

# STRmix Limited Unveils New Version of FaSTR™ DNA

*FaSTR™ DNA v1.2 Features Review Module, ScanPoint View Mode*

WASHINGTON, DC, UNITED STATES, October 3, 2024 /EINPresswire.com/ -- The [STRmix](#) Team has released a new version of FaSTR™ [DNA](#). This introduces major improvements including the



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addition of a new Review Module which enables the comparison of two analyzed projects to create a final reviewed project.

FaSTR™ DNA v1.2, like its predecessor, combines an intuitive, user-friendly graphical interface with easily understandable and laboratory-customizable rules to rapidly analyze raw DNA data generated by capillary electrophoresis instruments and standard STR DNA profiling kits, and assign a number of contributors (NoC) estimate.

In addition to the new Review Module, the latest version of

FaSTR™ DNA also introduces, among other improvements, known artifact detection and optional new viewing modes for scanpoint view and individual channel zoom, allowing users to independently zoom the y-axis for different channels. FaSTR™ DNA v1.2 also reworks the filtering of the analysis file list by including additional filters for sample type and status, and the ability to search sample names.

When used in conjunction with STRmix™ (sophisticated [forensic software](#) which resolves mixed DNA profiles previously regarded as too complex or degraded to interpret) and DBLR™ (which enables users to undertake superfast database searches, visualize the value of DNA mixture evidence, determine whether there is a common donor, and calculate any kinship relationship conceivable), FaSTR™ DNA delivers an end-to-end analysis, interpretation, and intelligence solution, completing the full workflow.

“The development of FaSTR™ DNA v1.2, and in particular the new Review Module, was driven through extensive engagement with the end user community to ensure the feature set is targeted to real world needs and is useful for casework operations,” says Dr Meng-Han Lin, Senior Scientist, STRmix Team.

In addition to those features mentioned above, FaSTR™ DNA v1.2 contains a number of other new features including the ability to:

- Add more than one sample with the same name to the project;
- View the method details from within the Analysis window;
- Model stutters using allele-specific stutter exceptions (same as STRmix™);
- Customize detailed labels; and
- Set a zoom level for PDF Sample Reports.

FaSTR™ DNA works by applying a set of fully configurable rules to streamline the analysis of STR DNA profiles. In some instances, DNA analysis is more complex, and automated heuristics (analysis rules) alone may not be able to resolve all profiles. Where the intervention of a DNA analyst is required, FaSTR™ DNA readily provides all details related to possible ambiguity of a peak (i.e. stutter type, stutter ratio, composite stutter, pull-up proportion, N/shoulder peak, peak morphology, stochastic homozygous threshold, heterozygote imbalance) and signals a requirement for the DNA analyst to make a decision. It then records and highlights changes made by the analyst.

The algorithms used for analysis in FaSTR™ DNA are conceptually adapted from the proven approach of OSIRIS analysis software (National Center for Biotechnology Information).

To see a brief overview of FaSTR™ DNA v1.2, visit <https://vimeo.com/1007497807/85d479cea3?share=copy>

For more information on FaSTR™ DNA v1.2, visit <https://www.strmix.com/fastr>.

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