AmpFLSTR® SEfiler™ Kit Template 8

This compact disk contains the following Genotyper® software template files for use on Windows NT® computers and Macintosh® computers with AmpFLSTR® products. Copy the appropriate template file(s) onto your computer. Genotyper® software version requirements for each template file are indicated below.

TEMPLATES FOR WINDOWS NT® COMPUTER

TEMPLATE NAME ON DISK

AmpFLSTR® SEfiler™ Kit Template v1

SEfiler V1

TEMPLATES FOR MACINTOSH® COMPUTER

TEMPLATE NAME ON DISK

AmpFLSTR® SEfiler™ Kit Template v2

SEfiler V2

- AmpFLSTR® SEfiler $^{\mathbb{M}}$ Kit Template v1 requires Genotyper $^{\mathbb{B}}$ Software v3.7. The computer requirement for Genotyper $^{\mathbb{B}}$ Software v3.7 is a Windows NT $^{\mathbb{B}}$, 4.0, Service Pack 4 or 5 operating system.
- AmpFLSTR® SEfiler $^{\mathbb{M}}$ Kit Template v2 requires Genotyper $^{\mathbb{R}}$ Software v2.5.2 or higher. The minimum system requirement for Genotyper $^{\mathbb{R}}$ Software v2.5.2 is a Power Macintosh $^{\mathbb{R}}$ computer running Mac OS 8.x or 9.1.
- The Kazam macros within a color have been rearranged so that the steps for loci with more stringent sample allele stutter filters are executed first. All Kazam macros have stutter filters ordered to avoid removal of labels for preceding loci from subsequent filters (Kinsey and Hormann, 2000).
- Proximal filtering is 3.25 bp to 4.75 bp.

Filtering

Filtering is left to right along the electropherogram.

Filtering compares Peak A to next labeled peak, peak B. The label will be removed from Peak A if Peak B meets both criteria:

- 1. Peak B is higher than peak A by the specified percentage (F value).
- 2. Peak B is within the specified size (bp) proximity range relative to Peak A.
- A = stutter peak
- B = allele peak
- $F = [(B-A)/A] \times 100$ where F is the filter value used in Genotyper® software
- $S = A/B \times 100$ where S is the conventional calculation of stutter percentage
- F = (10,000/S)-100
- S = 100/(0.01F +1)
- The Kazam macro for AmpFLSTR® SEfiler™ Kit use stutter filters calculated from the highest observed stutter at a particular locus plus three (3) standard deviations. This calculation is consistent with that used for the Kazam macros for AmpFLSTR® Blue™ Kit, AmpFLSTR® Green™ I Kit, Profiler® Kit, Profiler Plus™ Kit, COfiler™ Kit, SGM Plus® Kit, and CODIS COPP, which all use consistent stutter filters for common loci.

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Minus A (-A) filtering is not included.

Kazam w/Allele Control, Kazam (20%) w/Allele Control Two additional Kazam macros are provided in the AmpFLSTR® SEfiler $^{\text{TM}}$ Kit Template for use when running the AmpFLSTR® SEfiler $^{\text{TM}}$ Allele Control. To enable these macros to function effectively, identify the allele control sample with the words 'allele control' in the green sample/color info field of the sample sheet/plate record. This allows the macro to identify this sample and label appropriately.

Reference

Kinsey, P., and Hormann, S. 2000. "Modification of the stutter position label-filtering macro in the PE Biosystems Genotyper" Version 2.5 software package: Resolution of stutter-filter back talk." Forensic Science Communications 2(3).

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