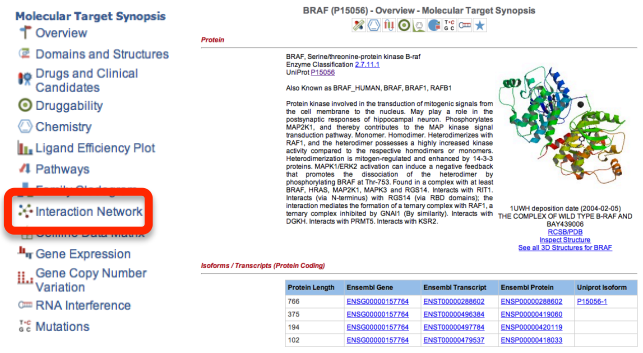
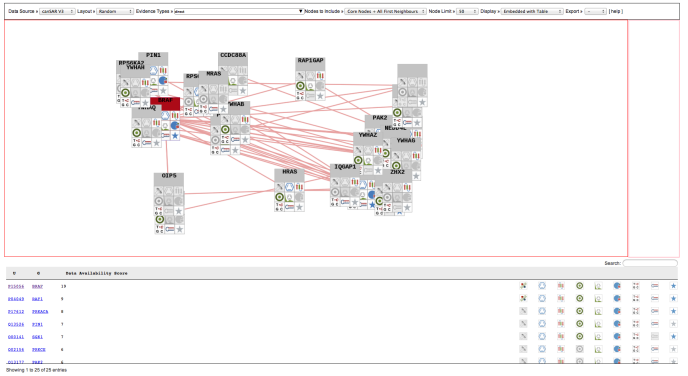
Target interaction network

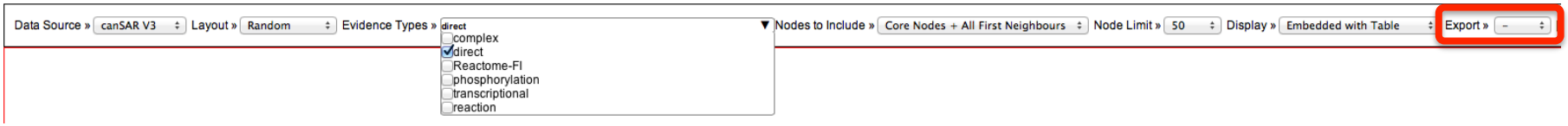




Select 'Interaction Matrix' on the molecular target synopsis side menu.

This will display a network of interactions between the target protein (red) and other proteins. The canSAR human interactome is comprised of the following key data sources:

1) Non-predictive interactions from the IMEx consortium (Orchard et al., 2012)
2) Protein interactions from HPRD (Peri et al., 2003)
3) Phosphorylation reactions from Phosphosite (Hornbeck et al., 2015)
4) Crystallographically-resolved protein binding interfaces from PDBePISA (Krissinel and Henrick, 2007) with complexation significance score greater than zero or interface binding site area greater than 400 square angstrom
5) Functional interaction definitions from Reactome (Milacic et al 2012)
6) Transcriptional signalling events from TFactS (Essaghir et al., 2010)



Use the drop down menus above the network to select the source of interactions displayed (canSAR V3 or STRING), to change the network layout, number and type of nodes displayed and more. The network view can be exported as an image (Export -> PNG) or as a network file for use in Cytoscape (Export -> JSON). Note: JSON files can only be imported into Cytoscape 3.1.0+.