Poster # 37 This poster contains some good graphics of some of the variations of the hydrolysate analysis. It is important to note that we currently support three different separations of AccQ•Tag derivatized AA's. The glycoprotein analysis shown quantitates a wide variety of AA's not found in hydrolyzed samples as well as identification of amino sugars. The use of Nle as an internal standard and U.V. detection of are also shown. Finally, analysis of Trp is also shown, this is only useful when using U.V. detection.

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Protein Compositional Analysis Using a Novel Precolumn Derivatizing Reagent, 6-Aminoquinolyl-N-Hydroxysuccinimidyl Carbamate

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The analysis of recombinant proteins is a critical step in the approval and continued production of these macromolecules as biotherapeutics and diagnostics. A number of analytical procedures must be carried out to fully characterize such complex analytes, amino acid analysis being one of the more complicated quantitative procedures to perform accurately and reproducibly. We have recently reported on a new pre-column derivatization procedure for protein hydrolysate analysis using a novel reagent, 6-Aminoquinolyl-N-hydroxysuccinimidyl carbamate (AQC)1. This highly fluorescent tag reacts rapidly and quantitatively with both primary and secondary amines to form stable urea derivatives readily amenable to chromatographic analysis. Recombinant samples are often glycosylated and the N-and O-linked oligosaccharides contain one or more acetylated aminosugars. The hexosamines resulting from acid hydrolysis are derivatized by most common pre-column reagents, and consequently these derivatives must be resolved from the amino acid derivatives to allow for quantitative analysis. These are derivatized in the same simple, one-step procedure used for amino acids and have developed chromatographic conditions that provide for high resolution, high accuracy analysis of glycosylated proteins as well as a variety of other important sample types such as hydrolyzed collagen-type proteins. Quantitative compositional results superior to other pre-column derivatization methods will be shown. These are essentially equivalent to ion-exchange analysis, with the significant benefit that sample sizes can be up to two orders of magnitude smaller.