Instructions for Providing your Sequence

Before we can perform any analysis on your "known" protein, the following information must be sent to us by email. Incomplete information will likely cause an incorrect analysis, increase the costs and delay the analysis.

- **Submit to us the *exact* sequence of the mature protein or construct you expect your sample to have.** A *single* amino acid mistake in the sequence you send us will adversely affect the results you obtain. The most common mistake that researchers make is to send us the public database entry when in fact their sample had differences such as known his-tags, cleaved signal sequences, GST-fusions, etc. Research the molecule you are sending and indicate the true amino- and carboxy- termini and any known or predicted modifications.
- **Send the sequence as single letter amino acid code in the text of an email.** Please do *not* send as an attachment. The sequence should be in the body text of the email, no numbers or characters other than the sequence itself, .FASTA configuration.

Email the sequence to: **proteomics@fas.harvard.edu**

- **In the same email, indicate project specifics, such as species, construct, vector, or expression system.** We must know all species that are involved. For example, you may have a human gene being expressed in e. coli as a GST fusion.
- **For phosphorylation or other modification site experiments, in the email:**
  1. **Make a clear distinction between (a)** requests to find *any* site of the modification versus **(b)** requests to prove/disprove specific (known or putative) sites of modification. *Our analysis strategy is quite different for each.*
  2. **If specific residues are of interest (b - above),** indicate them in the email.
  3. **If you are surveying for *any* site (a - above)**, please research the literature and indicate what is known or predicted by motif.
  4. Indicate the conditions that may cause your modification, e.g. expected kinase(s), exposure to UV, etc.
  5. If there are tags or relevant domains, indicate the residues at which they begin and end.
- **Above all, we need to know what you know**. Anything not indicated above but germane to the project should also be in the email. This is also a good place to indicate items above that you *do not* know, e.g. "we do not know where the exact amino-terminus begins."