Barber, M., Bordoli, R. S., Sedgwick, R. D., and Tyler, A. N. (1981). *J. Chem. Soc. Chem. Commun.* 325–327.
Barinaga, C. J., Edmonds, C. G., Udseth, H. R., and Smith, R. D. (1989). *Rapid Commun. Mass Spectrom.* **3**, 160–164.
Biemann, K. (1988). *Biomed. Environ. Mass Spectrom.* **16**, 99–111.
Biemann, K. (1990). *In* McCloskey, J. A. (ed.), *Methods in Enzymology*, Vol. 193 (Academic Press, San Diego), pp. 455–479.
Biemann, K., and Scoble, H. A. (1987). *Science* **237**, 992–998.
Hunt, D. F., Zhu, N. Z., and Shabanowitz, J. (1989). *Rapid Commun. Mass Spectrom.* **3**, 122–124.
Johnson, R. S., and Biemann, K. (1989). *Biomed. Environ. Mass Spectrom.* **18**, 945–957.
Juhasz, P., Papayannopoulos, I. A., and Biemann, K. (1992). *In* Smith, J. A., and Rivier, J. E. (eds.), *Peptides: Chemistry and Biology* (Escom, Leiden), pp. 558–559.
Karas, M., and Hillenkamp, F. (1988). *Anal. Chem.* **60**, 2299–2301.
McCloskey, J. A. (ed.). *Methods in Enzymology*, Vol. 193 (Academic Press, San Diego).
Meng, C. K., Mann, M., and Fenn, J. B. (1988). *Z. Phys. D.* **10**, 361–368.
Papayannopoulos, I. A., and Biemann, K. (1991). *J. Am. Soc. Mass Spectrom.* **2**, 174–177.
Wada, Y., Matsuo, T., and Sakurai, T. (1989). *Mass Spectrom. Rev.* **8**, 379–434.

**Brian T. Chait,[1] Rong Wang,[1] and Stephen B. H. Kent.[2] A New Approach for Sequencing Peptides and Proteins.** ([1] The Rockefeller University, New York, New York 10021; [2] Scripps Research Institute, LaJolla, California, U.S.A.)

In the present paper, we describe a new approach for sequencing peptides and proteins that has the potential for greatly speeding up this type of analysis. The method has two steps:

*Step 1.* The production by chemical means of a complete set of peptide fragments, where each fragment shares a common terminus. For example:

$$\begin{array}{lll} 1\text{–}2\text{–}3\text{–}4 & \ldots & (n-1)-n \\ 2\text{–}3\text{–}4 & \ldots & (n-1)-n \\ 3\text{–}4 & \ldots & (n-1)-n \\ & & \vdots \\ & & (n-1)-n \\ & & n \end{array}$$

*Step 2.* Measurement by matrix-assisted laser desorption (Beavis and Chait, 1990; Hillenkamp *et al.*, 1991) of this complete set of peptides. The sequence of amino acids is then deduced directly from the accurately determined mass differences between adjacent peaks in the mass spectrum. A number of different approaches for the production of the required ensemble of peptides (step 1) are being evaluated and will be discussed. The second step of the procedure was thoroughly tested on peptide mixtures generated during the stepwise solid-phase synthesis of the 99-residue protein HIV-1 protease. After each consecutive amino acid coupling step, a fraction of the peptide resin was removed and pooled. Three important observations were made during the analysis of these peptide mixtures: (a) complex mixtures of more than 30 peptide components could be analyzed by matrix-assisted laser desorption using an appropriate matrix; (b) the masses of the components of a mixture were determined with an accuracy of 1 part in 10,000 for peptides with molecular masses of up to 7000 $\mu$; and (c) aliquots of a peptide mixture produced intense molecule ion signals for components present in amounts of much less than 1 pmol/$\mu$l. These findings demonstrate that sequences of peptides can be readily inferred from the spectra of such mixtures.

*References*

Beavis, R. C., and Chait, B. T. (1990). *Anal Chem.* **62**, 1836–1840.
Hillenkamp, F., Karas, M., Beavis, R. C., and Chait, B. T. (1991). *Anal. Chem.* **63**, 1193A–1203A.

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Calcium plays a major role in cellular regulation and is mediated by a range of calcium-binding proteins. The annexins are a superfamily of calcium and phospholipid binding proteins containing repeated domain structures that are characterized by the endonexin fold (Burgoyne and Geisow, 1989). Purification of two calcium-dependent phospholipid and membrane proteins from bovine brain has recently been described (Donato *et al.*, 1990). These have been termed CaBP33 and CaBP37. The proteins co-purify on phenyl-Sepharose but can be separated on DEAE-Sepharose; on sodium dodecylsulphate polyacrylamide gel electrophoresis (SDS-PAGE), they migrate at 33 and 37 kD, respectively. Other workers have observed proteins