Method Biography



2023-GBL-EN-100951-v1

Disclaimer

Biomek Automated Workstations are not intended or validated for use in the diagnosis of disease or other conditions.

The Cytiva[™] Sera-Xtracta HMW kit is intended for research use only. It is not intended for use in any clinical or *in vitro* procedures for diagnostic purposes.

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Cytiva[™] Sera-Xtracta High Molecular Weight Kit

Kit Highlights:

- The Cytiva[™] Sera-Xtracta ٠ HMW kit is designed to rapidly extract and purify genomic DNA from whole blood and minimize shearing.
- The kit is optimized for ٠ processing 50-200µL of whole blood.
- The resulting genomic DNA ٠ extracted from the blood samples is of a purity and quality compatible with most molecular biology techniques.

Illustrated procedure INPUT Blood Proteinase K Lysis buffer Blood Cell Lvsis INCUBATE 30 min Silica beads Genomic Binding buffer DNA Binding MAGNET Wash 1 buffer RESUSPEND Bead Washes Wash 1 (x2)



Fig 1, Workflow diagram of the Cytiva™ Sera-Xtract gDNA process.

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ASPIRATE

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DNA

Automated Method Description:

The Cytiva[™] Sera-Xtracta HMW Kit on Biomek i7 Dual-Hybrid automated workstation method allows the user to extract genomic DNA from up to 96 blood samples at a time. The method requires only one user interaction (two if the user chooses to incubate their plate off-deck), and it uses multichannel plate stamping to avoid potential column effects.



Fig 2. A. Biomek i7 Dual-Hybrid workstation. B. Diagram of the deck layout employed in this method.







Fig 3. Overview of the Cytiva™ Sera-Xtracta HMW Kit workflow.





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Major	24	48	96	
Process	Samples	Samples	Samples	
Instrument Setup	30 Min	30 Min	30 Min	
Reagent	14 Min 55	26 min 11	48 min 56	
Aliquoting	sec	sec	sec	
Blood Cell	35 Min 30	35 Min 30	35 min 30	
Lysis	sec	sec	sec	
gDNA	14 Min 28	14 Min 28	14 min 28	
Binding	sec	sec	sec	
First Wash	19 Min 29	19 Min 29	19 min 29	
	sec	sec	sec	
Second	23 Min 49	23 Min 49	23 min 49	
Wash	sec	sec	sec	
Elution	18 min 36	18 Min 36	18 min 36	
	sec	sec	sec	
Total time	2 hr, 36	2 hr, 48	3 hr 10 min	
	min, 47 sec	min 3 sec	48 sec	

Table 1. Estimated duration of each step of the automated protocol.

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Demonstrated Method Interface Makes it Easy to Run

Biomek Method Launcher

- 1. Makes method available outside of the editor
- 2. Protects against accidental changes from multiple users



Fig 4. Biomek Method Launcher Interface.





Demonstrated Method Interface Makes it Easy to Run

Method Option Selector (MOS) Dynamic, HTMLdriven interface allows the user to select a number of options to configure the workflow as desired.

Beckman Coulter [®] Cytiva [™] Sera-Xtracta HMW Kit							
Optimized for Biomek i-Series	Automated by Beckman Coulter, Inc						
Method Options							
Enter Number of Samples: 96 8-96 samples							
Enter the Sample Volume in Microliters: 200 50-200 microliters							
Incubation Method Incubate on-deck with Inheco Incubator •							
Start run							

Fig 5. Cytiva™ Sera-Xtracta HMW Kit method option selector.





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Demonstrated Method Interface Makes it Easy to Run

MOS options that enable flexibility, reduce errors and provide greater walk-away time

- 1. Enter Number of Samples: Input the number of samples to run. The Cytiva[™] Sera-Xtracta gDNA automated method accepts 8-96 samples in multiples of 8 (one column of the plate).
- **2.** Specify the sample input volume: Set sample volume from 50µL to 200µL. The sample volume in each well must be uniform.
- **3. Select the desired process for incubating the sample plate during lysis:** Choose from three different incubation options:
 - 1. Incubate on-deck: Incubate via an integrated Inheco Deep Well Single Plate Incubator©
 - 2. Incubate on-deck: Incubate via an on-deck Inheco Thermoshake AC Peltier
 - 3. Incubate off-deck: System is paused at the incubation step by Biomek software to allow the user to remove the plate from the deck and manually incubate. The user replaces the plate to the deck after incubation is complete.



Demonstrated Method Interface Makes it Easy to Run

Guided Labware Setup and Reagent Calculation

- Provides clear instructions for setup
- Reduces setup errors
- GLS diagrams may be printed or saved as a PDF for future reference



Fig 6. Guided Labware Setup interface with reagent calculations.





Experimental Details:

Two vials of human de-identified blood were collected a day prior to the experiment; one tube preserved with EDTA and the other with sodium-citrate. Blood samples were kept at 4°C and then were brought to room temperature approximately 30 minutes prior to the run.

8 samples of blood preserved in EDTA and 8 samples of blood preserved in sodium-citrate were simultaneously processed in an automated run, for a total of 16 samples. Each well contained 200µL of blood. Samples were alternated by row according to their preservative to control for potential column effects that would affect blood samples of one preservative differently than those of the samples with the other preservative.

Cell lysis was performed on-deck with the Inheco Single Plate Incubator[®]. 100µL of end product per sample was eluted into elution buffer. Yields were measured with a ThermoFisher Qubit Broad Range Assay[®], and 260/280 and 260/230 ratios were measured via a ThermoFisher NanoDrop[®] system.





Average yields, A260/A280, and A260/A230 products derived from EDTA- and sodium citrate-derived samples are listed below along with their respective standard deviations. While EDTA-preserved blood produced a higher variation in yields, sodium citrate-preserved blood had a lower average yield overall. The protocol notes sample yield may vary depending on the agent used to preserve the blood samples, which may explain this deviation between resultant yields. One sample from blood preserved with sodium citrate was discarded as its gDNA yield was calculated to be an outlier.

Preservative	Average Yield (ng/µL)	Yield St. Dev (ng/μL)	Average A260/A280	A260/A280 St. Dev	Average A260/A230	A260/A230 St. Dev
EDTA	91.74167	30.87936	1.925	0.030956959	2.15	0.165931713
Sodium Citrate	54.77143	12.09351	1.92	0.029277002	2.001428571	0.341401673

Table 2. Averages and standard deviations of yield, A260/280, and A260/230 ratios by blood preservative of initial samples.

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Demonstrated Data

Α

Yields (ng/µL) Average concentration $(ng/\mu L)$ 140 120 100 100 80 ng/µL 80 60 60 ng/µL 40 40 20 20 0 0 **FDTA** Sodium 📕 EDTA 📃 Sodium AVG conc (ng/µL) 91.74166667 54.77142857 Fig 7. Yields from automated runs of the method. A. Average yield of blood

Fig 7. Yields from automated runs of the method. A. Average yield of blood samples preserved in EDTA (n=8) and sodium citrate (n=7). B. Distribution of yields of the aforementioned samples.

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B

Demonstrated Data



Fig 8. A. Average 260/280 ratios of samples derived from blood preserved in EDTA (n=8) and sodium citrate (n=7). B. 260/280 ratios from the EDTA and sodium citrate samples.





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Demonstrated Data



Fig 9. A. The average 260/230 ratios of samples derived from blood preserved in EDTA (n=8) and sodium citrate (n=7). B. Distribution of the 260/230 ratios of the samples.



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