

STRmix[™] Now Being Used to Interpret Crime Scene Evidence in 91 U.S. Labs

Software Has Produced Usable DNA Evidence in More Than 690,000 Cases Worldwide

WASHINGTON, DC, UNITED STATES, February 25, 2025 /EINPresswire.com/ -- <u>STRmix</u>[™] – sophisticated <u>forensic</u> <u>software</u> capable of resolving mixed <u>DNA</u> profiles previously regarded as too complex or degraded to interpret –



is now being used to interpret crime scene evidence by 91 forensic organizations in the U.S.

Since its launch in 2012, STRmix[™] has produced usable, interpretable, and legally admissible DNA evidence in more than 690,000 criminal cases worldwide. The software has been

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Forensic analysts using STRmix[™] are able to combine DNA profiles from different kits and compare profiles against a person of interest in order to calculate a likelihood ratio." John Buckleton DSc, FRSNZ particularly effective in resolving violent crime and sexual assault cases, as well as cold cases in which evidence originally dismissed as inconclusive was able to be reexamined.

The newest U.S. lab to use STRmix[™] is the Maryland State Police Forensic Sciences Division. STRmix[™] will support the Division's mission to serve as the model laboratory for analyzing forensic evidence in Maryland. Maintaining ISO 17025 accreditation and compliance with all oversight requirements, the Division collaborates with other labs and

agencies to maximize the forensic services available, promote state-of-the-science operations through continuing education and routine evaluation of procedures, eliminate backlogs and initiate cases upon submission, and maximize the public's return on investment.

In addition to its use in the U.S., STRmix[™] is being employed by 29 forensic laboratories internationally, including labs in Canada, the United Kingdom, Europe, Asia, the Middle East, the Caribbean, New Zealand, and Australia.

STRmix[™] works by matching mixed DNA profiles directly against a database – a tremendous

advance for those cases in which there are no suspects and DNA from multiple contributors is present in a single sample.

"Forensic analysts using STRmix[™] are able to combine DNA profiles from different kits in the same interpretation and compare profiles against a person of interest in order to calculate a likelihood ratio, enabling the resolution of previously unresolvable DNA mixtures regardless of the number of contributors," explains STRmix[™] co-developer John Buckleton DSc, FRSNZ, Principal Scientist at the New Zealand Institute of Environmental Science and Research (ESR).

The latest version of STRmix[™], introduced in December 2024, builds on previous versions of the software, while adding several significant new features. These include support for peak label probabilities in varNOC calculations and inclusion of results collation tools for database searches, and interpretations and likelihood ratios (LRs) in the Reporting module.

STRmix[™] v2.12 also features the ability to visualize the evidence input in a stylized plot and ignore loci from the graph if required; extension to the Visualize Weights module to include the ability to visualize genotypes corresponding to person(s) of interest and evidence; and improvements to the varNOC LR assignment calculation.

In addition to STRmix[™], the STRmix team has developed three related software applications:

• DBLR[™], an application which when used with STRmix[™] allows forensic laboratories to undertake extensive kinship analysis, carry out rapid database searches, visualize the value of their DNA mixture evidence, and carry out mixture-to-mixture matches;

• FaSTR[™] DNA, expert forensic software which seamlessly integrates with STRmix[™] (when in use) to rapidly analyze raw DNA data generated by genetic analyzers and standard profiling kits and assigns a number of contributors (NoC) estimate; and

• STRmix[™] NGS, fully continuous mixture interpretation and likelihood ratio generation software for profiles generated using Next Generation Sequencing (NGS).

In combination with STRmix[™], FaSTR[™] DNA and DBLR[™] complete the full workflow from analysis to interpretation and database matching, while STRmix[™] NGS broadens the range of profile types that can be interpreted.

For more information about STRmix[™], visit <u>http://www.strmix.com</u>.

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