

## Method development for heavy metal analysis in biological samples on dual instrumentation; graphite furnace atomic absorption (GFAA) and total reflection X-ray fluorescence (TXRF)

Michelle Lund, Martina Schmeling, Bruce Gaynes, Susanne Tidow-Kebritchi  
Department of Chemistry and Biochemistry; Loyola University Chicago

Contact email: [mlund@luc.edu](mailto:mlund@luc.edu)

Detection of heavy metals within biological samples can be very difficult due to the complexity of its matrix. This can often lead to either false positives, artificially high or low values, or completely hinder the signal leading to no quantification. Therefore, method development remains an important factor in experimental design since it can account for these problems and generate a method that produces accurate, precise, reliable and reproducible results. In this study an in-depth look was taken for the quantification of heavy metals in biological materials on both total-reflection X-ray fluorescence (TXRF) and graphite furnace atomic absorption (GFAA). The method developed proved not only to be reliable and reproducible but also can be applied to multiple different biological materials including; *Escherichia coli*, *saccharomyces cerevisiae*, and human cataract cell pellets.

Having a standardized method for the analysis of heavy metals in biological samples can have a widespread positive influence in the certain fields of study such as; toxicology studies, food pathogen detection, trace of pollutants and bioaccumulation studies.

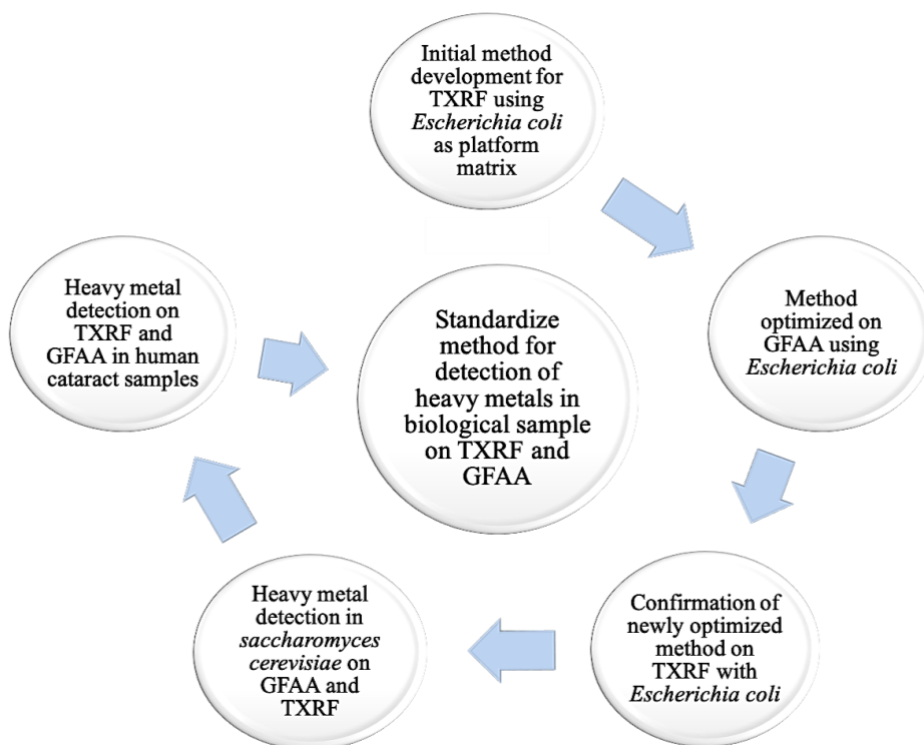


Figure 1: Overview of how the standardize method for the detection of heavy metals within biological samples was constructed