



# Keck Biotechnology Resource Laboratory

## Yale Automated MALDI-MS Protein Identification Sample Submission Form

Order Date: 

MM	DD	YY	

Your Name: \_\_\_\_\_  
Last Name First Name MI

PI Name: \_\_\_\_\_  
Last Name First Name MI

Department: \_\_\_\_\_ Yale Cancer Center Member?  YES  NO

Room #: \_\_\_\_\_ Building: \_\_\_\_\_

Telephone: (\_\_\_\_) \_\_\_\_\_ - \_\_\_\_\_ Fax: (\_\_\_\_) \_\_\_\_\_ - \_\_\_\_\_ E-mail: \_\_\_\_\_

**Yale Charging Instructions:**

Project	Task	Award	Expenditure Type	Organization
			8 3 3 6 2 0	

Check here if NBC Member

**Preparation of Samples for Automated MALDI-MS Protein Identification by Peptide Mass Database Searching**

- Excise the stained bands and/or spots from the gel in such a manner to avoid removing excess gel that does not contain any protein.
- Place each band (which must be less than 2 mm x 10 mm x 1.5 mm in size) or spot into an individual well (beginning with the A1, B1, C1, D1, etc wells) in a Corning Costar #3363 V-bottom polypropylene 96 well plate. We suggest that you include at least one spot or band which derives from an area of your gel which should not contain protein and which can serve as a control.
- The minimum number of samples (including the control) that may be submitted in each plate is 8, which must be in wells A1 through H1. Please note that your samples will be identified by the Keck Laboratory only by the plate name you assign and then by their individual well designation. No liquid should be present in these wells. After covering the plates with a Corning #3080 Storage Mat III, they should be securely wrapped in Parafilm to prevent the mat from coming off and then stored at -20 degrees prior to shipment.
- Please especially note that only about 5% of each sample will be subjected to MALDI-MS. If this 5% aliquot will contain substantially less protein than the minimum recommended amount of 100 fmol, we suggest you utilize the "Manual" MALDI-MS Protein Identification Service and request that a larger fraction of the sample be subjected to MALDI-MS.

Description of Samples Submitted in 96 Well Plates for MALDI-MS Protein Identification		
96 Well Plate Name	Number of Samples in Plate	MW Range to be Searched (Default is 15,000 – 150,000)

If any of the above samples represent a potential biohazard, please explain below. Contact the Protein Chemistry/Mass Spectrometry Resource *before* shipment of radioactive samples – which cannot be submitted to Automated MALDI-MS Protein Identification. The Keck Laboratory recommends that SDS PAGE-purified samples destined for protein identification be submitted as Coomassie Blue or Colloidal Coomassie Blue (not silver) stained gel bands as described on the Website.

How many weeks would be required to replace these samples?: \_\_\_\_\_

Other information: \_\_\_\_\_

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