

GenoProof® Mixture 1.3

GenoProof® Mixture – our expert program for analyses of forensic DNA samples and complex mixtures of DNA – provides the following new functionalities:

EasyRead Technology

With GenoProof® Mixture Version 1.3 the raw data analysis of fsa files has been fundamentally revised and optimized in terms of usability, robustness and speed. This new **EasyRead technology** enables to read in almost any file without any manually adjustments. With it, especially problems in size matching and ladder calibration can be reduced significantly. The EasyRead technology includes the following features.

Peak Detection Based on Polynomials

The usage of polynomial functions result in a higher sensitivity in peak detection in comparison to using linear functions. Thus, a higher resolution can be achieved and peaks can be separated clearly.

Size Matching and Allele Matching on Heuristics

The **EasyRead technology**, in comparison to other analysis methods, does not assign peaks just continuously to the sizes of size standards, but finds the best solution for size matching with help of an optimization function with the following characteristics:

- Inclusion of all available fragments
- Consideration of the heuristic parameters distance and equal heights of the fragments

Hence, even early terminated runs are correctly identified.

Optimized parameters of raw data analysis

The new parameter smoothing was introduced. It represses high-frequency signal noise and optimizes the peak shape in its width and height. Thus, the number of false detected peaks is reduced.

The greater (coarser) the smoothing is set the rounder the peaks appear. Indeed, they lose in height in the process. Therefore, only a fine smoothing is recommended for analysis of standard data.

Improved Display of Electropherograms and optimization of print functions

Display of electropherograms has been optimized in terms of speed and optical finesse. Additional GenoProof® Mixture 1.3 provides new printing options for electropherograms. Now the user can choose between a high print quality and a faster output.

Separate Calculation of RMNE and Likelihood Ratio

The calculation of RMNE and likelihood ratio is now carried out separately. Therefore, RMNE calculations can also be performed if no hypotheses have been formed.

2p rule for allelic dropouts

In case of consideration of allelic dropouts, the 2p rule can be used for calculation of probability of identity.

Alternative Population

In case that allele frequencies for specific markers are not available in the respective population, you can choose an alternative population for these several markers.

Change in quality information

In the quality information a warning is shown in case of spectral overlaps. Furthermore, the quality information tab is actualized after every re-analysis.

Inspired?

Are you interested in GenoProof® Mixture 1.3 or do you want to update your version? Please contact us by calling the telephone number +49 (0) 351-88382808 or e-mail to sales@qualitytype.de.

For further information or in order to download a trial version please click [here](#).