

University of Bern Will Use STRmix™ to Clarify Crimes, Examine Crime Scene Traces

Forensic Software Has Proven Highly Effective in Resolving Violent Crime, Sexual Assault Cases

PORIRUA, NEW ZEALAND, November 25, 2024 /EINPresswire.com/ -- The Department of [Forensic Molecular Biology](#) at the University of Bern's Institute of Forensic Medicine has added [STRmix™](#)



STRmix™ matches mixed DNA profiles directly against a database, a tremendous advance for cases in which there are no suspects and DNA from multiple contributors is present in a single sample."

John Buckleton DSc, FRSNZ

forensic software to its array of scientific testing solutions for clarifying crimes and examining crime scene traces and comparators on behalf of police and judicial authorities.

Touted for its ability to resolve mixed [DNA](#) profiles previously regarded as too complex or degraded to interpret, STRmix™ has generated a highly successful track record since its introduction in 2012, producing usable, interpretable, and legally admissible DNA evidence in more than 690,000 criminal cases worldwide.

STRmix™ has proven to be a particularly effective solution

for examining violent crime and sexual assault cases, as well as cold cases in which evidence initially dismissed as inconclusive was able to be reexamined.

The Department of Forensic Molecular Biology at the University of Bern analyzes crime scene traces – including biological material such as blood, saliva, sperm, skin cells, and hair – from a wide range of trace carriers on behalf of police and judicial authorities. The resulting DNA profiles are transmitted to the Federal DNA Database and compared with DNA profiles (traces or persons) that have already been stored.

In order to clarify offenses and parentage issues, as well as the identification of deceased or missing persons, the Department also creates DNA profiles from buccal mucosal swabs (WSA) or other comparative materials, depending on the case. In addition, the Department carries out parentage analyses, including special or more complex kinship investigations, on behalf of authorities and private individuals.

The Institute of Forensic Medicine is one of 150 institutes at the University of Bern. The university, founded in 1834, is ranked as one of the top 150 universities in the world. With about 19,000 students, the university is the third largest university in Switzerland.

With the addition of the Department of Forensic Molecular Biology, STRmix™ is now being used in 120 forensic laboratories worldwide. This includes 20 forensic labs throughout Europe, the United Kingdom, Asia, the Middle East, Canada, and the Caribbean, all nine state and territory forensic laboratories in New Zealand and Australia, and 90 forensic labs in the U.S.

“This ability of STRmix™ to use more of the information in a DNA profile, coupled with its proven effectiveness in interpreting DNA results faster than the previous binary interpretation method, helps to explain why STRmix™ is so widely used today by forensic labs around the world,” says John Buckleton DSc, FRSNZ, Principal Scientist at the New Zealand Institute of Environmental Science and Research (ESR) and a co-developer of STRmix™.

Buckleton explains that 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,” Buckleton explains.

In addition to STRmix™, the STRmix team has developed and previously launched 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. STRmix™ NGS, meanwhile, broadens the range of profile types that can be interpreted.

For more information, visit <http://www.strmix.com>.

Ray Weiss
Pugh & Tiller PR
+1 410-303-5019
[email us here](#)

This press release can be viewed online at: <https://www.einpresswire.com/article/763007927>

EIN Presswire's priority is source transparency. We do not allow opaque clients, and our editors try to be careful about weeding out false and misleading content. As a user, if you see something we have missed, please do bring it to our attention. Your help is welcome. EIN Presswire, Everyone's Internet News Presswire™, tries to define some of the boundaries that are reasonable in today's world. Please see our Editorial Guidelines for more information.

© 1995-2024 Newsmatics Inc. All Right Reserved.