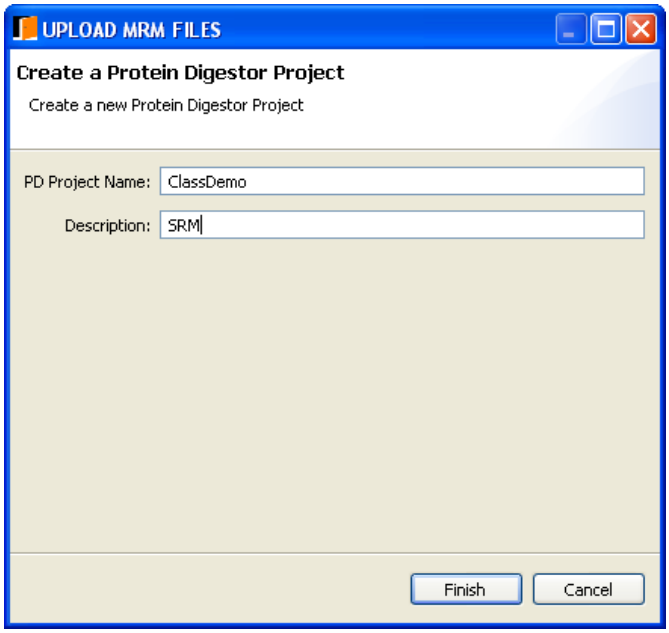
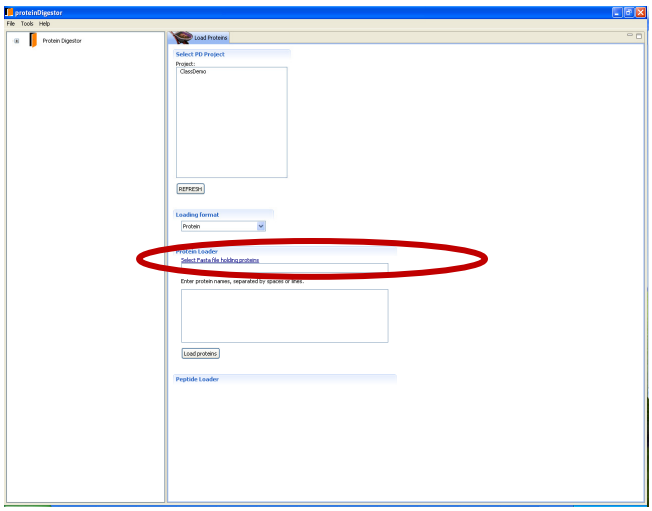
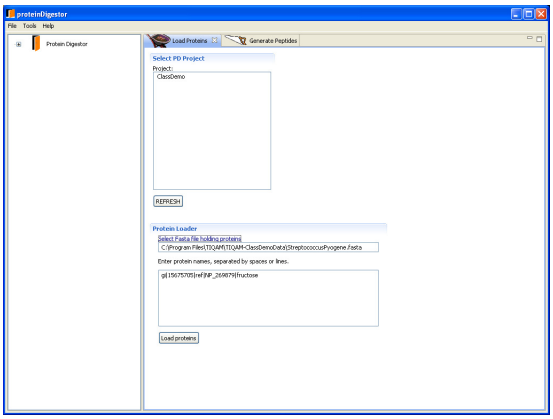
TIQAM-Digestor tutorial



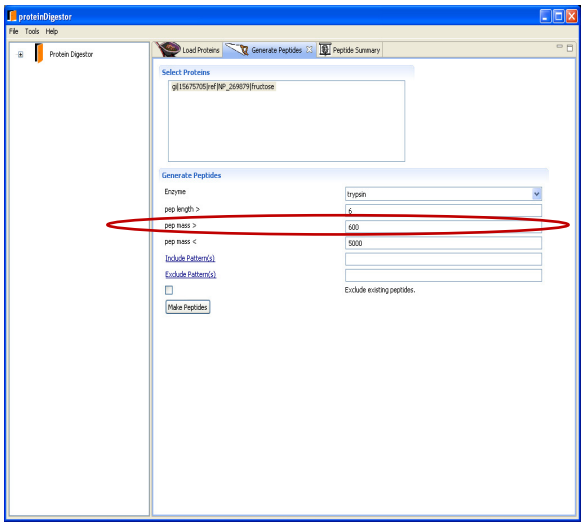
1. Double Click Short cut of TIQAM-Digestor
2. **File >> New >> Create new PD project**
3. Type PD Project Name and Description as shown in the screen then click **"Finish"**



4. Click **"Select Fasta file holding proteins in Protein Loader"** Select StreptococcusPyogene.fasta in the "My Document/TIQAM-ClassDemoData"

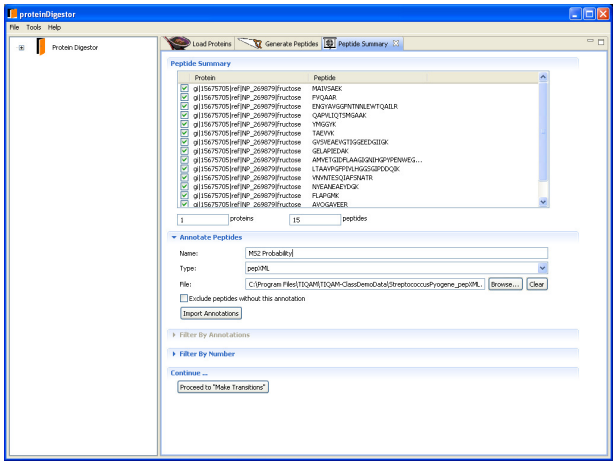


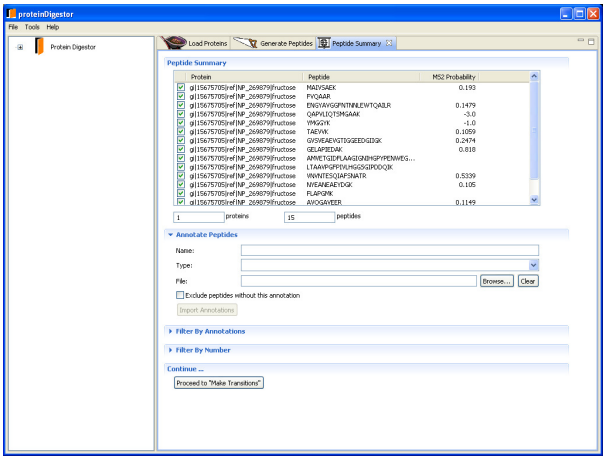
5. Fructose-bisphosphate aldolase will be loaded as it is shown in the left figure. Click ClassDemo in **"Select PD Project"** tab, then click **"Load Proteins"** button

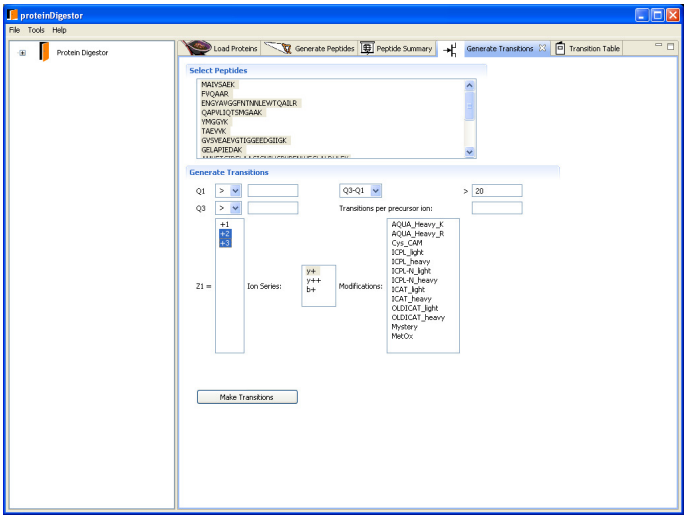


6. Change "pep mass >" query to be 600 as shown in the left figure and then click **"Make Petides"** button

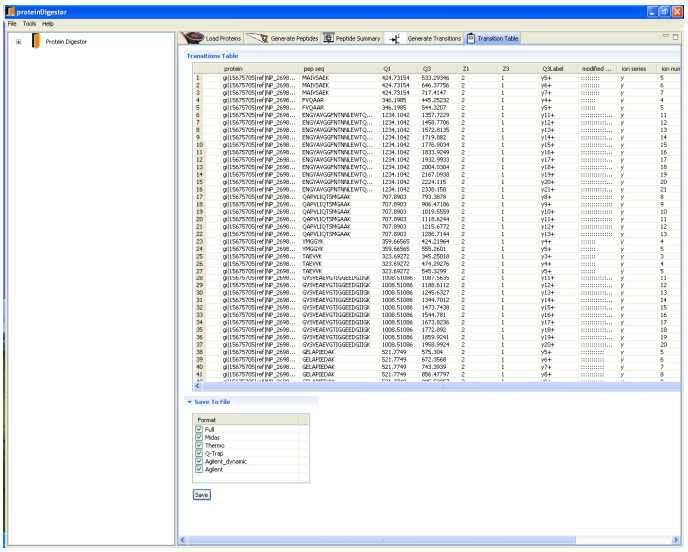
7. Click **"Annotate Peptides"** tab and type in Name filed and select Type field and select File StreptococcusPyogene_pepXML.xml using **"Brower"** button shown in the left bottom figure. The clock **"Import Annotations"** button to see the right bottom figure.







8. Click "Proceed to Make Transitions" button it will show Generate Transitions page as you see in the left figure. Select +2 and +3 in z1 column while holding down shift key then click **"Make Transitions"**



9. It will show Transition Table, click "Save to File" tab then it will show **"save"** button (shown in the left figure) and save as StreptococcusPyogene_Digestor in "My Document/TIQAM-ClassDemoData".

10. Exercise

Open the exported file StreptococcusPyogene.txt in Excel and order by CE (Collision Energy). Is there any correlation with Mass?

Could you think of way to get better Retention time for schedule SRM?