



Keck Biotechnology Resource Laboratory Yale Amino Acid Analysis Sample Submission Form

(Protein/Peptide Concentration and Composition Analysis - Radioactive Samples Cannot Be Accepted)

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

Description of Samples

(Use separate forms for samples that are not all in or were not all dried from the same buffer)

Name (6 letters)	Number of Analyses Requested*				Estimated Amount (micrograms)	Form (solution, dry, gel or PVDF)	Total volume for solution samples (μl)	Predicted Monomer Mass
	Normal	PAO	MSA	No Hydrolysis				

* Normal hydrolysis gives poor recovery of cysteine and tryptophan, if these residues need to be quantified it is best to request prior performic acid oxidation (PAO) and hydrolysis with methanesulfonic acid (MSA) respectively. However, since the latter two procedures may result in poor recoveries of several other amino acids, all three kinds of analyses are generally required to quantify all 18 naturally occurring amino acids. No hydrolysis will permit quantitation of the "free" amino acid background.

E-mail Results? (Check if Yes):

If samples are submitted in solution please give the composition of the buffer:

If samples are submitted dry, give the method of precipitation or the volume and composition of the buffer that was dried:
