

From STRING to Cytoscape: stringApp

Input table

A	B	C	D	E	F	G	H	I	J	
1	UniProt	Gene name	Peptides	Sequence coverage [%]	5 min ratio exp. 1	5 min ratio exp. 2	5 min log ratio	10 min ratio exp. 1	10 min ratio exp. 2	10 min log ratio
2	Q99880	HIST1H2BL	5	35.7	0.27	0.04	-2.66	0.24	0.08	-2.66
3	Q8TER5	ARHGEF40	34	28.3	3.65	4.09	1.95	2.64	3.24	1.56
4	Q8IZ07	ANKRD13A	12	19.2	2.22	1.99	1.07	1.99	2.25	1.08
5	P62805	HIST1H4A	11	57.3	0.36	0.05	-2.31	0.65	0.11	-1.39
6	Q08380	LGALS3BP	14	28.2	0.09	0.13	-3.16	0.12	0.14	-2.98
7	O00750	PIK3C2B	35	24.2	4.49	4.77	2.21	4.64	5.27	2.31
8	O00443	PIK3C2A	29	17.8	2.32	2.07	1.13	2.39	2.41	1.26
9	Q9UJ41	RABGEF1	6	6.5	1.67	1.50	0.67	1.86	2.36	1.08
10	Q8TC07	TBC1D15	12	19.1	1.27	1.44	0.43	1.78	2.39	1.06
11	Q9UN70	PCDHGC3	9	12.7	1.29	1.05	0.23	1.65	1.78	0.78
12	Q75VX8	GAREML	26	37.5	8.59	5.97	2.86	9.71	7.57	3.11
13	P42336	PIK3CA	21	22.8	4.43	4.95	2.23	6.09	5.92	2.59
14	P27986	PIK3R1	19	28.2	4.13	3.61	1.95	4.97	5.83	2.43
15	O00459	PIK3R2	21	40.2	3.88	3.77	1.94	4.59	4.89	2.24
16	P42338	PIK3CB	12	13.4	3.68	2.72	1.68	4.86	3.88	2.13
17	Q96S55	WRNIP1	16	29.8	1.42	1.59	0.59	1.86	2.44	1.10
18	Q15276	RABEP1	22	31.1	1.34	1.51	0.51	1.73	2.31	1.02
19	P16234	PDGFRA	24	24.3	1.52	1.75	0.71	1.10	1.36	0.30
20	Q06124	PTPN11	27	48.4	1.22	1.44	0.41	1.31	2.08	0.76
21	P36896	ACVR1B	4	10.1	1.09	0.87	-0.03	2.80	2.18	1.32
22	Q6ZNH5	ZNF497	2	3.8	0.44	0.69	-0.82	2.13	15.14	3.11
23	P06702	S100A9	9	74.6	0.17	0.05	-3.17	0.07	0.05	-4.12
24	Q13410	BTN1A1	3	9.3	0.27	0.10	-2.44	1.38	0.19	-0.34
25	O95757	HSPA4L	15	21.2	0.20	0.33	-1.93	0.30	0.63	-1.12
26	O14492	SH2B2	5	9.5	6.55	6.69	2.73	7.05	10.85	3.16
27	P19174	PLCG1	69	50	5.63	7.23	2.69	6.06	8.07	2.82
28	Q9H706	GAREM	17	23.9	4.72	4.61	2.22	4.14	5.78	2.31

[Search](#)[Download](#)[Help](#)[My Data](#)

Welcome to STRING

Protein-Protein Interaction Networks
Functional Enrichment Analysis

ORGANISMS

5090

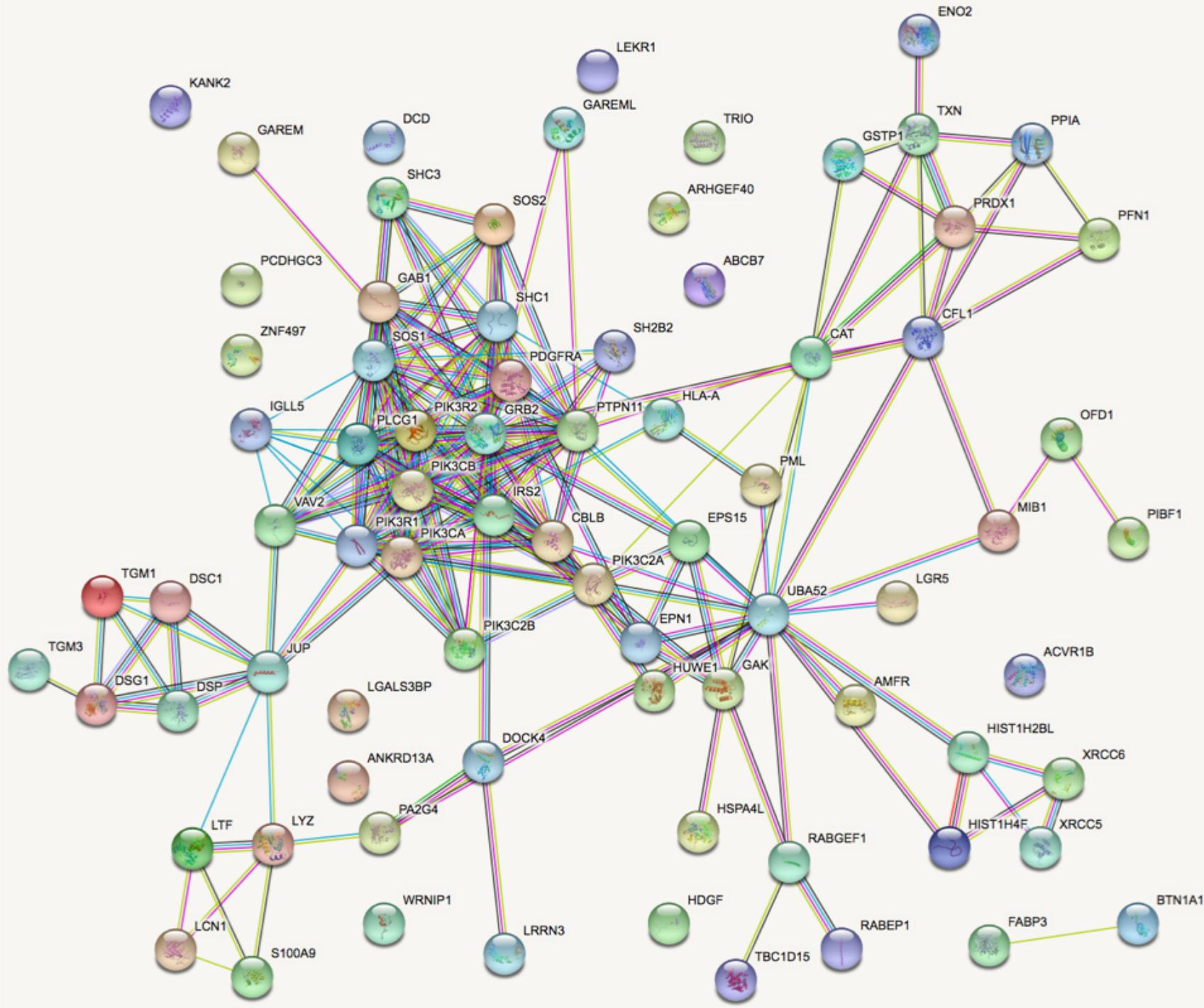
PROTEINS

24.6 mio

INTERACTIONS

>2000 mio

[SEARCH](#)



From STRING to Cytoscape

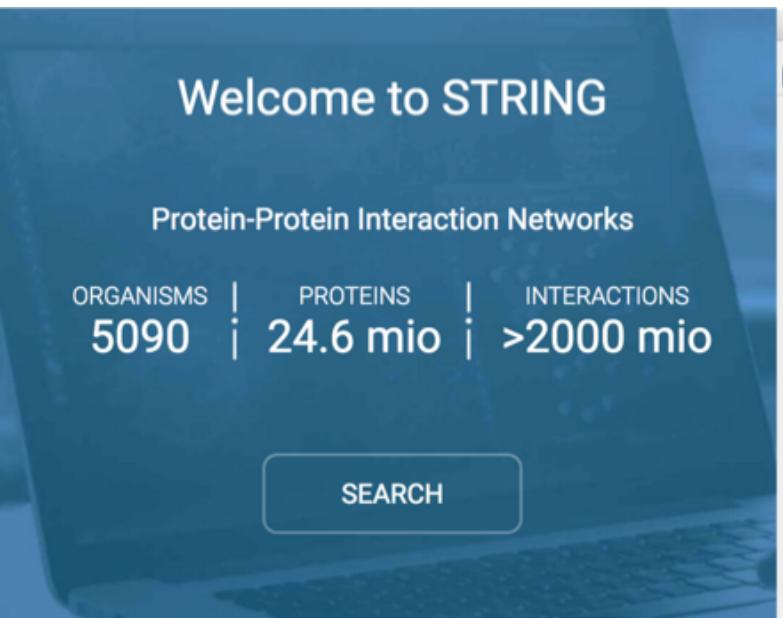
Welcome to STRING

Protein-Protein Interaction Networks

ORGANISMS | PROTEINS | INTERACTIONS

5090 | 24.6 mio | >2000 mio

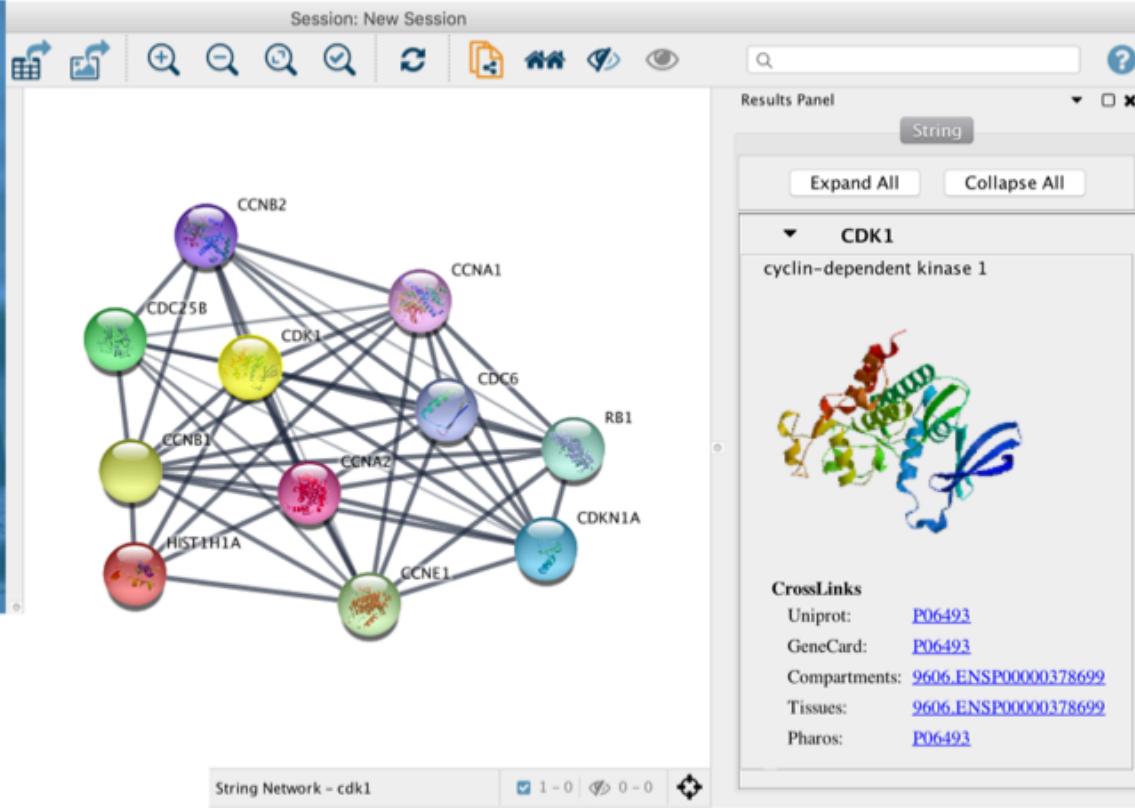
SEARCH



 **stringApp**
Import and augment Cytoscape networks from STRING

★★★★★ (15) 43854 downloads | posts | citations 

Session: New Session

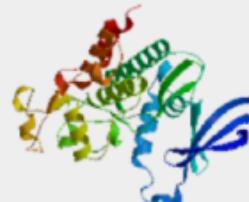


Results Panel

String

Expand All Collapse All

▼ CDK1
cyclin-dependent kinase 1



CrossLinks

Uniprot:	P06493
GeneCard:	P06493
Compartments:	9606.ENSP00000378699
Tissues:	9606.ENSP00000378699
Pharos:	P06493

String Network - cdk1

1 - 0 0 - 0

STRING protein query

Import Network from Public Databases

Data Source: STRING: protein query

Species: Homo sapiens

All proteins of this species

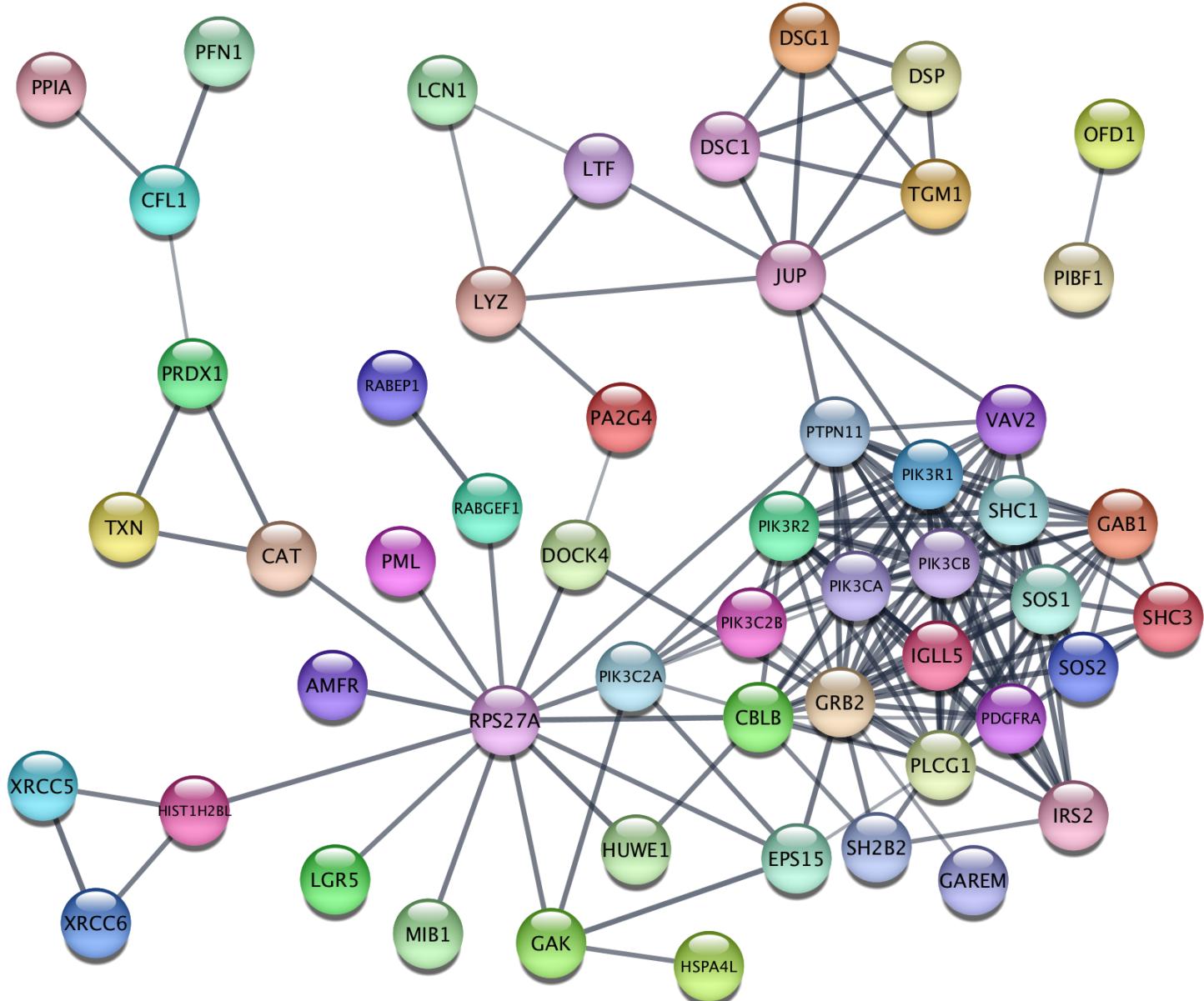
Enter protein names or identifiers:

Q99880
Q8TER5
Q8IZ07
P62805
Q08380
O00750
O00443
Q9UJ41
Q8TC07
Q9UN70
Q75VX8
P42336
P27986
O00459
P42338
Q96S55
Q15276
P16234
Q06124
P36896
Q6ZNH5
P06702
Q13410
O95757

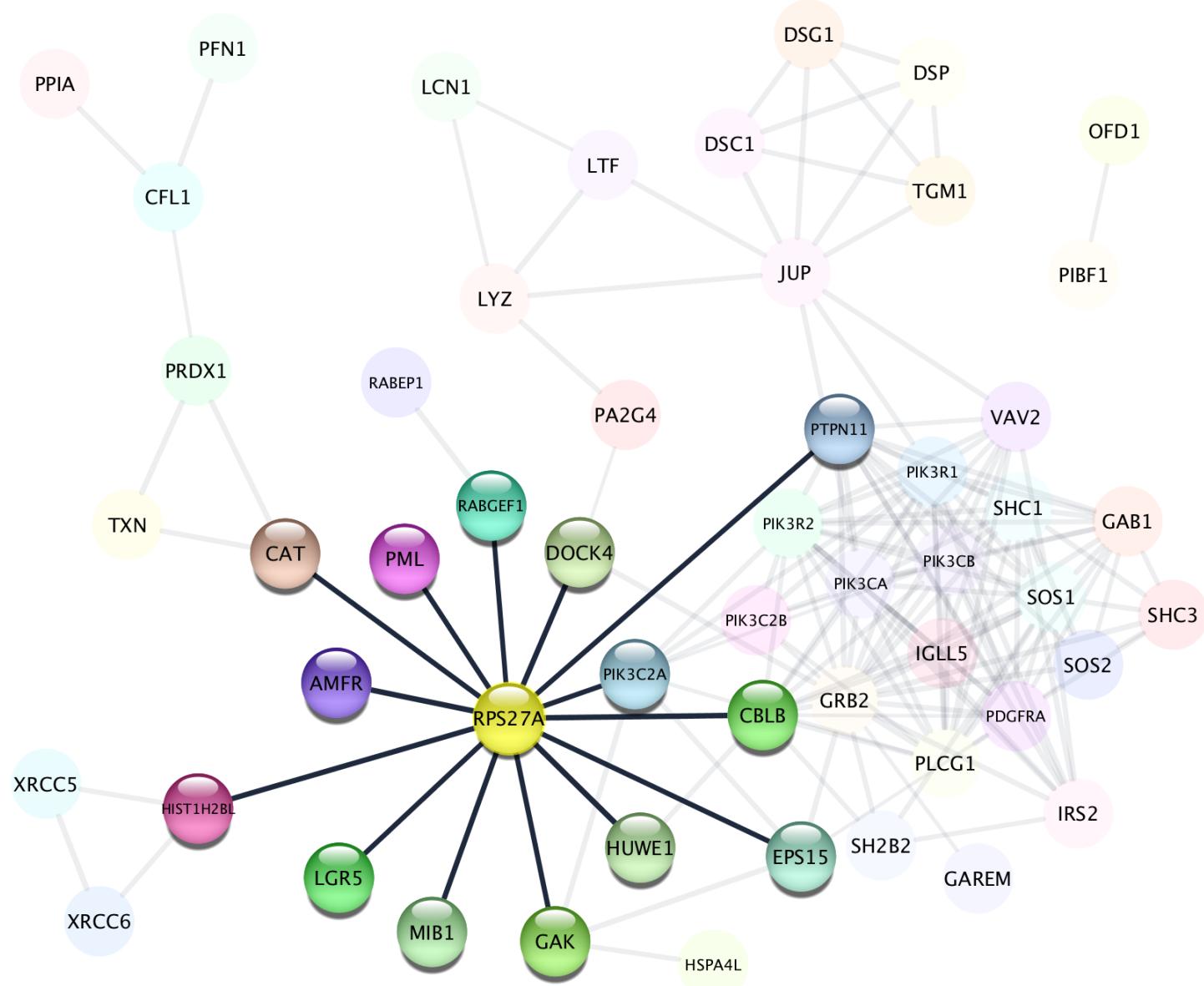
Confidence (score) cutoff: 0.60

Maximum number of interactors: 0

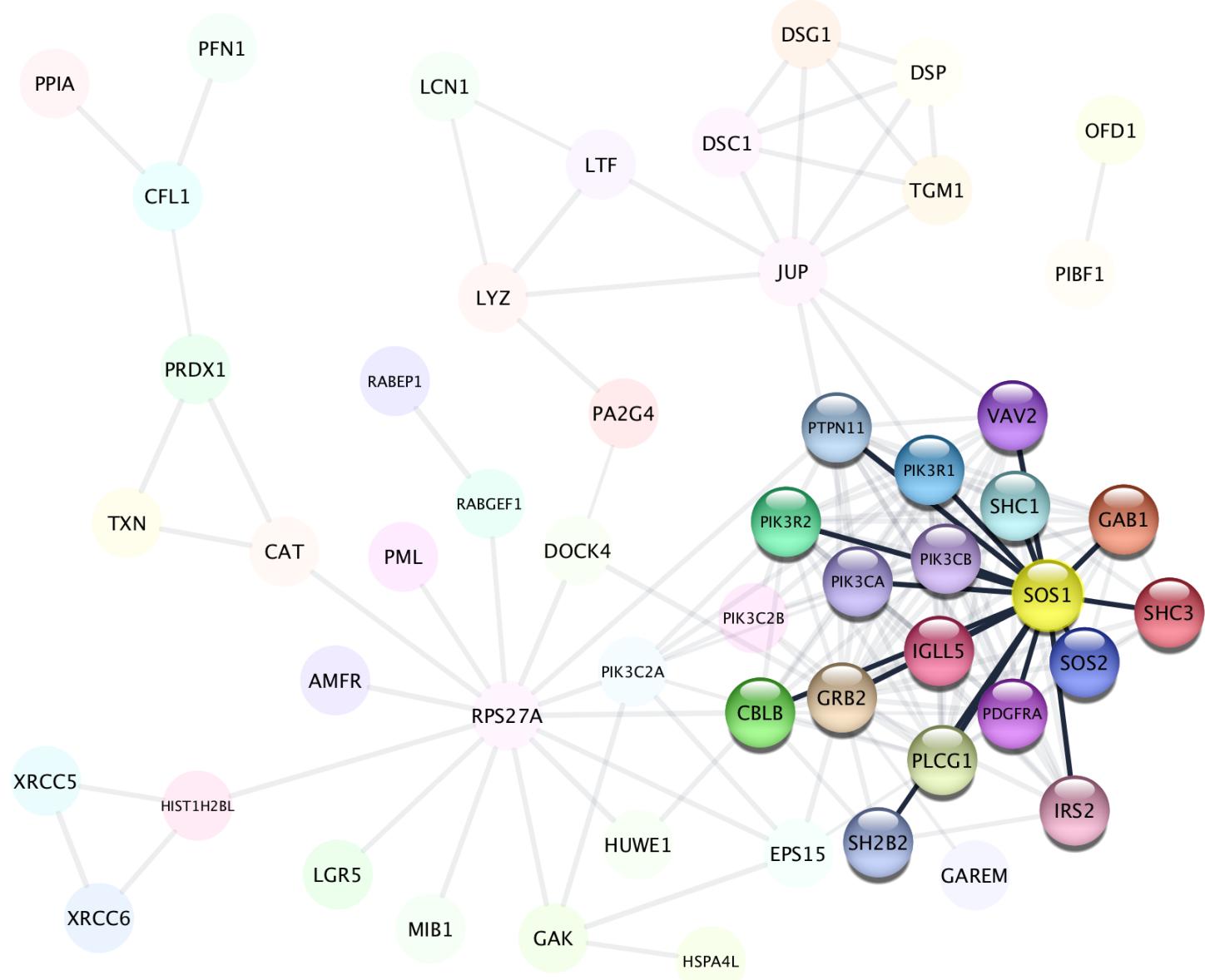
STRING network in Cytoscape



First neighbors



First neighbors



Additional node annotations

Table Panel

The screenshot shows a 'Table Panel' interface with a toolbar at the top containing icons for settings, search, and file operations. Below the toolbar is a table with various columns representing protein annotations. The first four columns are highlighted with a black border: 'display name', 'stringdb canonical name', 'stringdb description', and 'stringdb sequence'. The remaining columns are: 'compartment cytosol', 'compartment nucleus', 'tissue blood', and 'target family'. The data rows include entries for GAK, PDGFRA, PIK3C2A, PIK3C2B, PIK3CA, PIK3CB, PIK3R1, LGR5, AMFR, and CAT. The 'target family' column indicates Kinase for most proteins except CAT, which is a GPCR.

display name	stringdb canonical name	stringdb description	stringdb sequence	compartment cytosol	compartment nucleus	tissue blood	target family
GAK	O14976	Cyclin G associated kinase; Ass...	MSLLQSALDFLAG...	4.670617	1.557458	1.990326	Kinase
PDGFRA	P16234	Platelet-derived growth factor r...	MGTSHPAFLVLGC...	2.004486	4.507324	4.52719	Kinase
PIK3C2A	O00443	Phosphatidylinositol 4-phospha...	MAQISSNSGFKEC...	4.771678	4.591553	2.945786	Kinase
PIK3C2B	O00750	Phosphatidylinositol 4-phospha...	MSSTQGNGEHWK...	4.62589	4.504065	4.417402	Kinase
PIK3CA	P42336	Phosphatidylinositol 4,5-bispho...	MPPRPSSGELWGIH...	4.756729	3.294534	2.731771	Kinase
PIK3CB	P42338	Phosphatidylinositol 4,5-bispho...	MCFSFIMPPAMAD...	4.489296	4.381225	2.334249	Kinase
PIK3R1	Q8N1C5	Phosphatidylinositol 3-kinase 8...	MSAEGYQYRALY...	4.712311	4.448957	2.619943	Kinase
LGR5	O75473	Leucine-rich repeat containing ...	MDTSRLGVLLSLP...	2.411035	2.679854	2.163659	GPCR
AMFR	Q9UKV5	Autocrine motility factor recept...	MPLLFLERFPWPSL...	3.890287	3.084065	4.180633	
CAT	P04040	Catalase; Occurs in almost all ae...	MADS RDPASDQM...	4.777516	3.554507	4.751272	

Below the table are navigation tabs: Node Table, Edge Table, Network Table, STRING Enrichment, and STRING Publications.

- Protein information from STRING

Additional node annotations

Table Panel

display name	stringdb canonical name	stringdb description	stringdb sequence	compartiment cytosol	compartiment nucleus	tissue blood	target family
GAK	O14976	Cyclin G associated kinase; Ass...	MSLLQSALDFLAG...	4.670617	1.557458	1.990326	Kinase
PDGFRA	P16234	Platelet-derived growth factor r...	MGTSHPAFLVLC...	2.004486	4.507324	4.52719	Kinase
PIK3C2A	O00443	Phosphatidylinositol 4-phospha...	MAQISSNSGFKEC...	4.771678	4.591553	2.945786	Kinase
PIK3C2B	O00750	Phosphatidylinositol 4-phospha...	MSSTQGNGEHWK...	4.62589	4.504065	4.417402	Kinase
PIK3CA	P42336	Phosphatidylinositol 4,5-bispho...	MPPRPSSGELWGIH...	4.756729	3.294534	2.731771	Kinase
PIK3CB	P42338	Phosphatidylinositol 4,5-bispho...	MCFSFIMPPAMAD...	4.489296	4.381225	2.334249	Kinase
PIK3R1	Q8N1C5	Phosphatidylinositol 3-kinase 8...	MSAEGYQYRALY...	4.712311	4.448957	2.619943	Kinase
LGR5	O75473	Leucine-rich repeat containing ...	MDTSRLGVLLSLP...	2.411035	2.679854	2.163659	
AMFR	Q9UKV5	Autocrine motility factor recept...	MPLLFLERFPWPSL...	3.890287	3.084065	4.180633	
CAT	P04040	Catalase; Occurs in almost all ae...	MADS RDPASDQM...	4.777516	3.554507	4.751272	GPCR

- Protein information from STRING
- TISSUES & COMPARTMENTS scores

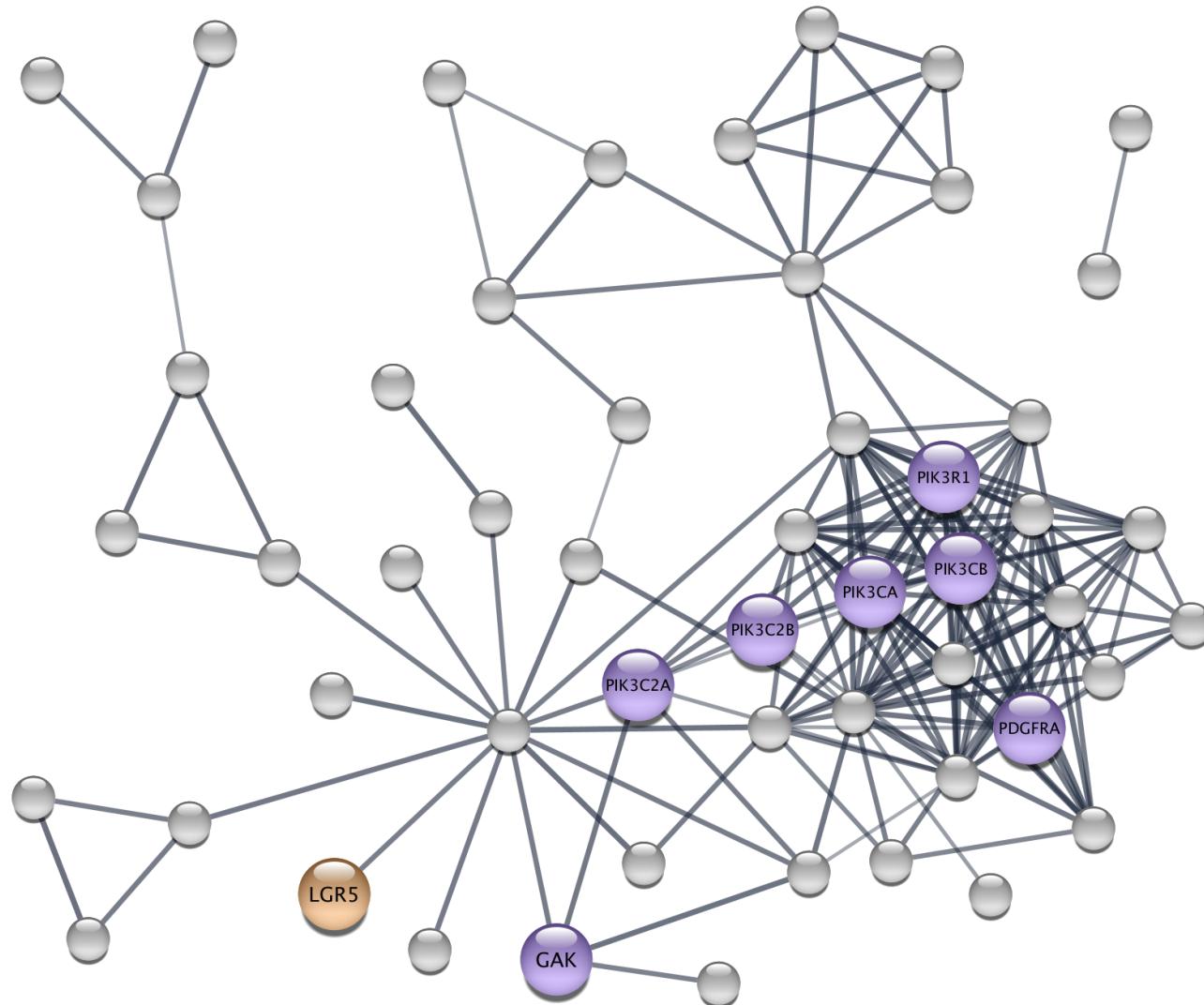
Additional node annotations

Table Panel

display name	stringdb canonical name	stringdb description	stringdb sequence	compartment cytosol	compartment nucleus	tissue blood	target family
GAK	O14976	Cyclin G associated kinase; Ass...	MSLLQSALDFLAG...	4.670617	1.557458	1.990326	Kinase
PDGFRA	P16234	Platelet-derived growth factor r...	MGTSHPAFLVLC...	2.004486	4.507324	4.52719	Kinase
PIK3C2A	O00443	Phosphatidylinositol 4-phospha...	MAQISSNSGFKEC...	4.771678	4.591553	2.945786	Kinase
PIK3C2B	O00750	Phosphatidylinositol 4-phospha...	MSSTQGNGEHWK...	4.62589	4.504065	4.417402	Kinase
PIK3CA	P42336	Phosphatidylinositol 4,5-bispho...	MPPRPSSGELWGIH...	4.756729	3.294534	2.731771	Kinase
PIK3CB	P42338	Phosphatidylinositol 4,5-bispho...	MCFSFIMPPAMAD...	4.489296	4.381225	2.334249	Kinase
PIK3R1	Q8N1C5	Phosphatidylinositol 3-kinase 8...	MSAEGYQYRALY...	4.712311	4.448957	2.619943	Kinase
LGR5	O75473	Leucine-rich repeat containing ...	MDTSRLGVLLSLP...	2.411035	2.679854	2.163659	GPCR
AMFR	Q9UKV5	Autocrine motility factor recept...	MPLLFLERFPWPSL...	3.890287	3.084065	4.180633	
CAT	P04040	Catalase; Occurs in almost all ae...	MADSRDPASDQM...	4.777516	3.554507	4.751272	

- Protein information from STRING
- Scores from TISSUES & COMPARTMENTS
- Drug target information from Pharos database

Drug targets info visualization



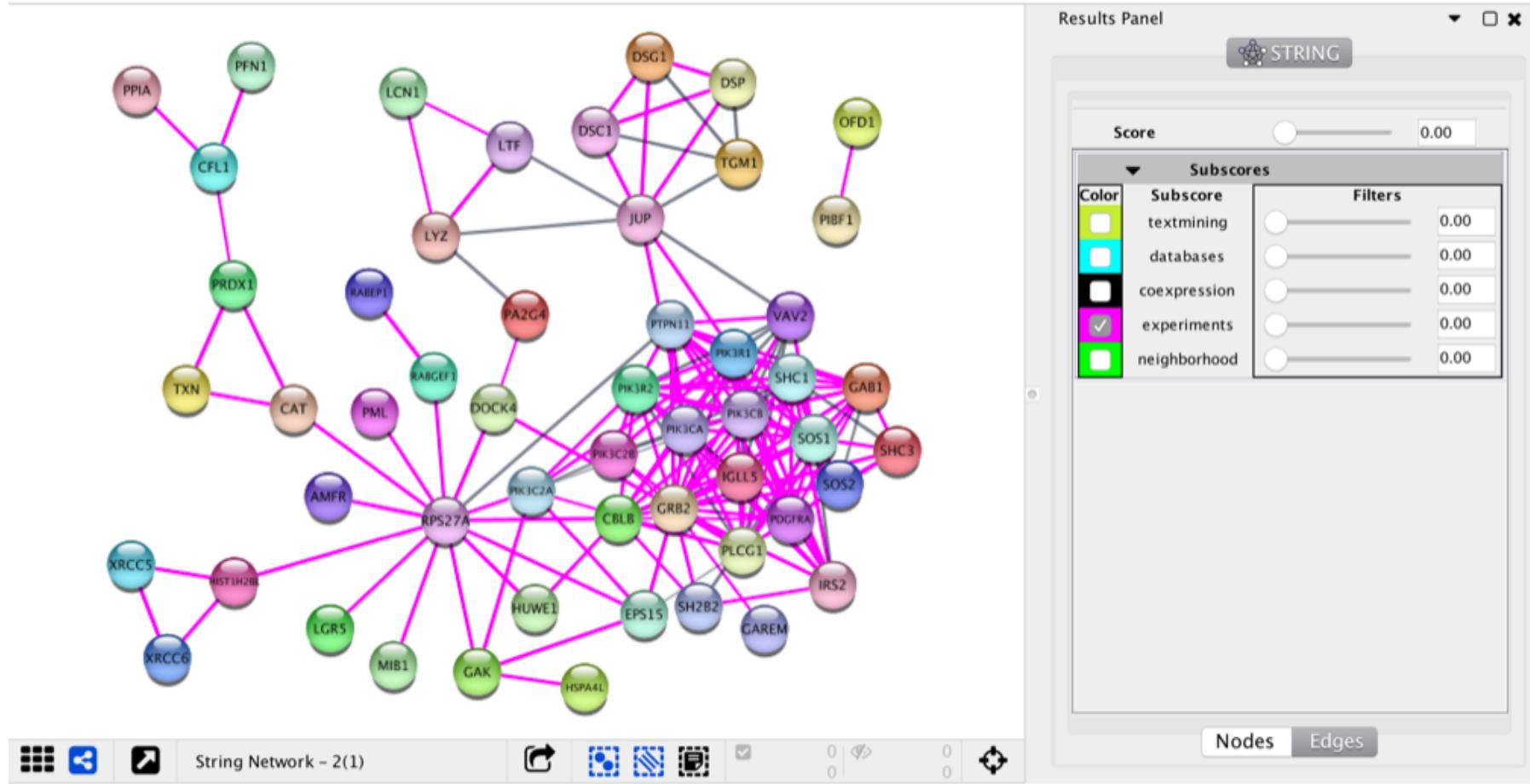
Additional edge annotations

Table Panel

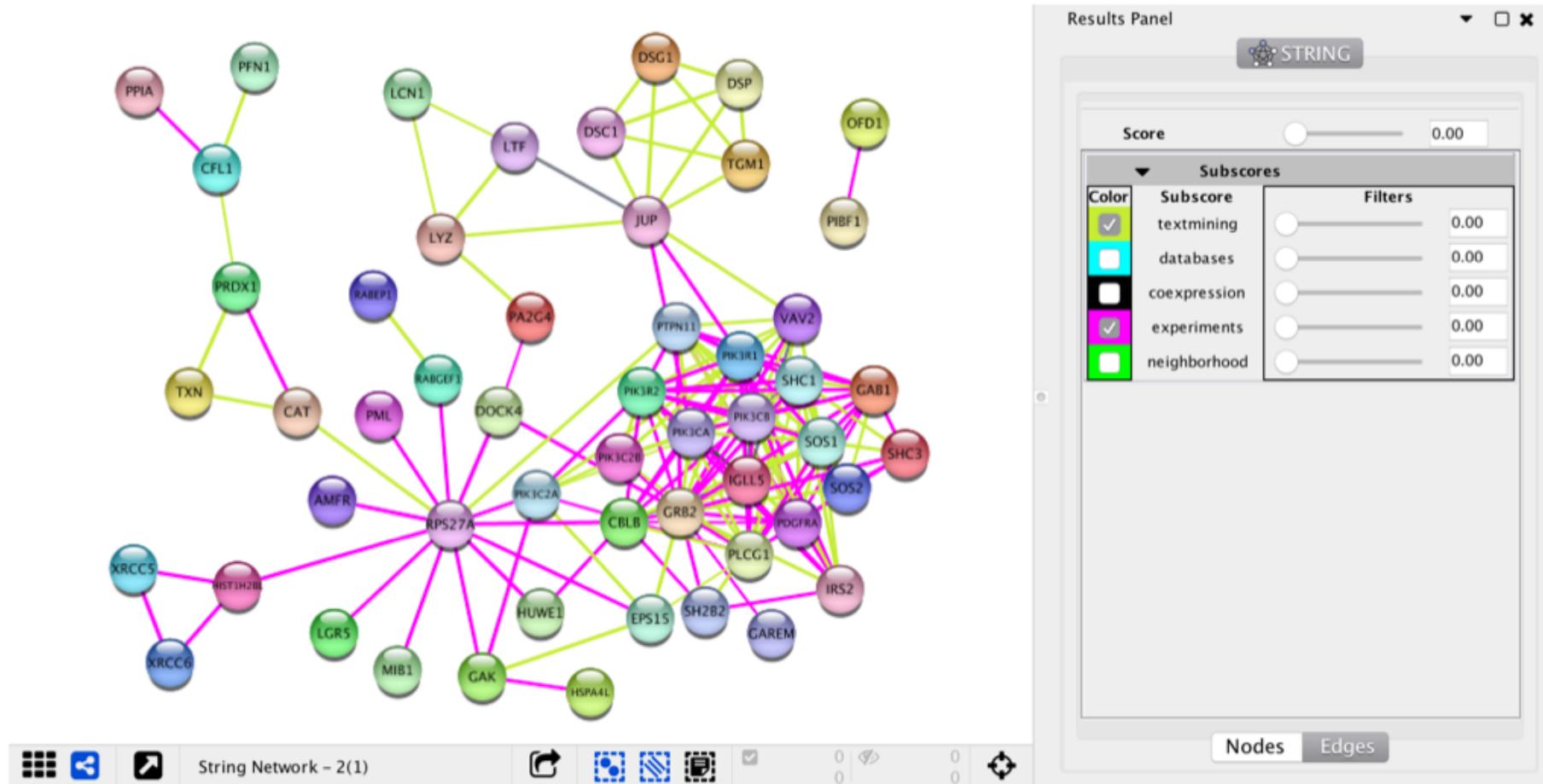
shared name	shared interaction	stringdb score	stringdb textmining	stringdb databases	stringdb coexpression	stringdb experiments	stringdb neighborhood
GAB1 (pp) SHC3	pp	0.86	0.186	0.8	0.062	0.194	
GAB1 (pp) GRB2	pp	0.996	0.829	0.9	0.052	0.829	
GAB1 (pp) SOS1	pp	0.977	0.338	0.9	0.061	0.687	
GAB1 (pp) SHC1	pp	0.975	0.577	0.9	0.062	0.46	
GAB1 (pp) PIK3R1	pp	0.952	0.186	0.9	0.05	0.46	
PIK3CA (pp) CBLB	pp	0.909	0.067	0.9	0.062	0.085	
PIK3CA (pp) PIK3CB	pp	0.911	0.128	0.9	0.062		
PIK3CA (pp) PTPN11	pp	0.949	0.498	0.9	0.063	0.061	
PIK3CA (pp) PIK3C2B	pp	0.916	0.185	0.9	0.062		
PIK3CA (pp) VAV2	pp	0.904	0.056	0.9	0.066		

Node Table Edge Table Network Table STRING Enrichment STRING Publications

Highlight edge evidence



Highlight edge evidence



Users experimental data

	A	B	C	D	E	F	G	H	I	J
1	UniProt	Gene name	Peptides	Sequence coverage [%]	5 min ratio exp. 1	5 min ratio exp. 2	5 min log ratio	10 min ratio exp. 1	10 min ratio exp. 2	10 min log ratio
2	Q99880	HIST1H2BL	5	35.7	0.27	0.04	-2.66	0.24	0.08	-2.66
3	Q8TER5	ARHGEF40	34	28.3	3.65	4.09	1.95	2.64	3.24	1.56
4	Q8IZ07	ANKRD13A	12	19.2	2.22	1.99	1.07	1.99	2.25	1.08
5	P62805	HIST1H4A	11	57.3	0.36	0.05	-2.31	0.65	0.11	-1.39
6	Q08380	LGALS3BP	14	28.2	0.09	0.13	-3.16	0.12	0.14	-2.98
7	O00750	PIK3C2B	35	24.2	4.49	4.77	2.21	4.64	5.27	2.31
8	O00443	PIK3C2A	29	17.8	2.32	2.07	1.13	2.39	2.41	1.26
9	Q9UJ41	RABGEF1	6	6.5	1.67	1.50	0.67	1.86	2.36	1.08
10	Q8TC07	TBC1D15	12	19.1	1.27	1.44	0.43	1.78	2.39	1.06
11	Q9UN70	PCDHGC3	9	12.7	1.29	1.05	0.23	1.65	1.78	0.78
12	Q75VX8	GAREML	26	37.5	8.59	5.97	2.86	9.71	7.57	3.11
13	P42336	PIK3CA	21	22.8	4.43	4.95	2.23	6.09	5.92	2.59
14	P27986	PIK3R1	19	28.2	4.13	3.61	1.95	4.97	5.83	2.43
15	O00459	PIK3R2	21	40.2	3.88	3.77	1.94	4.59	4.89	2.24
16	P42338	PIK3CB	12	13.4	3.68	2.72	1.68	4.86	3.88	2.13
17	Q96S55	WRNIP1	16	29.8	1.42	1.59	0.59	1.86	2.44	1.10
18	Q15276	RABEP1	22	31.1	1.34	1.51	0.51	1.73	2.31	1.02
19	P16234	PDGFRA	24	24.3	1.52	1.75	0.71	1.10	1.36	0.30
20	Q06124	PTPN11	27	48.4	1.22	1.44	0.41	1.31	2.08	0.76
21	P36896	ACVR1B	4	10.1	1.09	0.87	-0.03	2.80	2.18	1.32
22	Q6ZNH5	ZNF497	2	3.8	0.44	0.69	-0.82	2.13	15.14	3.11
23	P06702	S100A9	9	74.6	0.17	0.05	-3.17	0.07	0.05	-4.12
24	Q13410	BTN1A1	3	9.3	0.27	0.10	-2.44	1.38	0.19	-0.34
25	O95757	HSPA4L	15	21.2	0.20	0.33	-1.93	0.30	0.63	-1.12
26	O14492	SH2B2	5	9.5	6.55	6.69	2.73	7.05	10.85	3.16
27	P19174	PLCG1	69	50	5.63	7.23	2.69	6.06	8.07	2.82
28	Q9H706	GAREM	17	23.9	4.72	4.61	2.22	4.14	5.78	2.31

Users exp. data as node attributes

Table Panel

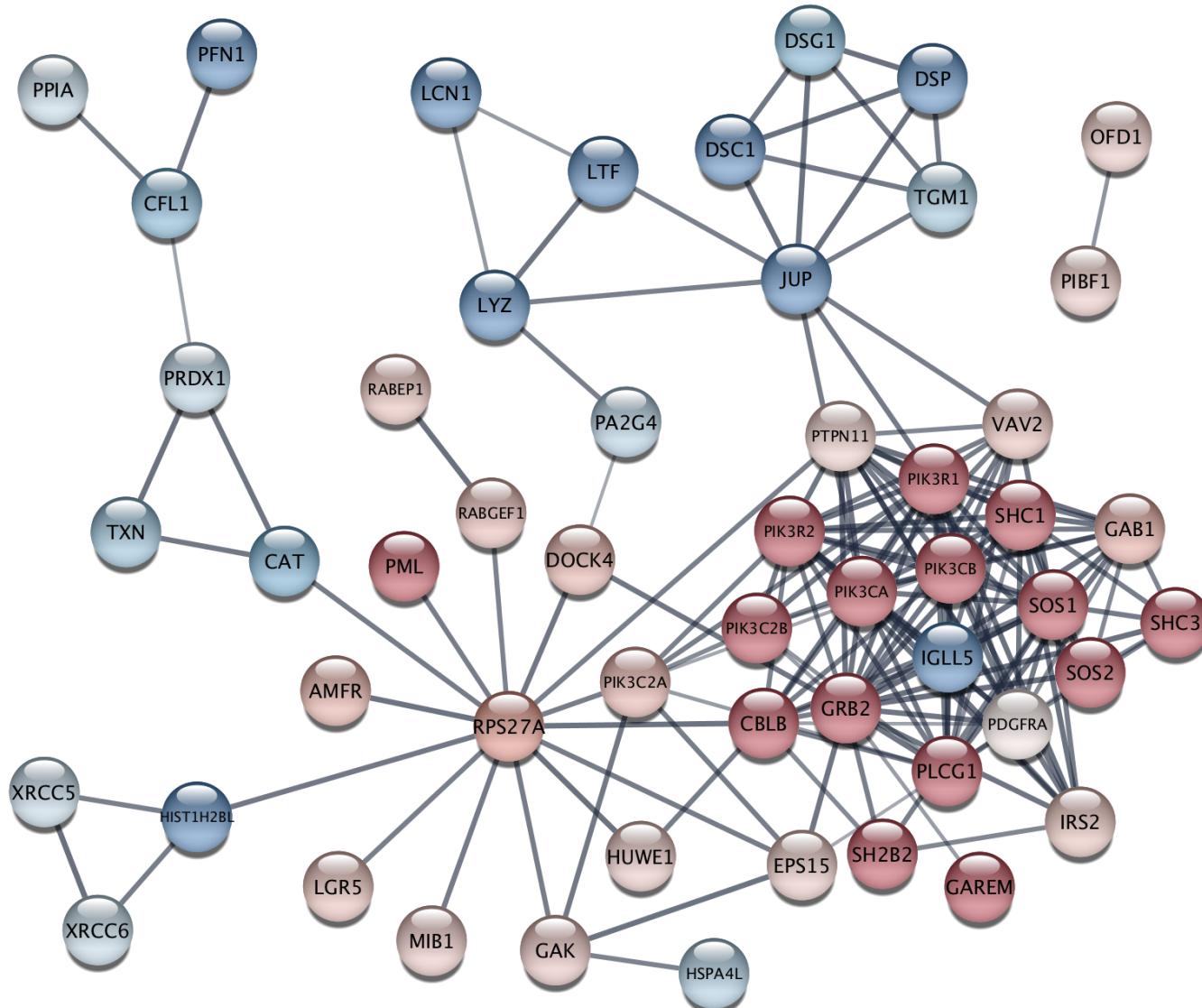
The screenshot shows a 'Table Panel' window with a title bar and a toolbar at the top. The toolbar includes icons for settings, search, add, delete, and refresh, along with a formula input field ($f(x)$) and a refresh button.

The main area is a data grid with the following columns:

query term	Gene name	Peptides	Sequence coverage [%]	10 min log ratio	5 min log ratio	Gene name length
O14976	GAK	25	23.3	0.94	0.38	3
P16234	PDGFRA	24	24.3	0.3	0.71	6
O00443	PIK3C2A	29	17.8	1.26	1.13	7
O00750	PIK3C2B	35	24.2	2.31	2.21	7
P42336	PIK3CA	21	22.8	2.59	2.23	6
P42338	PIK3CB	12	13.4	2.13	1.68	6
Q8N1C5	PIK3R1	19	28.2	2.43	1.95	6
O75473	LGR5	16	22.5	1.0	0.61	4
Q9UKV5	AMFR	8	19.1	1.33	1.51	4

Below the table are several navigation tabs: Node Table, Edge Table, Network Table, STRING Enrichment, and STRING Publications.

Users data mapped to node colors



Functional enrichment

Table Panel

PPI Enrichment: 1.0E-16

category	chart color	term name	description	FDR value	# genes	# background genes	genes
GO Process		GO.0007173	epidermal growth factor receptor s...	2.62E-18	13		52 [PLCG1, GAB1, PIK...
Reactome Pathways		HSA-8853659	RET signaling	3.22E-16	11		38 [PIK3R2, PLCG1, G...
KEGG Pathways		hsa01521	EGFR tyrosine kinase inhibitor resi...	1.13E-15	12		78 [SOS2, PIK3R2, PL...
KEGG Pathways		hsa04012	ErbB signaling pathway	1.13E-15	12		83 [SOS2, PIK3R2, PL...
KEGG Pathways		hsa04722	Neurotrophin signaling pathway	1.13E-15	13		116 [SOS2, PIK3R2, PL...
KEGG Pathways		hsa05214	Glioma	4.44E-15	11		68 [SOS2, PIK3R2, PL...
KEGG Pathways		hsa04072	Phospholipase D signaling pathway	5.65E-15	13		145 [SOS2, PIK3R2, PL...
GO Process		GO.0007169	transmembrane receptor protein t...	2.73E-14	19		499 [PIK3R2, PLCG1, P...
GO Process		GO.0007167	enzyme linked receptor protein sig...	2.96E-14	21		698 [PIK3R2, PLCG1, P...
KEGG Pathways		hsa04650	Natural killer cell mediated cytotox...	3.2E-14	12		124 [SOS2, PIK3R2, PL...

Node Table Edge Table Network Table STRING Enrichment STRING Publications

Functional enrichment

Table Panel

PPI Enrichment: 1.0E-16

category	chart color	term name	description	FDR value	# genes	# background genes	genes
GO Process		GO.0007173	epidermal growth factor receptor s...	2.62E-18	13		52 [PLCG1, GAB1, PIK...
Reactome Pathways		HSA-8853659	RET signaling	3.22E-16	11		38 [PIK3R2, PLCG1, G...
KEGG Pathways		hsa01521	EGFR tyrosine kinase inhibitor resi...	1.13E-15	12		78 [SOS2, PIK3R2, PL...
KEGG Pathways		hsa04012	ErbB signaling pathway	1.13E-15	12		83 [SOS2, PIK3R2, PL...
KEGG Pathways		hsa04722	Neurotrophin signaling pathway	1.13E-15	13		116 [SOS2, PIK3R2, PL...
KEGG Pathways		hsa05214	Glioma	4.44E-15	11		68 [SOS2, PIK3R2, PL...
KEGG Pathways		hsa04072	Phospholipase D signaling pathway	5.65E-15	13		145 [SOS2, PIK3R2, PL...
GO Process		GO.0007169	transmembrane receptor protein t...	2.73E-14	19		499 [PIK3R2, PLCG1, P...
GO Process		GO.0007167	enzyme linked receptor protein sig...	2.96E-14	21		698 [PIK3R2, PLCG1, P...
KEGG Pathways		hsa04650	Natural killer cell mediated cytotox...	3.2E-14	12		124 [SOS2, PIK3R2, PL...

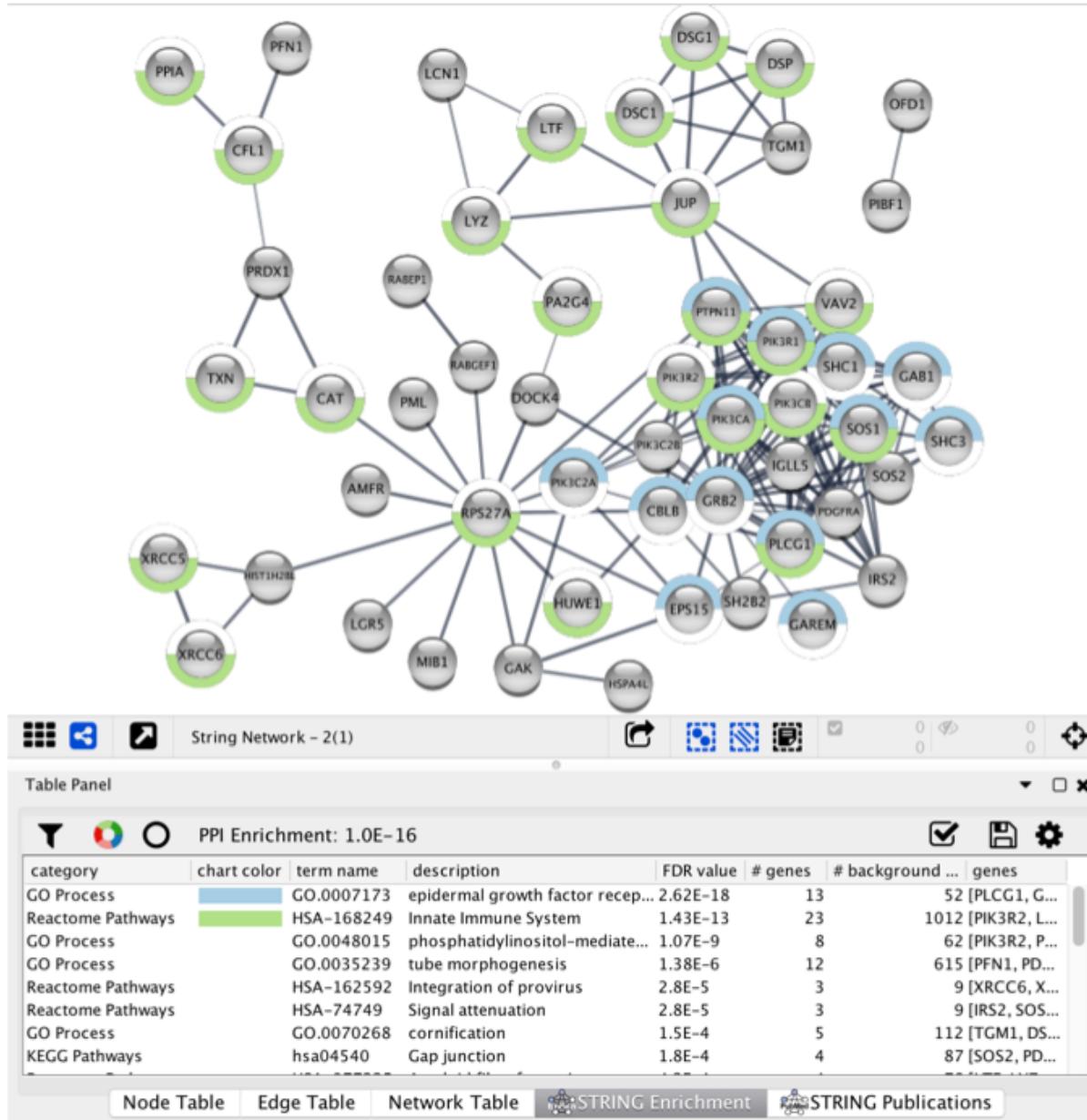
Node Table Edge Table Network Table STRING Enrichment STRING Publications

Table Panel

PMID	year	description	FDR value	# genes	# background...	genes
29693170	2018	Inflammatory genes are novel prognostic biomarkers for col...	2.94E-7	6		13 [PLCG1, PTPN...
29587761	2018	Evaluation of oxidative stress biomarkers in idiopathic pulm...	4.96E-5	5		29 [CAT, PDGFRA...
29229958	2017	EGFR feedback-inhibition by Ran-binding protein 6 is disrupt...	2.94E-7	8		56 [PLCG1, PDGF...
28934129	2017	A Comprehensive Survey of the Roles of Highly Disordered P...	5.56E-6	7		64 [PIK3R2, PIK3...
28857471	2017	Identification of a Potent Phosphoinositide 3-Kinase Pan Inhi...	2.22E-5	5		19 [PIK3CA, PIK3...
28475121	2017	HGFMet Signaling in Cancer Invasion: The Impact on Cytoskel...	4E-5	6		56 [HUWE1, PTPN...
28355572	2017	Precise Temporal Profiling of Signaling Complexes in Primary...	4.56E-5	5		27 [SOS2, CBLB, ...
29332342	2017	Study on the association between PI3KAKTmTOR signaling p...	4.56E-5	4		8 [PIK3R2, PIK3...
27625010	2017	Identification of new key genes for type 1 diabetes through c...	6.45E-5	4		10 [PLCG1, XRCC...
27025927	2016	Changes in Gab2 phosphorylation and interaction partners i...	1.93E-7	7		26 [PIK3R2, PIK3...

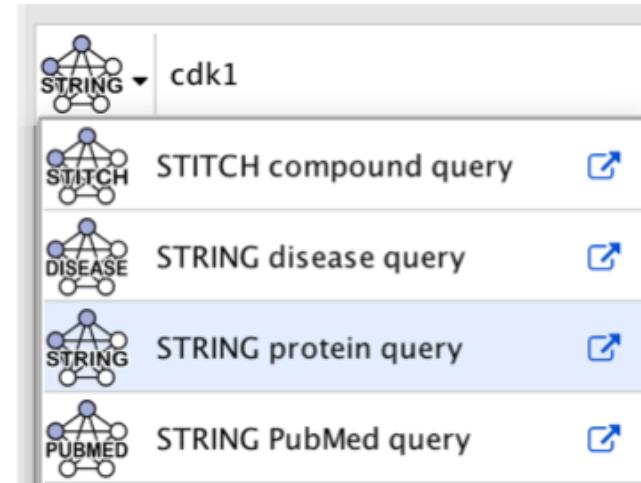
Node Table Edge Table Network Table STRING Enrichment STRING Publications

Functional enrichment



stringApp queries

- **STRING protein query**
 - Queries the STRING database for protein-protein associations for **one** protein or for a **list** of protein identifiers
- **STRING compound query**
 - Queries the STITCH database for protein-compound interactions
- **STRING disease query**
 - Queries the DISEASES database for disease-associated proteins and STRING for interactions between them
- **STRING PubMed query**
 - Retrieves STRING interactions for proteins co-occurring with the query term in PubMed



Install Cytoscape v3.7.2

<https://cytoscape.org/download.html>