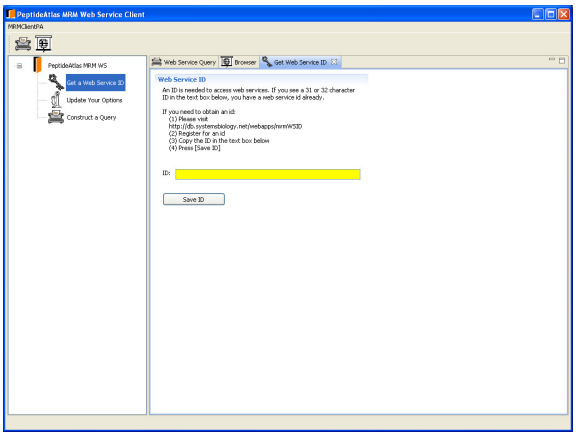
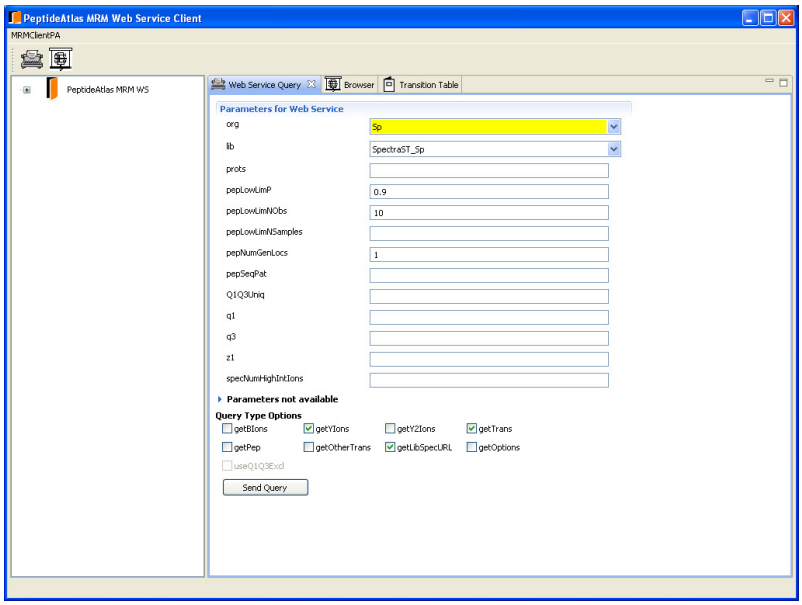
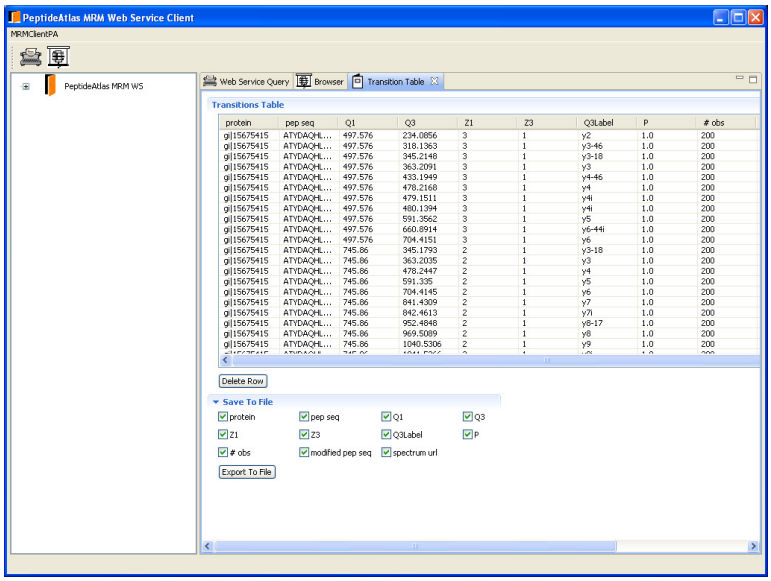
TIQAM-PeptideAtlas tutorial



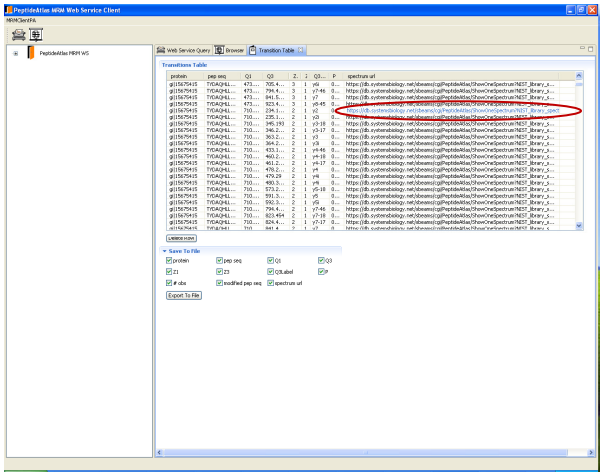
1. Double Click short cut of TIQAM-PeptideAtlas
2. Click "**PeptideAtlas MRM WS**" in the left panel shown in the left panel
3. Follow instruction in **"Get Web Service ID"** using a any web brower.
4. Cut and paste ID obtained from the http://db.systemsbiology.net/webapps/mrmWSID to the **"Web Service ID"** then Click **"Save ID"** button.
5. Click back to **"Web Service Query"** tab on the top shown in the left figure.
6. Select Sp in **"org"** drop down menu and SpectraST_Sp in **"lib"** drop down menu for Streptococcus Pyogenes library. Currently, it shows Hs (Human) and Sc (yeast) consensus library is available.
7. Fill 0.9 in "**pepLowLimP"** text box for lower limit of peptide prophet and 10 in **"pepLowLimNObs"** text box for lower limit of number of observation and 1 in**"pepNumGenLocs"** text box to get unique protein mapping by selecting one for genome chromosomal locations. Then select getYIons , getTrans, getLibSpecURL as shown in the left figure. Click **"Send Query"**

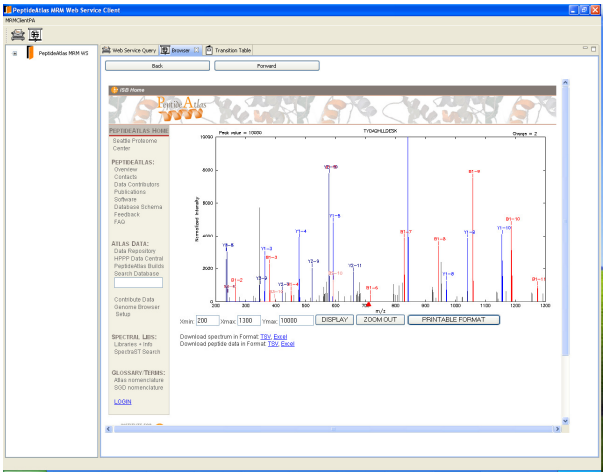




8. You will see the resulted Transition Table. Click "Save To File" tab and click "Export To File" and give file name "Streptococcu_TIQAM_PA_out.csv" and click "save" button as shown in the left.

9. Scroll the table to the right to see spectrum url. Click spectrum url shown in the below left figure (any url belong to TYDAQHLLDESK will be ok). Then select **"Brower"** tab at the top to exam the spectra shown in the below right figure.





10. Exercise

What Q3 would you pick for peptide TYDAQHLLDESK transition?

Open the exported file using Excel. How many transitions did you get?