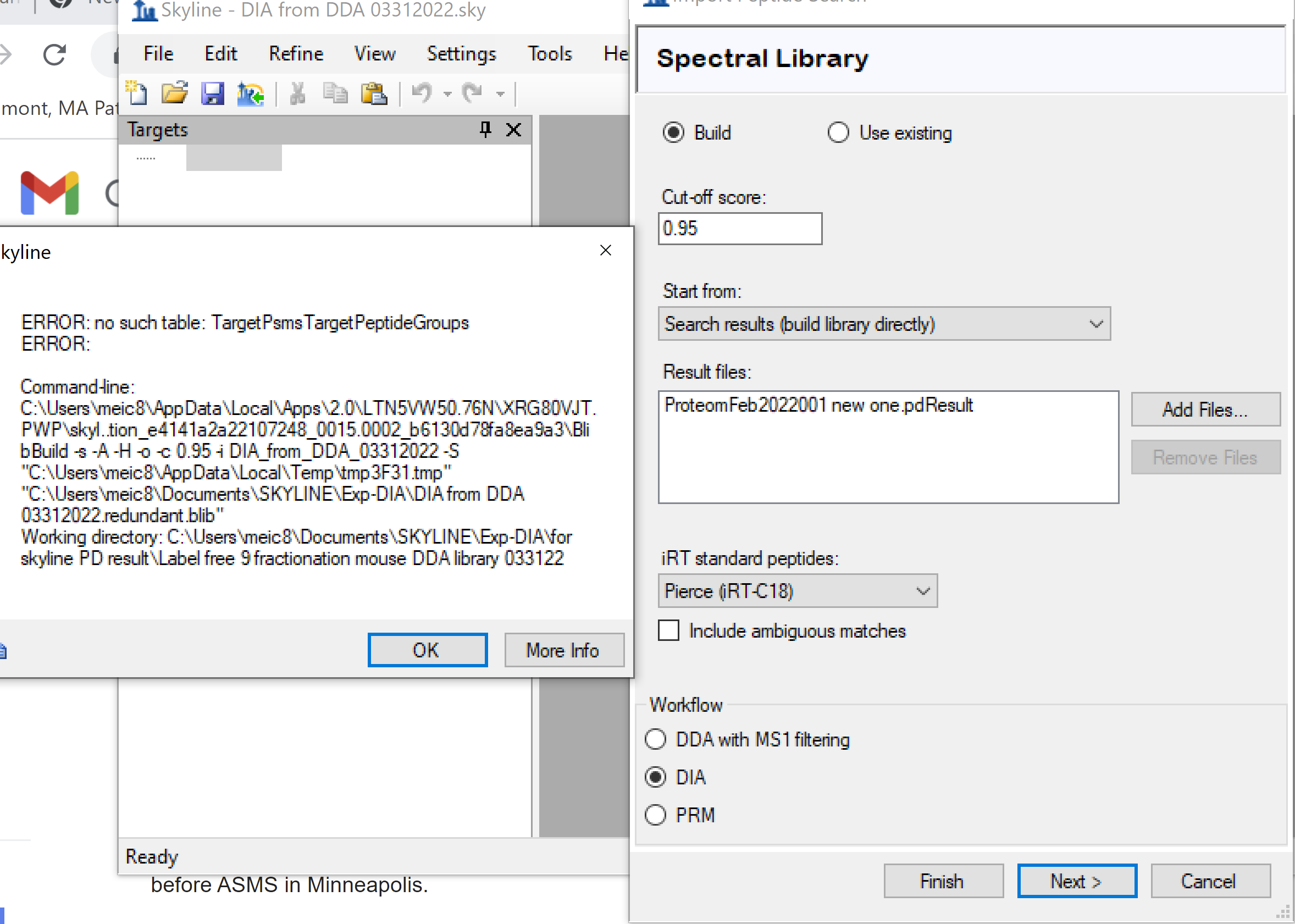
**Question 1)** I am trying to import my DDA result file into Skyline to build a DDA library for DIA analysis. It is a Proteome discoverer result file from several fractions, and PD has integrated them into one file. When I import the PD file, I got the following error message. What should I do?



I am wondering if the **Settings** (**Peptide Settings** and **Transition Settings**) are supposed to set as **defaults** before building a DDA library for DIA analysis.

**Question 2**) This question is related to settings for PRM. In the **Library** under **Peptide Settings**, I want to “**Build**” a library from a Proteome Discovery result file I generated. But I got the similar error message as above:

