

Tabloid Proteome

Version 2.0

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1. How to search the online Tabloid Proteome database

With the online Tabloid Proteome, you can search for protein association in five ways: Protein Search, Gene Search, Pathway Search, Disease Search and Tissue Search.

Tabloid Proteome is a database of protein association network generated using publically available mass spectrometry based experiments in PRIDE. These associations represent a broad scala of biological associations between pairs of proteins that goes well beyond mere binary protein interactions. [More info](#)

Protein Search

> Single Protein Search

> Two Protein Search

> Multiple Protein Pair Search

Gene Search

> Single Gene Search

> Two Gene Search

> Multiple Search

Pathway Search

Disease Search

Tissue Search

PROTEIN SEARCH

[Q13330](#), [P08134](#)

Select species:

Homo sapiens (Human)

Jaccard Similarity Threshold ?

0.4

Search

1.1. Protein Search

1.1.1. Search with one protein

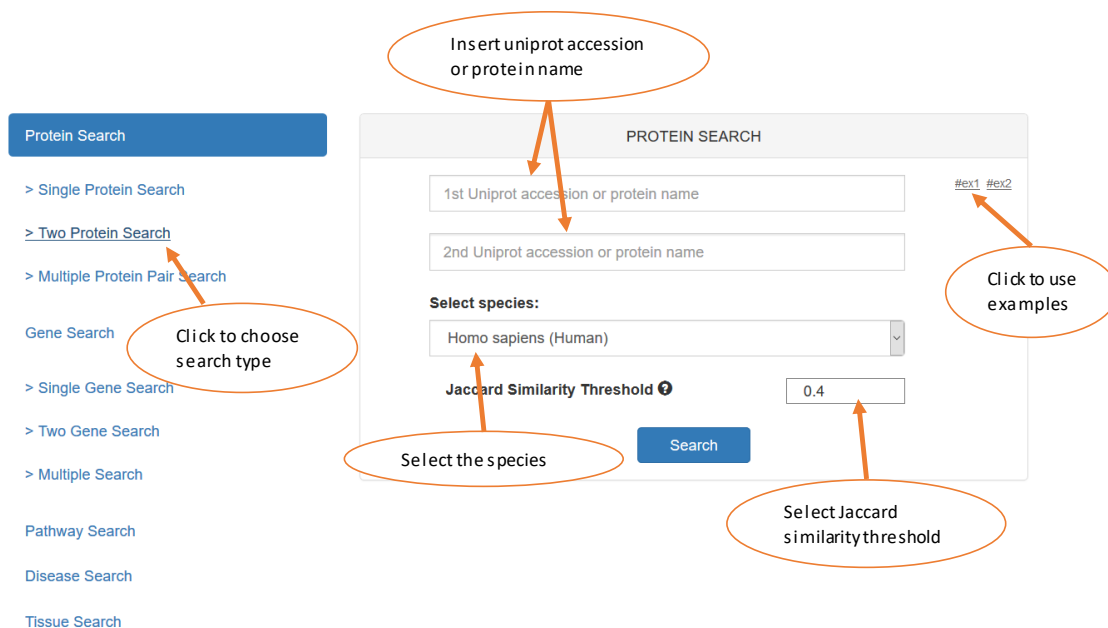
To search for one protein, you can use **Single Protein Search** tab in the search page. You can search the database by either using UniProt Accession or protein name. Upon search you will see associating partner of the searched protein, as per our protein association pipeline. If you would like to try some cases, you could also use the given examples, in the upper right corner of the search box to initiate the searches. After defining the protein select the Jaccard similarity threshold, to filter your result, which will show you all the associating protein pair with minimum defined Jaccard similarity score threshold. The recommended threshold is 0.4. Now, from the **Select species** dropdown box, select the species for the protein search. For the example cases select Human.

Tabloid Proteome is a database of protein association network... available mass spectrometry based experiments in PRIDE. These associations represent a broad scale of biological associations as well beyond mere binary protein interactions. [More info***](#)

The screenshot shows the 'Protein Search' interface. On the left is a sidebar with search options: 'Protein Search' (selected), '> Single Protein Search', '> Two Protein Search', '> Multiple Protein Pair Search', 'Gene Search', '> Single Gene Search', '> Two Gene Search', '> Multiple Search', 'Pathway Search', 'Disease Search', and 'Tissue Search'. The main area is titled 'PROTEIN SEARCH' and contains a search form. The form has a text input field labeled 'Uniprot accession or protein name' with the example 'Q13330, P08134' in the top right corner. Below this is a 'Select species:' dropdown menu currently showing 'Homo sapiens (Human)'. To the right of the dropdown is a 'Jaccard Similarity Threshold' input field with the value '0.4'. A blue 'Search' button is at the bottom right of the form. Five orange callout boxes with arrows point to specific elements: 'Insert uniprot accession or protein name' points to the input field; 'Click to choose search type' points to the 'Single Protein Search' link in the sidebar; 'Click to use examples' points to the example text 'Q13330, P08134'; 'Select the species' points to the 'Select species:' dropdown; and 'Select Jaccard similarity threshold' points to the '0.4' input field.

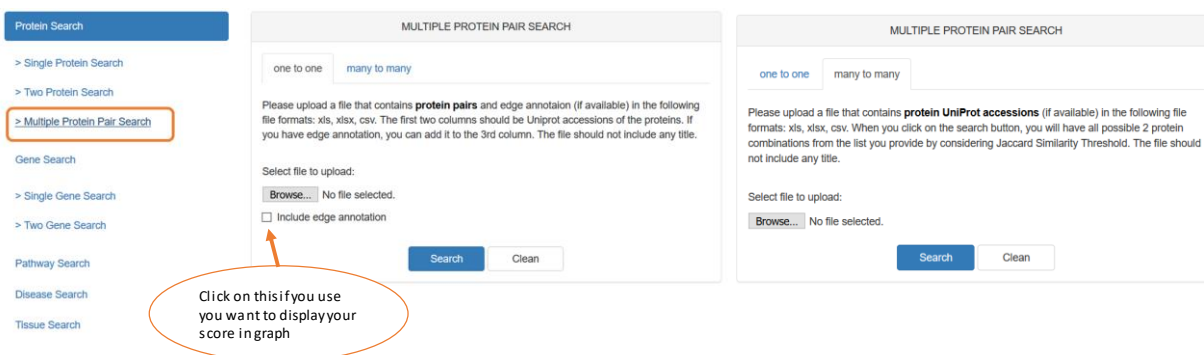
1.1.2. Search with two proteins

To search for a protein pair (or two protein), you can use **Two Protein search** tab in the search page. Two protein search is similar to single protein search, however, here you can check if there exists any possible biological association between two proteins. You can use either UniProt accession or protein name to initiate the search. Then select the Jaccard similarity threshold and species. You can also use examples provided in the upper right corner to initiate the search. For example use human as species.



1.1.3. Multiple protein search

To search for more than two proteins, select the **Multiple Protein Pair Search** tab, which further provides two different ways to search for protein pairs either via **one to one** search or a **many to many** search. At the moment, multiple search only support searches with UniProt accession. You can upload file in any of the three format xls, xlsx, csv (**without header**).



One to one search is similar to **Two Protein search**, where you can upload more than one pair in a file (UniProt Accessions), to the database to initiate the search. Here each row is one pair and entry in first column is protein1

and second column is protein2. You can also define the third column with your own score which will be displayed later on the graph in graph view. If you do define the third column, don't forget to click on the **include edge annotation** checkbox.

MULTIPLE PROTEIN PAIR SEARCH

one to one **many to many**

1st Uniprot Accession	2nd Uniprot Accession	Edge Annotation
Q9UKL0	Q92769	
Q8W009	Q12873	0.53
Q12873	Q13330	0.43

Jaccard Similarity Threshold ⓘ 0.4

Select file to upload:
 Browse... No file selected.
☒ Include edge annotation

Search Clean

However, **many to many** search is designed to search for all possible associating partner within a list of proteins (UniProt accession). For which you can upload a file with a single column of proteins accession. Each protein in the list will be searched with every other entry in the database for their association.

MULTIPLE PROTEIN PAIR SEARCH

one to one **many to many**

Uniprot Accessions

- P63000
- P51148
- P18085
- P62491

Jaccard Similarity Threshold ⓘ 0.4

Select file to upload:
 Browse... No file selected.

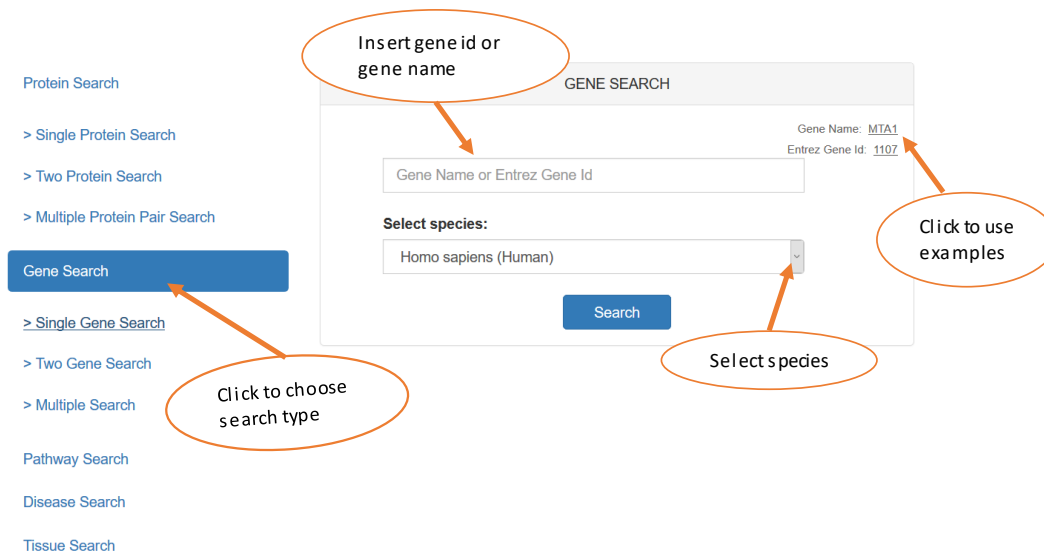
Search Clean

1.2. Gene Search

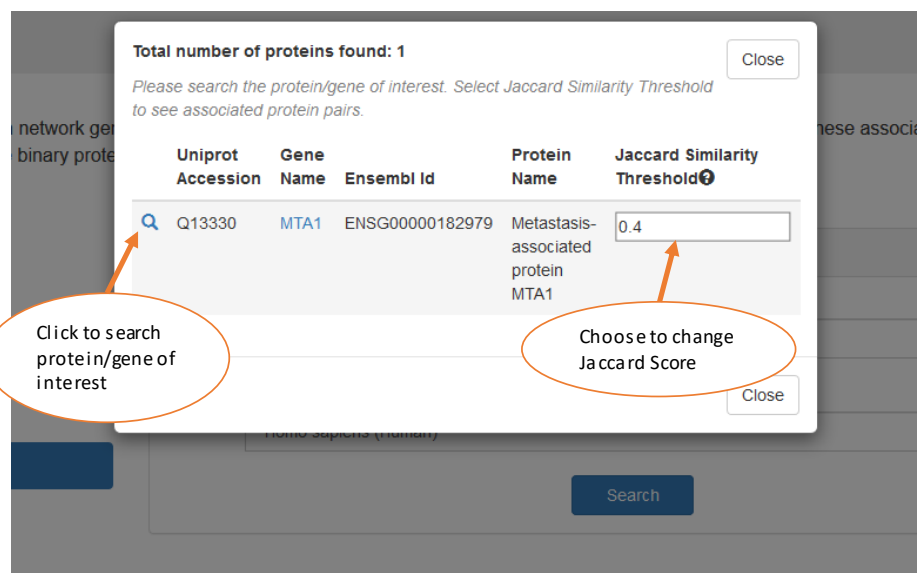
You can also search Tabloid Proteome either using gene name or NCBI RefSeq GeneID. Similar to Protein based search, Gene based searches are also allowed for more than one gene using **Single Gene search**, **Two Gene search** and **Multiple search** options.

1.2.1. Search with one gene

To search with one gene, click on **Single Gene Search** tab. Then in the search bar enter either a gene name or NCBI RefSeq GeneID. You can also use examples provided in the upper right corner to initiate the search. Here you also need to define the species that you are searching for, human for example cases.



Upon search, you will see a selection window, showing all possible proteins found for the entered gene. You can initiate your search by clicking on the search button next to one of protein accession. In this window you can also change for Jaccard similarity threshold.



1.2.2. Search with two genes

Similar to the one gene search, you can also search with two genes, using **Two Gene Search** tab, by either using gene name or NCBI RefSeq GeneID. Here you also need to define the species that you are searching for. You can also use examples provided in the upper right corner to initiate the search.

Protein Search

- > Single Protein Search
- > Two Protein Search
- > Multiple Protein Pair Search

Gene Search

- > Single Gene Search
- > Two Gene Search
- > Multiple Search

Pathway Search

Disease Search

Tissue Search

Insert gene ID or gene name

MTA1

CHD3

Select species:

Homo sapiens (Human)

Search

Click to use examples

Select the species

Click to choose search type

The next window will show you (if exists) protein pair for your queried genes with their Jaccard similarity score. Click on the search button next to the protein pair to get more information about the protein pair (as shown below).

Total number of protein pairs found: 1

Please select the protein/gene pair of interest

1st Uniprot Accession	1st Gene Name	1st Protein Name	2nd Uniprot Accession	2nd Gene Name	2nd Protein Name	
Q13330	MTA1	Metastasis-associated protein MTA1	Q12873	CHD3	Chromodomain-helicase-DNA-binding protein 3 (CHD-3) (EC 3.6.4.12) (ATP-dependent helicase CHD3) (Mi-2 autoantigen 240 kDa protein) (Mi2-alpha) (Zinc finger helicase) (hZFH)	0.43

Click here to search

1.2.3. Search with multiple genes

To search for more than two genes, select the **Multiple Gene Search** tab. Here you can upload the list of genes either gene name or gene ID, in any of the three format xls, xlsx, csv (**without header**).

Protein Search

- > Single Protein Search
- > Two Protein Search
- > Multiple Protein Pair Search

Gene Search

- > Single Gene Search
- > Two Gene Search
- > Multiple Search

Pathway Search

Disease Search

Tissue Search

GENE SEARCH

Please upload a file that contains **gene names** (if available) in the following file formats: xls, xlsx, csv. The file should not include any title.

Select file to upload:

Browse... example_gene_multiple.txt

Search Clean

Once the file is uploaded, it allows you to select the species for the list of genes.

Protein Search

> Single Protein Search
> Two Protein Search
> Multiple Protein Pair Search

Gene Search

> Single Gene Search
> Two Gene Search
> Multiple Search

Pathway Search
Disease Search
Tissue Search

GENE SEARCH

Uniprot Accessions

PIR
MTA1
CHD3
GATAD2B

Select species:

Homo sapiens (Human)

Select file to upload:

Browse...

example_gene_multiple.txt

Search

Clean

Upon initiating the search, it will display a selection window, where you can select the gene for which you would like to initiate the search for. Here you can also change the Jaccard similarity threshold.

Total number of proteins found: 5

Close

Please search the protein/gene of interest. Select Jaccard Similarity Threshold to see associated protein pairs.

	Uniprot Accession	Gene Name	Ensembl Id	Protein Name	Jaccard Similarity Threshold
	Q13330	MTA1	ENSG00000182979	Metastasis-associated protein MTA1	0.4
	Q13330	CHD3	ENSG00000170004	Chromodomain-helicase-DNA-binding protein 3 (CHD-3) (EC 3.6.4.12) (ATP-dependent helicase CHD3) (Mi-2 autoantigen 240 kDa protein) (Mi2-alpha) (Zinc finger helicase) (hZFH)	0.4
	Q8WXI9	GATAD2B	ENSG00000143614 ENSG00000261992	Transcriptional repressor p66-beta (GATA zinc finger domain-containing protein 2B) (p66/p68)	
	Q8TDI0	CHD5	ENSG00000116254	Chromodomain-helicase-DNA-binding protein 5 (CHD-5) (EC 3.6.4.12) (ATP-dependent helicase CHD5)	0.4
	Q96ST3	SIN3A	ENSG00000169375	Paired amphipathic helix protein Sin3a (Histone deacetylase complex subunit Sin3a) (Transcriptional corepressor Sin3a)	0.4

Click to initiate the search

If required change the threshold

Search

Clean

1.3. Pathway search:

You can also search for all associated protein pairs available in Tabloid Proteome, for the particular pathway. The search can be initiated either by unique Reactome ID or pathway name.

Protein Search

> Single Protein Search

> Two Protein Search

> Multiple Protein Pair Search

Gene Search

> Single Gene Search

> Two Gene Search

> Multiple Search

Pathway Search

Disease Search

Tissue Search

PATHWAY SEARCH

Pathway name: NOD1/2 Signaling Pathway

Reactome accession: R-HSA-114604

Reactome accession or pathway name

Search

Insert Reactome accession or pathway name

Click to use examples

Click to choose search type

After the selection of the pathway, in the next window you can see multiple pathway entries. Select for your pathway of interest and click on the down arrow on the right side of the pathway name. If your entered pathway is not leaf pathway, then upon clicking on dropdown arrow, you will see protein pairs with their Jaccard Similarity score, under different leaf pathways. Then select one of these pair to initiate the protein pair search (as shown in the image below).

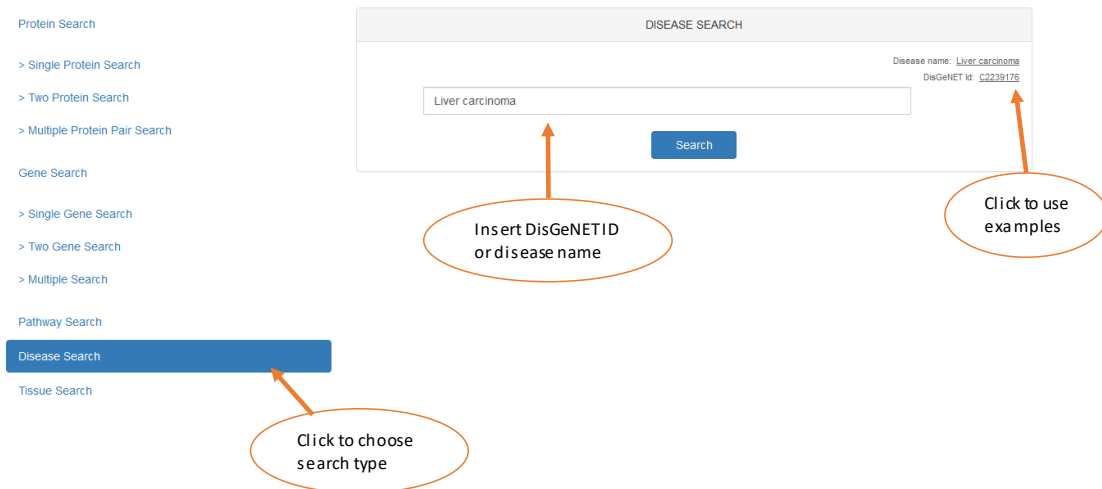
Pathway Name	Reactome Accession
Toll Like Receptor 3 (TLR3) Cascade	R-HSA-168164
TICAM1, RIP1-mediated IKK complex recruitment	R-HSA-168927

1st Uniprot Accession	1st Protein Name	2nd Protein Name	Jaccard Similarity
P61088	Ubiquitin-conjugating enzyme E2 N (EC 2.3.2.23) (Bendless-like ubiquitin-conjugating enzyme) (E2 ubiquitin-conjugating enzyme N) (UbcN13) (Ubiquitin carrier protein N) (Ubiquitin-protein ligase N)	P13044	Ubiquitin-conjugating enzyme E2 variant 1 (UEV-1) (CROC-1) (TRAF6-regulated IKK activator 1 beta Uev1A)
Q13404	Ubiquitin-conjugating enzyme E2 variant 1 (UEV-1) (CROC-1) (TRAF6-regulated IKK activator 1 beta Uev1A)	P61077	Ubiquitin-conjugating enzyme E2 D3 (EC 2.3.2.23) (E3-independent) E2 ubiquitin-conjugating enzyme D3 (UbcD3) (Ubiquitin carrier protein D3) (Ubiquitin-conjugating enzyme E2(17kD 3)) (Ubiquitin-conjugating enzyme E2-17 kDa 3) (Ubiquitin-protein ligase D3)
P62837	Ubiquitin-conjugating enzyme E2 D2 (EC 2.3.2.23) (E3-independent) E2 ubiquitin-conjugating enzyme D2 (UbcD2) (Ubiquitin carrier protein D2) (Ubiquitin-conjugating enzyme E2(17kD 2)) (Ubiquitin-conjugating enzyme E2-17 kDa 2) (Ubiquitin-protein ligase D2) (p53-regulated ubiquitin-conjugating enzyme 1)	Q13404	Ubiquitin-conjugating enzyme E2 variant 1 (UEV-1) (CROC-1) (TRAF6-regulated IKK activator 1 beta Uev1A)
P61088	Ubiquitin-conjugating enzyme E2 N (EC 2.3.2.23) (Bendless-like ubiquitin-conjugating enzyme) (E2 ubiquitin-conjugating enzyme N) (UbcN13) (Ubiquitin carrier protein N) (Ubiquitin-protein ligase N)	P61077	Ubiquitin-conjugating enzyme E2 D3 (EC 2.3.2.23) (E3-independent) E2 ubiquitin-conjugating enzyme D3 (UbcD3) (Ubiquitin carrier protein D3) (Ubiquitin-conjugating enzyme E2(17kD 3)) (Ubiquitin-conjugating enzyme E2-17 kDa 3) (Ubiquitin-protein ligase D3)
P62837	Ubiquitin-conjugating enzyme E2 D2 (EC 2.3.2.23) (E3-independent) E2 ubiquitin-conjugating enzyme D2 (UbcD2) (Ubiquitin carrier protein D2) (Ubiquitin-conjugating enzyme E2(17kD 2)) (Ubiquitin-conjugating enzyme E2-17 kDa 2) (Ubiquitin-protein ligase D2) (p53-regulated ubiquitin-conjugating enzyme 1)	P61088	Ubiquitin-conjugating enzyme E2 N (EC 2.3.2.23) (Bendless-like ubiquitin-conjugating enzyme) (E2 ubiquitin-conjugating enzyme N) (UbcN13) (Ubiquitin carrier protein N) (Ubiquitin-protein ligase N)

1st Uniprot Accession	1st Protein Name	2nd Uniprot Accession	2nd Protein Name	Jaccard Similarity
P61088	Ubiquitin-conjugating enzyme E2 N (EC 2.3.2.23) (Bendless-like ubiquitin-conjugating enzyme) (E2 ubiquitin-conjugating enzyme N) (UbcN13) (Ubiquitin carrier protein N) (Ubiquitin-protein ligase N)	Q13404	Ubiquitin-conjugating enzyme E2 variant 1 (UEV-1) (CROC-1) (TRAF6-regulated IKK activator 1 beta Uev1A)	0.38
P61088	Ubiquitin-conjugating enzyme E2 N (EC 2.3.2.23) (Bendless-like ubiquitin-conjugating enzyme) (E2 ubiquitin-conjugating enzyme N) (UbcN13) (Ubiquitin carrier protein N) (Ubiquitin-protein ligase N)	P09429	High mobility group protein B1 (High mobility group protein 1) (HMG-1)	0.24
Q13404	Ubiquitin-conjugating enzyme E2 variant 1 (UEV-1) (CROC-1) (TRAF6-regulated IKK activator 1 beta Uev1A)	P09429	High mobility group protein B1 (High mobility group protein 1) (HMG-1)	0.2
P61088	Ubiquitin-conjugating enzyme E2 N (EC 2.3.2.23) (Bendless-like ubiquitin-conjugating enzyme) (E2 ubiquitin-conjugating enzyme N) (UbcN13) (Ubiquitin carrier protein N) (Ubiquitin-protein ligase N)	P0CG47	Polyubiquitin-B [Cleaved into: Ubiquitin]	0.19
P61088	Ubiquitin-conjugating enzyme E2 N (EC 2.3.2.23) (Bendless-like ubiquitin-conjugating enzyme) (E2 ubiquitin-conjugating enzyme N) (UbcN13) (Ubiquitin carrier protein N) (Ubiquitin-protein ligase N)	P0CG48	Polyubiquitin-C [Cleaved into: Ubiquitin]	0.19
P61088	Ubiquitin-conjugating enzyme E2 N (EC 2.3.2.23) (Bendless-like ubiquitin-conjugating enzyme) (E2 ubiquitin-conjugating enzyme N) (UbcN13) (Ubiquitin carrier protein N) (Ubiquitin-protein ligase N)	P62987	Ubiquitin-60S ribosomal protein L40 (CEP52) (Ubiquitin A-52 residue ribosomal protein fusion product 1) [Cleaved into: Ubiquitin, 60S ribosomal protein L40 (Large ribosomal subunit protein eL40)]	0.19
P62979	Ubiquitin-40S ribosomal protein S27a (Small ribosomal subunit protein eS31) [Cleaved into: Ubiquitin, 40S ribosomal protein S27a (Small ribosomal subunit protein eS31)]	P61088	Ubiquitin-conjugating enzyme E2 N (EC 2.3.2.23) (Bendless-like ubiquitin-conjugating enzyme) (E2 ubiquitin-conjugating enzyme N) (UbcN13) (Ubiquitin carrier protein N) (Ubiquitin-protein ligase N)	0.19

1.4. Disease search:

Similar to the pathway search, you can also search for the associated protein pairs available in the Tabloid Proteome for particular disease. Tabloid Proteome include all human diseases from DisGeNET database. Here you can search, by clicking on 'Disease Search', either by using the disease name or unique DisGeNET ID.



After the selection of the disease, in the next window it will show you, all possible disease entries found for your search (as shown below). With the down arrow you can check for all possible associated protein pairs with minimum 0.4 Jaccard similarity score. With the protein pair of interest, you can initiate the search, by clicking on the search button next to the Unique DisGeNET Id. For protein pairs less than 0.4 can be accessed via API, (for more detail refer here <http://iomics.ugent.be/tabloidproteome/tabloidApi.html>)

Please click on the disease of interest to find relevant proteins, and search the relevant protein pairs

Disease Name	DisGeNet Id			
Precursor cell lymphoblastic lymphoma	C0079748	<div> <div>click to search relevant protein pairs</div> <div>click to close protein pairs under this disease</div> </div>		
1st Uniprot Accession	1st Protein Name	2nd Uniprot Accession	2nd Protein Name	Jaccard Similarity
Q P08196	CD4 cell-surface antigen heavy chain (H2hc) (H2 heavy chain antigen) (Lymphocyte activation antigen 4F2 large subunit)	P33993	DNA replication licensing factor MCM7 (EC 3.6.4.12) (CDC47 homolog) (P1 1-MCM3)	0.18
Q P42672	40S ribosomal protein S27 (Metalloprotein-stimulin 1) (MPS-1)	P33993	DNA replication licensing factor MCM7 (EC 3.6.4.12) (CDC47 homolog) (P1 1-MCM3)	0.15
Q P08196	CD4 cell-surface antigen heavy chain (H2hc) (H2 heavy chain antigen) (Lymphocyte activation antigen 4F2 large subunit)	P08196	Large neutral amino acids transporter small subunit 1 (H2F light chain) (H2F LC) (CD98 light chain) (Integral membrane protein F-85) (L-2-amino acid transporter 1) (L-2AT1) (Solute carrier family 7 member 5) (h.s. system x ^{ag})	0.15
Precursor B-lymphoblastic lymphoma/leukemia	C0862030			
Precursor B-lymphoblastic lymphoma stage II	C0862039			
Precursor B-lymphoblastic lymphoma	C0855146			
Precursor T cell lymphoblastic leukemia/lymphoblastic lymphoma	C1301359			
adult lymphoblastic lymphoma	C0278721			
Precursor T-cell lymphoblastic lymphoma	C1292758			

Close

1.5. Tissue Search

The online Tabloid Proteome also allows user to restrict their search for associated protein pair with the tissue annotations, included from The Human Protein Atlas. The tissue based searches can be initiated by selecting one of the provided 53 tissue names, from the drop down menu, for example lungs as, as shown in the figure below.

Protein Search

> Single Protein Search

> Two Protein Search

> Multiple Protein Pair Search

Gene Search

> Single Gene Search

> Two Gene Search

> Multiple Search

Pathway Search

Disease Search

Tissue Search

TISSUE SEARCH

Choose a tissue

Choose a tissue

adrenal gland

appendix

bone marrow

breast

bronchus

caudate

cerebellum

cerebral cortex

cervix, uterine

colon

duodenum

endometrium 1

endometrium 2

epididymis

esophagus

fallopian tube

gallbladder

hair

heart muscle

Threshold

0.4

Search

Select tissue

Set Jaccard score

After selecting the on the tissue from the drop down menu, first select the Jaccard Similarity threshold and then click on the search button. Upon clicking on the search button, the next window will show all associated protein pairs annotated to be present in the searched tissue (as shown in figure below), according to The Human Protein Atlas.

Jaccard similarity threshold is set as 0.4 for this search. If you want to see more results with lower threshold, please contact us.

Total number of protein pairs found: 653

1st Uniprot Accession	1st Protein Name	2nd Uniprot Accession	2nd Protein Name	Jaccard Similarity	Tissue Name
P40227	T-complex protein 1 subunit zeta (TCP-1-zeta) (Acute morphine dependence-related protein 2) (CCT-zeta-1) (HTR3) (Tcp20)	P48643	T-complex protein 1 subunit epsilon (TCP-1-epsilon) (CCT-epsilon)	0.49	lung
P40227	T-complex protein 1 subunit zeta (TCP-1-zeta) (Acute morphine dependence-related protein 2) (CCT-zeta-1) (HTR3) (Tcp20)	P17987	T-complex protein 1 subunit alpha (TCP-1-alpha) (CCT-alpha)	0.47	lung
P40227	T-complex protein 1 subunit zeta (TCP-1-zeta) (Acute morphine dependence-related protein 2) (CCT-zeta-1) (HTR3) (Tcp20)	Q99832	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta) (HIV-1 Nef-interacting protein) [Cleaved into: T-complex protein 1 subunit eta, N-terminally processed]	0.51	lung
P40227	T-complex protein 1 subunit zeta (TCP-1-zeta) (Acute morphine dependence-related protein 2) (CCT-zeta-1) (HTR3) (Tcp20)	P50990	T-complex protein 1 subunit theta (TCP-1-theta) (CCT-theta) (Renal carcinoma antigen NY-REN-15)	0.44	lung
P40227	T-complex protein 1 subunit zeta (TCP-1-zeta) (Acute morphine dependence-related protein 2) (CCT-zeta-1) (HTR3) (Tcp20)	P78371	T-complex protein 1 subunit beta (TCP-1-beta) (CCT-beta)	0.47	lung

It is suggested to use Jaccard similarity coefficient of 0.4 for web search, lower threshold might take longer to retrieve annotation. However, protein pairs less than 0.4 can be accessed via API, (for more detail refer here help section or

<http://iomics.ugent.be/tabloidproteome/tabloidApi.html>)

2. Search Results

If the protein(s) searched either through protein, gene, pathway or search, pathway search is present in the database and have association with any another protein, Tabloid Proteome will provide result in two forms; Data Table and Graph View.

2.1. Data Table

Data table view gives association information between two or more proteins. If searched for one protein, the resulting table will show you one or more rows, depending on the association found for the searched protein. In the data table, each row represents the possible biological connection for each partner proteins (as shown below). For the double protein search, the resulting table will provide user with one row, showing possible biological connection between two proteins.

Protein Association Data Table

Download

Graph View

1st protein #	2nd protein #	1st protein name #	2nd protein name #	2nd protein gene name #	Jacc similarity score #	Interaction #	Ensembl paralog #	# common complex #	# common pathway #	# common projects #	# common diseases #		
Q13330	Q8TD90	Metastasis-associated protein MTA1	MTA1	Chromodomain-helicase-DNA-binding protein 5 (CHD-5) (EC 3.6.4.12) (ATP-dependent helicase CHD5)	CHD5 KIAA0444	0.43	yes	no	0	0	5	20	▼
Q13330	Q12873	Metastasis-associated protein MTA1	MTA1	Chromodomain-helicase-DNA-binding protein 3 (CHD-3) (EC 3.6.4.12) (ATP-dependent helicase CHD3) (M-2 autotantigen 240 kDa protein) (M2-alpha) (Zinc finger helicase) (hZFH)	CHD3	0.43	yes	no	3	3	6	2	▼
Q13330	Q8IX09	Metastasis-associated protein MTA1	MTA1	Transcriptional repressor p66-beta (GATA zinc finger domain-containing protein 2B) (p66p68)	GATAD2B KIAA1150	0.48	yes	no	0	3	7	8	▼
Q13330	Q96373	Metastasis-associated protein MTA1	MTA1	Paired amphipathic helix protein Sin3a (Histone deacetylase complex subunit Sin3a) (Transcriptional repressor Sin3a)	SIN3A	0.4	yes	no	1	0	6	9	▼

Click on the UniProt accession link to go to UniProt website

Click on headers to sort the table

Click on a row to see detailed information about the association

UniProt accession column (blue) provides direct link to UniProt website. You can also sort each column with high to low score or with alphabetical order. With the click on each protein pair, you can find more information about the association between two proteins (as shown in image below) like Interactions, Projects, Pathways, Complexes, Disease, and GO.

Protein Association Data Table

Download

Graph View

1st protein #	2nd protein #	1st protein name #	2nd protein name #	2nd protein gene name #	Jacc similarity score #	Interaction #	Ensembl paralog #	# common complex #	# common pathway #	# common projects #	# common diseases #		
Q13330	Q8TD90	Metastasis-associated protein MTA1	MTA1	Chromodomain-helicase-DNA-binding protein 5 (CHD-5) (EC 3.6.4.12) (ATP-dependent helicase CHD5)	CHD5, KIAA0444	0.43	yes	no	0	0	5	20	▼
Q13330	Q12873	Metastasis-associated protein MTA1	MTA1	Chromodomain-helicase-DNA-binding protein 3 (CHD-3) (EC 3.6.4.12) (ATP-dependent helicase CHD3) (M-2 autotantigen 240 kDa protein) (M2-alpha) (Zinc finger helicase) (hZFH)	CHD3	0.43	yes	no	3	3	6	2	▼
Q13330	Q8IX09	Metastasis-associated protein MTA1	MTA1	Transcriptional repressor p66-beta (GATA zinc finger domain-containing protein 2B) (p66p68)	GATAD2B, KIAA1150	0.48	yes	no	0	3	7	8	▼

Interactions

Interact : yes

BioGRID : yes

Interact Confidence

0.35

Interact Detection

M0007_anti tag immunoprecipitation

Interact Interaction Type

M0014_association

Common Projects

▼

Pathways

▼

Complexes

▼

GO

▼

Diseases

▼

Q13330	Q8TD90	Metastasis-associated protein MTA1	MTA1	Paired amphipathic helix protein Sin3a (Histone deacetylase complex subunit Sin3a) (Transcriptional corepressor Sin3a)	SIN3A	0.4	yes	no	1	0	6	9	▼
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click on the row to close the details

click on the icon to close the panel

click on the icon to open the panel

With the further click on the expandable buttons, at the end of each row, you can get more information about each type of association, in separate section. More information about each section is described below.

2.1.1. Interactions

Interaction section gives information about protein-protein interaction between two proteins. All the information about the interaction is collected from IntAct and BioGRID database. If the interaction is found in the IntAct database, then more information about the interaction is shown in this section (as shown in image below).

Interactions		
IntAct : yes BioGRID : no		
Intact Confidence	Intact Detection	Intact Interaction Type
0.59	MI0398_two hybrid pooling approach	MI0915_physical association
0.59	MI0018_two hybrid	MI0915_physical association
0.59	MI0663_confocal microscopy	MI0403_colocalization

2.1.2. Common Projects

Common Projects section shows all common projects between two proteins (shown in image below). By clicking on one of the project accessions (marked with [blue](#)), it will redirect to PRIDE website.

Common Projects					
No	Project Accession	Keywords	Tissue	Tags	Instruments
1	PXD000314	Sequential IMAC, human lung cancer tissue, phosphoproteomics	cell culture, lung		instrument model
2	PXD001572	DNA sensing, protein interactions, iFOX	cell culture	Biomedical	LTQ Orbitrap Velos
3	PRD000711	Not available	293T cells	Technical, PRIME-XS Project	instrument model, LTQ Orbitrap Velos

2.1.3. Pathways

Pathways section shows the common pathways found between two proteins, according to Reactome database. By clicking on Reactome accession (marked in [blue](#)), it will re-direct to Reactome's 'Pathway Browser' page.

Pathways			
No	Reactome Accession	Pathway Name	Evidence Code
1	R-HSA-1445148	Translocation of GLUT4 to the plasma membrane	TAS
2	R-HSA-75035	Chk1/Chk2(Cds1) mediated inactivation of Cyclin B:Cdk1 complex	TAS
3	R-HSA-5625740	RHO GTPases activate PKNs	TAS
4	R-HSA-5628897	TP53 Regulates Metabolic Genes	TAS

2.1.4. Complexes

Complexes section, as shown below in the image, will provide you with list of complexes where both proteins are present, according to CORUM database. Here, with the click to Pubmed Id, it will re-direct to the link to PubMed webpage and click on the CORUM id, (marked in blue) will re-direct to the CORUM database.

2.1.5. GO

Complexes								
No	Corum Id	Complex Name	Complex Comment	Cell Line	Disease Comment	Subunit Comment	Pubmed Id	Purification Method
1	5199	Kinase maturation complex 1	None	None	None	None	14743216	MI:0676- tandem affinity purification
2	5615	Emerin complex 52	Complexes are named on the basis of their S300 elution fraction number. Subunits 9-22 were	None	Emerin is involved in Emery-Dreifuss muscular dystrophy	None	17620012	MI:0004- affinity chromatography technologies, MI:0226- ion exchange

GO		
Molecular Function		
No	MF Id	MF Name
Biological Process		
No	BP Id	BP Name
1	GO:0061024	membrane organization
2	GO:1900740	positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway
3	GO:0006605	protein targeting
Cellular Component		
No	CC Id	CC Name
1	GO:0005739	mitochondrion
2	GO:0016020	membrane
3	GO:0005925	focal adhesion
4	GO:0070062	extracellular exosome

Under this section, you can find information regarding common Biological Process, Molecular Function and Cellular Component of two proteins, defined by GO. These three information is provided with three different subsection with the respective names (as shown in image below). All section includes GO Id (marked with blue) which will re-direct to EMBL-EBI Gene Ontology service.

2.1.6. Disease

In the disease section, you can find the list of diseases, where both proteins are found to be involved in. All the information about the disease and protein involved in each disease are collected from DisGeNET database. With the click on the DisGeNET ids (marked with blue), it will re-direct to DisGeNET search webpage.

Diseases		
No	Disgenet Id	Disease Name
1	C0025202	melanoma
2	C2239176	Liver carcinoma
3	C0242379	Malignant neoplasm of lung
4	C0376358	Malignant neoplasm of prostate

2.2. Graph View

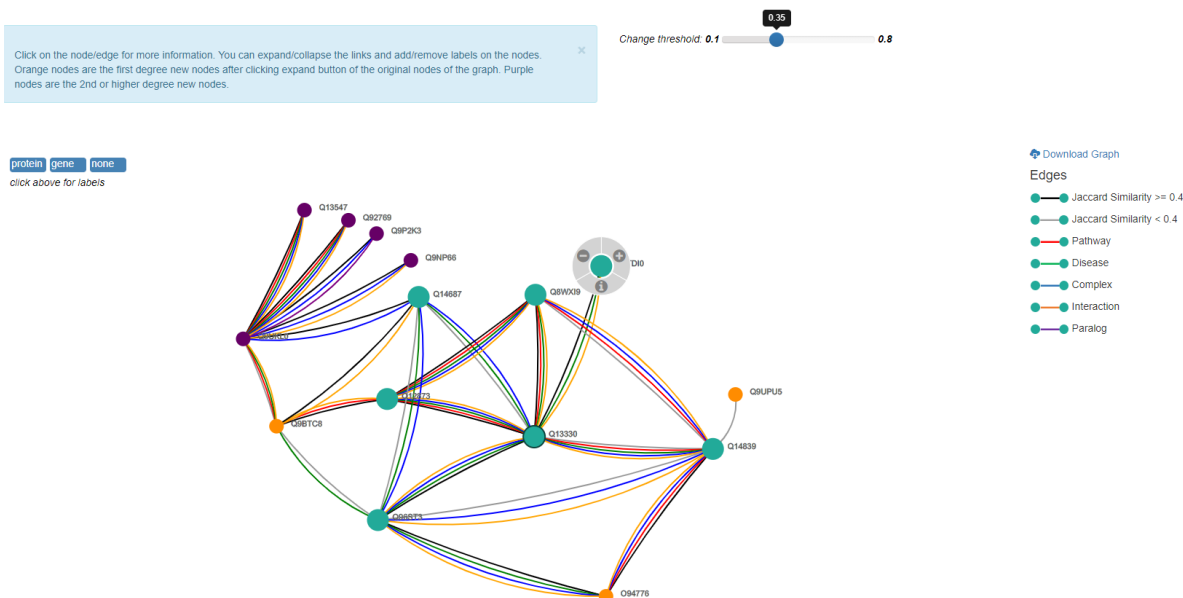
In Tabloid proteome, you can also visualize your results in form of graph, where each node represent proteins and edges represents associations. The link to the graph can be accessed through the upper right corner of the Data Table result page.

PROTEIN ASSOCIATION DATA TABLE								
protein name	2nd protein name	2nd protein gene name	Jacc similarity score	Interaction	Ensembl paralogs	# common complex	# common pathway	# common projects
AQ	14-3-3 protein epsilon (14-3-3E)	YWHAE	0.4	yes	yes	3	5	43
AQ	14-3-3 protein beta/alpha (Protein 1054) (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into:	YWHAH	0.46	yes	yes	2	5	

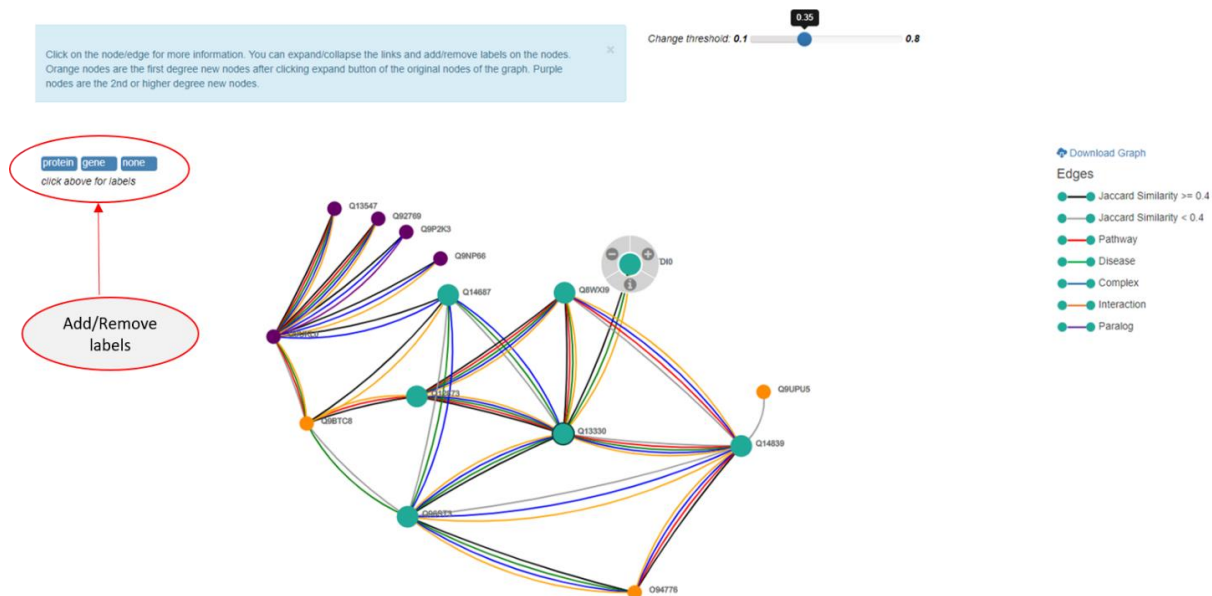
Download Graph View

Click to go to Graph View

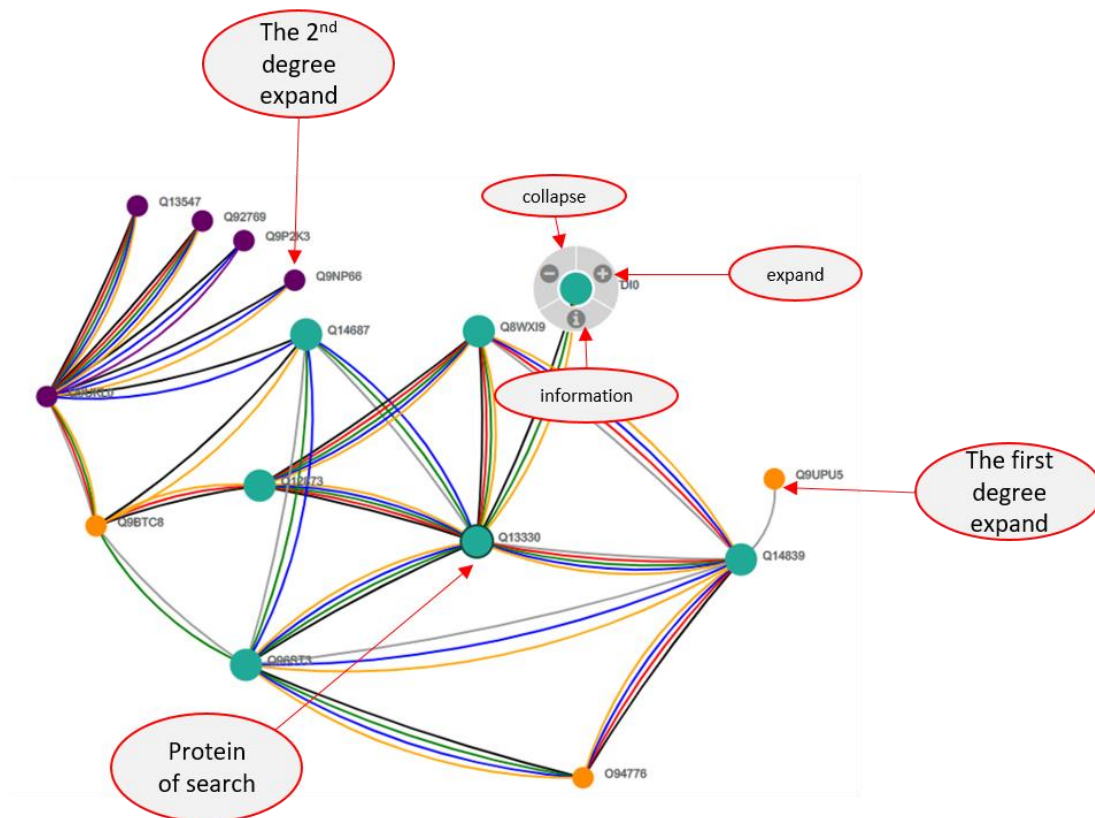
On this page, you can see dynamic graph representation of your search. All nodes and edges are repositionable. After/before changing position of the graph you can download as an image (.png) by clicking on “Download Graph” link (as shown below). For more information about the proteins and their relations, you need to click on the node or edge. You can also expand the node to see the relations with other nodes. If you want to go back to original graph you can click on the collapse button.



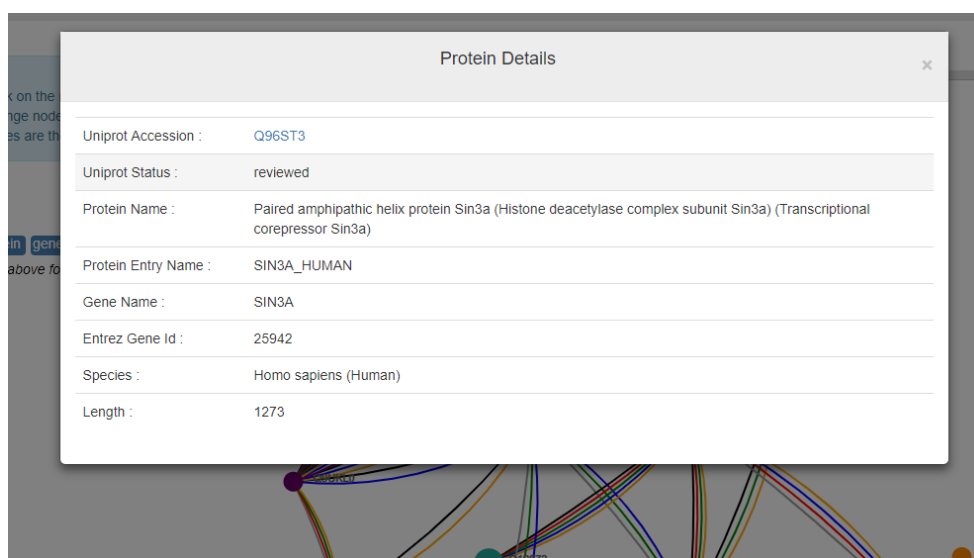
With default the nodes will be shown without any label. You can add UniProt accession with “protein” button and add gene name with “gene” button on the left hand side of the panel, as highlighted in the red in the image below. By clicking on the “none” button you can remove all labels.



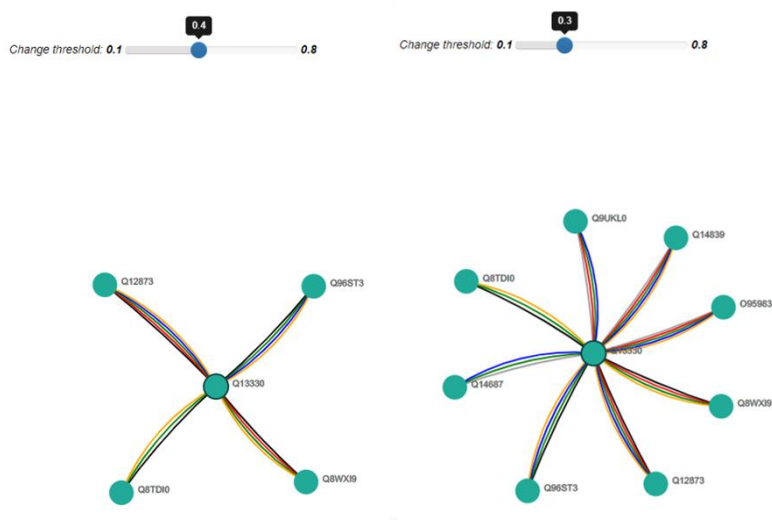
With the click on the node, there will be 3 options: Expand or collapse the relations and protein information. To remove the buttons around the node, click on the node again.



Protein of the search is highlighted with gray circle. Orange nodes are the first degree new nodes after clicking expand button of the one of the original nodes of the graph. Purple nodes are 2nd or higher degree new nodes. The graph is expandable as much as possible. If you want to remove the new nodes and new links, collapse button will remove all related links and nodes except the original search. When the click on the information button, a pop up window will appear which will show more information about the protein, derived from UniProt database (as shown in the image below). With the click on the UniProt accession (marked with blue), it will re-direct to the Swissprot/UniProt webpage. Similarly, click on Gene Id (marked with blue), it will re-direct to detailed view of the gene on NCBI Gene & Expression website.

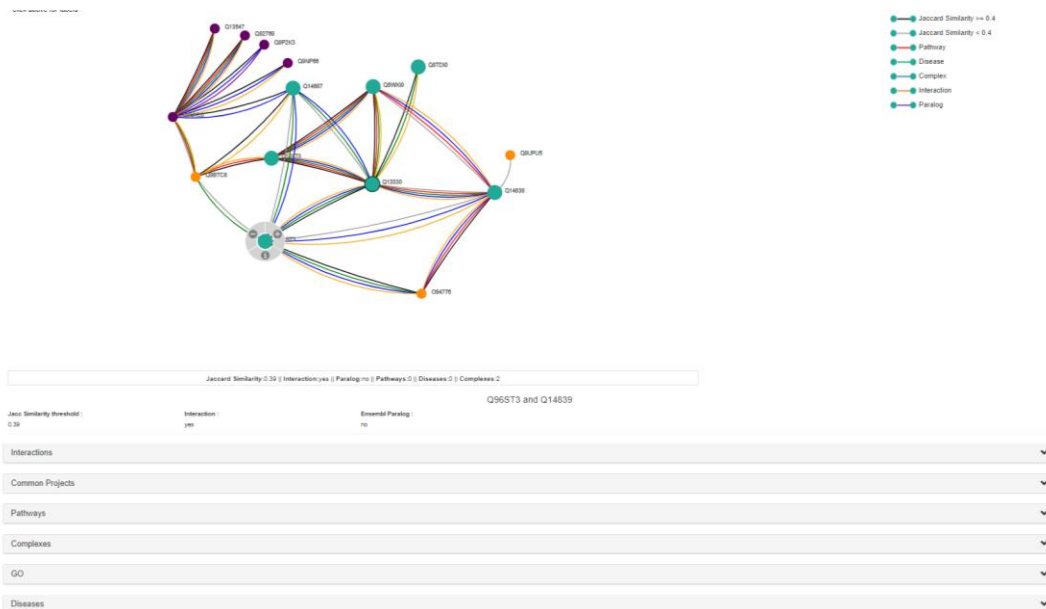


Another new feature of this version is to be able to change Jaccard Similarity threshold and see the change on the graph immediately. User can change the threshold by using slider on top of the graph.

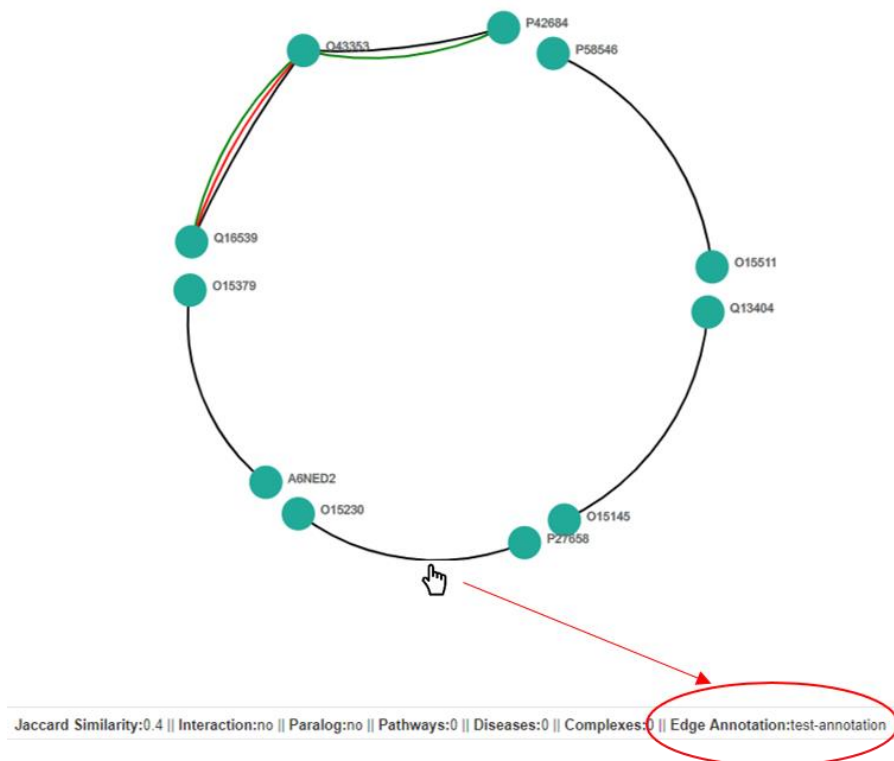


The edges between the proteins represents biological association. When user hovers on the edge, different biological association between proteins are visible below the graph. Edge with black color represent the Jaccard similarity association found with our method which is 0.4 and above, and gray color shows association having Jaccard similarity score smaller than 0.4. This information is also shown in a panel, on the right side of the graph (as shown in the image below).

For more information about association, you can click on the edge, it will show brief information about the association, with six sub-sections; Interactions, Projects, Pathways, Complexes, Diseases, and GO (at the bottom of the graph). Each sub-section, contains same information as provided in the Data Table page (explained in more detail under section 2.1.1 to 2.1.6).

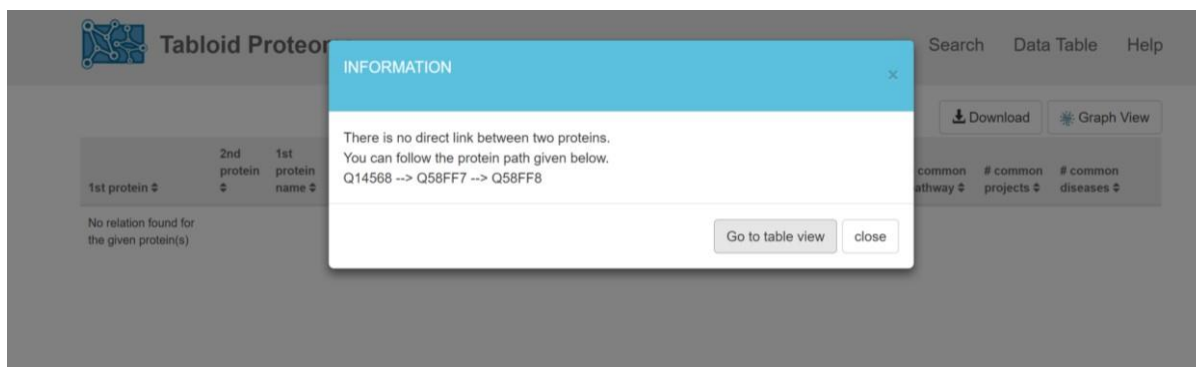


For multiple protein search, if edge annotation is added, then it will be shown below the graph when user hover on the edge. Graph shown below shows an example of the multiple protein search with added annotation.



2.3. Special case

In the double protein search, if this pair does not contain any direct biological connection in the database, Tabloid proteome will try to check for indirect association between the proteins. If the searched pair contains any indirect association, you will show a pop up window for the possible connection (as shown in the image below).



For further click on the “Data Table” option, you can view the result about the search in the Data Table view, with all information explained above. With the Data Table view, you can go to Graph View, to visualize you result with the same information and changes, as explained above.

3. Downloads

From Tabloid proteome, you can download the results, in two form; tab delimited format for the table or as an image. Tab delimited or CSV format can be downloaded from the upper right corner of Data table result page.

Total number of protein pairs found: 16
 1 protein pair(s) cannot be found.
 Please click on the protein pair of interest

Click to download in CSV or TSV format

Download ▾ Graph View

TSV format
 CSV format

Protein Association Data Table

1st protein	2nd protein	1st protein name	1st protein gene name	2nd protein name	2nd protein gene name	Jacc similarity threshold	Interaction	Ensembl paralogs	# common complex	# common pathway	# common projects	# common diseases	
P20292	P13688	Arachidonate 5-lipoxygenase-activating protein (FLAP) (MK-886-binding protein)	ALOX5AP FLAP	Carcinoembryonic antigen-related cell adhesion molecule 1 (Biliary glycoprotein 1) (BGP-1) (CD antigen CD66a)	CEACAM1 BGP BGP1	0.44	no	no	0	0	2	7	▼
P40199	P31997	Carcinoembryonic antigen-related cell adhesion molecule 6 (Non-specific crossreacting antigen) (Normal cross-reacting antigen) (CD antigen CD66c)	CEACAM6 NCA	Carcinoembryonic antigen-related cell adhesion molecule 8 (CD67 antigen)	CEACAM8 CGM6	0.5	yes	yes	0	2	3	2	▼

As mention above, you can also download the graph view from the upper left corner of the graph view page.

Click on the node/edge for more information. You can expand/collapse the links and add/remove labels on the nodes. Orange nodes are the first degree new nodes after clicking expand button of the original nodes of the graph. Purple nodes are the 2nd or higher degree new nodes.

Change threshold 0.1 0.35 0.8

protein gene none
 click above for labels

Download Graph

You can download the graph as an image

Edges

- Jaccard Similarity >= 0.4
- Jaccard Similarity < 0.4
- Pathway
- Disease
- Complex
- Interaction
- Paralog

4. Citation

If you are using Tabloid Proteome, do not forget to cite us.

Surya Gupta, Kenneth Verheggen, Jan Tavernier, and Lennart Martens

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Gupta*,S., Turan*,D., Tavernier,J. and Martens,L.

The online Tabloid Proteome: an annotated database of protein associations

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DOI: <https://doi.org/10.1093/nar/gkx930> PMID: 29040688