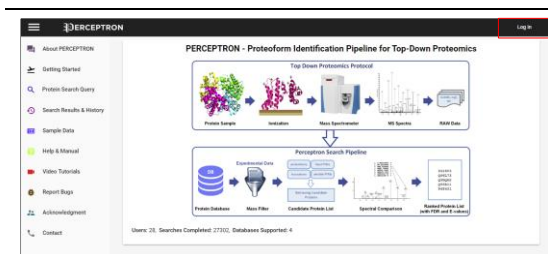
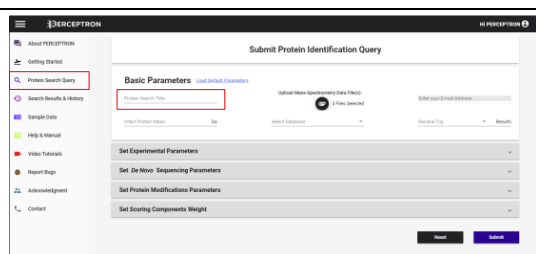


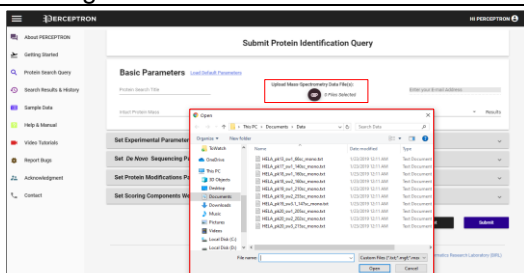
# Step-by-Step Guidelines for using PERCEPTION



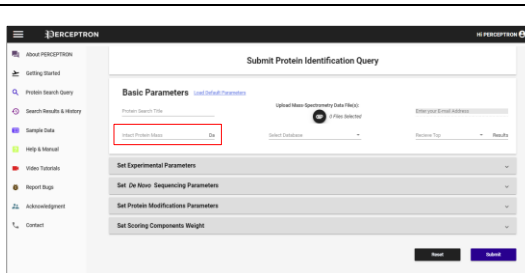
**Step 1:** Login PERCEPTION using an existing email account.



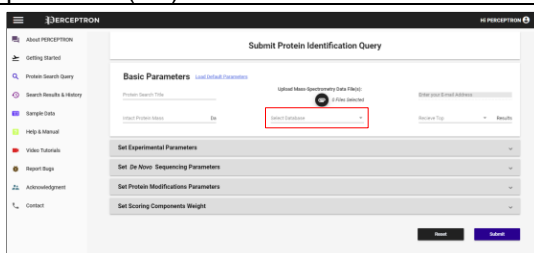
**Step 2:** Go to the 'Protein Search Query' and enter 'Protein Search Title' to start search.



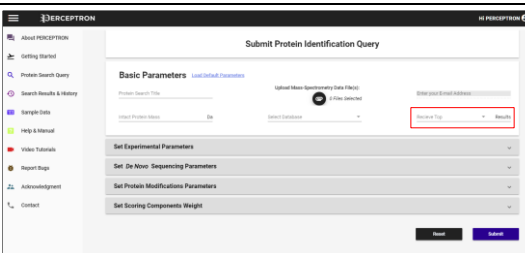
**Step 3:** Browse and upload Data file(s). Upload one file (.mzXML/ .mzML/ .MGF/ .txt) to perform single file search or add multiple peak-lists (.txt) to search in batch mode.



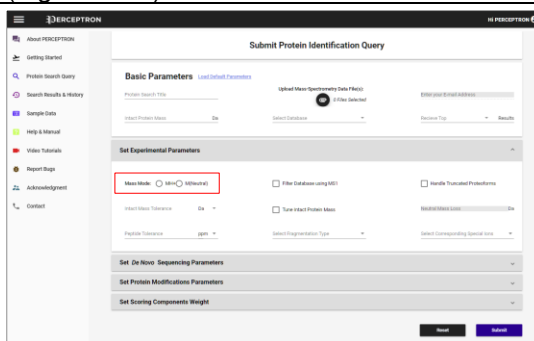
**Step 4:** Click on 'Intact Protein Mass' to enter mass of precursor ion (MS1).



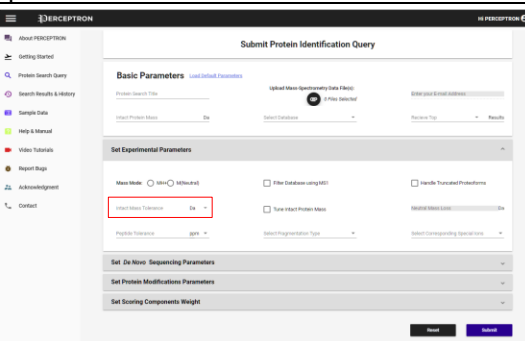
**Step 5:** Select a Database to search from (e.g. Human).



**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).

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**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.

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

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

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

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**Step 15:** Select the complementary specificity from the drop down menu.

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**Step 16:** Select 'Enable FRT Filtering' to allow search for FRT modified peptides.

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**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'.

Protein Rank	Protein Name	Protein ID	Molecular Weight	Terminal Modification	No. of Modification(s)	Protein Score
1	Protein 1	P12345	11271.2518	No	2	0.0868
2	Protein 1	P12345	11447.6576	No	2	0.0828
3	Protein 2	L12345	11506.8545	No	2	0.0810
4	Protein 3	Q12345	11708.0892	No	2	0.0844
5	Protein 4	P12345	11546.0892	No	2	0.0840
6	Protein 5	P12345	10851.8405	No	2	0.0816
7	Protein 6	H12345	11171.4752	No	2	0.0824
8	Protein 7	A12345	11239.9304	No	2	0.0823
9	Protein 8	C12345	11357.8892	No	2	0.0821
10	Protein 9	P12345	11587.7025	No	2	0.0815
11	Protein 10	Q12345	11465.7075	No	2	0.0815

**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.