

# New NIST reference material for peptide analysis

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The National Institute of Standards and Technology (NIST) has issued its first-ever reference material designed to improve the performance and reliability of experiments to measure the masses and concentrations of peptides in biomolecular samples. The new reference material is expected to be an important tool in the analysis of proteins, both for disease diagnosis and drug discovery.

Proteomics—the study of proteins and the roles they play in biology—is one of the most fertile fields of modern medical research. Proteins typically are very large molecules, built of hundreds or thousands of amino acids, but they can be divided into smaller units, chains of about 50 or fewer amino acids. These are peptides. The usual way to analyze proteins is to chop them into their constituent peptides (generally with enzymes that cut through them at specific sites), sort the various peptides out using a chemical separation technique like high performance liquid chromatography (HPLC), and then determine the mass of each peptide using mass spectroscopy.

One big uncertainty in this process is that the peptide fragments differ in size, electrical charge and physical properties (such as the speed in which they separate under HPLC.) Chemists are accustomed to using well-known reference samples as chemical rulers to calibrate their analysis instrumentation, but until now there have been no such reference samples of peptides.

The need for this peptide reference material has been long recognized by

the Association of Biomolecular Resource Facilities (ABRF), a non-profit standards organization created by representatives from industry firms, universities and government agencies. In collaboration with NIST, the ABRF created a Peptide Standards Project Committee to design and characterize three synthetic peptides to serve as the basis for a NIST peptide reference material. NIST RM 8327, "Peptide Reference Material for Molecular Mass and Purity Measurements," consists of three peptides from 11, 14 and 26 amino acid residues in length, with net charges of -3, -1 and +3. These three synthetic peptides were designed to provide long-term stability (do not contain methionine, cysteine and tryptophan), a range of purities, a range of molecular masses, protease cleavage sites, and contain tyrosine to enable concentration analysis by UV spectroscopy.

Source: National Institute of Standards and Technology (NIST)

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