

Liquid Chromatography

Flexar PDA Plus Detector



A Definitive Solution to Confirm Peak Identity

In liquid chromatography using UV/Vis detector, peak identification is usually based on relative retention time. With the ability to scan samples at superior data acquisition rate (up to 200 Hz) and unmatched wavelength accuracy of ± 0.5 nm, the Flexar™ PDA Plus™ Detector and Chromera® chromatography data system can store reliable spectra in an integrated spectral library. This feature offers another way of identifying peaks by matching any peak spectrum to spectra in the library. When a match is made the name of the matching spectrum in the library will be appended to the corresponding peak in the sample. This capability increases confidence in peak identification, as it is well known that the same relative retention time does not necessarily mean the components are the same.

The spectra at the peak apexes of a sunscreen standard solution (*Figure 1*) are stored in a spectral library (*Figure 2*). The peaks of a solution of sunscreen lotion are compared to the stored spectra and matches are made confirming peaks identities (*Figure 3*).

Chromatographic conditions:

Mobile phase: 10 % A (1.25% acetic acid in water)
90% B (acetonitrile)
Sample diluent: Acetonitrile
Flow/injection: 0.6 mL/min; 2 μ L volume
Flush solvent: 75:25 methanol/water
Analytical wavelength: 325 nm
Column: Brownlee™ SPP C-18, 100 x 3 mm, 2.7 μ m
at ambient temp. (Cat # N9308410)
Chromera® version 4.0, 5 pts/sec sampling rate

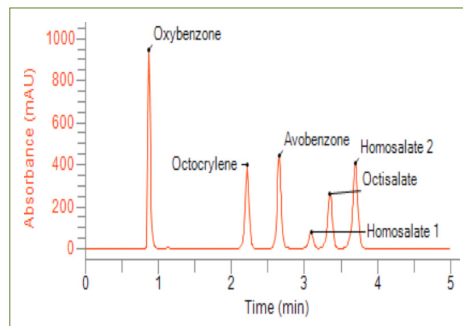


Figure 1: Chromatogram from the analysis of a sunscreen standard solution.

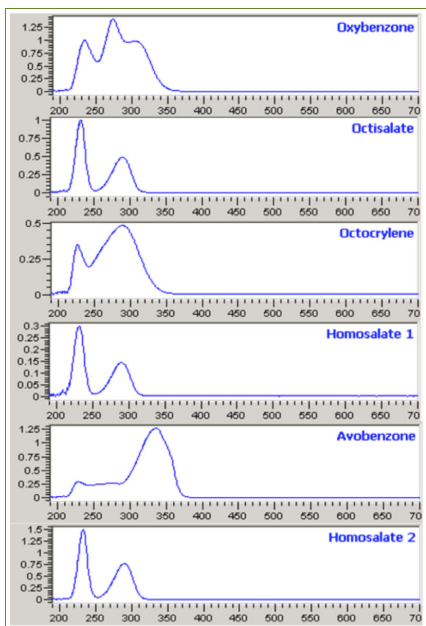


Figure 2: Stored spectra from the sunscreen standard solution.

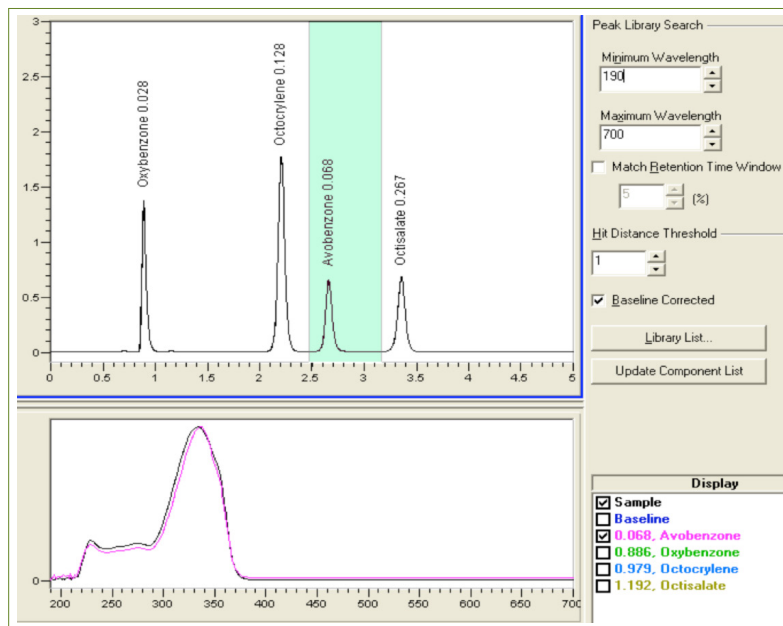


Figure 3: Peak identification based on spectral library.

The Flexar PDA Plus detector, through Chromera or third party chromatographic data system software, by combining identification by retention time and identification by matching spectra, enables a definitive identification of peaks, therefore providing greater confidence in analysis results.