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■ Identifying Cap-1 and Unreacted Groups

Fig. 3 shows the component chromatogram of analyzed samples obtained by spiking Cap-1 group (0.5 µg) with the unreacted group at 10 % (w/w). The mass chromatogram is displayed as a component chromatogram, based on MS1 spectra and by combining signals from different valences and

isotopes. Fig. 4 shows the multivalent ion analysis for the Cap-1 group. Both Cap-1 and unreacted groups were detected with a mass error of less than 1 Da compared to the theoretical molecular weight value.

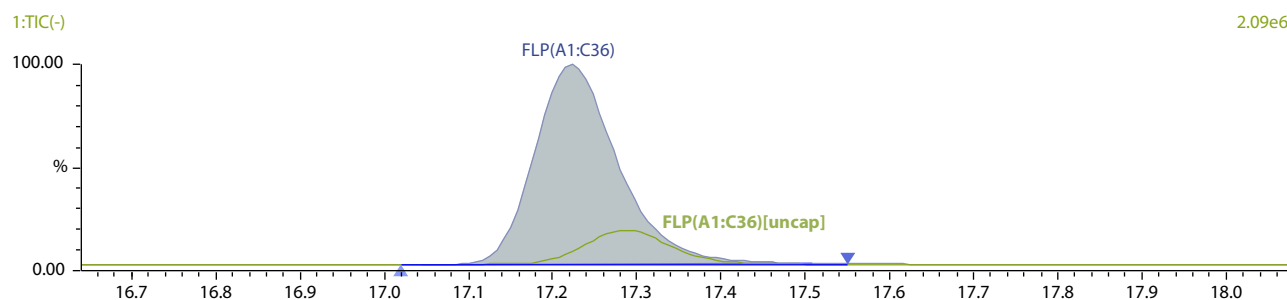


Fig. 3 Component Chromatograms of the Cap-1 Group and the Unreacted Group
FLP (A1:C36) indicates the Cap-1 group, and FLP (A1:C36)[uncap] indicates the unreacted group.

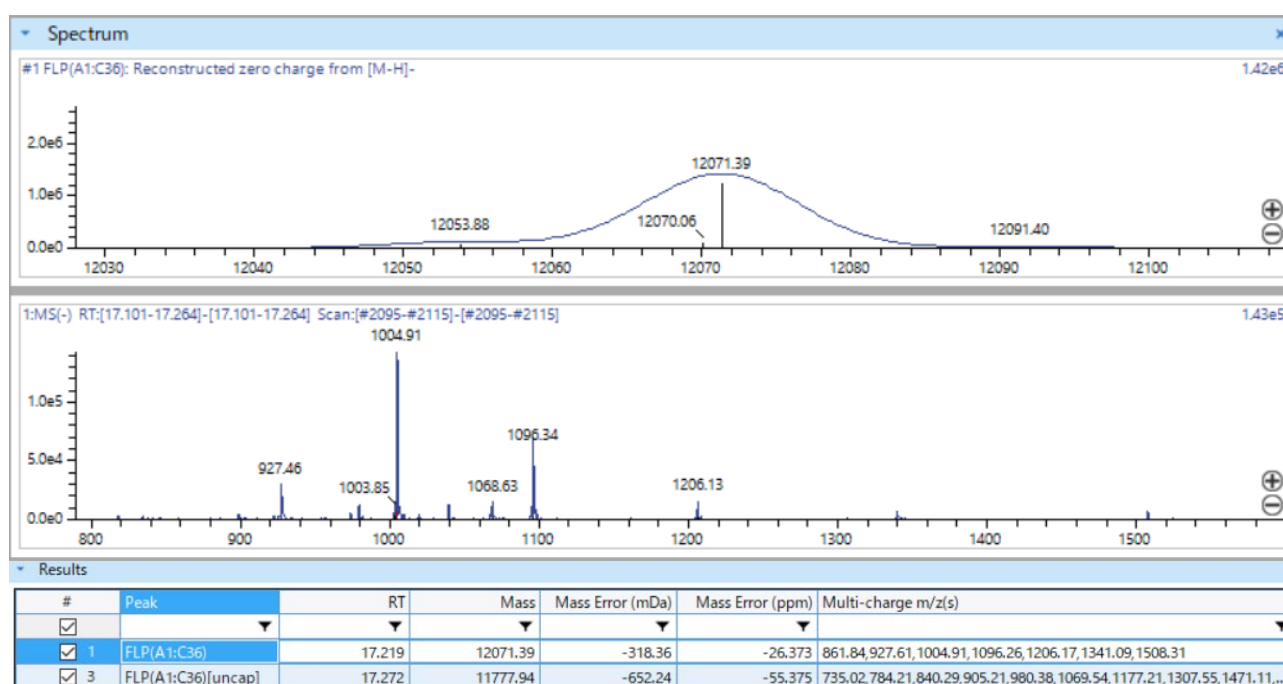


Fig. 4 Results of Multivalent Ion Analysis
Top: Deconvoluted mass spectrum; Center: Mass spectrum; Bottom: Identification results

■ Conclusion

In this study, molecular weight identification of 5' cap modified mRNA was performed using the LCMS-2050 mass spectrometer and LabSolutions Insight Biologics software. Both Cap-1 and unreacted groups were detected with a mass error of less than 1 Da compared to the theoretical molecular weight value. The LCMS-2050 demonstrated it is easy to use and similar to operate as an LC, making it suitable for confirming molecular weights such as for quality controls.

Related Applications

1. Analysis of mRNA 5' Cap Structure Using a Quadrupole Time-of-Flight Mass Spectrometer
[Application News No.01-00733-EN](#)
2. Simple Analysis of Impurities in Oligonucleotide Therapeutics Using a Single Quadrupole Mass Spectrometer
[Application News No.01-00656-EN](#)

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