

Automated Axiom™ Analysis (AutoAx)

New features in v3.0

- AutoAx now supports *https*.
- Configurations have been updated to enable:
 - Library packages to be installed and/or deleted from the server.
 - The modification of disc usage thresholds.
- Current disc usage can be revealed by hovering the mouse cursor over the AutoAx Taskbar icon.

Companion tool issues resolved in v3.0

- The **Automated Axiom Sample File Uploader** is now *https* compatible.
- The **GCC File Uploader** can now upload to *https* servers.

Resolved issue in v2.0.3

- BloodGenomiX Reporter has been updated to improve the calling of the INFI antigen. NEG is now reported if a marker reports a GG genotype.

New features in v2.0.2

- The **Configurations** window in all AutoAx installations now include a BloodGenomiX Reporter **Licensing** tab/button. For more information about a BloodGenomiX Reporter license, contact your Thermo Fisher Sales Representative.
- BloodGenomiX Reporter includes sample sex to accurately type antigens on chromosome X.

New features in v2.0

- Automated Axiom v2.0 has a brand-new user interface that features three easy-to-use window tabs: Batches, Workflow Setup and Multiplate.
 - **Batches** is the primary window tab and dashboard. It is divided into three separate panes (left, middle, and right):
 - The left pane displays the batches as individual information cards. This pane can be viewed in full screen mode by clicking its expand arrow button.
 - The middle pane displays the details of the selected batch. It includes a pop-up Marker Metrics Summary, expanded Plate Plots, and configurable Sample Metrics and Probeset Summary tables.
 - The right pane displays batch parameters and input values of a highlighted/selected card.

- **Workflow Setup** window tab features Analysis and Extension panes.
 - Exports are now labeled as *Extensions* and are included for arrays that support them (Allele Translation, and HLA).
 - **Reset to Defaults** enables users to reset to factory or previous custom settings.
 - **Multiplate** batches can be setup in the Multiplate window tab.
 - If the plate is already located on the Server, Automated Axiom automatically starts the analysis after the multiplate batch is created. **Note:** A manual start option is available.
 - Multiplate batches can be created prior to scanning.
 - Multiplate Normalization is now enabled.
- Parallelization of analyses is now enabled. Queued analyses are no longer performed one at a time. For details on batches performed at the same time, see the *Automated Axiom Performance Testing* metrics table below.

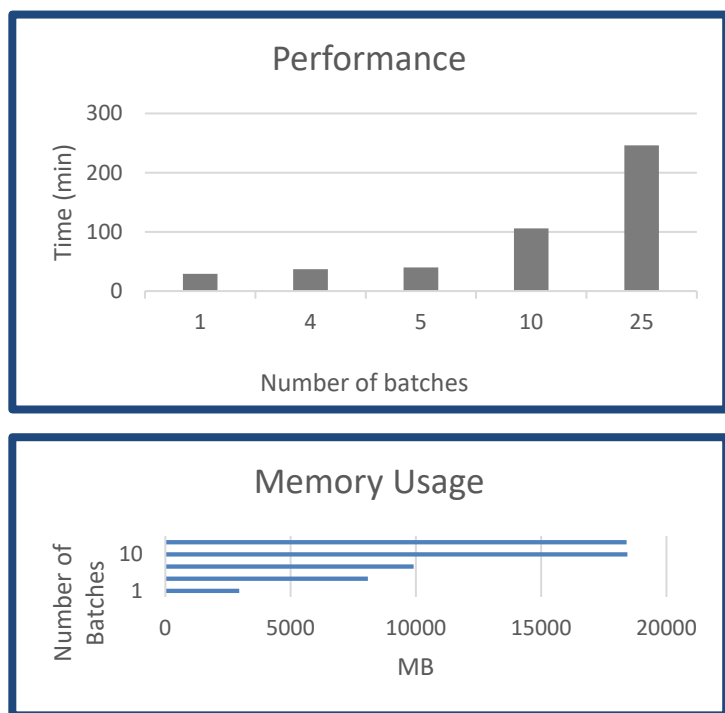
Automated Axiom Performance Testing

Number of analyses started at same time	Array type	Workflow	Number of Plates per Batch	Time	CPU (%) up to...	Memory (MB) up to...
1 batch	PMRA	Best Practices	1	44m	5.7	2275
1 batch	PMRA	Best Practices with HLA and AxLE Extensions	1	1h 8m	20.6	6638
1 batch	PMRA	Best Practices with AxLE Extension	50	20h 41m	5.5	5151
2 batches	Transfusion-focused research 384 array	BloodGenomiX Reporter	4	1h 53m	20.7	4014
	BovMD	Best Practices	10			
4 batches	Transfusion-focused research 384 array	BloodGenomiX Reporter	4	5h 58m	30.6	4799
	PMRA	Best Practices with AxLE Extension	20			
	BovMD	Best Practices	10			
	Transfusion-focused research 384 array	BloodGenomiX Reporter	1			
10 batches	PMRA	Best Practices with AxLE Extension	50	48h 5m	43.3	40466

Note: Automated Axiom Performance Testing was performed on a system with 2 cores: 20 threads (2 per 64GB RAM and 2GB Swap).

- BloodGenomiX Reporter is a new research-orientated workflow enabled for blood transfusion arrays. Its analysis includes Best Practices, Contamination QC, HLA, and Extended Blood Typing. The final output file is configured for easy integration.

Note: The following graphs illustrate performance testing results of a Blood GenomiX Reporter workflow run that utilized a *Transfusion-focused research 384* array.



Note: Memory Usage: *Number of Batches* = Number of single plate analyses running in parallel.

- AutoAx v2.0 directory structure now includes a Transfers folder. Mapping a drive to this folder enables direct copying rather than requiring a download from the Batches window tab.
- Downloaded data can now be configured.

Known issues and limitations in v3.0

- When two users are editing a template in the analysis or extension pane at the same time, edits made by one of the two users may not be saved.
- Running Automated Axiom on a virtual machine has been validated, however, it is critical the Checklist is properly followed and AutoAx is the only application currently running.
- Archive scheduling for the GeneTitan™ is highly recommended. Archiving batches and rootdata should be an on-going scheduled routine. See **Archiving** in the *Automated Axiom User Guide* (P/N MAN0030173) for details.
- When batches are run using the ContaminationQC Extension, **ContaminationQC** will not be displayed in the Sample Metrics Table.
- A value entered in the Analysis pane's Inbred File Value field does not reset after clicking on the **Reset to Defaults** button. To reset, click on the **Use value for all samples** check box, change the value to 0, then click outside the value field to save.
- When exporting single sample VCF formats, the VCF Extension card may display an error message even though the export was successful.