

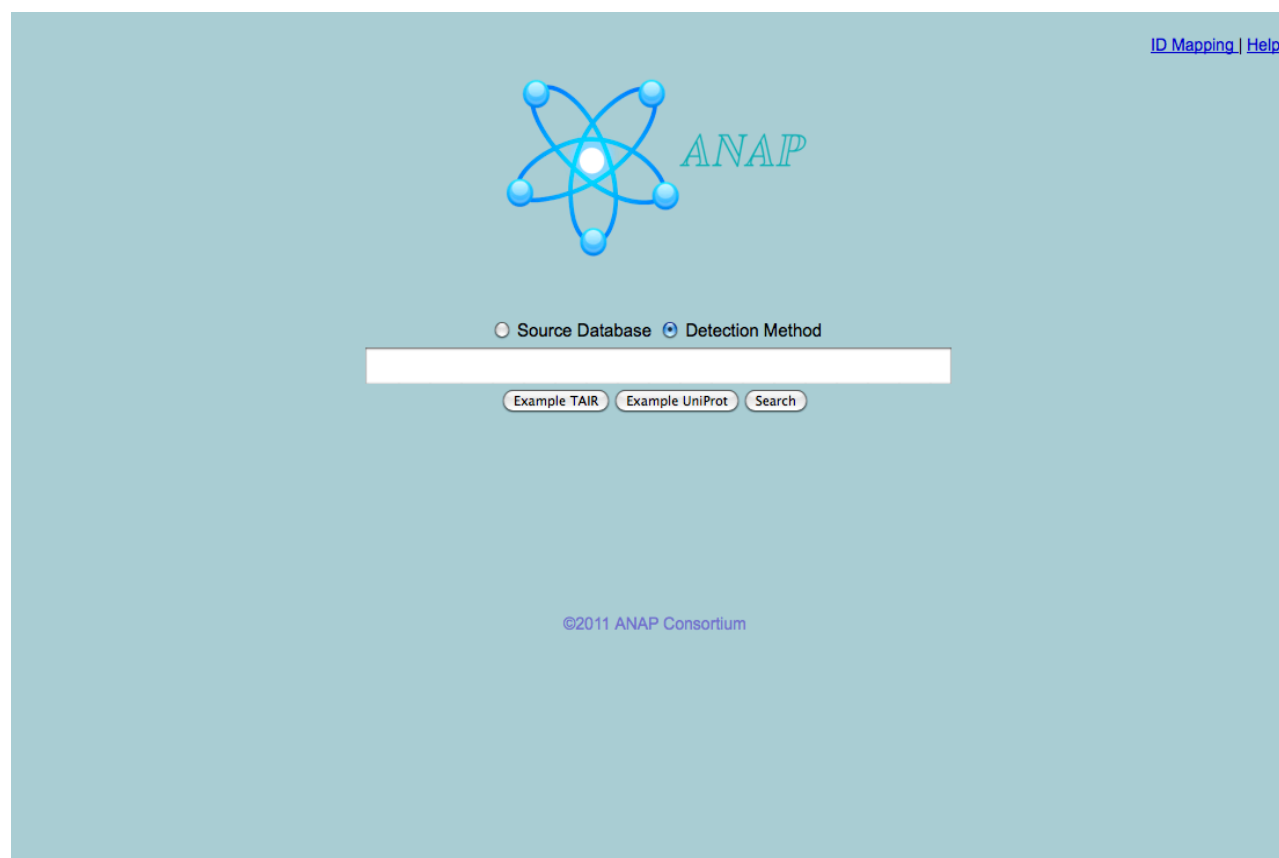
ANAP User Guide

The ANAP tool has many useful network biology functions that are demonstrated in this user guide.

1. The ANAP tool

http://gmdd.shgmo.org/Computational-Biology/ANAP/ANAP_V1.0/

The ANAP tool is very easy to use, and has an intuitive interface. When you open the front webpage, you are presented with a web form in which you load in your AGI codes or Uniprot identifiers, and then select the interaction type source database or detection method. The search button will then search the whole of the ANAP dataset for all the protein interactions from the integration, and the nearest neighbours. The Help link at the top of the ANAP input page links to videos that visually show you how to use the tool. The links between the proteins in the network can be presented in different ways by selecting source database or detection method. This does not affect the network that is generated, but gives information relating to the data that has been used for network construction.

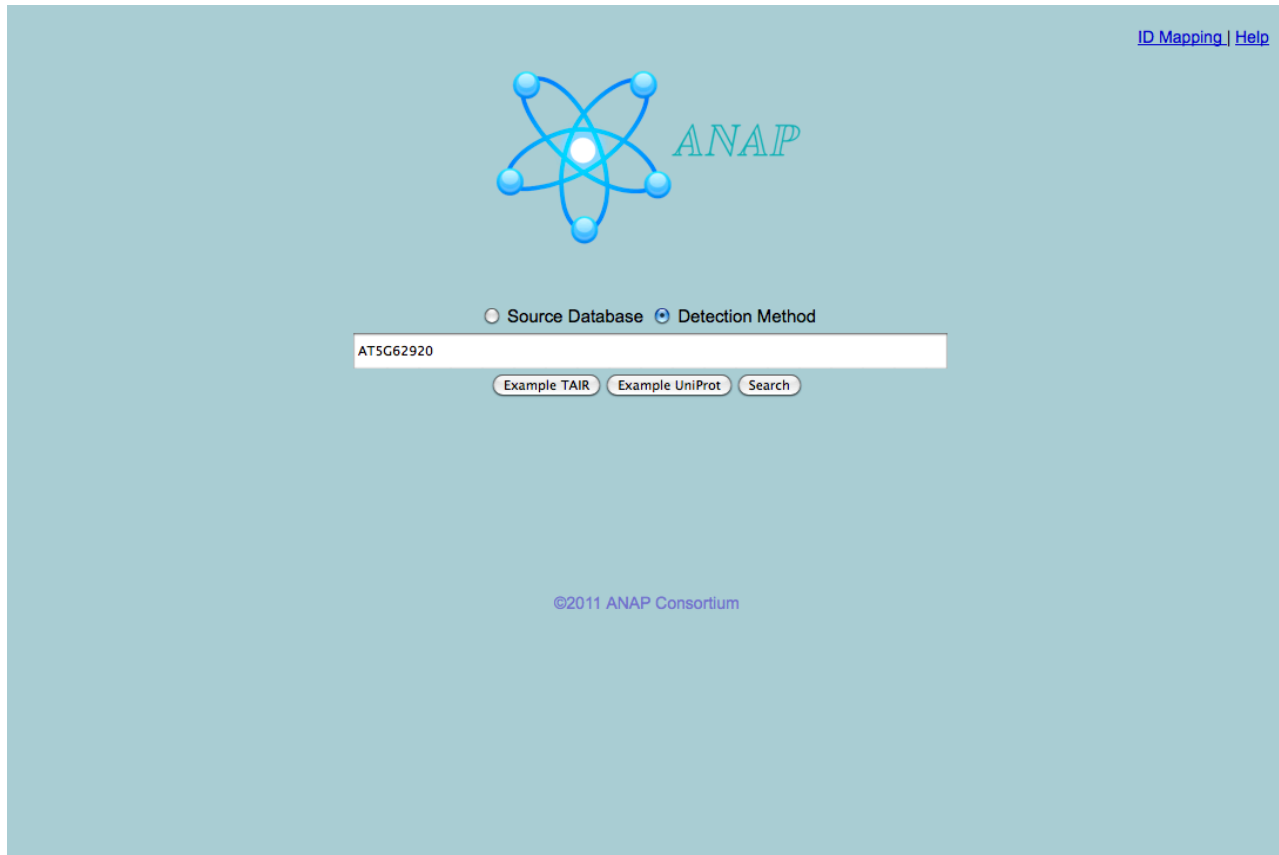


2. One identifier search

Try an initial search using one AGI identifier, this will show you how the tool works.

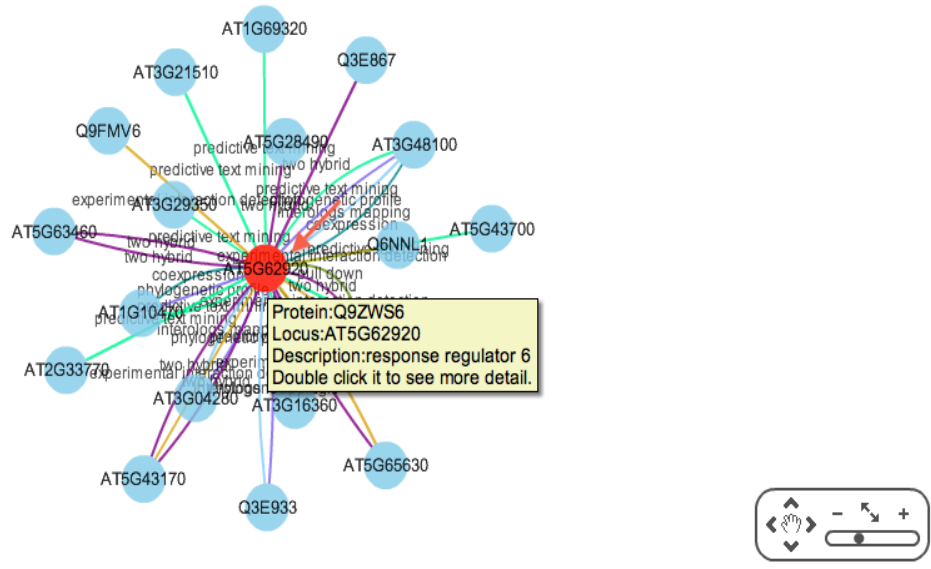
AT5G62920 - this is an ARR6 Response regulator.

Add this identifier in the box, and click search. You can also add Uniprot codes to the box, ANAP handles both type of identifier.



The screenshot displays the ANAP web interface. At the top right, there are links for [ID Mapping](#) and [Help](#). The central logo features a stylized atomic structure with the text "ANAP" to its right. Below the logo, there are two radio buttons: "Source Database" (unselected) and "Detection Method" (selected). A search input field contains the text "AT5G62920". Below the input field are three buttons: "Example TAIR", "Example UniProt", and "Search". At the bottom center, the copyright notice "©2011 ANAP Consortium" is visible.

The resulting network shows the query node highlighted in red, and all the interaction nodes with it in light blue. The multiple edges and colours represent the different interaction methods that prove these set of protein interactions occur. If you hover your mouse over a node, a box will pop up showing you the uniprot and AGI identifiers and a gene description.



Change the Colour

New ANAP Search Clear Search in Network Clear UP-Regulate Map Clear

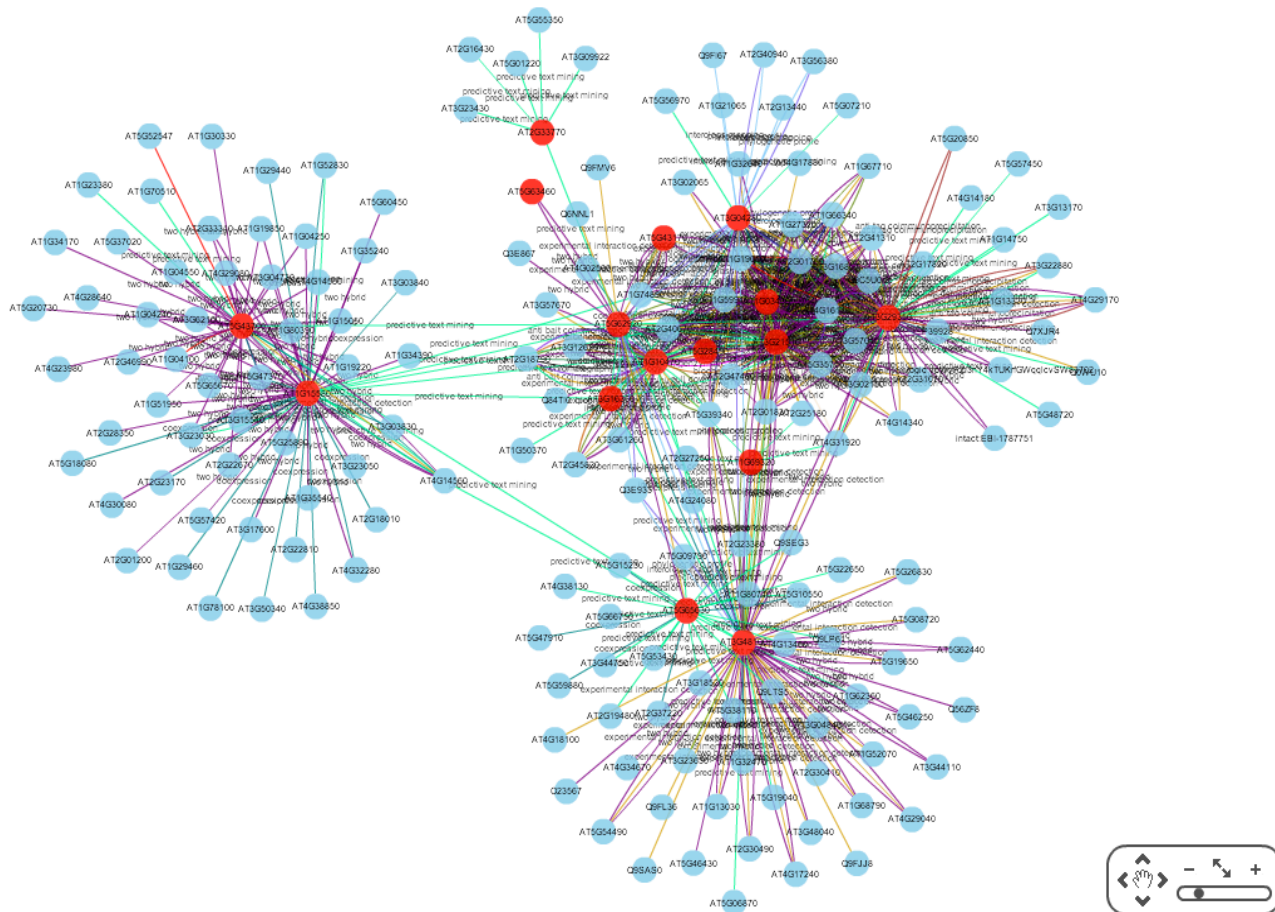
The network has 20 nodes and 44 edges!

Home Save Network to PNG PDF SVG SIF GRAPHML XGMML Evidence Source Database Interaction Detection Method Depth Search

ANAP has a set of functions which can be seen at the bottom of the output screen. You can save a network in PDF, PNG, SVG, SIF, GRAPHML and XGMML format. This tool is fully supported by Cytoscape, the widely used network visualisation and analysis tool. The GRAPHML can be imported into other network analysis tools.

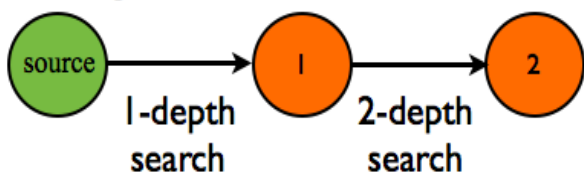
You can move the nodes around the page, you have to highlight the nodes you wish to move, and drag them by hovering over a node and dragging. Other functions include a list of the evidence, links to the source database and interaction detection method. There is a depth search function, which allows you to move out 1 nearest neighbour in terms of the protein interaction network.

The resulting network can be increased one nearest neighbour using the depth search function (see below).



Depth search is defined as the number of paths out from an original node. It can also be named as nearest neighbours, which means the nodes connected to the source node (see below).

paths out from the source node to the target nodes



3. Analysing a Cytokinin protein interaction network

To show an example network in ANAP, we are using a subset of cytokinin genes, and selecting up-regulated genes from the AtGenExpress microarray experiments as an example of how to analyse protein interaction data using ANAP.


This example gene list contains 24 genes from a Cytokinin signalling pathway (Dortay *et al.* 2006). The following table which is directly from the paper supplementary data, lists those genes and the protein interactions.

Interacting pair	Method	References
ETR1 – AHP1, AHP2, AHP3	Yeast two-hybrid	[1]
AHK1 – AHP2	Yeast two-hybrid	[1]
AHK4 – AHP1, AHP2, AHP3, AHP5	<i>E. coli</i> – LacZ	[2]; [3]
AHP1 – ETR1, ARR1, ARR2, ARR3, ARR4, ARR8, ARR9, ARR10	Yeast two-hybrid, phospho-relay	[4]; [1]; [5]; [6]; [7]; [8]
AHP2 – ETR1, AHK1, AHK4, ARR1, ARR2, ARR3, ARR4, ARR8, ARR9, ARR10, ARR11	Yeast two-hybrid, phospho-relay, quenching	[4]; [3]; [8]; [7]; [9]; [1]; [5]
AHP3 – ETR1, AHK4, ARR1, ARR2, ARR8, ARR9, ARR10	Yeast two-hybrid, quenching	[4]; [3]; [7]; [1]; [5]
AHP4 – ARR1, ARR2	Yeast two-hybrid	[5]
AHP5 – AHK4, ARR1, ARR2, ARR22	Yeast two-hybrid, phospho-relay, quenching	[3]; [5]; [10]
ARR3 – AHP1, AHP2	Phospho-relay	[6]; [7]
ARR4 – AHP1, AHP2	Phospho-relay, yeast two-hybrid	[6]; [1]; [7]
ARR8 – AHP1, AHP2, AHP3	Yeast two-hybrid	[1]
ARR9 – AHP1, AHP2, AHP3	Yeast two-hybrid	[1]
ARR1 – AHP1, AHP2, AHP3, AHP4, AHP5	Yeast two-hybrid	[4]; [5]
ARR2 – AHP1, AHP2, AHP3, AHP4, AHP5	Yeast two-hybrid	[4]; [8]
ARR10 – AHP1, AHP2, AHP3	Yeast two-hybrid	[4]; [7]
ARR11 – AHP2	Phospho-relay	[9]
ARR22 – AHP5	Phospho-relay	[10]

Please highlight the following 23 Cytokinin pathway AGI codes, and add to the ANAP search box.

**AT2G40670 AT1G74890 AT1G19050 AT5G62920 AT3G48100 AT1G10470 AT2G01830
AT2G41310 AT2G17820 AT3G57040 AT1G59940 AT3G21510 AT4G31920 AT1G27320
AT1G66340 AT5G39340 AT2G01760 AT3G29350 AT1G67710 AT1G03430 AT5G35750
AT4G16110 AT3G16857**

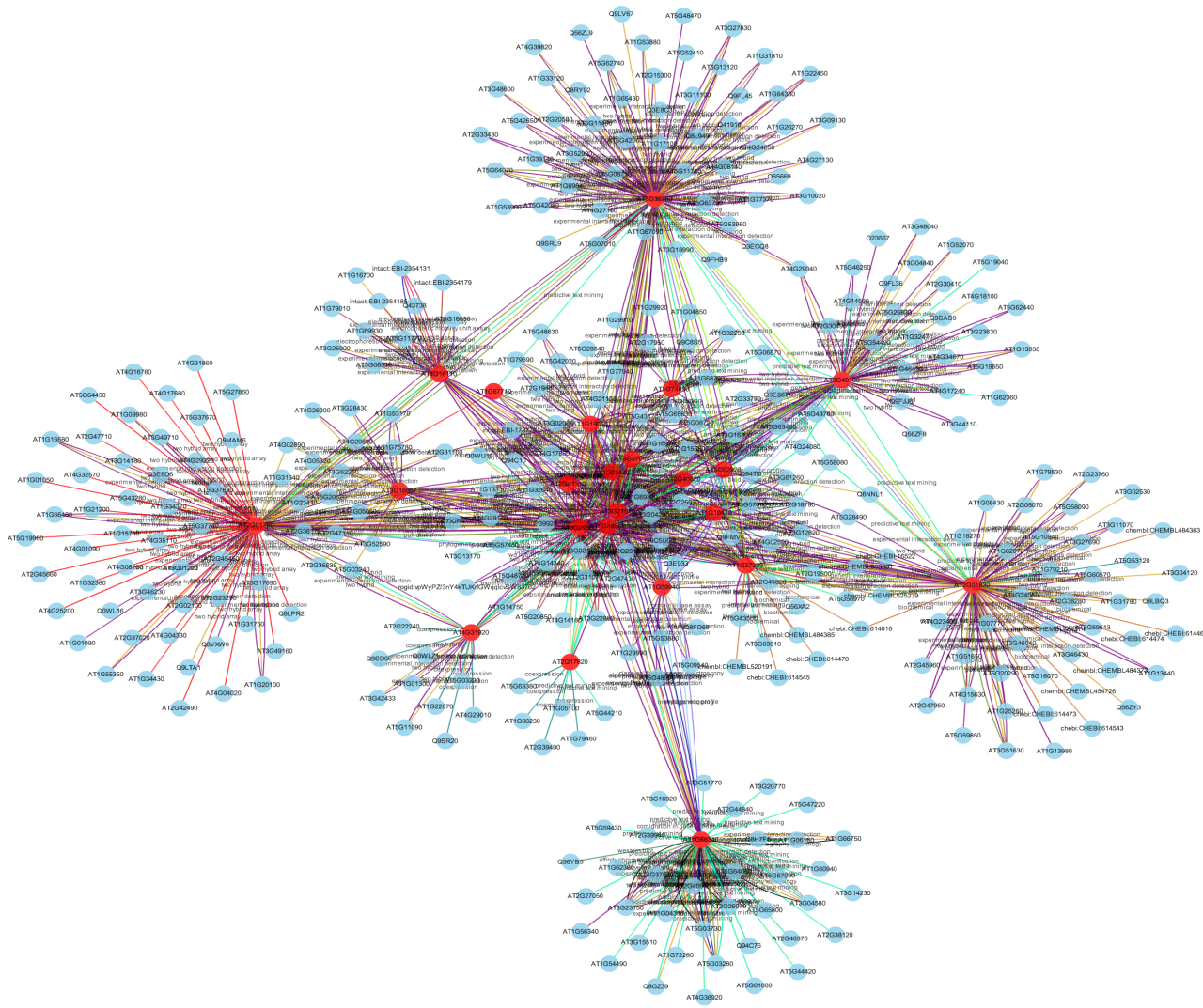
[ID Mapping](#) | [Help](#)

ANAP

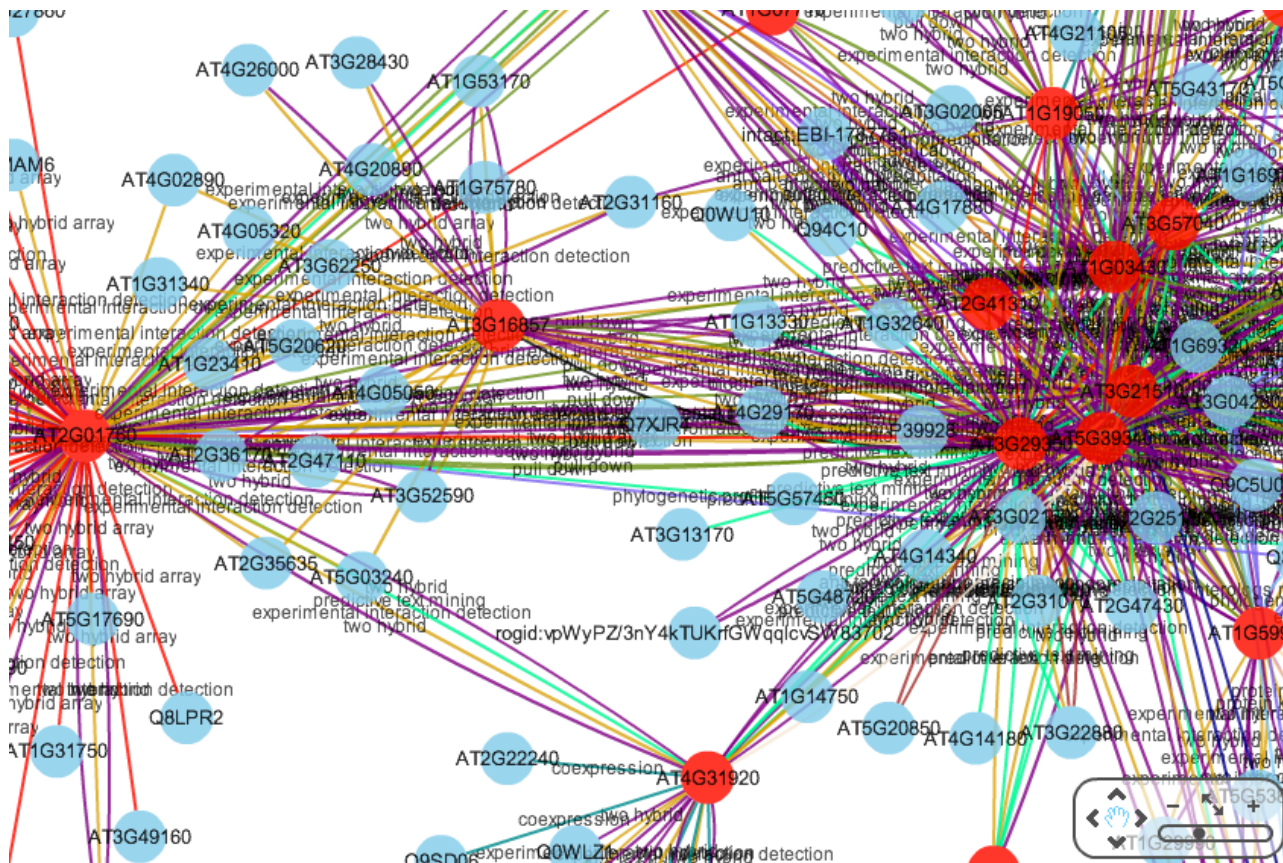
Source Database Detection Method

9350 AT3G48100 AT3G57040 AT4G16110 AT4G31920 AT5G35750 AT5G39340 AT5G62920

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You can zoom into the network (see below) and inspect the various proteins that are identified in the network. The methods that found the interactions are labelled on the edges.



You can map up or down-regulation of the corresponding genes onto the protein interaction network, or a customised list of genes.

You can colour the nodes on the network based on a AGI identifier list, which can be genes of interest to map microarray data.

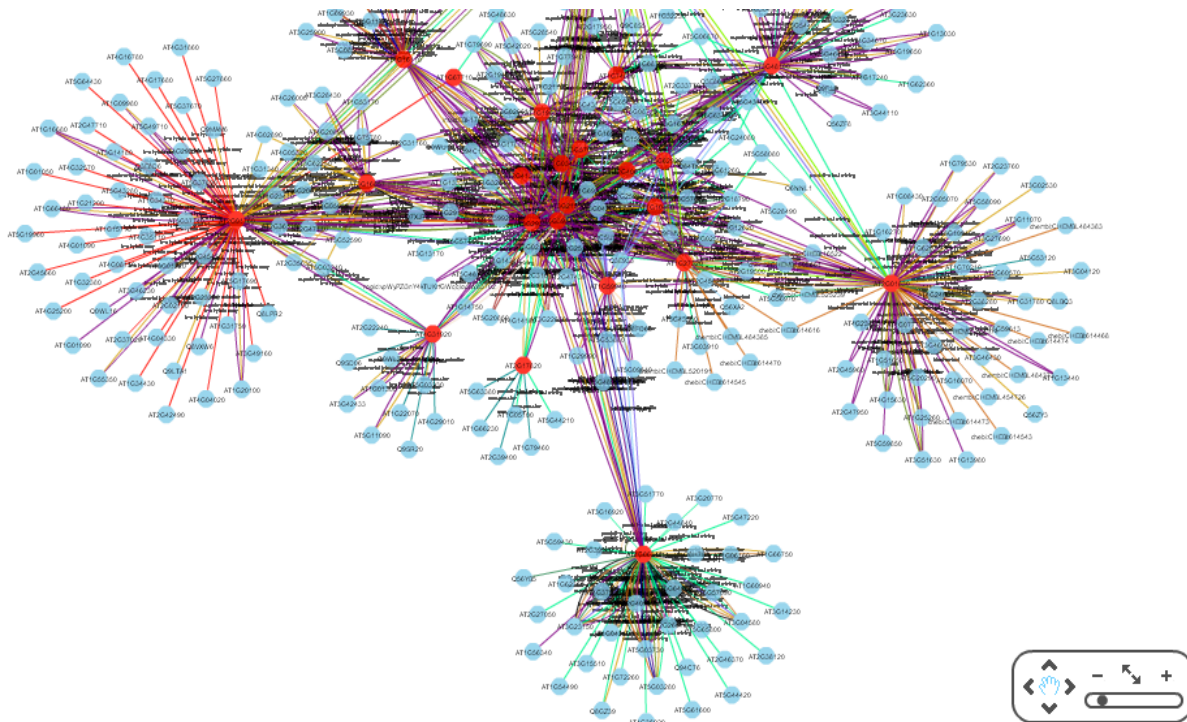
The following table shows the 24 genes from Dortay *et al.* 2006, the AGI mapping identifiers, the Affy probe identifiers, the microarray log2-fold results and annotation. There were 11 genes (coloured red) out of the 24 genes which were up-regulated 2-fold or more in AtGenExpress Cytokinin treated microarray dataset (Goda *et al.* 2008). There was one down-regulated gene which is highlighted in blue in the table below.

probe id	log2-fold	p-value	AGI	Uniprot	Gene name
266078_at	3.208401906	2.61E-09	AT2G40670	Q9SHC2	ARR16 (response regulator 16)
262212_at	3.133437919	6.25E-10	AT1G74890	Q7G8V2	ARR15 (RESPONSE REGULATOR 15)
259466_at	2.437820275	1.82E-09	AT1G19050	Q9ZWS7	ARR7 (RESPONSE REGULATOR 7)
247406_at	2.423036628	1.47E-09	AT5G62920	Q9ZWS6	ARR6 (RESPONSE REGULATOR 6)
252374_at	2.405448208	4.89E-09	AT3G48100	O80366	ARR5 (ARABIDOPSIS RESPONSE REGULATOR 5)
263236_at	1.921933777	1.51E-09	AT1G10470	O82798	ARR4 (RESPONSE REGULATOR 4)
263599_at	1.888694217	5.25E-08	AT2G01830	Q9C5U0	WOL (WOODEN LEG)

266372_at	1.415694245	1.28E-08	AT2G41310	O80365	ATRR3 (RESPONSE REGULATOR 3)
264790_at	1.324142919	1.19E-07	AT2G17820	Q9SXL4	ATHK1 (HISTIDINE KINASE 1)
251665_at	1.203165362	1.86E-07	AT3G57040	Q9ZWJ9	ARR9 (RESPONSE REACTOR 4)
262915_at	1.132317547	6.53E-07	AT1G59940	Q9ZWS9	ARR3 (RESPONSE REGULATOR 3)
258184_at	0.385262241	0.001027767	AT3G21510	Q9ZNV8	AHP1 (HISTIDINE-CONTAINING PHOSPHOTRANSMITTER 3)
253500_at	0.019787927	0.801095111	AT4G31920	Q9C5U2	ARR10 (ARABIDOPSIS RESPONSE REGULATOR 10)
264448_at	- 0.035530686	0.706114366	AT1G27320	Q9C5U1	AHK3 (ARABIDOPSIS HISTIDINE KINASE 3)
260133_at	- 0.041333474	0.614271634	AT1G66340	P49333	ETR1 (ETHYLENE RESPONSE 1)
249473_at	- 0.065345712	0.386032485	AT5G39340	Q9ZWS6	AHP3/ATHP2 (HISTIDINE-CONTAINING PHOSPHOTRANSMITTER 3)
265869_at	- 0.113195597	0.197058747	AT2G01760	Q8L9Y3	ARR14 (ARABIDOPSIS RESPONSE REGULATOR 14)
256744_at	- 0.167316734	0.047145049	AT3G29350	Q9SB04	AHP2 (HISTIDINE-CONTAINING PHOSPHOTRANSMITTER 2)
245186_at	-0.31796334	0.019346406	AT1G67710	Q9FXD6	ARR11 (RESPONSE REGULATOR 11)
264838_at	- 0.405169888	5.64E-05	AT1G03430	Q8L9T7	AHP5 (HISTIDINE-CONTAINING PHOSPHOTRANSFER FACTOR 5)
249693_at	- 0.417876529	0.000692231	AT5G35750	Q9SAZ5	AHK2 (ARABIDOPSIS HISTIDINE KINASE 2)
245477_at	- 0.687547107	3.14E-05	AT4G16110	O49397	ARR2 (ARABIDOPSIS RESPONSE REGULATOR 2)
257649_at	- 0.730396253	4.80E-06	AT3G16857	Q940D0	ARR1 (ARABIDOPSIS RESPONSE REGULATOR 1) [2 probes for AGI]
256790_at	- 1.261328062	7.98E-08	AT3G16857	Q940D0	ARR1 (ARABIDOPSIS RESPONSE REGULATOR 1) [2 probes for AGI]

Please highlight the following 11 up-regulated genes and add to the 3rd microarray mapping ANAP search box.

**AT2G40670 AT1G74890 AT1G19050 AT5G62920 AT3G48100 AT1G10470 AT2G01830
AT2G41310 AT2G17820 AT3G57040 AT1G59940**



Change the Colour

New ANAP Search

Search in Network

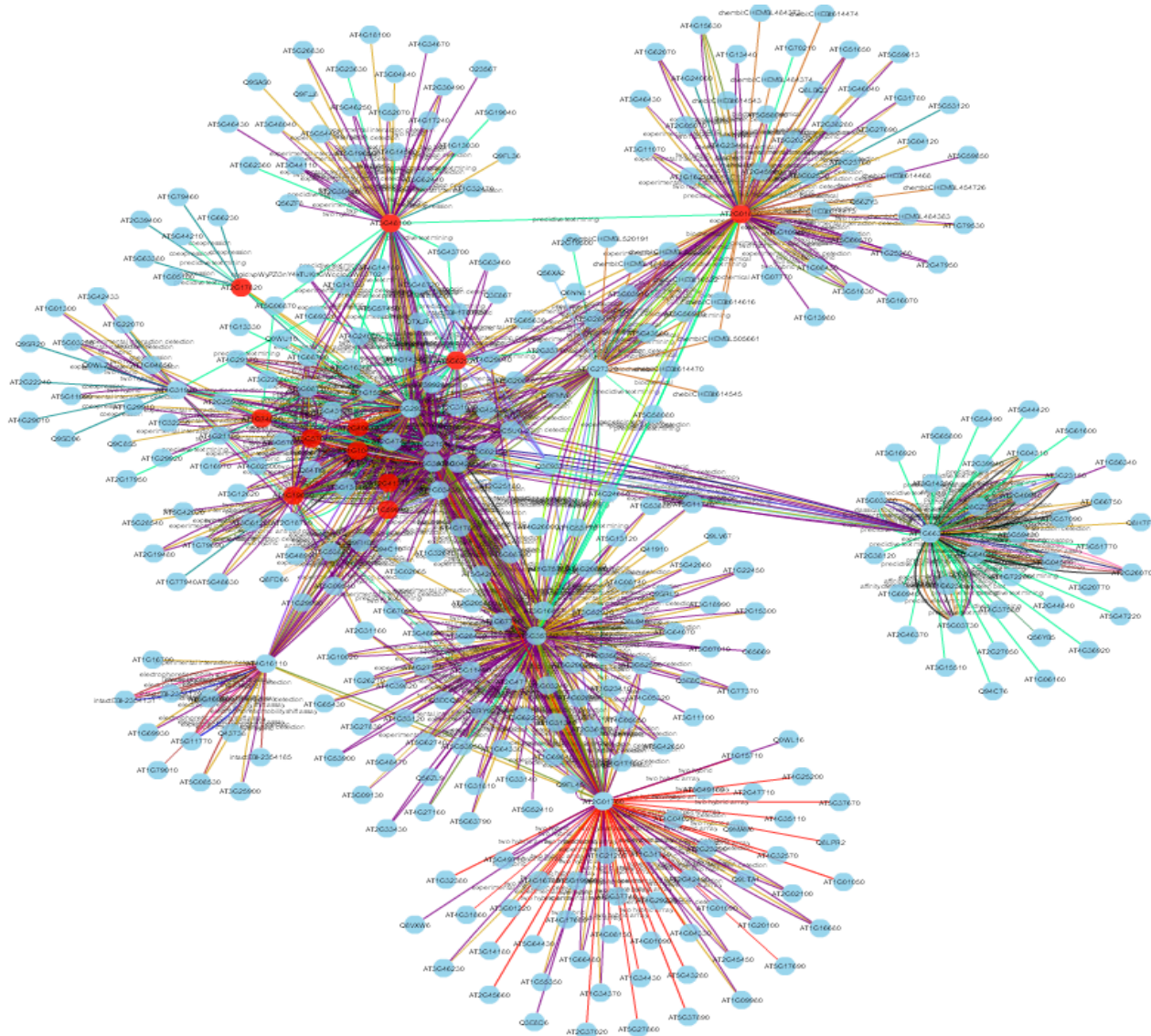
UP-Regulate

The network has 362 nodes and 1759 edges!

Home
 Save Network to
 PNG
 PDF
 SVG
 SIF
 GRAPHML
 XGMML

Evidence
 Source Database
 Interaction Detection Method
 Depth Search

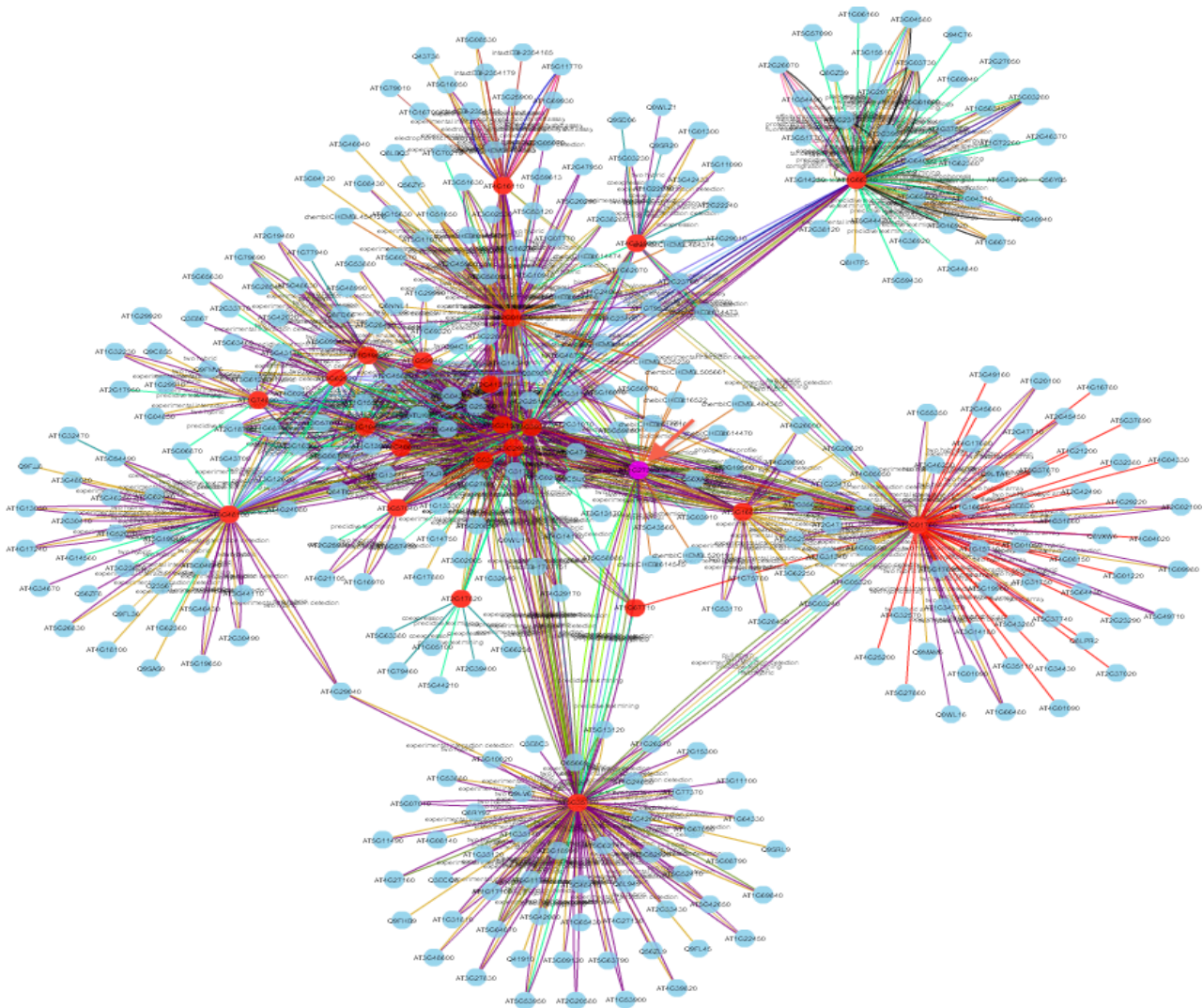
The following network shows the 11 up-regulated genes coloured in red and mapped onto the protein interaction network, and you can see they are interlinked with the inner cluster.



Please highlight the following AGI code, and add to the 2nd search in network ANAP search box.

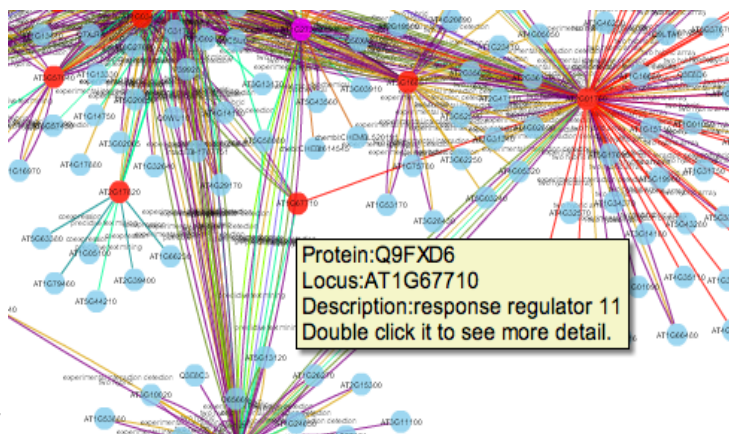
AT4G29040

You can map on proteins that you are interested in, that protein is highlighted in the network as a pink node (see below).

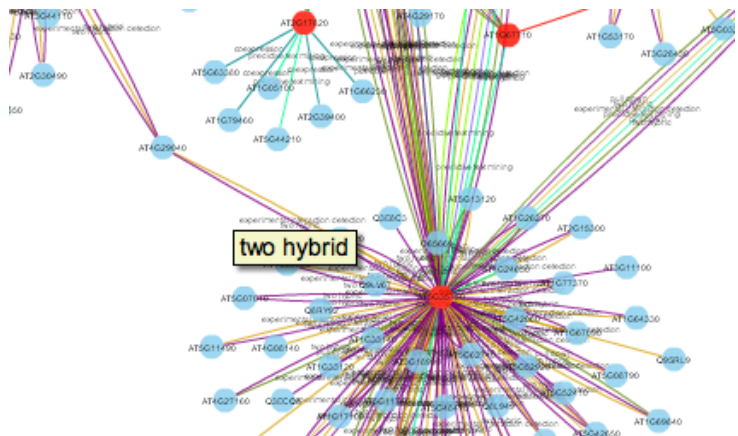


4. More ANAP functions

ANAP has more functions that extend the capability of the tool. One function allows you to see the AGI and Uniprot identifiers in more detail when you click on a node (see below).



If you click on an edge, you will see the edge type. This is useful for highly interconnected networks with many edges.



Double click on any node in the network, and the ANAP tool opens the AGI identifier in more detail with the TAIR website (see below).

Gene Search

Home Help Contact About Us Login/Register

Search Browse Tools Portals Download Submit News ABRC Stocks

Locus: AT4G29040

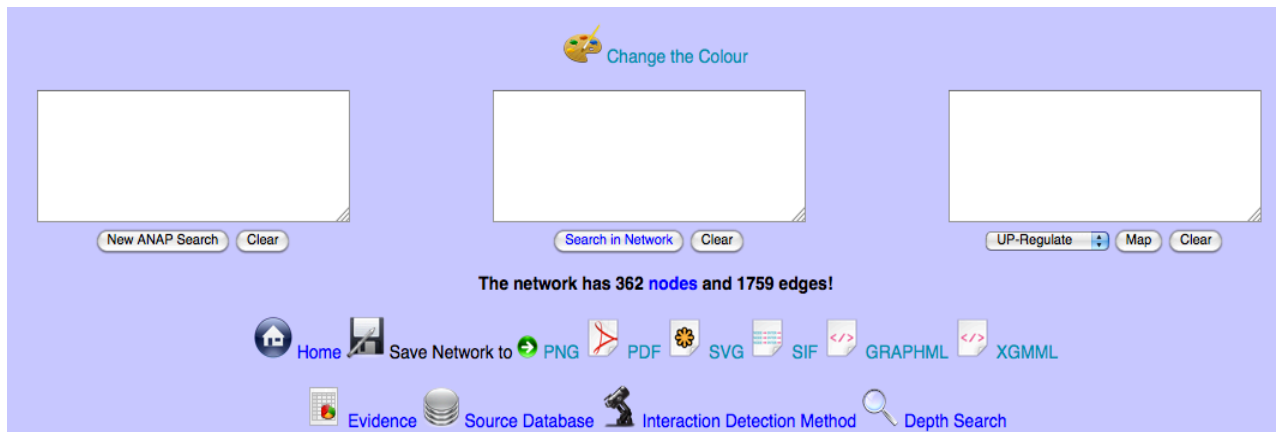
Date last modified: 2011-12-06
 TAIR Accession: Locus:2119926
 Representative Gene Model: [AT4G29040.1](#)
 Gene Model Type: protein_coding
 Other names: F19B15.70, F19B15_70, REGULATORY PARTICLE AAA-ATPASE 2A, RPT2A
 Description: RPT2a encodes the 26S proteasome subunit. It is required for root meristem maintenance, and regulates gametogenesis.

Map Detail Image

Annotations

category	relationship type	keyword
GO Biological Process	has protein modification of type	N-terminal protein myristoylation
GO Biological Process	involved in	ATP catabolic process, female gamete generation, lateral root primordium development, leaf morphogenesis, maintenance of root meristem identity, male gamete generation, meristem growth, meristem structural organization, phylome development, proteasomal ubiquitin-dependent protein catabolic process, proteasome assembly, response to cadmium ion, response to heat, response to misfolded protein, root cap development, root development, root morphogenesis, shoot development, ubiquitin-dependent protein catabolic process
GO Biological Process	not involved in	proteasome core complex assembly
GO Cellular Component	is subunit of	proteasome complex
GO Cellular Component	located in	membrane, nucleus, proteasome regulatory particle, base subcomplex
GO Cellular Component	not located in	cytosol
GO Molecular Function	has	ATPase activity
Growth and Developmental Stages	expressed during	4 anthesis, 4 leaf senescence stage, C globular stage, D bilateral stage, E expanded cotyledon stage, F mature embryo stage, LP:02 two leaves visible, LP:04 four leaves visible, LP:06 six leaves visible, LP:08 eight leaves visible, LP:10 ten leaves visible, LP:12 twelve leaves visible, petal differentiation and expansion stage
Plant structure	expressed in	carpel, cauline leaf, collective leaf structure, cotyledon, cultured plant cell, flower, flower bud, hypocotyl, inflorescence apical meristem, inflorescence meristem, leaf apex, leaf lamina base, megagametophyte, microgametophyte, pedicel, petal, petiole, plant embryo, pollen, quiescent center, root, root initial cell, root meristem, root tip, seed, sepal, shoot apex, shoot apical meristem, shoot system, stamen, stem, vascular leaf

The menu at the bottom of the page with the ANAP output has several interesting features.



You can save network as a variety of formats, which include PNG, PDF, SVG, SIF, GRAPHML and XGMML format.

There are extra features along the bottom which include evidence, source database, interaction detection method and depth search.

(a) **Evidence** - Clicking on this downloads an excel file with all the information about the interactions in the query network. The figure below shows you the columns, which include the node AGI codes, interaction detection method, species molecule A, species molecule B, pubmed identifier and source database.

Get the Evidence example file -> [here](#) <-

	A	B	C	D	E	F	G	H
1	Name molecule A	Name molecule B	Interaction Detection Method	Species molecule A	Species molecule B	PubMed Identifier	Source Database	
2	AT1G01300	AT4G31920	experimental interaction detect	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:18642946	STRING	
3	AT1G03430	AT1G10470	experimental interaction detect	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	STRING	
4	AT1G03430	AT1G10470	pull down	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	iRefIndex	
5	AT1G03430	AT1G10470	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	APID	
6	AT1G03430	AT1G10470	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	iRefIndex	
7	AT1G03430	AT1G10470	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:18642946	APID	
8	AT1G03430	AT1G10470	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:18642946	BioGrid	
9	AT1G03430	AT1G10470	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:18642946	IntAct	
10	AT1G03430	AT1G10470	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:18642946	iRefIndex	
11	AT1G03430	AT1G19050	experimental interaction detect	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	STRING	
12	AT1G03430	AT1G19050	pull down	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	iRefIndex	
13	AT1G03430	AT1G19050	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	IntAct	
14	AT1G03430	AT1G19050	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	iRefIndex	
15	AT1G03430	AT1G27320	experimental interaction detect	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	STRING	
16	AT1G03430	AT1G27320	pull down	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	IntAct	
17	AT1G03430	AT1G27320	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	IntAct	
18	AT1G03430	AT1G27320	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	iRefIndex	
19	AT1G03430	AT1G32640	experimental interaction detect	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:12826627	STRING	
20	AT1G03430	AT1G32640	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:12826627	APID	
21	AT1G03430	AT1G32640	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:12826627	BIND	
22	AT1G03430	AT1G32640	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:12826627	BioGrid	
23	AT1G03430	AT1G32640	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:12826627	iRefIndex	
24	AT1G03430	AT1G59940	experimental interaction detect	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	STRING	
25	AT1G03430	AT1G59940	pull down	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	iRefIndex	
26	AT1G03430	AT1G59940	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	APID	
27	AT1G03430	AT1G59940	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	iRefIndex	
28	AT1G03430	AT1G67710	experimental interaction detect	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	STRING	
29	AT1G03430	AT1G67710	pull down	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	iRefIndex	
30	AT1G03430	AT1G67710	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	APID	
31	AT1G03430	AT1G67710	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	iRefIndex	
32	AT1G03430	AT1G74890	experimental interaction detect	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	STRING	
33	AT1G03430	AT1G74890	pull down	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	IntAct	
34	AT1G03430	AT1G74890	pull down	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	iRefIndex	
35	AT1G03430	AT1G74890	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	IntAct	
36	AT1G03430	AT1G74890	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	iRefIndex	
37	AT1G03430	AT2G01760	experimental interaction detect	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	STRING	
38	AT1G03430	AT2G01760	pull down	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	IntAct	
39	AT1G03430	AT2G01760	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	IntAct	
40	AT1G03430	AT2G01830	experimental interaction detect	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	STRING	
41	AT1G03430	AT2G01830	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	APID	
42	AT1G03430	AT2G01830	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	IntAct	
43	AT1G03430	AT2G25180	experimental interaction detect	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:11158442	STRING	
44	AT1G03430	AT2G40670	experimental interaction detect	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	STRING	
45	AT1G03430	AT2G40670	pull down	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	iRefIndex	
46	AT1G03430	AT2G40670	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	IntAct	
47	AT1G03430	AT2G40670	two hybrid	Arabidopsis thaliana	Arabidopsis thaliana	pubmed:16965536	iRefIndex	

(b) **Source database** - Clicking on this opens a new webpage which shows the source database that contained the interaction.


```

AT1G01300    STRING    AT4G31920
AT1G03430    STRING    AT1G10470
AT1G03430    iRefIndex AT1G10470
AT1G03430    APID      AT1G10470
AT1G03430    iRefIndex AT1G10470
AT1G03430    APID      AT1G10470
AT1G03430    BioGrid   AT1G10470
AT1G03430    IntAct    AT1G10470
AT1G03430    iRefIndex AT1G10470
AT1G03430    STRING    AT1G19050
AT1G03430    iRefIndex AT1G19050
AT1G03430    IntAct    AT1G19050
AT1G03430    iRefIndex AT1G19050
AT1G03430    STRING    AT1G27320
AT1G03430    IntAct    AT1G27320
AT1G03430    IntAct    AT1G27320
AT1G03430    iRefIndex AT1G27320
AT1G03430    STRING    AT1G32640
AT1G03430    APID      AT1G32640
AT1G03430    BIND      AT1G32640
AT1G03430    BioGrid   AT1G32640
AT1G03430    iRefIndex AT1G32640
AT1G03430    STRING    AT1G59940
AT1G03430    iRefIndex AT1G59940
AT1G03430    APID      AT1G59940
AT1G03430    iRefIndex AT1G59940
AT1G03430    STRING    AT1G67710
AT1G03430    iRefIndex AT1G67710
AT1G03430    APID      AT1G67710
AT1G03430    iRefIndex AT1G67710
AT1G03430    STRING    AT1G74890
AT1G03430    IntAct    AT1G74890
AT1G03430    iRefIndex AT1G74890
    
```

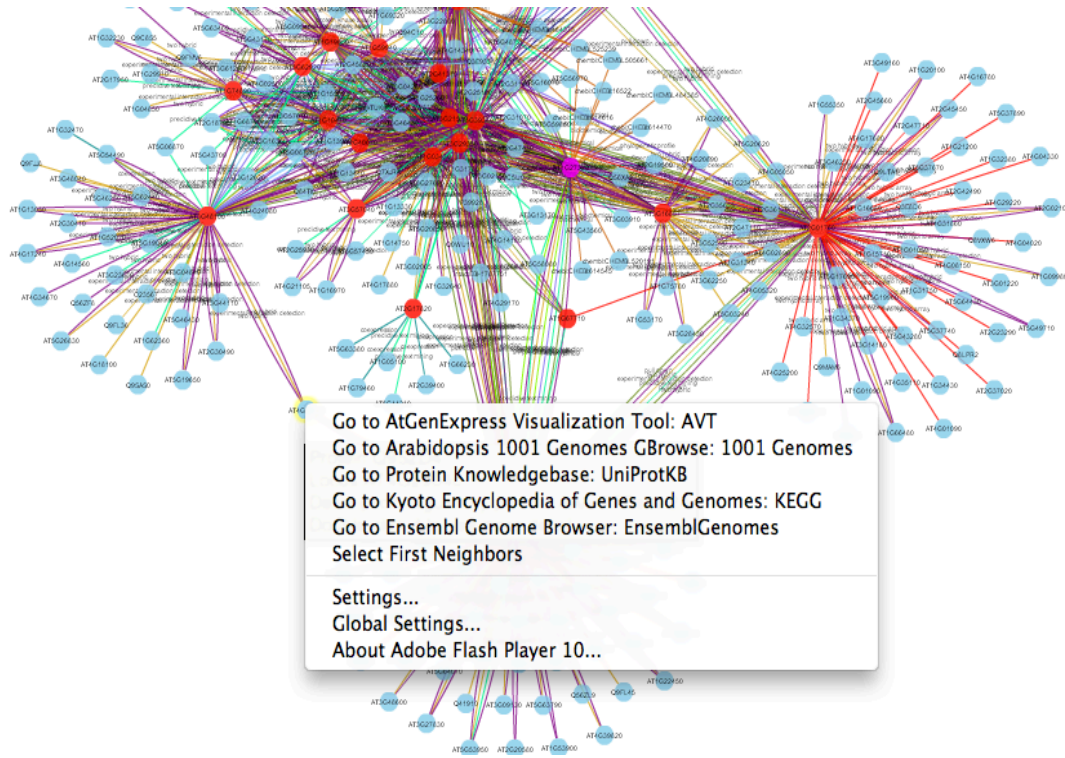
(c) **Interaction detection method** - Clicking on this opens a new webpage which shows the different interaction methods. For example, 2 hybrid, affinity chromatography technology, etc.

```

AT1G01300    experimental interaction detection    AT4G31920
AT1G03430    experimental interaction detection    AT1G10470
AT1G03430    pull down    AT1G10470
AT1G03430    two hybrid   AT1G10470
AT1G03430    two hybrid   AT1G10470
AT1G03430    two hybrid   AT1G10470
AT1G03430    two hybrid   AT1G10470
AT1G03430    two hybrid   AT1G10470
AT1G03430    experimental interaction detection    AT1G19050
AT1G03430    pull down    AT1G19050
AT1G03430    two hybrid   AT1G19050
AT1G03430    two hybrid   AT1G19050
AT1G03430    experimental interaction detection    AT1G27320
AT1G03430    pull down    AT1G27320
AT1G03430    two hybrid   AT1G27320
AT1G03430    two hybrid   AT1G27320
AT1G03430    experimental interaction detection    AT1G32640
AT1G03430    two hybrid   AT1G32640
AT1G03430    two hybrid   AT1G32640
AT1G03430    two hybrid   AT1G32640
AT1G03430    experimental interaction detection    AT1G59940
AT1G03430    pull down    AT1G59940
AT1G03430    two hybrid   AT1G59940
AT1G03430    experimental interaction detection    AT1G67710
AT1G03430    pull down    AT1G67710
AT1G03430    two hybrid   AT1G67710
AT1G03430    two hybrid   AT1G67710
AT1G03430    experimental interaction detection    AT1G74890
AT1G03430    pull down    AT1G74890
AT1G03430    two hybrid   AT1G74890
AT1G03430    two hybrid   AT1G74890
AT1G03430    experimental interaction detection    AT2G01760
    
```

5. Links to other databases

If you right click on any node, a window will pop with links to several databases including AtGenExpress, 1001 genomes browser, UniProt, KEGG and Ensembl Genome browsers. There is also the function to select first nearest neighbour to that node.



(a) Link to AtGenExpress

AtGenExpress Visualization Tool (AVT)

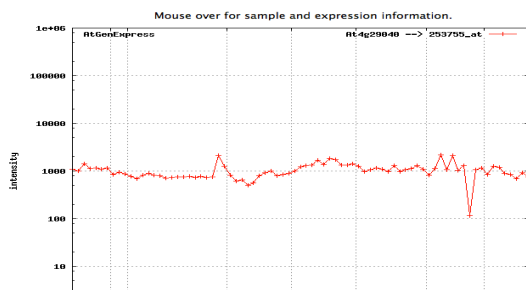
Select experiment: AtGE Development

Select normalization: Absolute values only create tab-delimited file

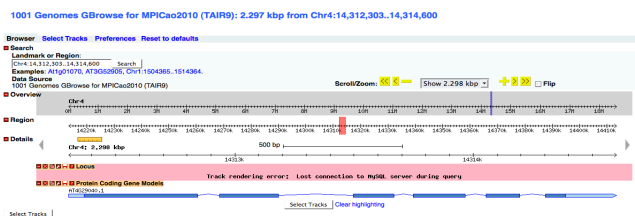
Select genes: Run Clear

enter desired AGI or Affymetrix identifiers (comma separated), e.g., AT5G61850, AT5G57090, At1G29910, 254595_at then press "Run"

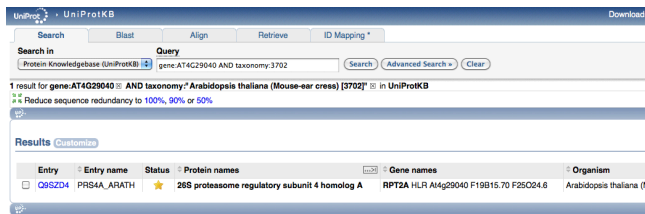
AtGenExpress Development



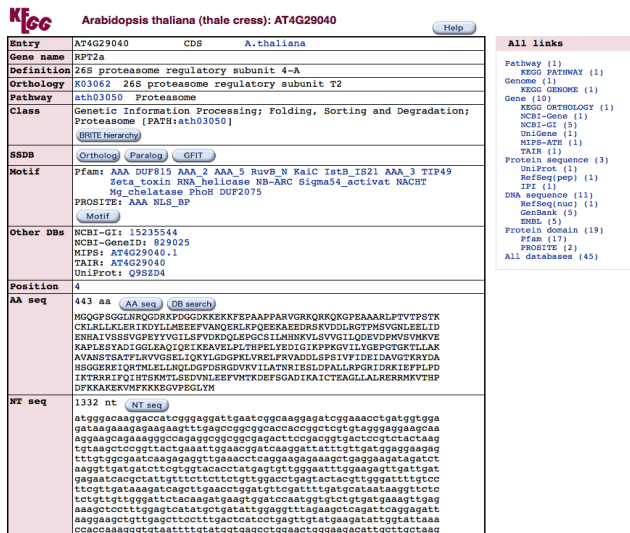
(b) Link to Arabidopsis 1001 Genomes GBrowse



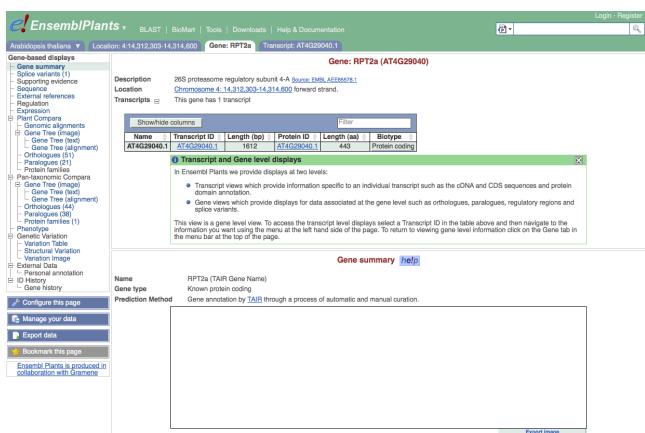
(c) Link to UniProt database



(d) Link to KEGG



(e) Link to Ensembl Genome Browser



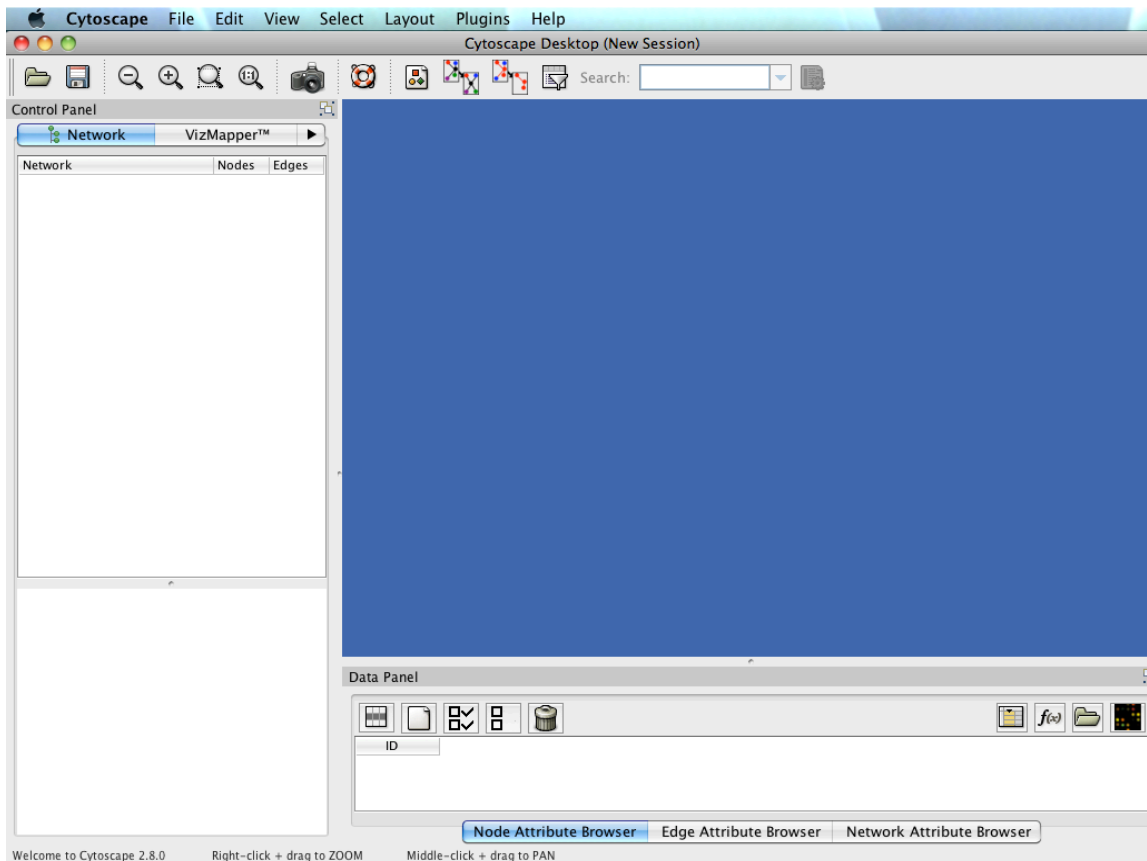
6. Importing the ANAP Cytokinin protein interaction network into Cytoscape

Cytoscape is the main network visualisation and analysis software tool (Cline *et al.* 2009) that is fully supported by ANAP, so results can be saved in a format and imported into Cytoscape. Cytoscape is useful when analysing very large networks since internet browsers have problems displaying very large networks and there are also many supporting analysis plugins.

First download Cytoscape from the following website:-

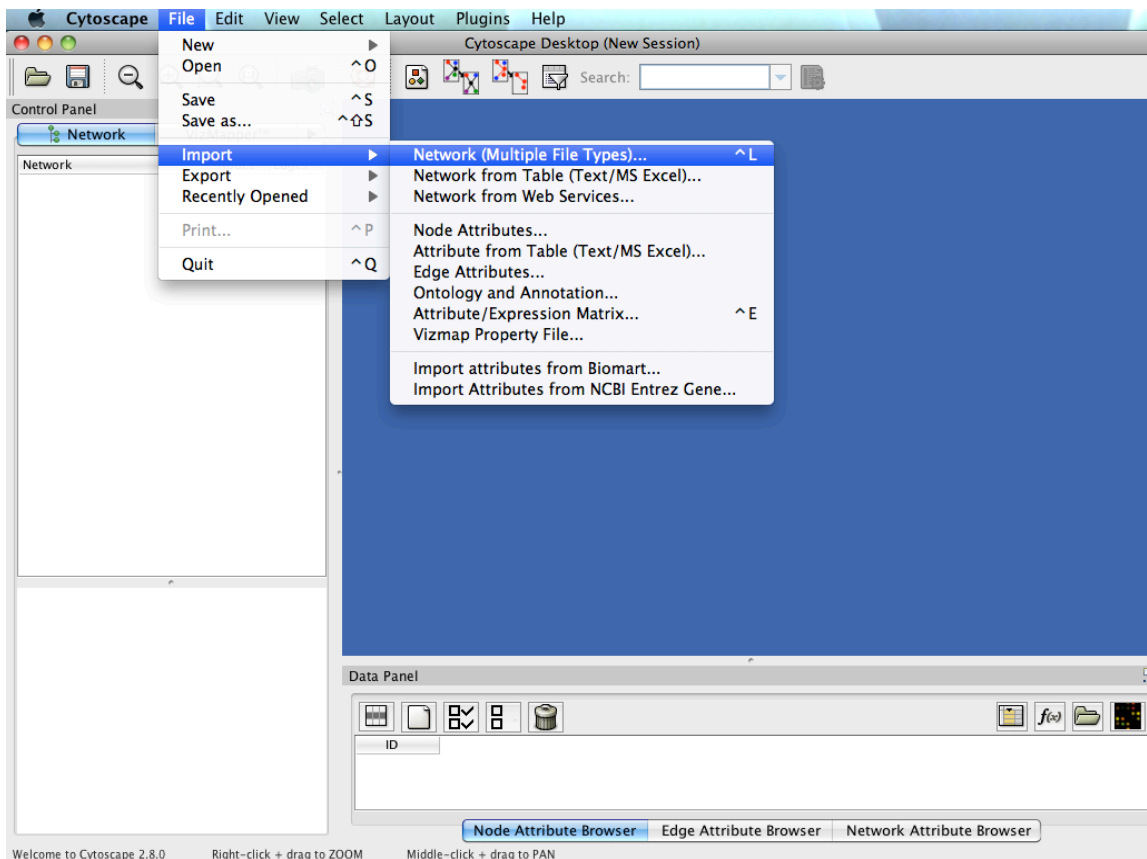
<http://www.cytoscape.org/>

Install Cytoscape onto your computer.

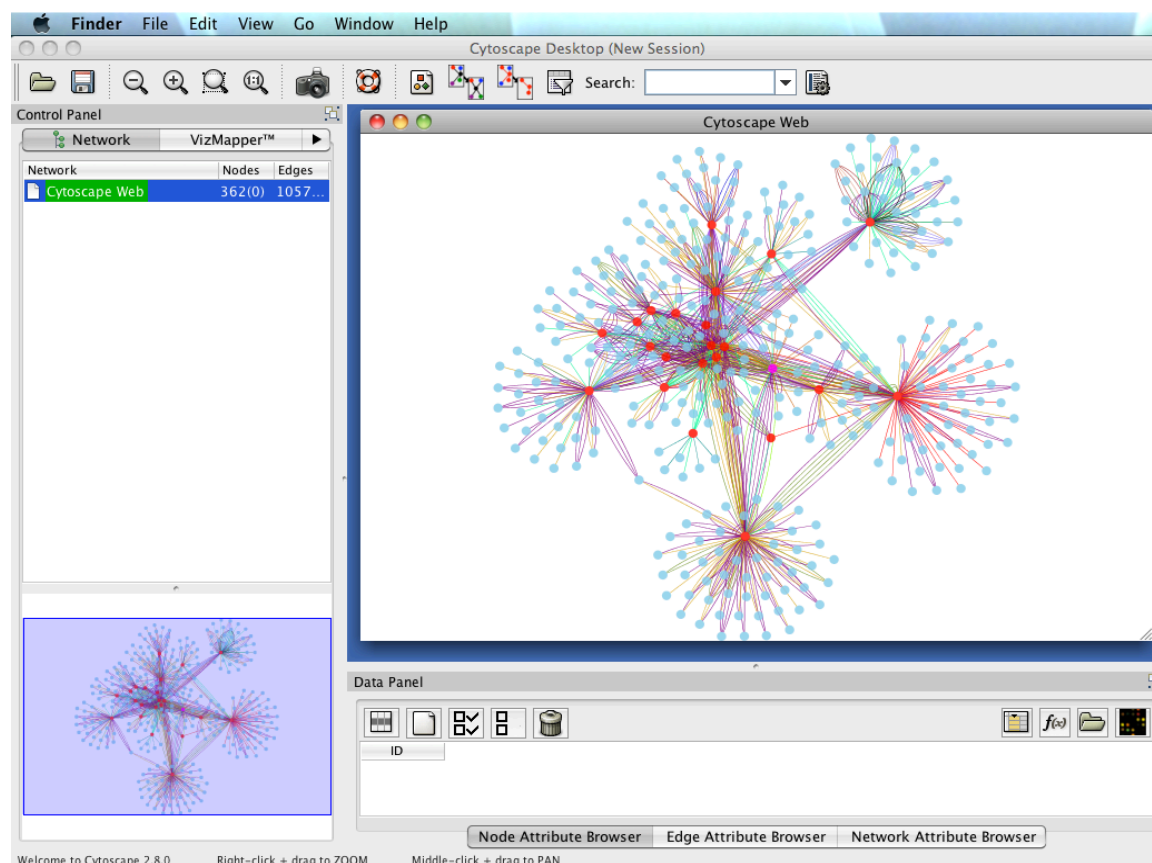


Please use the XGMML file from using this user guide, or download it -> [here](#) <-

Import the ANAP generated XGMML file into Cytoscape (see below).



The imported network retains the node and edge colouring of ANAP using the XGMML file (see below).



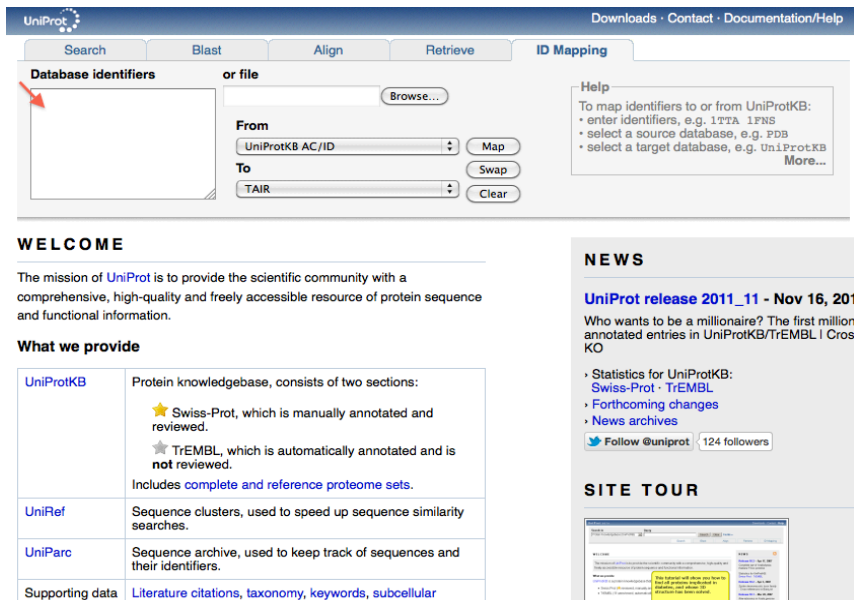
Cytoscape has many interesting features which complement the ANAP tool, these include expression data mapping, being able to render very large networks, and a wide variety of analysis functions.

You can create a node attributes file easily in a text editor, which will map the AGI codes to protein identifiers.

The ANAP tool uses both Uniprot identifiers (e.g. B4G294) and AGI codes (e.g. AT2G40670), and these can be easily interconverted the id mapping function at the Uniprot website.

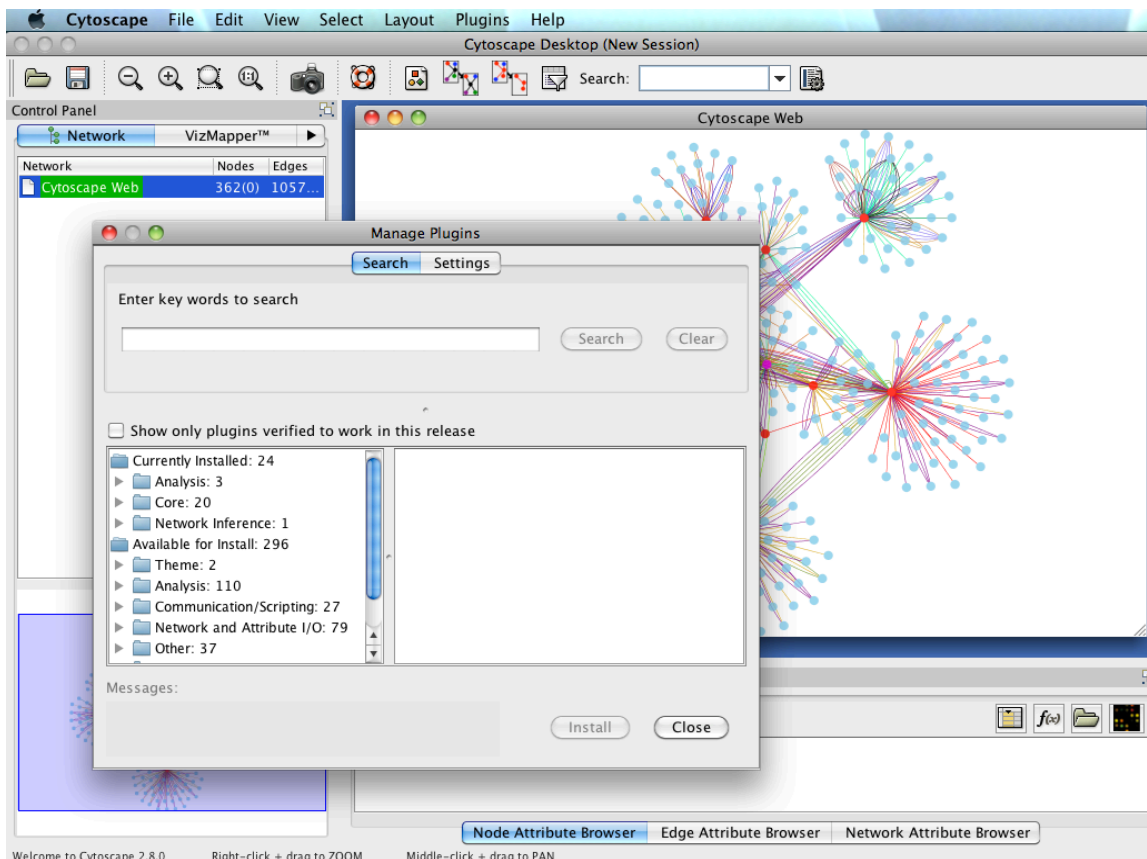
<http://www.uniprot.org/>

Select the Uniprot accession and TAIR id boxes, add list of identifiers in the large box, and click "map".



The resulting output will have a list of Uniprot to AGI conversions, highlight and save in either a text file or in excel. This is useful for when you want to create a Cytoscape mapping node attribute file.

Cytoscape offers a very large number of plugins that can be downloaded using the Cytoscape plugin menu (see below).



The full Cytoscape tutorial can be found here:

http://www.cytoscape.org/documentation_users.html

You have successfully completed the ANAP user guide.

If you have any questions, queries about the tool or suggestions for added functionality, please email the ANAP developer [Congmao Wang](#) (Zhang lab, Shanghai Jiao Tong University, China) or [Dr. Zoe Wilson](#) (School of Biosciences, University of Nottingham, UK).

Here is a link to videos that explain ANAP's functionality as a step by step process.

http://gmdd.shgmo.org/Computational-Biology/ANAP/ANAP_V1.0/help/help.html

6. References

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