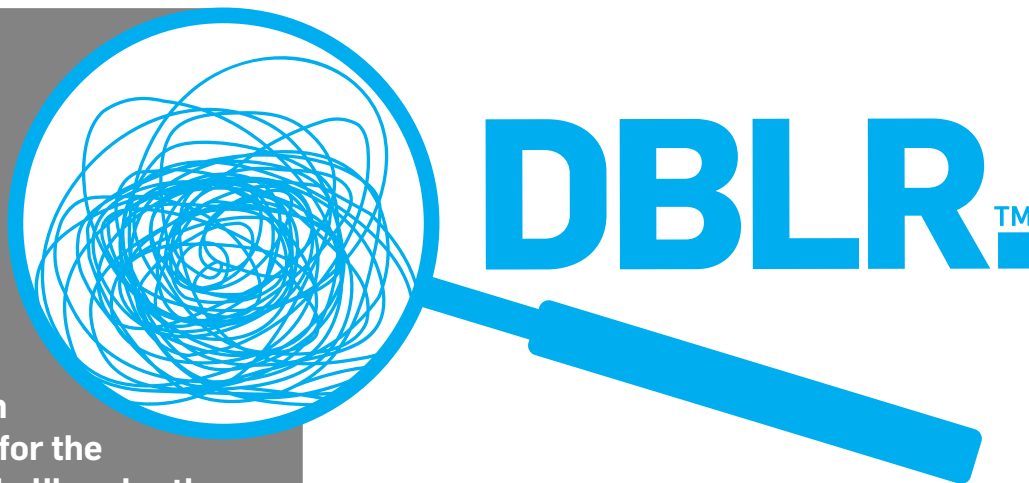


*From the
team that
brought you
STRmix™*

DBLR™ (database
likelihood ratios) is an
application designed for the
rapid calculation of likelihood ratios
(LRs) using STRmix™ deconvolutions.



www.STRmix.com

FAST DBLR™ calculates millions of LRs in seconds.

ACCESSIBLE DBLR™ runs on a user's PC, without the
need for high-speed computing.

ENABLING DBLR™ enables you to get more value from
your DNA evidence.

WITH DBLR™ YOU WILL BE ABLE TO:

- Achieve superfast database searches.
- Visualise the value of your DNA mixture evidence.
- Undertake mixture to mixture matches.

WHAT CAN DBLR™ DO?

- Undertake direct comparison of one or many components of a forensic DNA mixture to a database of known individuals (i.e. "Who contributed to the profile?").
- Carry out familial searching for a range of different relationships including siblings, half-siblings, parents, and children (i.e. "Is there a relative of the donor in the database?").
- Search for common contributors between mixed DNA profiles (mixture to mixture comparisons).
- Determine the profiles of the most likely contributors to a profile.
- Visualise the value of evidence by calculating expected LRs for one or many components of forensic DNA profiles for true and non-contributors using randomly generated individuals.
- Manage automated searches for one or many DNA profiles against one or many databases of known individuals.
- Manage databases of known contributors and STRmix™ deconvolutions from unsolved casework for easy matching.

HOW DOES DBLR™ WORK?

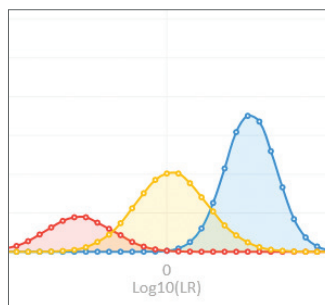
DBLR™ uses efficient algorithms for the fast calculation of LRs.

VALIDATION

DBLR™ has been extensively validated by the STRmix™ team based at ESR, New Zealand.

SPECIFICATIONS

DBLR™ is designed to run on an individual DNA analyst's PC.



ID	Search Name	Profile Database	# Deconvolutions	# Matches
19	GlobalFiler threshold 1	GP 1 million	1	22
Displaying 22/22 matches				
Previous Matches	Deconvolution	Reference ID1	Reference ID2	LR
▶ 686	L1.KAG6K7VAB.41	Random	77928	1.68308E+001
▶ 686	L1.KAG6K7VAB.41	Random	76542	2.03703E+001
▶ 686	L1.KAG6K7VAB.41	Random	112939	5.96656E+001
▶ 686	L1.KAG6K7VAB.41	Random	186729	2.97658E+001
▶ 686	L1.KAG6K7VAB.41	Random	221816	1.84802E+001
▶ 686	L1.KAG6K7VAB.41	Random	298966	1.78186E+003
▶ 686	L1.KAG6K7VAB.41	Random	307761	7.08050E+001
▶ 686	L1.KAG6K7VAB.41	Random	332865	3.67899E+001
▶ 686	L1.KAG6K7VAB.41	Random	343310	9.72803E+001
▶ 686	L1.KAG6K7VAB.41	Random	377650	2.71295E+002
▶ 686	L1.KAG6K7VAB.41	Random	507282	1.60802E+001
▶ 686	L1.KAG6K7VAB.41	Random	527888	7.70232E+002
▶ 686	L1.KAG6K7VAB.41	Random	558359	4.74342E+001
▶ 686	L1.KAG6K7VAB.41	Random	602117	3.18974E+001
▶ 686	L1.KAG6K7VAB.41	Random	609528	4.18378E+002
▶ 686	L1.KAG6K7VAB.41	Random	617190	4.63347E+001
▶ 686	L1.KAG6K7VAB.41	Random	687340	1.12944E+001

PUBLISHED DATA

The following papers describe the mathematics and application of DBLR™:

- [1] Slooten K. Identifying common donors in DNA mixtures, with applications to database searches. *Forensic Science International: Genetics* 2017;26:40-7.
- [2] Kruijver M, Bright J-A, Kelly H, Buckleton J. Exploring the probative value of mixed DNA profiles. *Forensic Science International: Genetics* 2019;41: 1-10.
- [3] Bright J-A, Taylor D, Kerr Z, Buckleton J, Kruijver M. The efficacy of DNA mixture to mixture matching. *Forensic Science International: Genetics* 2019;41: 64-71.
- [4] Taylor D, Rowe E, Kruijver M, Abarno D, Bright J-A, Buckleton J. Inter-sample contamination detection using mixture deconvolution comparison. *Forensic Science International: Genetics* 2019; 40: 160-167.

CONTACT

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INSTITUTE OF ENVIRONMENTAL SCIENCE AND RESEARCH (ESR)

ESR uses the power of science to solve complex problems with the potential to affect the lives of all New Zealanders. It is the sole source provider of forensic services to the New Zealand Police while its comprehensive knowledge of the presence and interpretation of DNA is utilised across the country and around the world.