

# 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

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# Welcome to STRING

Protein-Protein Interaction Networks  
Functional Enrichment Analysis

ORGANISMS

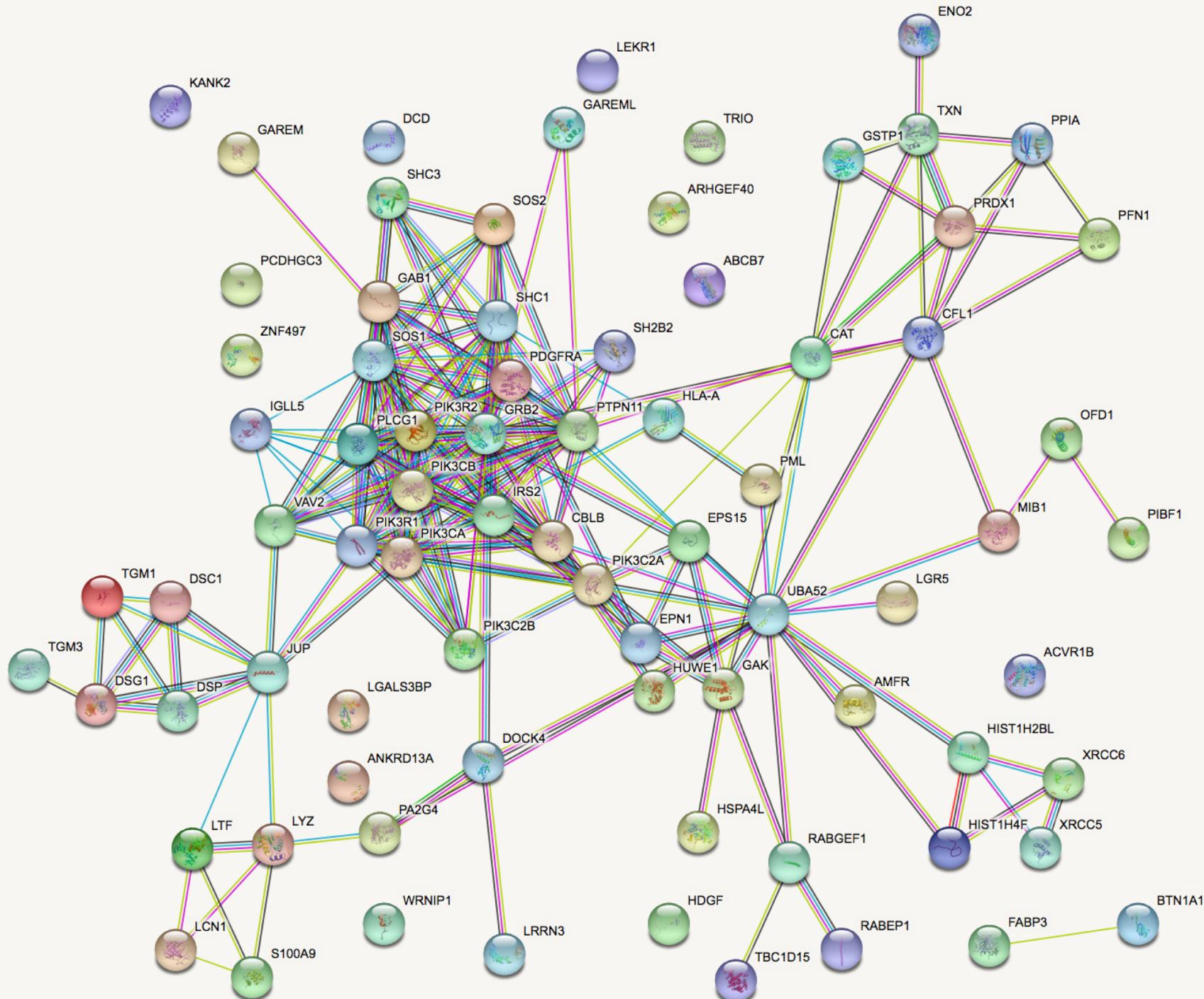
**5090**

PROTEINS

**24.6 mio**

INTERACTIONS

**>2000 mio**[SEARCH](#)



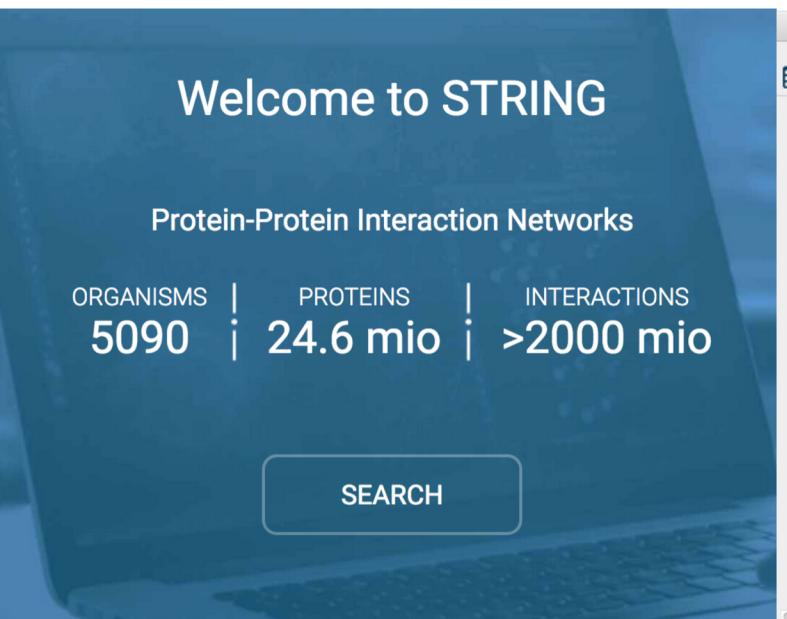
# From STRING to Cytoscape

Welcome to STRING

Protein-Protein Interaction Networks

ORGANISMS | PROTEINS | INTERACTIONS  
5090 | 24.6 mio | >2000 mio

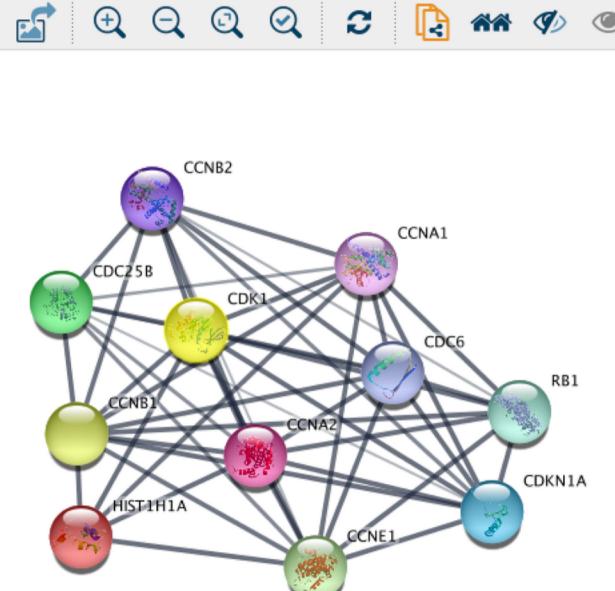
SEARCH



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

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

Session: New Session

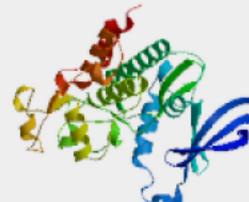


Results Panel

String

Expand All   Collapse All

▼ CDK1  
cyclin-dependent kinase 1



CrossLinks

Uniprot:	<a href="#">P06493</a>
GeneCard:	<a href="#">P06493</a>
Compartments:	<a href="#">9606.ENSP00000378699</a>
Tissues:	<a href="#">9606.ENSP00000378699</a>
Pharos:	<a href="#">P06493</a>

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

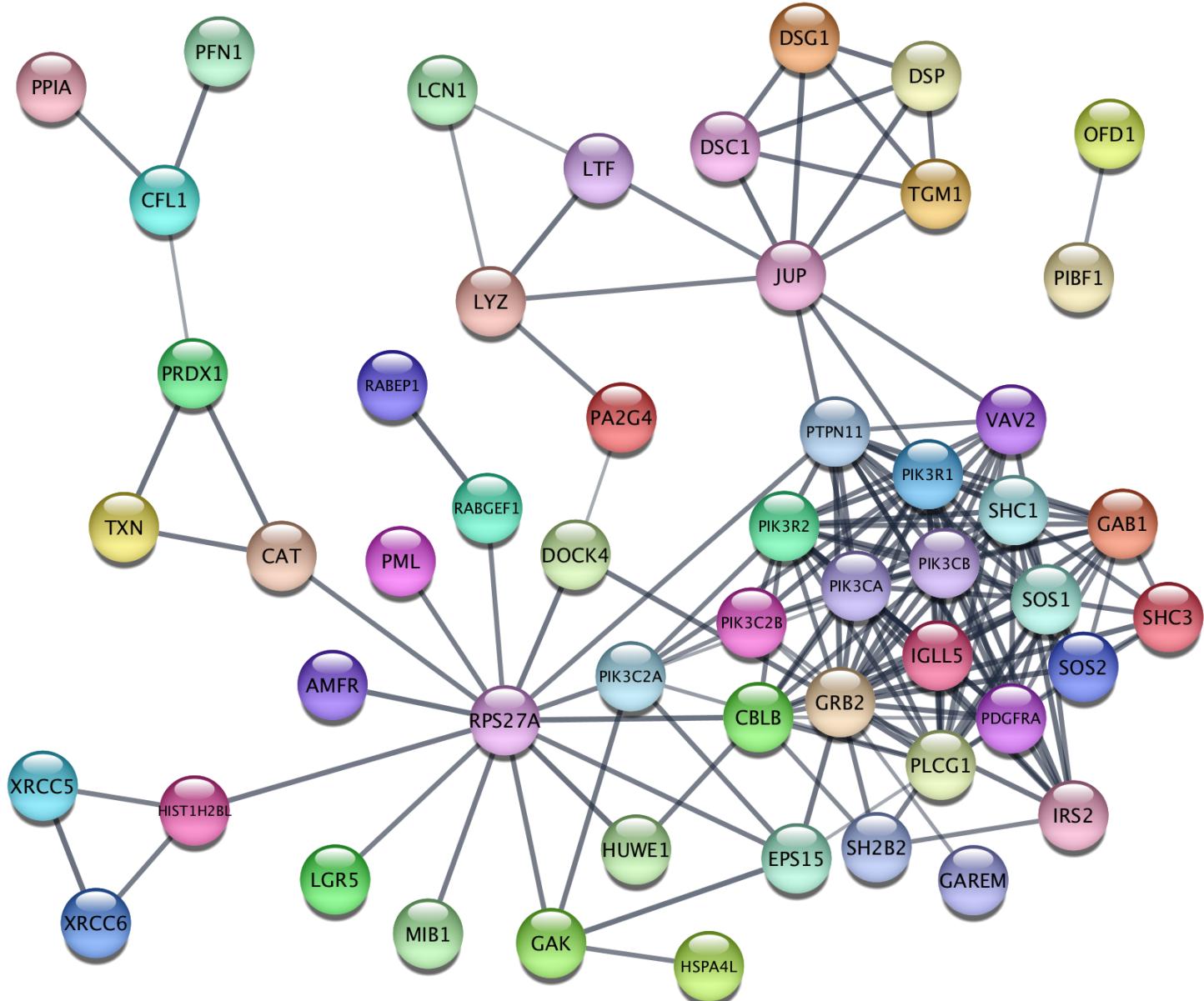
Enter protein names or identifiers:

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

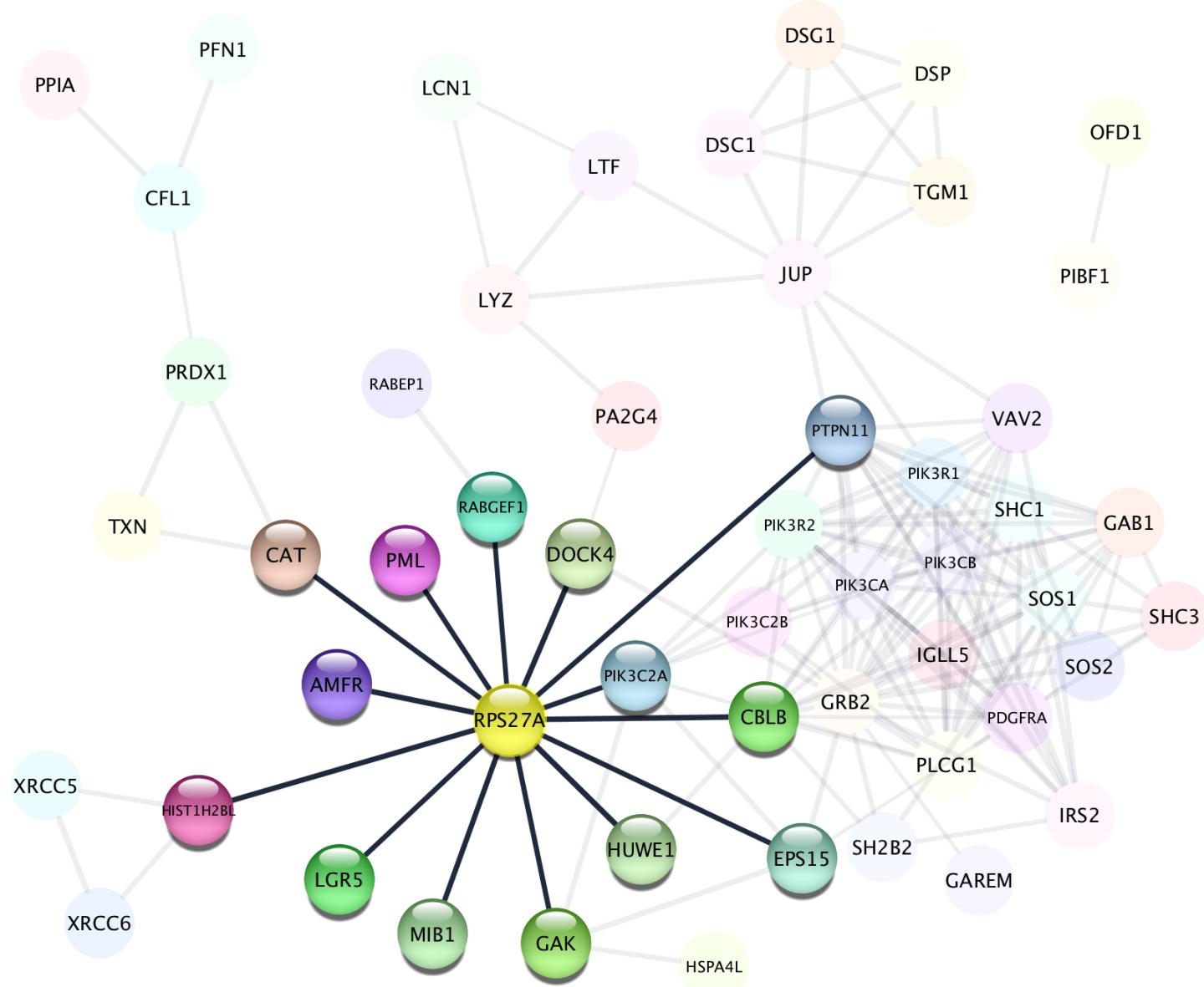
Confidence (score) cutoff:  0.60

Maximum number of interactors:  0

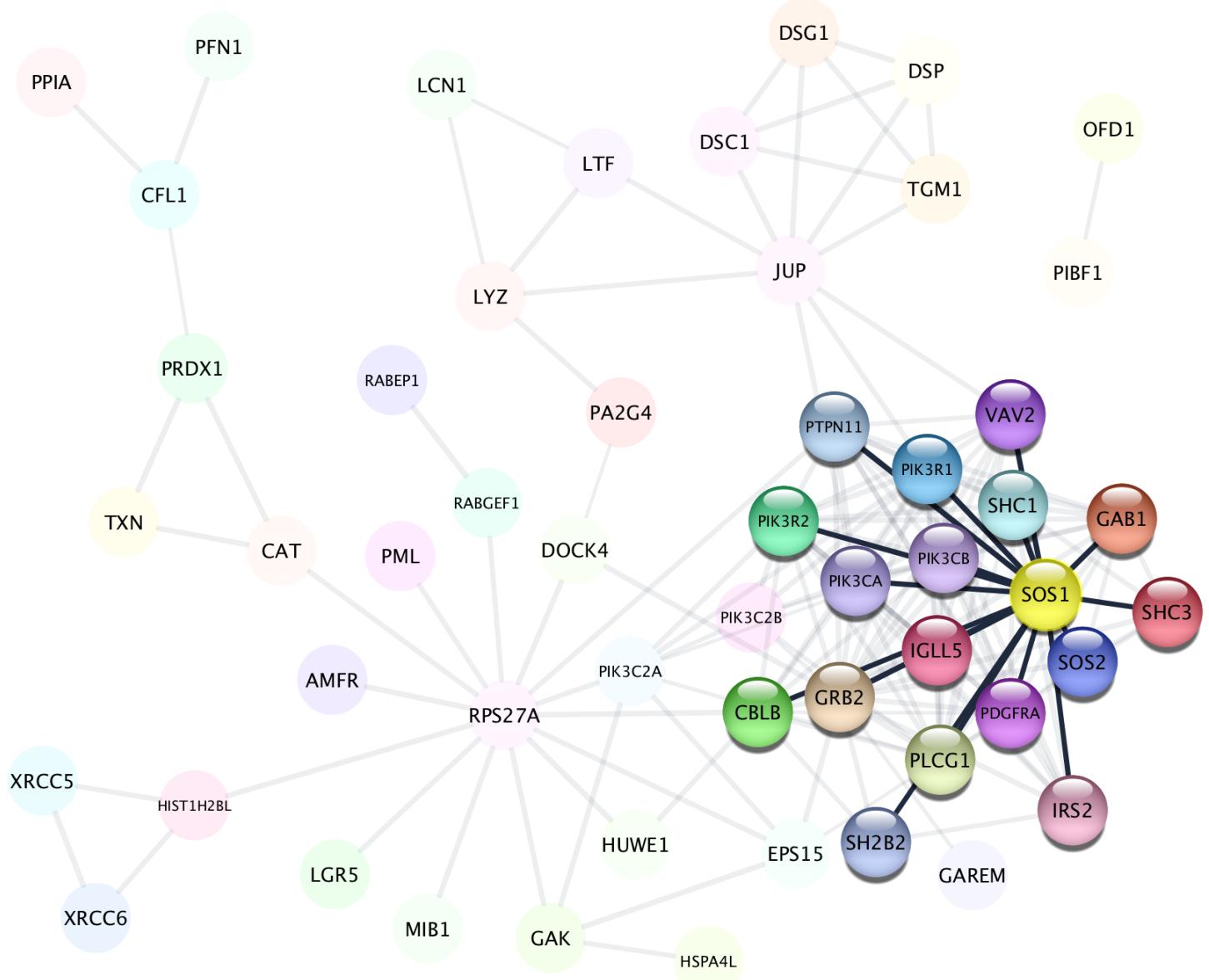
# STRING network in Cytoscape



# First neighbors



# First neighbors



# Additional node annotations

Table Panel

The screenshot shows a 'Table Panel' interface with a header bar containing icons for settings, search, and file operations. Below the header 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	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...	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...	MADSRDPASDQM...	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

The screenshot shows a 'Table Panel' interface with a header bar containing icons for settings, search, and file operations. Below the header is a table with columns for display name, stringdb canonical name, stringdb description, stringdb sequence, compartment (cytosol), compartment (nucleus), tissue (blood), and target family. A sidebar on the right lists target families: Kinase (10 entries) and GPCR (1 entry). At the bottom are navigation tabs: Node Table, Edge Table, Network Table, STRING Enrichment, and STRING Publications.

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	
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	GPCR

- Protein information from STRING
- TISSUES & COMPARTMENTS scores

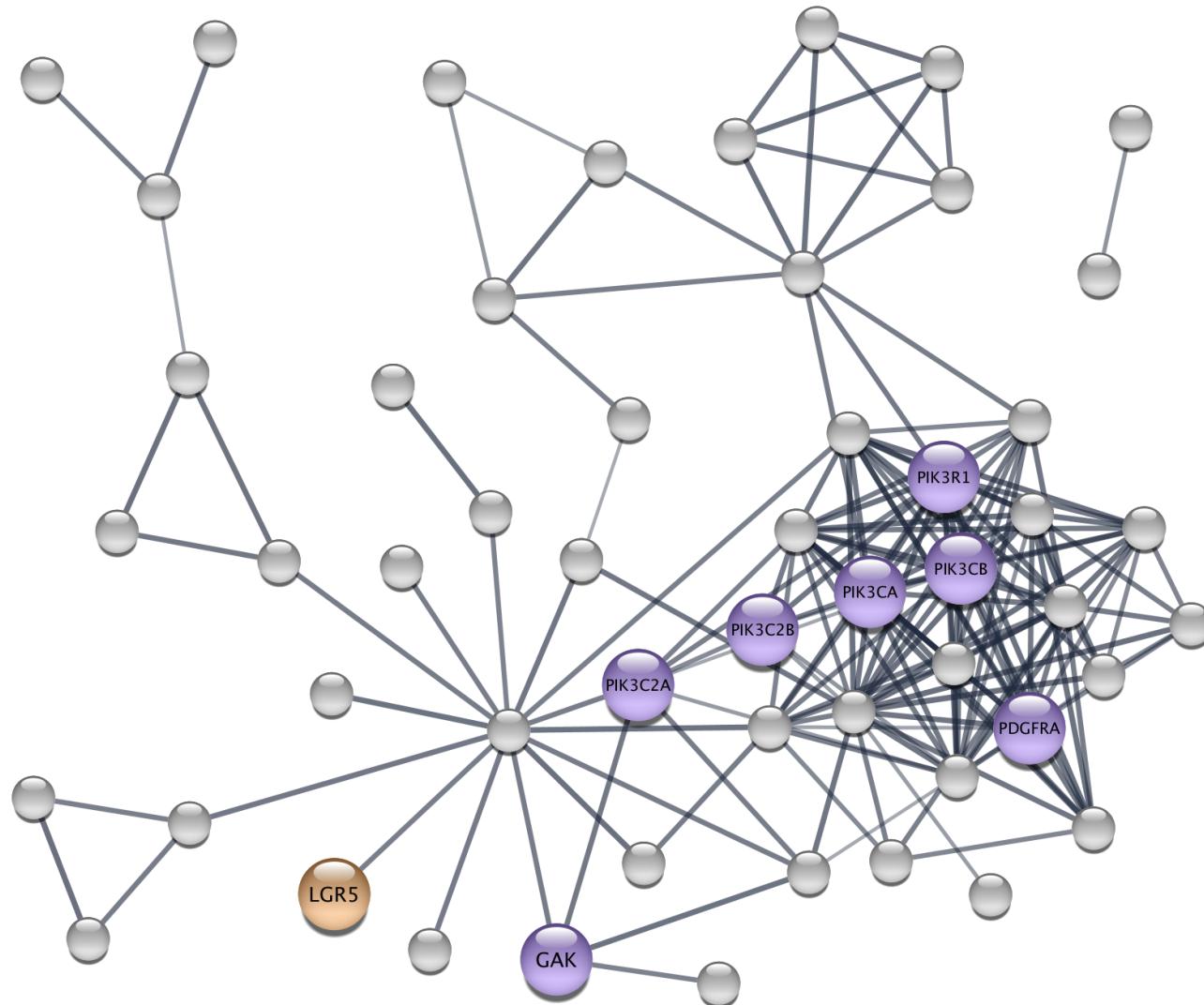
# Additional node annotations

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...	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...	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

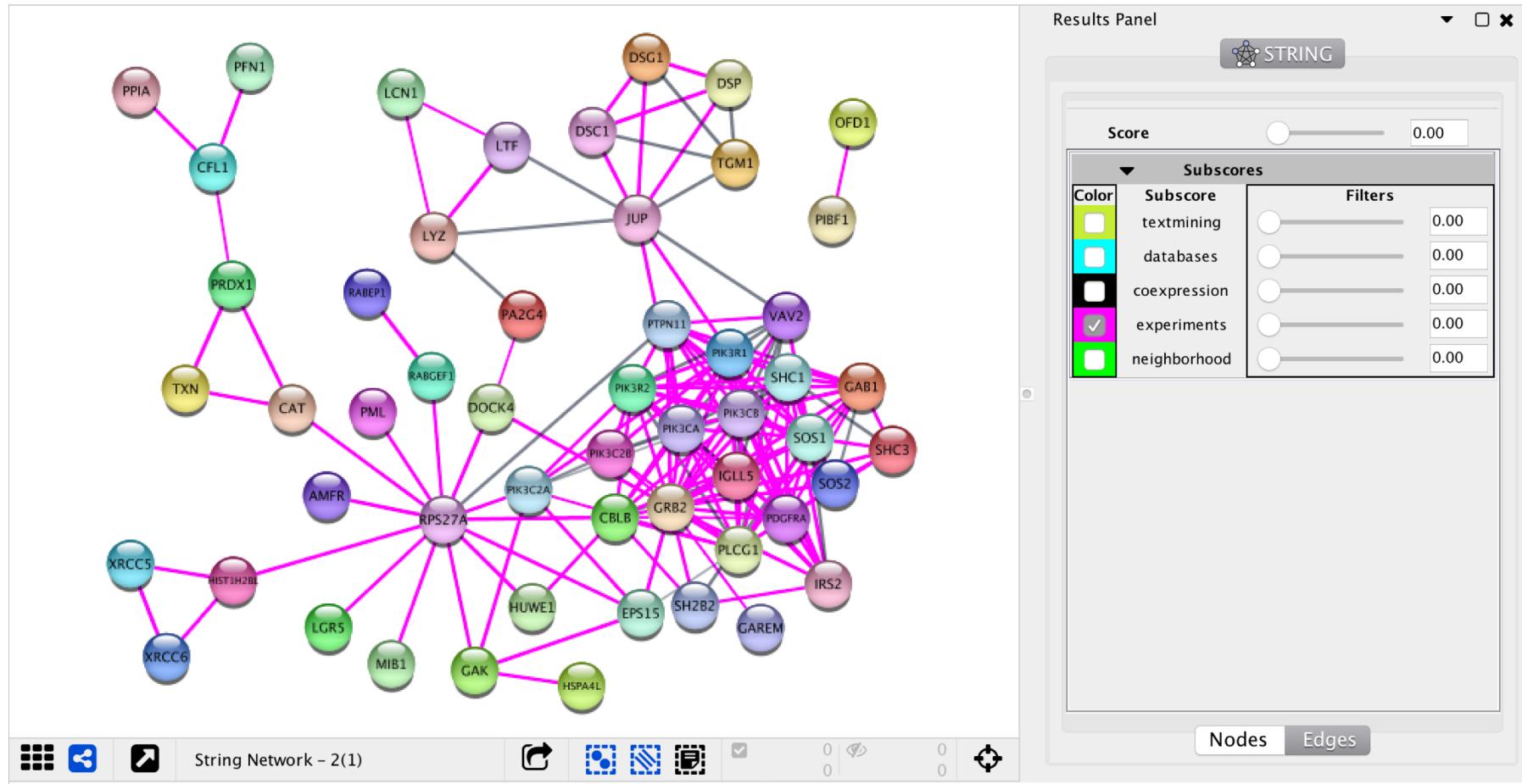
Table Panel

The screenshot shows a 'Table Panel' interface with various tools at the top: gear, square, plus, minus, trash, search, f(x), and refresh. Below is a table with two main sections: 'shared name' and 'shared interaction'. The 'shared name' section lists pairs like GAB1 (pp) SHC3, GAB1 (pp) GRB2, etc. The 'shared interaction' section lists all as 'pp'. The table is annotated with 'stringdb' scores across six databases: score, textmining, databases, coexpression, experiments, and neighborhood. A black box highlights the first row of these headers and the corresponding data for each database.

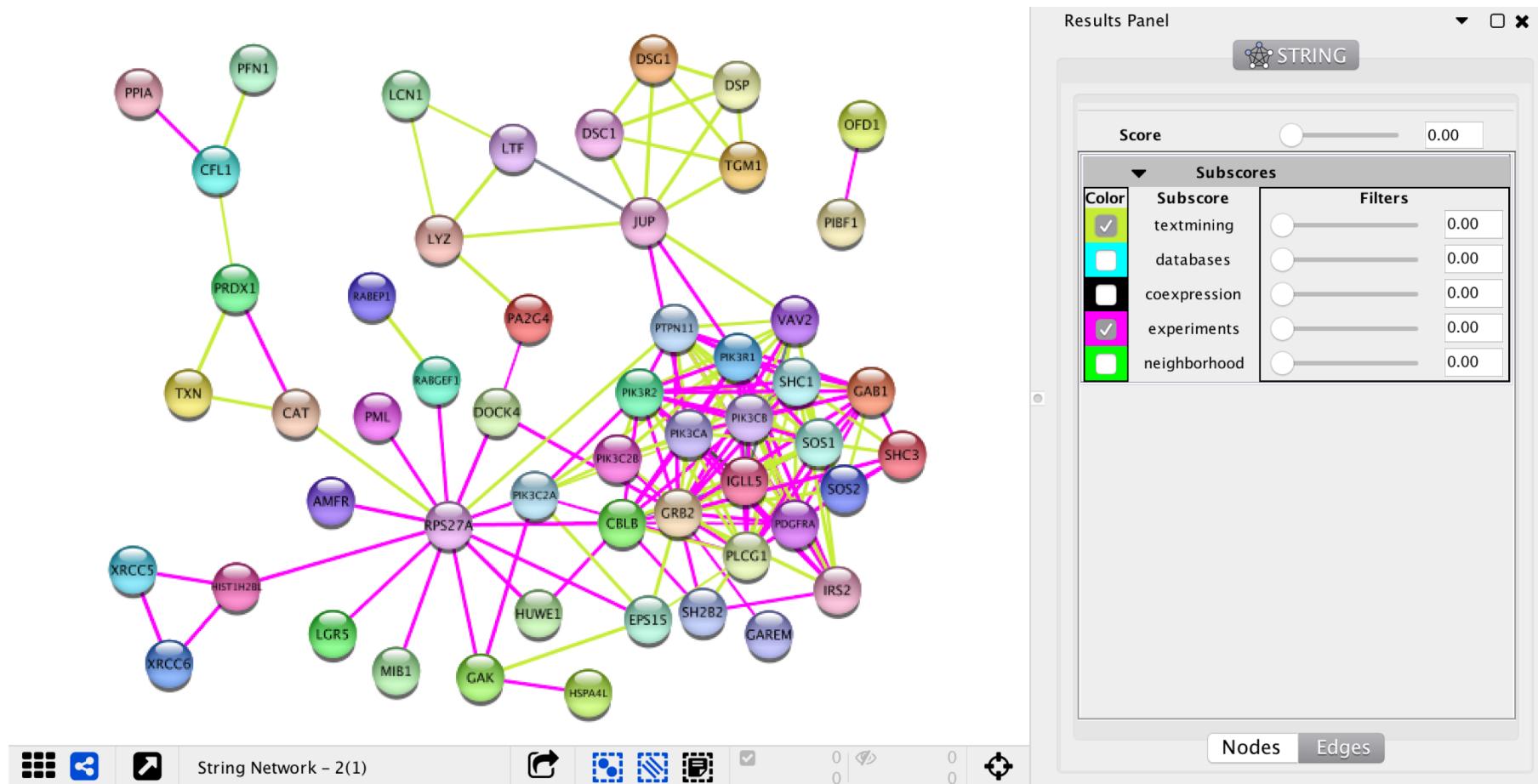
shared name	shared interaction	stringdb	stringdb	stringdb	stringdb	stringdb	stringdb
		score	textmining	databases	coexpression	experiments	neighborhood
GAB1 (pp) SHC3	pp	0.86	0.186	0.8	0.062	0.194	
GAB1 (pp) GRB2	pp	0.996	0.829	0.9	0.052	0.829	
GAB1 (pp) SOS1	pp	0.977	0.338	0.9	0.061	0.687	
GAB1 (pp) 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

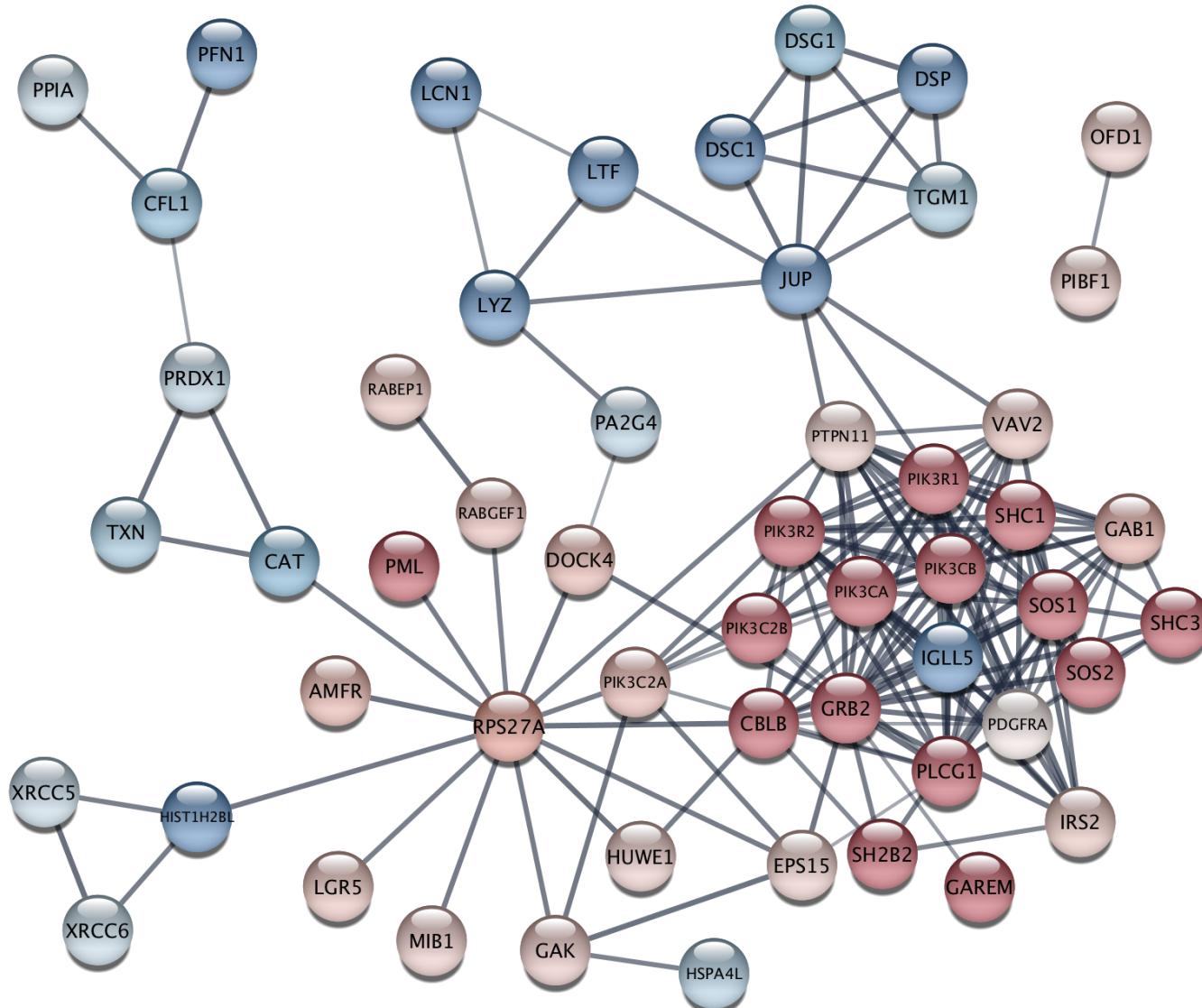
The screenshot shows a 'Table Panel' window with a title bar and a toolbar at the top. The toolbar includes icons for settings, search, add, delete, and refresh, along with a formula input field ( $f(x)$ ) and a refresh button.

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

At the bottom of the panel, there is a navigation bar with five tabs: Node Table, Edge Table, Network Table, STRING Enrichment, and STRING Publications. The 'Node Table' tab is currently selected.

# 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...

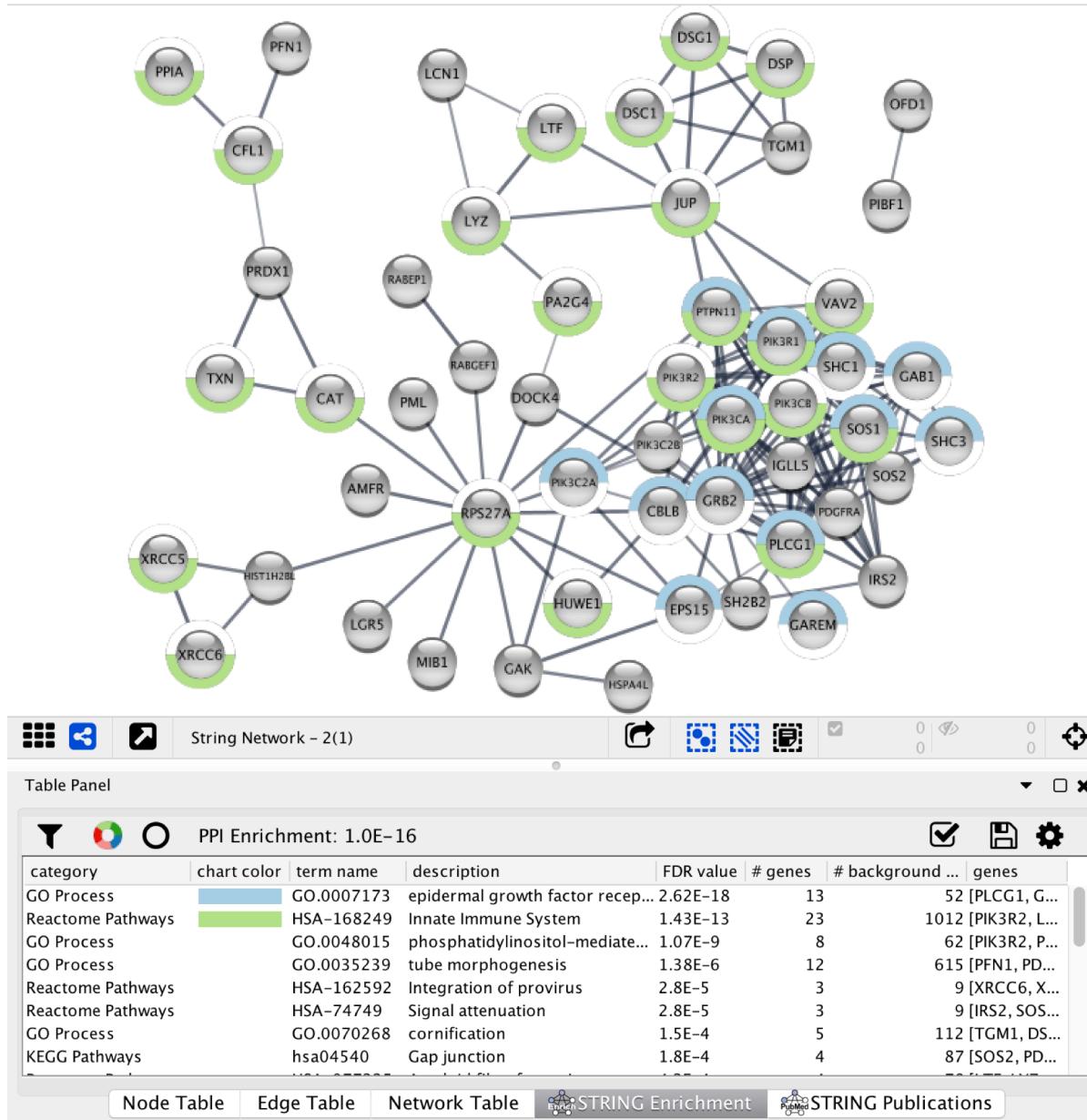
[Node Table](#) [Edge Table](#) [Network Table](#) [STRING Enrichment](#) [PubMed Publications](#)

Table Panel

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

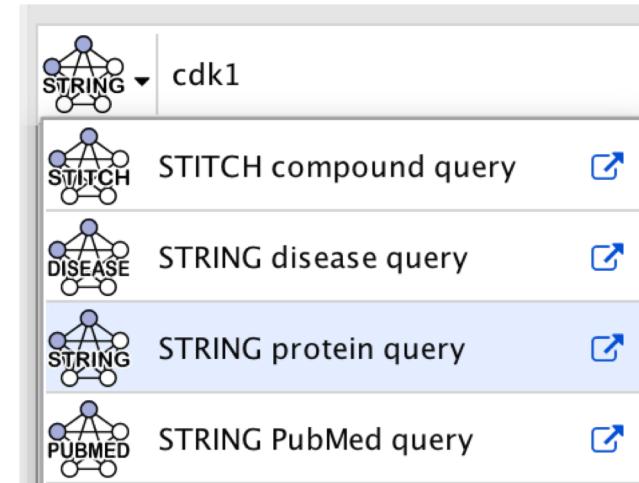
[Node Table](#) [Edge Table](#) [Network Table](#) [STRING Enrichment](#) [PubMed Publications](#)

# 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>