

ANALYSIS OF CASEWORK SAMPLES FROM SWEAT

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We describe here our approach for the validation of a method to analyze large casework samples, such as sweat stains, starting from the extraction steps, including a pre-filtering step with the PureYield™ Blue Columns, the DNA quantization with the Plexor® HY System, leading to accurate STR analysis with the PowerPlex® ESI/ESX and NGM/Identifiler Plus.

Due to the technology improvements, the success of the analysis of difficult traces has strongly increased. Subsequently, the request of these kind of investigation has got greater than in the past. In particular, we have analyzed a large number of “sweat traces”. These evidences are subjected to two main problems: the degradation of the DNA and the large surface from which the genetic material must be extracted (e.g. caps, clothes etc.), consequently, large volume extraction methods are required. In our lab, we have validated an extraction method involving the use of the Promega PureYield™ Blue Filter Columns, originally suited for a totally different purpose.

An accurate and reliable DNA quantification is crucial to address samples to the most appropriate PCR based STR analysis. We have validated the Plexor® HY Systems on the new Roche 480II RealTime thermal-cycler. The use of a multi-locus approach, peculiar to the Promega system, minimizes fake results caused by the DNA fragmentation/degradation and eventual mutational events.

Finally, we provide evidences that, mainly in case of Low Template samples, the use of a combination of two amplification set such as PowerPlex® ESI and PowerPlex® ESX or NGM/Identifiler Plus seemed to be a better approach than the classical Serial Multiple Amplification with the same system to get a much more reliable profile.