Database Information Instructions

The following is a requirement for correct and expeditious analysis of your sample(s). Please follow instructions below to e-mail the website and exact folder and filename of the sequence database for your organism of interest. Incorrect or incomplete information can jeopardize your results, increase the costs and delay the analysis.

If the sequence database for your organism is available on the web please send an e-mail to **proteomics@fas.harvard.edu** indicating:

1. The exact name and the URL (web address) of the **FASTA** format protein or nucleotide database.
(example: ftp://genome-ftp.stanford.edu/pub/yeast/data_download/sequence/GenBank/yeast_nrpep.fasta.Z).
2. **Be sure to test that you can download this database from the website you specify (and that it is downloadable as one file).**
3. Name and exact description of the database.
4. Tell us if this is a protein or nucleotide database.
5. Related species information of your sample and the database(s), i.e. if sequences for your organism are not available and the database is the closest related organism, indicate that.
6. Setup, search, analysis and reporting of each database is charged separately.

If the necessary database is private, unavailable on the web or requires concatenation of multiple source databases then please concatenate and send the database on CD to us at:

Harvard University
Mass Spectrometry and
Proteomics Resource Laboratory
52 Oxford St. Room B247
Cambridge MA 02138

All information provided by you is confidential.