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**Analyst® 1.4.2 HotFixes to May 2008  
Release Notes**

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## **Introduction**

Analyst® 1.4.2 HotFixes to May 2008 contains updated software components with the following fixes:

**1. Empty Audit Trail Archive if User Does Not Have Windows “Modify” Permissions on the Project:** For quantitation Results Tables and AAC Results Tables, this issue **cannot** occur. However, for project and instrument audit trails, in rare cases where the audit trail exceeds 1000 records (for instance, when there are a large number of subprojects), and the user has been denied “modify” permissions for the audit trail folder, a situation could occur where these audit trails became depopulated of archive events.

The audit trails for the project and instrument automatically archive after 1000 records are written. The audit trail is saved in the Project Information folder with a name indicating the type of audit trail and the date and time. A new audit trail is then created with the first record giving the path of the previously archived audit trail.

In previous versions of the Analyst software, if the user both did not have Windows “modify” permissions and was not explicitly given “delete” permissions, an empty archive file was created that did not show the audit trail records. With this HotFix, neither “modify” nor “delete” rights are required to successfully archive audit trail files. However, Windows read and write access is still required.

**2. Area Discrepancy Between the Results Table and Peak Review:** In the Quantitation module, in rare cases, small discrepancies have been reported between the Results Table peak area and the peak review peak area. In sites that reported experiencing the issue, fewer than 1 in 2000 integrations were affected. The issue has been addressed. For more information, see **Technical Information Regarding the Area Discrepancy Issue**.

**3. Shimadzu FIA Quantitation Optimization Isocratic Method Not Recognized:** Following the installation of Analyst 1.4.2 Hotfixes to July 2007, attempting to perform FIA Quantitative Optimization with Shimadzu devices configured natively within Analyst caused a message to appear informing the user that an isocratic method was needed. This occurred even when an isocratic method was provided. This issue is resolved and users can once again use Shimadzu devices to perform FIA Quantitative Optimization.

**4. Record Modified Flag Does Not Accurately Reflect the Modification Status of the Sample:** In previous versions of the Analyst software, incorrect behavior of the record modified flag was found in the following scenarios:

- (i) The Record Modified flag for a manually integrated Analyte Peak is set to “off” when the integration parameters for its Internal Standard peak are modified and globally updated.
- (ii) The Record Modified flag remains checked “on” for some Analyte peaks even after the integration method for all samples is reset using the “Update Method” operation.

This behavior has been corrected and the record modified flag is now set properly for these scenarios.

## **Package Contents**

This HotFix contains one self-extracted executable program called **Analyst 1.4.2 HotFixes to May 2008.exe** that can be downloaded from the Applied Biosystems web site:

<http://www.appliedbiosystems.com/support/software/lcmsms/updates.cfm>

The fixes in this update will also be included in the next release of the Analyst software.

## **Requirements**

Analyst 1.4.2 HotFixes to May 2008 requires the following to be installed:

- Windows 2000 (SP3 or SP4) or Windows XP (SP2) operating system
- Analyst 1.4.2 software
- Analyst 1.4.2 HotFixes to November 2006
- Analyst 1.4.2 HotFixes to July 2007

## **Before Installing**

Before installing Analyst 1.4.2 HotFixes to May 2008:

- Read these Release Notes.
- Back up the Analyst Data folder to a safe location. Backing up data is recommended before installing any software.
- Make sure that you have administrator privileges for the computer on which you want to install the software. Contact your IT group if you are unsure of your access rights.
- Deactivate all Analyst 1.4.2 hardware profiles.
- Make sure that the Analyst 1.4.2 software and all AAO applications are not running.

### **Files Added / Updated**

This HotFix updates the following files:

- In the “\Program Files\Analyst\Bin\” folder:
  - Analyst.exe
  - AuditTrailCommon.dll
  - PEUtils.dll
  - QuantIntegration.dll
  - QuantOptimizeWizard.dll
  - QuantPeakReview.ocx

This HotFix adds the following files:

- In the “\Program Files\Analyst\Help\” folder:
  - Analyst 1.4.2 HotFixes to May 2008 – Release Notes.pdf

## **Installation Instructions**

To install Analyst 1.4.2 HotFixes to May 2008:

**Note:** Install the Analyst 1.4.2 software, Analyst 1.4.2 HotFixes to November 2006, and Analyst 1.4.2 HotFixes to July 2007 before installing Analyst 1.4.2 HotFixes to May 2008.

1. Download Analyst 1.4.2 HotFixes to May 2008 from the Applied Biosystems website at:  
<http://www.appliedbiosystems.com/support/software/lcmsms/updates.cfm>
2. Log on to the computer as a user with local administrator privileges.
3. Start the Analyst 1.4.2 software, deactivate any active hardware profiles, and then close the Analyst software.
4. Browse to the folder on your hard drive where you saved the downloaded HotFix file.
5. Double-click **Analyst 1.4.2 HotFixes to May 2008.exe** to extract:
  - Analyst 1.4.2 HotFixes to May 2008.msi: An installer file
  - UpdateInfo.exe: A HotFix/patch information utility
  - HowToUseUpdateInfo.doc: A document detailing the usage of the HotFix/patch information utility

By default, these files extract to the C:\Analyst 1.4.2 HotFixes to May 2008 folder.

6. Browse to the folder where you extracted the Analyst 1.4.2 HotFixes to May 2008 installer files.
7. Double click **Analyst 1.4.2 HotFixes to May 2008.msi**.  
The HotFix Installer wizard opens.
8. Follow the instructions provided in the wizard.

## **Known Problems and Limitations**

The following patches are removed during the installation of the HotFix as their functionality is included in the HotFix:

- Analyst 1.4.2 Patch for Agilent DAD
- Analyst 1.4.2 Patch for Shimadzu FIA Quantitative Optimization.

## **Common Questions and Validation Concerns**

To obtain answers to questions about any of our products, report problems, or suggest improvements, visit <http://www.appliedbiosystems.com>. For on-site service, support, and training, visit [www.appliedbiosystems.com/support/contact/](http://www.appliedbiosystems.com/support/contact/).

### **Does Analyst 1.4.2 HotFixes to May 2008 affect any other functions?**

No, the changes in this HotFix do not affect any other Analyst software functionality.

### **Can I uninstall this HotFix?**

Yes, this HotFix includes an automatic uninstaller. To uninstall:

1. On the Windows desktop, click **My Computer > Control Panel > Add/Remove Programs**.
2. Select **Analyst 1.4.2 HotFixes to May 2008**, and then click **Change/Remove Programs**.

This procedure uninstalls the HotFix from the computer and restores the files to their previous settings (with Analyst 1.4.2 HotFixes to July 2007).

### **Has this HotFix been fully tested?**

Yes, it has undergone formal testing and meets the requirements for release.

### **How can I tell if Analyst 1.4.2 HotFixes to May 2008 has already been installed?**

A utility exists that can be used to determine if the HotFix is installed. Run the UpdateInfo.exe utility, included in the downloadable version of the HotFix, by double clicking it. When complete, all HotFixes and patches for the Analyst 1.4.2 software that have been installed on the system are displayed. As this utility is updated with every release, you must run the version that comes with the download. Previous versions of the utility cannot identify the most recent updates. The document HowToUseUpdateInfo.doc provides the details of this utility.

Alternately, in the Control Panel, double-click **Add/Remove Programs** and, in the currently installed programs, find the entry **Analyst 1.4.2 HotFixes to May 2008** to determine if it is installed.

### **What is the impact on my Validation?**

If you work in a regulated environment, validate the software according to your company's policies. As this is a HotFix, no new functionality has been added to the software. Specific validation information is not included with this HotFix; however, the decision to validate this HotFix is subject to your internal change control policy and the specific requirements of your previous validation of the Analyst software. Validation services are available through Applied Biosystems Professional Services. For more information, contact [softwarevalidation@appliedbiosystems.com](mailto:softwarevalidation@appliedbiosystems.com).

### Technical Information Regarding the Area Discrepancy Issue

Integration data is displayed in Results Tables using stored results from the original integration. The peak review displays the results of a re-integration of the data using the same peak-finding parameters. In situations where the issue is manifest, the area on the Results Table and the area on the chromatogram will differ slightly.

When using the Analyst Classic integration algorithm, in cases where a “shoulder peak” occurs (i.e., a large peak with a second peak rising on the back shoulder of the first peak), the Analyst Classic integration algorithm uses an exponential approximation of the first peak to “skim” the second peak from the underlying shoulder. This method is called “exponential skimming”. Conversely, if the second peak is not a “shoulder peak”, the software performs an integration to the baseline.

A second peak is considered part of a shoulder peak if the ratio of the main peak height to the shoulder peak height is more than a user specified value (the default value is 5) and if certain other criteria are met (see the descriptions of the **Exponential Peak Ratio**, **Exponential Adjusted Ratio**, and **Exponential Valley Ratio** parameters in the Analyst software documentation for details).

If the experimental ratio is *exactly* equal to the specified value, previous versions of the Analyst software would occasionally round inconsistently during initial integration. This could result in the peak not being exponentially skimmed during the original integration but skimmed when displayed in the peak review, and hence in different peak areas. This issue has been corrected so that rounding is now consistently and correctly to the nearest value.

<p><b>Note:</b> In cases where the discrepancy occurs, the chromatogram reviewed at the time the Results Table was saved are correct. In the rare case where the new rounding results give a slightly different value for the peak area, do not save the results again unless the chromatogram is reviewed a second time.</p>
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