stringApp

Import and augment Cytoscape networks from STRING

★★★★★ (16) 52104 downloads | helpdesk | citations | discussions

Details | Release History

Categories: annotation, automation, data visualization, disease, enrichment analysis, gene-disease association, gene function prediction, import, interaction database, network generation, online data import, PPI-network, visualization

stringApp imports protein-protein and protein-chemical interaction data from STRING, Viruses.STRING, STITCH, DISEASES and from PubMed text mining into Cytoscape. Users provide a list of one or more gene, protein, compound, disease, or PubMed queries, the species, and a confidence score and *stringApp* will query the database and return the matching network. Currently, four different queries are supported:

- STRING: protein query -- enter a list of protein names (e.g. gene symbols or UniProt identifiers/accession numbers) to obtain a STRING network for the proteins
- STRING: PubMed query -- enter a PubMed query and utilize text mining to get a STRING network for the top N proteins associated with the query
- STRING: disease query -- enter a disease name to retrieve a STRING network of the top N proteins associated with the specified disease
- STITCH: protein/compound query -- enter a list of protein or compound names to obtain a network for them from STITCH

CYTOSCAPE 3

Download

Version 1.5.0

Released 10 Sep 2019

Works with Cytoscape 3.7

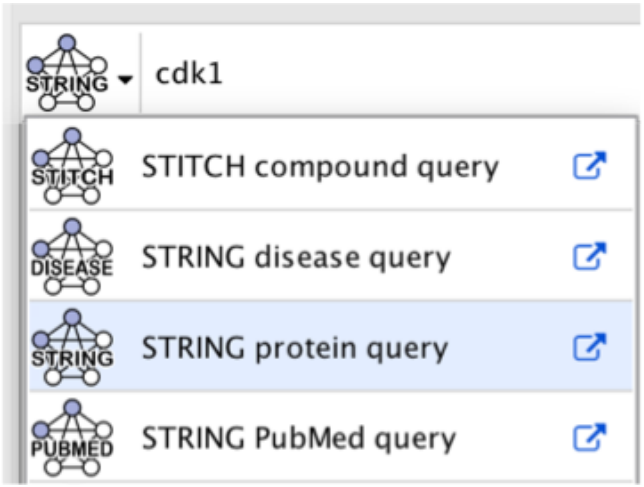
Download Stats Click here

RESOURCES

- Ask a question
- Search helpdesk
- Search BioStars
- Website
- Tutorial
- Cite this App
- Code Repository
- Automation Support
- E-mail

stringApp

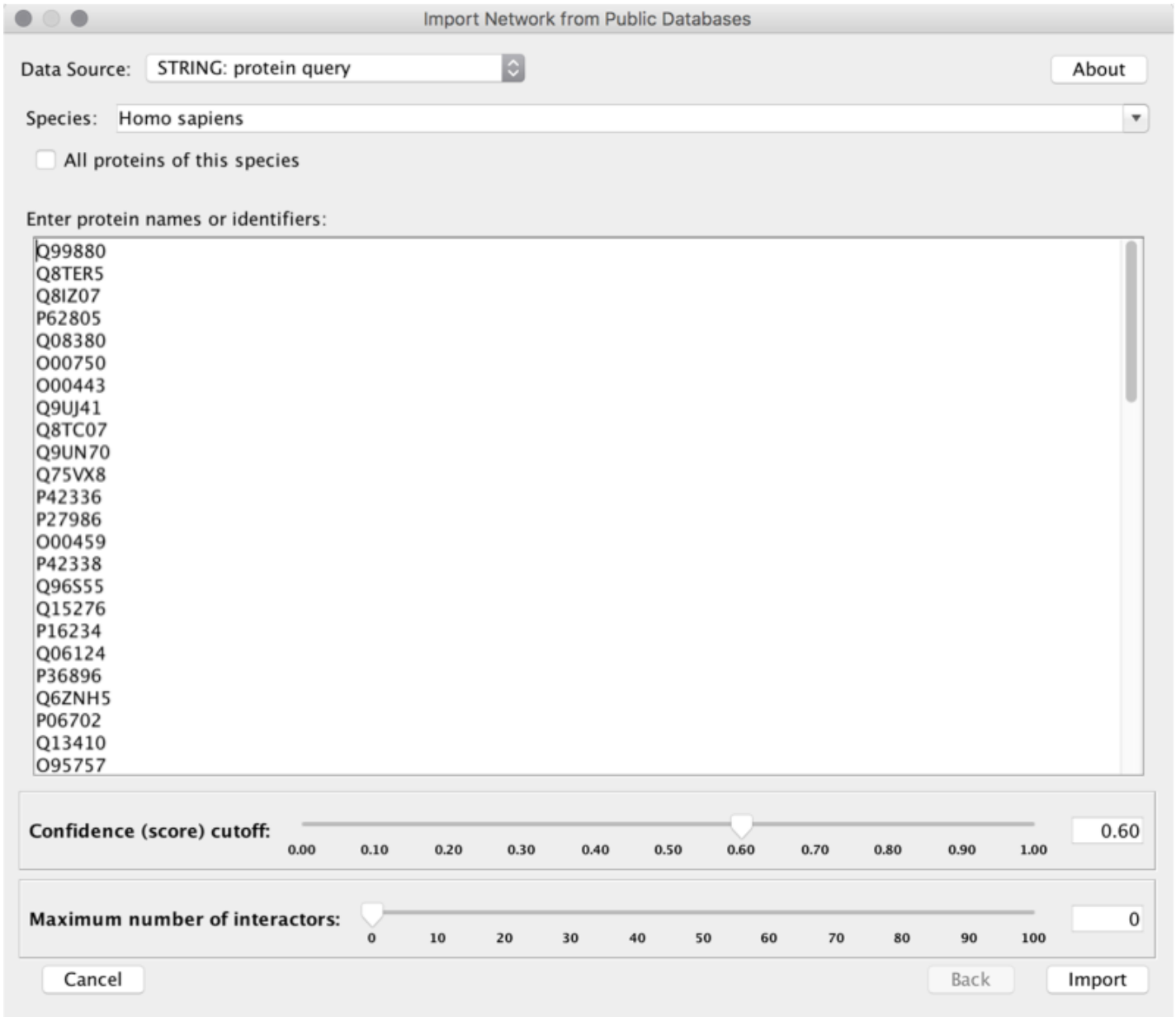
- STRING **protein** query
  - Queries the STRING database for protein-protein associations for **one** protein or for a **list** of protein identifiers
- STRING **compound** query
  - Queries the STITCH database for protein-compound interactions



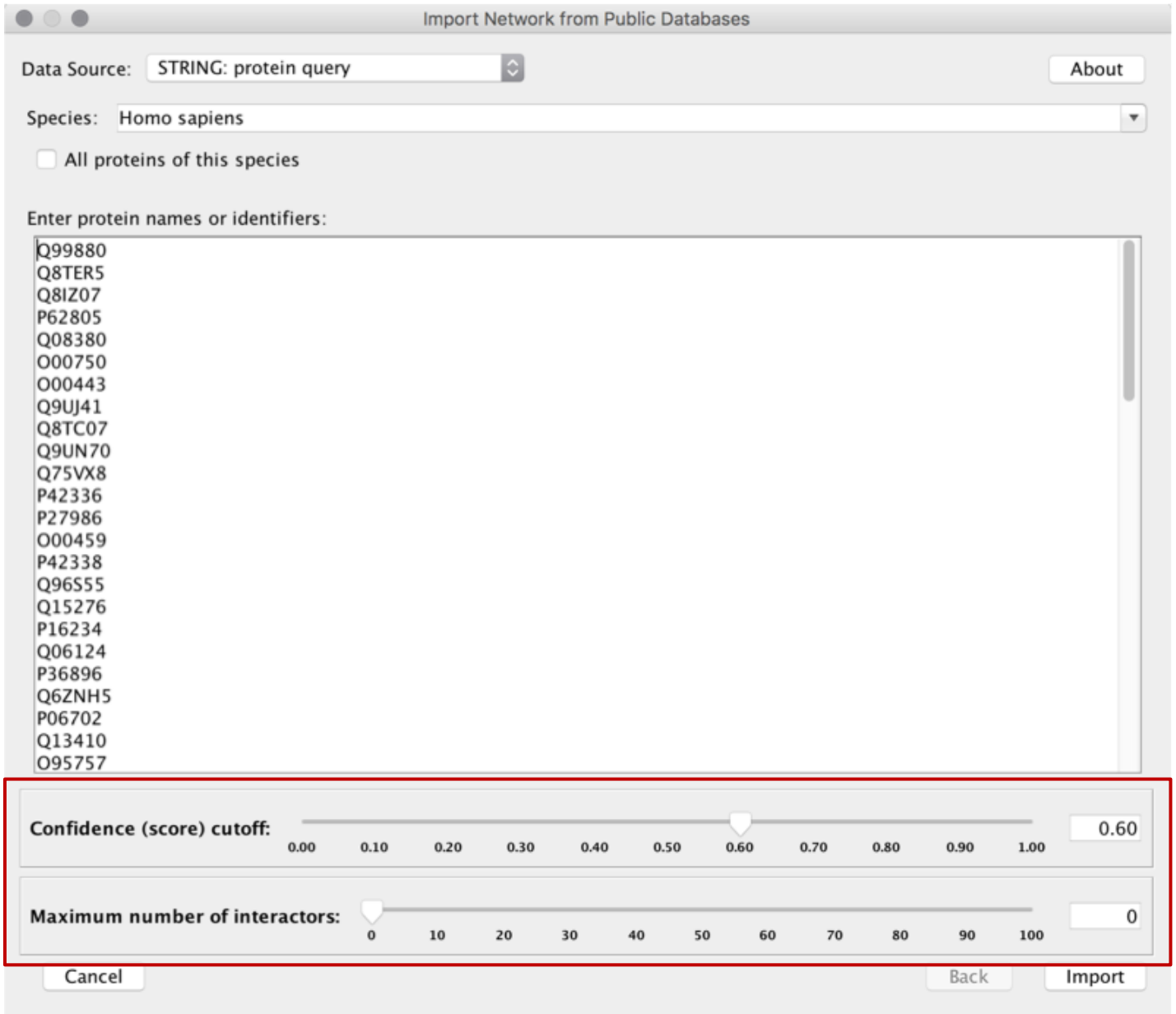
Input table

	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

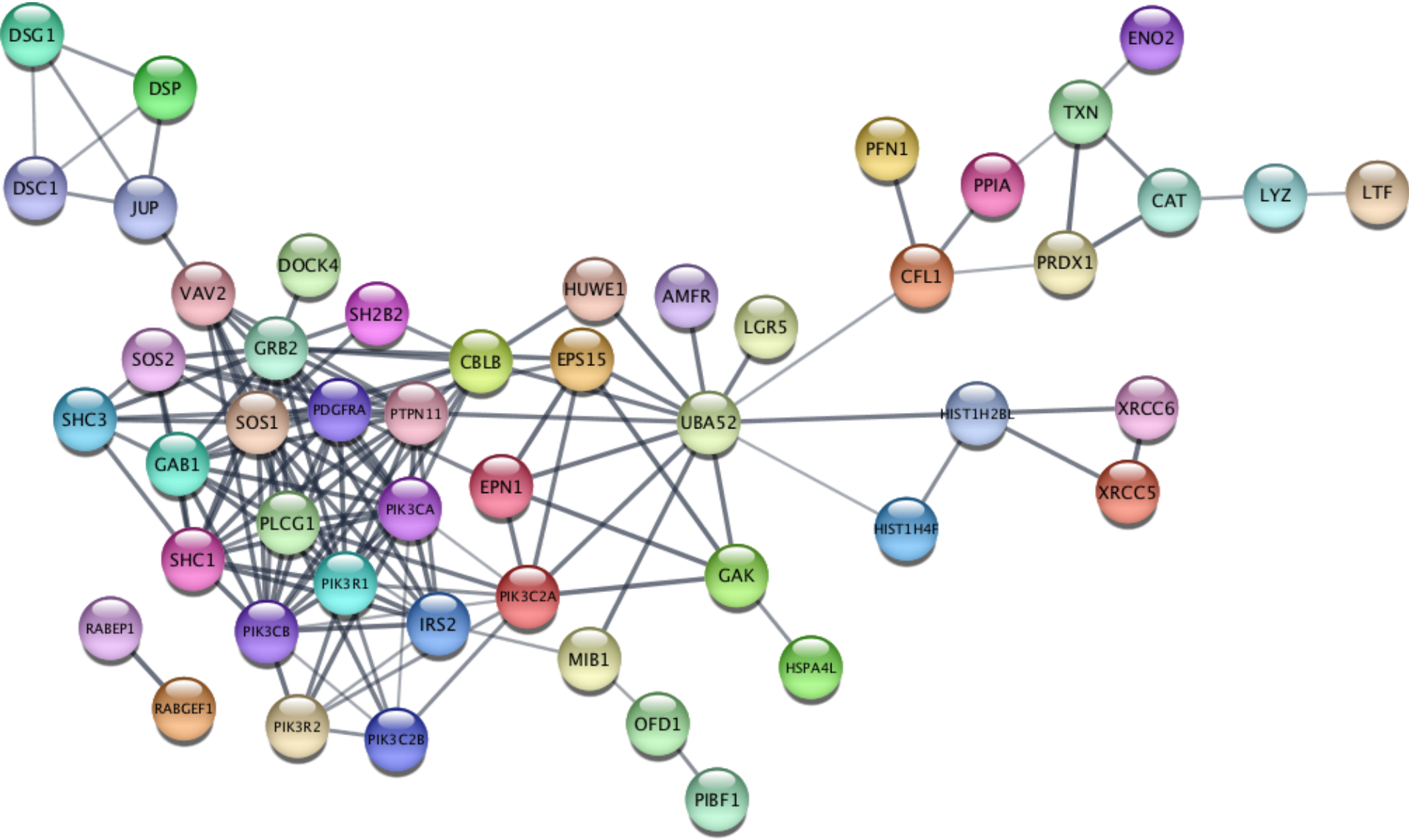
STRING protein query



STRING protein query

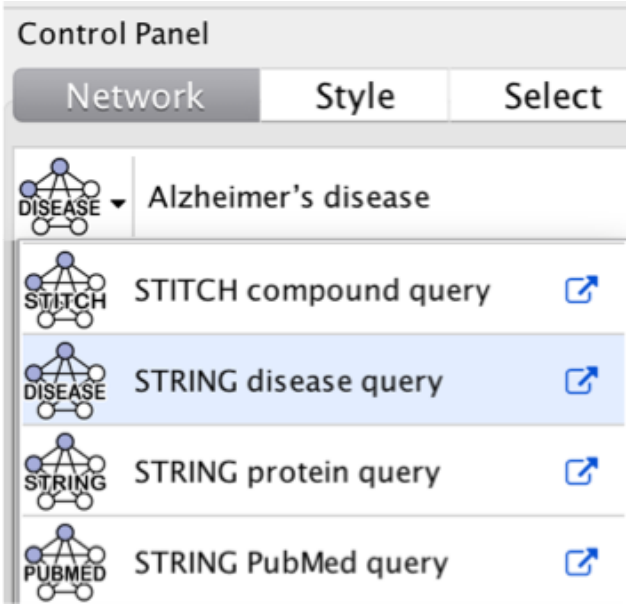


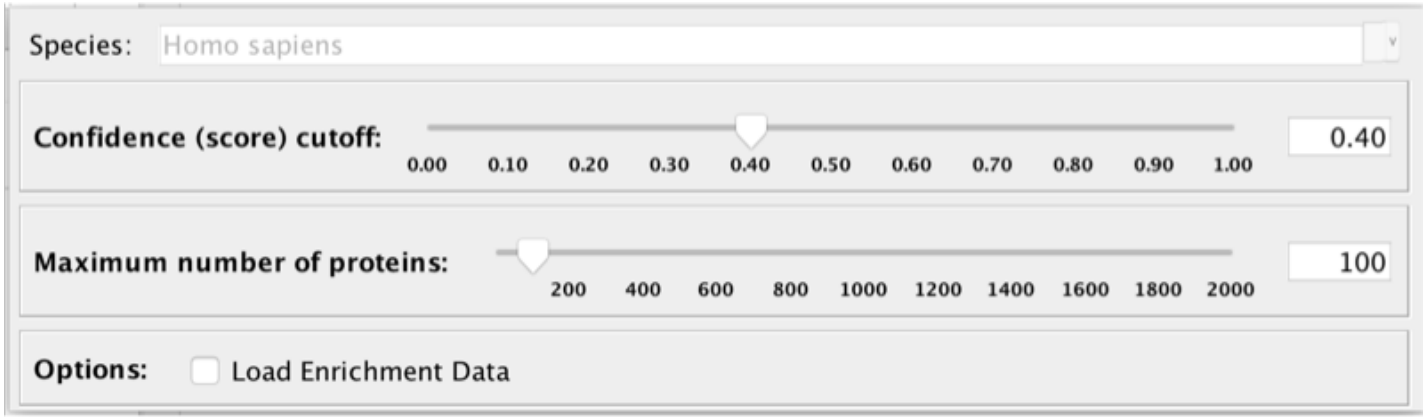
STRING network in Cytoscape



stringApp

- 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





Additional data as node attributes

Table Panel

display name	stringdb canonical name	stringdb description	stringdb sequence	stringdb species	compartment cytoskeleton	compartment cytosol	tissue blood
PHF1	O43189	Polycomb-like prot...	MAQPPRLSRSGAS...	Homo sapiens	5.0	0.326524	0.766667
EDAR	Q9UNE0	Tumor necrosis fac...	MAHVGDCTQTPW...	Homo sapiens		0.328125	0.750488
IL6	P05231	B-cell stimulatory f...	MNSFSTSAFGPVA...	Homo sapiens	2.617751	2.977923	4.0
CREB1	P16220	Cyclic AMP-respon...	MTMESGAENQQS...	Homo sapiens	1.709787	1.861972	3.449199
MS4A5	Q9H3V2	Membrane-spanni...	MDSSTAHSPVFLV...	Homo sapiens			
YWHAQ	P27348	Tyrosine 3-monoo...	MEKTELIQKAKLA...	Homo sapiens	2.200642	4.573817	4.794277
AKT1	P31749	V-akt murine thym...	MSDVAIVKEGWLH...	Homo sapiens	4.742235	5.0	3.61311
ADAM10	O14672	Disintegrin and me...	MVLLRVLILLLSWA...	Homo sapiens	0.905751	0.670166	4.566774
BIN1	O75514	Box-dependent my...	MAEMGSKGVTAG...	Homo sapiens	4.193255	4.589923	4.468784
NCSTN	Q92542	Nicastrin; Essential ...	MATAGGGSGADP...	Homo sapiens	2.584858	0.28125	1.411382
NRGN	Q92686	Neurogranin (prote...	MDCCTENACSKP...	Homo sapiens	1.019197	4.181165	2.951829
GIG25	Q6NSC9	Serpin peptidase in...	MERMLPLLALGLL...	Homo sapiens	2.315754	1.121397	3.634819
SYP	P08247	Major synaptic vesi...	MLLLADMDVVNQ...	Homo sapiens	3.11418	1.395096	1.911957

Node Table | Edge Table | Network Table

- Protein information from STRING
- Assignment of TISSUES & COMPARTMENTS scores
- Pharos drug target information

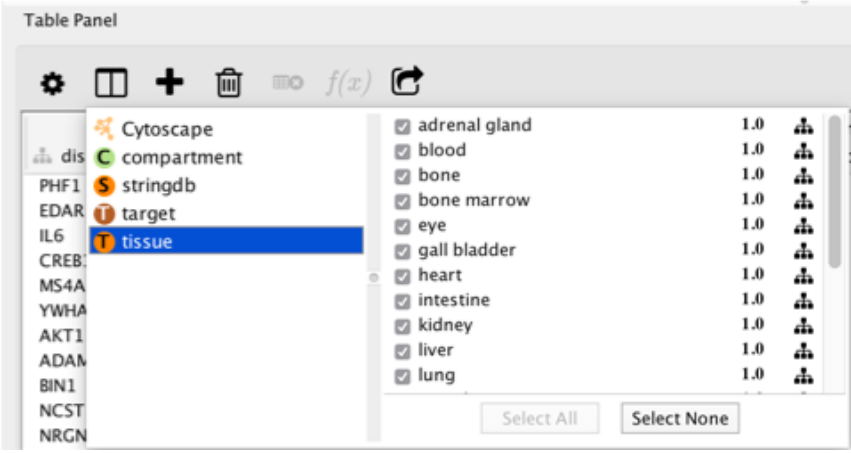
Additional data as node attributes

Table Panel

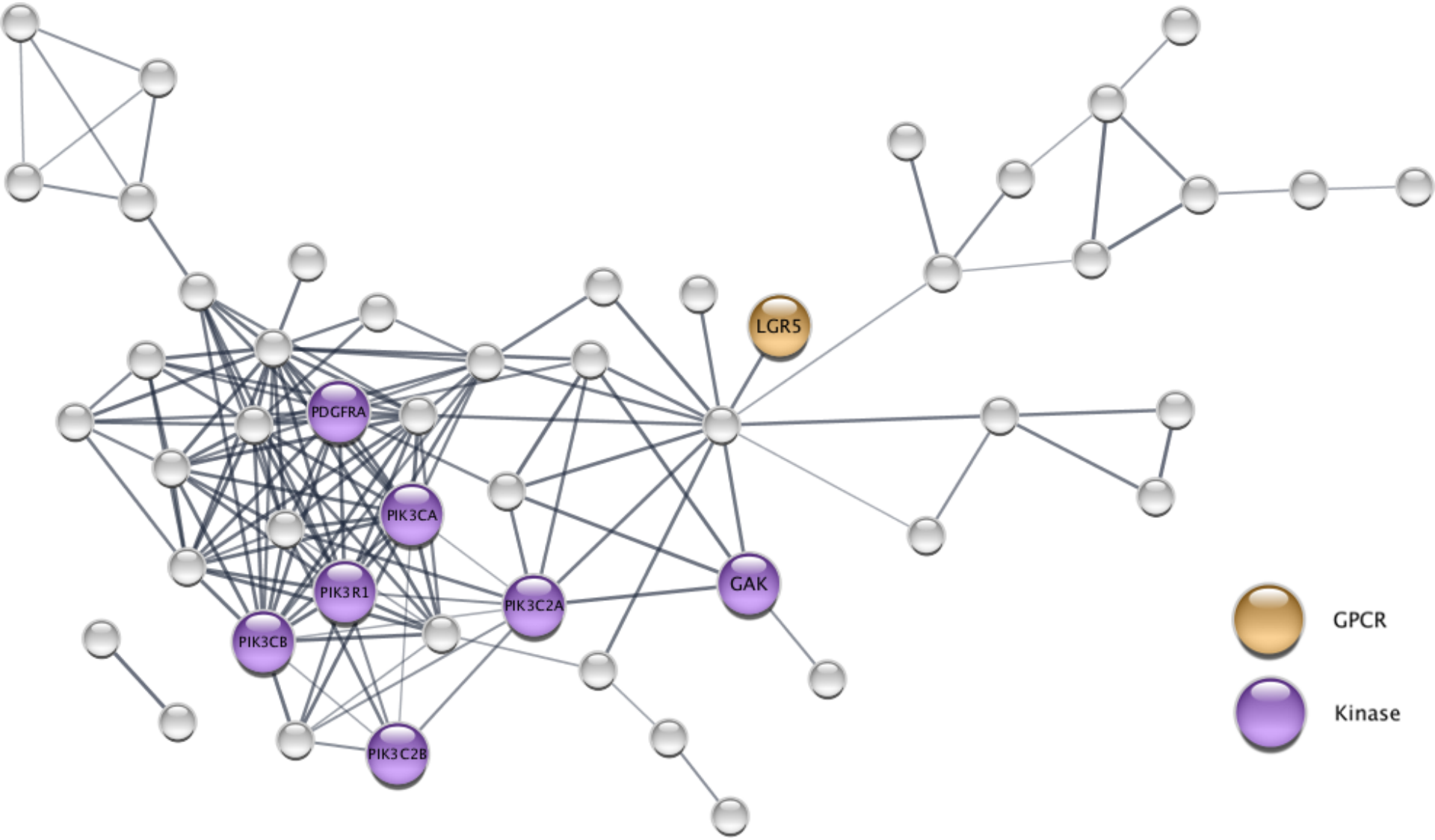
display name	stringdb canonical name	stringdb description	stringdb sequence	stringdb species	compartment cytoskeleton	compartment cytosol	tissue blood
PHF1	O43189	Polycomb-like prot...	MAQPPRLSRSGAS...	Homo sapiens	5.0	0.326524	0.766667
EDAR	Q9UNE0	Tumor necrosis fac...	MAHVGDCTQTPW...	Homo sapiens		0.328125	0.750488
IL6	P05231	B-cell stimulatory f...	MNSFSTSAFGPVA...	Homo sapiens	2.617751	2.977923	4.0
CREB1	P16220	Cyclic AMP-respon...	MTMESGAENQQS...	Homo sapiens	1.709787	1.861972	3.449199
MS4A5	Q9H3V2	Membrane-spanni...	MDSSTAHSPVFLV...	Homo sapiens			
YWHAQ	P27348	Tyrosine 3-monoo...	MEKTELIQKAKLA...	Homo sapiens	2.200642	4.573817	4.794277
AKT1	P31749	V-akt murine thym...	MSDVAIVKEGWLH...	Homo sapiens	4.742235	5.0	3.61311
ADAM10	O14672	Disintegrin and me...	MVLLRVLILLLSWA...	Homo sapiens	0.905751	0.670166	4.566774
BIN1	O75514	Box-dependent my...	MAEMGSKGVTAG...	Homo sapiens	4.193255	4.589923	4.468784
NCSTN	Q92542	Nicastrin; Essential ...	MATAGGGSGADP...	Homo sapiens	2.584858	0.28125	1.411382
NRGN	Q92686	Neurogranin (prote...	MDCCTENACSKP...	Homo sapiens	1.019197	4.181165	2.951829
GIG25	Q6NSC9	Serpin peptidase in...	MERMLPLLALGLL...	Homo sapiens	2.315754	1.121397	3.634819
SYP	P08247	Major synaptic vesi...	MLLLADMDVVNQ...	Homo sapiens	3.11418	1.395096	1.911957

Node Table | Edge Table | Network Table

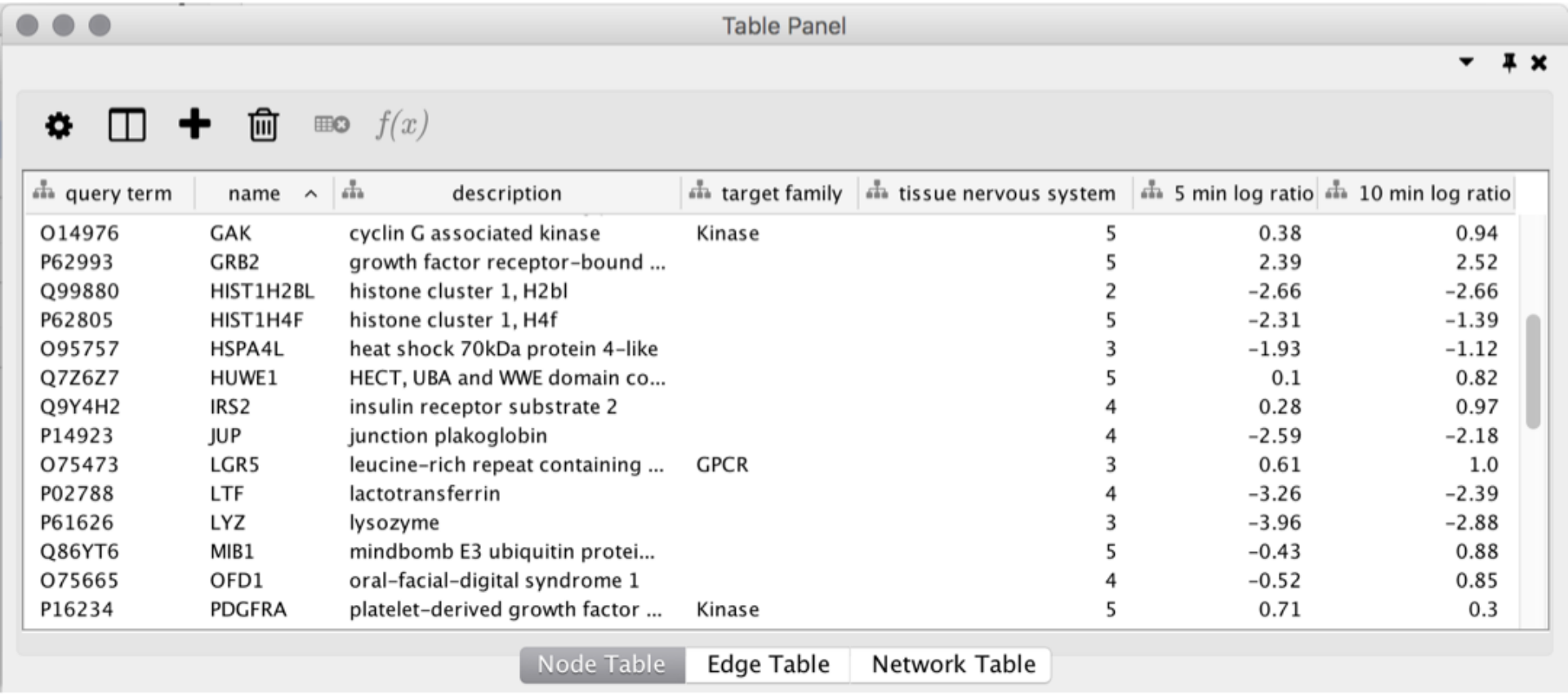
- Protein information from STRING
- Assignment of TISSUES & COMPARTMENTS scores
- Pharos drug target information
- Attributes are grouped into so called **namespaces** *(tissue::blood)*



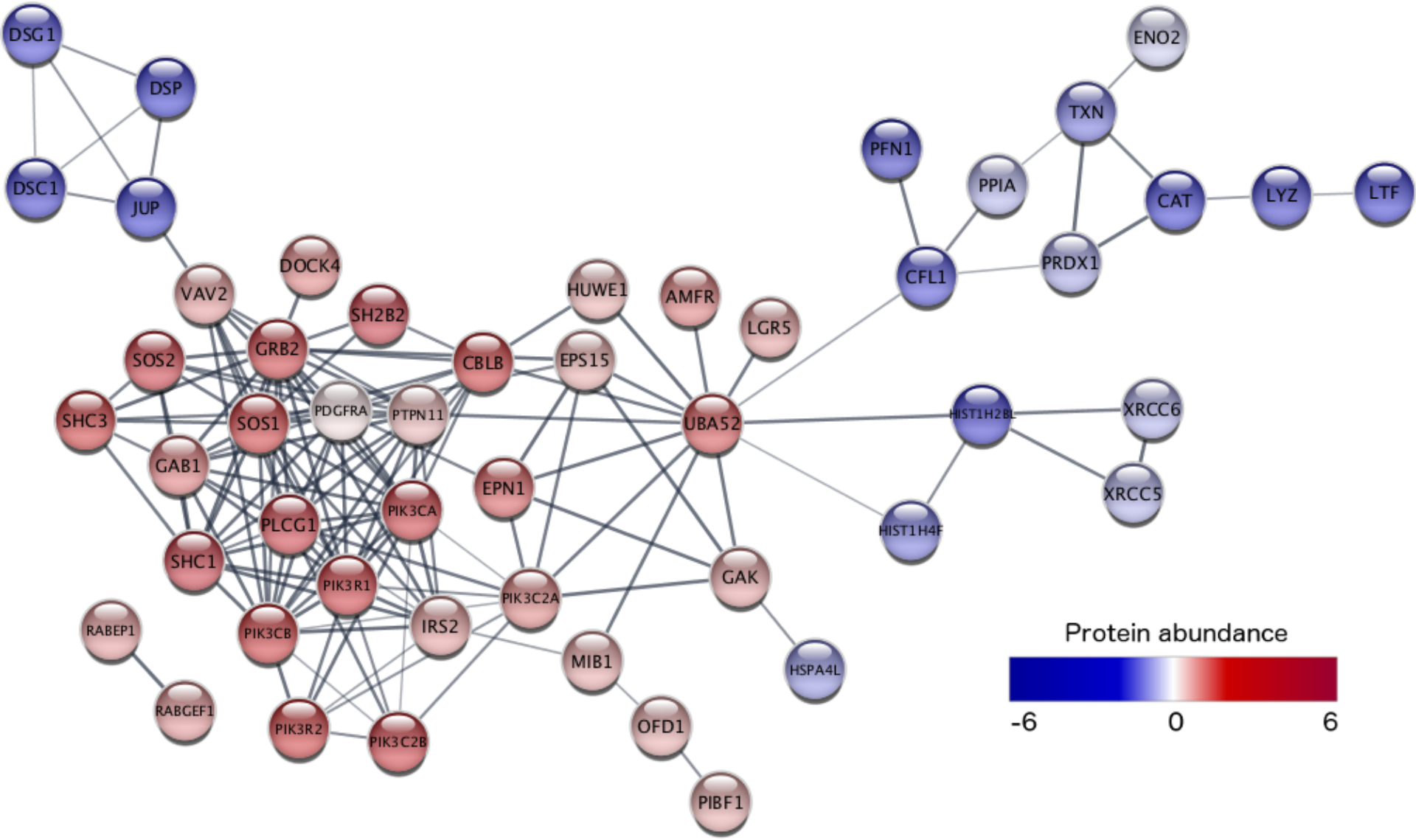
Pharos data mapped to node colors



Users data as node attributes

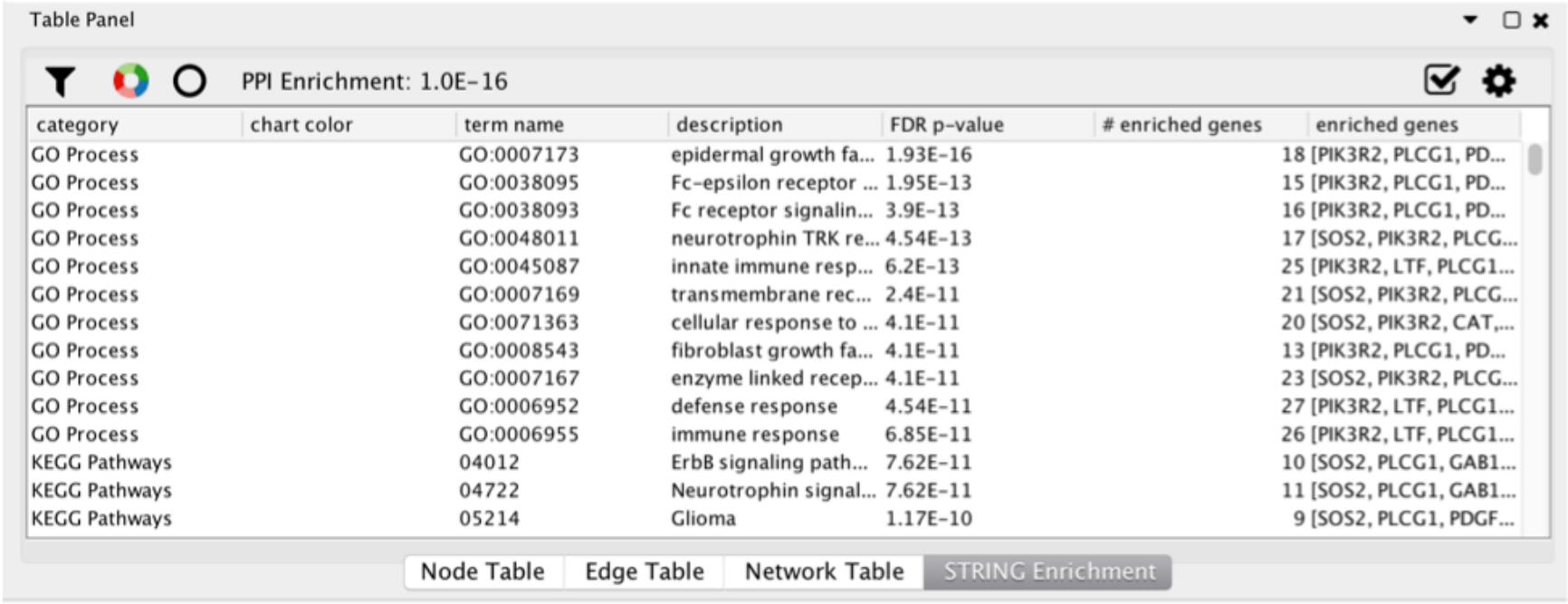


Users data mapped to node colors



Functional enrichment analysis

- Different categories: Gene Ontology terms, KEGG & Reactome Pathways, Protein domains (Pfam, InterPro), Uniprot keywords, PubMed Publications
- Filtering options
- Visualization of the most significant terms



category	chart color	term name	description	FDR p-value	# enriched genes	enriched genes
GO Process		GO:0007173	epidermal growth fa...	1.93E-16	18	[PIK3R2, PLCG1, PD...
GO Process		GO:0038095	Fc-epsilon receptor ...	1.95E-13	15	[PIK3R2, PLCG1, PD...
GO Process		GO:0038093	Fc receptor signalin...	3.9E-13	16	[PIK3R2, PLCG1, PD...
GO Process		GO:0048011	neurotrophin TRK re...	4.54E-13	17	[SOS2, PIK3R2, PLCG...
GO Process		GO:0045087	innate immune resp...	6.2E-13	25	[PIK3R2, LTF, PLCG1...
GO Process		GO:0007169	transmembrane rec...	2.4E-11	21	[SOS2, PIK3R2, PLCG...
GO Process		GO:0071363	cellular response to ...	4.1E-11	20	[SOS2, PIK3R2, CAT,...
GO Process		GO:0008543	fibroblast growth fa...	4.1E-11	13	[PIK3R2, PLCG1, PD...
GO Process		GO:0007167	enzyme linked recep...	4.1E-11	23	[SOS2, PIK3R2, PLCG...
GO Process		GO:0006952	defense response	4.54E-11	27	[PIK3R2, LTF, PLCG1...
GO Process		GO:0006955	immune response	6.85E-11	26	[PIK3R2, LTF, PLCG1...
KEGG Pathways		04012	ErbB signaling path...	7.62E-11	10	[SOS2, PLCG1, GAB1...
KEGG Pathways		04722	Neurotrophin signal...	7.62E-11	11	[SOS2, PLCG1, GAB1...
KEGG Pathways		05214	Glioma	1.17E-10	9	[SOS2, PLCG1, PDGF...

Functional enrichment analysis

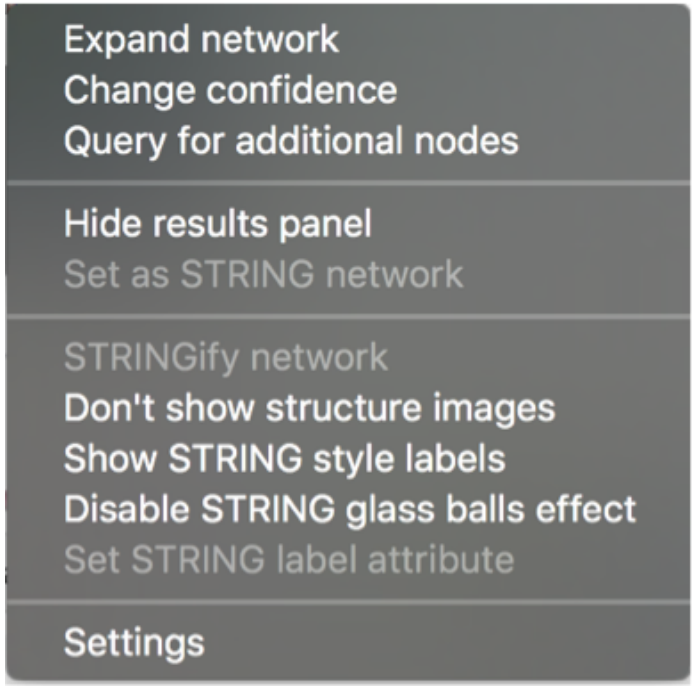
Table Panel

PPI Enrichment: 1.0E-16

category	chart color	term name	description	FDR p-value	# enriched genes	enriched genes
GO Process		GO:0007173	epidermal growth fa...	1.93E-16	18	[PIK3R2, PLCG1, PD...
GO Process		GO:0038095	Fc-epsilon receptor ...	1.95E-13	15	[PIK3R2, PLCG1, PD...
GO Process		GO:0038093	Fc receptor signalin...	3.9E-13	16	[PIK3R2, PLCG1, PD...
GO Process		GO:0048011	neurotrophin TRK re...	4.54E-13	17	[SOS2, PIK3R2, PLCG...
GO Process		GO:0045087	innate immune resp...	6.2E-13	25	[PIK3R2, LTF, PLCG1...
GO Process		GO:0007169	transmembrane rec...	2.4E-11	21	[SOS2, PIK3R2, PLCG...
GO Process		GO:0071363	cellular response to ...	4.1E-11	20	[SOS2, PIK3R2, CAT,...
GO Process		GO:0008543	fibroblast growth fa...	4.1E-11	13	[PIK3R2, PLCG1, PD...
GO Process		GO:0007167	enzyme linked recep...	4.1E-11	23	[SOS2, PIK3R2, PLCG...

Node Table | Edge Table | Network Table | STRING Enrichment

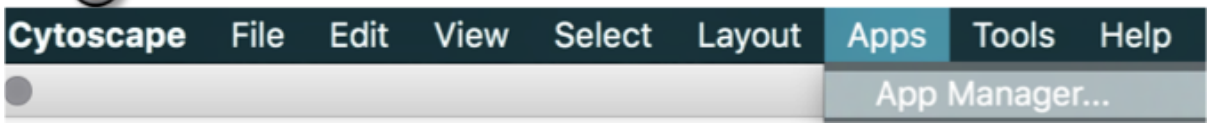
More stringApp features

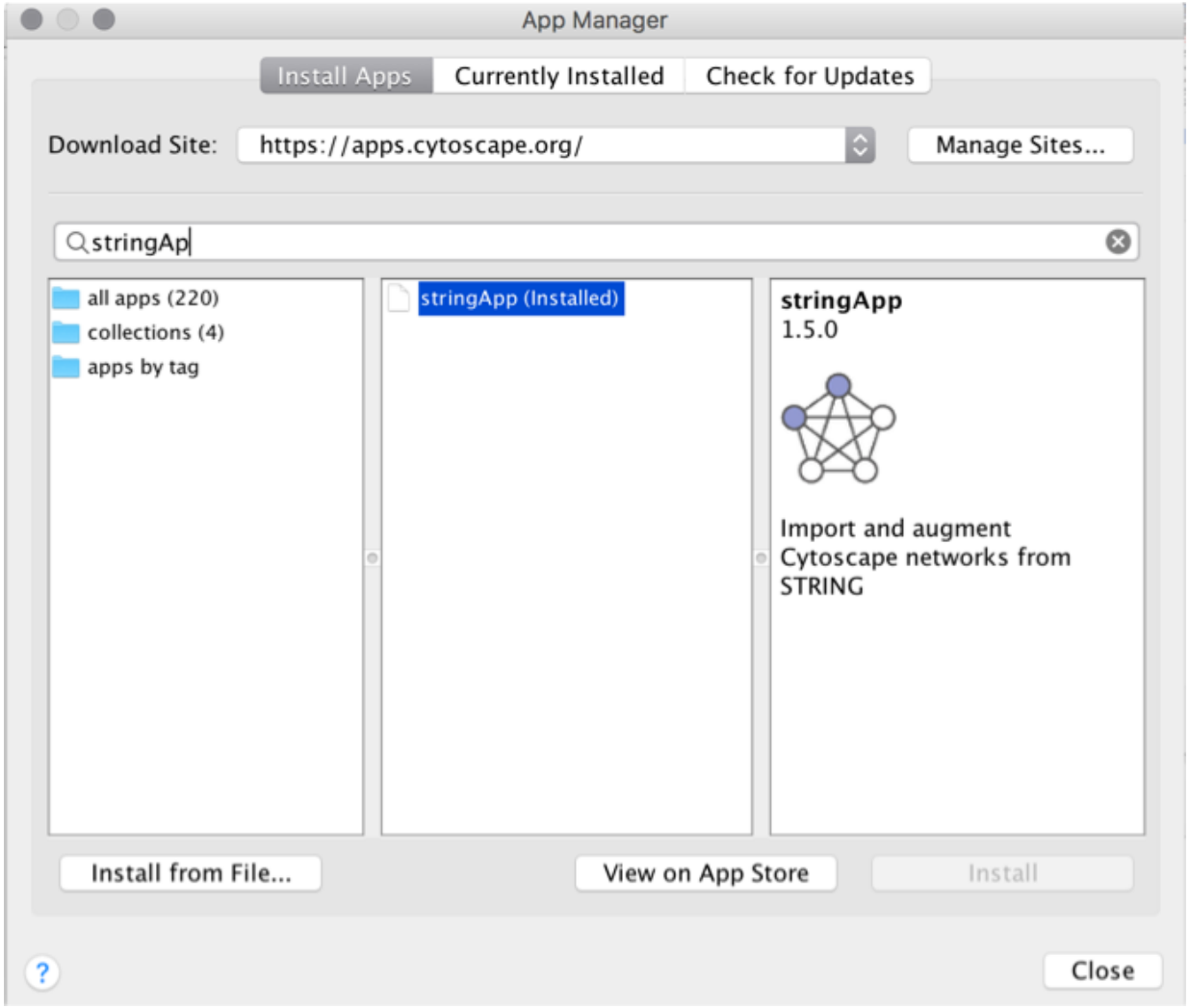


- Change confidence level of interactions
- Expand network by a user defined number of additional interactors
- Query virus-host interactions
- Explore node and edge attributes from the new Results Panel
- Stringify networks not created with the stringApp
- Retrieve enriched publications

Do you want to try it out yourself?

Install apps





Getting to know the stringApp

Exercises 2 & 3

http://jensenlab.org/training/stringapp/