IntAct – Basic search

1. Go to the IntAct webpage. http://www.ebi.ac.uk/intact/
2. Search for LRRK1.
3. How many binary interactions have you found?
   Click on “customize view”, and check in the species A and B columns.
   What taxons can you find among the interaction partners?
   How many interactions are left after filtering out the spoke interactions?
   Check the graph view.
   Have a closer look on the interaction partners. How many partners are there? What other types of interaction partners does it have? List a few detection methods they were identified with.
   Now choose all proteins and click “search interactions”. How many interactions do you find now? What are missing compared to the “LRRK1” results?
4. Search for “LRRK1 and DAPK1”
   Click on the “EBI-“ interaction identifier.
   Now you can see publication data and the experiment description.
   What was the interaction method they used?
   Go down to the “Interactions” and the “Participants” paragraphs.
   What kind of interaction is this? Which partner was the bait? Click on the red “F” in the DAPK and LRRK1 lines. What is a “ha tag” and a “myc tag”? Click on the links!

IntAct – Combined search

1. There's no interactions found to the query “Q95JH6”. Go to the www.ebi.ac.uk/tools/sss page, choose NCBI-BLAST search on proteins, paste in the sequence and start the search. The result is a summary tabe.
2. Have a look at the "Tool Output" to see the alignments, the "Visual Output" tabs for a visualisation of the sequence similarity and the "Functional Predictions" to look for structural-functional similarity.
3. Go back to the Summary Table. Can you find close species that has the "Molecular Interaction" annotation listed? How many interactions belong to this protein?

BioGrid

1. Search for the human ACTA1 protein!
   How many interactors and interactions did you find?
   How many of the interactions
   - are physical / genetic?
   - come from high / low through methods?
   How many publications are there?

Check the "Interactions" tab, what kind of experiments do you find there?
Go to the "Network" tab and try out the different filters, evidences, and layouts.
Check out the "Chemicals" and "PTM Sites" tabs as well.

STRING

1. Go to the webpage http://string-db.org/
2. Search for the human TYMS. You can see a protein network in an interactive display. The spheres are not empty: STRING imports the known or predicted structure of preoteins from the PDB and the Swiss-Model. You can drag the circles and click on them for more information.
3. Go to the "Data Settings" and set the minimum required interaction score to the highest confidence, and the max numer of interacotrs to 20. See the legend to understand what the lines of different colors mean. Which interaction of TYMS has the most evidence?
4. In the "View Settings" switch to condifence mode. (Note: as you can see, there are other display options, like you can diasable the structure previews or hide node labels.)
   Since we set the confidence score to the highest creiterium, the edges are thick and similar. Set the score back to a lower requirement, and see if new lines appeared.
5. From the "Evidence" tab chose "Coexpression", and see the pattern. Repeat the query for the mouse TYMS protein. Which protein is the TYMS expression level most correlated with?