FaSTR™

www.STRmix.com/FaSTR

FaSTR™ DNA is expert forensic software that rapidly analyses DNA profiles and assigns a Number of Contributors, ensuring consistency and efficiency in DNA analysis. Developed by the makers of the highly successful STRmix™, it simplifies the analysis of DNA profiles generated by genetic analysers and standard profile testing kits.

RAPIDLY ANALYSE DNA PROFILES

FaSTR™ DNA is designed by scientists for scientists, combining a sophisticated and user-friendly graphical interface with easily understandable, transparent and laboratory customisable rules for DNA profile analysis.

INTUITIVE

FaSTR™ DNA's interface helps streamline the otherwise time-consuming workflow of calling alleles.

INTELLIGENT

FaSTR™ DNA incorporates artificial neural networks (ANN) for the independent classification of peaks detected [1].

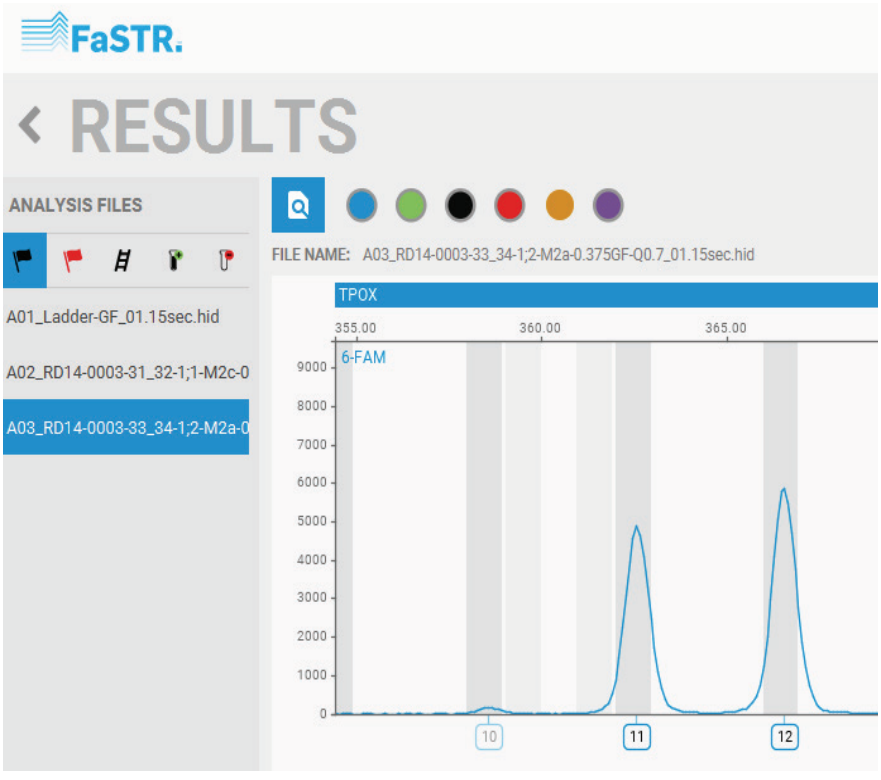
INTEGRATED

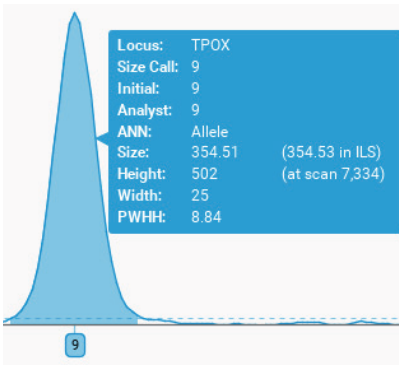
FaSTR™ DNA's in-built Number of Contributors (NoC) estimator allows seamless integration with STRmix™ to make the analysis and interpretation process even easier.

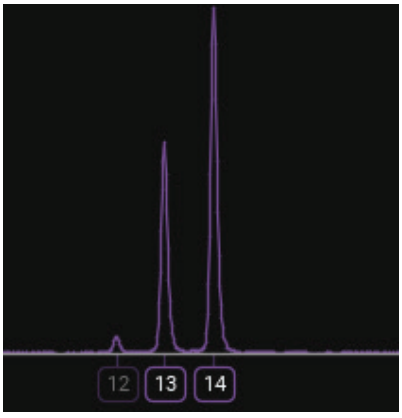
The software has been developed by New Zealand's Institute of Environmental Science and Research (ESR), with Forensic Science South Australia (FSSA).

WITH FASTR™ DNA YOU WILL BE ABLE TO:

- analyse raw DNA results more rapidly, particularly high throughput samples such as DNA database samples
- fully configure settings
- estimate the Number of Contributors to a mixture
- seamlessly integrate with STRmix™ (when in use) for even greater speed and efficiency from analysis to interpretation
- easily generate informative epg reports
- customise export templates







[1] D. Taylor, A. Harrison, D. Powers, Artificial neural network system to identify alleles in reference electropherograms. FSI Genetics 30 (2017) 114-126.

ABOUT FASTR™ DNA

FaSTR™ DNA is an expert system that allows professional DNA analysts to simplify the analysis of DNA profiles generated by genetic analysers and standard profile testing kits.

FaSTR™ DNA enables forensic laboratories to:

- expedite the otherwise time-consuming process of calling alleles
- ensure consistency in DNA analysis and NoC estimation, which is critical to meeting quality assurance criteria.

FaSTR™ DNA applies a set of fully configurable rules to analyse many DNA profiles automatically. But DNA analysis is complex, and the rules alone cannot resolve all profiles. At times, the DNA analyst must intervene. FaSTR™ DNA signals when this human intervention (expert judgment) is required.

As forensic provider to New Zealand Police and custodian of New Zealand's National DNA Database, ESR understands the need for speed, accuracy, and simplicity. In developing FaSTR™ DNA, particular attention has been paid to simplifying the procedure. Reliable results can now be gained with minimal effort.

FaSTR™ DNA can analyse profiles generated using the most commonly used instruments and multiplex kits. The software is configurable, with easy addition of new kits, dye colours and internal size standards.

FaSTR™ DNA proposes the Number of Contributors to a profile using an easily replicable decision tree process. Utilising all information within the profile, FaSTR™ DNA can optionally be coupled with STRmix™ (www.strmix.com/strmix) for seamless interpretation of complex mixed DNA profiles.

CONFIGURATION PARAMETERS

The analysis settings can be general or specific to each profile kit type and locus. FaSTR™ DNA contains easily customisable default kits and methods. You can also create (and save) customised sets of parameters appropriate to different types of DNA samples (e.g. single source samples and crime-scene samples).

SPECIFICATIONS

For guidance on hardware and/or software specifications please go to www.strmix.com/fastr/specifications

HOW DOES FASTR™ DNA WORK?

DNA analysis is a process of identifying alleles. The alleles appear as peaks in an electropherogram (EPG) and are identified from their locations within the EPG. The locations are determined using internal size standards and 'ladders'.

FaSTR™ DNA contains the size-standard and ladder data for commonly-available testing kits. Additional kits and size standards can easily be added by importing panel, bin, and size standard information, or by manual entry.

Based on an adaptation of the methods implemented in OSIRIS DNA [2], FaSTR™ DNA applies a set of fully configurable rules to identify and label alleles and reject artefacts within the EPGs of test samples.

THE ANALYSIS PROCESS

EPGs are produced by genetic analysers in the form of .fsa or .hid data files. FaSTR™ DNA analyses EPG data by:

1. Dynamic baselining of the EPG data
2. Detection and assignment of size-standard peaks for the accurate sizing of peaks in the allelic ladder and test sample
3. Size alignment of peaks detected in the allelic ladder with peaks detected in the test sample to apply allele calls
4. Applying a set of analysis rules to distinguish artefactual from allelic peaks
5. Optionally carrying out NoC estimation
6. Exporting the results as configurable outputs

OUTPUTS

FaSTR™ DNA displays the results of its analysis (the 'DNA profile'), as a labelled EPG and as a table of loci and peak designations. With FaSTR™ DNA you can:

- Easily print EPGs and include snapshots of areas of interest
- Export the data to STRmix™ or the CODIS tool or a data table
- Save the analysis as a 'project' for future reference.

CONTACT

FOR MORE INFORMATION ABOUT FASTR™ DNA PLEASE E-MAIL:

support@fastrdna.com

STRMIX LIMITED

STRmix Limited is a subsidiary of ESR, founded to better serve international users of STRmix™.

INSTITUTE OF ENVIRONMENTAL SCIENCE AND RESEARCH (ESR)

ESR is New Zealand's Crown Research Institute specialising in science for communities. ESR uses world-leading science to safeguard our health, keep our communities safer, protect our food-based economy, and improve the health of our water and natural environment.

FORENSIC SCIENCE SOUTH AUSTRALIA (FSSA)

FSSA provides services to some of South Australia's largest government departments and undertakes award-winning research in forensic science.

[2] *R.M. Goor, L. Forman Neall, D. Hoffman, S.T. Sherry, Mathematical approach to analysis of multiplex DNA profiles, Bull Math Biol 73(8) (2011) 1909-1931*