

STRmix Will Present at 31st ISFG Congress

Presentations Will Focus on Probabilistic Genotyping, LR Behavior of Y-STR Profiles

WASHINGTON, DC, UNITED STATES, August 14, 2026 /EINPresswire.com/ -- [STRmix](#) will have major presence when the International Society for [Forensic](#) Genetics (ISFG), an international

association promoting scientific knowledge in the field of genetic markers analyzed for forensic purposes, holds its 31st Congress in Montréal from August 17-21.

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Dr. Hannah Kelly

In addition to its booth on the exhibition floor, STRmix team members will present a talk entitled “Likelihood Ratio Behavior for Mixed and Low Template Y-STR Samples in the Haplotype-Centered Method” as part of the Congress Program, and participate in a Poster Session on [“Probabilistic Genotyping of Y-STR Profiles.”](#)

Founded in 1968, ISFG represents more than 1,100

members from over 60 countries. Regular meetings, which are held at both regional and international levels, are designed to provide a comprehensive overview of the latest scientific developments, technological innovations, and practical applications in the field.

Attendees at the 31st ISFG Congress can expect a dynamic mix of plenary sessions, keynote presentations, panel discussions, workshops, and poster sessions, all aimed at fostering knowledge and interdisciplinary collaboration.

The STRmix Poster Session, “Probabilistic Genotyping of Y-STR Profiles,” will explore whether a probabilistic genotyping method can address the challenges associated with the interpretation of Y-STR profiles, particularly in complex mixtures with multiple male contributors. These challenges are compounded by the lack of consensus-driven interpretation frameworks, and the variability in how laboratories handle stochastic effects, PCR artifacts, and multi-copy loci, leading to subjectivity in reported casework.

To be presented by Emma Marie, Data Analyst with STRmix, the poster session will provide early results of a sensitivity and specificity study for a range of mixed Y-STR profiles of varying quality and quantity. The Poster Session will be held on Wednesday, August 19, beginning at 10:49 a.m.

The final day of the ISFG Congress, August 21, will feature the talk, “Likelihood Ratio Behavior for

Mixed and Low Template Y-STR Samples in the Haplotype-Centered Method,” at 12:15 p.m. To be presented by STRmix Science Leader Dr. Hannah Kelly, the talk will provide results of the Haplotype Centered Likelihood Ratio (HC-LR), a method that allows locus-specific haplotype weights to be incorporated into a likelihood ratio for Y-STR data.

The results, according to Dr. Kelly, “will demonstrate that the HC-LR decreases appropriately as uncertainty in the contributing haplotypes increases. As the information in the sample decreases, the likelihood ratios trend toward one. This highlights the suitability of the method for integration with a probabilistic Y-STR interpretation framework.”

Since its introduction in 2012, STRmix™ has proven to be a highly effective tool in producing usable, interpretable, and admissible DNA results in more than 700,000 criminal cases worldwide. It has been particularly effective in helping to resolve violent crime and sexual assault cases, as well as cold cases in which evidence was originally dismissed as inconclusive.

The worldwide success of STRmix™ has led the team behind its development to create and regularly update three related software application:

- FaSTR™ DNA, expert forensic software which seamlessly integrates with STRmix™ (when in use) to rapidly analyze raw DNA data and assign a number of contributors (NoC) estimate;
- DBLR™, an application which when used with STRmix™ allows forensic laboratories to undertake extensive kinship analysis, carry out rapid database searches and mixture-to-mixture matches, and visualize the value of their DNA mixture evidence;
- STRmix™ NGS, fully continuous mixture interpretation and likelihood ratio generation software for profiles generated using Next Generation Sequencing.

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 ISFG, visit <https://isfg2026.ca/>. For more information about STRmix™, visit <http://www.strmix.com>.

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