

2016

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# ANDSystem

ANDVisio user's guide

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# Information explosion in biology

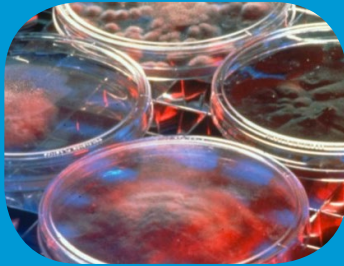
GENOMICS



PROTEOMICS



METABOLOMICS



OVER 23 MILLION OF BIOLOGICAL PUBLICATIONS, THOUSANDS OF BIOLOGICAL DATABASES



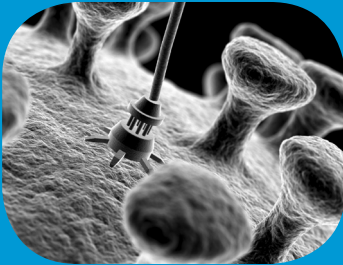
OVER 10 MILLION OF PATENTS



PHARMACOLOGY



BIOTECHNOLOGY



NANOTECHNOLOGY



AGROBIOLOGY

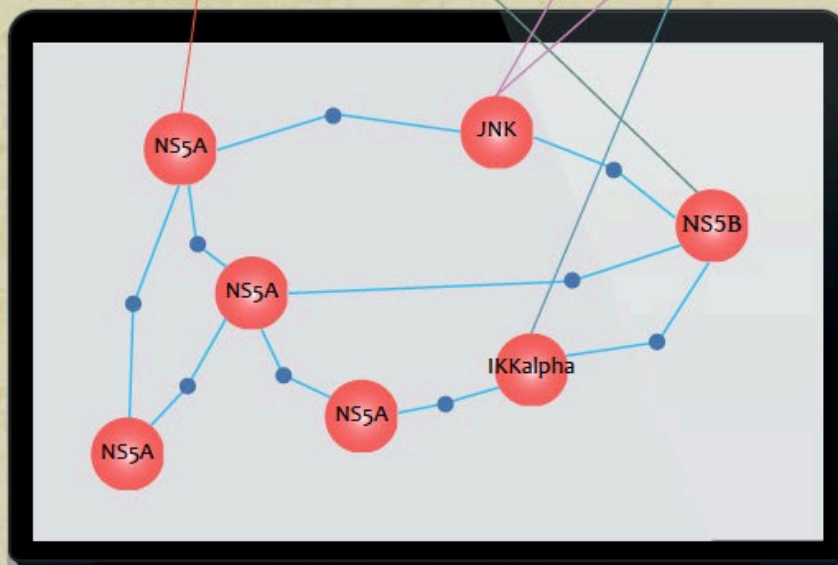
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*Illustration of the automated reconstruction process of the associative network describing HCV life cycle with text-mining module of ANDSystem*

Hepatitis C virus (HCV) NS5B protein is a membrane-associated phosphoprotein that possesses an RNA-dependent RNA polymerase activity. We recently reported that NS5A protein interacts with TRAF2 and modulates tumor necrosis factor alpha (TNF-alpha)-induced NF-kappaB and Jun N-terminal protein kinase (JNK). Since NS5A and NS5B are the essential components of the HCV replication complex, we examined whether NS5B could modulate TNF-alpha-induced NF-kappaB and JNK activation. In this study, we have demonstrated that TNF-alpha-induced NF-kappaB activation is inhibited by NS5B protein in HEK293 and hepatic cells. Furthermore, NS5B protein inhibited both TRAF2- and IKK-induced NF-kappaB activation. Using coimmunoprecipitation assays, we show that NS5B interacts with IKKalpha. Most importantly, NS5B protein in HCV subgenomic replicon cells interacted with endogenous IKKalpha, and then TNF-alpha-mediated IKKalpha kinase activation was significantly decreased by NS5B. Using in vitro kinase assay, we have further found that NS5B protein synergistically activated TNF-alpha-mediated JNK activity in HEK293 and hepatic cells. These data suggest that NS5B protein modulates TNF-alpha signaling pathways and may contribute to HCV pathogenesis.

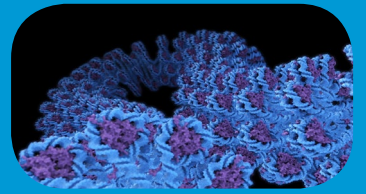


● proteins

- activity upregulation
- activity downregulation
- complex formation

# Statistics of dictionaries stored in the ANDCell database

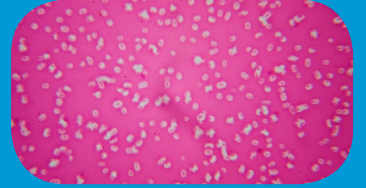
Proteins / 566.249



Genes / 15.480.756



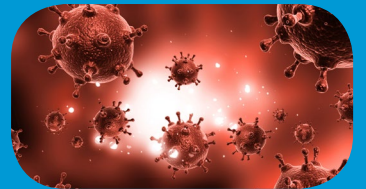
Diseases / 15.500



Metabolites / 46.226



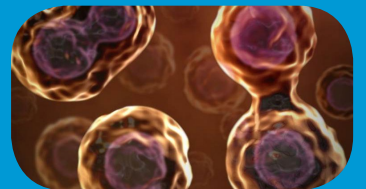
Organisms / 21.981



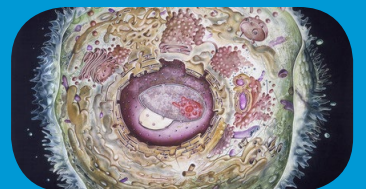
microRNAs / 28.645



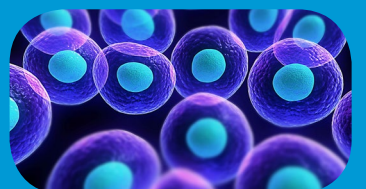
Processes / 26.645



Cell components / 3.680



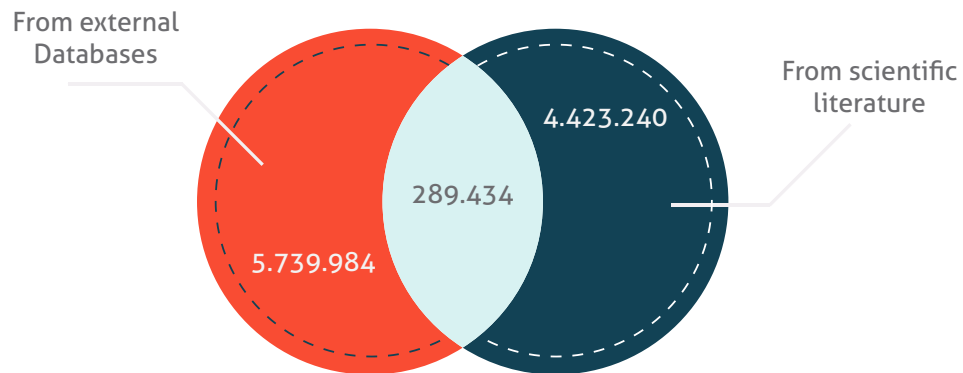
Cells and Tissues / 2.507



# General statistics on interactions

statistics on molecular-genetic interactions from ANDCell database of ANDSystem

Association	3.755.191	Activity downregulation	16.030
Involvement	4.504.760	Expression upregulation	14.706
Interaction	588.260	Activity upregulation	14.085
Expression	442.973	Expression downregulation	11.651
Catalyze	361.953	Degradation downregulation	4.805
Regulation	99.392	Activity regulation	4.805
Downregulation	71.069	Degradation upregulation	3.459
Upregulation	62.633	Coexpression	2.265
Transport regulation	58.226	Cleavage	905
Treatment	56.207	Degradation regulation	385
Expression regulation	48.234	Catalyze modification	62
Conversion	38.897		
<b>Total</b>		<b>10.161.038</b>	



# ANDVisio configuration

Step 1. Select Options and press Settings

The screenshot shows the ANDVisio application window with the 'Options' dialog box open. The 'Options' dialog has three tabs: 'Database connection', 'Colors', and 'Common'. The 'Database connection' tab is active, showing 'MySQL settings' with fields for Host, Port (3306), Username, Password, and Database name. Below this, the 'Use webservice' checkbox is checked, and the 'Webservice settings' section contains a 'Webservice address' field with the URL 'http://www-bionet.sccc.ru/andcell/services/ANDService', and fields for Username and Password. The 'Use proxy' checkbox is unchecked. The 'Proxy settings' section has fields for Host, Port (3128), Username, and Password. At the bottom of the dialog are 'Save' and 'Cancel' buttons. In the background, the main application window shows a search bar, a toolbar, and a status bar with the text 'Conected' and the same URL as the webservice address.

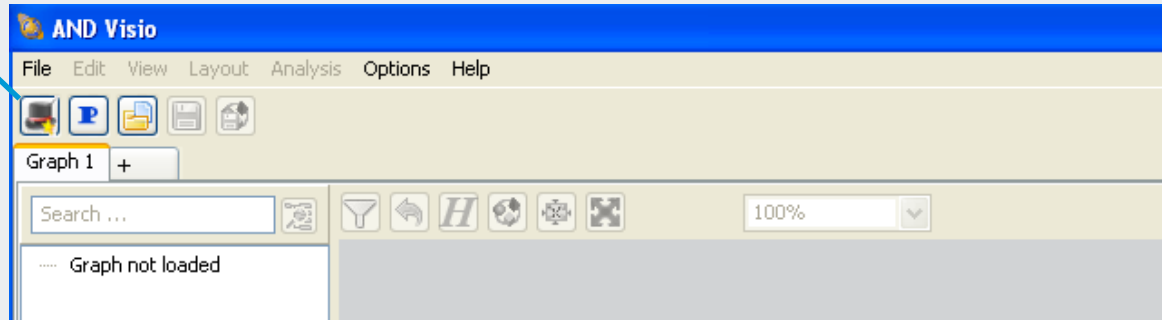
Step 2. Type your  
Username and Password  
in the  
Webservice settings

Step 3. Press Save button



# ANDVisio Network reconstruction

Press hat icon to start a  
Query Wizard



1. Type name of object

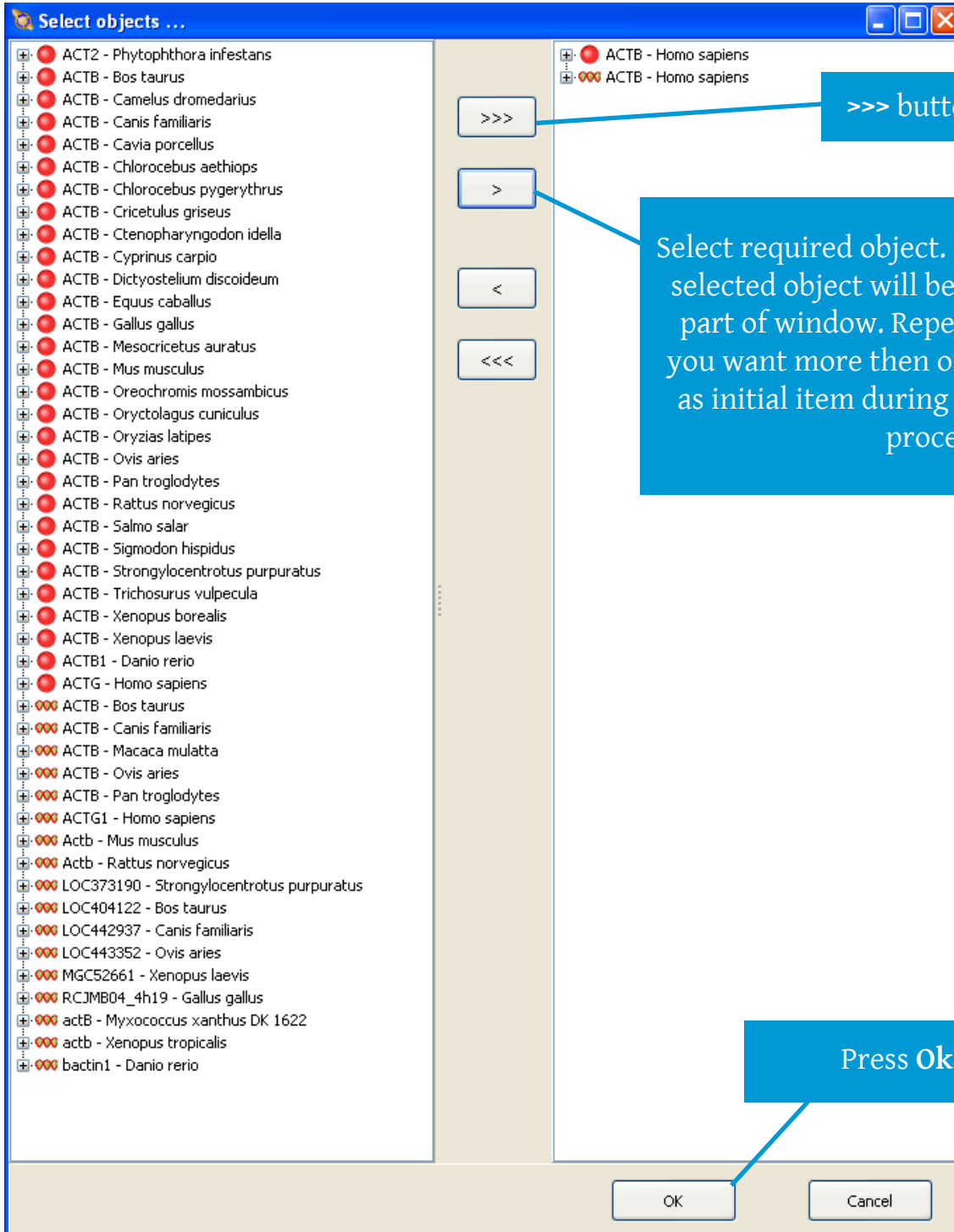
2. Here an object type can be specified

3. This field allows to specify a level of the reconstructed network.  
level 0: no neighbors, only the initial object  
level 1: level 0 plus neighbors directly connected with initial object  
level 2: level 1 plus all neighbors directly connected with any objects from level 1

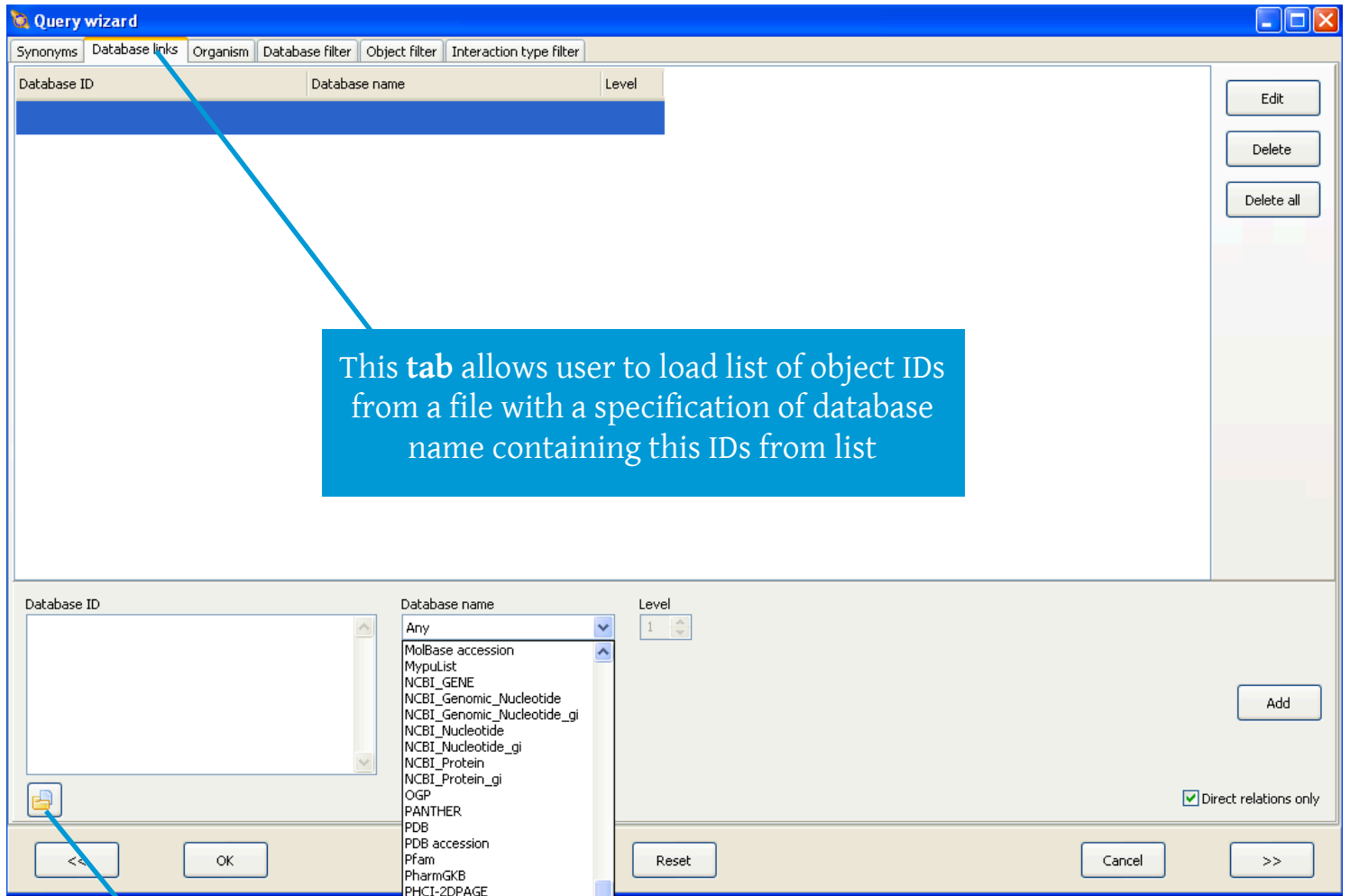
4. Check **Direct relations only** if only the reconstruction of level 1 network without interactions between neighbors is required

5. Press **Add** button to be proceeded

# ANDVisio Network reconstruction



# ANDVisio Network reconstruction



IPI00020091  
IPI00003919  
IPI00883772  
IPI00902579  
IPI00946417  
IPI00382926  
IPI00029260

# ANDVisio Network reconstruction

Query wizard

Synonyms Database links **Organism** Database filter Object filter Interaction type filter

Organism

Homo sapiens

Edit

Delete

Delete all

Organism

Add

<< OK Reset Cancel >>

This tab allows to add organisms

1. Type the name of organism

2. Press the **Add** button

Query wizard

Synonyms Database links Organism **Database filter** Object filter Interaction type filter

Databases

EC  miRNA

Ensembl  NCBI\_GENE

GO  PubMed

HAMAP  TRRD

IntAct  UniProt

InterPro  UniProt Knowledgebase keywords

mint

Check all

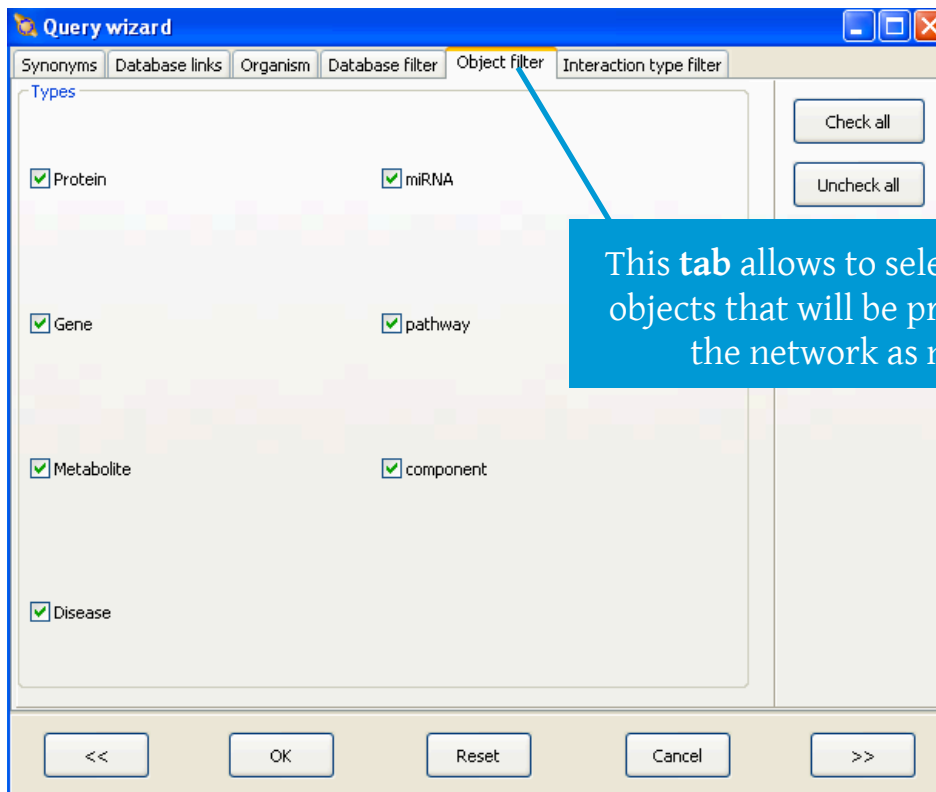
Uncheck all

<< OK Reset Cancel >>

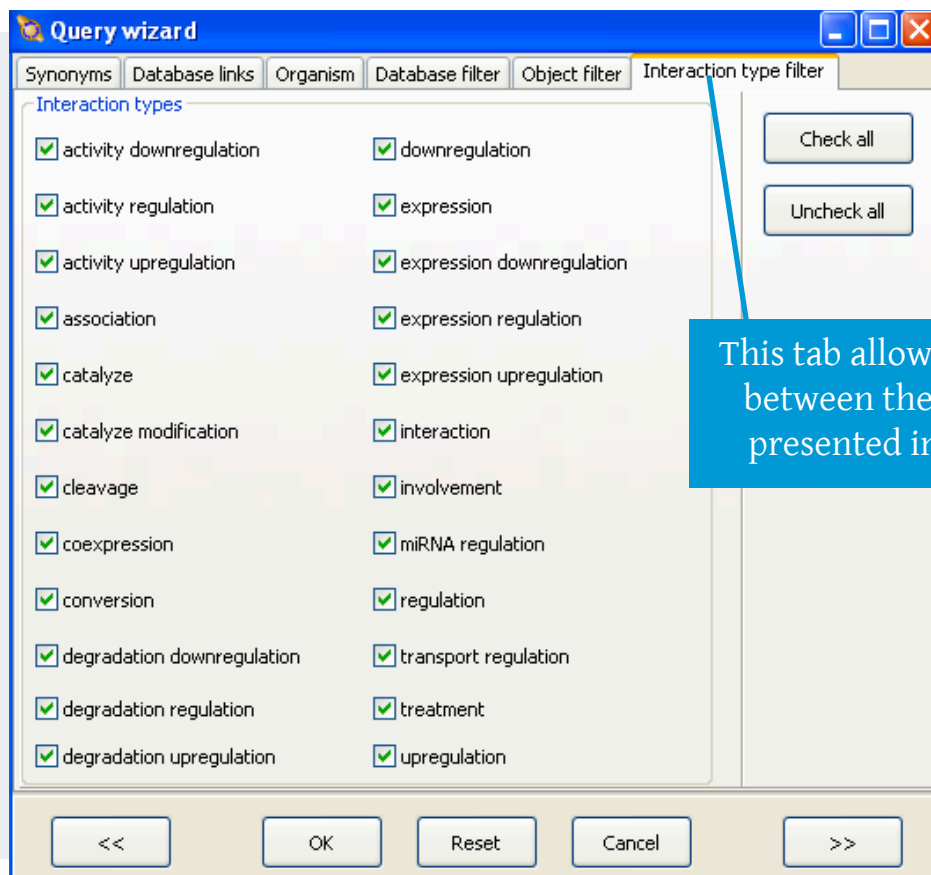
This tab allows to select databases from where interactions were extracted



# ANDVisio Network reconstruction



This **tab** allows to select types of objects that will be presented in the network as nodes

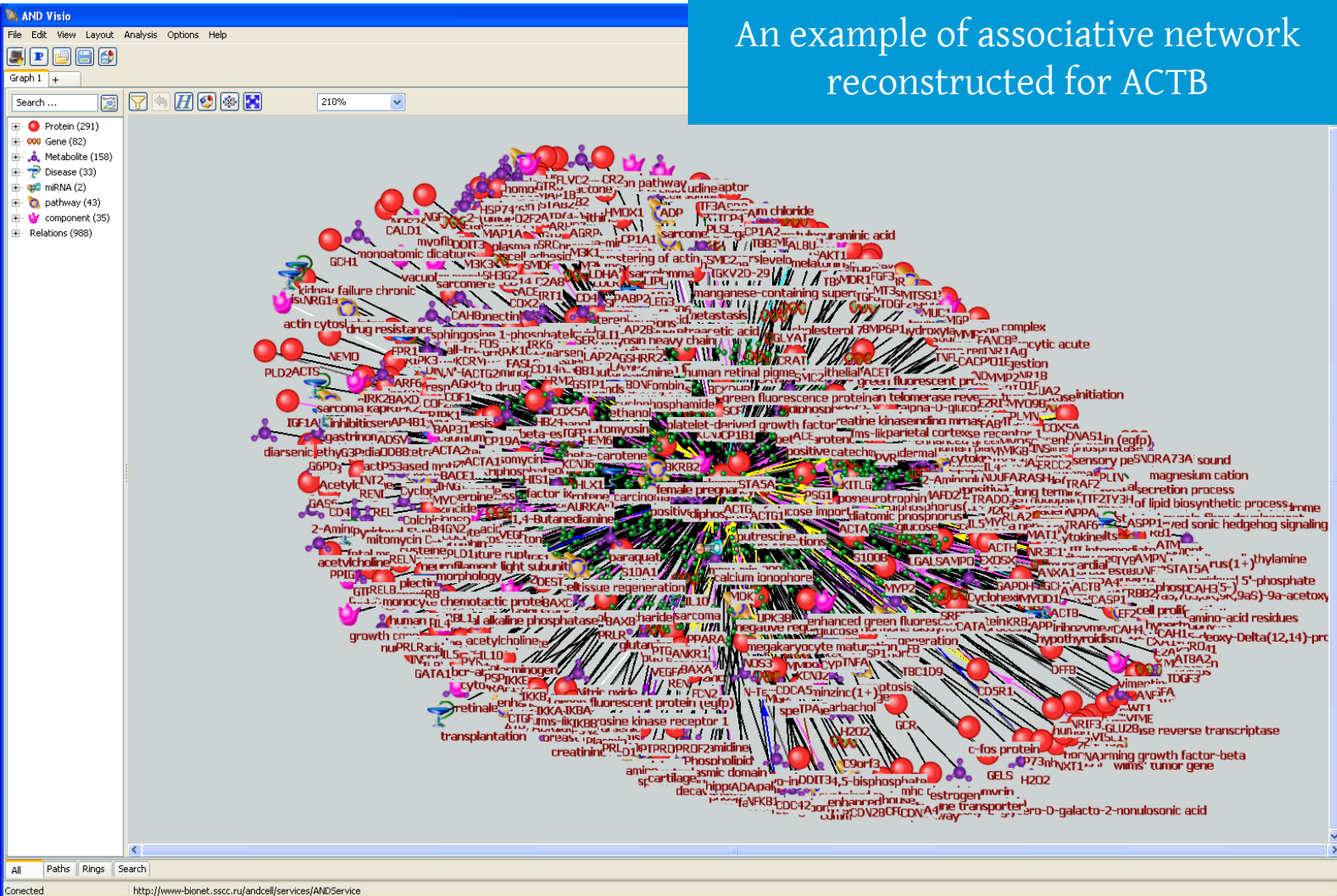


This **tab** allows to specify types of interactions between the objects, that will be presented in the network as edges, objects

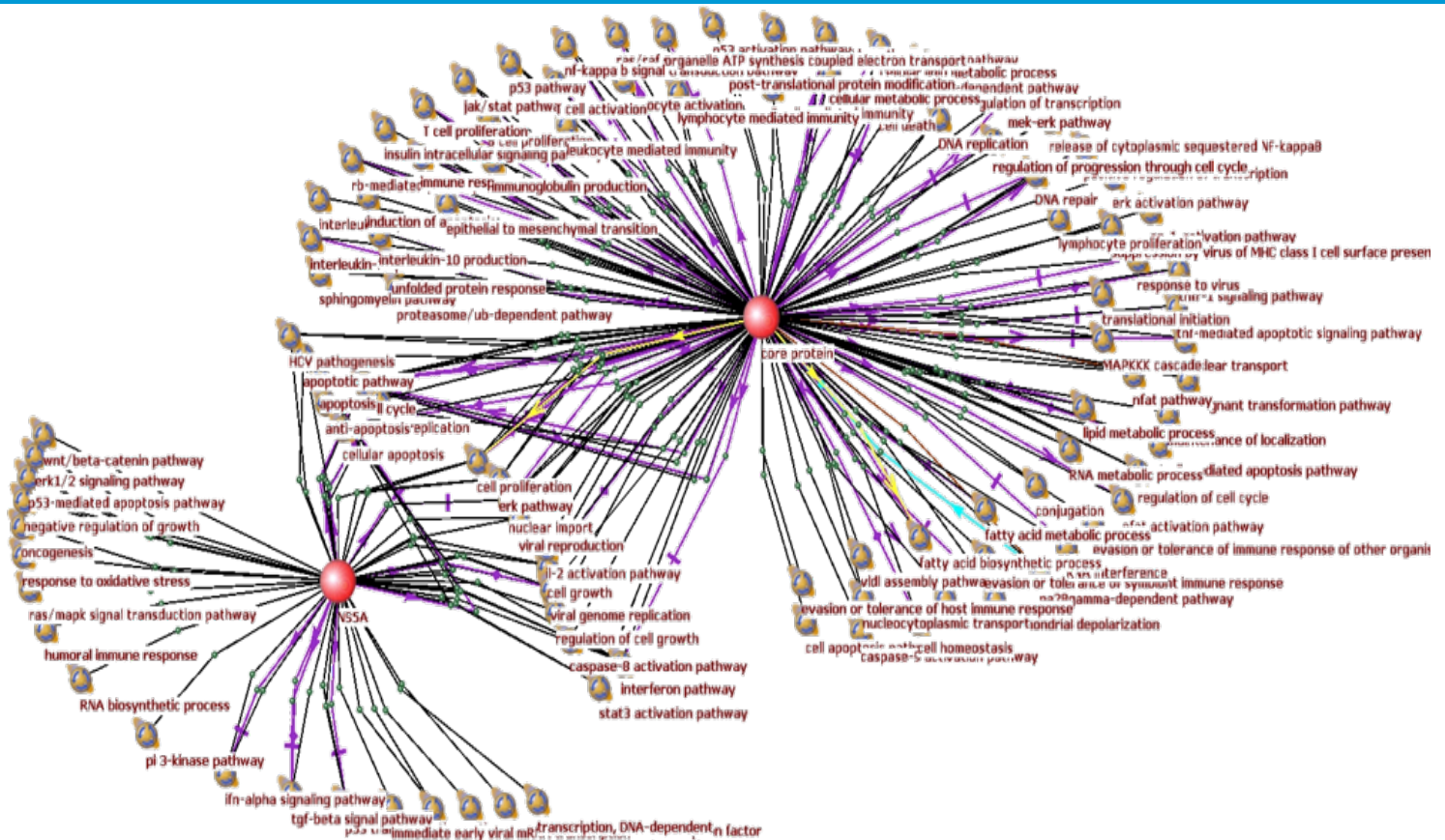
# ANDVisio

## Examples of reconstructed networks

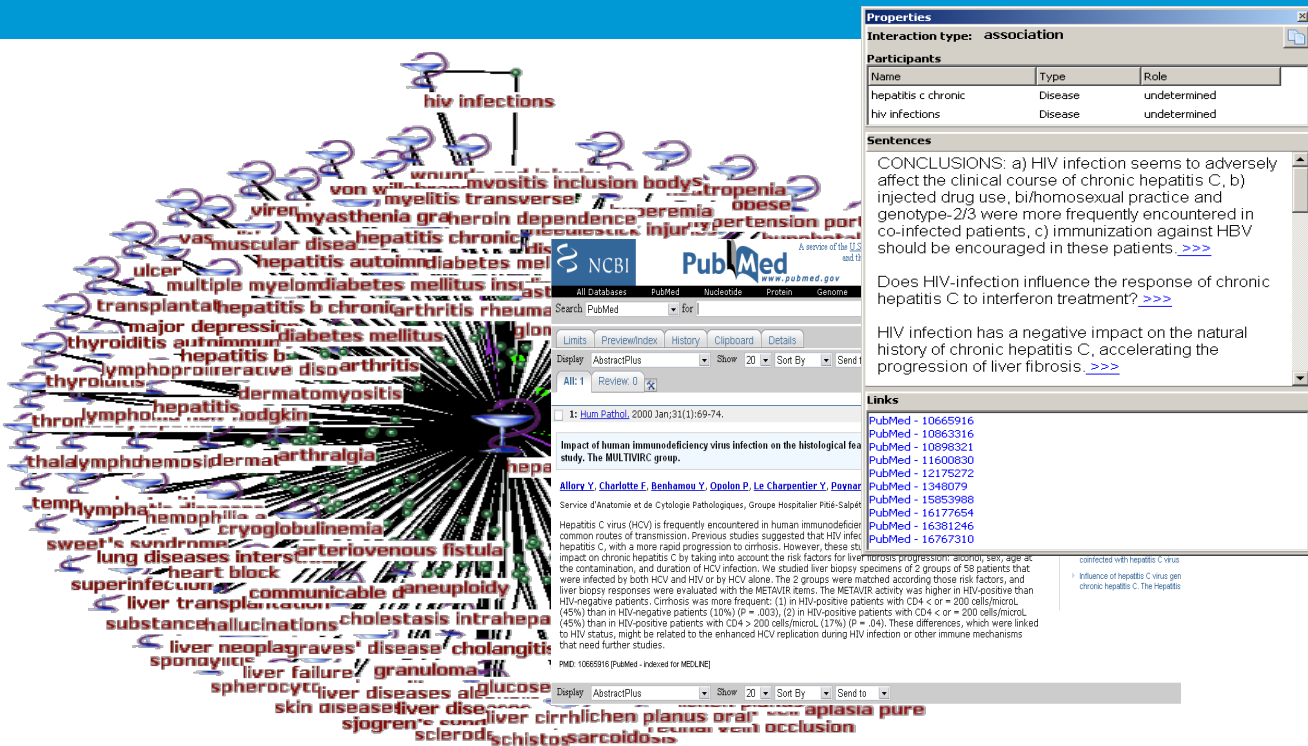
An example of associative network reconstructed for ACTB



# An example of the reconstruction of interactions between HCV proteins (NS5A and Core protein) and molecular-biological processes with the help of ANDVisio



# An example of the associative network of interactions of Hepatitis C virus with other diseases, obtained with the help of ANDVisio



**Properties**

Interaction type: association

**Participants**

Name	Type	Role
hepatitis c chronic	Disease	undetermined
hiv infections	Disease	undetermined

**Sentences**

CONCLUSIONS: a) HIV infection seems to adversely affect the clinical course of chronic hepatitis C, b) injected drug use, bi/homosexual practice and genotype-2/3 were more frequently encountered in co-infected patients, c) immunization against HBV should be encouraged in these patients. >>>

Does HIV-infection influence the response of chronic hepatitis C to interferon treatment? >>>

HIV infection has a negative impact on the natural history of chronic hepatitis C, accelerating the progression of liver fibrosis. >>>

**Links**

- PubMed - 10665916
- PubMed - 10863316
- PubMed - 10899321
- PubMed - 11600830
- PubMed - 12175272
- PubMed - 1348079
- PubMed - 15853988
- PubMed - 16177654
- PubMed - 16381246
- PubMed - 16767310



# ANDVisio

## Main window description

By right-clicking the node and selecting **Property** in the appeared menu a window with node's properties will appear

By right-clicking the edge and selecting **Property** in the appeared menu a window with edge's properties will be shown

Holding a **Shift** key on the keyboard allows to do a multiple selection of objects

The screenshot displays the ANDVisio main window with a complex network graph. On the left, a legend lists object types: Protein (291), Gene (82), Metabolite (158), Disease (33), miRNA (2), pathway (43), component (35), and Relations (988). The graph contains numerous nodes and edges, with labels such as CALD1, NDS2A, NGF, HSP74K6, and MTSS1. Three windows are open:

- Node Properties (MTSS1 - Homo sapiens):** Shows details for the MTSS1 node, including its organism (Homo sapiens), synonyms (FL344694, KIAA0429, metastasis suppressor 1, etc.), and links to external databases like EMBL and GO.
- Edge Properties (Interaction type: association):** Shows details for an association edge between ACTG and MTSS1. The table below lists the participants:
- Legend:** Lists various biological object types and their counts.

Name	Type	Role
ACTG	Protein	undetermined
MTSS1	Protein	undetermined



# ANDVisio Main window description

This buttons allows to save network in the different formats or as image

This button allows to load saved network

This button allows to undo last action

This dropdown list allows to change scale of the network, also scaling can be performed with scroll wheel of the mouse

This button allows to expand the network by adding relations between selected object and his neighbours

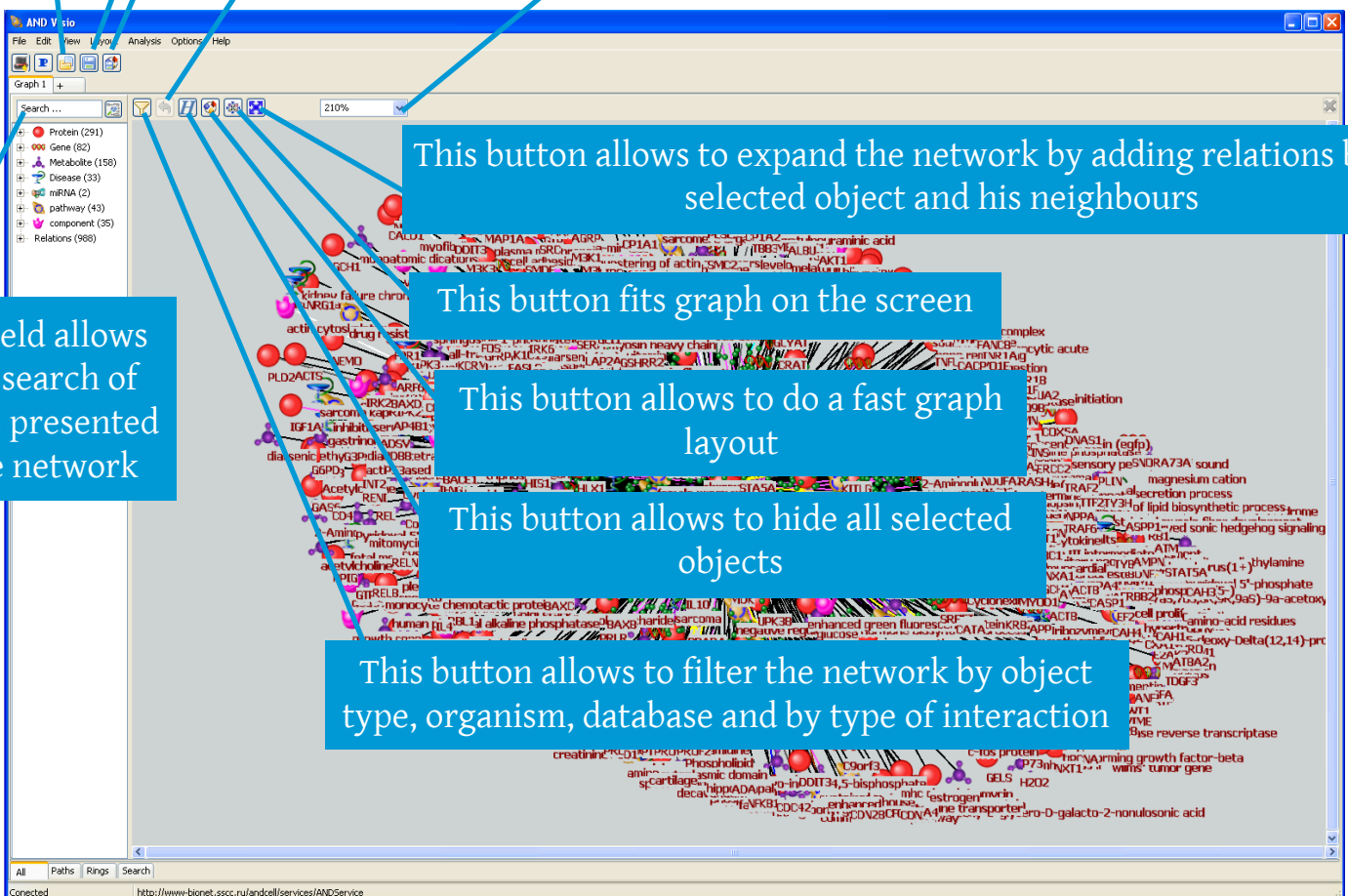
This button fits graph on the screen

This button allows to do a fast graph layout

This button allows to hide all selected objects

This button allows to filter the network by object type, organism, database and by type of interaction

This field allows to do search of objects presented in the network



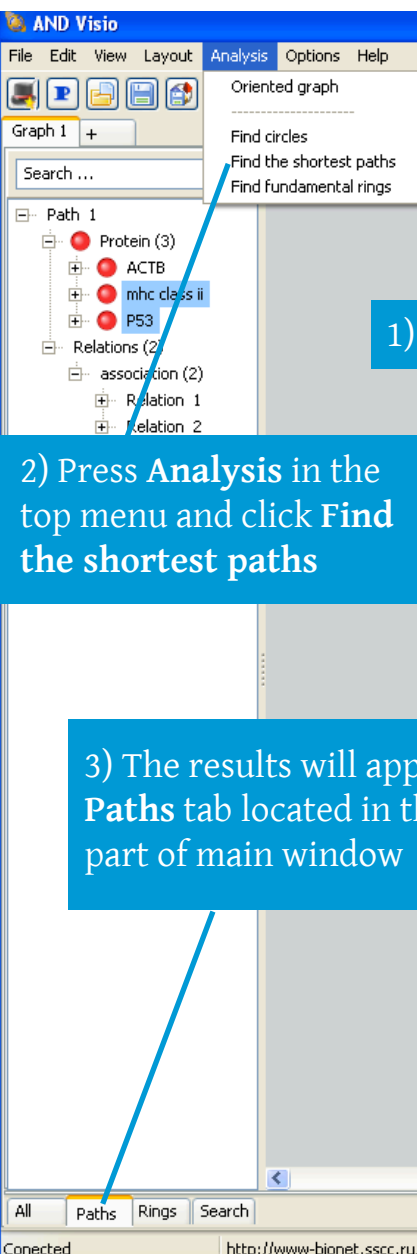


# ANDVisio

## Search of the shortest paths

ANDVisio provides a search of cycles, fundamental rings and the shortest paths between objects

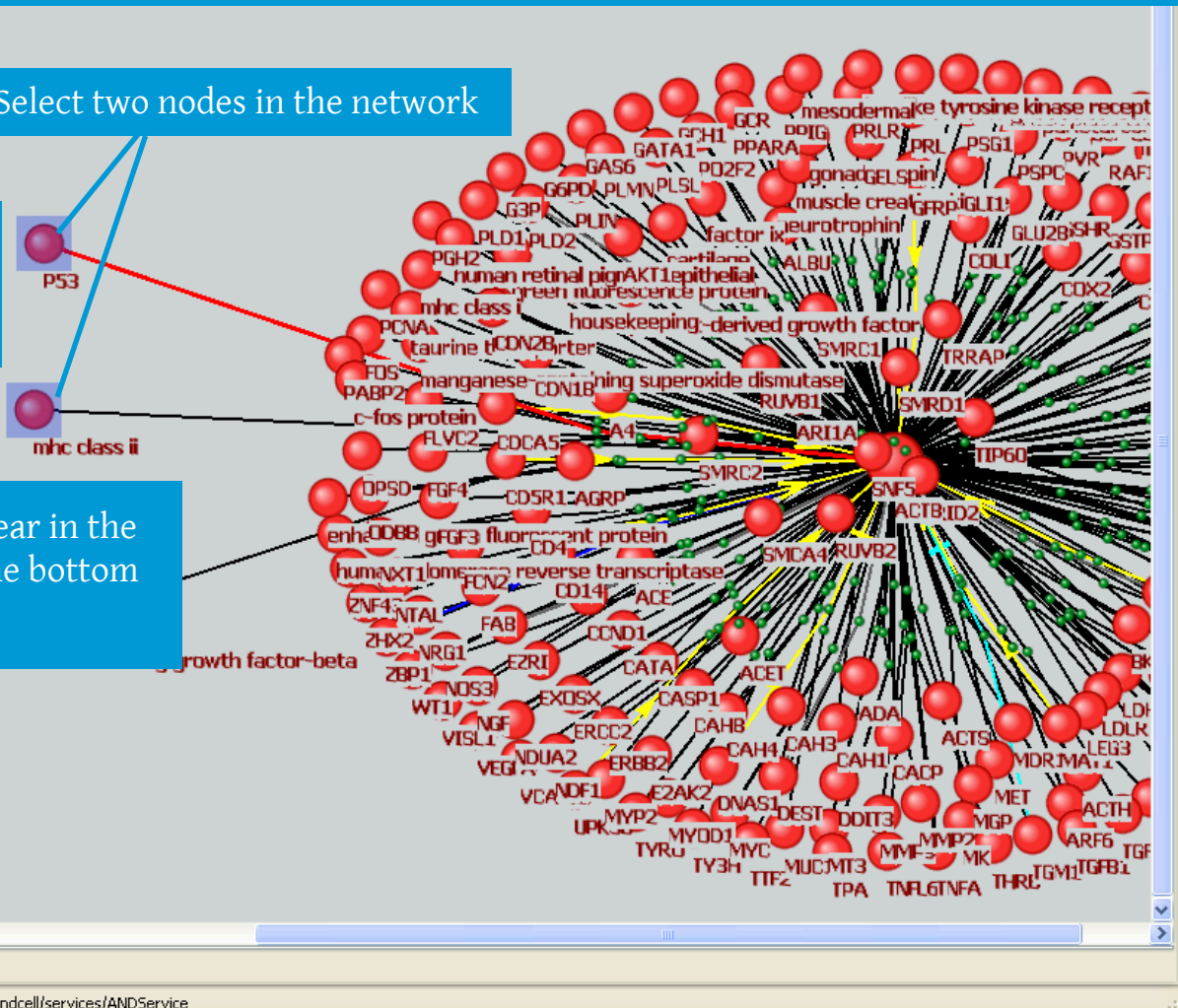
To find a shortest path between two objects:



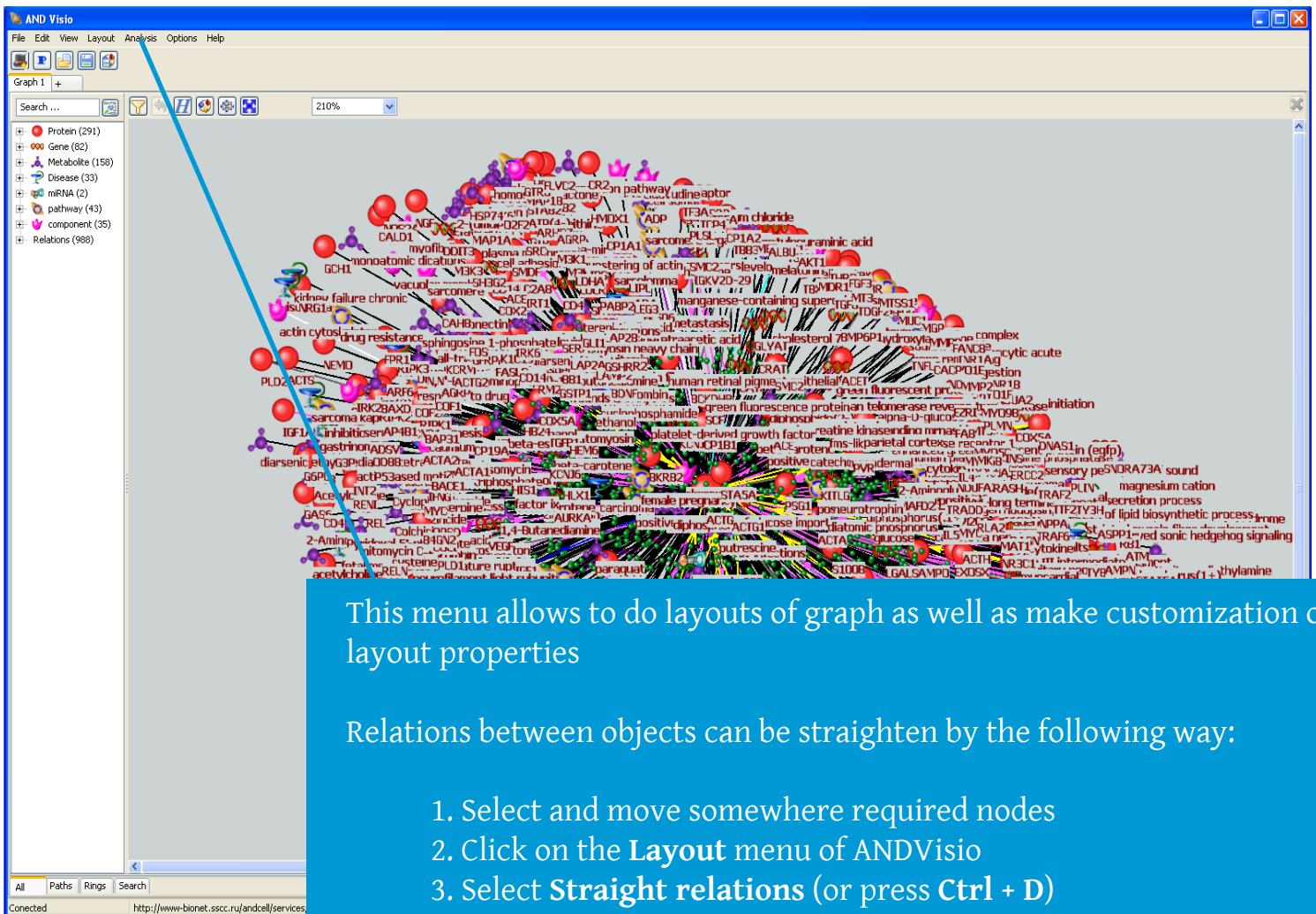
1) Select two nodes in the network

2) Press **Analysis** in the top menu and click **Find the shortest paths**

3) The results will appear in the **Paths** tab located in the bottom part of main window



# ANDVisio Graph Layout



AND Visio

File Edit View Layout Analysis Options Help

Graph 1 +

Search ... 210%

Protein (291)  
Gene (82)  
Metabolite (158)  
Disease (33)  
miRNA (2)  
pathway (43)  
component (35)  
Relations (988)

This menu allows to do layouts of graph as well as make customization of layout properties

Relations between objects can be straightened by the following way:

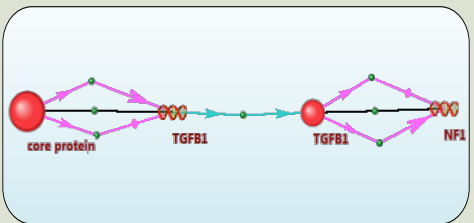
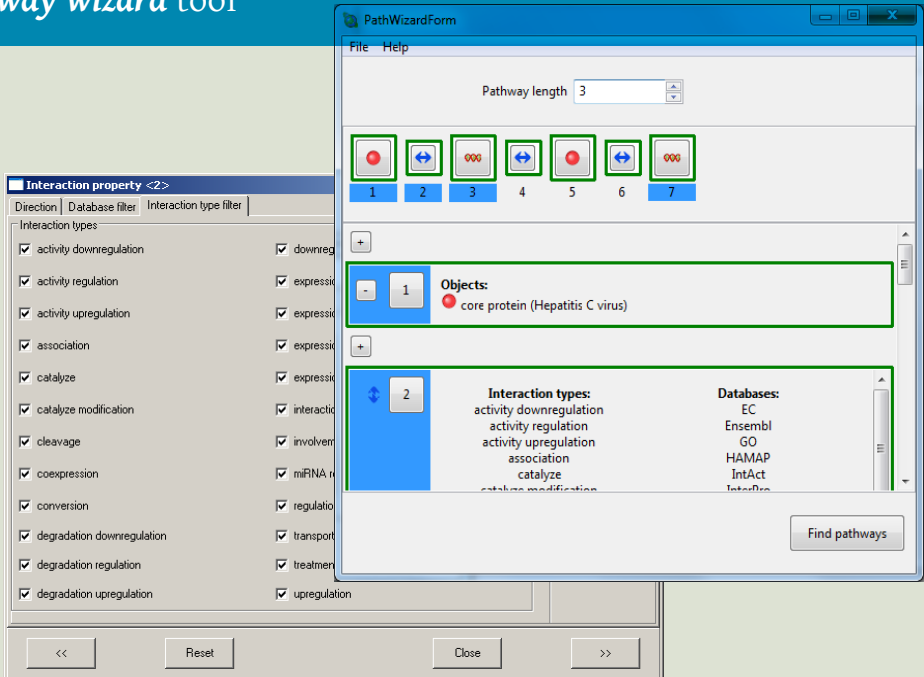
1. Select and move somewhere required nodes
2. Click on the **Layout** menu of ANDVisio
3. Select **Straight relations** (or press **Ctrl + D**)

As the result - the layout will be recalculated in accordance with straighten relations between selected objects.

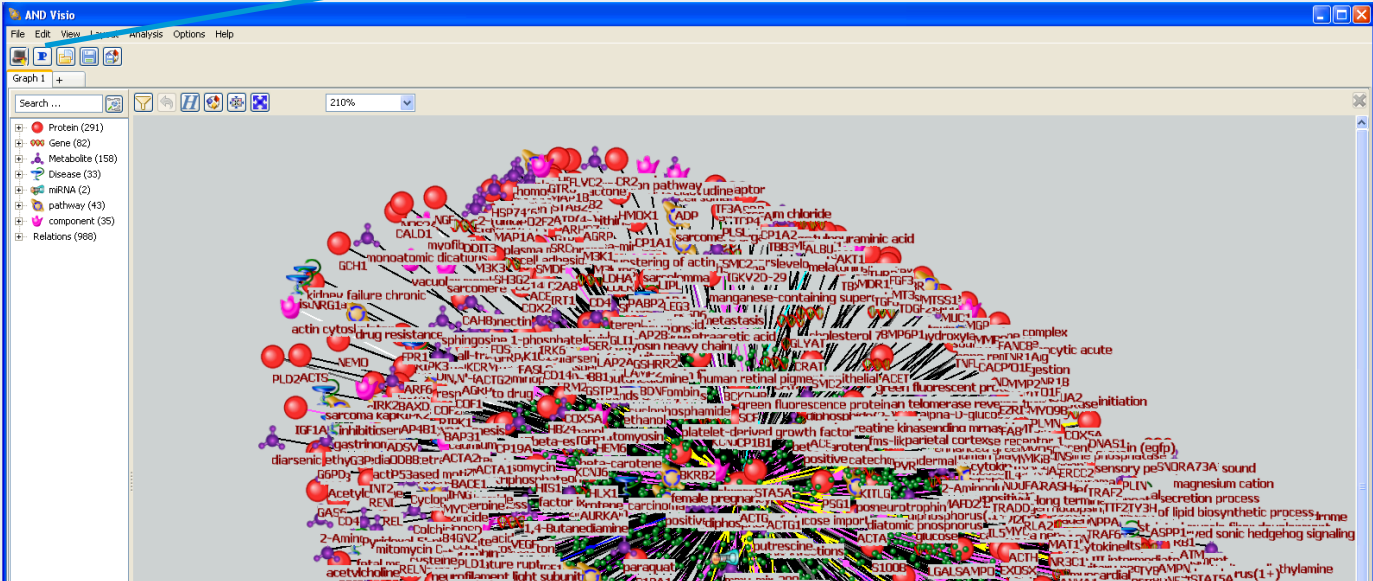


# ANDVisio Pathway wizard

ANDVisio allows to search pathways through ANDCell database even when some participants are unknown with the help of built-in *Pathway wizard* tool



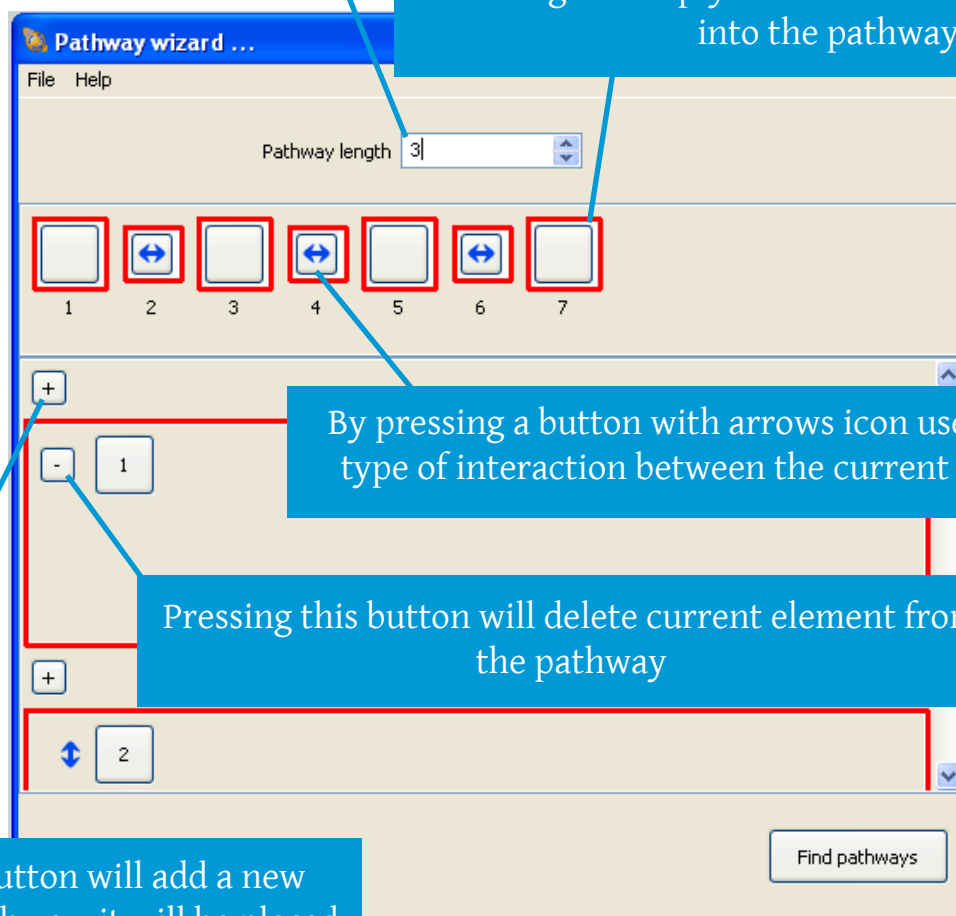
Press this button to start a *Pathway wizard*



# ANDVisio Pathway wizard

This field allows to specify length of pathway

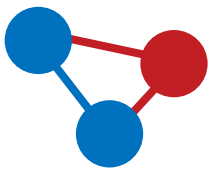
Pressing the empty button allows user to add object into the pathway



By pressing a button with arrows icon user can specify a type of interaction between the current pair of objects

Pressing this button will delete current element from the pathway

Pressing this button will add a new element to the pathway, it will be placed before the current object or interaction



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