

- The LC/MS/MS data was collected with a Thermo LTQ ion trap mass spectrometer. Approximately 20-40% of your sample was used in this analysis. The remaining amount is available for further analysis (looking for post-translational modifications, confirming weak protein identifications, etc.)
- A Sequest search of the LC/MS/MS data was done using the NCBI non-redundant protein database (see: <ftp://ftp.ncbi.nih.gov/blast/db/FASTA/nr>). If we did the in-gel digestion for your samples, the trypsin enzyme was used (unless otherwise specified). Please note that if a species subset of this protein database was used in the search, its species database name will appear at the top right of the protein identification list (see “database searched”).
- The attached report for each sample is broken into two halves. At top is a list of protein identifications for that sample, ranked in order of confidence in identification. Note that for confident protein identification we generally expect at least 4 unique peptides listed for a given protein. Those protein identifications that have less than 4 unique peptides listed under them are not necessarily false positives but they would need further experiments to confirm or disprove the identification (contact us to discuss how to do this). The second half of the report is the details (protein sequence, coverage, post-translational modifications, and molecular weight) of the protein identifications, ranked in the same order as the first half. The dark green horizontal lines below your protein sequence are the peptides observed. The light green bands are oxidized Methionines (very common in in-gel digestions and not something to be concerned about).
- If your expected protein was not identified it could be due to several reasons including its sequence may not exist in the protein database we searched. If you can provide us with a database for the species of your sample in FASTA format we can search your data against that database and report the results to you again. Also, you can do a protein BLAST search (<http://www.ncbi.nlm.nih.gov/blast/>, use protein blast or blastp) of any peptide or protein sequence or identifier (such as gi or protein accession number) to find out if it may have come from another homologous protein. Weak protein identifications can be validated by targeting (in further mass spectrometry experiments) the peptides from the protein. Please call to discuss details of this procedure.
- Let us know if the protein identifications are not in agreement with your expectations and please call or email ([tucf-proteomics@tufts.edu](mailto:tucf-proteomics@tufts.edu)) if you have any questions. Lastly, if you include our results in a publication, feel free to contact us for the experimental text and please let us know the publication name and journal for our records. Thanks.

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# HOW TO INTERPRET YOUR REPORT

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Note: Any protein identification that has "rubber elongation factor" in it is protein name can be ignored as it is from the gloves used during the in-gel digestion procedure

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