

In Chromatography, Like in Life, All Interactions Matter

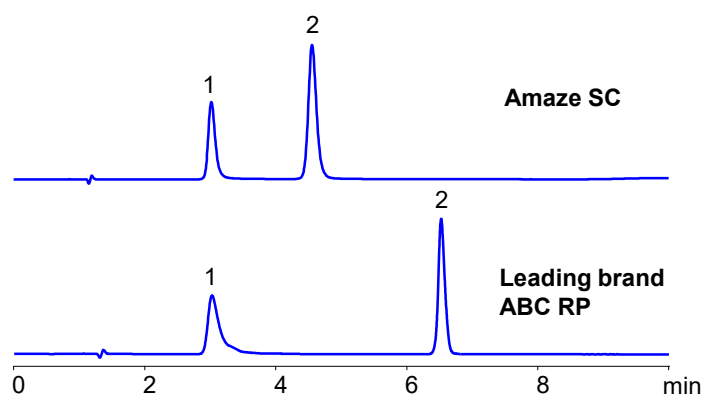


Fig. 1 HPLC Analysis of 4-Carboxyphenylboronic Acid on Amaze SC Mixed-Mode and Single Mode RP Columns

1. 4-Carboxyphenylboronic Acid
2. Benzoic acid

Dimensions: 3.0 x 100 mm, 3 μ m, 100A
Mobile phase: ACN/water/ H_3PO_4
Flow: 0.6 ml/min
Detection: 255 nm
Sample: 1 mg/ml
Injection: 2 μ L

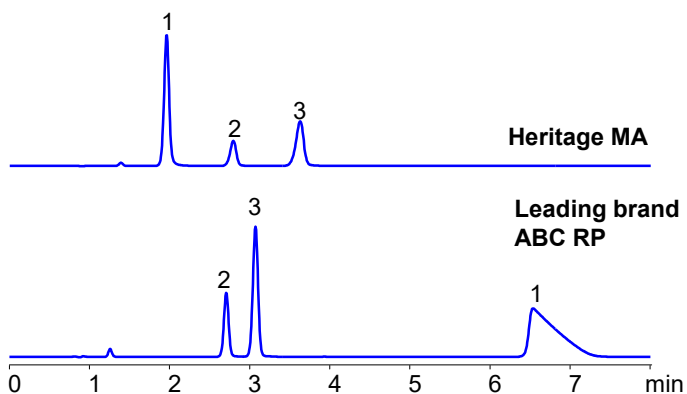


Fig. 2 HPLC Analysis of Cetylpyridinium on Heritage MA Mixed-Mode Column and Single Mode RP Columns

1. Cetylpyridinium
2. Biphenyl
3. Phenanthrene

Dimensions: 3.0 x 100 mm, 3 μ m, 100A
Mobile phase: ACN/water/TFA
Flow: 0.6 ml/min
Detection: 255 nm
Sample: 1 mg/ml
Injection: 2 μ L

Application Notes

Different interactions between analytes and stationary phases exist for almost every compound. Even if you are using strictly RP or HILIC columns, there are some strong and residual weak mechanisms of interaction always present. Most of the column manufacturers are trying to eliminate these "unwanted" interactions to provide a better efficiency and peak shape. "Optimized" ligand loading, base-deactivation, end-capping, double end-capping, and other tricks are used to eliminate such "undesired" interactions, but sometimes it is impossible to fight the nature of the analyte which produces poor peak shape in single-mode chromatography. While single-mode chromatography remains a perfect choice for some analytes and provides good robustness (toluene, benzoic acid in applications below) for more complex compounds you need something different - our mixed-mode columns. HELIX Chromatography is embracing multiple interactions. We know how to control every interaction to improve resolution and peak shape. All interactions matter and it is important when you decide what column and conditions to use. Aromatic boronic acids and hydrophobic basic surfactants are two examples where the nature of compounds affects the peak shape.