QIAGEN workflows for any sample type and application

Keith Elliott
QIAGEN has hundreds of years of experience in HID

- Research and product development
- Validation
- High throughput DNA workflows
- Specialist casework processing
- Auditing
- Process improvement
- Private and public labs, academia
- All corners of the world
Workflows in human ID and forensics

Traditional workflow for casework and reference sample on CE

Sample to Insight

QIAGEN's automated workflows for forensic applications
QIAGEN’s Automated Workflows for Database Samples
Reference samples: Buccal swabs

Up to 196 samples per day, 2 operators

- Up to 91 samples may be processed in a single run
- Automatic distribution of PCR Mastermix
- Automatic addition of PCR positive control
- Up to 4 ladder positions automatically reserved in the plate for optimal positioning at CE Set-up
- Ladder positions can be defined by custom plate layouts (QIAGEN Apps lab, or QIAgility Data Handling tool)

Investigator STR GO!
Lysis Buffer

Investigator GO! PCR Kits
- 24plex GO!
- IDplex GO!
- ESSplex SE GO!

QIAgility for PCR setup

QIAgility for CE setup
Reference samples: Buccal swabs

Up to 384 samples per day, 1 operators

Investigator GO! PCR Kits
- 24plex GO!
- IDplex GO!
- ESSplex SE GO!

STAR Q Swab AS
for swab lysis and PCR setup

QI Agility for CE setup

• Integrating swab lysis and liquid handling in one workflow
• Full traceability of samples including export to and import from LIMS systems
Buccal cells on Puritan swab

Profile example Investigator 24plex GO! Kit

1 swab lysed in 500 µl Investigator GO! Lysis buffer, 2 µl as template
Validation with Investigator 24plex GO! Kit

**Study setup and results**

- Swabs from 20 different donors in 4 replicates each
- Checkerboards with alternating water samples
  - Total of 80 buccal samples and x-contamination controls
- 100% full profiles at 200 RFU threshold
- No sample carry over observed
Find out more…

Read the application note on the STAR Q Swab AS
Reference samples: FTA

Up to 384 samples per day, 2 operators (automated/semi-automated punch)

- Up to 91 samples may be processed in a single run
- Automatic distribution of PCR Mastermix
- Automatic addition of PCR positive control
- Up to 4 ladder positions automatically reserved in the plate for optimal positioning at CE set-up
Reference samples: FTA

Up to 384 samples per day, 1 operator

Investigator GO! PCR Kits
- 24plex GO!
- IDplex GO!
- ESSplex SE GO!

STAR Q Punch AS
for punching and PCR setup

QIAgility for CE setup

- Integrating card handling, punching and liquid handling into one workflow
- Identification of samples and calculation of optimal punch position
- Full traceability of samples including export to and import from LIMS systems
Buccal cells on GE Healthcare EasiCollect card

Profile example Investigator 24plex GO! Kit

1.2 mm punch amplified using 27 cycle protocol
Validation with Investigator 24plex GO! Kit

Study setup and results

• 44 cards from 22 different donors, 3 cleaning punches
• 3 independent runs using checkerboards with alternating water samples
• 98.5 % full profiles at 200 RFU threshold (2 partial, total of 6 alleles missed)
• No peaks above 200 RFU in negative samples
Application Note

Highthroughput Investigator® 24plex GOI PCR setup from EasCollect®+ FTA cards using the STAR Q Punch AS

Kath Heintz, Bernd Huber, Stefan Schiewer, Katha Lauerfuss and Richard Bühl

Introduction
The increasing utilization of DNA databases as an investigative tool in criminal investigations has resulted in a need for sensitive and selective sample extraction for DNA profiling. However, the use of these databases is limited by the number of samples available for processing. Moreover, the analysis of large numbers of samples in laboratories requires significant resources allocation. The availability of automated processes allows for the efficient extraction of DNA from multiple samples. The STAR Q Punch AS kit from Hamilton Robotics is a versatile, high-throughput instrument that enables the efficient processing of large numbers of samples.

Methods

Highthroughput assay setup for the Investigator® 24plex GOI Kit from Bode Buccal 2 Assambed Cassette samples using the STAR Q Punch AS

Kristin H. Wiegandt, Lidiya S. Kuznetsova, Daniel S. Whistle, Robert A. Burns, Lone Andersen, Kevin Miller, Kath Heintz

1 Bode Caliper-Fomacard, 10430 Commerce Road, Suite 107, Boston, MA 02199, USA
2 Hamilton Robotics, 6070 Energy Way, Sunnyvale, CA 94089, USA
3 QIAGEN GmbH, 41476 Hilden, Germany

Introduction
Since its first applications in forensic science in the 1980s, the impact of DNA testing on criminal justice has been profound. As of June 2016, there were over 100 million DNA databases in use worldwide, with over 100 million profiles stored. A comprehensive database of DNA samples is critical for the effective and efficient use of DNA profiling in criminal investigations. The Investigator® 24plex GOI Kit from Bode Buccal 2 Assambed Cassette samples enables the simultaneous extraction of DNA from large numbers of samples. The STAR Q Punch AS kit from Hamilton Robotics is a versatile, high-throughput instrument that enables the efficient processing of large numbers of samples.

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Methods

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3 QIAGEN GmbH, 41476 Hilden, Germany
QIAGEN’s Automated Workflows for Casework Samples
Workflows in human ID and forensics

Traditional workflow for casework and reference sample on CE

- **Sample**
- **Pretreatment**
  - Instruments: Tissue Lyser II
  - Kits: Investigator ® Lyse&Spin Basket Kit
- **Sample preparation**
  - Instruments: QIAcube ®, EZ1 ® Adv XL Instrument, QIAsymphony ® SP, STAR Q SP/AS
  - Kits: QIAamp ® DNA Investigator Kit, EZ1 DNA Investigator Kit, QIAsymphony DNA Investigator Kit, STAR Lyse&Prep Kit
- **Assay setup**
  - Instruments: QIAsymphony AS, QIAgility ®, STAR Q SP/AS
- **Quantification**
  - Instruments: RotorGene ® Q
- **STR analysis**
  - Autosomal STR kits:
    - Investigator 24plex QS
    - Investigator ESSplex SE QS
    - Investigator IDplex Plus
    - Investigator ESSplex Plus
  - Supplementary autosomal STR kits:
    - Investigator HDplex
    - Investigator Triplex DSF
    - Investigator Triplex ASF QS
  - Human gonosomal STR kits:
    - Investigator Argus Y-12 QS
    - Investigator Argus X-12 QS
  - Human bi-allelic Marker Kits:
    - Investigator DIPplex
Casework samples: low- to medium-throughput

Up to 56 samples per day, 2 operators

- EZ1 Adv XL: most successful sample prep automation on the market
- QIAgility: protocols for quantification setup on the Rotor-Gene Q and AB7500 incl.
- Data exported directly from QIAgility to downstream quant and CE instruments

Speed and workflow flexibility with high yields and high-quality DNA
EZ1: Fast processing with high sensitivity

Different dilutions of blood extracted on the EZ1 Advanced, Investigator trace protocol

Full profiles obtained for all dilutions
High-performance DNA from forensic samples using the EZ1 DNA Tissue Kit together with the EZ1 DNA Forensic Card protocols

Moritz Hagg, Silvie Falkier*, Ingo Evers*, and Finn Hohbergman*
Institut für Rechtsmedizin der Charité Berlin, DNA Labor, Berlin, Germany
* QIAGEN AS, Oslo, Norway

Introduction
Forensic science demands the efficient preparation of small amounts of DNA from a wide range of low-volume and high samples. Repeatability isolation of pure DNA is critical for successful downstream analysis. Sample throughput demands for forensic science continue to increase because of the introduction of DNA standards and the expanding volume of casework samples. Automating time-consuming and labor-intensive sample prep can increase both repeatability and throughput.

Materials and methods
Samples were mixed with 190 µl Buffer O2 and 10 µl Proteinase K. For absorbent sample, distilled water was added to a final sample volume of 300 µl. The samples were incubated at 56°C for 15 minutes with mixing. After incubation, any solid material was removed from the tubes using sterile forceps. Samples were processed using the LabRobot EZ1 workstation, the EZ1 DNA Tissue Kit, and the time Sample Protocol encoded in the EZ1 DNA Forensic Card. Purified DNA was eluted in 100 µl water and quantified by absorbance (A260) corrected for background (A230).

Dried blood samples (10 µl paper drops, each of 3.75 mm diameter) were processed using the Dried Blood Protocol.

Results
The quantitative amplification and detection of small amounts of DNA is invaluable for casework analyses, especially in mixed samples. DNA purified from dried blood samples performed well in sensitive real-time PCR (Figure 1).

Multiple PCR of STR loci allows high-definition typing of specimens and has become an indispensable tool in forensic analysis. STR results (Figure 2) show clean and easily interpretable quantitative STR profiles obtained using DNA from hair demonstrating the high quality of DNA obtained using the LabRobot EZ1 system.

Table 1: Yield of DNA from a Range of Samples

<table>
<thead>
<tr>
<th>Sample type</th>
<th>DNA yield (µg)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Blood sample</td>
<td>0.7 ± 0.2</td>
</tr>
<tr>
<td>Blood sample</td>
<td>0.1 ± 0.2</td>
</tr>
<tr>
<td>Hair</td>
<td>0.1 ± 0.2</td>
</tr>
</tbody>
</table>

Figure 1: Real-time quantitative PCR using DNA from dried blood. Purified DNA (10 µl) was used in each of 30 replicate 25-µl real-time PCR reactions. The DNA obtained from the dried blood sample was spiked into a reference sample, and the DNA yield was normalized using the LabRobot EZ1 system.

Customer Application Notes: LMI Berlin
A scalable solution that grows with your lab

Up to x-fold 56 samples per day, 2 operators

- Multiple EZ1 Adv XL
- QIAgility for quant setup, normalization and PCR setup
- QIAgility for CE setup

- If space is limited
- Four EZ1 Instruments can be combined via 1 PC to collect data files
- If individual analysts require dedicated workflows
Premium sample workflow

Up to 56 specialist samples per day, 2 operators

- EZ1 Adv XL
- QIAgility for quant setup, normalization and PCR setup
- QIAgility for CE setup

- Combined with higher throughput automation for a dedicated specialist sample workflow
  - Bones, telogen hair, urgent cases, ‘major crime’
Automated purification of DNA from bones of a Bronze Age family using the BioRobot® EZ1 workstation

Sebastian Schmidt, and Serina Hamel
Department of Human Biology and Human Ecology, Institute of Zoology and Anthropology, University of Göttingen, Germany.

This BioRobot EZ1 workstation was used with the EZ1 DNA Tissue Kit and the EZ1 DNA Forensic Card to successfully purify DNA from 350-year-old bones. STR analysis and sequencing of mitochondrial DNA established genetic relationships within a Bronze Age family.

DNA from 350-year-old bones is a rare and valuable tool for anthropologists investigating recent samples. Since DNA is a relatively stable molecule it can survive for thousands of years, with varying degrees of degradation, depending on the storage conditions.

An archaeological site of 40 people from the Bronze Age, the bones had been relatively well preserved for approximately 3000 years due to the constant cool temperature and isotopic conditions of the cave, which is very similar with a cave dwelling. Many of the bones were covered with greyer matter, a type of calcium phosphate from skeletal muscle that didn't affect the bone. The greyer matter layer was undamaged, indicating that nobody had come across the area for approximately 300 years.

Bronze Age human remains are seldom found in central Europe as they are commonly preserved. When the site was first excavated in the 1990s, it was thought to represent a site of human sacrifice. However, lack of signs of violence on the bones plus the mixture of different genera and a wide range of ages and deaths suggest a different explanation. DNA analysis indicates that the remains from a deceased family clan, consisting of at least 5 generations. This suggests that the site is actually a family burial chamber. Analysis of tooth discs of the site may provide a better understanding of the frequency of human sacrifices in Bronze Age Europe and alternative burial practices.

We have established the first genetic family tree based on DNA analysis of 2 generations in the Bronze Age bone. In this report, we present genotyping data for 3 individuals comprising one family from the Bronze Age bone. Automated purification of DNA from Bronze Age bones using the BioRobot EZ1 workstation.
A comparison of three automated DNA extraction methods for forensic casework

Christina Valgren, Sara Wester, Odd Zahrtland National Laboratory of Forensic Science, 35-3390
Received 20 August 2000; accepted 15 August

Abstract

Manual QIAamp® DNA blood kits and automated QIAamp® DNA blood kits are used as routine methods of the Swedish National Laboratory of Forensic Science, RRL. The routine method is time consuming and involves hazardous chemicals. The aim of this study was to find an automated DNA purification system to replace the manual method. 

1. Introduction

Manual QIAamp® DNA blood kits [1] and automated QIAamp® DNA blood kits (QIAamp® DNA blood kit and QIAamp® DNA blood kit) are used as routine methods of the Swedish National Laboratory of Forensic Science, RRL. The aim of this study was to find an automated DNA purification system to replace the manual method.

2. Materials and methods

The following methods were examined and compared to each other and to the manual method used routinely: QIAamp® DNA Blood Kit, QIAamp® DNA Blood Kit and QIAamp® DNA Blood Kit.

3. Results and discussion

Four DNA extraction methods were used: QIAamp® DNA Blood Kit, QIAamp® DNA Blood Kit, QIAamp® DNA Blood Kit, and QIAamp® DNA Blood Kit. The results were compared to each other and to the manual method used routinely.

4. Conclusions

Three DNA extraction methods were used: QIAamp® DNA Blood Kit, QIAamp® DNA Blood Kit, and QIAamp® DNA Blood Kit. The results were compared to each other and to the manual method used routinely.
Casework samples: medium- to high-throughput

Up to 120 samples per day, 2 operators

- Fully automated workflow from sample purification to PCR setup (integrated operation)
- SP and AS module also can be used separately (independent operation)
- Continuous loading of new samples during run
- Run consists of 4 batches of 1–24 samples
Casework samples: medium- to high-throughput

Up to 120 samples per day with reduced PCR volume, 2 operators

Workflow approach
- For laboratories requiring high throughput AND reduced volume (10 µl) PCR
- QIAgility offers flexibility in pipetting small sample volumes
QIAsymphony: throughput and sensitivity

Saliva purification

<table>
<thead>
<tr>
<th>Sample volume</th>
<th>Elution Vol</th>
<th>Yield</th>
<th>PCR input</th>
<th>PCR cycles</th>
</tr>
</thead>
<tbody>
<tr>
<td>10 µl</td>
<td>50 µl</td>
<td>145 ng</td>
<td>0.5 ng</td>
<td>30</td>
</tr>
<tr>
<td>1.0 µl</td>
<td>50 µl</td>
<td>12 ng</td>
<td>0.5 ng</td>
<td>30</td>
</tr>
<tr>
<td>0.1 µl</td>
<td>50 µl</td>
<td>1.3 ng</td>
<td>390 pg</td>
<td>30</td>
</tr>
</tbody>
</table>

Full profiles obtained for all starting volumes
Customer application note: Bode Cellmark Forensics

ApplicationNote

High-throughput DNA sample prep using the QIAsymphony® SP instrument: An overview of workflow optimization at Bode Cellmark Forensics™

Amy Jeangros, Jonathan Donovan, Anke Poohrow, Lesley Eithinger, Mario Scheer and Keith Elliott
1 Bode Cellmark Forensics, Lorton, VA USA 2 QIAGEN GmbH, Hilden, Germany

We describe Bode Cellmark Forensics (Bode Cellmark) workflow optimization, an established best practice, in achieving the highest possible throughput, with the QIAsymphony SP platform. The most optimized workflow ensures over 500 cases can be processed with only 2 operators using QIAsymphony SP instruments. This is achieved while maintaining the high success rate demanded of crucial casework samples.

Introduction

Bode Cellmark has grown to become one of the leading US DNA testing laboratories in the US, with an international reputation for high-throughput, high-quality analysis of casework samples. Bode Cellmark handles an average annual volume of around 10,000 casework samples from a wide range of challenging samples, including trace DNA and various tissue types. An overview of the types of samples collected each year to Bode Cellmark can be seen in Figure 1.

High-throughput DNA processing workflows for casework samples, such as those collected from shooters, are now widespread. However, implementation of such high-throughput processing for casework samples entails a number of specific challenges which must be overcome. These include achieving yields of high-quality, nicked-free DNA, comparable with manual extraction methods. In addition, a rigorous, robust protocol, and a workflow with a minimal number of manual handling steps, must be identified for all sample types.

Sample to Insight
Casework samples: Medium- to high-throughput

Up to 192 samples per day, 2–3 operators

- Optimized for use with the new QIAGEN Investigator STAR Lyse&Prep Kit
- Highest throughput QIAGEN workflow
- Optional QIAgility for PCR setup to maximize capacity of STAR Q SP/AS for sample prep
Extraction of inhibitory matrices

- Cuttings from fabric with old engine oil
- Swabs soaked in soil or sand slurry
- 1 µl blood from two donors applied
- Investigator Quantiplex HYres Kit quantification – no inhibition observed as indicated by IC

---

**Yield**

<table>
<thead>
<tr>
<th></th>
<th>STAR Q SP/AS</th>
<th>QIAsymphony</th>
</tr>
</thead>
<tbody>
<tr>
<td>fabric donor1</td>
<td>50 ± 5</td>
<td>50 ± 5</td>
</tr>
<tr>
<td>fabric donor2</td>
<td>60 ± 5</td>
<td>60 ± 5</td>
</tr>
<tr>
<td>sand</td>
<td>40 ± 5</td>
<td>40 ± 5</td>
</tr>
<tr>
<td>soil</td>
<td>30 ± 5</td>
<td>30 ± 5</td>
</tr>
</tbody>
</table>

**Quantiplex IC**

<table>
<thead>
<tr>
<th></th>
<th>STAR Q SP/AS</th>
<th>QIAsymphony</th>
</tr>
</thead>
<tbody>
<tr>
<td>fabric donor1</td>
<td>25 ± 2</td>
<td>25 ± 2</td>
</tr>
<tr>
<td>fabric donor2</td>
<td>26 ± 2</td>
<td>26 ± 2</td>
</tr>
<tr>
<td>sand</td>
<td>27 ± 2</td>
<td>27 ± 2</td>
</tr>
<tr>
<td>soil</td>
<td>28 ± 2</td>
<td>28 ± 2</td>
</tr>
<tr>
<td>standards</td>
<td>29 ± 2</td>
<td>29 ± 2</td>
</tr>
</tbody>
</table>
Customer application notes from Dublin and Netherlands Forensic Institute

Application Note

QIAGEN’s DNA Investigator® chemistry on the Hamilton® Microlab® STAR™ Liquid Handling Workstation

Brian O’Brien, Denis Koppert, Chris Elliott, and Anda Ploem
Netherlands Forensic Institute, The Hague, The Netherlands

QIAGEN’s automated workflows for forensic applications

Introduction
QIAGEN’s DNA Investigator® chemistry has been optimized for high-throughput sample preparation. The QIAGEN DNA Investigator® chemistry features the reagent for automated sample preparation, which is designed to provide optimal performance at each step of the workflow. The reagent is designed to work with a variety of sample types, including forensic, forensic, and other sample types.

The QIAGEN DNA Investigator® chemistry is based on a modular design approach, which allows for easy customization and scalability. The chemistry is designed to be used with a variety of robotic systems, which can be integrated with the QIAGEN DNA Investigator® chemistry to provide a high-throughput solution.

High-Throughput DNA Extraction from Forensic Trace Samples Using QIAGEN Investigator® Chemistry and the Hamilton® Autosampler

Brian O’Brien, Denis Koppert, Chris Elliott, and Anda Ploem
Netherlands Forensic Institute, The Hague, The Netherlands

Application Note

QIAGEN’s automated workflows for forensic applications
Casework: sexual assault samples

Up to 48 differential wash samples per day, 2 operators

- Fully automated differential fraction separation and sperm pellet lysis
- Up to 12 samples/run
- The QIAcube can be used up front of other automation workflows
Automated “manual” processing: the QIAcube diff. wash workflow

- 6 samples
- 12 samples
- 24 samples

24 samples in one day
QIAcube for automated differential wash

Yield and RFU

- **Linearity Diff Wash: Epithelial Fraction**
  - Data points for different dilutions showing yield in ng.

- **Linearity Diff Wash: Sperm Fraction**
  - Similar data points as above, showing yield in ng.

- **Total RFU QIAcube vs Manual**
  - Comparison of RFU for different fractions, showing female and male alleles.

- **Total RFU QIAcube vs Manual Differentials**
  - Additional comparison showing exponential fits with $R^2$ values.
Feasibility of using the QIAGEN QIAcube to help Automate the Differential Extraction Process

April Leon1, Mark Guilliano2 and Angelo Delta Manna3

1 Alabama Department of Forensic Sciences, Birmingham AL, 2 QIAGEN, Germantown, MD

Abstract

A modified version of the QIACube process and automated extraction protocol for forensic applications was evaluated in this study. The QIAcube includes a magnetic bar to facilitate the extraction of DNA from a variety of specimen types, such as hair, bone, and tissue. The study aimed to assess the feasibility of using the QIAcube to automate the differential extraction process, specifically focusing on the extraction of DNA from different specimen types. The study involved the development of a protocol and the evaluation of the efficiency and effectiveness of the QIAcube in automating the DNA extraction process.

Introduction

The QIACube process is designed to automate the extraction of DNA from a variety of specimen types, including hair, bone, and tissue. The study evaluated the feasibility of using the QIAcube to automate the differential extraction process, focusing on the extraction of DNA from different specimen types. The study aimed to assess the efficiency and effectiveness of the QIAcube in automating the DNA extraction process.

Methodology

The study involved the development of a protocol and the evaluation of the efficiency and effectiveness of the QIAcube in automating the DNA extraction process. The protocol included the following steps:

1. Specimen preparation: The specimens were prepared by adding the appropriate buffer to the specimen and incubating it for a specific time period.
2. Enzyme digestion: The specimen was incubated with the enzyme solution to facilitate the digestion of the specimen.
3. DNA purification: The specimen was purified using the QIAcube, which facilitated the extraction of DNA from the specimen.
4. DNA quantification: The quality and quantity of the extracted DNA were assessed using a DNA quantification assay.

Conclusion

The results of the study demonstrated the feasibility of using the QIACube to automate the differential extraction process, specifically focusing on the extraction of DNA from different specimen types. The study showed that the QIAcube is a viable tool for automating the DNA extraction process, which can significantly improve the efficiency and effectiveness of the process. The study also highlighted the importance of developing a protocol that can be used to automate the extraction process, which can be used to improve the accuracy and reliability of the results.

Acknowledgments

The authors would like to acknowledge the Alabama Department of Forensic Sciences for providing the specimen types used in the study. The study was supported by QIAGEN, and the authors would like to thank QIAGEN for their support.

References

### Overview

QIAGEN offers a broad portfolio of automated sample preparation solutions for low-to high-throughput workflows.

<table>
<thead>
<tr>
<th>Instrument</th>
<th>Max. throughput (samples/day)</th>
<th>Technology</th>
</tr>
</thead>
<tbody>
<tr>
<td>QIAcube</td>
<td>48</td>
<td>Spin columns</td>
</tr>
<tr>
<td>EZ1</td>
<td>56</td>
<td>Magnetic bead cartridge</td>
</tr>
<tr>
<td>QIAsymphony SP/AS</td>
<td>120</td>
<td>Magnetic bead cartridge</td>
</tr>
<tr>
<td>STAR Q SP/AS</td>
<td>192</td>
<td>Magnetic bead</td>
</tr>
</tbody>
</table>

QIAGEN’s sample preparation automation portfolio

QIAGEN’s automated workflows for forensic applications
# QIAGEN’s assay setup automation portfolio

## Overview

<table>
<thead>
<tr>
<th>Instrument</th>
<th>qPCR AS</th>
<th>Normalization</th>
<th>STR AS</th>
<th>CE</th>
</tr>
</thead>
<tbody>
<tr>
<td>QIAgility</td>
<td>32 min</td>
<td>100 min (combined norm.+STR setup)</td>
<td>35 min</td>
<td></td>
</tr>
<tr>
<td>QIAsymphony AS</td>
<td>30 min</td>
<td>23 min</td>
<td>30 min</td>
<td>N/A</td>
</tr>
<tr>
<td>STAR Q SP/AS</td>
<td>&lt;45 mins</td>
<td>0-60 mins*</td>
<td>&lt;30 mins</td>
<td>N/A</td>
</tr>
</tbody>
</table>

*Time for 96 samples; QIAgility for 80 samples; *dependent on dilutions required*

---

**QIAGEN offers a broad portfolio of automation solutions for assay setup, normalization and CE plate set up**
QIAGEN’s automated casework workflows

Summary

• A wide range of automation solutions: optimization of your workflow regardless of throughput
  ◦ EZ1 for medium throughput, scalable workflows and premium samples
  ◦ QIAsymphony for medium- to high-throughput, maximum process safety and workflow integration
  ◦ STAR Q platforms for highest throughput with no compromise on quality
  ◦ QIAcube for differential wash

• All workflows underpinned by QIAGEN’s Investigator ISO 18385-compliant kits and assays
  ◦ High yields of inhibitor-free DNA from sample prep
  ◦ High sensitivity assays in all required formats, with Quality Sensor

• Trusted by hundreds of customers worldwide with their most valuable casework samples
Thank You!

For up-to-date licensing information and product-specific disclaimers for QIAGEN products, see the respective QIAGEN kit handbook or user manual. QIAGEN kit handbooks and user manuals are available at www.qiagen.com or can be requested from QIAGEN Technical Services or your local distributor.

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