

# Journal of Visualized Experiments

## Pyrosequencing for Microbial Identification and Characterization

--Manuscript Draft--

<b>Manuscript Number:</b>	JoVE50405R2
<b>Full Title:</b>	Pyrosequencing for Microbial Identification and Characterization
<b>Article Type:</b>	Methods Article - JoVE Produced Video
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<b>Abstract:</b>	Pyrosequencing is a versatile technique that facilitates microbial genome sequencing that can be used to identify bacterial species, discriminate bacterial strains and detect genetic mutations that confer resistance to anti-microbial agents. The advantages of pyrosequencing for microbiology applications include rapid and reliable high-throughput screening and accurate identification of microbes and microbial genome mutations. Pyrosequencing involves sequencing of DNA by synthesizing the complementary strand a single base at a time, while determining the specific nucleotide being incorporated during the synthesis reaction. The reaction occurs on immobilized single stranded template DNA where the four deoxyribonucleotides (dNTP) are added sequentially and the unincorporated dNTPs are enzymatically degraded before addition of the next dNTP to the synthesis reaction. Detection of the specific base incorporated into the template is monitored by generation of chemiluminescent signals. The order of dNTPs that produce the chemiluminescent signals determines the DNA sequence of the template. The real-time sequencing capability of Pyrosequencing technology enables rapid microbial identification in a single assay. In addition, the pyrosequencing instrument, PyroMark Q24, can analyze the full genetic diversity of anti-microbial drug resistance, including typing of SNPs, point mutations, insertions, and deletions, as well as quantification of multiple gene copies that may occur in some anti-microbial resistance patterns.
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<b>Author Comments:</b>	This submission includes animations that need editing by JOVE. I plan to mail the animation files with time stamps for editing to the JOVE office. Because of the large size of these files, I will mail the files on a USB drive. Please let me know if this is okay to do, and provide the name of the individual who should receive the files.  Authors Response: The authors plan to include an animation of the pyrosequencing

	reaction at the end of the Introduction section. The animation will be provided by the author, but we request that JOVE edit the Quick Time movie file to include the times between 0:07 to 1:49. I will attempt to include the file with this resubmission.
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Title: Pyrosequencing for Microbial Identification and Characterization

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Key Words: Pyrosequencing, DNA, Microbe, Sequencing, Genomics, Next-Generation

Short Abstract:

Pyrosequencing is a versatile technique that facilitates microbial genome sequencing that can be used to identify bacterial species, discriminate bacterial strains, and detect genetic mutations that confer resistance to anti-microbial agents. In this video, the procedure for microbial amplicon generation, amplicon pyrosequencing, and DNA sequence analysis will be demonstrated.

Long Abstract:

Pyrosequencing is a versatile technique that facilitates microbial genome sequencing that can be used to identify bacterial species, discriminate bacterial strains and detect genetic mutations that confer resistance to anti-microbial agents. The advantages of pyrosequencing for microbiology applications include rapid and reliable high-throughput screening and accurate identification of microbes and microbial genome mutations. Pyrosequencing involves sequencing of DNA by synthesizing the complementary strand a single base at a time, while determining the specific nucleotide being incorporated during the synthesis reaction. The reaction occurs on immobilized single stranded template DNA where the four deoxyribonucleotides (dNTP) are added sequentially and the unincorporated dNTPs are enzymatically degraded before addition of the next dNTP to the synthesis reaction. Detection of the specific base incorporated into the template is monitored by generation of chemiluminescent signals. The order of dNTPs that produce the chemiluminescent signals determines the DNA sequence of the template. The real-time sequencing capability of Pyrosequencing technology enables rapid microbial identification in a single assay. In addition, the pyrosequencing instrument, **PyroMark Q24**, can analyze the full genetic diversity of anti-microbial drug resistance, including typing of SNPs, point mutations, insertions, and deletions, as well as quantification of multiple gene copies that may occur in some anti-microbial resistance patterns.

**~~NOTE: Animations will be mailed separately because of the large file sizes.~~**

**Introduction:**

Pyrosequencing is a rapid and accurate method to sequence nucleic acids that is based on the principle of "sequencing by synthesis". "Sequencing by synthesis" involves using a single strand DNA template to synthesize the complementary strand one base at a time, and detecting the incorporated base (A, T, G, or C) at each step by detection of a chemiluminescent signal. The pyrosequencing reaction includes template DNA, dNTPs (dATP, dGTP, dTTP, dCTP), DNA polymerase, ATP sulfurylase, luciferin, luciferase, and apyrase. The synthesis reaction is initiated by the addition of one of the four dNTPs and DNA polymerase to the single stranded biotinylated template DNA. DNA polymerase incorporates the complementary dNTP onto the template, with the subsequent release of pyrophosphate (Figure 1). ATP sulfurylase proportionately converts the pyrophosphate to ATP. ATP acts as a catalyst for the luciferase-mediated conversion of luciferin to oxyluciferin, which generates light (Figure 2). The intensity of light is proportionate to the number of nucleotides incorporated and determines if one or more specific dNTP's (dATP, dTTP, dGTP, or dCTP) is present on the template strand sequentially (Figure 3). Any unincorporated dNTP is degraded by apyrase prior to addition of the next dNTP for continuation of the synthesis reaction. This "sequencing by synthesis" reaction is repeated with addition of each of the four dNTPs until the DNA sequence of the single stranded DNA template is determined.

[To view an animation of the pyrosequencing reaction click HERE \(Note: include animation time between 0:07-1:49\).](#)

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## Procedure:

**Introduction:** A single bacterial colony should be used to inoculate an appropriate culture broth that is incubated overnight. A bacterial pellet is then processed to **purify harvested** genomic DNA using a commercially available genomic isolation kit. The purified genomic DNA should have a 260/280 (nm) ratio >1.8 to assure that the sample is free of protein contamination. The amount of genomic DNA required for generation of the pyrosequencing template is 10-20 ng

### A. Amplification of the Template (*PyroMark PCR Handbook*; [www.qiagen.com/handbooks](http://www.qiagen.com/handbooks) (1) )

#### Setting up the PCR reaction

NOTE: One primer must be biotinylated at its 5' end, and it's recommended that it be HPLC purified for **Pyrosequencing** template preparation. We recommend the PyroMark Assay Design Software 2.0 for PCR and sequence primer design **because of its ease of use and algorithms** that are optimized for short-read sequencing, however, Primer-BLAST ([http://www.ncbi.nlm.nih.gov/tools/primer-blast/index.cgi?LINK\\_LOC=BlastHome](http://www.ncbi.nlm.nih.gov/tools/primer-blast/index.cgi?LINK_LOC=BlastHome)) from NCBI can also be used for primer design. ~~We recommend the use of CorallLoad Concentrate for best PCR performance.~~

1. Thaw all required solutions (listed in Table 1) and mix each thoroughly. Set up the reaction according to Table 1. All work can be done at room temperature.

NOTE: **PyroMark** The PCR Master Mix contains  $MgCl_2$  for a final concentration of 1.5 mM, which provides satisfactory results in most cases. If a higher  $Mg^{2+}$  concentration is required, up to 3.5  $\mu l$  of 25 mM  $MgCl_2$  can be added to a reaction.

2. Thoroughly mix the reaction mix by gently pipetting up and down, then dispense appropriate volumes into PCR tubes.
3. Add template DNA ( $\leq 500$  ng/reaction) to each PCR tube. We recommend 10 ng of genomic DNA.
4. Program the thermal cycler according to Table 2. A final hold at 4°C is recommended for convenience. If using a thermal cycler without a heated lid, overlay reactions with 100  $\mu l$  mineral oil.
5. Place the PCR tubes in the cycler and start the cycling program.

### B. Vacuum Workstation Protocol

#### Immobilizing the Biotinylated PCR products

1. Make a master mix according to Figure 4.

NOTE: Before pipetting, gently shake the bottle of streptavidin-coated Sepharose

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beads to ensure a homogenous suspension.

2. Depending on the volume of PCR product used, dispense 60–75 µl master mix into each well of a PCR plate to give a total volume of 80 µl per well.
3. Add 5-20 µl biotinylated PCR product to each well.
4. Seal the wells with strip caps and agitate the PCR plate at 1400 rpm for 5-10 minutes at room temperature (15-25°C) using an orbital shaker.

#### Denaturation of DNA and addition of sequencing primer

1. Dilute the sequencing primers to 0.3 µM with **PyroMark Annealing Buffer** and dispense 25 µl into each well of a **reaction PyroMark Q24 Plate**. Position the plate on the workstation.
  2. Fill the workstation troughs according to the Figure 5 diagram.
  3. Turn on the vacuum pump, and make sure the switch on the vacuum tool is set to **on** (Figure 6). Flush the filter probes with high-purity water (Milli-Q 18.2 MW x cm or equivalent) in trough 5 (Figure 5). Refill the trough with fresh high-purity water for use in step 12.
  4. Working quickly, position the PCR plate with beads on the workstation. Ensure that both plates are in the same orientation as when the samples were loaded.
  5. With the vacuum switch ON, lower the vacuum tool into the wells of the PCR plate for 20 seconds or until all volume has been aspirated. The beads will be captured by the vacuum tool (Figure 7).
  6. With the vacuum still ON, flush the tool with 70% ethanol (trough 1) for 20 seconds or until all volume has been aspirated.
  7. With vacuum ON, flush the tool with denaturation solution (trough 2) for 20 seconds or until all volume has been aspirated.
- NOTE: The Denaturation Solution contains sodium hydroxide, which is an eye and skin irritant. Always wear a lab coat, gloves, and protective goggles.
8. With vacuum ON, flush the tool with wash buffer (trough 3) for 20 seconds or until all volume has been aspirated.
  9. With vacuum ON, raise the vacuum tool to beyond 90° vertical for 5 seconds, to allow all liquid to drain out of the vacuum tool. Turn the pump OFF, and align the vacuum tool with the **reaction PyroMark Q24** plate. Lower the vacuum tool into the wells and gently shake from side to side to release the beads into the **wells containing** sequencing primer.
  10. In order to clean the vacuum tool, agitate the filter probes in high-purity water (trough 4) for 10 seconds.
  11. Switch the vacuum ON and flush the tool with high-purity water (trough 5) for 20 seconds or until all volume has been aspirated.

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12. Raise the vacuum tool to beyond 90°C vertical for 5 seconds, then switch the vacuum OFF and store in the “Parking” position.

#### Annealing sequencing primer to DNA strands

1. Place the reaction PyroMark Q24 Pplate in a pre-warmed Pplate Hholder.
2. Heat the Pyrosequencing samples plate on a heating block at 80°C for 2 minutes.
3. Remove the plate from the holder and place on the counter to cool at room temperature for 5 minutes.

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### C. Pyromark Q24 Operation

#### Loading the PyroMark Q24 Instrument

NOTE: Switch on the instrument using the power switch located above the power cord. Startup can take up to 1 minute.

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1. Fill a cartridge according to the instructions provided in the *PyroMark Gold Q24 Reagents Handbook (2)*. To determine volumes needed, set up a run file in the instrument PyroMark Q24 Ssoftware, and under the Tools menu select Pre Run Information
2. If the instrument was already on, ensure that it is not performing a run and then open the lid. An audible warning signal will be emitted if the lid is opened when it is unsafe to do so.
3. Open the cartridge gate and insert the cartridge with the label facing forward (Figure 8). Ensure that the cartridge is properly inserted (a line should be visible at the front) and close the gate.
4. Open the plate-holding frame and position the plate with samples inside the instrument.
5. Close the plate-holding frame and the instrument lid (Figure 9).

#### Starting a run

1. Insert the USB stick with the run files created with the instrument PyroMark Q24 Ssoftware into the USB port at the front of the instrument.
2. Select “Run” in the main menu and press “OK”.
3. Use the scroll arrows to select the desired run file and press “Select”.

NOTE: The instrument will begin dispensing reagents when all preset pressure and temperature levels are reached (this may take several minutes). NOTE: During a run, the instrument screen displays the Ppyrogram of the selected well in real-time. Use the scroll arrows to view the Ppyrogram of other wells.

#### Completing a run

1. When the instrument confirms that the run is finished and the run file has been

saved to the USB stick, press "Close".

2. Remove the USB stick. If it was removed before the run finished, insert the USB stick. Select "Administration" and then "Copy Unsaved Runs".
3. The run file can now be opened and analyzed using the instrument PyroMark Q24 Software and compared to a library of known microbes using the Identifire software.

### Representative Results:

The results of a typical pyrosequencing run using the Qiagen-IdentiFire 1.0 software shows the location of the forward and reverse primers used for amplicon generation, and the sequencing primer used for the pyrosequencing reaction within the conserved 16S ribosomal sequence (Figure 10). The hypervariable sequence between the primer sites allows for bacterial identification of a large number of bacterial species using the conserved sequencing primer (5'-TACATGCAAGTCGA). As an internal quality control, the DNA sequence bracketing the variable region can be checked to assure that the correct DNA region has been analyzed. The pyrosequencing software allows for comparison and alignment of the generated sequence to an internal database of bacterial ribosomal sequences for bacterial identification. In addition, a sequence can be analyzed to determine mutations that confer antibiotic drug resistance. For example, analysis of mutations in the 23S ribosomal genes of *Helicobacter pylori* demonstrates two mutation patterns (GAA or AGA) that confer antibiotic resistance (Figure 11). Analysis of multiple isolates from the same patient can be concurrently assayed to track the emergence of drug resistance over time to aid in epidemiological investigations of microbial drug resistance outbreaks.

### Discussion:

Several new next generation sequencing methods have been commercialized. Three of the most widely used methods are ion semiconductor sequencing, single molecule real time sequencing, and sequencing by synthesis (SBS). Each of these methods depends on sequencing by synthesis but employ novel platforms for detection of the incorporated nucleotides. In ion semiconductor sequencing, a single strand of DNA serves as a template for the sequencing strand. Polymerase and nucleotides are added sequentially as in pyrosequencing. When a nucleotide is added to the growing DNA strand, a hydrogen ion is released. The hydrogen ion is detected by a field effect transistor based sensor (Rothberg 2011).

Single molecule real time sequencing depends on the zero mode wave guide (ZMW) (13) The ZMW is a small structure where a single polymerase molecule is attached to the bottom of the well. It is illuminated in such a way that a fluorescent molecule can be detected. Each nucleotide is tagged with a fluorescent molecule. As a fluorescently tagged nucleotide is incorporated, a detector identifies the nucleotide. When the next nucleotide is added, the fluorescent molecule is cleaved. (14)

Sequencing by synthesis (SBS) uses a unique method to amplify the target DNA such that clusters of unique sequences are generated (15). Single stranded templates are



generated and then the complementary strand is synthesized. Each nucleotide is labeled with a fluorescent molecule and after each base addition the fluorescence of the added base is recorded.

Acknowledgements: This project was supported in part by Johns Hopkins University, Office of the Provost through the *Gateway Science Initiative* and Qiagen Inc.

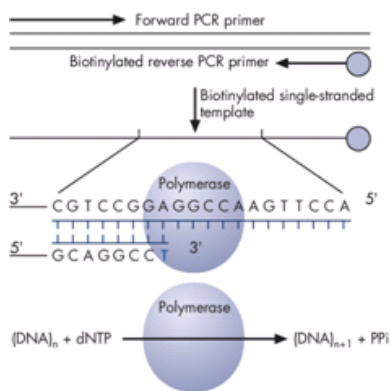
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Disclosures: Authors Ahmed, Durocher, Jessen and Vardi are employees of Qiagen Inc. that produces reagents and instruments used in this article.

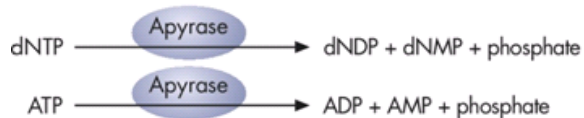
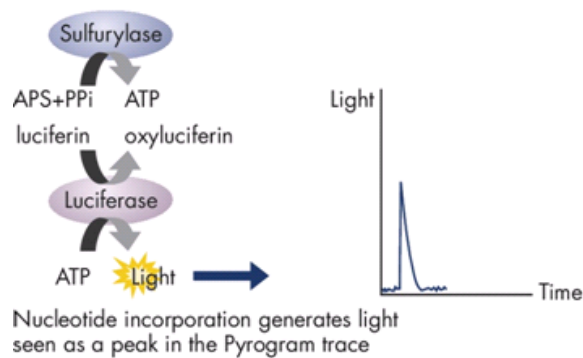
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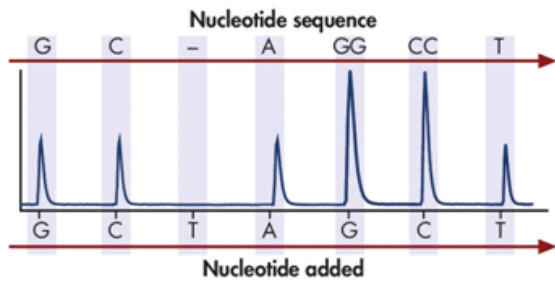
14. J. Eid, A. Fehr, et al. Real-Time DNA Sequencing from Single Polymerase Molecules. *Science* 323:133-138 (2009)
15. [http://www.illumina.com/technology/sequencing\\_technology.ilmn](http://www.illumina.com/technology/sequencing_technology.ilmn) (accessed 10-28-12)



**Figure 1. Biotinylated PCR product is used as a template to incorporate dNTPs by DNA polymerase, leading to the generation of pyrophosphate (PPi).**



**Figure 2. ATP sulfurylase proportionately converts pyrophosphate to ATP. ATP acts as a catalyst for the luciferase-mediated conversion of luciferin to oxyluciferin, which generates light that is proportional to the amount of ATP. The light is recorded as peak on the pyrogram trace and indicates nucleotide incorporation. The unincorporated dNTPs are degraded by apyrase before the next dNTP is added for continuation of the synthesis.**



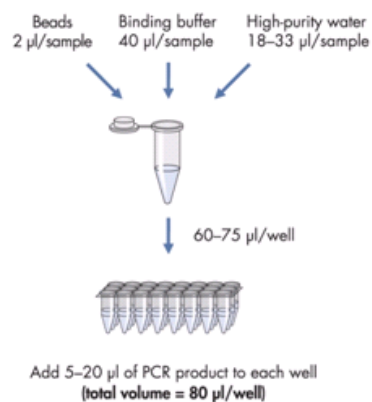
**Figure 3.** The intensity of light generated indicates if one or more specific dNTP's (dATP, dTTP, dGTP, or dCTP) was incorporated onto the template strand sequentially.

Table 1 PCR Reaction Mixture

Component	Volume per reaction	Final concentration
PyroMark PCR Master Mix, 2x	12.5 µl	1x
CoralLoad Concentrate, 10x	2.5 µl	1x
25 mM MgCl <sub>2</sub> (optional)	Variable	≥ 1.5 mM
Q-Solution, 5x (optional)	5 µl	1x
Primer A/Primer B	Variable/Variable	0.2 µM/0.2 µM
RNase-free water	Variable	–
<b>Total volume (after adding template DNA)</b>	<b>25 µl</b>	

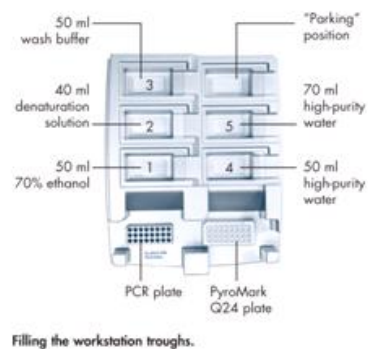
Table 2 PCR Cycle Specifications

			Additional comments
Initial PCR activation step	15 min	95°C	HotStartTaq DNA Polymerase is activated
3 step cycling:			
Denaturation	30 s	94°C	
Annealing	30 s	60°C 56°C	For genomic DNA For bisulfite converted DNA
Extension	30 s	72°C	
Number of cycles	45		
Final extension	10 min	72°C	



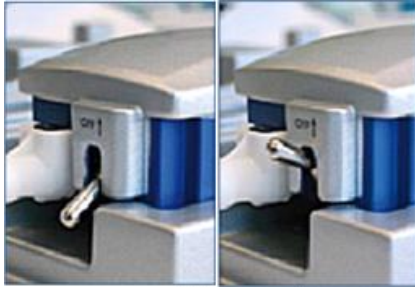
Preparing the master mix to immobilize the PCR products.

**Figure 4. Flow chart for preparation of PCR master mix to amplify and immobilize the biotinylated PCR product.**



**Figure 5. PyroMark workstation, with PCR plate, PyroMark plate, and trough locations.**





**Figure 6. Locations of the Vacuum switch ON and OFF positions.**



**Figure 7. Vacuum tool. Proper handling of the vacuum tool.**



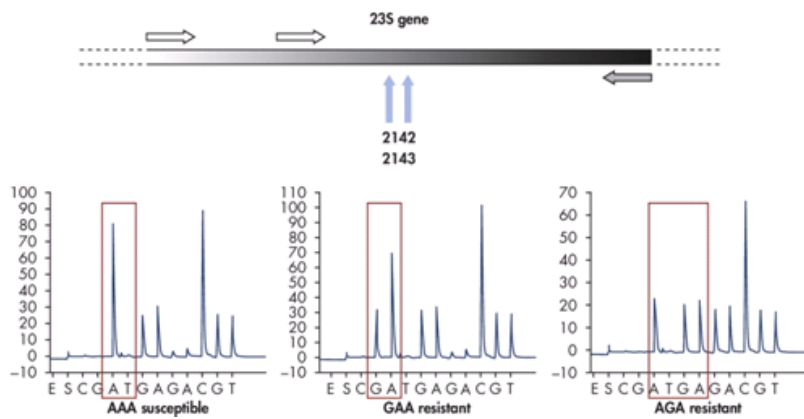
**Figure 8. Cartridge gate opened with cartridge in place.**



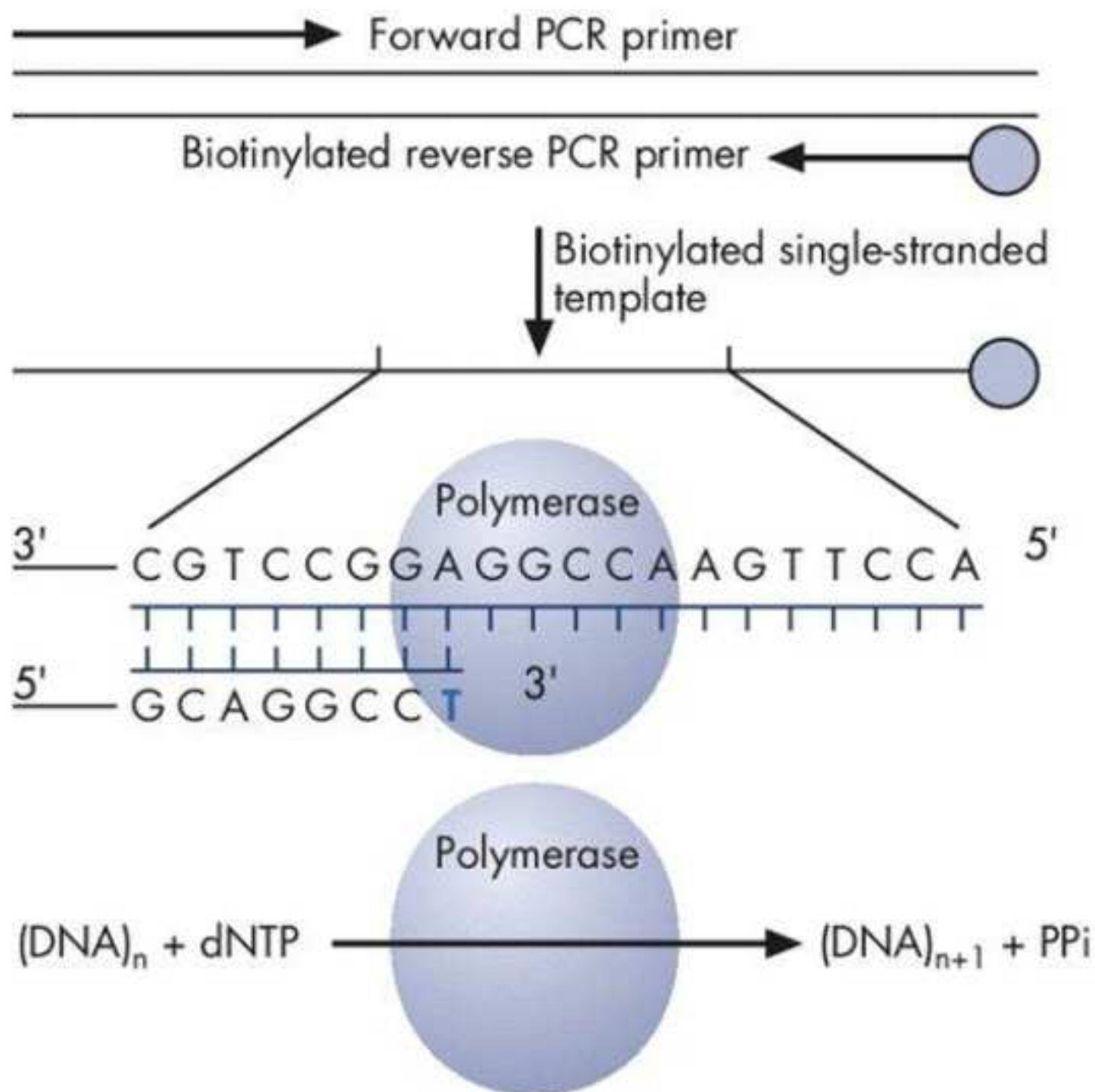
**Figure 9. Cartridge properly inserted with gate closed**



Figure 10: Pyrosequencing based bacterial identification results. PCR primers are designed for conserved regions of the DNA template, and the sequencing primer is positioned immediately upstream of a well-characterized identifying hypervariable DNA sequence within the amplicon (shown in blue).

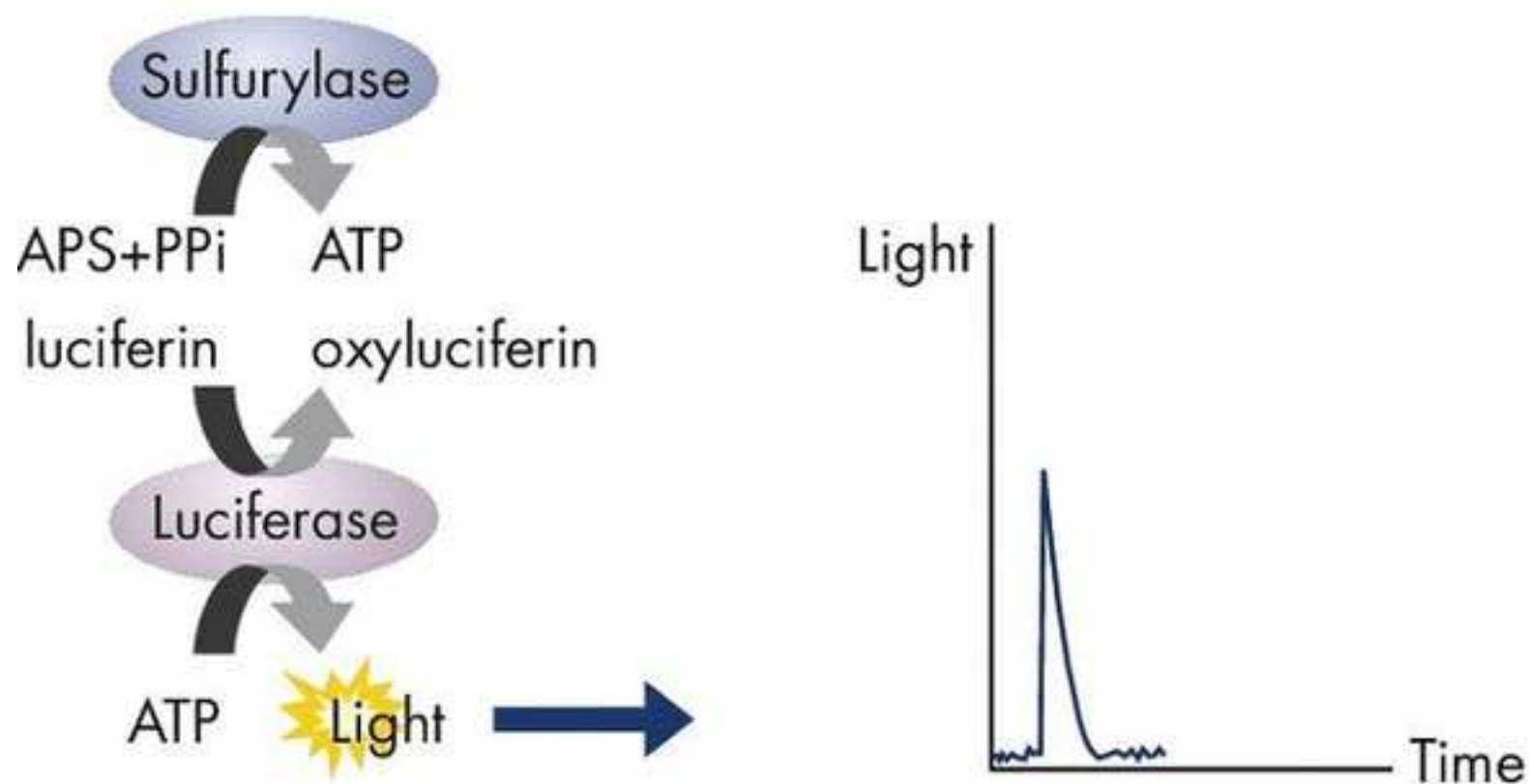


**Figure 11.** Detection of antibiotic drug resistance in *Helicobacter pylori* using pyrosequencing. Analysis of mutations in the 23S genes that confer antibacterial resistance in *Helicobacter pylori* containing GAA or AGA sequences.

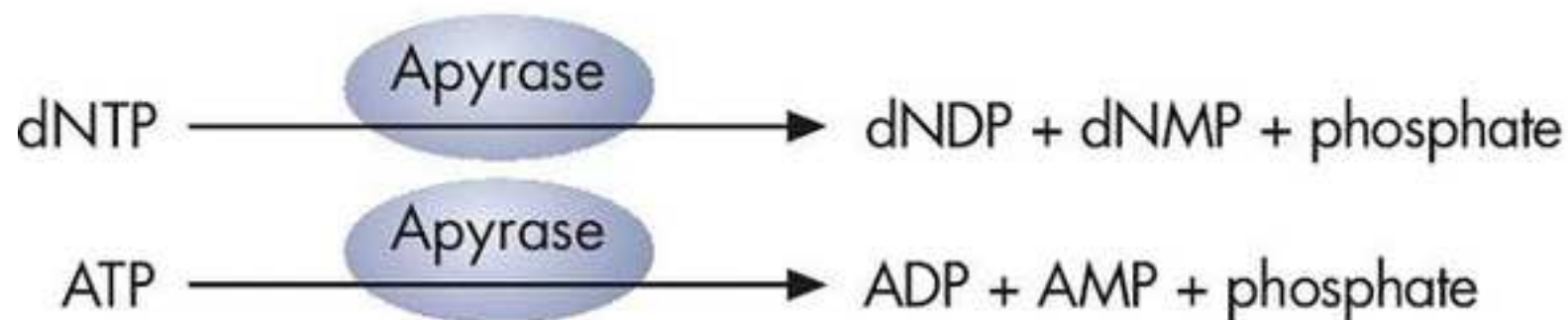


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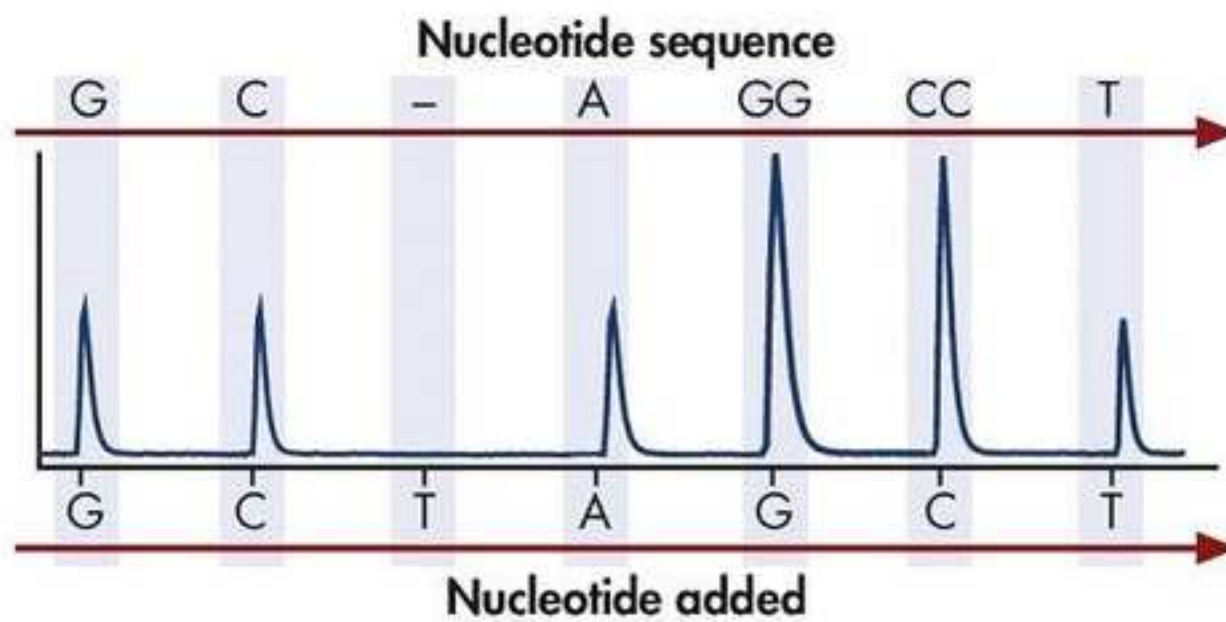
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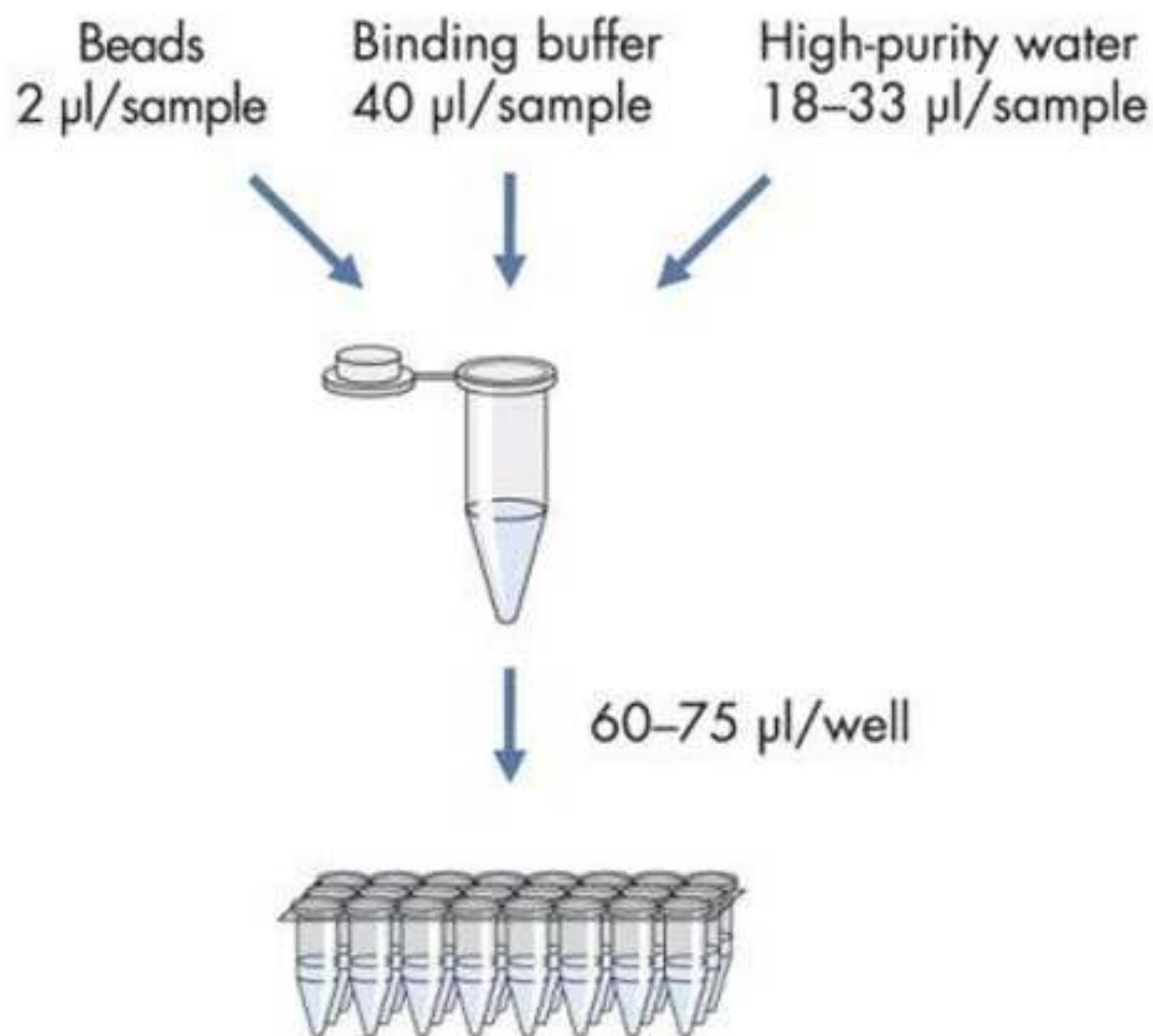


Nucleotide incorporation generates light  
seen as a peak in the Pyrogram trace



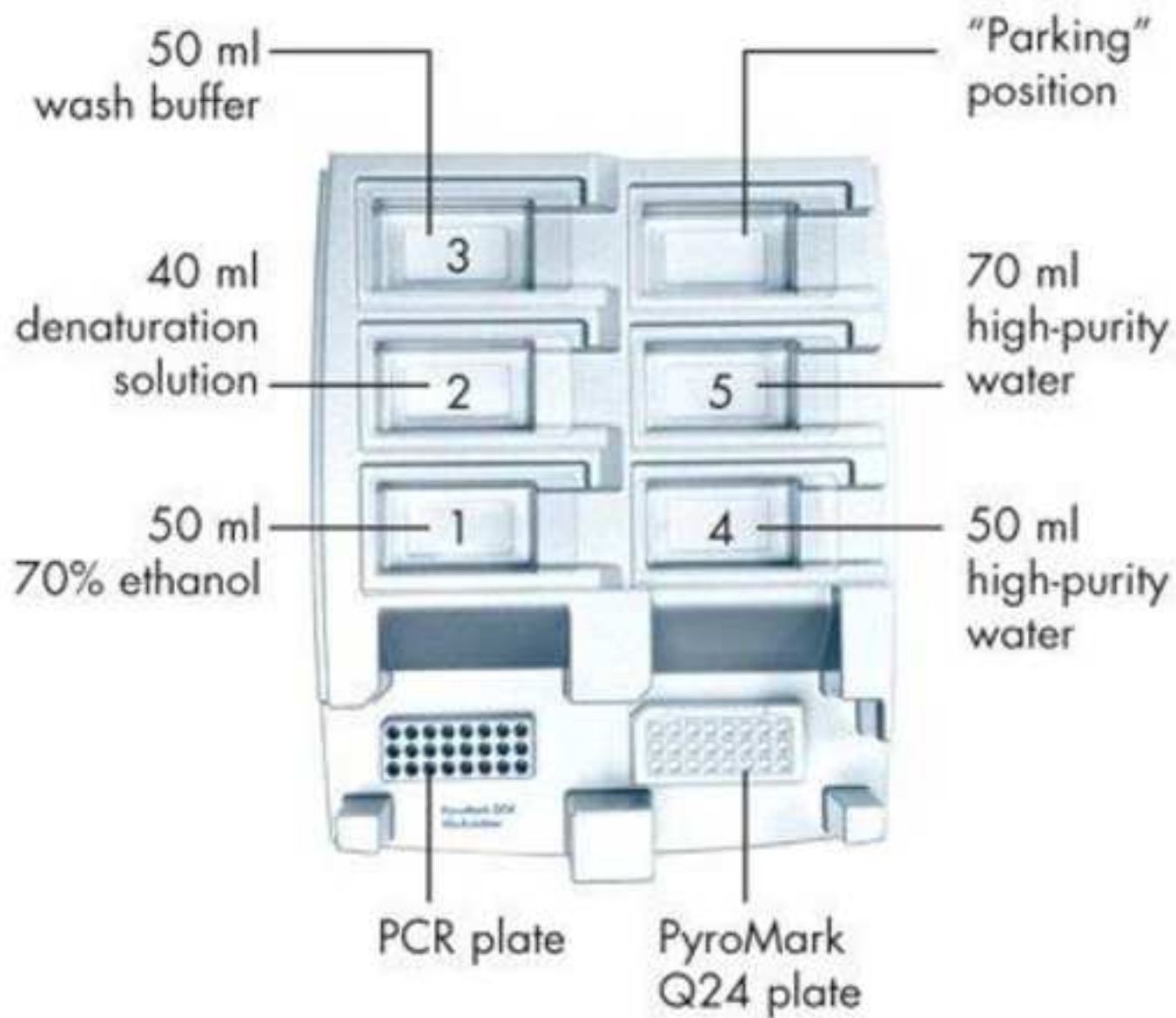






Add 5–20  $\mu\text{l}$  of PCR product to each well  
(total volume = 80  $\mu\text{l}$ /well)

**Preparing the master mix to immobilize the PCR products.**



**Filling the workstation troughs.**

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\*Figure

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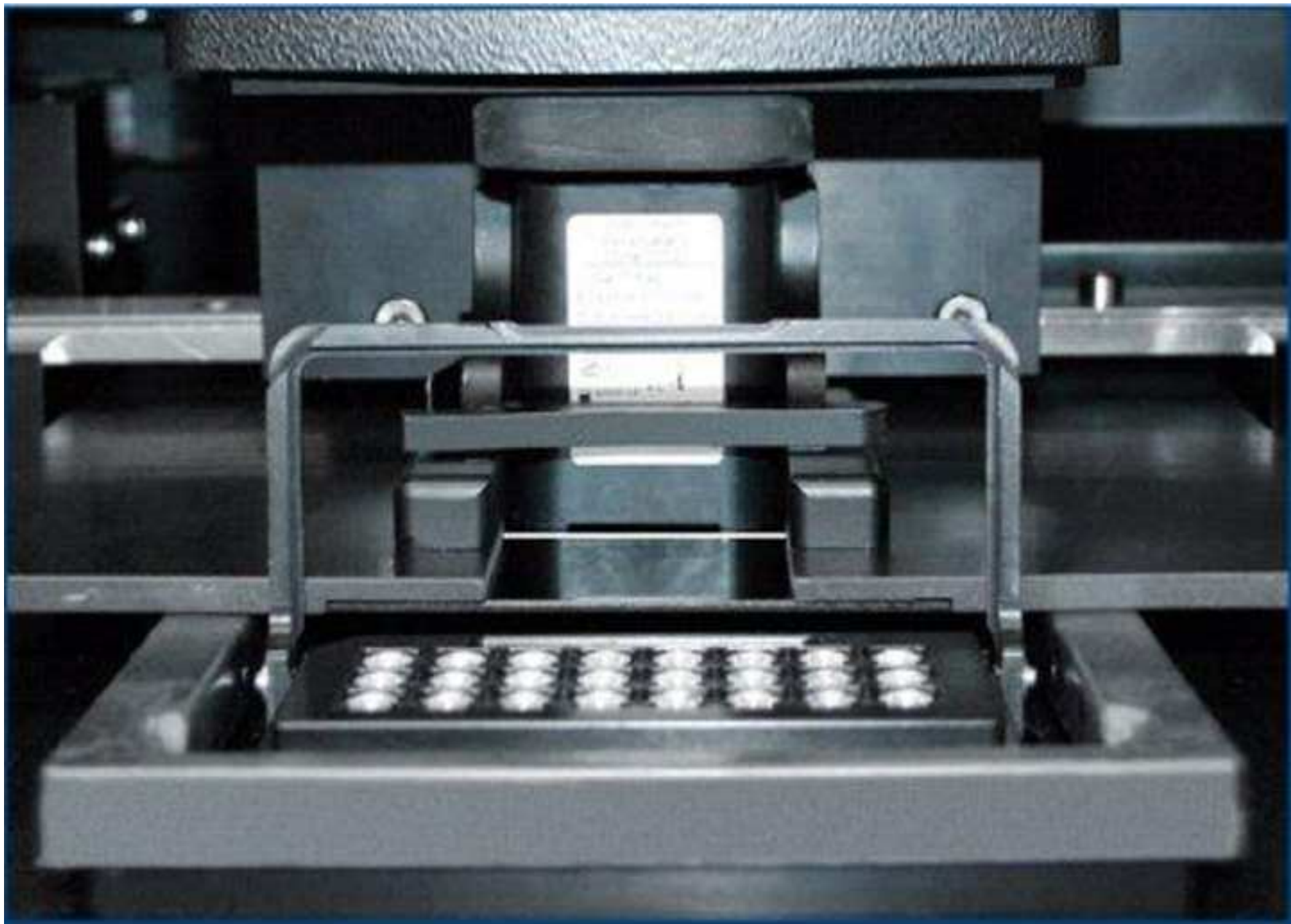
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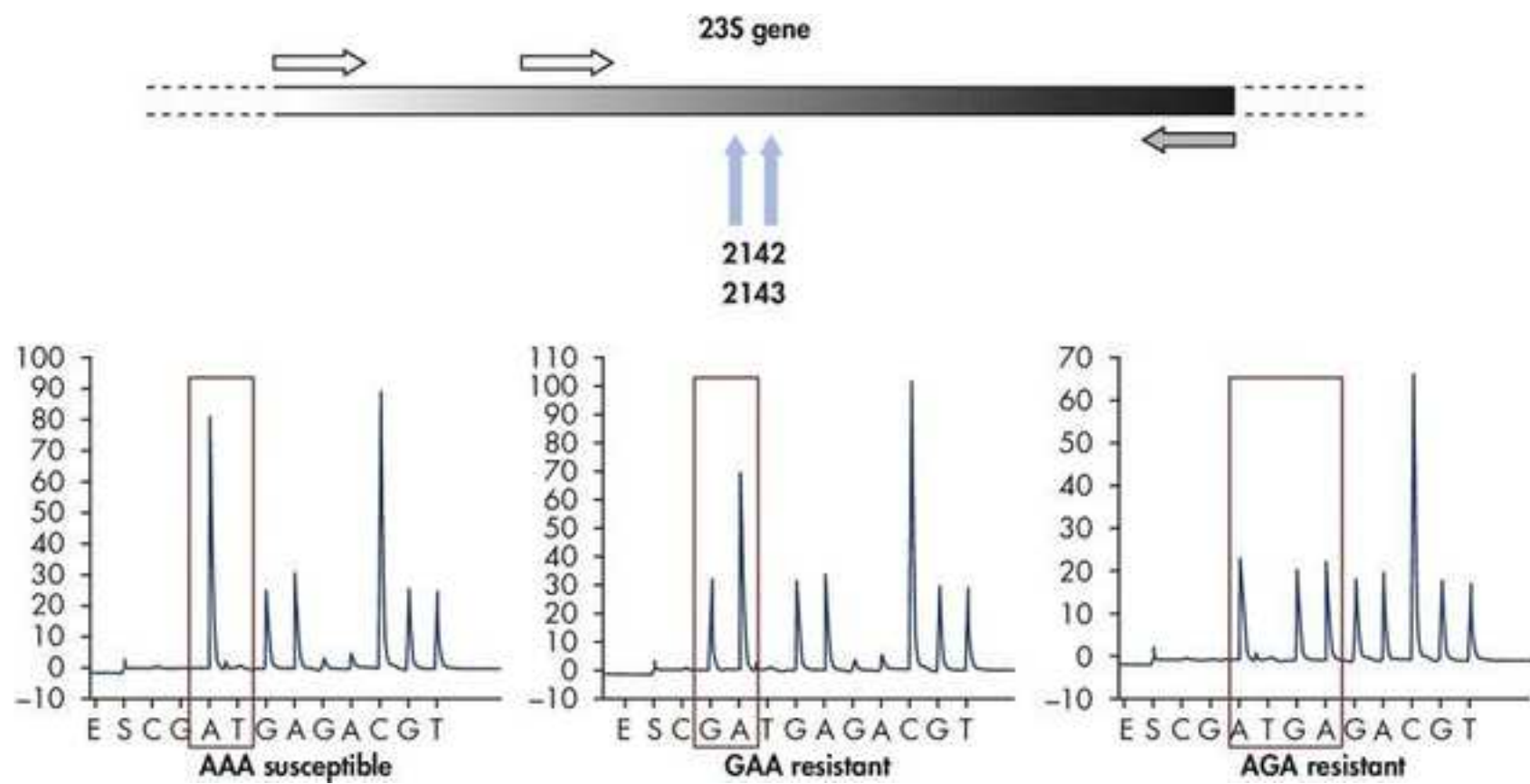


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Component	Volume per reaction
PyroMark PCR Master Mix, 2x	12.5 $\mu$ l
CoralLoad Concentrate, 10x	2.5 $\mu$ l
25 mM MgCl <sub>2</sub> (optional)	Variable
Q-Solution, 5x (optional)	5 $\mu$ l
Primer A/Primer B	Variable/Variable
RNase-free water	Variable
<b>Total volume (after adding template DNA)</b>	<b>25 <math>\mu</math>l</b>

			Additional comments
Initial PCR activation step	15 min	95°C	HotStartTaq DNA Polymerase is activated
3 step cycling:			
Denaturation	30 s	94°C	
Annealing	30 s	60°C 56°C	For genomic DNA For bisulfite converted DNA
Extension	30 s	72°C	
Number of cycles	45		
Final extension	10 min	72°C	

Animated/Video Figure

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\*Table of Reagents/ Materials Used  
[Click here to download Table of Reagents/ Materials Used: Pyro-JoVE\\_Materials.xlsx](#)

Name of Reagent/Material	Company	Catalog Number	Comments
PyroMark PCR Master Mix, 2x	Qiagen	978703	
CoralLoad® Concentrate, 10x	Qiagen	978703, 978705	
Q-Solution®, 5x	Qiagen	978703, 978705	
MgCl <sub>2</sub> , 25 mM	Qiagen	978703, 978705	
RNase-Free Water	Qiagen	129112	
Primers	Qiagen	978776 or 978777	Primers should be purchased from an established manufacturer (i.e. QIAGEN Pyromark Custom As: primers should be dissolved in TE to provide a st
Pyromark Gold Q24 Reagents	Qiagen	970802	
High-purity water (Milli-Q® 18.2 MΩ x cm or equivalent)			
Streptavidin Sepharose® High Performance Beads	GE Healthcare	17-5113-07	
PyroMark Annealing Buffer	Qiagen	979009	
PyroMark Denaturation Solution	Qiagen	979007	
PyroMark Wash Buffer	Qiagen	979008	
PyroMark Q24	Qiagen	9001514	
PyroMark Q24 Cartridge	Qiagen	979202	
PyroMark Q96 HS Tip Holder Box	Qiagen	979105	
PyroMark Q24 Vacuum Workstation	Qiagen	9001516	
PyroMark Q24 Plate Holder	Qiagen	9022273	
Orbital shaker	Fisher	11-675-297	
Heat block	Fisher	11-718Q	

d oligonucleotide  
says, IDT, etc). Lyophilized  
tock solution of 100  $\mu$ M.



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Pyrosequencing for Microbial Identification & Characterization

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Date:

9/27/2012

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January 25, 2013

17 Sellers Street

Cambridge, MA 02139

Dear Dr. Singh:

Thank you for the opportunity to resubmit the article "Pyrosequencing for Microbial Identification and Characterization" for consideration to be published in the Journal of Visualized Experiments (JOVE). The authors have added our responses to the editorial and reviewer comments below.

Editorial comment: The protocol length is over our three page limit, so please use highlighting to define a total of three pages of protocol to be included in the video.

Authors Response: The three pages have been highlighted in the revised submission.

Editorial Comment: 50405 (resub) - Previous issues (10/4) has been partially addressed. Conditional pass for commercialization, and for required author clarification. \*The Pyromark name has been removed in a few places but is still extensively used (12 times in the 3 pages of protocol).

Authors Response: The Pyromark name has been removed 8 more times from the revised protocol.

Editorial Comment: \*There is a note from the author on Aries: "This submission includes animations that need editing by JOVE. I plan to mail the animation files with time stamps for editing to the JOVE office. Because of the large size of these files, I will mail the files on a USB drive. Please let me know if this is okay to do, and provide the name of the individual who should receive the files." We need more information on what they are asking for before we can agree. Are they asking us to incorporate their own animations into the video, or for us to (re)create animations for them? What sort of animations?

Authors Response: The authors plan to include an animation of the pyrosequencing reaction at the end of the *Introduction* section. The animation will be provided by the author, but we request that JOVE edit the Quick Time movie file to include the times between 0:07 to 1:49. I will attempt to include the file with this resubmission.

Editorial Comment: \*The length is borderline, 3 pages if subheadings and the introductory paragraph are removed. Authors should be careful to take length into consideration if they add material after peer review.

Authors Response: Highlighted text is less than three pages after removing and consolidating text.

Reviewer #1 Comment: I am not clear on the purpose of this article. To me, this work looks like a package insert describing a test, step by step. The authors did not indicate the intent of this work nor the reason of the study.

Authors Response: The purpose of this article is to present the theory and application of the pyrosequencing technology for microbial DNA sequencing and analysis, which has been explained in the *Introduction* and *Results* sections of this submission. The protocol is written step by step to mirror the manufacturer's instructions to assure proper sample preparation and instrument operation, which will give the highest possible success rate when using this technology.

Reviewer #2 Comment: The abstract should be rewritten to emphasize the findings and conclusions rather than providing a description of the technique and its advantages. The results and discussion section should focus on the sequence data obtained, and how the instrument and technique are useful for rapid identification of mutational changes. There are 11 figures, mostly describing the technique and instrument, but only two figures for the results. The discussion section included three paragraphs that describe the next generation sequencing methods and did not address the findings and their importance in this research.

Authors Response: This submission is not a research or hypothesis based study and therefore this submission did not focus on the results or conclusions from a single organism or DNA sequence. The authors believe the abstract accurately reflects the purpose of this submission.

The purpose of the submission is to present the theory, step-by-step procedure, and analysis of microbial DNA sequencing using the pyrosequencing technology. The discussion section describes other emerging and next generation sequencing technologies besides pyrosequencing, and it did not address a research question or hypothesis.

Reviewer #3:

I thought this article presented a very clear picture of the techniques involved in performing Pyrosequencing. I could easily operate the instrument with the instructions that were provided. I was pleased to see the antibiotic resistance determination described in the paper. This is a very critical area of medicine right now and the rapid determination of the correct bacterial strain could prevent time wasted on using the incorrect therapeutic intervention. One of the primary

reasons for incorrect diagnoses is the time in which it takes to type bacterial pathogens by conventional means.

Authors Comments: None

Regards

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