SOFTWARE
RELEASE NOTES
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HLA Fusion™Research Software, Version 3.3Service Pack
Catalog #FUSREPGRX
RUOFor ResearchUseOnly. Not for use in diagnostic procedures.
DESIGNATED USERS
This service packis for the users of HLA Fusion Research(FUSREPGRX)3.0, 3.2and 3.2Hot Fix 1
software. Please review the New Features, Enhancements, and Bug Fixes as outlined below to verify
the relevance of this softwarerelease to your environment.
RELEASE CONTENTS
1.The HLA Fusion Software release,Researchv3.3service pack is located on the One
Lambda Download
site:http://download.onelambda.com/pub/tray_info/Windows/HLA_Fusion_Catalogs/Docume
nt/
2.The service packexecutable for upgrading HLA Fusion Researchv3.0, v3.2,andv3.2Hot
Fix 1 toResearchv3.3is HLA Fusion Research 3.3.exe found in either of these files:
HLA FusionResearch3.3.zip
HLA FusionResearch3.3.rar
Download and save the appropriate file on your computer, depending on your system
requirements.
3.The installation instructions for the service packare found in the following document:
HLAFusion Researchv3.3Install Guide_EN.pdf
NEW FEATURES
C1qassay is now available inLABXpress Moduleby clicking on the Assay type
dropdown box(Sample > Create Plate Design).When you click on C1qassay type,
the Test namedropdown box displays the following tests:
oMixed Bead Mix
oClass I Bead Mix
oClass II Bead Mix
oClass I & Class II Bead Mix
oClass I Single Antigen Beads
oClass II Single Antigen Beads
oClass I Single Antigen Supplemental Beads
oClass II Single Antigen Supplemental Beads
oMulti Bead Mix
oMICA Single Antigen Beads
Note: C1qassay can berunonlyin the Plate driven –Custommode.
ACombinebuttonhas been added totheConsenSyssummary screen. This allows
youto perform combined analysis between ConsenSys samples and LABType or
SSPsamples. Note that the sample ID, loci, and nomenclature mustallmatch.

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• User Reports Export and Import Template options have been added to allow
exporting and importing of report templates. The following is an example of the necessary steps to export a user report template: (Reports > Specialty > User Reports > Setup > Pick field > Save as Template > Export). This new feature creates two files using the same name that is in the setup, which can then be imported using the Import button. You have the option of changing the name and
the location of the exported templates, but neither the content nor the format of the exported files can be edited or updated manually. The person receiving an e-mailed template clicks on Import and selects that template.

• An Export and Import Data Template option has been added to allow exporting
and importing of data templates. The following is an example of the necessary steps to export an export data template: (Reports > Specialty> Export Data > Pick field
> Save as Template > Export). This new feature creates a text file that can then be imported into the Export Data module. You have the option of changing the name
and the location of the exported template, but neither the content nor the format of
the exported files can be edited or updated manually. The person receiving the e-mailed template clicks on Import and selects that template.

• We have added a BML – ABCDR Allele Pair report that allows the following data to
be exported in .csv format:

1. Sample ID
2. For A, B, C, DRB1 locus: (1) Assigned Allele Pair and (2) Assigned Serology

o The format is:
tanaka0803,A*24:02,A24,A*33:01,A33,B*52:01,B*52,B*15:18,B*71,C*01:02, Cw1,C*03:03,Cw9,DRB1*09:01,DR9,DRB1*04:05,DR4

• Additional Export format options are now available for the following BmT reports:
LABType, MicroSSP, LABScreen, and ABDR; these reports all support the following format options: .txt, .csv, and .xml.

• You can generate a report that only includes the following fields: SampleID,
assigned KIR genotypes, and positive possible alleles associated with the assigned KIR genotypes.

o Anything labeled as a “final assignment” will be treated as a positive allele.

• Additional tests have been added to the Plate Designer (for LABScreen, and C1q),
which also can be exported directly to the Luminex software.

• You can apply the type of secondary Ab used per sample in the Plate Designer
when using the sample work list (Utilities > General Settings > Secondary Antibodies). The secondary Ab will be identified by a color indicator in the center of the well. The assigned secondary Ab will also be reflected in Plate Design and Plate Detail screens as an additional tab labeled Secondary Ab (Sample > Create Plate Design) once it has been setup. By default, the secondary antibody assigned is IgG. You can click on the well to change that default assignment.

• The Legend icons and the Xs on the Line Graph (time scale) are now squares
(Patient Info > Ab Tracking).

• A template name can now be assigned to multiple catalogs. During session import
you can select a catalog from a list of active catalogs that are associated with the template name. If the template is associated with more than one catalog a dialog box appears and prompts you to select a specific catalog.

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• A Cancel Import button has been added to the Catalog Template Association pop-
up. If you do not want to continue with the import, you can cancel it and return to the
previous screen

ENHANCEMENTS

• The system now issues an alert when you attempt to generate a Custom SSP
Report, SSP Report, Molecular Custom, or a Custom Typing Result by Sample report if there are more than 10,000 allele pairs in the selected samples. This
number is an internal benchmark to keep the report time under 60 seconds. A
warning message appears advising you it may take a significant amount of time to
generate the report. You have the option to not include the allele pairs, which will
then speed up the time to generate the report. Note that time may vary based on
your computer configuration.

o When the message appears, click Cancel, go to the Custom Report Setup Screen,
and deselect the “Possible Allele Pairs” field, which allows the system to generate
the report in a shorter amount of time.

• The following enhancements have been made to the ConsenSys SBT Module:

o ConsenSys Engine:
• Updated the engine to avoid EPG intensity adjustment to the first
several bases in EPG.
o Sequence Alignment:
• Updated primer orientation and coverage parameters to correctly
align class I exon 4 and 5. For example, seq close to primer will be aligned (5R won’t get aligned to 4).
o A02/2402 Mistyping:
• Updated the capacity of the SBT module to hold allele pairs.
o SBT/SSO Toggle Function:
• Updated functionality to switch between SBT, SSO, and combined
typing result in the Allele Pairs window without retaining unwanted results. Also, incorporated a screen color change to clearly distinguish between SBT, SSO and combined results.
o Allele Sequence Comparison Feature:
• Updated this feature to visualize the differences between the called
allele sequence and the sequence of choice.
o Ab1 File Change:
• Updated this feature to allow addition of Ab1 file during analysis
session.
o Allele Pair Window Display:
• Updated the display engine to highlight alleles containing unreported
sequence in the covered exon(s).
BUG FIXES

• Corrected a problem with exporting a batch or a multi-batch directly onto the
Luminex xPONENT 3.1 software. Customers were receiving an error message from xPONENT 3.1 stating the XY heater was out of range even if the XY heater was disabled. Note that the XY heater turns itself off when running the analysis.

• Corrected a problem in the ConsenSys Session Summary. After using the RA
function to “Add Selected Kits to Comment,” when user attempted to reanalyze the data again and clicked on Analysis button the following error message displayed:
"The index file could not be opened. Please check the xml doc by opening it in Internet Explorer."

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NOTES

• The software supports all sizes of gel images provided the image can be resized to
fit on the screen, and sized so that the report can print it out. The software will generate an error message if it cannot resize the gel image, and if necessary will temporarily resize the gel image for preview and reporting. The software may
generate an exception if the user does not have the appropriate level of software
rights or enough disk space for temporary storage.

• Microsoft SQL Server client driver is required to use the ConsenSys module. If it is
not installed the driver can be downloaded from the Microsoft website.

• The NMDP Rpt + Export report includes the locus value for SBT samples.

• Users are suggested to export or print a report to mitigate the truncation issues that may
appear in the report viewer

• The plate designer layout view report generates first blank page. This will be addressed in
the future release.

SYSTEM REQUIREMENTS

• One of the following operating systems:
 Microsoft Windows 7
 Microsoft Windows XP
• For Windows XP systems, Microsoft Windows Installer 3.1
• Microsoft SQL Server 2005 or SQL Server 2005 Express
• Microsoft .NET Framework Version 3.5
• Visual JSharp (version must match the .NET Framework version you are using)
• Pentium 3, Pentium 4, or Pentium 5 Processor
• 4 GB hard disk space
• 512 MB RAM (minimum)
• 8-bit graphics adapter and display (for 256 simultaneous colors)
• VGA display with 1280 x 960 resolution (minimum)
• Mouse, or another Windows compatible pointing device; mouse with wheel required for
certain products

Note: Regardless of where you install HLA Fusion, as much as 400MB of space on your local hard drive may be required for temporary installation files as well as any other programs you may be using.

OTHER COMPONENTS (RECOMMENDED)
• Microsoft Windows supported graphics accelerator card
• Microsoft Windows supported printer
• Microsoft Excel 2000 or 2003
• Microsoft Word 2000, 2003, or other text editing or word processing program
• WinZip

®

Software 9.0 or higher
• Adobe

®

Reader

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REVISION HISTORY
Date Revision Revision Description
0 03/27/2014 Original release