



“Golden Rules” for Protein and Peptide Handling

- Take your unprotected hands away from microsamples or you will find keratin, glycine, alanine, ...
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- Take your unprotected hands away from microsamples...
- Avoid any unnecessary sample transfer.
- Minimize the number of purification steps.
- Avoid purification steps, which increase the sample volume, especially during the late stages of a purification scheme.
- Take a suitable detergent if needed to purify or stabilize your protein. E.g. if you are preparing a protein sample for mass spectrometry analysis, be aware that only octylglucoside (max. 0.1%) is compatible.
- Adjust column dimensions to your sample size.
- An individual peptide (in a proteolytic digest) has a concentration limit, usually between 100 and 500 fmol/μl, below which it is irreversibly adsorbed to surfaces.
- Therefore, keep the sample volume as small as possible and the peptide concentration as high as possible, respectively.
- Work fast, because even at -80°C peptide samples are not completely stable.
- Keep your protein protected from oxygen (especially important for mass spectrometry).
- Use quartz glassware for water and all buffer solutions to minimize contamination of mass spectrometry samples with sodium and potassium.
- Excise a PVDF-blotted or spotted protein band precisely, it improves the initial and repetitive yield during sequence analysis.

Partially adapted from:

Kellner R., Lottspeich, F., and Meyer, H.E. Microcharacterization of Proteins (Second Edition).

DIRECTOR: HENRIETTE REMMER, PH. D.
EMAIL: hremmer@umich.edu
PHONE: (734) 936-1624 FAX: (734) 936-2638

2560 MSRB II
1150 W. MEDICAL CENTER DRIVE
ANN ARBOR, MI 48109-0674