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Application of LEDA Algorithm for the characterization of Isomers in Simultaneous Degradation Study in Human Plasma by HPLC-MS/MS

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Design and synthesis of new candidate drugs produces a large number of compounds that must be qualified and tested to evaluate their characteristics and potential applications. Therefore, many studies will be scheduled and, consequently, it will be necessary to arrange specific, reliable, fast and relatively cheap analytic methods to support this research.
For these reasons, a tandem mass spectrometry (MS/MS) approach in isomer recognition by playing with the "energetic dimension" of the experiment was proposed[1]. The chromatographic set up (HPLC) was tuned to minimize the run time, without requiring high efficiency or resolution between the isomers. Then, the MS/MS properties to solve the signal assignment were explored by performing a series of energy resolved experiments in order to optimize the parameters, and by applying an interesting post-processing data elaboration tool (LEDA)[2-4]. The reliability of this approach was evaluated, determining the accuracy and precision of the quantitative results through analysis of the isomer mixture solutions. Next, the proposed method was applied in a chemical stability study of human plasma samples through the simultaneous addition of each pair of isomers. In the studied case, only one of the isomers suffered of enzymatic hydrolysis; therefore, the influence of the stable isomer on the degradation rate of the other was verified. In order to monitor this process correctly, it must be possible to distinguish each isomer present in the sample, quantify it, and plot its degradation profile. The reported results demonstrated the effectiveness of the LEDA algorithm in separating the isomers, without chromatographic resolution, and monitoring their behavior in human plasma samples.

References

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