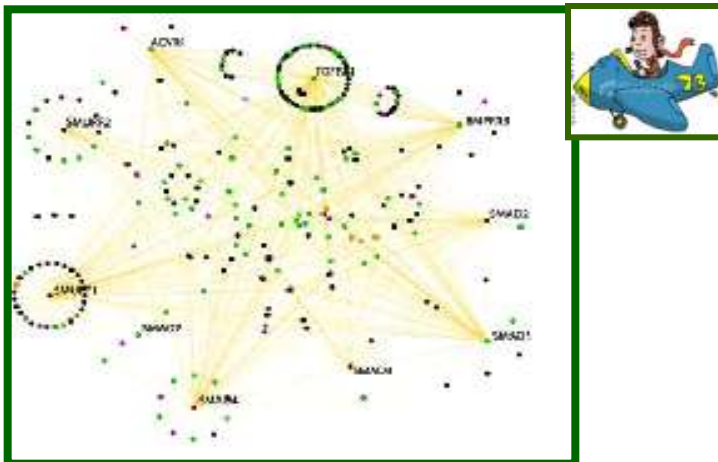
Útvonal-hálózatok felfedezésének megközelítései és módszerei



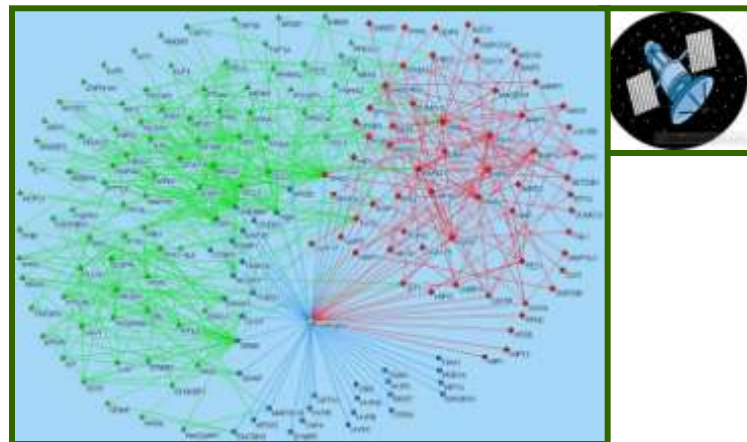
Kis útvonalak kémiai pontos felderítései



Nagyobb útvonalak általános szerkezetének megismerései

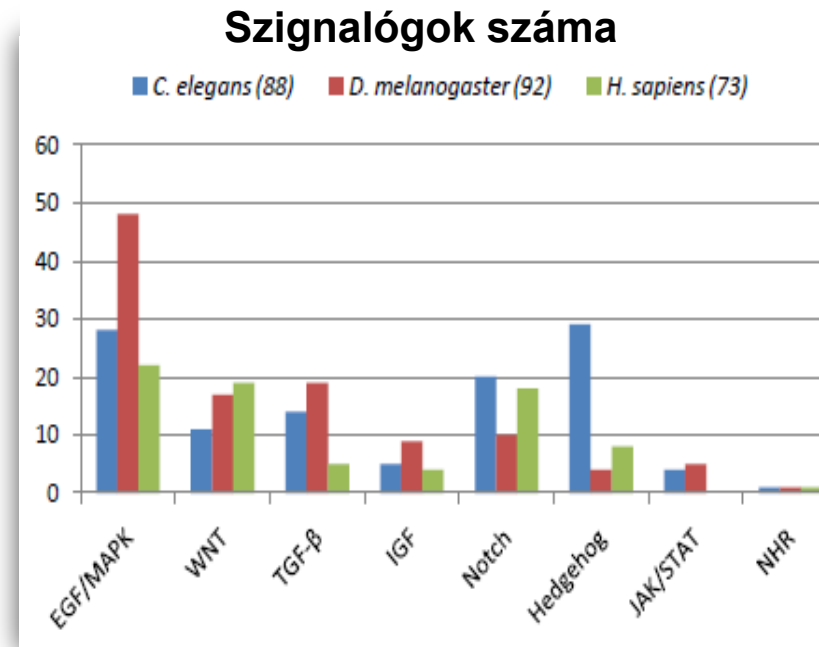
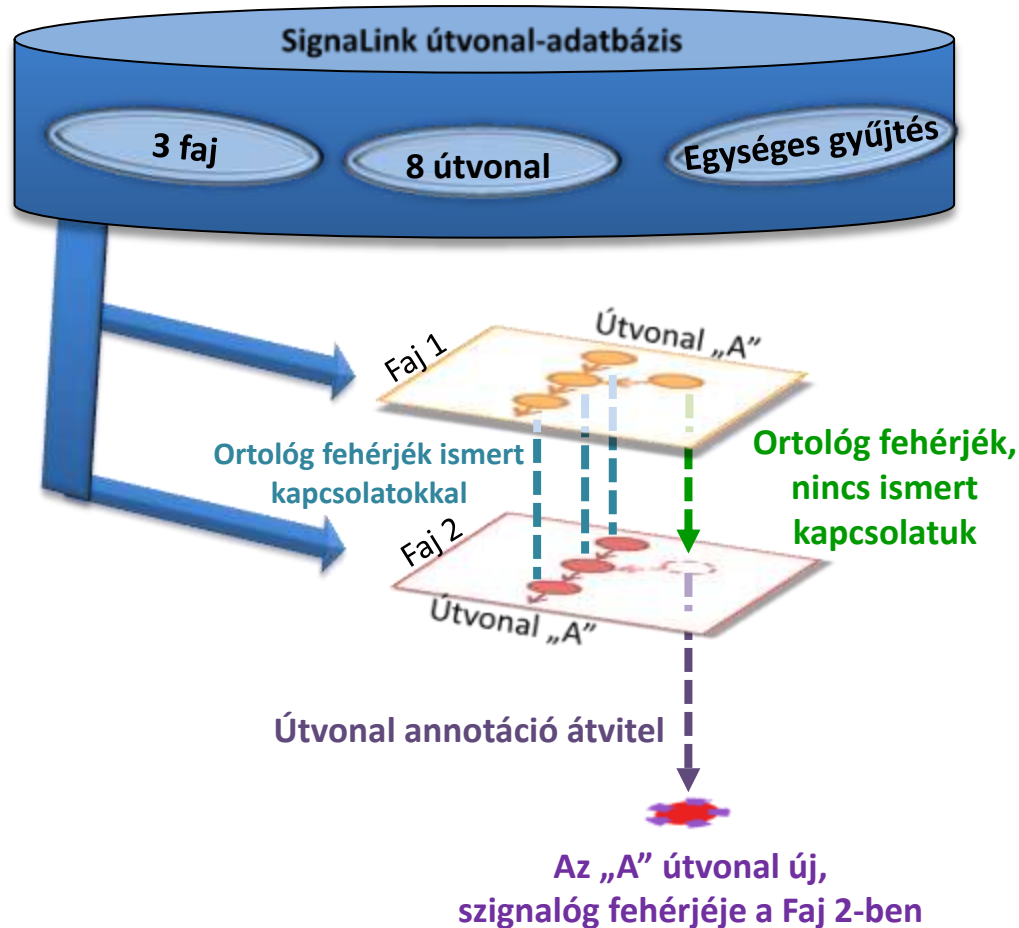


Útvonalhálózatok felderítése

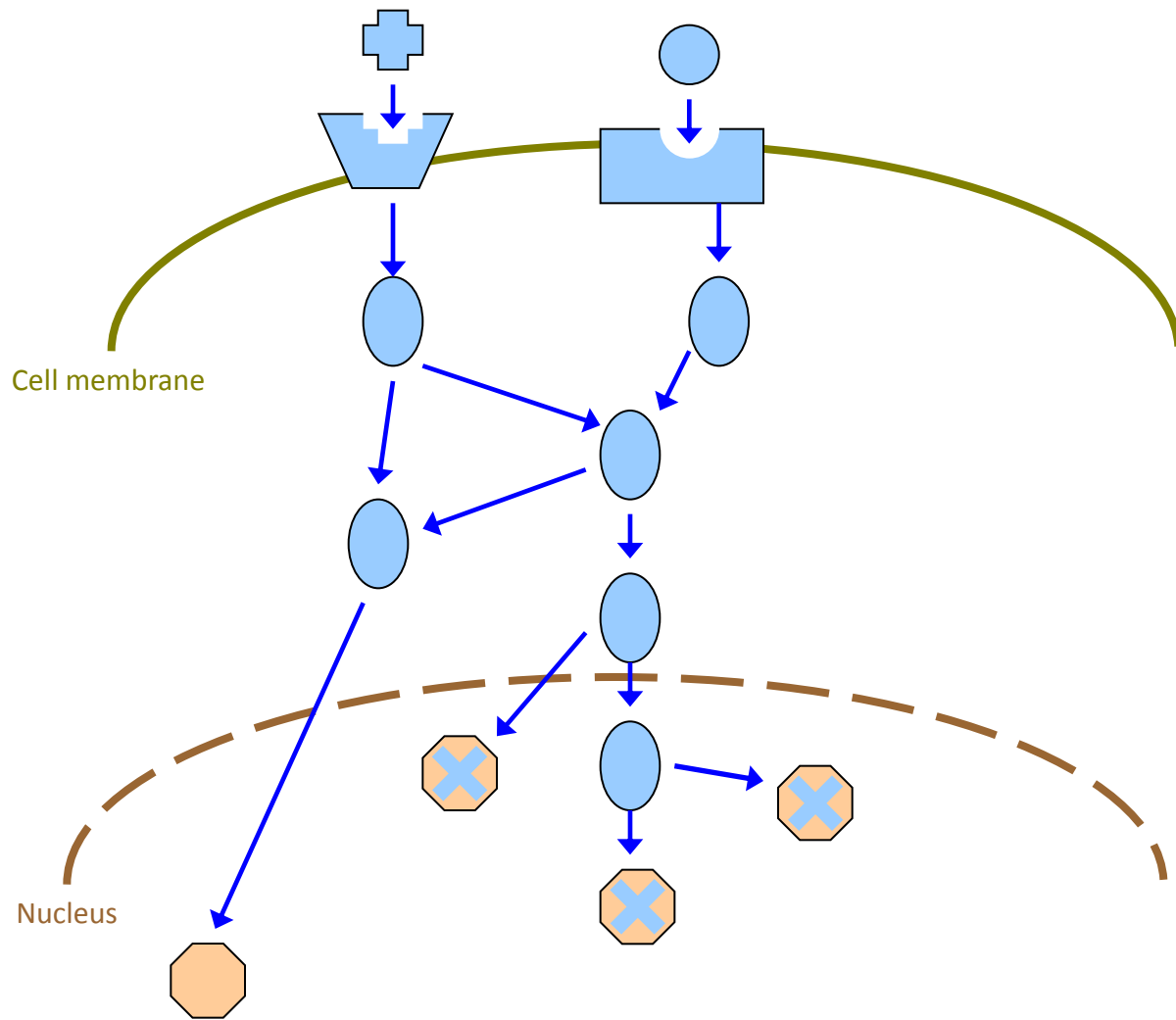


A sejt teljes hálózata


Szignálógok: ortológia alapján jószolt új jelátviteli komponensek




Jelátviteli és regulációs hálózatok - adatbázisok



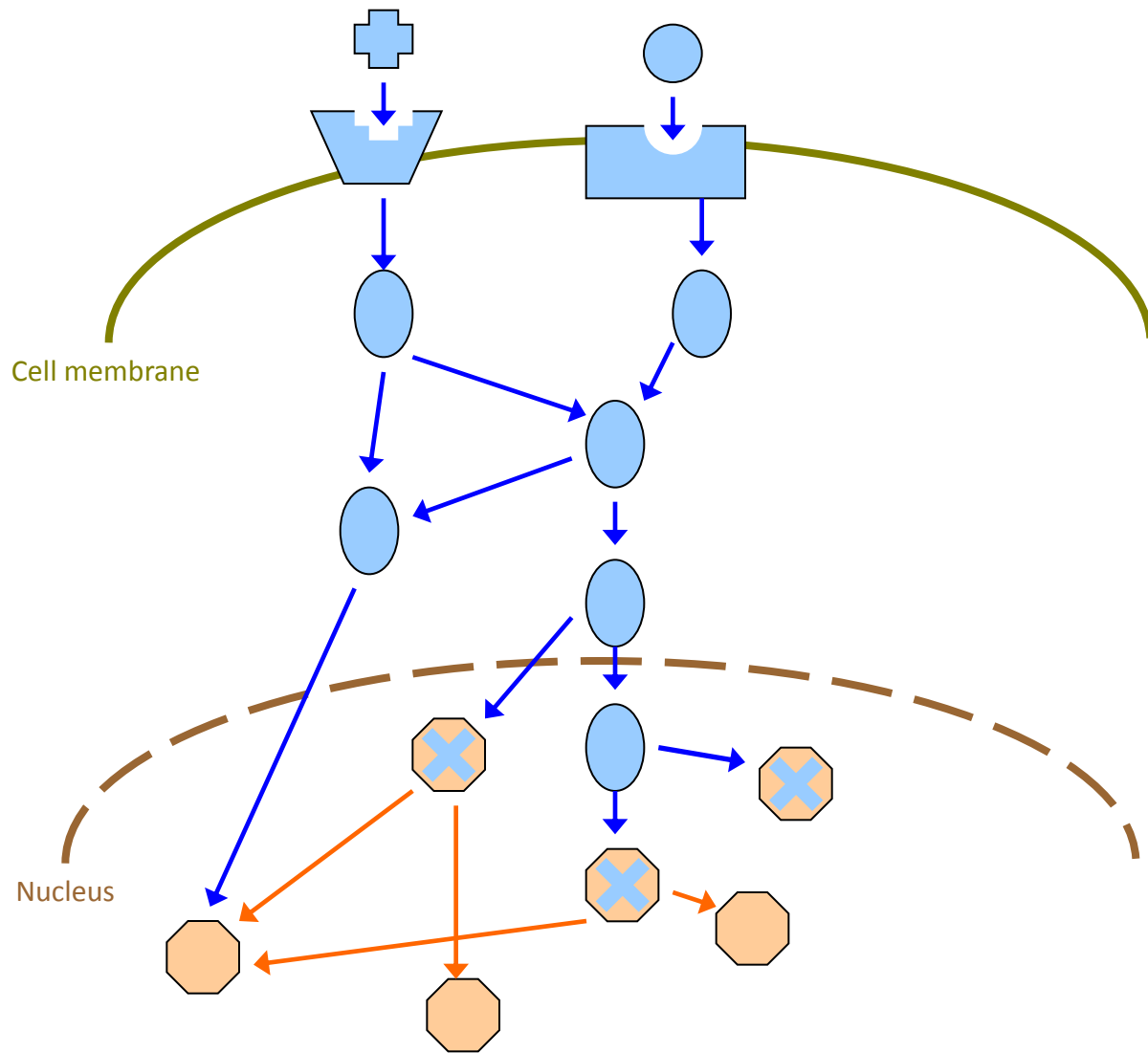
Legends:

 Signaling elements


 Transcription factors


Types of networks:

 Network of signaling pathways

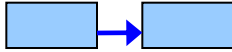


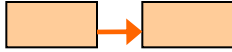
Legends:

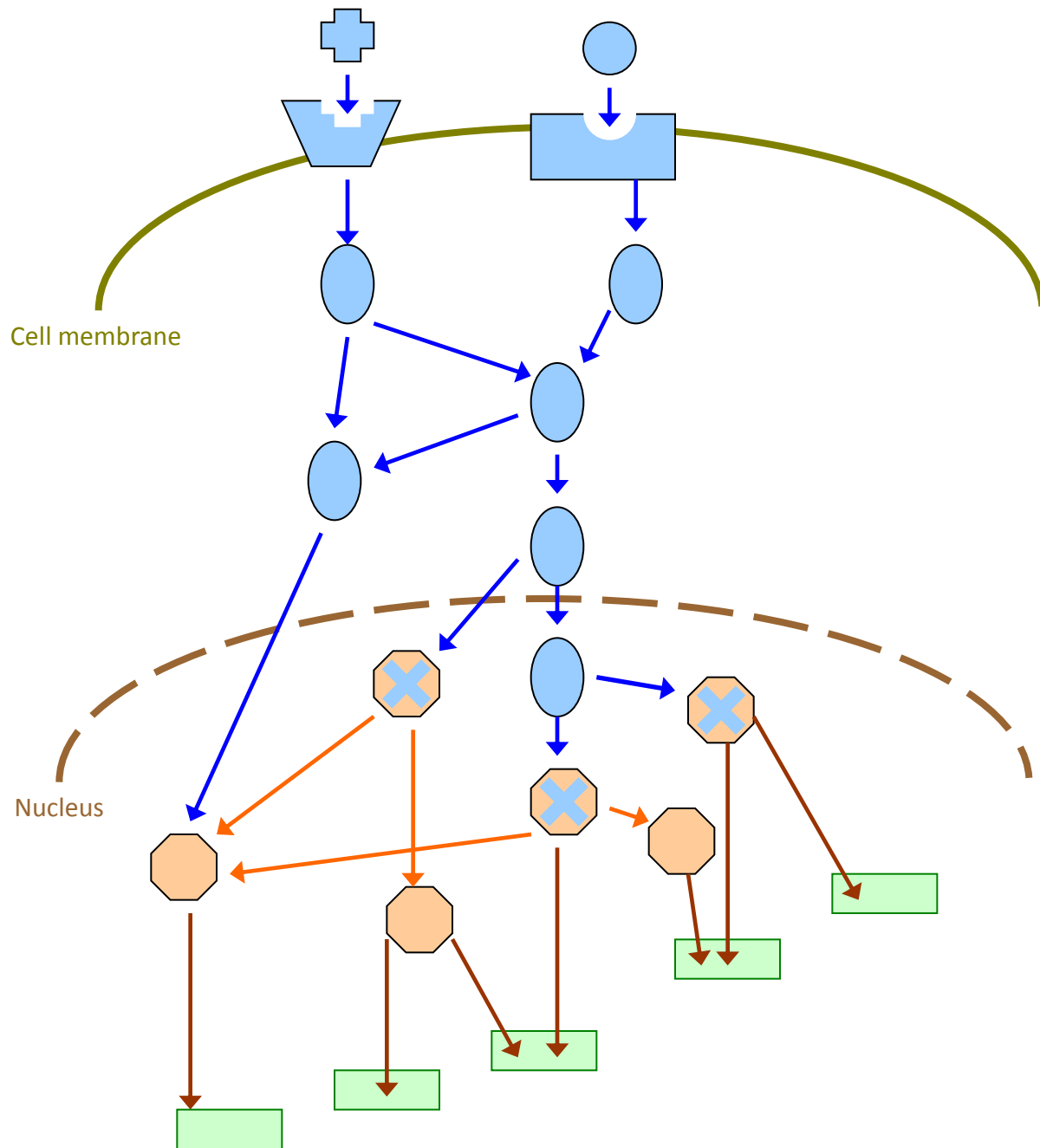
 Signaling elements

 Transcription factors

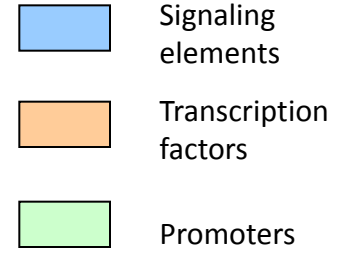
Types of networks:

 Network of signaling pathways

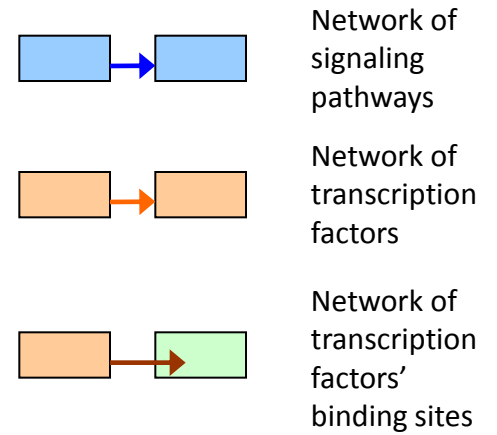
 Network of transcription factors

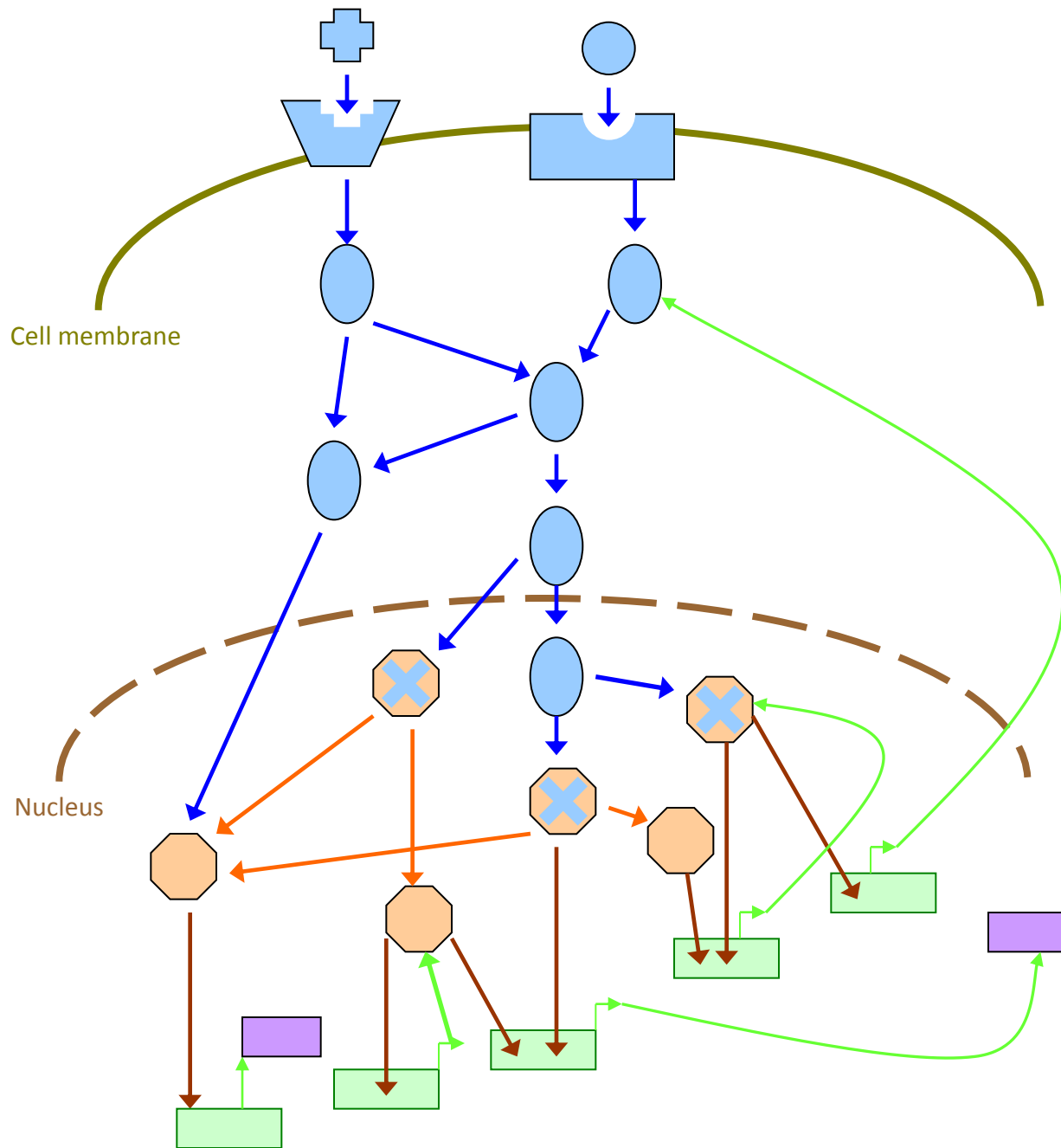


Legends:

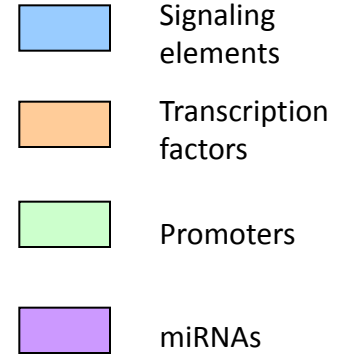


Types of networks:

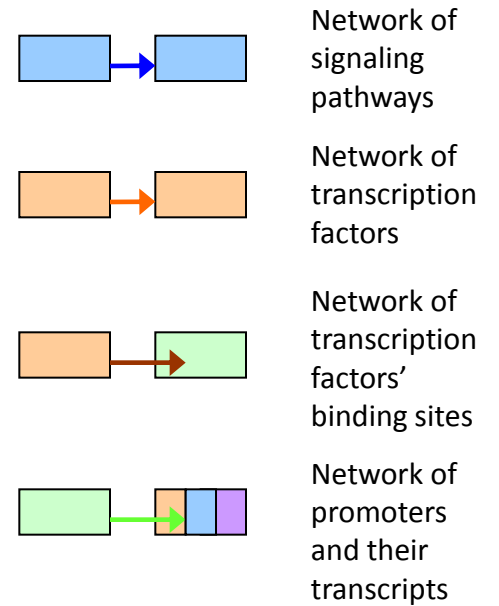


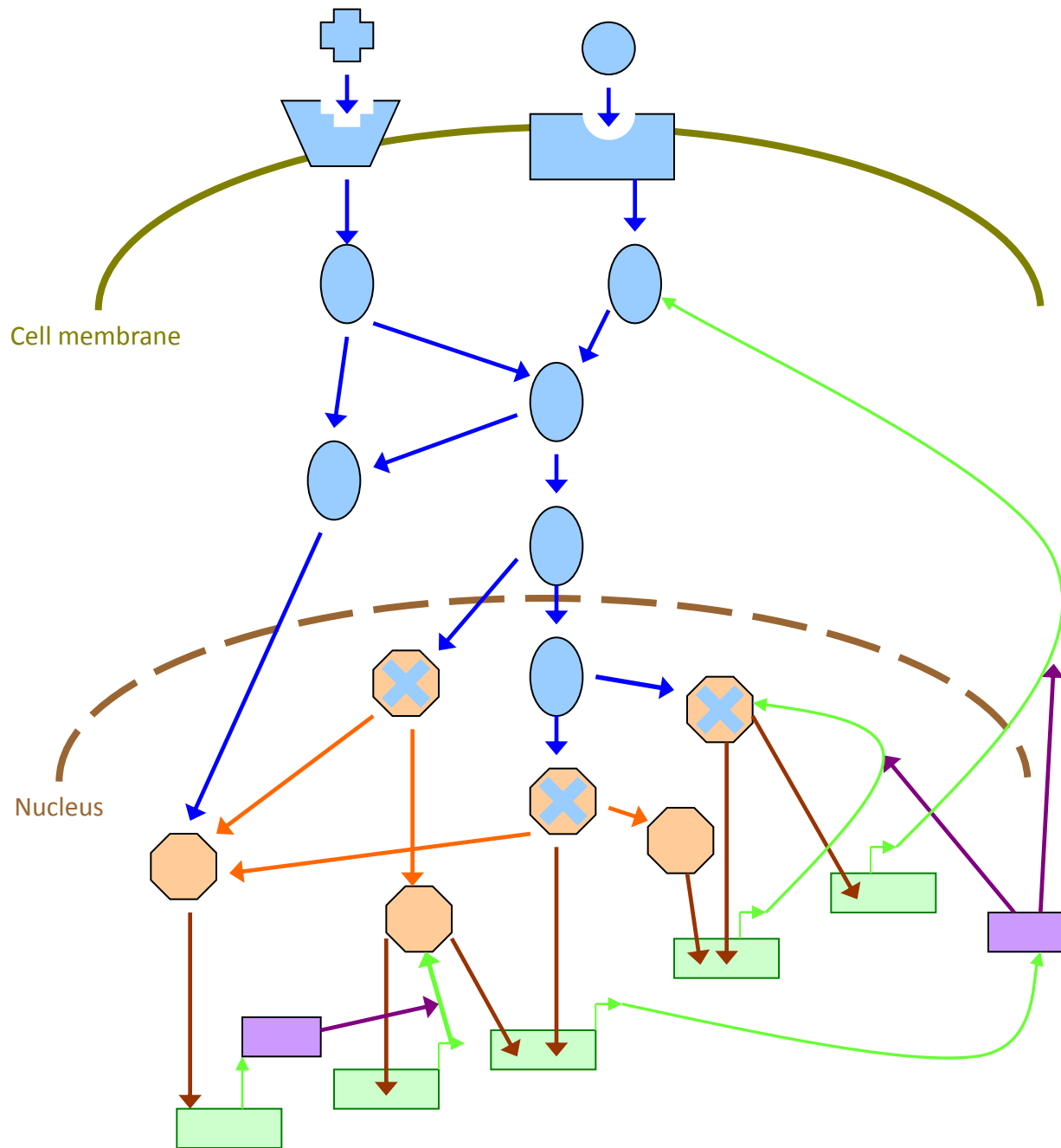


Legends:

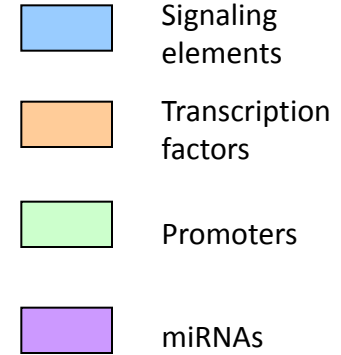


Types of networks:

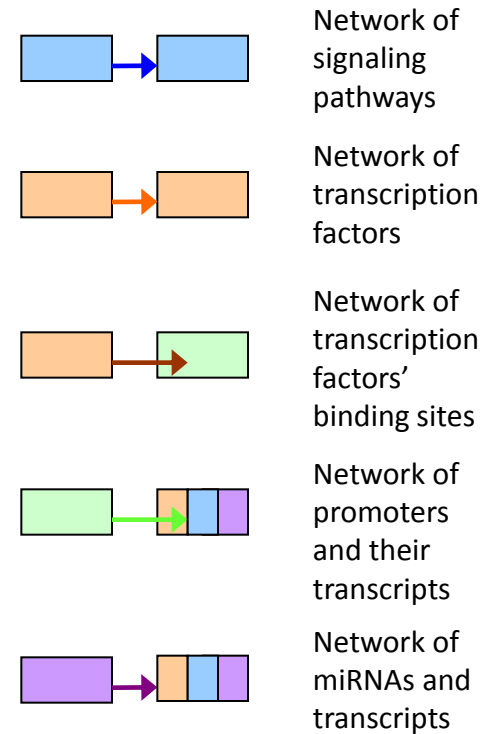




Legends:



Types of networks:



- KEGG
- Reactome
- Signalink
- ...

Component data

- wTF2.1
- FlyTF
- A census of human TFs

•MPromDB

- miRBase
- miROrtho

Legends:



Signaling elements



Transcription factors



Promoters

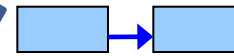


miRNAs

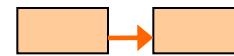
•Fantom4

- ABS
- TRED
- RedFly
- EdgeDB
- JASPAR
- TFe

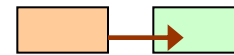
Types of networks:



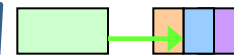
Network of signaling pathways



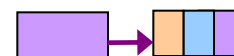
Network of transcription factors



Network of transcription factors' binding sites



Network of promoters and their transcripts



Network of miRNAs and transcripts

Interaction data

- MPromDB
- miRGen
- PutMir

- miRecords
- TarBase



[» Japanese](#)

KEGG Home

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KEGG: Kyoto Encyclopedia of Genes and Genomes

A grand challenge in the post-genomic era is a complete computer representation of the cell, the organism, and the biosphere, which will enable computational prediction of higher-level complexity of cellular processes and organism behaviors from genomic and molecular information. Towards this end we have been developing a bioinformatics resource named KEGG as part of the research projects of the Kanehisa Laboratories in the Bioinformatics Center of Kyoto University and the Human Genome Center of the University of Tokyo.

● Main entry point to the KEGG web service

[KEGG2](#) [KEGG Table of Contents](#) [Update notes](#) [Help](#)

● Data-oriented entry points

[KEGG PATHWAY](#) Pathway maps and pathway modules [Pathway maps](#)
[KEGG BRITE](#) Functional hierarchies and ontologies [Brite hierarchies](#)
[KEGG DISEASE](#) Human diseases
[KEGG DRUG](#) Drugs
[KEGG ORTHOLOGY](#) KO system and ortholog annotation
[KEGG GENES](#) Genes and proteins
[KEGG GENOME](#) Genomes
[KEGG LIGAND](#) Chemical compounds, glycans, and reactions

● Organism-specific entry points

[KEGG Organisms](#) Select (example) [hsa](#)

● Other entry points

[KEGG Atlas](#) New interface to navigate pathway maps
[KEGG GLYCAN](#) Glycome informatics resource
[KEGG COMPOUND](#) Knowledge base for biochemical compounds
[KEGG REACTION](#) Knowledge base for biochemical reactions
[KEGG PLANT](#) Knowledge base for plant natural products
[KAAS](#) KEGG automatic annotation server

http://Reactome.org

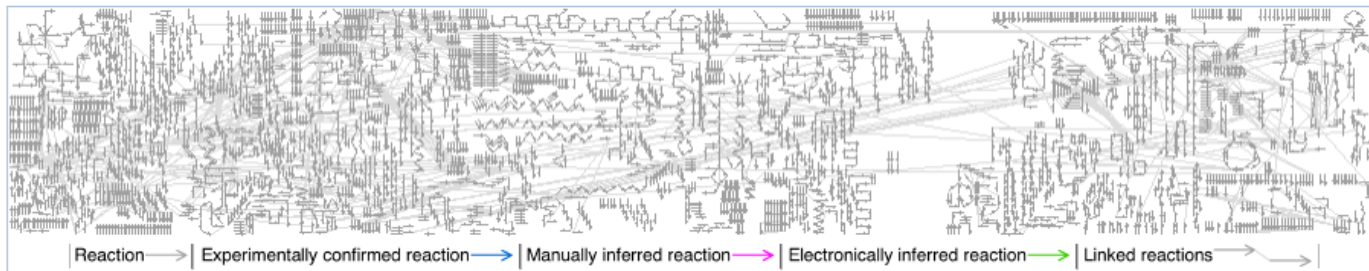


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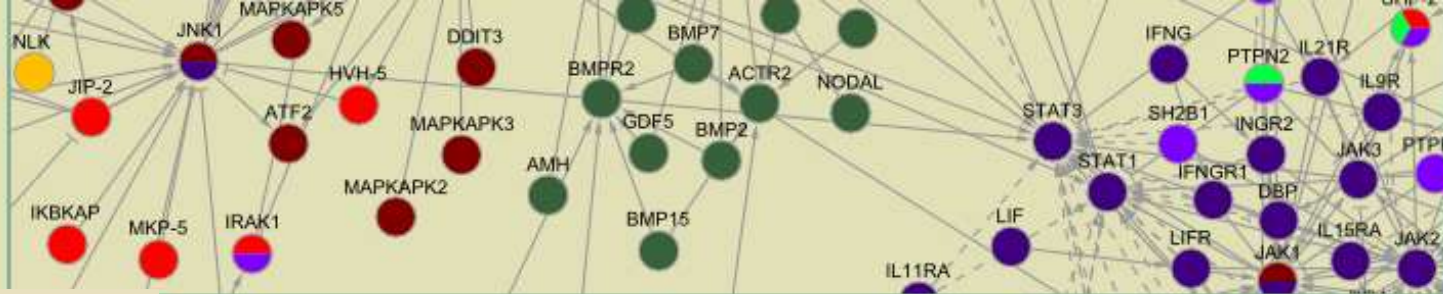
Search for: in **Homo sapiens**

Reactome - a curated knowledgebase of biological pathways

The data displayed is for **Homo sapiens** Use the menu to change the species. Check for cross-species comparison.



Apoptosis	Axon guidance	Biological oxidations	Botulinum neurotoxicity
Cell junction organization	Cell Cycle Checkpoints	Cell Cycle, Mitotic	DNA Repair
DNA Replication	Diabetes pathways	Electron Transport Chain	Gap junction trafficking and regulation
Gene Expression	Hemostasis	HIV Infection	Influenza Infection
Integration of energy metabolism	Integrin cell surface interactions	Metabolism of lipids and lipoproteins	Membrane Trafficking
Metabolism of amino acids and derivatives	Metabolism of carbohydrates	Metabolism of nitric oxide	Metabolism of nucleotides
Metabolism of polyamines	Metabolism of porphyrins	Metabolism of proteins	Metabolism of RNA
Metabolism of vitamins and cofactors	Muscle contraction	mRNA Processing	Myogenesis
Pyruvate metabolism and Citric Acid (TCA) cycle	Regulation of beta-cell development	Regulatory RNA pathways	Signaling by BMP
Signaling by EGFR	Signaling by FGFR	Signaling by GPCR	Signaling by PDGF
Signaling in Immune system	Signaling by Insulin receptor	Signalling by NGF	Signaling by Notch
Opioid Signalling	Signaling by Rho GTPases	Signaling by TGF beta	Signaling by VEGF
Signaling by Wnt	Synaptic Transmission	Telomere Maintenance	Transcription
Transmembrane transport of small molecules			



<http://Signalink.org>




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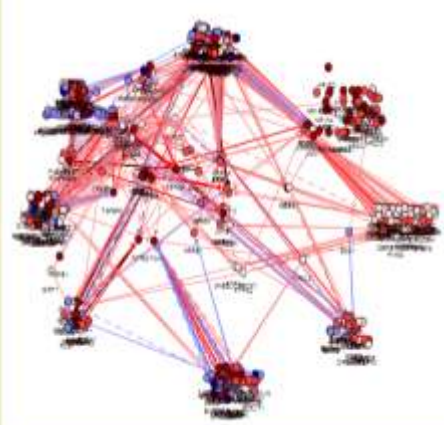
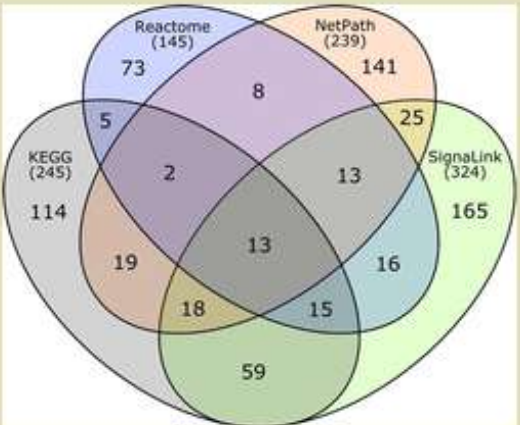
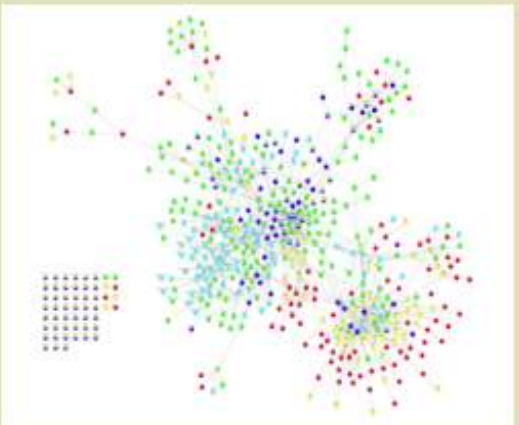
Signalink
an integrated signaling resource

- Features**
- **Biochemically defined** pathways, all major developmental signaling mechanisms included
 - **Manual curation criteria** & identical depth of detail for the entire database
 - **Multi-pathway proteins:** proteins can belong to more than one pathway
 - **Proteins are classified** by pathway position (core/non-core) and section (ligand, receptor, mediator, etc.)
 - **Interactions** are directed and **labeled** with PubMed IDs of experimental evidence

- Curation:** manual, uniform, documented
- Predictions:** pathway members, drug targets
- Experiments:** validate novel pathway members

- With Signalink you can
- **Browse** signaling pathways, cross-talks and multi-pathway proteins
 - **Download** species- and pathway-specific information in several formats
 - **Design** genetic/biochemical **experiments** to verify predicted pathway member proteins
 - **Model** tissue- or disease-specific signaling processes by merging Signalink with expression data
 - **Discover** novel signaling drug target candidates

Species			
Proteins²	560	344	646
<i>predicted²</i>	118	133	121
Interactions²	237	233	991
Pathways²	EGF/MAPK Hh IGF/Ins JAK/STAT IHR Notch TGF Wnt/Wingless		
Data sources	<i>170 pathway-based reviews</i> Total: 941 papers Online sources		



http://fantom.gsc.riken.jp/4/ppi_module/

Mammalian atlas of combinatorial transcriptional regulation

Protein-protein interactions between transcription factors

- Gene centric view
- Network view

Conserved subnetworks

Conserved PPI modules between human and mouse, by qRT-PCR and PPI.

Supplemental material




1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama City, Kanagawa, 230-0045, Japan, RIKEN Omics Science Center
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Transcription factor Encyclopedia

<http://www.cisreg.ca/cgi-bin/tfe/home.pl>



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Legend
• Indicates articles that have been assigned to authors to annotate. • Indicates articles that can be viewed.

Beta-Hairpin-Ribbon Group (open)

Transcription Factor T-Domain (open)

- EOMES**
human
- Eomes**
mouse
- TBR1**
human
- Tbr1**
mouse
- TBX21**
human
- Tbx21**
mouse

Helix-Turn-Helix Group (open)

Arid Domain Family (open)

- ARID3a** human
- Arid3a** mouse

Homeodomain Family (open)

- Arx**
mouse
- CDX2**
human
- Cfxc2**
mouse

- ZBTB16**
human

Other (open)

Stat Protein Family (open)

- STAT1**
human
- Stat1**
mouse

Other Alpha-Helix Group (open)

High Mobility Group (Box) Family (open)

- SOX10**
human
- Sox10**
mouse
- Sox2**
mouse
- SOX8**
human
- Sox8**
mouse
- SOX9**
human
- Sox9**
mouse

MLL

myeloid/lymphoid or mixed-lineage leukemia
(trithorax homolog, Drosophila)

By [Michaela Liedtke](#)

The article completion score for this TF is 100%. [Refresh score](#) [Download scoring guide](#) and [see what's missing](#)

Summary | Structure | TFBS | Targets | Protein | Interactions | Genetics | Expression | Ontologies | Papers

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Overview

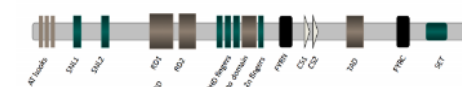
The mixed lineage leukemia (MLL) gene encodes a complex DNA-binding protein with histone H3 lysine 4 (H3K4) methyltransferase activity (Fig. 1)^{1,2} H3K4 methylation is associated with transcriptionally active chromatin, and MLL is therefore thought to epigenetically control gene expression through modification of chromatin structure rather than classical sequence-specific DNA-binding transcription factor function. In addition to its H3K4 methyltransferase activity, MLL has also been shown to bind to specific CpG clusters within gene loci protecting them from methylation ultimately resulting in maintenance of transcription expression.¹³ MLL is a structural and functional homologue of Drosophila trithorax, a homeotic regulator, and has been implicated in epigenetic regulation of transcription that is critical for normal embryonic development and hematopoiesis as well as the pathogenesis of leukemia.^{14,15} The MLL protein is post-translationally cleaved by the protease caspase 1 into two subunits that directly interact and form the core structure of the MLL multi-protein transcriptional complex (Fig. 2). The complex contains additional proteins that mediate DNA-binding, histone modification, transcription factor and co-regulator function and RNA-processing.¹⁶ Among the most widely studied targets of MLL transcriptional regulation are Hox genes. However, MLL associates with thousands of promoters, typically of genes occupied by RNA polymerase II which is required for normal transcriptional initiation and elongation, providing further evidence for MLLs global role as a transcriptional regulator.

The MLL gene is a frequent target for chromosomal rearrangements found in clinically aggressive human acute leukemias of myeloid, lymphoid or mixed lineage in children and adults. Reciprocal chromosomal translocations fuse the N-terminal ~1400 amino acids of MLL in frame to one of over 50 partner proteins of various function including nuclear transcription factors and cytoplasmic proteins. All MLL fusion proteins retain the amino-terminal AT-hoops and the CoG domain of MLL, thus preserving DNA binding activity. In contrast, the plant homeodomain fingers, a region with transactivating potential, and the H3K4 methyltransferase domain are lost.¹⁷ Although deletion of the carboxy-terminal region of MLL would be predicted to result in abrogation of transcription and histone methyltransferase functions, transforming MLL fusion proteins act as transcriptional regulators that can bind DNA and induce aberrant expression of downstream MLL targets such as Hox genes. This points to a disturbance in the epigenetic regulation of gene expression as the main mechanism for leukemogenesis induced by MLL rearrangements. The precise mechanism for this aberrant transcriptional activity is not known, but involves formation of a transcriptional core complex by the chimeric MLL oncoprotein and recruitment of other chromatin modifiers including the H3K79 methyltransferase MLL2/11L and the H3K9 methyltransferase SUV39/11L.^{18,14}

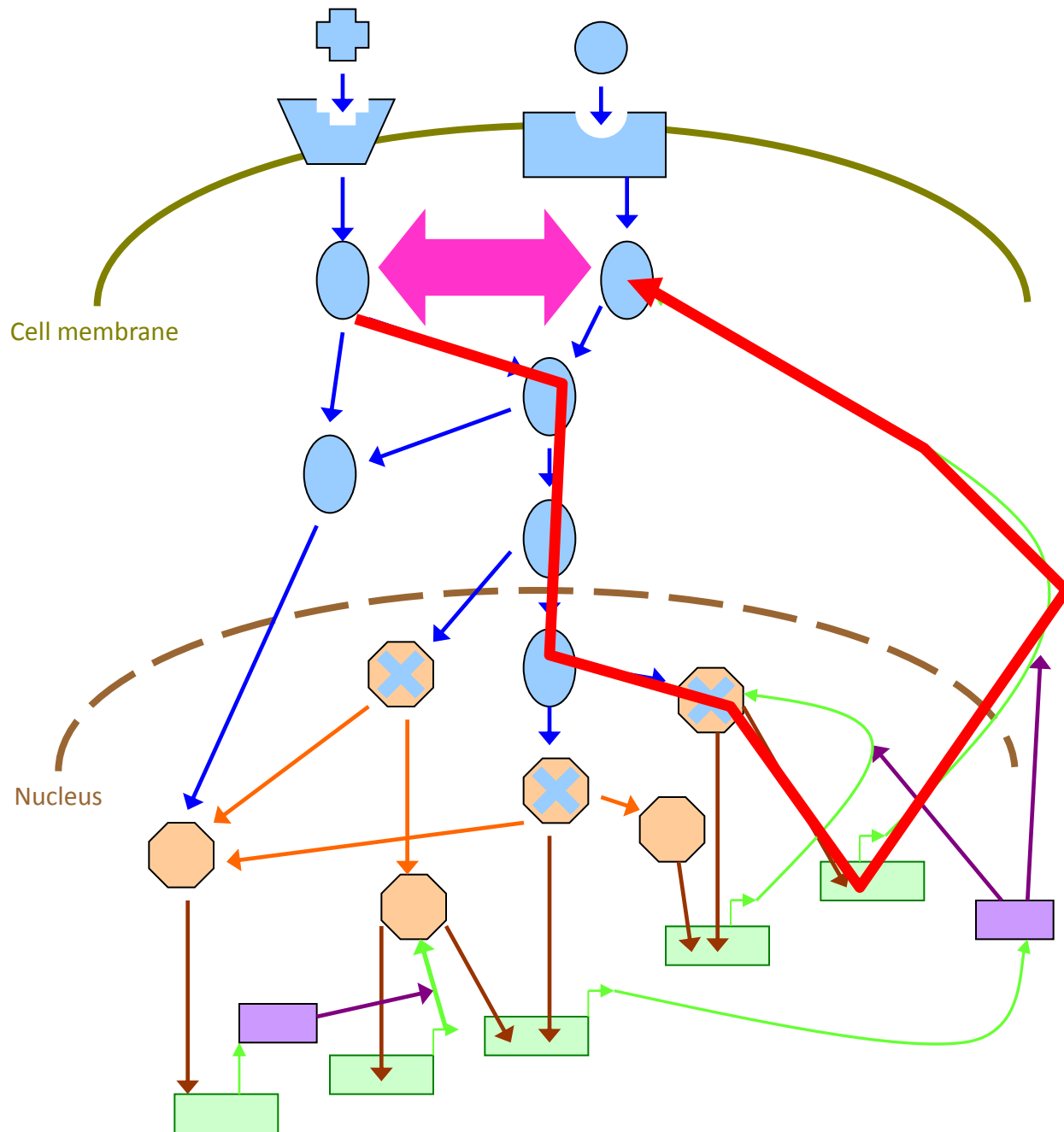
References

1. Tsuchida CC et al. Involvement of a homolog of Drosophila trithorax by 11q23 chromosomal translocations in acute leukemias. *Cell*. 2003;115:1021-1030. [PMID: 14528343]
2. Dhuriy H et al. MLL protects CpG clusters from methylation within the HoxD gene, maintaining transcript expression. *Proc Natl Acad Sci U S A*. 2005;102:1217-1222. [PMID: 15451149]
3. Yu SD et al. Altered Hox expression and segmental identity in MLL-mutant mice. *Nature*. 2003;425:823-828. [PMID: 14774020]
4. Hoss JL et al. Defects in yolk sac hematopoiesis in MLL-null embryos. *Blood*. 2003;102:1759-1765. [PMID: 12822121]
5. Daver A and Kallita TH. The versatile mixed lineage leukemia gene MLL and its many associations in leukemogenesis. *Biom. Cancer Res.*. 2002;17:95E. [PMID: 15283522]
6. Knicker AV and Armstrong SA. MLL translocations, histone modifications and leukemia stem-cell development. *Nat. Rev. Cancer*. 2002;1:82-95. [PMID: 15071180]
7. Okada Y et al. MLL2/11L links histone methylation to leukemogenesis. *Cell*. 2002;110:7-18. [PMID: 12851023]
8. Chung H et al. Protein arginine-methyltransferase-dependent oncogenesis. *Nat. Cell Biol.*. 2002;4:229-235. [PMID: 11981130]





Figures



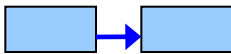



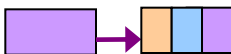
Géninterakciós hálózatok



Legends:

-  Signaling elements
-  Transcription factors
-  Promoters
-  miRNAs

Types of networks:

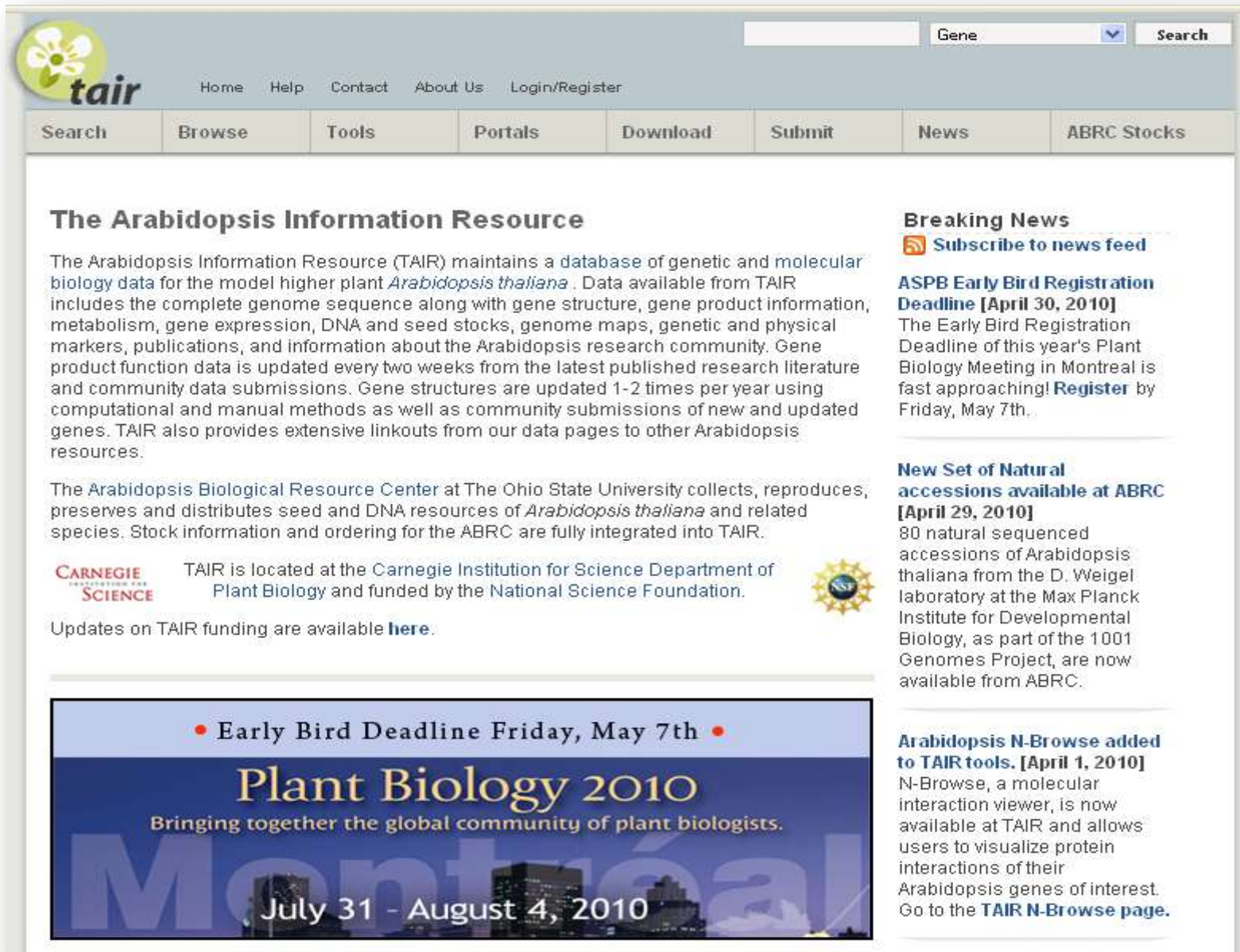
-  Network of signaling pathways
-  Network of transcription factors
-  Network of transcription factors' binding sites
-  Network of promoters and their transcripts
-  Network of miRNAs and transcripts

Gén és géninterakciós adatbázisok

- *A. thaliana*
- *E. coli*
- *S. cerevisiae*
- *D. discoideum*
- *C. elegans*
- *D. melanogaster*
- *M. musculus*
- *H. sapiens*



http://www.arabidopsis.org





The screenshot shows the TAIR website homepage. At the top left is the TAIR logo, a stylized flower. To its right is a search bar with the text "Gene" and a dropdown arrow, followed by a "Search" button. Below the logo is a navigation menu with links: Home, Help, Contact, About Us, and Login/Register. A secondary navigation bar contains buttons for Search, Browse, Tools, Portals, Download, Submit, News, and ABRC Stocks. The main content area is divided into several sections. The first section is titled "The Arabidopsis Information Resource" and contains a paragraph describing the database. The second section is titled "Breaking News" and includes a "Subscribe to news feed" link and a "ASPB Early Bird Registration Deadline [April 30, 2010]" announcement. The third section is titled "New Set of Natural accessions available at ABRC [April 29, 2010]" and describes 80 natural accessions. The fourth section is titled "Arabidopsis N-Browse added to TAIR tools. [April 1, 2010]" and describes a new molecular interaction viewer. At the bottom is a large banner for "Plant Biology 2010" in Montreal, with the dates "July 31 - August 4, 2010".


The Arabidopsis Information Resource

The Arabidopsis Information Resource (TAIR) maintains a database of genetic and molecular biology data for the model higher plant *Arabidopsis thaliana*. Data available from TAIR includes the complete genome sequence along with gene structure, gene product information, metabolism, gene expression, DNA and seed stocks, genome maps, genetic and physical markers, publications, and information about the Arabidopsis research community. Gene product function data is updated every two weeks from the latest published research literature and community data submissions. Gene structures are updated 1-2 times per year using computational and manual methods as well as community submissions of new and updated genes. TAIR also provides extensive linkouts from our data pages to other Arabidopsis resources.

The Arabidopsis Biological Resource Center at The Ohio State University collects, reproduces, preserves and distributes seed and DNA resources of *Arabidopsis thaliana* and related species. Stock information and ordering for the ABRC are fully integrated into TAIR.

 TAIR is located at the Carnegie Institution for Science Department of Plant Biology and funded by the National Science Foundation. 

Updates on TAIR funding are available [here](#).

Breaking News
 [Subscribe to news feed](#)

ASPB Early Bird Registration Deadline [April 30, 2010]
The Early Bird Registration Deadline of this year's Plant Biology Meeting in Montreal is fast approaching! **Register** by Friday, May 7th.

New Set of Natural accessions available at ABRC [April 29, 2010]
80 natural sequenced accessions of *Arabidopsis thaliana* from the D. Weigel laboratory at the Max Planck Institute for Developmental Biology, as part of the 1001 Genomes Project, are now available from ABRC.

Arabidopsis N-Browse added to TAIR tools. [April 1, 2010]
N-Browse, a molecular interaction viewer, is now available at TAIR and allows users to visualize protein interactions of their *Arabidopsis* genes of interest. Go to the [TAIR N-Browse page](#).

Plant Biology 2010
Bringing together the global community of plant biologists.
Montreal
July 31 - August 4, 2010

http://www.ecocyc.org

About EcoCyc

Project Overview
User Guide
Guided Tour
Instructional Videos
Publications
Update History
Steering Committee
Credits

Information

Gene Cross-References
Unsequenced Enzymes
Conferences
Web Links

Services

Join EcoCyc Mailing List
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Faster EcoCyc Search
Metabolic Posters
Genome Posters
Web Services

ECOCYC PROJECT OVERVIEW

EcoCyc is a bioinformatics database that describes the genome and the biochemical machinery of *E. coli* K-12 MG1655. The long-term goal of the project is to describe the molecular catalog of the *E. coli* cell, as well as the functions of each of its molecular parts, to facilitate a system-level understanding of *E. coli*. EcoCyc is an electronic reference source for *E. coli* biologists, and for biologists who work with related microorganisms.

This page provides an overview of the data content of EcoCyc. See also the list of [data sources from which EcoCyc integrates data](#).

Genome. EcoCyc contains the complete genome sequence of *E. coli*, and describes the nucleotide position and function of every *E. coli* gene. A staff of five full-time curators updates the annotation of the *E. coli* genome on an ongoing basis using a [literature-based curation](#) strategy. Mini-review summaries of *E. coli* gene products can be found in EcoCyc protein and RNA pages. Users can retrieve the nucleotide sequence of a gene, and the amino-acid sequence of a gene product.

Regulation. EcoCyc describes several types of *E. coli* cellular regulation:

- **Substrate-level enzyme regulation:** Provided for hundreds of *E. coli* enzymes.
- **Transcriptional regulation and operon organization:** EcoCyc contains the most complete description of the regulatory network of any organism, including *E. coli* [operons](#), promoters, transcription factors, transcription-factor binding sites, attenuators, and small-RNA regulators. The transcriptional regulatory information in EcoCyc and [RegulonDB](#) is curated by the group of [Dr. Adolfo Collado-VIDES](#) at the UNIAAM; both databases therefore have the same data content on transcriptional regulation of gene expression. Actual curation of the data occurs within EcoCyc, and the information is periodically propagated to [RegulonDB](#).
- **Attenuation:** Curation of regulation by attenuation began in 2008.
- **Regulation by small RNAs:** Curation of small RNA-based regulation began in 2008.

Membrane transporters. EcoCyc annotates *E. coli* transport proteins, and the associated [transport reactions](#) that they mediate.

Metabolism. EcoCyc describes all known [metabolic pathways](#) and signal-transduction pathways of *E. coli*. It describes each metabolic enzyme of *E. coli*, including its cofactors, activators, inhibitors, and subunit structure. See also the [MetaCyc project](#).

Database links. EcoCyc is linked to other biological databases containing protein and nucleic acid sequence data, bibliographic data, protein structures, and descriptions of different *E. coli* strains.

Literature-Based Curation. Curation is the process of manually refining and updating a bioinformatics database. The EcoCyc project uses a *literature-based* curation approach in which database updates are based on evidence in the experimental literature. EcoCyc is largely up to date with respect to its curation activities. As of March 2010, EcoCyc has encoded information from more than 19,000 publications.

Curators collect gene, protein, pathway, and compound names and synonyms. They classify genes and gene products using the Gene Ontology and MultiFun ontology, and they classify pathways within the Pathway Tools pathway ontology. Protein complex components and the stoichiometry of these subunits are captured; cellular localization of polypeptides and protein complexes is entered, as are experimentally determined protein molecular weights; enzyme activities and any enzyme prosthetic groups, cofactors, activators, or inhibitors are captured. Operon structure and gene regulation information are encoded. Textual summaries with extensive citations are authored by curators. Within the summaries for proteins, RNAs, pathways, and operons, curators capture additional information not captured in the highly structured database fields of EcoCyc. For example, curators use the free-text summary sections to capture phenotypes caused by mutation, depletion, or overproduction of each gene product; any genetic interactions known; protein domain architecture and structural studies; similarity to other proteins; or any functional complementation experiments that have been described. Summaries can also be used to note cases in which the published reports present contradictory results. In such cases, both viewpoints will be presented with proper attribution. This approach assures that no information is lost.

Query and visualization. Scientists can use the [EcoCyc web site](#) or the [downloadable](#) Pathway Tools software to visualize the layout of genes within the *E. coli* chromosome, or of an individual biochemical reaction, or of a complete biochemical pathway (with compound structures displayed). The navigation capabilities of the software allow a user to move from a display of an enzyme to a display of a reaction that the enzyme catalyzes, or to the gene that encodes the enzyme.

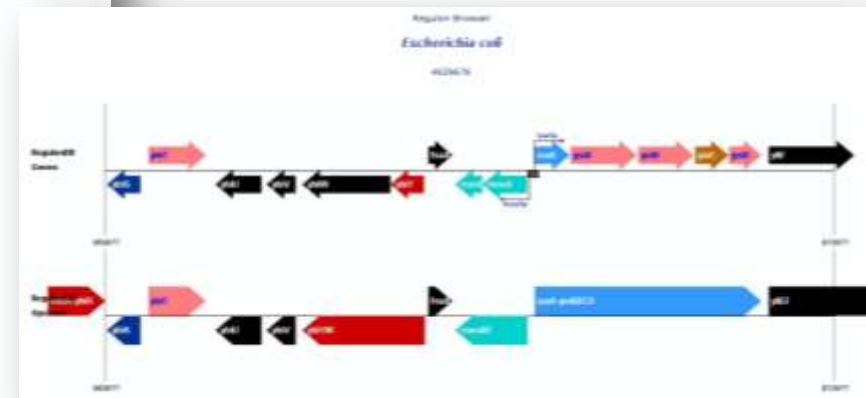
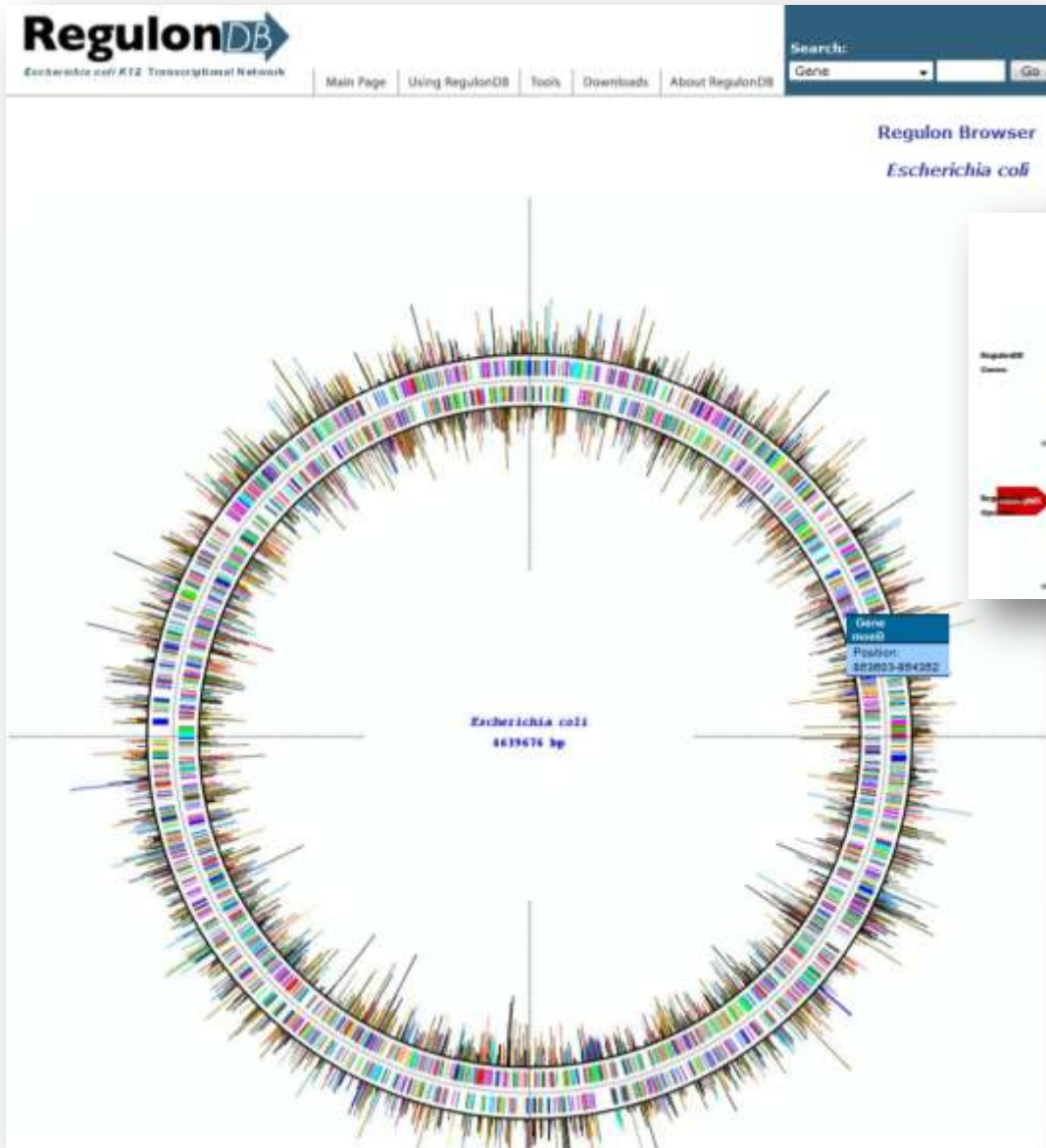
Analysis of omics data. EcoCyc provides four tools for analysis of omics datasets:

- The [Cellular Omics Viewer](#) allows metabolomics, gene expression, and proteomics data to be painted on a complete *E. coli* metabolic pathway map.
- The [Genome Omics Viewer](#) allows omics datasets to be visualized against the full *E. coli* genome map.
- The [Regulatory Omics Viewer](#) allows omics datasets to be painted onto the *E. coli* regulatory network. (Currently only available in the desktop version of Pathway Tools.)
- The [Genome Browser tracks](#) allow ChIP-chip data, and other positional data, to be viewed against regions of the *E. coli* genome.


Underlying software. The [Pathway Tools](#) software that underlies EcoCyc is not specific to *E. coli*, but has been applied to manage genomic and biochemical data for hundreds of organisms.

"EcoCyc" is pronounced "ee-ko-sike". It sounds like "ecology" and like "encyclopedia".

<http://regulondb.ccg.unam.mx/>







http://www.yeastgenome.org/



Saccharomyces Genome Database

Search

Site Map | Search Options | Help | Home |    

Community Info | Submit Data | BLAST | Primers | PatMatch | Gene/Seq Resources | Advanced Search | Community Wiki

SGD™ is a scientific database of the molecular biology and genetics of the yeast *Saccharomyces cerevisiae*, which is commonly known as baker's or budding yeast.

New and Noteworthy

- Search Options**
Advanced Search, Full-text Search (Textpresso), Search SGD web pages, Global Gene Hunter, Search Literature, and more.
- Help Resources**
Getting Started, Sitemap, FAQ, and more.
- Analysis & Tools**
BLAST, Gene/Seq Resources, Maps, and more.
- Homology & Comparisons**
PDB Homologs, Protein Domains/Motifs, Homologs, and more.
- Function & Expression**
Protein Info, Pathways, Expression Connection, and more.
- GO Resources**
GO Tutorial, What is GO?, GO Slim Mapper, GO Term Finder, and more.
- Community Info**
Search SGD colleagues, Find yeast labs, Conferences & Seminars, Community wiki, and more.
- Submit Data**
Gene Registry, Colleague update, Contact SGD, and more.
- Download Data**
FTP, Batch Download, Lab strains, Auxotrophic markers, Gene Names, Sequencing Tables, SGD Lite, and more.
- External Links**
General Yeast Topics, Protocols and Methods, and more.

- New Search Templates Added to YeastMine - November 12, 2010**
New pre-defined search templates have been added to [YeastMine](#) to query phenotype data, overlapping genes, intergenic regions and references curated to genes and/or literature topics. These [templates](#) can be accessed by clicking on the Templates tab and filtered by category using the pull down menu. With the addition of 11 templates in these categories, YeastMine can now be used to query the following datatypes: Chromosomal features, Protein features, GO annotations, Phenotypes, Interaction data and Literature. Please [email us](#) your comments and questions about YeastMine.

YeastMine is part of a joint project with [InterMine](#), the Rat Genome Database ([RGD](#)), and The Zebrafish Model Organism Database ([ZFIN](#)) to provide interoperability between the model organism databases via shared datatypes, such as Gene Ontology (GO) annotations or orthologs.
- SGD Curation News**
 - Genome Snapshot
 - New papers added to SGD this week.
 - View [Genome-wide Analysis papers](#) in SGD.
 - Do a [literature search](#).
 - [Table of Gene Summary Paragraphs](#) (new ones highlighted yellow).
- SGD Quarterly Newsletter - November 1, 2010**
SGD sends out its quarterly newsletter to colleagues designated as contacts in SGD. An [HTML version](#) of the newsletter is available. If you would like to receive this letter in the future please use the [Colleague Submission/Update](#) form to let us know.
- Yeast Biochemical Pathways Upgraded - October 5, 2010**
The [Yeast Biochemical Pathways](#) have been upgraded to [Pathway Tools version 14.0](#). This version offers a robust search system with auto-complete and filtering functionality to search for compounds, reactions, genes/proteins and pathways. In addition, the [Advanced Query](#) page has been enhanced to support structured queries to extract data. The yeastcyc14.0 data files that can be used with version 14.0 and the [biochemical_pathways.tab](#) file can be downloaded from [SGD's downloads page](#). Other features of interest are: 1) a downloadable [Yeast Biochemical Pathway Poster](#), which gives you an overview of the manually-curated pathways, and 2) the [Comparative Analysis Tool](#), which allows you to make comparisons between different pathway databases, and compute summary statistics on a single database.
- SGD on Facebook and Twitter - August 26, 2010**
SGD is now on Facebook and Twitter! ["Like" us](#) on Facebook or [follow @yeastgenome](#) on Twitter to get updates about new features, tips on using SGD, and interesting tidbits about yeast.

http://thebiogrid.org

BioGRID^{3.0}

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Welcome to the Biological General Repository for Interaction Datasets

BioGRID is an online interaction repository with data compiled through comprehensive curation efforts. Our current index is version **3.0.64** and searches **23,070** publications for **337,957** raw protein and genetic interactions from major model organism species. All interaction data are **freely** provided through our search index and available via download in a wide variety of standardized formats.

[INTERACTION STATISTICS](#)

[LATEST DOWNLOADS](#)

Search the BioGRID

Search by identifiers, keywords, and gene names...

All Organisms



[SUBMIT SEARCH](#)



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AREAS OF INTEREST TO HELP YOU GET STARTED



Build and Download Interaction Datasets

Create custom interaction datasets by protein or by publication. You can also download our entire dataset in a wide variety of standard formats.



Link To Us or Submit Interactions

Send us your datasets or link to the BioGRID directly from your own website or database. Full details on how to contribute are available here.



Online Tools and Resources

We've developed tools that make use of BioGRID data. Check out the list of tools to see if we can help you work with our data.



View Our Interaction Statistics

Find out how many organisms, proteins, publications, and interactions are available in the current release of the BioGRID.

BIOGRID FUNDING AND PARTNERS



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Dictyostelium discoideum

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Gene Page for rasD

Gene Summary Protein Information Gene Ontology Orthologs Phenotypes References BLAST


General Information

Gene Name	rasD
Name Description	ras = RAS Sarcoma viral oncogene homolog
Alternative Gene Names	ras, Del-ras, Ddras, rasA
Gene ID	DOB_G0292395
Gene Product	Ras GTPase
Description	expressed in pstAD cells and in upper cup during culmination
Community Annotations	Add an annotation for rasD Community Annotations Help

Genomic Information

Location: Chromosome 6 coordinates 2530991 to 2531851, Crick strand

Genomic Map: [Click on the map to browse the genome from this location]



Notes: The sequences from the Sequencing Center and GenBank

Gene Product Information

Protein Coding Gene	DOB0216195 (Curator reviewed) Derived from gene sequence. Supported by mRNA.
Protein Length	187 aa
Protein Molecular Weight	21,201.9 Da
More Protein Data	Protein sequence, domains and much more...
Sequence	Protein <input type="button" value="Get Fasta"/> <input type="button" value="BLAST"/>

Associated Sequences

GenBank Genomic Fragment	Z11804
GenBank mRNA	M62618
ESTs	DD815746 DD816340 DD816475 DD816476 DD816704 DD816704 more

Gene Ontology Annotations

View evidence and references

Molecular Function	GTPase activity (BS), GTP binding (BS), protein binding (FP), nucleotide binding (EA)
Biological Process	Ras protein signal transduction (BS), NOT cell death (DD), cytokinesis (DD), chemotaxis (MP), multicellular organismal development (MP), hematopoiesis (MP), phagocytosis (BP), small GTPase mediated signal transduction (EA)
Cellular Component	intracellular (EA), membrane (EA)

Strains and Phenotypes

View Phenotypic Information

rasD-rasD	alcohol aggregation
rasD	abnormal phagocytosis absent chemotaxis
rasD(G1T)	development arrests at mound stage development arrests at tipped mound stage
Additional Strains	rasD-fusD(rasD) jrc1(rasD G1P)

Links

Expression	In silico Expression Pattern dictyExpress (microarray) dictyExpress (RNA-Seq)
dictyBase Clonages	rasD Recombinants
External Resources	Interpro GenBank Protein UniProtKB PDB

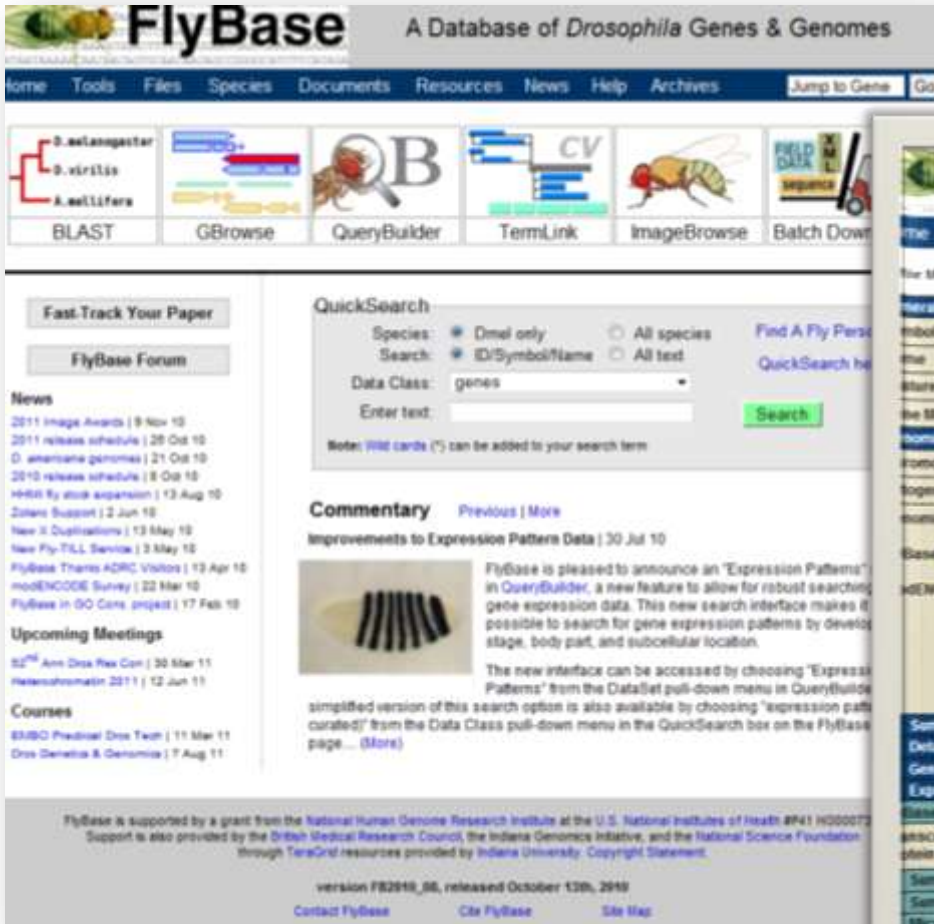
Summary

Curator Status: Basic annotations have been added to this gene. 11 MAR 2004 PF

Latest References: View complete list of references (17 papers)

- Brennwald, Spiegelskas & Weeks (2006) RAS PROTEINS HAVE MULTIPLE FUNCTIONS IN VEGETATIVE CELLS OF DICTYOSTELIUM. *Eukaryot Cell*
- Zhang, Charvet & Fird (2005) Spatiotemporal regulation of Ras activity provides directional sensing. *Cur Biol* 15:1587-93
- Kartick & van Haesbroek (2005) Highlighting the role of Ras and Rap during Dictyostelium chemotaxis. *Cell Signal* 20:1415-22
- Sacchi, Lorenza, Magdi & Belluzzi (2003) Theodora's Temporal Networks to represent temporal relationships in gene expression data. *J Biomed Inform* 40: N3-74
- Kartick, Robinson, Rao, Bhaugyal, Kuzler-Gambick, Weeks, Winkler & Van Haesbroek (2004) Characterization of the G20D-activated Rap1 pathway regulating adhesion and cell polarity in Dictyostelium discoideum. *J Biol Chem* 279:23267-75

http://flybase.org/



FlyBase A Database of *Drosophila* Genes & Genomes

Home Tools Files Species Documents Resources News Help Archives Jump to Gene Go

BLAST GBrowse QueryBuilder TermLink ImageBrowse Batch Down

Fast-Track Your Paper

FlyBase Forum

News

- 2011 Image Awards | 9 Nov 10
- 2011 release schedule | 29 Oct 10
- D. ananassae genomes | 21 Oct 10
- 2010 release schedule | 8 Oct 10
- HR68 fly stock expansion | 13 Aug 10
- Joblet Support | 2 Jun 10
- New X Duplication | 13 May 10
- New Fly-TLL Service | 3 May 10
- FlyBase Thru ADRC Visitors | 12 Apr 10
- modENCODE Survey | 22 Mar 10
- FlyBase in GO Core project | 17 Feb 10

Upcoming Meetings

- 52nd Ann Dros Res Con | 30 Mar 11
- Neurochromatin 2011 | 12 Jun 11

Courses

- EMBO Practical Dros Twin | 11 Mar 11
- Dros Genetics & Genomics | 7 Aug 11

QuickSearch

Species: Dmel only All species Find A Fly Person

Search: ID/Symbol/Name All text QuickSearch help


Data Class: genes

Enter text:

Note: Wild cards (*) can be added to your search term

Commentary Previous | More

Improvements to Expression Pattern Data | 30 Jul 10

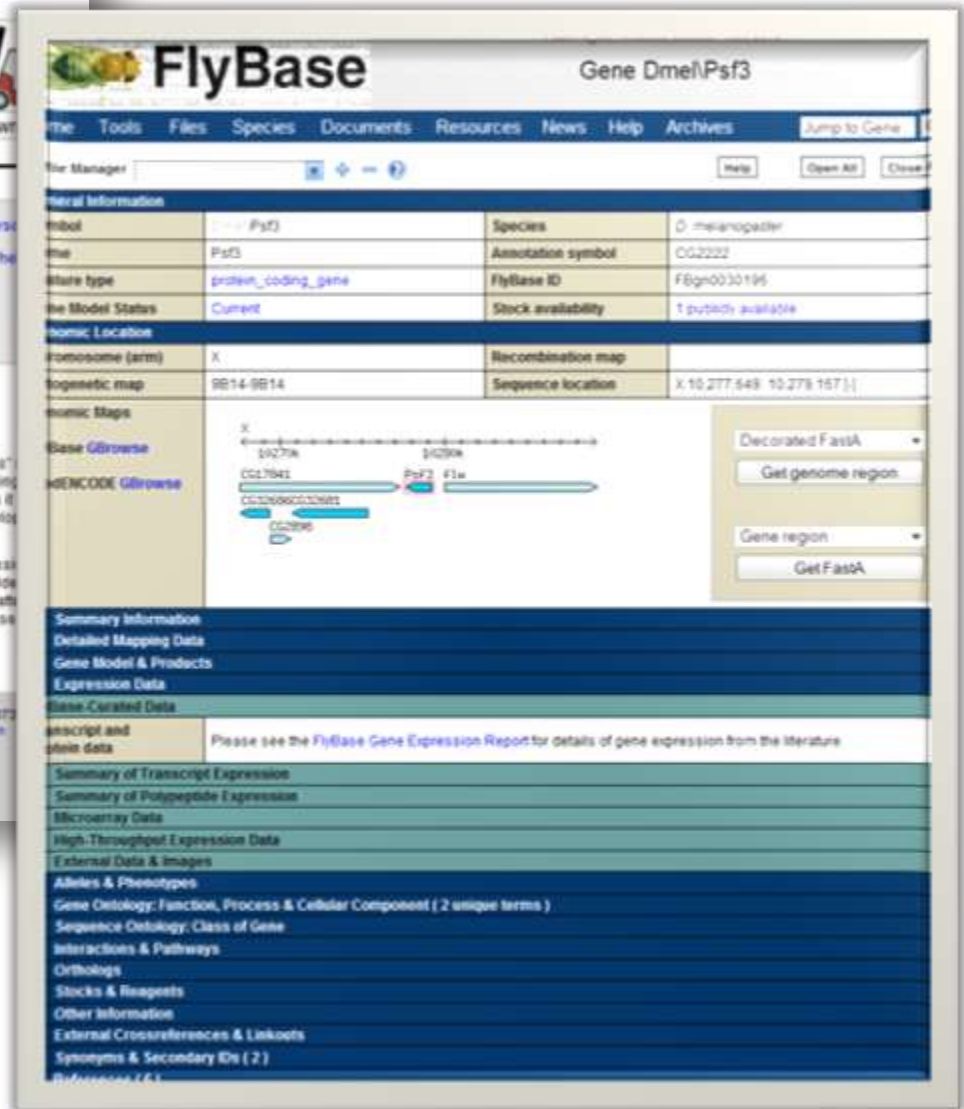


FlyBase is pleased to announce an "Expression Patterns" in QueryBuilder, a new feature to allow for robust searching gene expression data. This new search interface makes it possible to search for gene expression patterns by developmental stage, body part, and subcellular location.

The new interface can be accessed by choosing "Expression Patterns" from the Dataset pull-down menu in QueryBuilder. A simplified version of this search option is also available by choosing "expression pattern curated" from the Data Class pull-down menu in the QuickSearch bar on the FlyBase page... (More)

FlyBase is supported by a grant from the National Human Genome Research Institute at the U.S. National Institutes of Health #P41 HG000723. Support is also provided by the British Medical Research Council, the Indiana Genomics Initiative, and the National Science Foundation through TerraCred resources provided by Indiana University. Copyright Statement.

version FB2010_06, released October 13th, 2010
Contact FlyBase Cite FlyBase Site Map



FlyBase Gene Dmel\Psf3

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The Manager

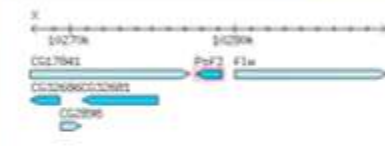
General Information

Symbol	Psf3	Species	D. melanogaster
Name	Psf3	Annotation symbol	CG2222
Feature type	protein_coding_gene	FlyBase ID	FBgn0030196
Gene Model Status	Current	Stock availability	1 publicly available

Chromic Location

Chromosome (arm)	X	Recombination map	
Genetic map	9B14-9B14	Sequence location	X:10,277,549-10,279,157[+]

Genomic Maps



Base GBrowse

ENCODE GBrowse

Decorated FastA

Gene region

Summary Information

- Detailed Mapping Data
- Gene Model & Products
- Expression Data
- Base Curated Data
- Transcript and protein data
- Summary of Transcript Expression
- Summary of Polypeptide Expression
- Microarray Data
- High-Throughput Expression Data
- External Data & Images
- Aliases & Phenotypes
- Gene Ontology: Function, Process & Cellular Component (2 unique terms)
- Sequence Ontology: Class of Gene
- Interactions & Pathways
- Orthologs
- Stocks & Reagents
- Other Information
- External Crossreferences & Linkouts
- Synonyms & Secondary IDs (2)
- References (6)

http://www.wormbase.org/

Find:

Gene Summary | Linkout Summary | Sequence Summary | Protein Summary | CDS Alignment | Genome Browser | GeneMap | Nearby Genes | Bibliography | Tree Display | AAL | Schemas | About Page

Gene Summary for let-60

Specify a gene using a gene name (*let-60*), a predicted gene id (*R1345.9*), or a protein ID (*CE02711*) *let-60*
[\[identification\]](#)[\[location\]](#)[\[function\]](#)[\[expression\]](#)[\[gene ontology\]](#)[\[genetics\]](#)[\[homology\]](#)[\[reagents\]](#)[\[bibliography\]](#)

IGs	Main name	Sequence name	Other name(s)	WB Gene ID
	<i>let-60</i> (<i>let-60</i>) We Person evidence: David Barker	ZK702.6	lin-34	WBGene0002335

Concise Description: *let-60* encodes a member of the GTP-binding RAS proto-oncogene family. *let-60* activity is required for viability, vulval development, oocyte development, germ line meiotic progression, posterior development of the hypodermis, chemotaxis, sex myoblast migration, and muscle membrane extension. *let-60* acts generally downstream of *let-23* with respect to vulval development and upstream of the MAPK pathway with respect to chemotaxis. *let-60* is expressed in neural, muscle, and hypodermal lineages. [\[Details\]](#)

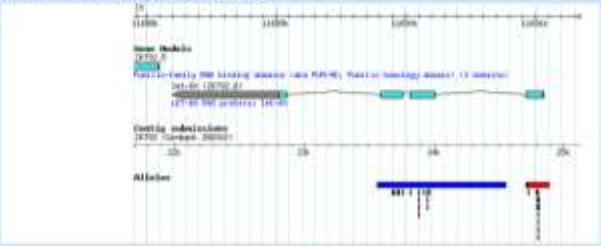
NCBI KOGs: Ras-related GTPase [KOG0395] [CMPare_WA001730]


Species: *Caenorhabditis elegans*

Gene model(s):

Gene Model	Status	Nucleotides (coding/transcript)	Protein	Amino Acids
ZK702.6 ¹	(confirmed by cDNA(s))	555/986 bp	WP.CE0037	184 aa

[Other sequences](#)
[Fastnotes](#)
[Revision History](#)

Location: Genetic Position: IV:5211-41, 9.004 cM [mapping data]
Genomic Position: IV:11091065..11098200 bp [view Genome Browser]
Genomic Environments:


Expression: Systemic expression patterns:

let-60 (ac:let-2) The vulval lineage. First detected in L3 larvae (before vulval induction). First strongly observed in P1-P6. Strong lacuonous stripes at VPCs begin dividing and fusion occurs in expressed through adulthood. First strongly observed in P1-P7. Strong staining in vul, vulB, vulC, vulD, vulE and vulF. Multilineage 11 (primarily after division of 10). [\[Details\]](#) [Exp009](#)
GFP-*let-60* localizes, in part, to the periphery of cells in embryos and during later stages of development. [\[Details\]](#) [Exp008](#)

Function: Phenotypic:
[Phenotypic Summary](#)
[RNAi Details](#)
The following phenotypes were observed via RNAi of *let-60*:

Experiment	Phenotype	Screen/Genotype	Clad ID
WB00040004753	sterile	lin-50;Sp10X	Silver 0 et al
WB00040011104	sterile; altered vulval induction; vulval induction	lin-50;let-394120	Silver 1 et al
WB00040007106	sterile; altered vulval induction; vulval induction	lin-50;let-120	Cowan J et al
WB00040004300	sterile	lin-50;let-120;1	Lohrle 0 et al
WB00040007100	slow growth; altered vulval induction	let-750;let-11	Styne AD et al
WB00040003073	sterile	lin-50;let-120	Gratchev D et al
WB00040004307	sterile; vulval induction; vulval induction	lin-50;let-120;1	Lohrle 0 et al
WB00040004301	sterile	lin-50;let-120;1	Silver 0 et al

Homology: Similarities: [Best BLASTP matches](#)

Species	Hit	Description	E-value	Length
<i>C. briggsae</i>	BP_CBP01499	gene CBG00092	6.6e-50	99.5%
<i>C. brennani</i>	CN_CN20628	gene CBN10834	9.3e-50	99.5%
<i>C. remanei</i>	RP_RP12904	gene CRE12606	2.6e-95	99.5%
<i>P. pacificus</i>	PP_PP11009		1.6e-82	99.5%
<i>B. malayi</i>	TR_LAMPY06	Ras protein <i>let-60</i> , putative	6.6e-78	99.5%
<i>H. sapiens</i>	ENSEMBL_ENSP00000308495	isoform 2B of GTPase KRas		
<i>C. carpio</i>	SW_Q8YH36	GTPase KRas		
<i>D. melanogaster</i>	FLYBASE_C06375	Flybase gene name is Ras85D-PA.		
<i>C. japonica</i>	JA_JA37659	gene C.JA02942		
<i>S. cerevisiae</i>	SGO_YOR101W	GTPase involved in G-protein signaling in the adenylate cyclase activating pathway, plays a role in membrane. homolog of mammalian RAS proto-oncogenes		
<i>C. elegans</i>	WP.CE03037	ras protein		

Interaction Summary

Interaction	Type	Interactor 1	Interactor 2	Effector to Effectuated
WBInteraction000040	Genetic	<i>let-60</i>	<i>sup-7</i>	Interactor 1 → 2
WBInteraction000060	Genetic	<i>let-60</i>	<i>gene</i>	Interactor 1 → 2
WBInteraction000080	Genetic	<i>lin-12</i>	<i>let-60</i>	Interactor 1 → 2
WBInteraction000090	Genetic	<i>let-60</i>	<i>lin-1</i>	Interactor 1 → 2
WBInteraction000070	Genetic	<i>let-60</i>	<i>let-23</i>	Interactor 1 → 2
WBInteraction000071	Genetic	<i>let-60</i>	<i>lin-10</i>	Interactor 1 → 2
WBInteraction000070	Genetic	<i>let-60</i>	<i>gene</i>	Interactor 1 → 2
WBInteraction000077	Genetic	<i>let-60</i>	<i>let-33</i>	Interactor 1 → 2
WBInteraction000113	Genetic	<i>let-60</i>	<i>let-21</i>	Interactor 1 → 2

http://www.ensembl.org

Names in Ensembl

- **ENSG###** Ensembl Gene ID
- **ENST###** Ensembl Transcript ID
- **ENSP###** Ensembl Peptide ID
- **ENSE###** Ensembl Exon ID

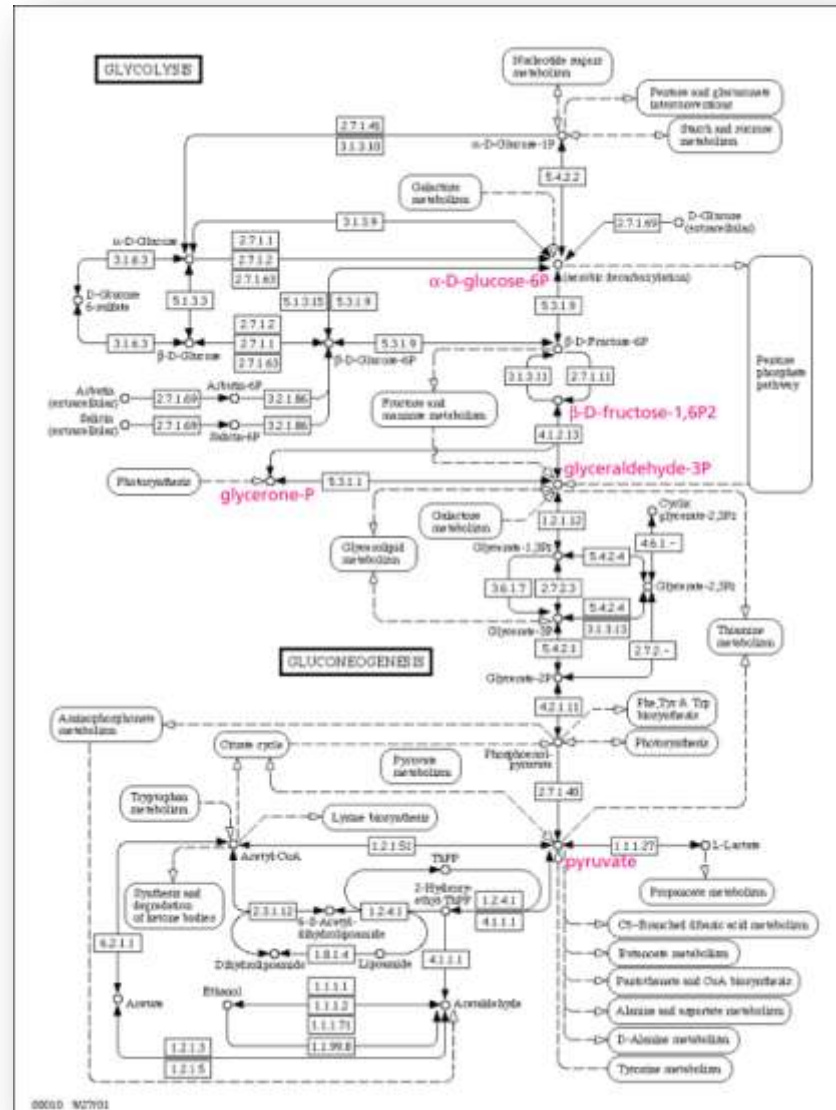
• For other species than human a suffix is added:
MUS (*Mus musculus*) for mouse: **ENSMUSG###**
DAR (*Danio rerio*) for zebrafish: **ENSDDARG###**, etc.

Name	Transcript ID	Length (bp)	Protein ID	Length (aa)	Biotype	CCDS
INSRR-001	ENST00000288195	5101	ENSP00000357170	1297	Protein coding	CCDS1300

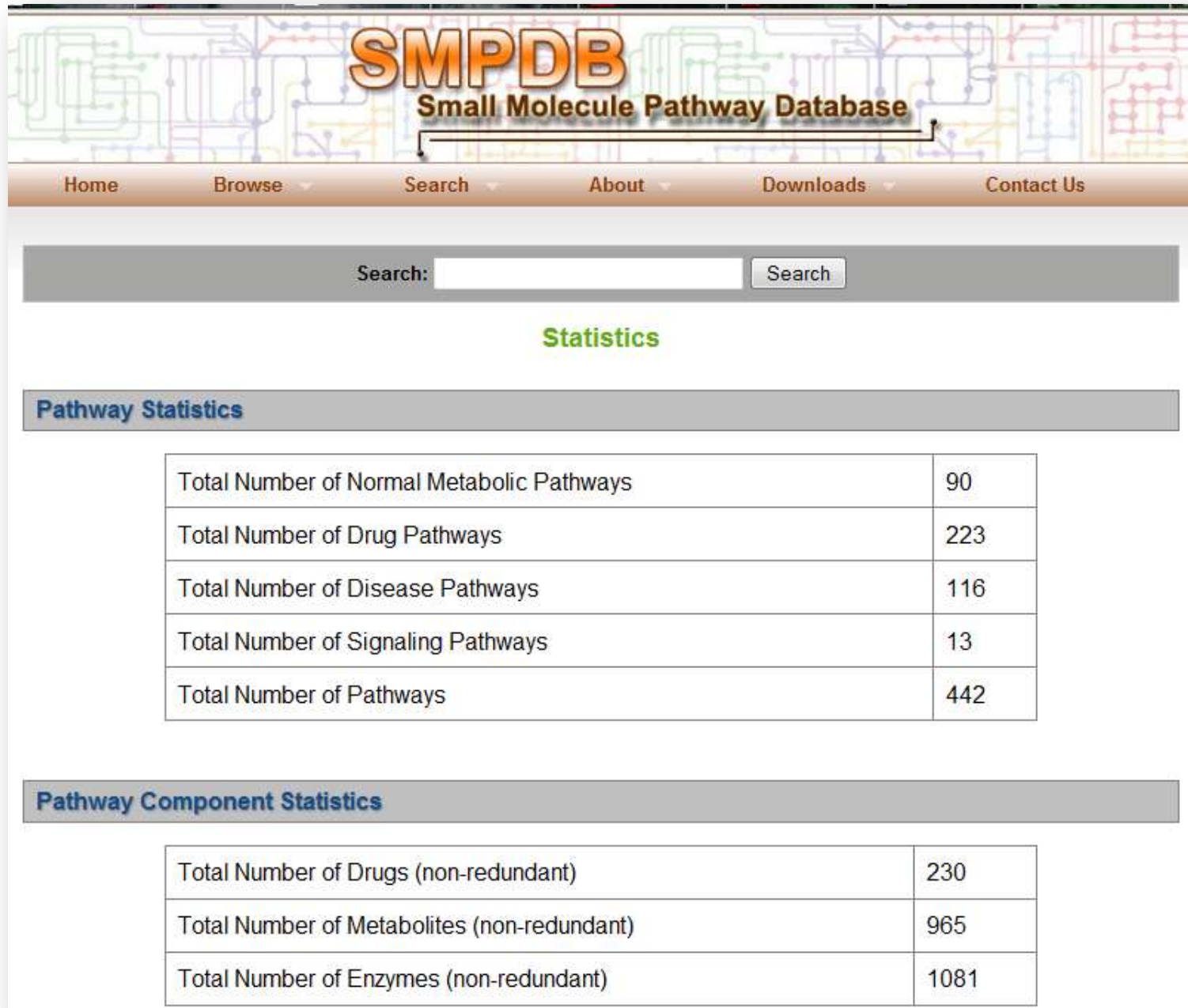
Transcript ID	UCSC Stable ID	CCDS	Human Protein Atlas	Wiki-Gene	UniProtKB/Swiss-Prot	RefSeq peptide	RefSeq DNA	Ensembl Gene	European Nucleotide	GO	GOSlim GOA	HGNC (curated)	IPi
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Metabolikus útvonal-adatbázisok

KEGG metabolikus útvonal-térkép



<http://smpdb.ca>



The image shows the homepage of the SMPDB (Small Molecule Pathway Database). The header features the logo 'SMPDB' in large orange letters, with 'Small Molecule Pathway Database' written below it. A navigation bar contains links for Home, Browse, Search, About, Downloads, and Contact Us. Below the navigation bar is a search bar with a 'Search' button. The main content area is titled 'Statistics' in green. Underneath, there is a section for 'Pathway Statistics' with a table listing the number of pathways in various categories. Below that is a section for 'Pathway Component Statistics' with a table listing the number of drugs, metabolites, and enzymes.

SMPDB Small Molecule Pathway Database

Home Browse Search About Downloads Contact Us

Search: Search

Statistics

Pathway Statistics

Total Number of Normal Metabolic Pathways	90
Total Number of Drug Pathways	223
Total Number of Disease Pathways	116
Total Number of Signaling Pathways	13
Total Number of Pathways	442

Pathway Component Statistics

Total Number of Drugs (non-redundant)	230
Total Number of Metabolites (non-redundant)	965
Total Number of Enzymes (non-redundant)	1081

Human Metabolome Database Version 2.5

Search: [\[Advanced\]](#)

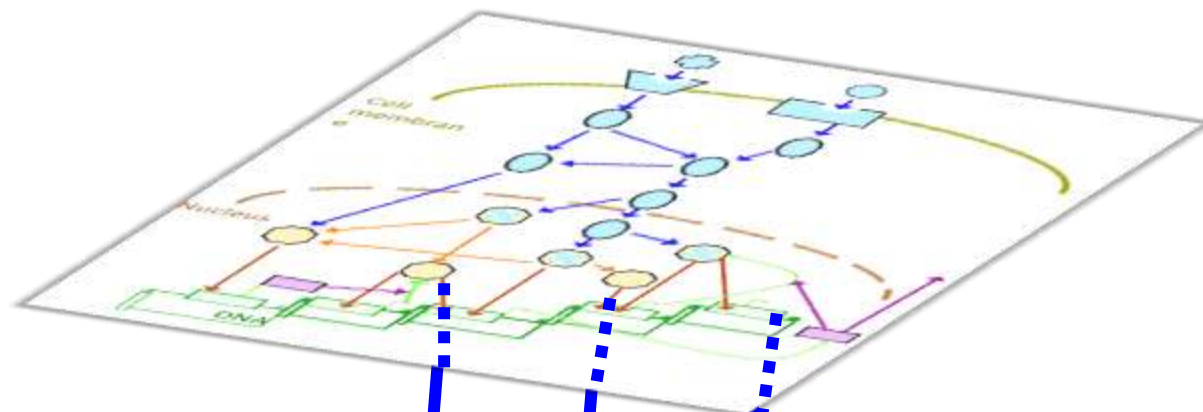
Statistics

General Statistics

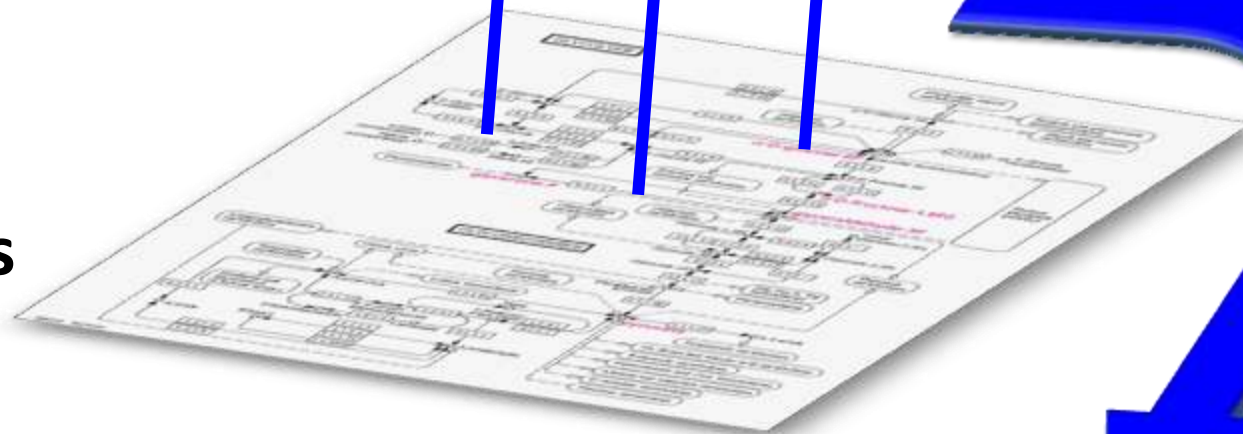
Description	Value
HMDB Compounds	8521
Compounds in the HML	1029
Synthesized Compounds	57
HMDB compounds with MS spectra	840
HMDB compounds with CNMR assigned spectra (2DHSQC only)	908
HMDB Compounds with HNMR assigned spectra	916
HMDB Compounds with a predicted HNMR spectrum	2989
HMDB Compounds with a predicted CNMR spectrum	2984
HMDB Identified Compounds in Urine	784
HMDB Identified Compounds in Blood	4229
HMDB Identified Compounds in CSF	1005
HMDB Identified Compounds in Other Biofluids	315
HMP Identified Compounds in Urine	232
HMP Identified Compounds in Blood	182
HMP Identified Compounds in CSF	84
Number of Associated Enzymes	7359
Number of Unique Synonyms	71782

Szintézis

**Jelátviteli és
regulációs
hálózat**



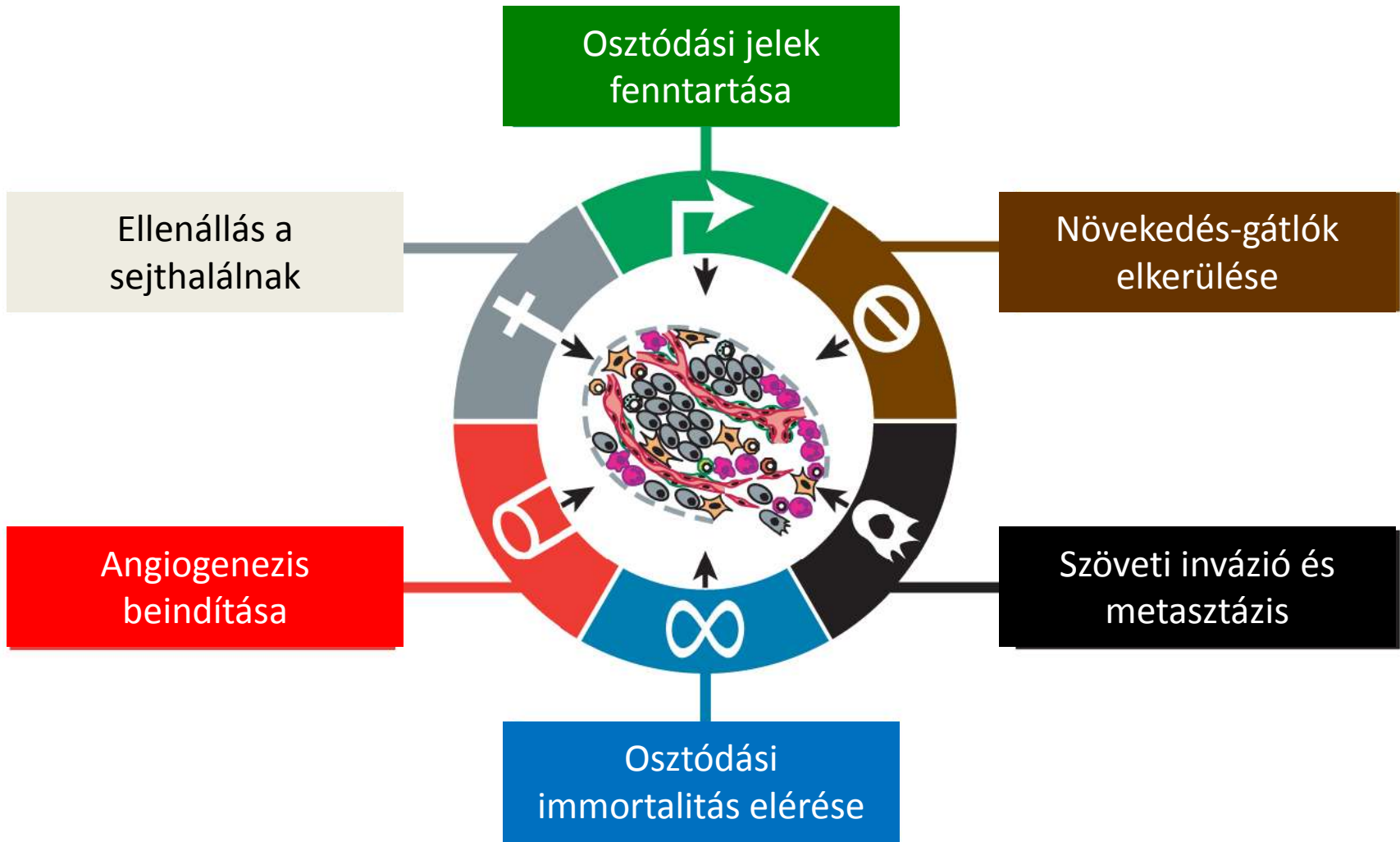
**Metabolikus
hálózat**



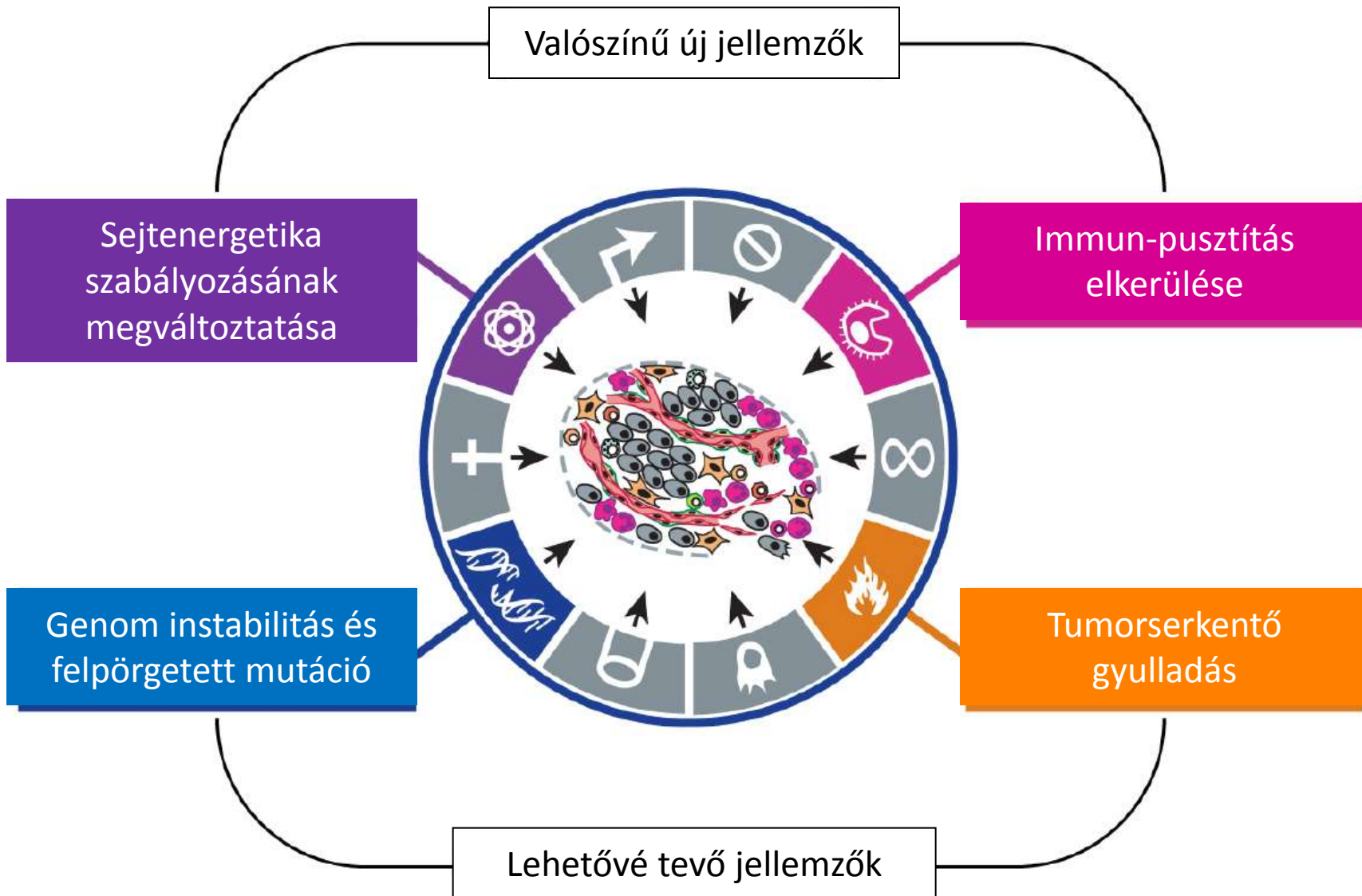
**Géninterakciós és
fehérjehálózat**



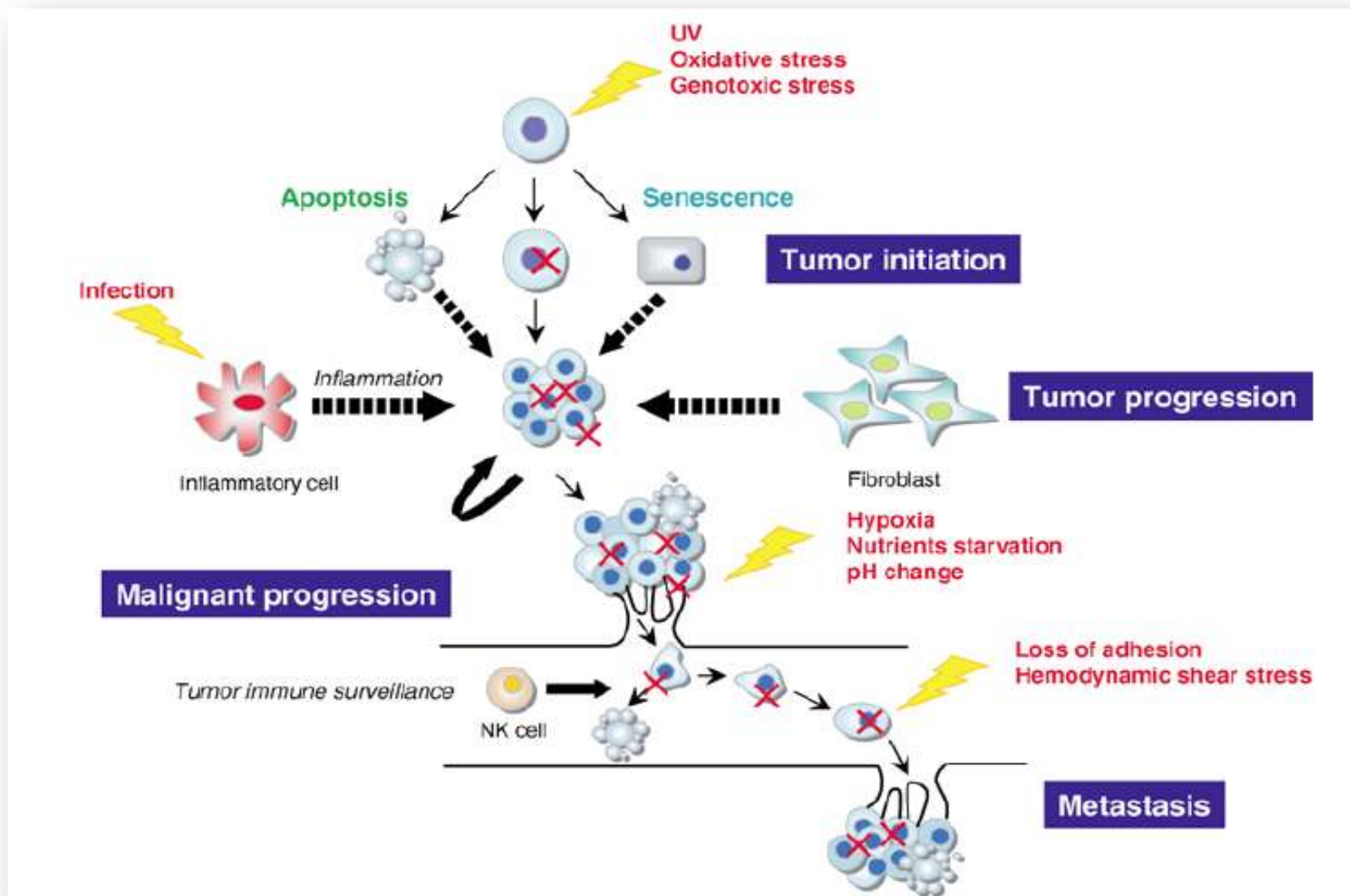
A rákos sejtek legfontosabb tulajdonságai 2000-ben



A rákos sejtek legfontosabb tulajdonságai 2011-ben



A rák és a stressz



Murakami et al., Cancer Sci 2007, 98:10.

Stress induced mutation

- Mismatch repair ↓
- Double-strand break repair (DSBR) – romló hatékonyság



Terápiák a rák ellen 2011-ben

