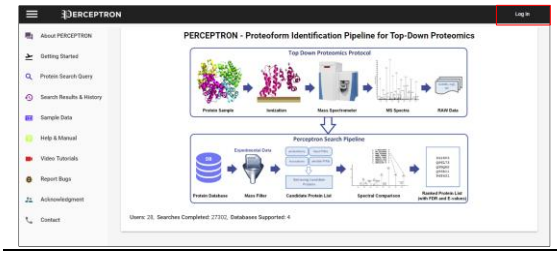
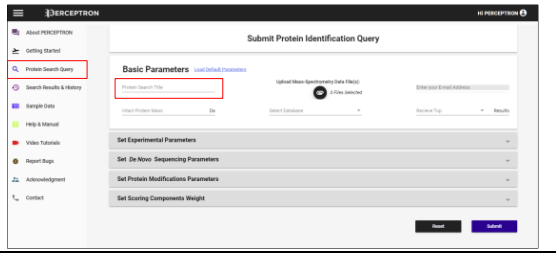
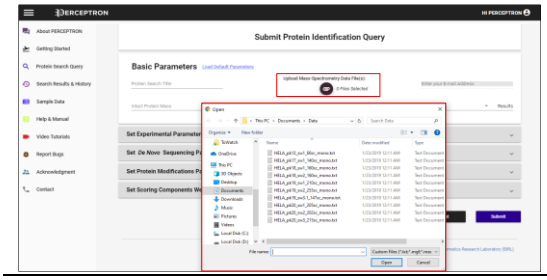
Step-by-Step Guidelines for using PERCEPTRON



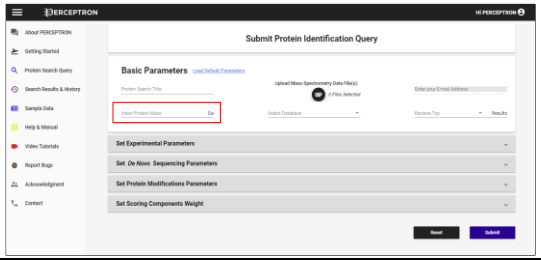
Step 1: Login PERCEPTRON using an existing email account.



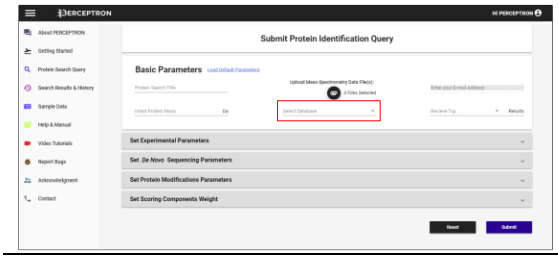
Step 2: Go to the 'Protein Search Query' and enter 'Protein Search Title' to start search.



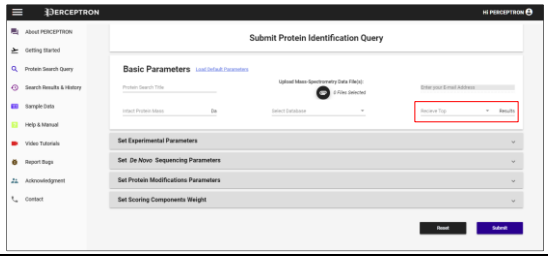
Step 3: Browse and upload Data file(s). Upload one file (.mzXML/ .mzML/ .MGF/ .txt/) to perform single file search or add multiple peak-lists (.txt) to search in batch mode.



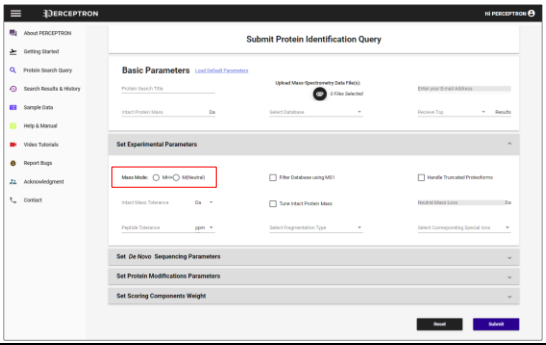
Step 4: Click on 'Intact Protein Mass' to enter mass of precursor ion (MS1).



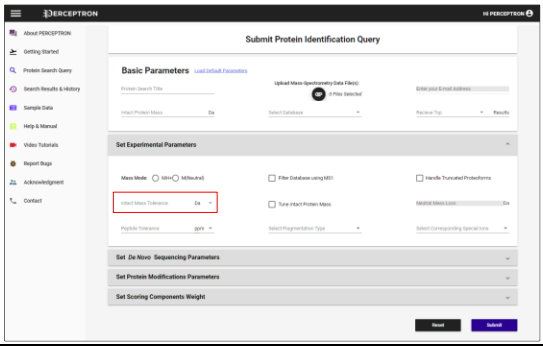
Step 5: Select a Database to search from (*e.g. Human*).



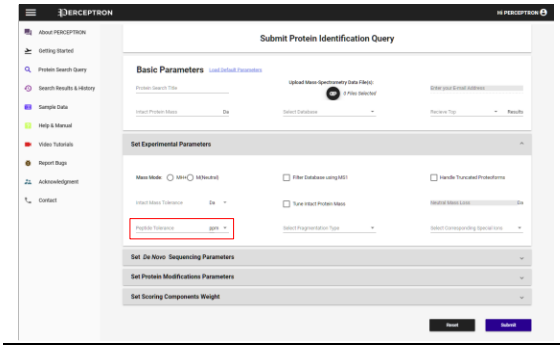
Step 6: Select the number of candidate proteins to be received via results email.

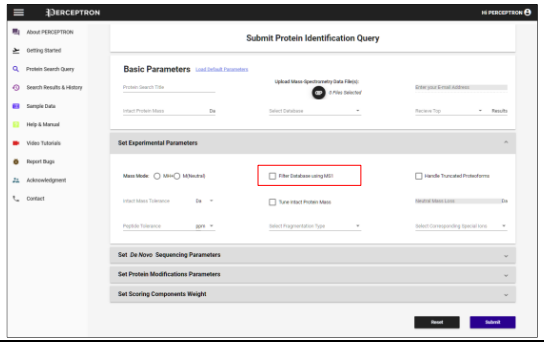


Step 7: Select the Mass Mode. MS data can only be provided in either m/z form with z = 1 (MH^+) or neutral masses (M(Neutral)).



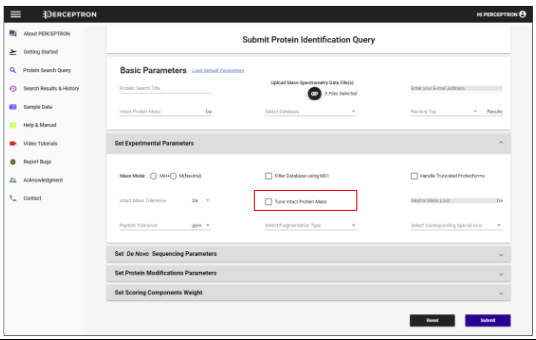
Step 8: Enter the desired 'Intact Mass Tolerance' and select its unit (Da or ppm).

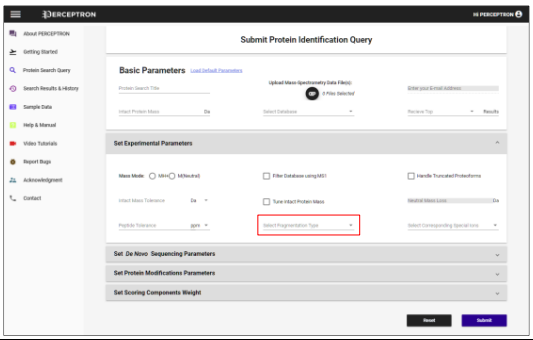




Step 9: Enter your desired 'Peptide Tolerance' and select its unit (Da or ppm).

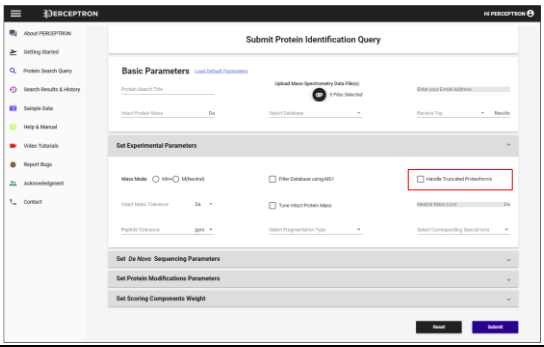
Step 10: Click 'Filter Database using MS1' to filter protein database on the basis of precursor ion mass (MS1).

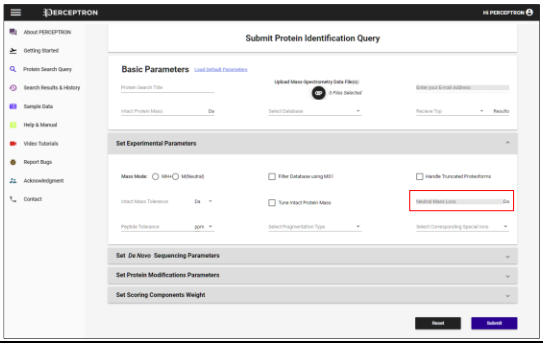




Step 11: Select 'Tune Intact Protein Mass' to allow for tuning of MS1 using MS2 data.

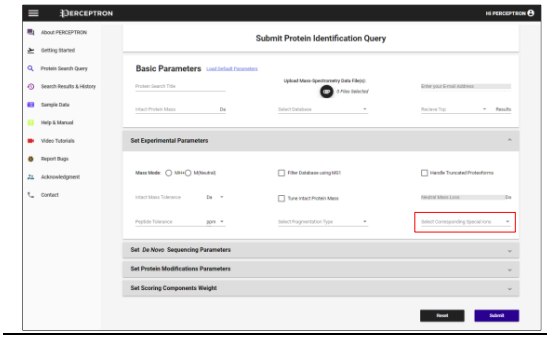
Step 12: Select the fragmentation type from the drop down menu.

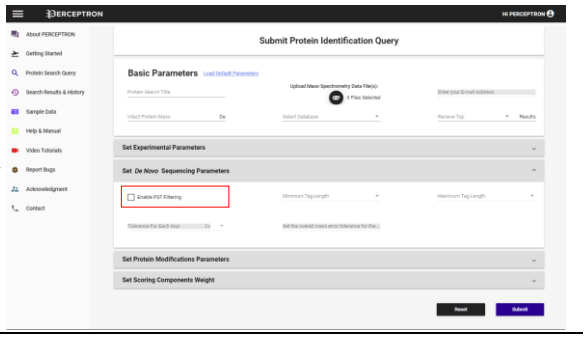




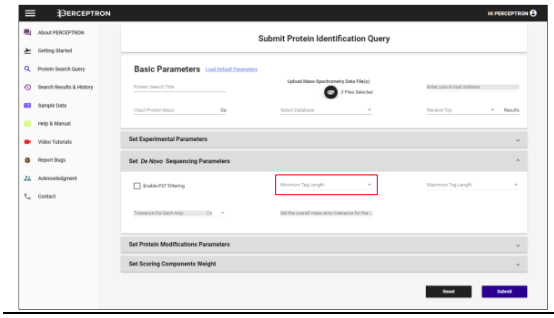
Step 13: Click 'Handle Truncated Proteoforms' to allow search for truncated proteoforms.

Step 14: Incorporate masses of neutral loss, if any.

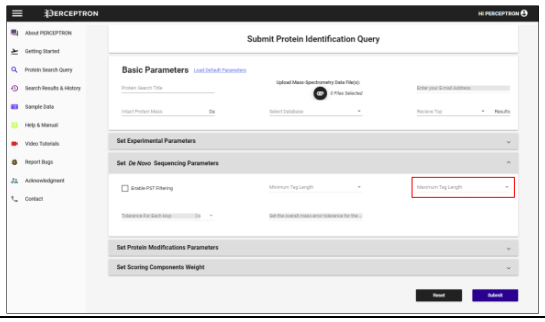




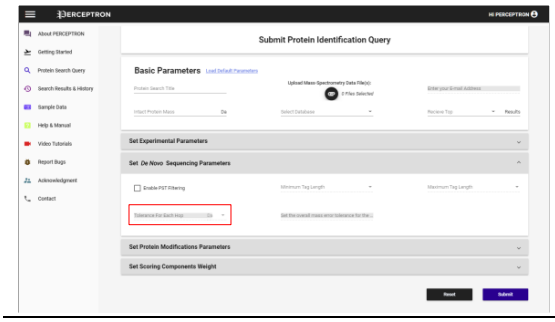
Step 15: Choose the corresponding special ions for the type of fragmentation method selected (i.e. a', b', y', z", a*, b*, y*, z' ions).



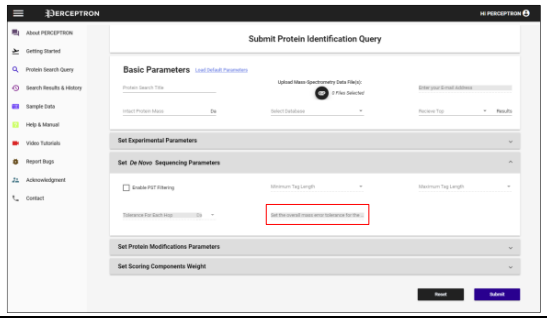
Step 16: Select 'Enable PST Filtering' to allow for peptide sequence tag (PST)-based search.



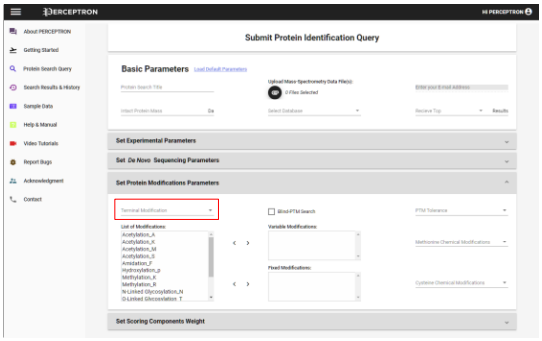
Step 17: Select your desired minimum PST tag length from the drop down menu.



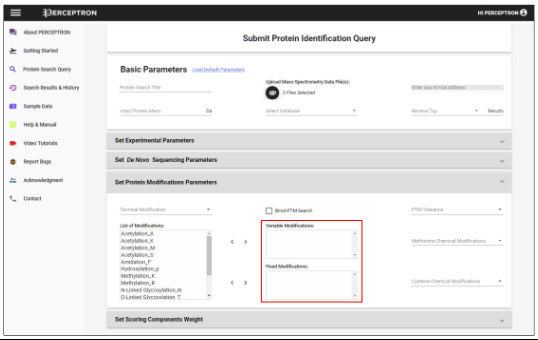
Step 18: Select your desired maximum PST tag length from the drop down menu.



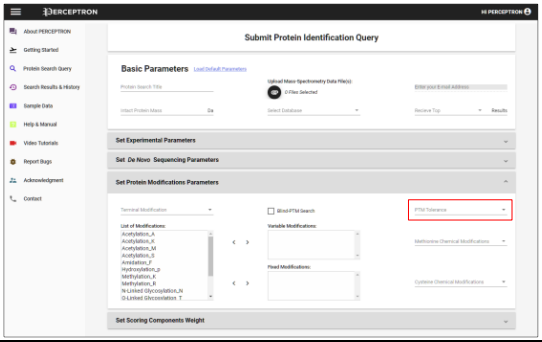
Step 19: Set the desired tolerance for each PST hop.



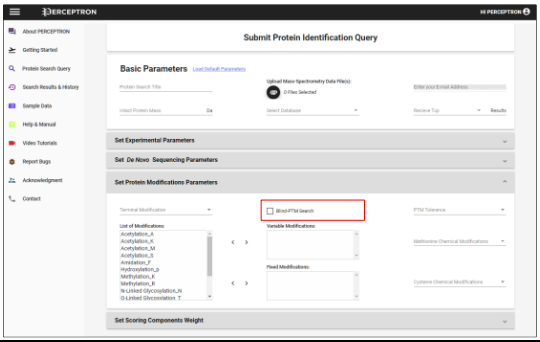
Step 20: Set the overall mass error tolerance for the entire PST.



Step 21: Select 'Terminal modifications' to be included in the search.



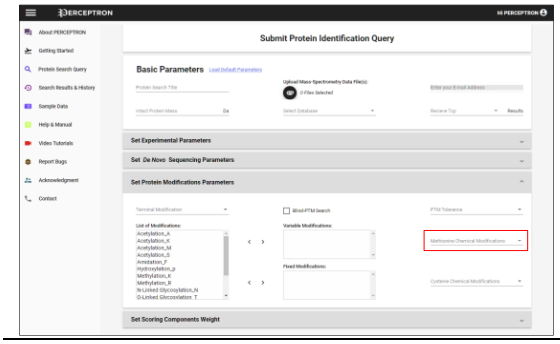
Step 22: Select 'Fixed' or 'Variable' post-translational modifications (PTMs) from the List of Modifications.



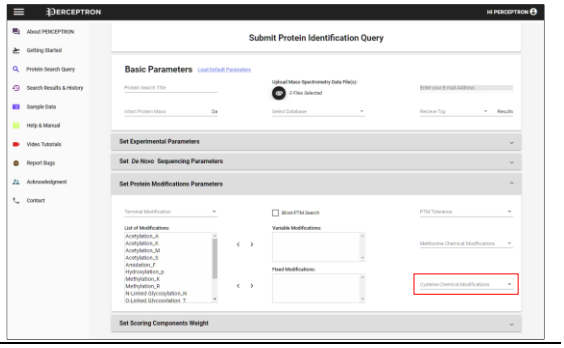
Step 23: Set the 'PTM tolerance'.

Step 24: To allow search for unknown post-translational modifications (PTMs), search for

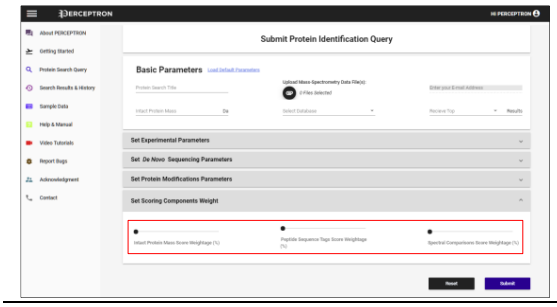
Blind PTMs instead of variable or fixed modifications. If ‘Blind-PTM Search’ is selected, there is no need to set PTM tolerance.



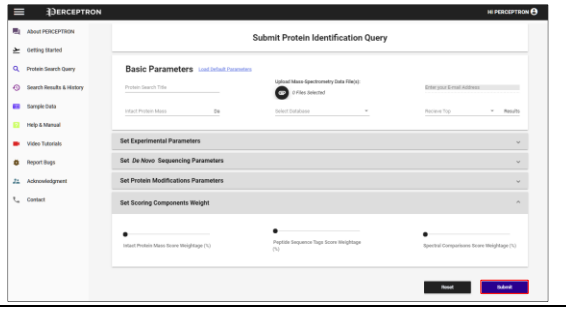
Step 25: Select the ‘Methionine Chemical Modifications’ from the drop down menu.



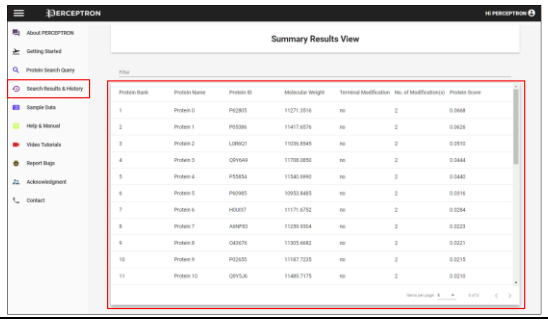
Step 26: Select the ‘Cysteine Chemical Modifications’ from the drop down menu.



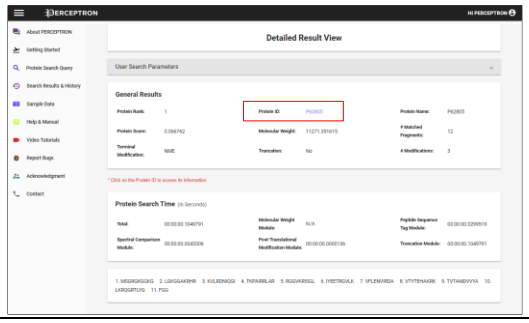
Step 27: Set the weights of the scoring components by moving the sliders.



Step 28: Submit the Protein Query Search by clicking on ‘Submit’.



Step 29: Click on ‘Search Results & History’ to see the search results. Click on any protein to see its Detailed Result View.



Step 30: Click on the Protein ID to see its UniProt view.