Using the interactive viewer

Source: select IP-MS data, SEC-MS data, or both, if nothing is selected both will be used

Interaction support:

IP+SEC: interactions found in IP-MS and SEC-MS

CORUM: interactions found in the CORUM interaction database

Direct: direct IP-MS interactions

RNA mediated: RNA-mediated IP-MS interactions

RNA shielded: RNA-shielded IP-MS interactions

Protein: search for a specific protein of interest (proteins are listed by their gene names). Use a comma-separated list to search for multiple proteins

Number of neighbors: how many degrees of separation from the searched proteins should be visualized

Clustering method: choose a clustering method, options are Louvain, Markov, and clusterOne

Clustering resolution: how large or small should the clusters be that are generated by the clustering method

Color node by: how should nodes be colored, options are life-cycle stage, location annotation (from Human Protein Atlas), and disease annotations (from DisGenNet)

Labels: should gene names be displayed on the network

Use Normalized Betweenness: betweenness centrality analysis is normalized to the ‘’traffic load’’ (e.g., number of interactions) between the life-cycle steps. If left unchecked the unnormalized betweenness centrality analysis is used.

Create Interactome: needs to be clicked any time selections are changed to create the updated network

Download: download the interactome table for the currently visualized network