



# **STRmix.<sup>TM</sup>**

## **RESOLVE MORE DNA MIXTURES.**

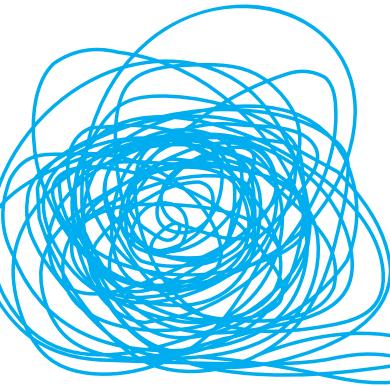
### **STRmix<sup>TM</sup> published data**

#### **Papers describing the biological model, mathematics, performance and validation of STRmix<sup>TM</sup>:**

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- [3] J.-A. Bright, D.A. Taylor, J. Curran, J.S. Buckleton, Degradation of forensic DNA profiles, *Australian Journal of Forensic Sciences*. 2013 45(4): 445-449.
- [4] J.-A. Bright, D.A. Taylor, J. M. Curran, J. S. Buckleton, Searching mixed DNA profiles directly against profile databases. *Forensic Science International: Genetics*. 2014; 9: 102-110.
- [5] D.A. Taylor. Using continuous DNA interpretation methods to revisit likelihood ratio behaviour. *Forensic Science International: Genetics*. 2014; 11: 144-153.
- [6] J.-A. Bright, J.M. Curran and J.S. Buckleton, The effect of the uncertainty in the number of contributors to mixed DNA profiles on profile interpretation. *Forensic Science International: Genetics*. 2014; 12: 208-214.
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- [12] D.A. Taylor and J.S. Buckleton, Do low template DNA profiles have useful quantitative data? *Forensic Science International: Genetics*. 2015; 16:13-6.
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- [15] J.-A. Bright, D.A. Taylor, C.E. McGovern, S.J. Cooper, L.J. Russell, D.V. Abarno and J.S. Buckleton, Developmental validation of STRmix<sup>TM</sup>, expert software for the interpretation of forensic DNA profiles. *Forensic Science International: Genetics*. 2016; 23:226-239.



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