

## Amino Acid Composition of Low Picomole Quantities of Peptides Using the PICO-TAG™ Amino Acid Analysis System

One of the major benefits of the PICO-TAG™ method is its high sensitivity. No other amino acid analysis technique provides the ability to routinely determine amino acid compositions with high accuracy, on submicrogram amounts of sample.

Researchers at Harvard Medical School recently published their work on the primary sequence of bovine Class 1 Heparin-Binding Growth Factor (HBGF-1)<sup>1</sup>. They reported the amino acid compositions of chymotryptic peptides from HBGF-1, as well as the composition of the intact protein, all determined using the PICO-TAG™ method. The peptides were isolated by reverse phase HPLC, and quantities ranging from 11 to 108 picomoles were used for PICO-TAG™ analysis. Results for two of the peptides are shown in the table below, along with the corresponding values from the sequence.

	Peptide C'-19a	Peptide C-11
pmoles analyzed	65	11
ASP	1.14 (1)	0.49
GLU	0.14	2.26 (2)
SER	1.04 (1)	1.00 (1)
GLY	2.99 (3)	1.64 (1)
HIS	0.89 (1)	
ARG	1.92 (2)	0.15
THR	0.98 (1)	1.83 (2)
ALA	0.16	0.21
PRO	1.11 (1)	0.16
TYR	0.03	0.29
VAL	0.98 (1)	
MET	0.02	
ILE	0.10	0.99 (1)
LEU	1.95 (2)	1.15 (1)
PHE	1.04 (1)	0.94 (1)
LYS	3.12 (3)	0.82 (1)

These results demonstrate that the PICO-TAG™ method provides at least an order of magnitude better sensitivity (real-life, useable sensitivity!) than any other commercially available amino acid method.

1. Daniel J. Strydom, J. Wade Harper, and Roy R. Lobb (1986) *Biochemistry* 25, 945-951.