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FSS-i^{3™} Expert Systems Software

With increased adoption of automation in forensic laboratories, the bottleneck for throughput has moved to analysis. With this shift comes increased interest in expert systems. Expert systems for the forensic community are defined as systems that increase the efficiency or effectiveness of genotyping samples in a laboratory by automatically interpreting nuclear STR data. Promega is now distributing the FSS-i^{3™} Expert Systems Software.

Is the FSS-i^{3™} software NDISapproved as an expert system?

Yes, the Florida Department of Law Enforcement has obtained approval from the National DNA Index System (NDIS) for database samples using Identifiler® reactions analyzed using an Applied Biosystems 3700 Genetic Analyzer and the FSS-i^{3™} Expert Systems Software. Additional efforts are underway in other labs to validate the software with other instrument platforms and STR systems.

Is it possible to create templates for other multiplex systems with the FSS-i^{3™} software?

With version 4.1.3 or newer versions of the software, it is possible to create new templates for new multiplexes. To do this, simply click on the green "+" symbol next to the list of multiplexes in the Multiplex Manager. You can create a new multiplex by editing an existing multiplex, such as PowerPlex® 16, or you can create a completely new multiplex. This ability is useful for labs that use multiplexes that are not commercially available or that use quadriplex systems, such as the *GenePrint*® Fluorescent STR Multiplex, F13A01, FESFPS, F13B, LPL (FFFL) System^(d,i), which are not included in the software.

When you create a new multiplex, the list of loci will be empty. To add specific loci, click "Templates" under "Ladders". This will bring up the Ladder Editor, where you can define the locus name, anchor positions, dye order and allele calls for each locus found within the ladder. For example, By Kimberly Huston Promega Corporation

the FFFL System contains the locus F13A01 in the fluorescein channel. Thus, you can add all alleles in the allelic ladder as well as alleles that you would like the software to designate.

Can I add frequent microvariant alleles to the virtual allelic ladder?

Yes. By simply selecting "Ladder Templates" and selecting the green "+" next to "Drag a new peak onto the graph", you can enter the specific virtual allele and its expected position relative to the first peak in the allelic ladder, known as the anchor peak (Figure 1). You can also drag the virtual



Figure 1. The Ladder Editor window.

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allele to the appropriate position within the allelic ladder. Make sure that the "Virtual Peak" box is checked. If this box is not checked, the software will expect to find the allele in the allelic ladder, and your ladder will fail the ladder check. Remember, the ladder check will ensure that all real peaks in the allelic ladder are present.

Can I save my analysis midway through a plate?

Yes. When first saving the analysis, select "File", then "Save As". The FSS-i^{3™} software will save the file with a .isf identifier. When the data set, also known as the batch, is re-opened, the software will resume with the sample that was active when the batch was saved.

There are different plate layouts that I can maintain for use with the i-ntegrity mode of the FSS-i^{3™} software. How do I make sure I am using the right one?

Many labs have different plate layouts that they use when injecting samples on a capillary electrophoresis instrument. The plate layout function helps manage multiple plate layouts. To use this function, multiple input templates need to be created (Figure 2). These input templates will determine what plate layout is used for the i-ntegrity software check.



Figure 2. The Edit Input Template window.





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What are the functions of the Plate Layout Manager?

The Plate Layout Manager is designed such that you can predetermine where the allelic ladders, positive and negative controls and blank wells are located in a plate (Figure 3). This helps when quickly scanning a plate that has gone through i-ntegrity. If a sample contains the same number of loci as another sample, they may have the same profile, which would result in further investigation. However, if they are both positive controls, this would be expected, and no further evaluation is necessary.

Can I have more than one positive control profile in the system?

Yes. The software can use multiple positive control profiles, as well as names, to check for positive control accuracy. Each additional control will be checked to ensure that there are no errors in the positive controls.

When troubleshooting a problem, Promega Technical Services Scientists may ask for your current Rulesets. Where do I find these, and how do I send them to Promega?

Rulesets, along with Multiplexes, Input and Output Templates, Plate Layouts and Ladder Templates, can be exported easily to a file and sent via e-mail to Promega. Rulesets are found within the Multiplex Manager and Plate Manager. When saving the exported files, use descriptive names. Promega Technical Services Scientists can then

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Figure 4. The iSTRess Export Tool.

import all of your templates into the software and check to ensure that all of the settings are correct. If they find an improvement, they will make it and send the improved files back to you. It is easy to import the modified files into your software. However, you must be logged in as an administrator to modify or import these files; this reduces the risk of accidental changes to validated settings.

I forgot my admin password. What should I do?

Contact the Promega FSS-i^{3™} software support line. We maintain a database of administrative passwords that are generated when we install the software. If you have changed the password, we can help you find the changed password.

Are output files from the FSS-i^{3™} software, version 4.1.3, compatible with laboratory information management systems (LIMS)?

Each license for the software includes an export tool (Figure 4), which can create output data in a format that is compatible with STACS, CMF 1.0 and CMF 3.2. In addition, output files can be generated in a .txt file, which is compatible with most LIMS systems.