

## SHORT TANDEM REPEAT (STR) MIXTURE ANALYSIS APPLICATION IN GENEMAKER®HID

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STR genotyping is instrumental in data analysis for a wide range of human identification applications, including missing persons, mass disasters and crime scene investigations. Expert systems greatly reduce the time needed to analyze data. GeneMarker HID has all of the features of an expert system as defined by the National Institute of Justice's Expert System Testbed (1).

However, very often samples from mass disasters and crime scene investigations are mixtures rather than single source. GeneMarker HID mixture analysis follows the recommendations of the DNA commission of the International Society of Forensic Genetics (2). GeneMarker HID identifies the presence of a mixture, designates allele peaks, identifies the number of potential contributors, estimates the relative ratio of the individuals contributing to the mixture, considers all possible genotype combinations and identifies those combinations that conform to the parameters set by the analyst (3, 4).

When a mixture of two contributors and single source samples are included in the same project, the mixture analysis tool automatically identifies any single source samples included in the mixture; providing information needed to exclude or include the single source samples. In the same mixture analysis screen, the analyst can use allele frequencies from major populations to have the program calculate likelihood ratios of samples that are included in the mixture; determining the likelihood that the sample in the mixture is from the individual in question or a random individual from the population.

GeneMarker HID combines the accuracy of an expert system for forensic DNA analysis and an integrated mixture analysis tool. The transition from raw data analysis to mixture analysis is user-friendly and intuitive; providing accurate analysis and significant time savings.

### References

<sup>1</sup>Phillips, N., R. Roby, J. Planz, A. Eisenberg. The relationship testing application of GeneMarker HID: automated pedigree and kinship analysis with database searching capabilities In: 19<sup>th</sup> Int. Symp. on Human Identification. 2008, Hollywood, CA.

<sup>2</sup>Gill, P., Brenner, C.H., Buckleton, J.S., Carracedo, A., Drawczak, M., Mayr, W.R., Morling, N., Prinz, M., Schneider, P.M. Weir, B.S. 2006. DNA commission of the International Society of Forensic Genetics: Recommendations on the interpretation of mixtures. *Forensic Sci. Int.* 160:90-101.

<sup>3</sup>Gill, P., R. Sparkes, R. Pinchin, T. Clayton, J. Witaker, J. Buckleton. 1998. Interpreting simple STR mixtures using allele peak areas. *Forensic Sci. Int.* 91:41-53.

<sup>4</sup>Clayton, T., J. Whitaker, R. Sparkes, P. Gill. 1998. Analysis and interpretation of mixed forensic stains using DNA STR profiling. *Forensic Sci. Int.* 91:55-70.