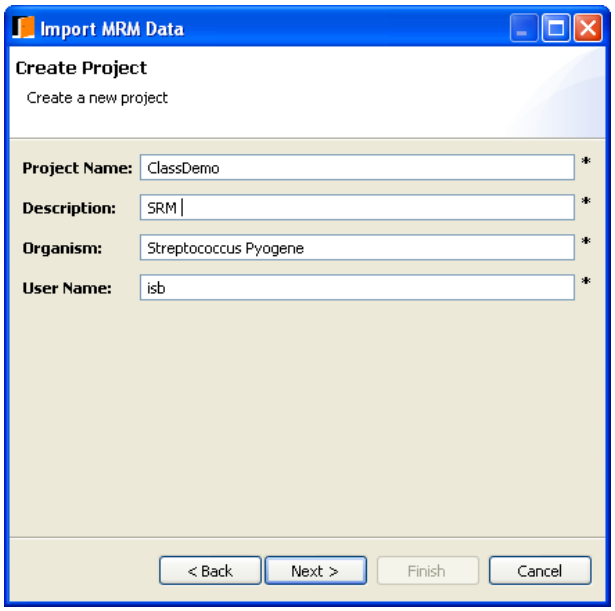
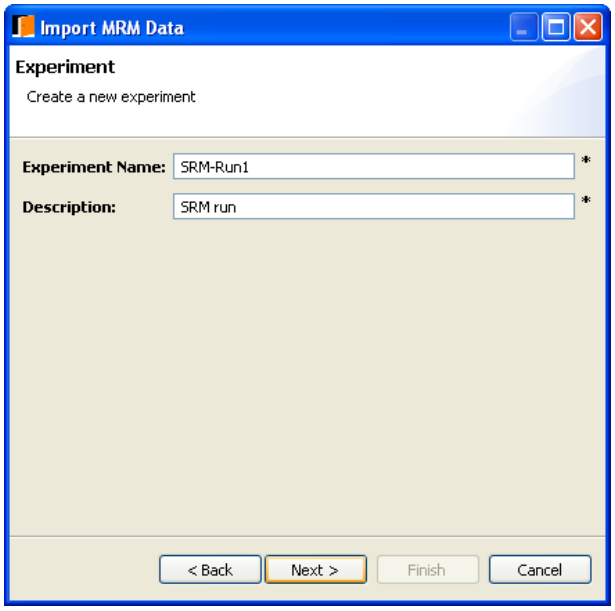
TIQAM-Viewer tutorial

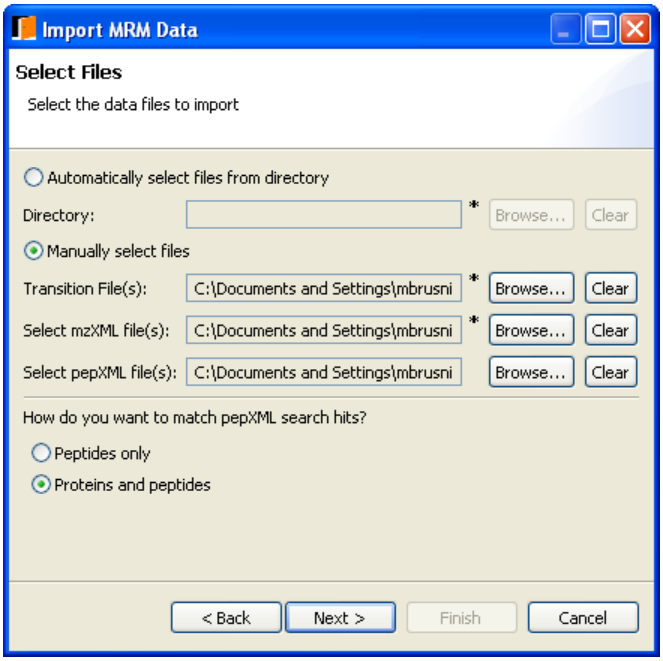




1. Double Click short cut of TIQAM-Viewer.
2. **File >> Import**

   Select **"A new project"**

   Click "**Next**"
3. Fill out the Create Project wizard as shown in the left figure
4. Click "**Next**"
5. Fill out the Experiment wizard as shown in the left figure



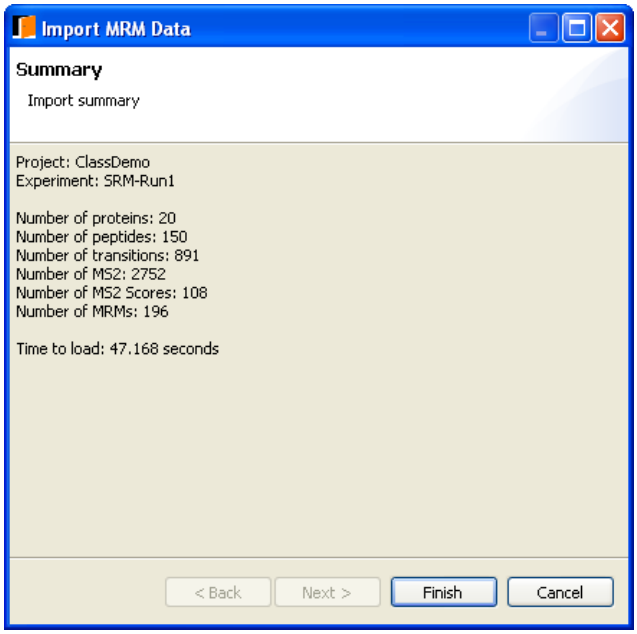
6. Click **"Manually select files"** and select the following files located in the "My Document/TIQAM-

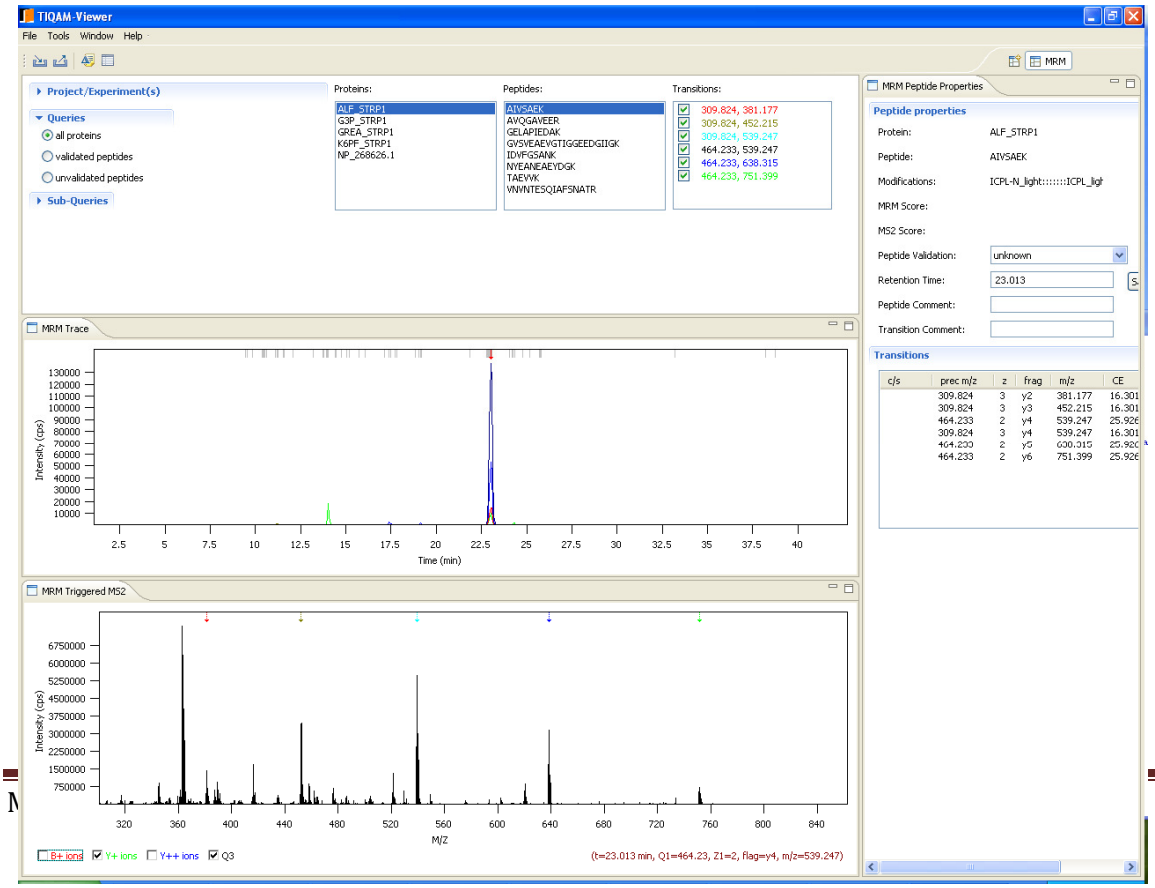
ClassDemoData" : Transition File (StreptococcusPyogene.csv), mzXML (0223House4.mzXML, 0223House5.mzXML), pepXML (StreptococcusPyogene_pep.xml). Select Peptides only before click "**Next**" .

7. When it's imported, it will show the summary dataset shown in the right figure

8. Click **"refresh"** button to show your imported project and experiment.

9. Select **"all proteins"** in Queries section and you will have the screen shown below





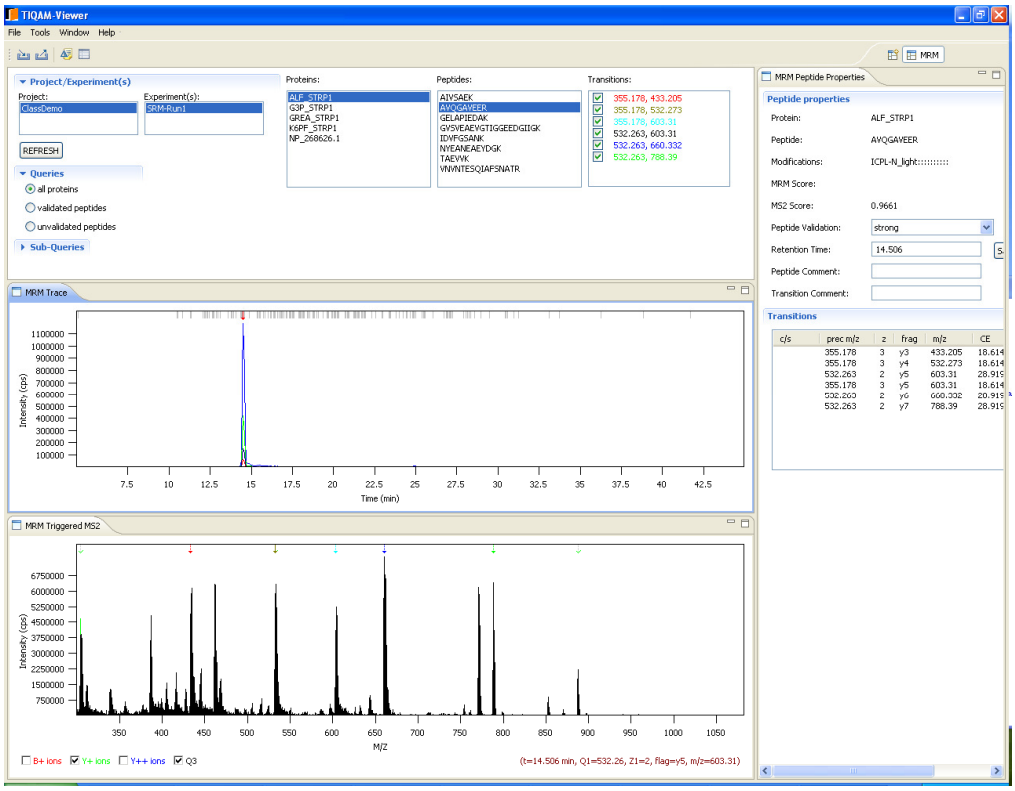
10. Exercise.

Go through the transitions and you can decide the level of validation whether the transition sets for a given peptide validate the peptide identification.

For example, the peptide AVQGAVEER of ALF_STRP1 Protein generates strong peptide (shown below figure). You can annotate this as strong category in Peptide Validation.

Which three transitions would you like to use for quantifying AVQGAVEER peptide? Please find your top three candidates from transitions table and write.

You may go through more peptides and proteins to see how you would like to annotate peptide validation and select best transitions.


TIQAM-Viewer
File Tools Window Help
MRM
Project/Experiment(s)
Project:
ClassDemo
Experiment(s):
SRM-Run1
REFRESH
Queries
all proteins
validated peptides
unvalidated peptides
Sub-Queries
Proteins:
ALF_STRP1
G3P_STRP1
GREA_STRP1
K6PF_STRP1
NP_268626.1
Peptides:
AIVSAEK
AVQGAVEER
GELAPIEDAK
GVSVEAEVGTIGGEEDGIIGK
IDVFGSANK
NYEANEAEYDGK
TAEVVK
VNVNTESQIAFSNATR
Transitions:
355.178, 433.205
355.178, 532.273
355.178, 603.31
532.263, 603.31
532.263, 660.332
532.263, 788.39
MRM Peptide Properties
Peptide properties
Protein: ALF_STRP1
Peptide: AVQGAVEER
Modifications: ICPL-N_light:::::::::
MRM Score:
MS2 Score: 0.9661
Peptide Validation: strong
Retention Time: 14.506
Peptide Comment:
Transition Comment:
Transitions
c/s prec m/z z frag m/z CE
355.178 3 y3 433.205 18.614
355.178 3 y4 532.273 18.614
532.263 2 y5 603.31 28.919
355.178 3 y5 603.31 18.614
532.263 2 y6 660.332 28.919
532.263 2 y7 788.39 28.919
MRM Trace
Intensity (cps)
Time (min)
MRM Triggered MS2
Intensity (cps)
M/Z
B+ ions
Y+ ions
Y++ ions
Q3
(t=14.506 min, Q1=532.26, Z1=2, flag=y5, m/z=603.31)