

# Use of the PowerPlex® ESX and ESI Fast Systems to Amplify Extracted DNA

INSTRUCTIONS FOR USE OF PRODUCTS DC1610, DC1611, DC1710, DC1711, DC1620, DC1621, DC1720 AND DC1721.

## Protocol for Amplification and Analysis of Extracted DNA

This document is a quick protocol for experienced users to amplify extracted DNA. Quick protocols are also available for amplifying DNA from storage card punches and swabs. For complete protocol information and troubleshooting tips, see the *PowerPlex® ESX 16 Fast System Technical Manual #TMD043*, *PowerPlex® ESX 17 Fast System Technical Manual #TMD040*, *PowerPlex® ESI 16 Fast System Technical Manual #TMD044* or *PowerPlex® ESI 17 Fast System Technical Manual #TMD041*, as appropriate. All manuals are available online at: [www.promega.com/protocols/](http://www.promega.com/protocols/)

### Before You Begin

Determine the concentration of genomic DNA for your samples. Note that different quantitation methods yield different quantitation values. We strongly recommend that you perform experiments to determine the optimal DNA template amount based on your DNA quantitation method.

**Optional:** Record the DNA template amount as optimized in your laboratory.

### PCR Setup

1. Thaw all pre-amplification components just prior to use.
2. Vortex the components thoroughly for 15 seconds. Centrifuge tube briefly, then vortex for 15 seconds before each use. Do not centrifuge after vortexing.
3. Determine the number of reactions including positive and negative controls. Add 1 or 2 reactions to this number.
4. Prepare the PCR amplification mix by combining the components as shown below.

Component	Volume per Reaction	x	Number of Reactions	=	Final Volume
Water, Amplification Grade	to a final volume of 25.0µl	x		=	
PowerPlex® ESI/ESX Fast 5X Master Mix	5.0µl	x		=	
PowerPlex® ESI or ESX Fast 10X Primer Pair Mix	2.5µl	x		=	
Template DNA (0.5ng)	up to 17.5µl				
<b>Total volume</b>	<b>25µl</b>				

5. Vortex the PCR amplification mix for 5–10 seconds, then add PCR amplification mix to each reaction well.
6. Add the template DNA.
7. For the positive amplification control, vortex the 2800M Control DNA, then dilute an aliquot to 0.5ng in the desired template DNA volume. Add 0.5ng of diluted DNA to a reaction well containing PCR amplification mix.
8. For the negative amplification control, add Water, Amplification Grade, or TE<sup>-4</sup> buffer instead of template DNA to a reaction well containing PCR amplification mix.
9. Seal the plate or cap the tube as appropriate. Briefly centrifuge the plate if desired.

### Additional Notes:

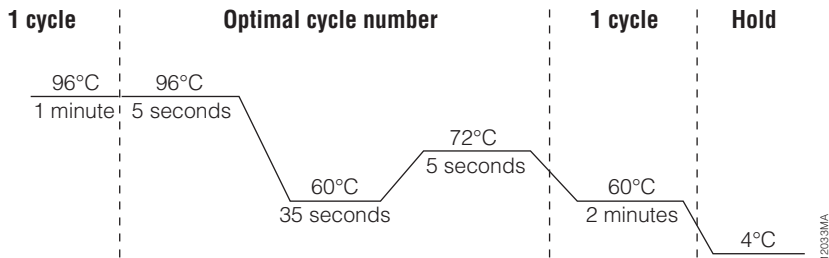
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## Thermal Cycling

The PowerPlex® ESX and ESI Fast Systems are designed for use with the GeneAmp® PCR System 9700 with a silver or gold-plated silver sample block with Max mode as the ramp speed.

1. Program the thermal cycler with the following conditions. Refer to the relevant technical manual for more information. For extracted DNA we recommend using 30 cycles. Optimize the cycle number as required.



**Figure 1. The thermal cycling protocol for the GeneAmp® PCR System 9700 thermal cycler.**

**Optional:** Record the cycle number as optimized in your laboratory.

2. Proceed with the analysis, or store amplified samples at  $-20^{\circ}\text{C}$  in a light-protected box until ready to analyze.

### Additional Notes:

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## Instrument Setup and Sample Preparation

 A passing spectral calibration must be generated using the PowerPlex® 5C Matrix Standard (Cat.# DG4850) prior to sample analysis. See the *PowerPlex® 5C Matrix Standard Technical Manual #TMD049* for more information.

### Instrument Setup

1. For the Applied Biosystems® 3500 or 3500xL Genetic Analyzer, we recommend preheating the oven at 60°C for at least 30 minutes prior to the first injection.
2. Use the following parameters when setting up the instrument. Refer to the instrument user's manual for additional details. Protocols for use with the Applied Biosystems® 310 Genetic Analyzer are available in the relevant PowerPlex® ESX or ESI Fast System Technical Manual. Instructions for generating a matrix can be found in the *PowerPlex® 5-Dye Matrix Standards, 310, Technical Bulletin #TBD023*.

Genetic Analyzer	Run Module	Dye Set	Injection Parameters <sup>1</sup>	Run Time
Applied Biosystems® 3500	HID36_POP4	Promega G5	1.2kV, 15 seconds	1,210 seconds
Applied Biosystems® 3500xL	HID36_POP4	Promega G5	1.2kV, 24 seconds	1,210 seconds
Applied Biosystems® 3130 and 3130xL	HIDFragmentAnalysis36_POP4	G5 <sup>2</sup>	3kV, 5 seconds	1,500 seconds
ABI PRISM® 3100 and 3100-Avant	HIDFragmentAnalysis36_POP4	G5 <sup>2</sup>	3kV, 5 seconds	1,500 seconds

<sup>1</sup>Injection time may be modified (2–24 seconds) to increase or decrease the observed peak heights.

<sup>2</sup>Confirm that the active dye set is the file generated for the PowerPlex® 5-dye chemistry.

**Optional:** Record the injection conditions as optimized in your laboratory.

### Additional Notes:

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## Instrument Setup and Sample Preparation (continued)

### Sample Preparation

Prepare samples for capillary electrophoresis immediately before loading.

1. Centrifuge the WEN Internal Lane Standard 500 ESS (WEN ILS 500 ESS) briefly, then vortex for 15 seconds before each use. Do not centrifuge after vortexing.
2. Calculate the number of samples including the number of allelic ladders per run. Add 1 or 2 reactions to this number.
3. Prepare a loading cocktail by combining and mixing the WEN ILS 500 ESS and Hi-Di™ formamide. You may need to optimize the volume of WEN ILS 500 ESS.

Component	Volume per Sample	×	Number of Samples	=	Final Volume
WEN ILS 500 ESS	0.5µl <sup>1</sup>	×		=	
Hi-Di™ formamide	9.5µl	×		=	

<sup>1</sup>The volume of WEN ILS 500 ESS can be adjusted to change the intensity of the size standard peaks based on laboratory preferences.

**Optional:** Record the volume of WEN ILS 500 ESS per sample as optimized in your laboratory.

4. Vortex the loading cocktail for 10–15 seconds, and pipet 10µl of formamide/internal lane standard mix into each well.
5. Add 1µl of amplified sample (or 1µl of the appropriate PowerPlex® ESX or ESI Fast System Allelic Ladder Mix). Cover wells with appropriate septa, and centrifuge plate briefly.
6. Denature samples at 95°C for 3 minutes, then immediately chill on crushed ice or in an ice-water bath for 3 minutes. Denature samples just prior to loading the instrument.
7. Place the plate assembly on the autosampler.
8. Start the capillary electrophoresis run.

### Data Analysis

The panels, bins and stutter text files needed for data analysis using GeneMapper® ID software, version 3.2, and GeneMapper® ID-X software, version 1.2 or higher, are available for download at:

[www.promega.com/resources/software-firmware/genemapper-id-software-panels-and-bin-sets/](http://www.promega.com/resources/software-firmware/genemapper-id-software-panels-and-bin-sets/)

For complete protocol information see the relevant PowerPlex® ESX or ESI Fast Technical Manual: *PowerPlex® ESX 16 Fast System Technical Manual #TMD043*, *PowerPlex® ESX 17 Fast System Technical Manual #TMD040*, *PowerPlex® ESI 16 Fast System Technical Manual #TMD044* or *PowerPlex® ESI 17 Fast System Technical Manual #TMD041*. These manuals are available online at:

[www.promega.com/protocols/](http://www.promega.com/protocols/)

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