

## **Standard Peptide Mixture**

Precise and Fast Equilibration Time



**Notes:** Peptides are distinguished from proteins on the basis of the number of amino acid residues. Generally this number is about 50 residues or fewer. Because of their smaller size, peptides do not have the same degree of complex folding that proteins do.

## **Method Conditions**

Column: Cogent Bidentate C8 300™, 5µm, 300Å

Catalog No.: 40008-75P-3M

Dimensions: 4.6 x 75 mm

Solvents: A: DI H<sub>2</sub>O/ 0.1% trifluoroacetic acid (TFA) B: Acetonitrile/ 0.1% TFA

Gradient:	time (min.)	%B
	0	9
	5	21
	20	27
	21	9

Post Time: 5 min

Flow rate: 1 mL/min

Detection: UV 214 nm

Peaks: 1. Gly-Tyr

2. Val-Tyr-Val

3. Methionine enkephalin

4. Angiotensin II

5. Leucine enkephalin

## Discussion

HPLC in various modes is a main technique for the characterization of peptides. Reverse Phase HPLC is employed for the initial analysis and the final large scale purification of peptides. The first step of the production of synthetic peptides usually involves an initial separation of the peptides in the mixture on an analytical scale. Next the purification and collection of the target peptide follows. The Figure shown here presents the use of RP-HPLC with a Cogent Bidentate C8 300 column in the separation of a five peptide mixture. The 300Å pore size of the sorbent is ideal for separation of small peptides chosen for the presented chromatogram. This column is a great choice for the gradient analysis of these due to the very fast equilibration time between injections (less than 5 minutes).

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