

How to Download the Protein-Protein Interaction (PPI) Data from STRING

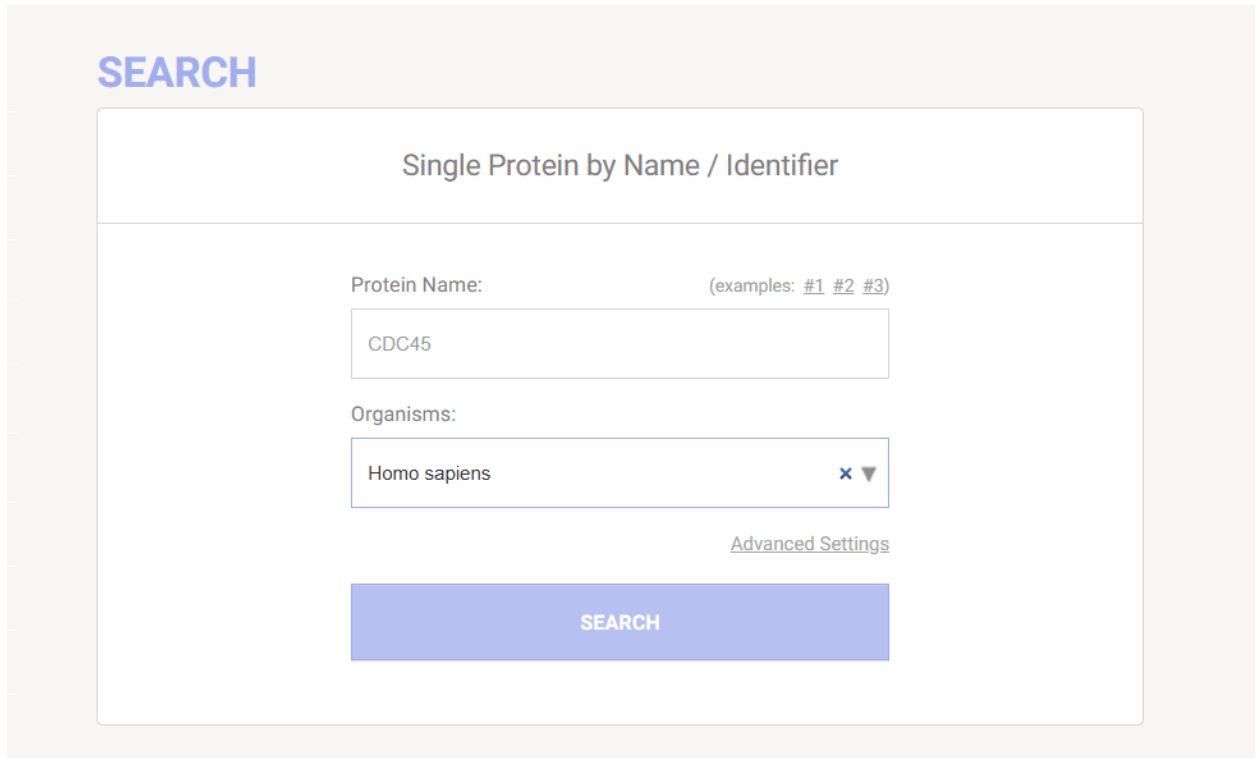
1) Go to the following link:

<https://string-db.org/cgi/network?taskId=bKEllqhE3Ntr&sessionId=bQYS56KsX3jK>

2) Click on the Search tab.

In the Protein name field, type CDC45.

In the Organism field, select Homo sapiens.



SEARCH

Single Protein by Name / Identifier

Protein Name: (examples: #1 #2 #3)

CDC45

Organisms:

Homo sapiens x ▼

[Advanced Settings](#)

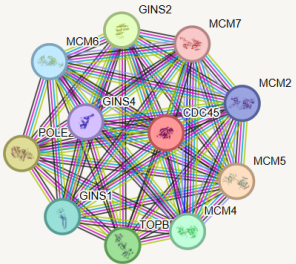
SEARCH

Then click Search.

3) Select the appropriate result and click Continue.

organism		protein
1) <input checked="" type="checkbox"/>	Homo sapiens	CDC45 - Cell division control protein 45 homolog; Required for initiation of chromosomal DNA replication; Belongs to the CDC45 family.
2) <input type="checkbox"/>	Homo sapiens	DTD1-2 - D-aminoacyl-tRNA deacylase 1; Possible ATPase involved in DNA replication, may facilitate loading of CDC45 onto pre-replication complexes. [<i>a.k.a. pqr-68, ENSG00000284776, Q9BW67</i>]

4) Navigate to the Exports tab.



Viewers > Legend > Settings > Analysis > Exports > Clusters > More > Less

Export your current network: [Send network to Cytoscape](#)

- ... as a bitmap image: [download](#) file format is 'PNG': portable network graphic
- ... as a high-resolution bitmap: [download](#) same PNG format, but at higher resolution
- ... as a vector graphic: [download](#) SVG: scalable vector graphic - can be opened and edited in Illustrator, CorelDraw, Dia, etc
- ... as short tabular text output: [download](#) TSV: tab separated values - can be opened in Excel and Cytoscape (lists only one-way edges: A-B)
- ... as tabular text output: [download](#) TSV: tab separated values - can be opened in Excel (lists reciprocal edges: A-B,B-A)
- ... as an XML summary: [download](#) structured XML interaction data, according to the 'PSI-MI' data standard
- ... protein node degrees: [download](#) node degree of proteins in your network (given the current score cut-off)
- ... network coordinates: [download](#) a flat-file format describing the coordinates and colors of nodes in the network
- ... protein sequences: [download](#) MFA: multi-fasta format - containing the aminoacid sequences in the network
- ... protein annotations: [download](#) a tab-delimited file describing the names, domains and descriptions of proteins in your network
- ... functional annotations: [download](#) a tab-delimited file containing all known functional terms of proteins in your network

5) Download the TSV file to use later in R or other data analysis tools.

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It is recommended to save this file in the same directory where your R script for building the PPI network is located

