

# Tabloid Proteome

Version 1.3

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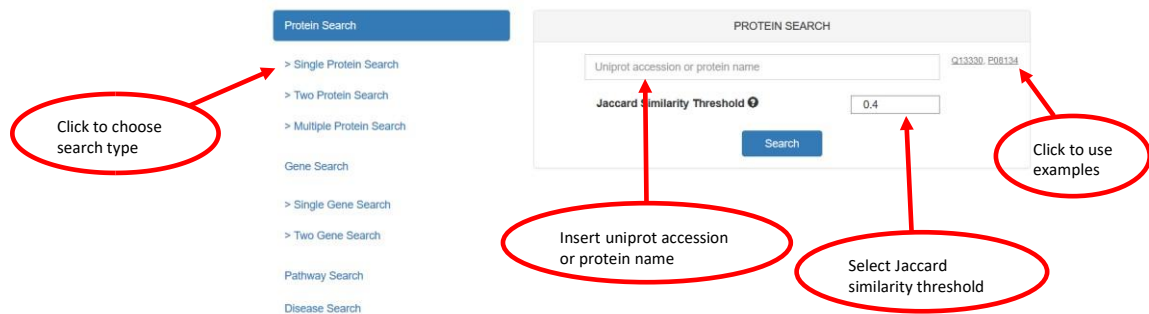
# 1. How to Search Tabloid Proteome

In order to perform the search, you can use the search box, provided in the search page. With the updated version of the Tabloid Proteome you can search for protein association in four ways; Protein Search, Gene Search, Pathway Search or Disease Search.

## 1.1. Protein Search

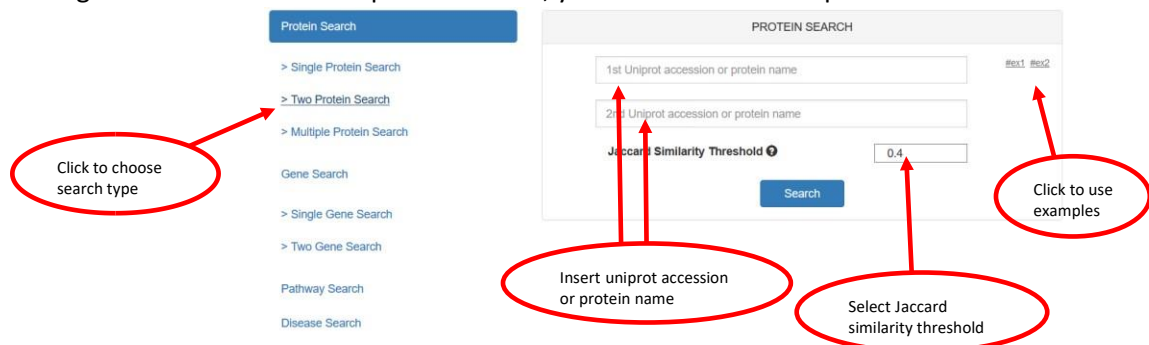
### 1.1.1. Search with one protein

You can search Tabloid Proteome with single protein, using Uniprot Accession or protein name. This will provide you with all possible partner of the protein that are found to be associated according to our analysis. Instead of using your own proteins, you can also use examples, provided in the upper right corner of the search box, to initiate the searches.



### 1.1.2. Search with two proteins

You can also start your search with two proteins, by using the 'Two Protein Search' tab in the search page. You need to define the Uniprot Accession or protein name of both proteins, as shown in image below. Similar to one protein search, you can also use examples.



### 1.1.3. Multiple protein search

If you have more than one protein pair to search, you can use 'Multiple Protein Search' tab under Protein Search. This will allow you to upload your own file with protein pairs as first and second

column. At the moment, multiple search only takes uniprot accession table (without header), with maximum three column.

Protein Search

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

Gene Search

- > Single Gene Search
- > Two Gene Search

Pathway Search
Disease Search

PROTEIN SEARCH

Please upload a file that contains protein pairs and edge annotation (if available) in the following file formats: xls, xlsx, csv. The first two columns should be Uniprot accessions of the proteins. If you have edge annotation, you can add it to the 3rd column. The file should not include any title.

Select CSV file to upload:

Browse...
No file selected.

Search

Moreover, if you would like to add your own annotation score in the resulting graph, you can include the score in the third column of the file, and click on button 'edge annotation'. You can upload file in any of the three format xls, xlsx, csv. If you have selected to add your own score, it will be shown in the third column upon upload, as shown below.

Protein Search

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

Gene Search

- > Single Gene Search
- > Two Gene Search

Pathway Search
Disease Search

PROTEIN SEARCH

1st Uniprot Accession	2nd Uniprot Accession	Edge Annotation
P20292	P13688	0.44
P40199	P31997	0.5
P01042	P02790	0.45
P08246	P24158	0.44

**Jaccard Similarity Threshold ?**

Select CSV file to upload:

Browse...
proteinAssociationTable.csv

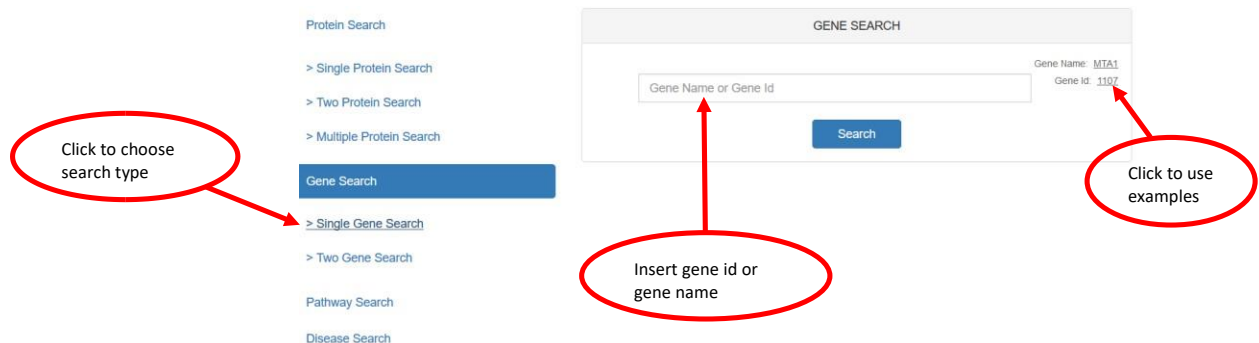
Search

## 1.2. Gene Search

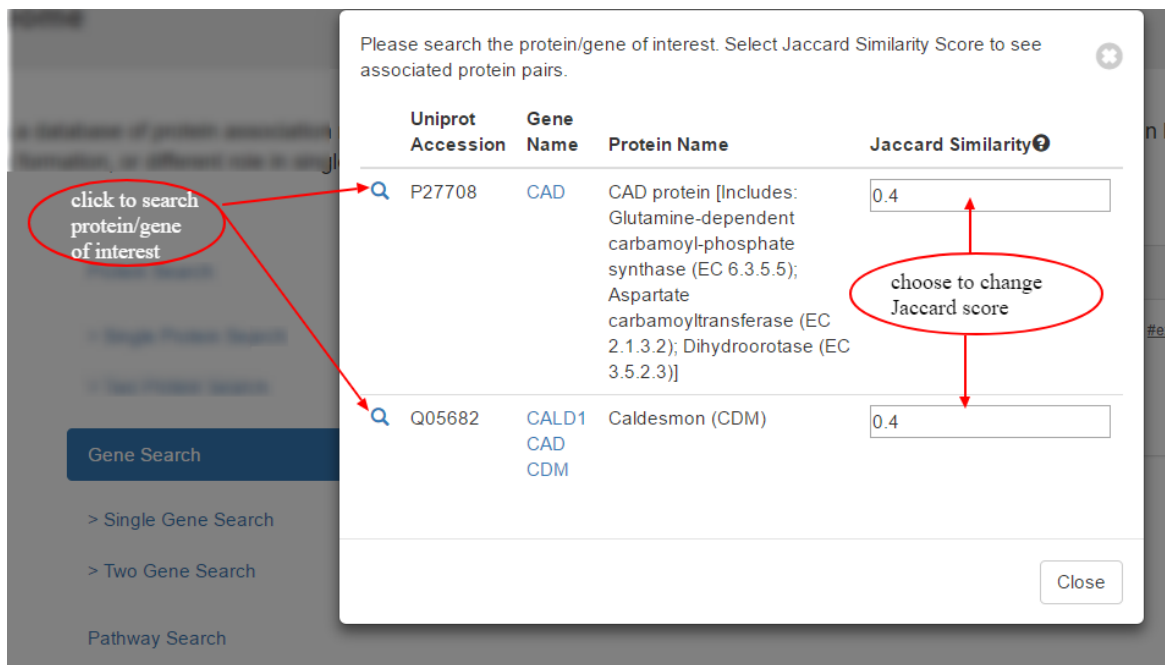
You can also search Tabloid Proteome either using gene name or NCBI RefSeq GeneID. Gene Search also allow you to search with up to two genes using with single or double gene search.

### 1.2.1. Search with one gene

To search with one gene, you can click on 'Single Gene Search' tab given under Gene Search. A search window for gene search will appear, as shown below. Here you can search for all possible proteins and their association with your gene of interest.

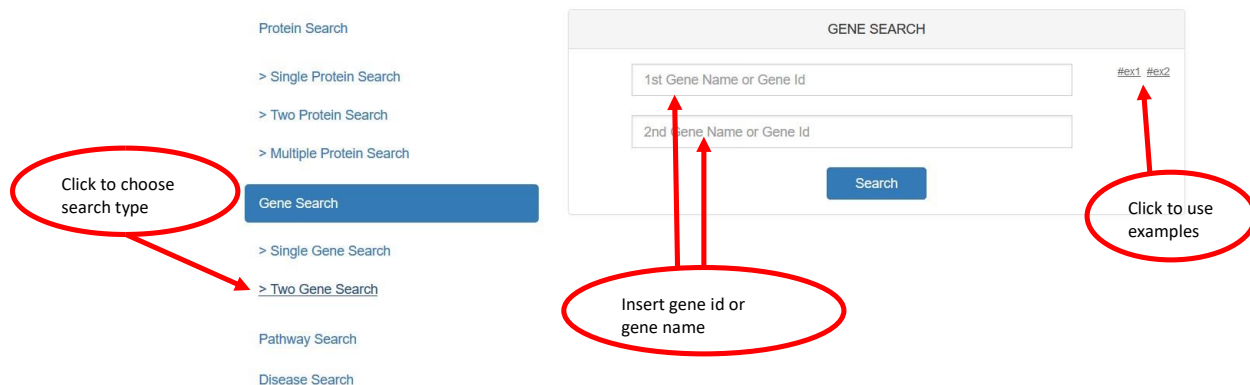


After clicking on search button, another window will appear, showing all possible proteins found for the entered gene. You can initiate your search by clicking on the search button next to the protein accession. In this window you can also change for Jaccard similarity threshold.



### 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.



The next window will allow you to search with your interesting protein pairs and with the search button next to the protein pair you can initiate the search (as shown below).

Total number of protein pairs found: 1

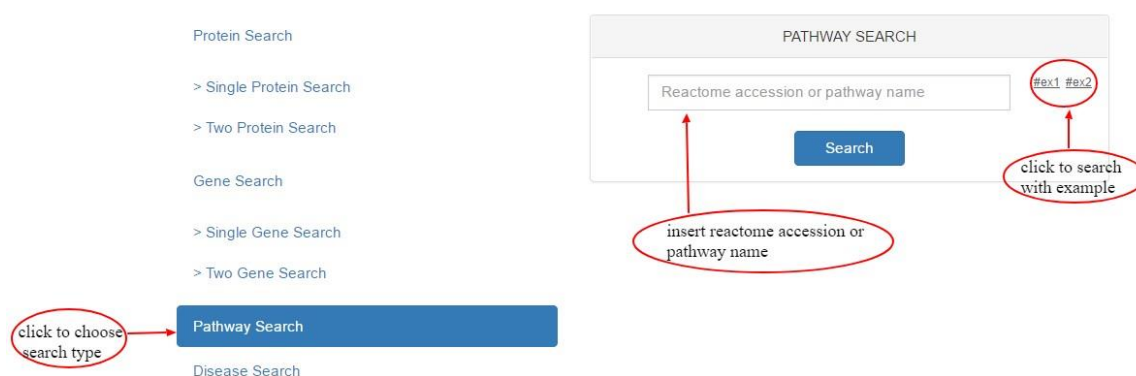
Please select the protein/gene pair of interest

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

A red circle around the magnifying glass icon with the text 'Click here to search' and an arrow pointing to it.

### 1.3. Pathway search:

You can also search for all associated protein pairs available in Tabloid Proteome, for the particular pathway. For the current version of Tabloid Proteome, only include lowest level of pathways from Reactome Database. The search can be initiated either by unique Reactome ID or pathway name.



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. The click on the down arrow will show you all possible protein pairs found in the Tabloid Proteome with

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

Pathway Name	Reaction Accession			
Signaling by FGFR3 point mutants in cancer	R:HSA-8653338			
<b>1st Uniprot Accession</b>	<b>1st Protein Name</b>	<b>2nd Uniprot Accession</b>	<b>2nd Protein Name</b>	<b>Jaccard Similarity</b>
P01112	GTPase HRas (H-Ras-1) [Hs-Ras] [Transforming protein p21 (c-H-ras) (p21ras)] [Cleaved into: GTPase HRas, N-terminally processed]	P01111	GTPase NRas (Transforming protein N-Ras)	0.29
P01111	GTPase NRas (Transforming protein N-Ras)	P01115	GTPase KRas (K-Ras-2) (K-Ras) (c-K-ras) [Cleaved into: GTPase KRas, N-terminally processed]	0.18
SMAD3 Phosphorylation Mutf Mutants in Cancer	R:HSA-3316356			
SMAD3 MH2 Domain Mutants in Cancer	R:HSA-3315487			
Constitutive Signaling by Aberrant PI3K in Cancer	R:HSA-2219530			
Signaling by FGFR3 fusions in cancer	R:HSA-8653334			
Constitutive Signaling by AKT1/IKK in Cancer	R:HSA-5674400			
SMAD4 MH2 Domain Mutants in Cancer	R:HSA-3311921			
Defective GALT12 causes colorectal cancer 1 (CRC51)	R:HSA-5683636			
TGFBRI1 KD Mutants in Cancer	R:HSA-3655532			
Loss of Function of FBXO7 in Cancer and NOTCH1 Signalling	R:HSA-2848697			
TGFBRI1 LBD Mutants in Cancer	R:HSA-3656335			
TGFBRI2 MH2 Framework Mutants in Cancer	R:HSA-3642279			
Constitutive Signaling by Ligand Responsive EGFR Cancer Variants	R:HSA-1236382			
TGFBRI2 Kinase Domain Mutants in Cancer	R:HSA-3646790			

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.

The screenshot shows the 'DISEASE SEARCH' section of a web application. On the left, a vertical menu lists search options: 'Protein Search', '> Single Protein Search', '> Two Protein Search', 'Gene Search', '> Single Gene Search', '> Two Gene Search', and 'Pathway Search'. The 'Disease Search' button in this menu is highlighted with a red circle and an arrow pointing to it with the text 'click to choose search type'. The main content area is titled 'DISEASE SEARCH' and contains a search input field with the placeholder text 'DisGeNET id or disease name'. An arrow points from a red circle containing the text 'Insert DisGeNET id or disease name' to this input field. To the right of the input field is a blue 'Search' button. Further right, there is a red circle containing the text '#BX1 #BX2' with an arrow pointing to it from another red circle containing the text 'click to search with example'.

<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	C0679748			
1st UniProt Accession	1st Protein Name	2nd UniProt Accession	2nd Protein Name	Jaccard Similarity
P01936	4F2 cell-surface antigen heavy chain (4F2c) (4F2 heavy chain antigen) (Lymphocyte activation antigen 4F2 large subunit) (Solute carrier family 3 member 2) (CD antigen CD98)	P33993	DNA replication licensing factor MCM7 (EC 3.6.4.12) (CDC47 homolog) (P1.1-MCM3)	0.18
P42573	40S ribosomal protein S27 (Metalloprotein-1) (MPS-1)	P33993	DNA replication licensing factor MCM7 (EC 3.6.4.12) (CDC47 homolog) (P1.1-MCM3)	0.15
P08196	4F2 cell-surface antigen heavy chain (4F2c) (4F2 heavy chain antigen) (Lymphocyte activation antigen 4F2 large subunit)	P33993	Large neutral amino acids transporter small subunit 1 (4F2 light chain) (4F2LC) (CD98 light chain) (Integral membrane protein F-10) (Lysine amino acid transporter 1) (NAT1) (Solute carrier family 7 member 5) (Lysine cotransporter)	0.15
Precursor B-lymphoblastic lymphoma/leukemia	C0862630			
Precursor B-lymphoblastic lymphoma stage II	C0862630			
Precursor B-lymphoblastic lymphoma	C0865146			
Precursor T cell lymphoblastic leukemia/lymphoblastic lymphoma	C1301369			
adult lymphoblastic lymphoma	C0278721			
Precursor T cell lymphoblastic lymphoma	C1262758			

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

Pathway Search

Disease Search

Tissue Search

TISSUE SEARCH

Choose a tissue

gallbladder

hair

heart muscle

hippocampus

hypothalamus

kidney

lactating breast

liver

lung

lymph node

nasopharynx

oral mucosa

ovary

pancreas

parathyroid gland

placenta

prostate

Search

After selecting of the on the tissue from the drop down menu, 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
Q	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
Q	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
Q	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
Q	P40227	T-complex protein 1 subunit zeta (TCP-1-zeta) (Acute morphine dependence-related protein 2) (CCT-zeta-1) (HTR3) (Tcp20)	P50980	T-complex protein 1 subunit theta (TCP-1-theta) (CCT-theta) (Renal carcinoma antigen NY-REN-15)	0.44	lung
Q	P40227	T-complex protein 1 subunit zeta (TCP-1-zeta) (Acute morphine dependence-related	P78371	T-complex protein 1 subunit beta (TCP-1-beta) (CCT-beta)	0.47	lung

Click here  
to search

It should be noted that, similar to disease search, here the results are also restricted to only protein pairs with at least Jaccard similarity coefficient of 0.4. 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 #	Jacc similarity score #	Interaction #	Ensembl paralogs #	# common complex #	# common pathway #	# common projects #	# common diseases #	
Q13330	Q8TD90	Metastasis-associated protein MTA1	Chromodomain-helicase-DNA-binding protein 5 (CHD-5) (EC 3.6.4.12) (ATP-dependent helicase CHD5)	0.43	yes	no	0	0	5	20	⌵
Q13330	Q12873	Metastasis-associated protein MTA1	Chromodomain-helicase-DNA-binding protein 3 (CHD-3) (EC 3.6.4.12) (ATP-dependent helicase CHD3) (M-2 autotargetin 240 kDa protein) (M2-apha) (Zinc finger helicase) (NCPH)	0.43	yes	no	3	3	6	2	⌵
Q13330	Q8VX09	Metastasis-associated protein MTA1	Transcriptional repressor p66-beta (GATA zinc finger domain-containing protein 2B) (p66p68)	0.48	yes	no	0	3	7	8	⌵
Q13330	Q96ST3	Metastasis-associated protein MTA1	Paired amphipathic helix protein Sin3a (Histone deacetylase complex subunit Sin3a) (Transcriptional corepressor Sin3a)	0.4	yes	no	1	0	6	9	⌵

click on headers to sort the table

Click on the Uniprot accession link to go to Uniprot website

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 #	Jacc similarity score #	Interaction #	Ensembl paralogs #	# common complex #	# common pathway #	# common projects #	# common diseases #	
Q13330	Q8TD90	Metastasis-associated protein MTA1	Chromodomain-helicase-DNA-binding protein 5 (CHD-5) (EC 3.6.4.12) (ATP-dependent helicase CHD5)	0.43	yes	no	0	0	5	20	⌵
Q13330	Q12873	Metastasis-associated protein MTA1	Chromodomain-helicase-DNA-binding protein 3 (CHD-3) (EC 3.6.4.12) (ATP-dependent helicase CHD3) (M-2 autotargetin 240 kDa protein) (M2-apha) (Zinc finger helicase) (NCPH)	0.43	yes	no	3	3	6	2	⌵
Q13330	Q8VX09	Metastasis-associated protein MTA1	Transcriptional repressor p66-beta (GATA zinc finger domain-containing protein 2B) (p66p68)	0.48	yes	no	0	3	7	8	⌵

click on the row to close the details

click on the icon to close the panel

click on the icon to open the panel

**Interactions**

IntAct : yes      BioGRID : yes

Intact Confidence: 0.35      Intact Detection: M0007\_antitag communsprecipitation      Intact Interaction Type: M0914\_association

**Common Projects**

**Pathways**

**Complexes**

**GO**

**Diseases**

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	<a href="#">PXD000314</a>	Sequential IMAC, human lung cancer tissue, phosphoproteomics	cell culture, lung		instrument model
2	<a href="#">PXD001572</a>	DNA sensing, protein interactions, IFX	cell culture	Biomedical	LTQ Orbitrap Velos
3	<a href="#">PRD000711</a>	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	<a href="#">R-HSA-1445148</a>	Translocation of GLUT4 to the plasma membrane	TAS
2	<a href="#">R-HSA-75035</a>	Chk1/Chk2(Cds1) mediated inactivation of Cyclin B:Cdk1 complex	TAS
3	<a href="#">R-HSA-5625740</a>	RHO GTPases activate PKNs	TAS
4	<a href="#">R-HSA-5628897</a>	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.

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	<a href="#">14743216</a>	MI:0676- tandem affinity purification
2	5615	Emerin complex 52	Complexes are named on the basis of their S300 elution fraction number. Subunits 8-22 were	None	Emerin is involved in Emery-Dreifuss muscular dystrophy	None	<a href="#">17620012</a>	MI:0004- affinity chromatography technologies, MI:0226- ion exchange

### 2.1.5. GO

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 EMBLEBI Gene Ontology service.

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

### 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	<a href="#">C0025202</a>	melanoma
2	<a href="#">C2239176</a>	Liver carcinoma
3	<a href="#">C0242379</a>	Malignant neoplasm of lung
4	<a href="#">C0376358</a>	Malignant neoplasm of prostate

## 2.2. Graph View

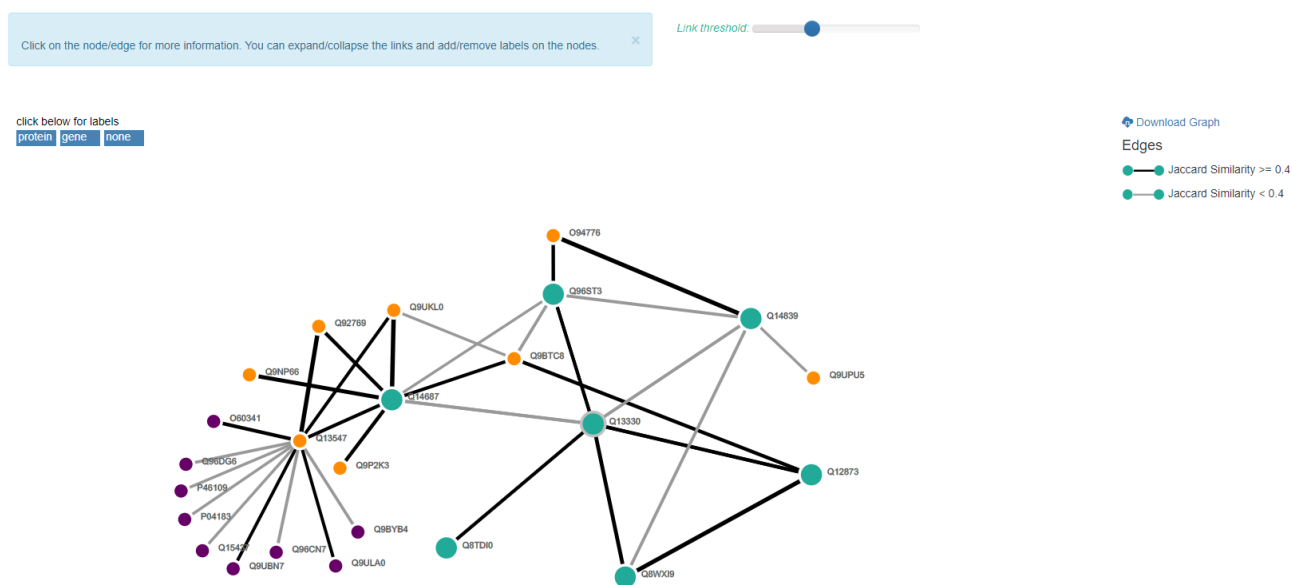
In Tabloid proteome, you can also visualize your results in form of graph, where each node represent proteins and edges represents associations. The link to the graph can be accessed through the upper right corner of the Data Table result page.

2nd protein name	2nd protein gene name	Jacc similarity score	Interaction	Ensembl paralog	# common complex	# common pathway	# common projects	# common diseases	
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	▼
Chromodomain-helicase-DNA-binding protein 3 (CHD-3) (EC 3.6.4.12) (ATP-dependent helicase CHD3) (M-2 autoantigen 240 kDa protein) (M2-alpha) (Zinc finger helicase) (hZFh)	CHD3	0.43	yes	no	3	3	6	2	▼
Transcriptional repressor p66-beta (GATA zinc finger domain-containing protein 2B) (p66/p66)	GATAD2B KIAA1150	0.48	yes	no	0	3	7	8	▼
Paired amphipathic helix protein Sin3a (Histone deacetylase complex subunit Sin3a) (Transcriptional corepressor Sin3a)	SIN3A	0.4	yes	no	1	0	6	9	▼

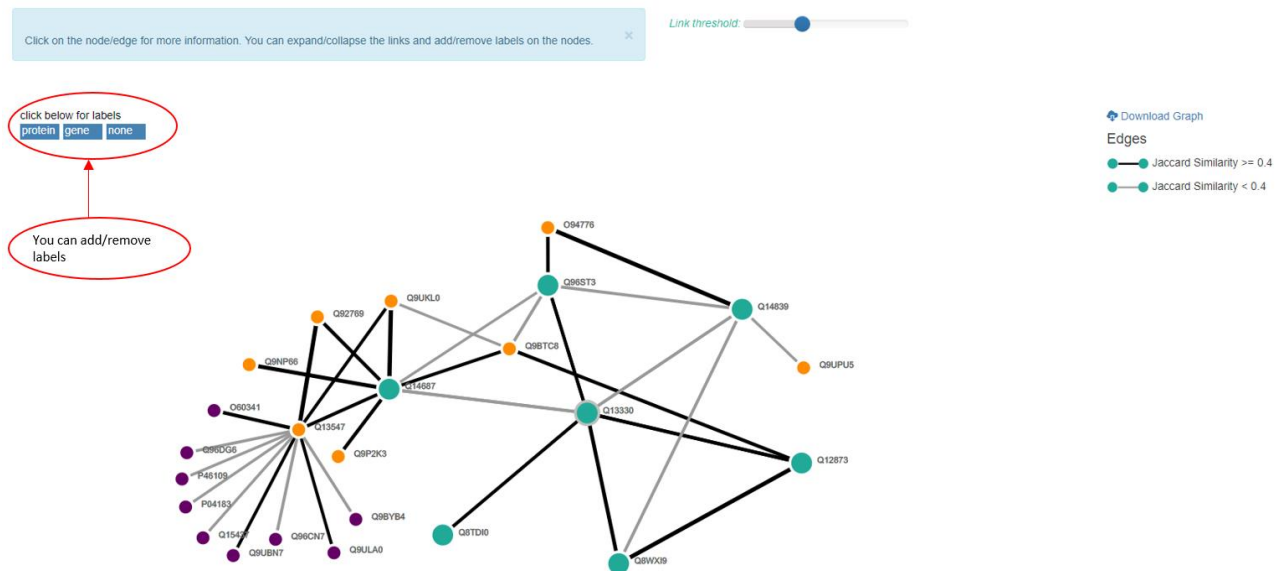
[Download](#) [Graph View](#)

Click to go to Graph View

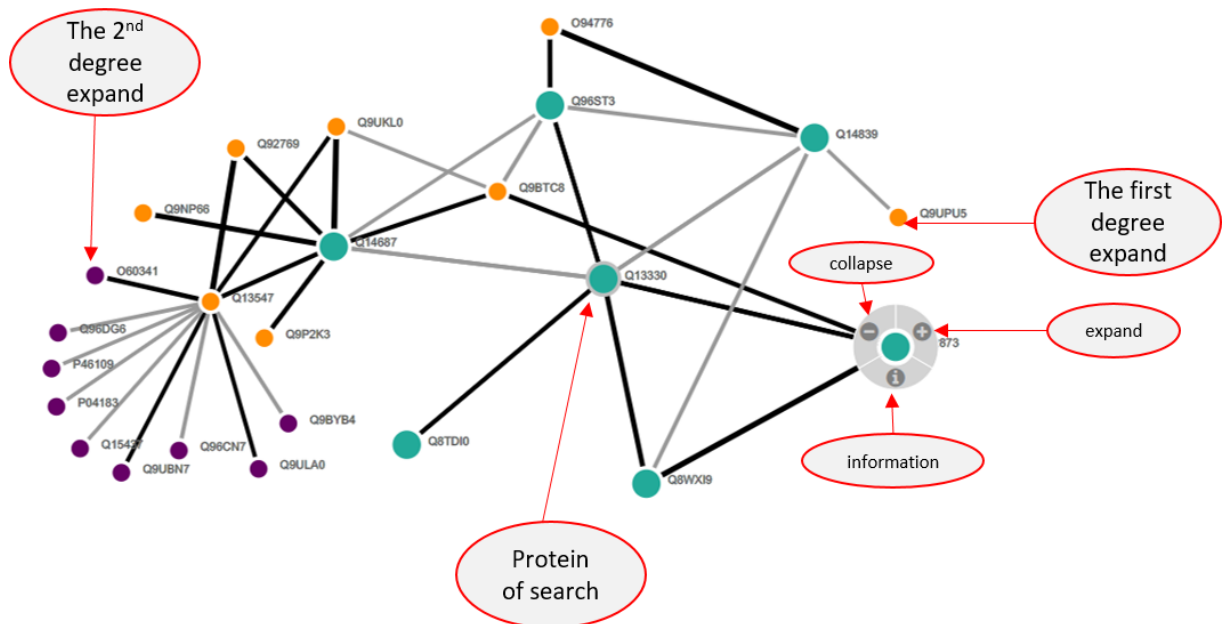
On this page, you can see dynamic graph representation of your search. All nodes and edges are repositionable. After/before changing position of the graph you can download as an image (.png) by clicking on “Download Graph” link (as shown below). For more information about the proteins and their relations, 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 2<sup>nd</sup> 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.

The screenshot shows a 'Protein Details' pop-up window with the following information:

Uniprot Accession :	<a href="#">Q96ST3</a>
Uniprot Status :	reviewed
Protein Name :	Paired amphipathic helix protein Sin3a (Histone deacetylase complex subunit Sin3a) (Transcriptional corepressor Sin3a)
Protein Entry Name :	SIN3A_HUMAN
Gene Name :	SIN3A
Entrez Gene Id :	<a href="#">25942</a>
Species :	Homo sapiens (Human)
Length :	1273

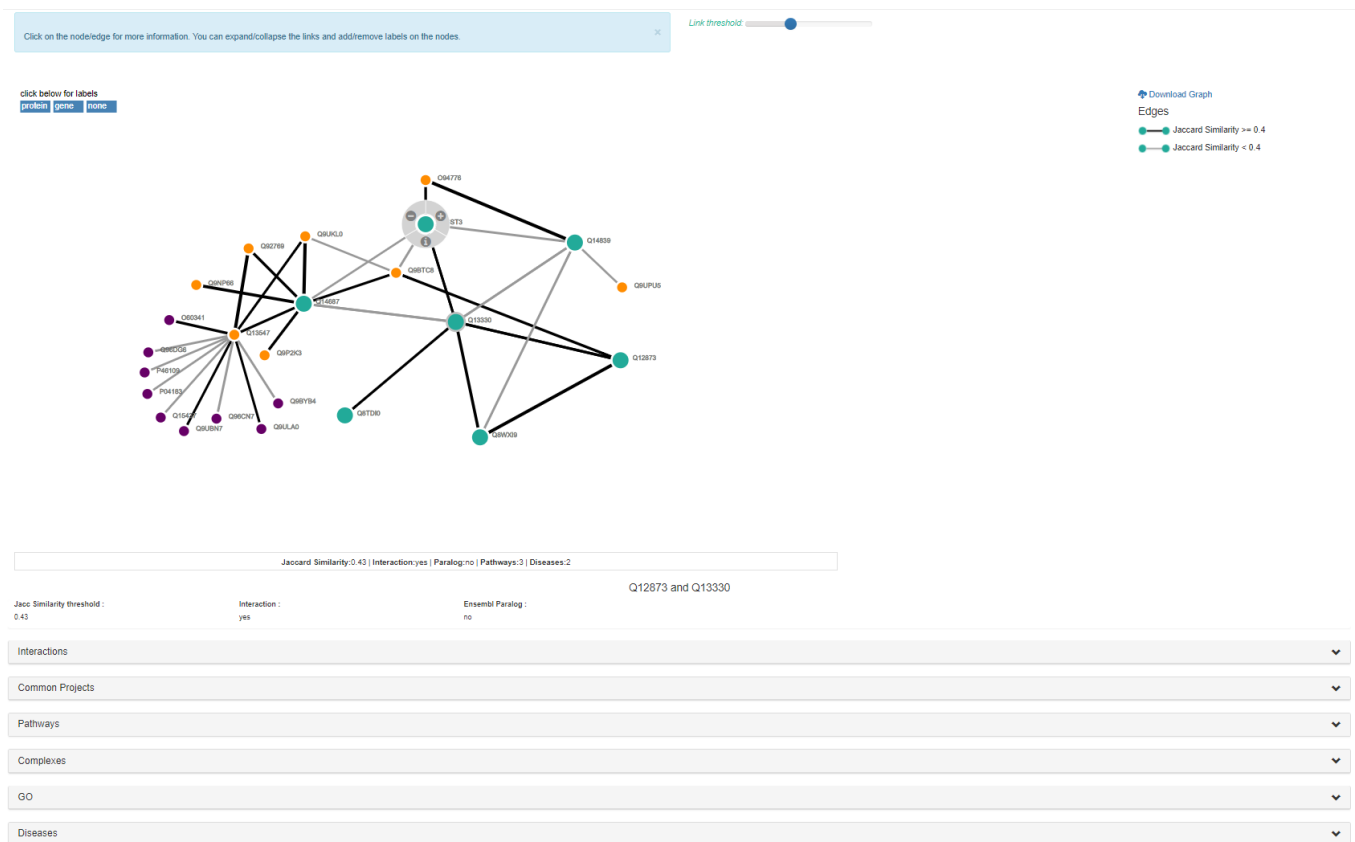
The background shows a network graph with nodes and edges, representing protein-protein interactions.

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.



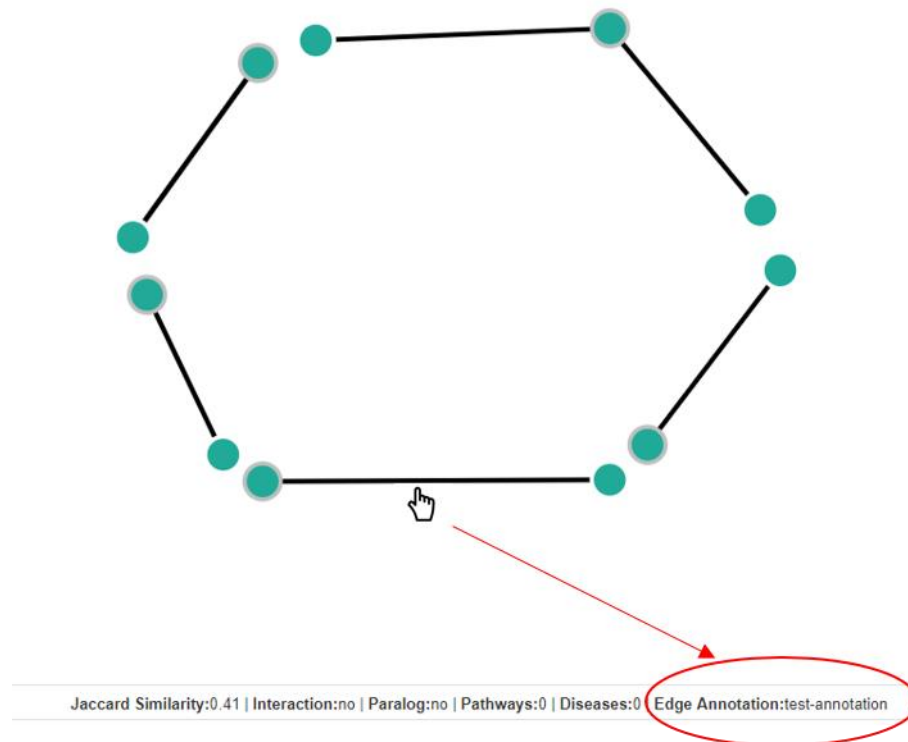
The edges between the proteins represents biological association. When user hovers on the edge, different biological association between proteins are visible below the graph. Edge with black color represent the Jaccard similarity association found with our method which is 0.4 and above, and gray color 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).



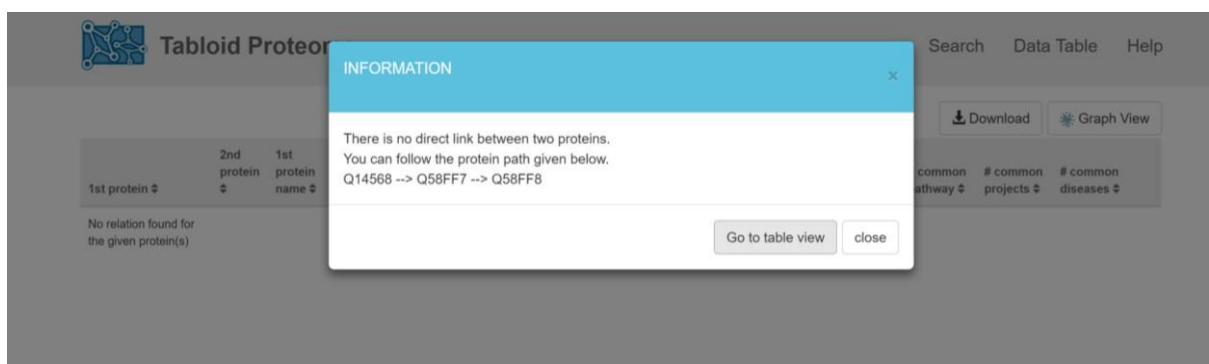
For multiple protein search, if edge annotation are added, then it will be shown below the graph when user hover on the edge. Graph shown below shows an example of the multiple protein search with added annotation.





### 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).



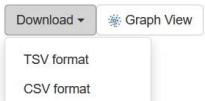
For further click on the “Data Table” option, you can view the result about the search in the Data Table view, with all information explained above. With the Data Table view, you can go to Graph View, to visualize you result with the same information and changes, as explained above.

### 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



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) (CD antigen CD86a)	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 CD88c)	CEACAM6 NCA	Carcinoembryonic antigen-related cell adhesion molecule 8 (CD67 antigen)	CEACAM8 CGM8	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.

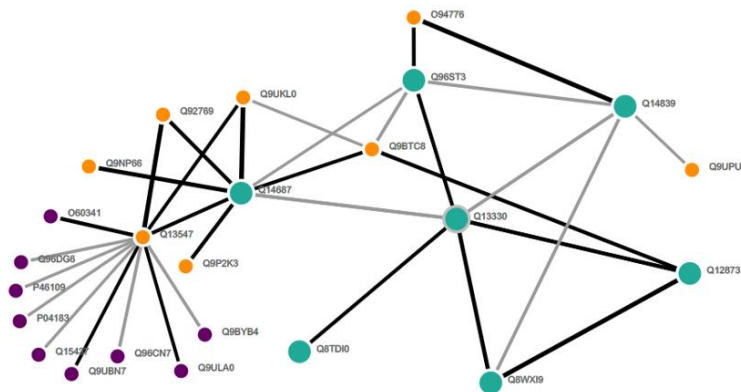
Link threshold:

click below for labels  
[protein](#) [gene](#) [none](#)

Download Graph

Edges  
●—● Jaccard Similarity  $\geq 0.4$   
●—● Jaccard Similarity  $< 0.4$

You can download the graph as an image



## 4. Citation

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

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

**Unbiased Protein Association Study on the Public Human Proteome Reveals Biological Connections between Co-Occurring Protein Pairs**

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

**The online Tabloid Proteome: an annotated database of protein associations**

*Nucleic Acids Res.*, 2017

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