

BigDye™ Terminator v1.1 Cycle Sequencing Kit

USER GUIDE

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B	16 July 2026	• The sequencing standards for spectral calibration were updated. • Expanded BigDye XTerminator™ Purification Kit instructions. • Minor edits were made for style and consistency.
A	28 June 2024	New user guide for the BigDye™ Terminator v1.1 Cycle Sequencing Kit. This document replaces Pub. No. 4337036.

The information in this guide is subject to change without notice.

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Product information

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IMPORTANT! Before using this product, read and understand the information in the “Safety” appendix in this document.

Product description

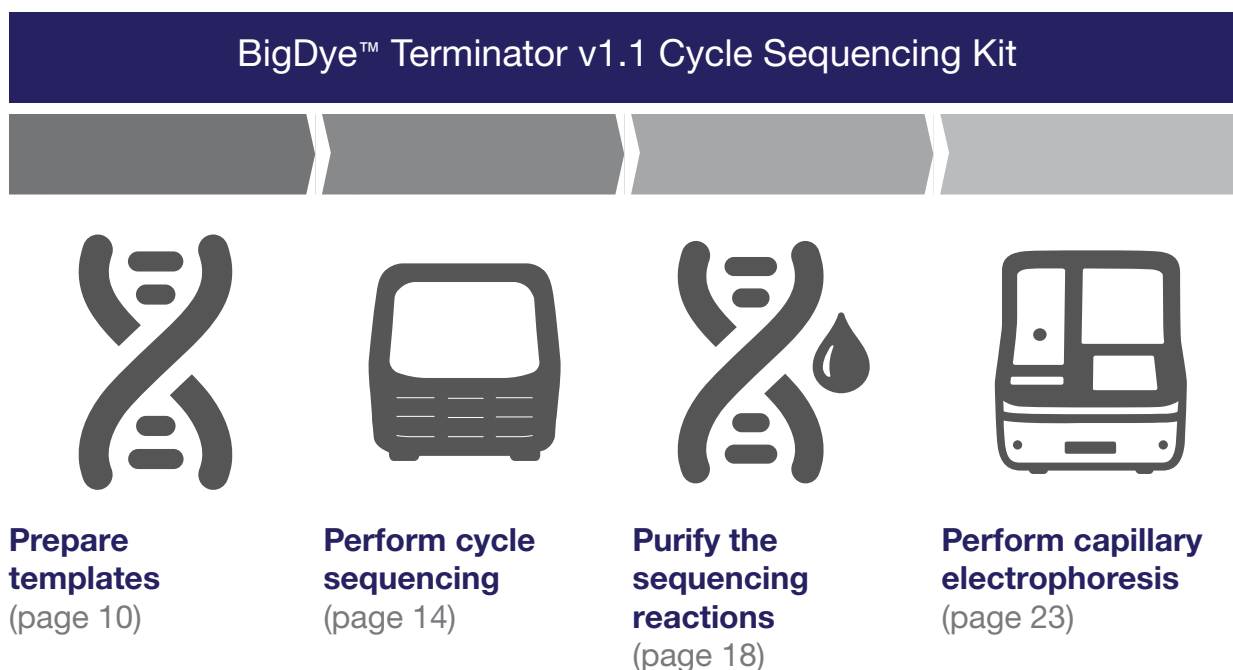
The BigDye™ Terminator v1.1 Cycle Sequencing Kit provides the reagents required for Sanger sequencing reactions in a pre-mixed format.

The kit reagents are suitable for performing fluorescence-based cycle sequencing reactions on single-stranded or double-stranded DNA templates, on PCR fragments, and on large templates (for example, BAC clones).

The kit includes BigDye™ Terminator v1.1/v3.1 Sequencing Buffer (5X), which is specifically optimized for use with the BigDye™ Ready Reaction mixes.

The kit has been designed to deliver optimal 5' resolution and basecalling in shorter fragments when used in combination with POP-6™ polymer and a 50cm array. When used in combination with Minor Variant Finder Software, the kit can also be used to detect variants as low as 5% in a sample (see *Minor Variant Finder Software User Guide* (Pub. No. [MAN0014835](#)).

Workflow



Kit contents and storage

Table 1 BigDye™ Terminator v1.1 Cycle Sequencing Kit

Contents	Cat. No. 4337449 (24 reactions)	Cat. No. 4337450 (100 reactions)	Cat. No. 4337451 (1,000 reactions)	Cat. No. 4337452 (5,000 reactions)	Storage
BigDye™ Terminator v1.1 Ready Reaction Mix	1 × 192 µL	1 × 800 µL	10 × 800 µL	2 × 20 mL	–25°C to –15°C Protect from light.
pREF-BDT™ Control DNA (200ng/µL)	1 × 30 µL	1 × 30 µL	1 × 250 µL	2 × 250 µL	
–21 M13 Control Primers (0.8 pmol/µL)	1 × 50 µL	1 × 50 µL	1 × 200 µL	2 × 200 µL	
BigDye™ Terminator v1.1 & v3.1 5X Sequencing Buffer ^[1]	1 × 1 mL	2 × 1 mL	1 × 12 mL	2 × 28 mL	4°C

^[1] Shipped separately from the rest of the kit.

Usage guidelines

- Avoid excess freeze-thaw cycles (no more than 10 cycles). If needed, aliquot reagents into smaller amounts.
- Before each use of the kit, thaw the frozen stocks.
 - Thaw on ice or at room temperature. (Do not heat.)
 - Keep the thawing stocks protected from light.
- Keep thawed materials on ice during use. Do not leave reagents at room temperature for extended periods.
- Protect dyes from light to avoid photobleaching.

IMPORTANT! After thawing, mix each stock thoroughly, then centrifuge briefly to collect all the liquid at the bottom of each tube.

Compatible sequencing instruments

This guide provides general instructions for using the kit to generate samples for these instruments. For more detailed instructions, see the appropriate instrument or chemistry guide.

The kit is compatible with the following Applied Biosystems™ genetic analyzers:

- SeqStudio™ Genetic Analyzer
- SeqStudio™ Flex Series Genetic Analyzer
- 3500/3500xL Genetic Analyzer
- 3730xL DNA Analyzer

Thermal cyclers

The protocols provided in this guide were optimized using Applied Biosystems™ thermal cyclers, including the:

- GeneAmp™ PCR System 9700 Dual 96-Well
- GeneAmp™ PCR System 9700 Dual 384-Well
- Veriti™ Thermal Cycler, 96-well Fast
- Veriti™ 384-Well Thermal Cycler

It is possible to use a different thermal cycler, although you may need to re-optimize the thermal cycling conditions. Ramping time is very important. If the thermal ramping time is too fast ($>1^{\circ}/\text{second}$), poor (noisy) data may result.

Required materials not supplied

Unless otherwise indicated, all materials are available through thermofisher.com. "MLS" indicates that the material is available from fisherscientific.com or another major laboratory supplier.

Catalog numbers that appear as links open the web pages for those products.

Item	Source
Reagents	
BigDye™ Terminator v1.1 Cycle Sequencing Kit	4337451
UltraPure™ DNase/RNase-Free Distilled Water	10977015
Hi-Di™ Formamide Note: Not required for BigDye XTerminator™ Purification Kit purification.	4311320 or 4440753
Sequencing and PCR primers (HPLC-purified recommended)	Primers can be designed and ordered with the Primer Designer™ Tool at http://www.thermofisher.com/primerdesigner . See "Primer Designer™ Tool" on page 45.
Laboratory supplies	
MicroAmp™ Clear Adhesive Film	4306311
MicroAmp™ Optical 96-Well Reaction Plate	N8010560
Plate Septa, 96 well	4315933
MicroAmp™ Optical 384-Well Reaction Plates	4343370
Digital Vortex-Genie™ 2 or equivalent	Scientific Industries, Inc. SI-A536
Centrifuge with swinging bucket (with PCR plate adapter)	MLS
Reagents for BigDye XTerminator™ Purification Kit purification (optional)	
BigDye XTerminator™ Purification Kit	4376486
Reagents for ethanol/EDTA purification (optional)	
0.5M EDTA, pH 8.0 for molecular biology	AM9260G
Ethanol, absolute, for molecular biology	MLS

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Prepare templates

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Control template

Include a control DNA template in every set of sequencing reactions. The results from the control help determine whether failed reactions are the result of poor template quality or sequencing reaction failure.

- pREF-BDT™ Control DNA is included with the kit as a double-stranded control (see Appendix C, “pREF-BDT™ Control DNA” for the partial sequence).

Note: The corresponding –21 M13 forward primer is also included.

- M13mp18 (Cat. No. [50-811-790](#)) is recommended as a single-stranded control.

Template preparation methods

Cycle sequencing can be performed directly from single- or double-stranded DNA, plasmids, cosmids, BACs, or purified PCR products. For high complexity DNA, PCR amplification of the target of interest before cycle sequencing is recommended.

For general guidelines on DNA isolation, see *DNA Sequencing by Capillary Electrophoresis Chemistry Guide Second Edition* (Pub. No. [4305080](#)) or *DNA Fragment Analysis by Capillary Electrophoresis User Guide* (Pub. No. [4474504](#)) for information on preparing single- and double-stranded templates.

DNA isolation of single- and double-stranded templates

For a comprehensive list of Thermo Fisher Scientific products available for DNA isolation, go to thermofisher.com/us/en/home/life-science/dna-rna-purification-analysis.

DNA isolation of BAC templates

With larger DNA targets such as bacterial artificial chromosomes (BACs), DNA template quality is important to the success of the sequencing reaction. Two methods have provided good sequencing results:

- Alkaline lysis; include extra phenol extraction and isopropanol precipitation if very clean DNA is desired
- Cesium chloride (CsCl) banding

For Thermo Fisher Scientific BAC DNA preparation products, see **Plasmid DNA Isolation** at thermofisher.com/us/en/home/life-science/dna-rna-purification-analysis.

DNA template amplification with PCR

PCR templates can also be used to perform reliable cycle sequencing. For optimal results, purify PCR templates before sequencing. In general, any method that removes unincorporated dNTPs and primers should work.

For a range of appropriate kits, go to thermofisher.com/us/en/home/life-science/dna-rna-purification-analysis, then click **Genomic DNA Extraction ▶ Isolation of DNA Fragments and PCR Clean-Up**.

For information about sequencing PCR templates, see the *DNA Sequencing by Capillary Electrophoresis Chemistry Guide Second Edition* (Pub. No. [4305080](#)).

Template quality

DNA quality can significantly influence the length of the fragment that can be amplified and the reproducibility of amplification from one sample to another. Even if the fragment successfully amplifies, poor quality DNA can result in decreased signal or increased background fluorescent noise from the sequencing reactions.

DNA quantity can also significantly affect amplification. For recommended quantities of DNA template per reaction, see “Template quantity” on page 13.

Factors affecting template quality

- **Type and amount of source material** – Influences the effectiveness and sensitivity of PCR amplification and the quality of sequencing results. The number of sequencing targets relative to the number of primer molecules can influence the efficiency and read-length of the sequencing reaction.
- **Contamination** – Can inhibit PCR amplification and cycle sequencing. Potential contaminants include:
 - Protein, RNA, or chromosomal DNA
 - Excess PCR primers, dNTPs, enzyme, and buffer components
 - Remaining salts, organic chemicals such as phenol, chloroform, and ethanol, or detergents.
 - Heparin – can partially or completely inhibit PCR amplification and cycle sequencing. Use the Dynabeads™ DNA DIRECT™ Blood Kit and the QIAamp™ Blood Kit (QIAGEN™, GmbH) to help remove heparin from heparin blood samples, leaving genomic DNA ready for PCR amplification.

Note: You can design primers using the free Primer Designer™ Tool at apps.thermofisher.com/apps/oligoperfect.

Determining template quality and quantity

Use a spectrophotometer to determine DNA quality and to check for protein contamination. Optimum absorbance ratios ($A_{260/280}$) are between 1.8 and 2.0.

If DNA and/or RNA contamination is suspected, run the sample on an agarose gel. A single band should be present for high-quality DNA.

For DNA quantification, A_{260} values can be converted into $\mu\text{g}/\mu\text{L}$ using Beer's Law:

- Concentration of single-stranded DNA = $A_{260} \times 33 \mu\text{g}/\mu\text{L}$.
- Concentration of double-stranded DNA = $A_{260} \times 50 \mu\text{g}/\mu\text{L}$.

Optical density (OD) measurements are used to determine template concentration. Highly concentrated ($\text{OD} > 1.0$) or very dilute ($\text{OD} < 0.05$) DNA samples can lead to inaccurate OD measurements. Dilute or concentrate the DNA if needed to obtain an OD value between 0.05 to 1.

Note: OD measurement is not a reliable method to determine template concentration following enzymatic PCR purification protocols. Instead, estimate PCR product purity and concentration using one of the following methods:

- Agarose gel
 - Quant-iT™ PicoGreen™ dsDNA Reagent (Cat. No. [P7581](#) or similar) for use on the Qubit™ quantification platform.
-

Template quantity

The table below lists the recommended quantity of template to use in a single cycle sequencing reaction. The quantity of PCR product is optimized to maximize the number of primer binding sites for the BigDye™ reaction and is dependent upon the length and purity of the PCR product.

Note: In general, higher DNA quantities give higher signal intensities.

Table 2 Recommended DNA quantities

DNA template	Quantity
PCR product:	
• 100–200 bp	1–3 ng
• 200–500 bp	3–10 ng
• 500–1000 bp	5–20 ng
• 1000–2000 bp	10–40 ng
• >2000 bp	20–50 ng
Single-stranded DNA	25–50 ng
Double-stranded DNA	150–300 ng
Cosmid, BAC	0.5–1.0 µg
Bacterial genomic DNA	2–3 µg

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Perform cycle sequencing

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Prepare the reactions

Set up the sequencing reactions

IMPORTANT! Protect dye terminators from light. Cover the reaction mix and sequencing plates with aluminum foil before use.

1. Completely thaw the contents of the BigDye™ Terminator v1.1 Cycle Sequencing Kit and your primers and store on ice.
2. Vortex the kit components for 2–3 seconds, then centrifuge briefly (2–3 seconds) with a benchtop microcentrifuge to collect contents at the bottom of the tubes.
3. Add components as indicated:

IMPORTANT! Change pipette tips after each transfer.

IMPORTANT! For control reactions, use 4 µL of the control primers for 20 µL and 10 µL reactions. Control primer concentration = 0.8pmol/µL.

Component	Standard reaction (20 µL)			Standard reaction (10 µL)		
	Quantity per reaction	Example Forward	Example Reverse	Quantity per reaction	Example Forward	Example Reverse
BigDye™ Terminator v1.1 Ready Reaction Mix	8 µL	8 µL	8 µL	4 µL	4 µL	4 µL
Forward primer (3.2 µM)	3.2 pmol	2 µL	—	3.2 pmol	1 µL	—
Reverse primer (3.2 µM)		—	2 µL		—	1 µL
Deionized water (RNase/DNase-free)	Varies based on template and primer volume	8 µL	8 µL	Varies based on template and primer volume	4 µL	4 µL

(continued)

Component	Standard reaction (20 µL)			Standard reaction (10 µL)		
	Quantity per reaction	Example Forward	Example Reverse	Quantity per reaction	Example Forward	Example Reverse
Template	See “Template quantity” on page 13	2 µL ^{[1],[2]}	2 µL ^{[1],[2]}	See “Template quantity” on page 13	1 µL ^{[1],[2]}	1 µL ^{[1],[2]}
Total volume	20 µL	20 µL	20 µL	10 µL	10 µL	10 µL

^[1] e.g. 150–300ng/µL of dsDNA^[2] Concentration of template may affect volume, if template volume differs, adjust the volume of water in the reaction mix.**Note:** Store on ice and protected from light.

- Seal the plate with MicroAmp™ Clear Adhesive Film.
- Vortex the plate for 2–3 seconds, then centrifuge in a swinging bucket centrifuge at 1,000 × g for 5–10 seconds to bring the contents to the bottom of the wells.

Note: Bubbles may be present in the wells, but they do not adversely affect the reaction.

Using BigDye™ Terminator v1.1 & v3.1 5X Sequencing Buffer to dilute sequencing reactions

Some cycle sequence reactions may be optimized using diluted BigDye™ Terminator Ready Reaction Mix. The BigDye™ Terminator Ready Reaction Mix is provided at a 2.5X concentration and can be diluted using BigDye™ Terminator v1.1 and v3.1 5X Sequencing Buffer to a final end reaction concentration of 1X.

Calculate the volume of BigDye™ Terminator v1.1 and v3.1 5X Sequencing Buffer to use:

$$0.5 * ((\text{total reaction volume})/2.5) - \text{volume of BigDye™ Terminator Ready Reaction Mix}$$

Note: Dilution of the BigDye™ Terminator v1.1 and v3.1 5X Sequencing Buffer without optimization, may cause deterioration of sequencing quality. We can not guarantee the performance of BigDye™ Terminator chemistry when it is diluted.

Component	Diluted reaction (0.5X)		
	Quantity per reaction	Example Forward	Example Reverse
BigDye™ Terminator v1.1 Ready Reaction Mix	4 µL	4 µL	4 µL
BigDye™ Terminator v1.1 & v3.1 5X Sequencing Buffer	2 µL	2 µL	2 µL
Forward primer (3.2 µM)	3.2 pmol	2 µL ^[1]	—
Reverse primer (3.2 µM)		—	2 µL ^[1]

(continued)

Component	Diluted reaction (0.5X)		
	Quantity per reaction	Example Forward	Example Reverse
Deionized water (RNase/DNase-free)	Varies based on template and primer volume	10 μ L	10 μ L
Template	See “Template quantity” on page 13	2 μ L ^{[2],[3]}	2 μ L ^{[2],[3]}
Total volume	20 μL	20 μL	20 μL

^[1] The control primer is provided at 0.8pmol/ μ L. Use 8 μ L to obtain a total primer quantity of 3.2 pmol per 20 μ L reaction. If primer volume differs, adjust the volume of water in the reaction mix.

^[2] e.g. 150-300ng/ μ L of dsDNA

^[3] Concentration of template may affect volume. If template volume differs, adjust the volume of water in the reaction mix.

Perform cycle sequencing

Run the sequencing reactions

1. Place the tubes or plate or plates in a thermal cycler and set the correct volume:
 - 20 μ L for microcentrifuge tubes or 96-well reaction plates
 - 10 μ L for 384-well reaction plates
2. Perform cycle sequencing:

Parameter	Stage/step				
	Incubate	25 cycles			Hold
		Denature	Anneal	Extend	
Ramp rate	—	1°C/second			
Temperature	96°C	96°C	50°C	60°C	4°C
Time (mm:ss)	01:00	00:10	00:05	04:00 ^[1]	Hold until ready to purify.

^[1] Shorter extension times can be used for short templates.

3. Briefly centrifuge the reactions.

STOPPING POINT Samples can be stored at 4°C overnight or at –20°C for up to a year.

Proceed to Chapter 4, “Purify the sequencing reactions”

4

Purify the sequencing reactions

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- Purify the sequencing reactions with ethanol/EDTA precipitation 21

Purifying the sequencing reactions is necessary to avoid the following issues.

Issue	Description
Unincorporated dye terminators	Residual dye terminators can negatively affect electrokinetic injections, obscure data in the first part of the sequence, and potentially interfere with accurate basecalling.
Excessive salts and dNTPs	High levels of salts and dNTPs can decrease peak height and signal intensity.

Two different methods to purify sequencing products are provided in this chapter. For a list of the required materials for each method, see “Required materials not supplied” on page 9.

Purify sequencing reactions with the BigDye XTerminator™ Purification Kit

This procedure is one example of the purification protocol using the BigDye XTerminator™ Purification Kit. It takes approximately 40 minutes to complete.

For detailed instructions and a complete list of options, see the *BigDye XTerminator™ Purification Kit User Guide* (Pub. No. [4374408](#)).

Note: Use disposable reagent reservoirs and an 8-channel P200 pipette, if available, to facilitate the clean-up process. Use wide bore pipet tips when pipetting the BigDye XTerminator™ reagent.

Note: If you use a 3730x/ DNA Analyzer, standard heat sealing techniques can be used. This protocol describes plate sealing with MicroAmp™ Clear Adhesive Film. The MicroAmp™ Clear Adhesive Film must be removed before loading the plate on the instrument.

1. Centrifuge the cycle-sequencing reaction plate at 1,000 × *g* for 1 minute.
2. Immediately before pipetting, mix the BigDye XTerminator™ Solution by inversion 10 times or until the solution is homogeneous.

3. Add the following components (in the order indicated) to each well of the reaction plate.

IMPORTANT! Remix the BigDye XTerminator™ Solution every minute to prevent phase separation.

Component	Volume per 10 µL reaction	Volume per 20 µL reaction
SAM solution	45 µL	90 µL
BigDye XTerminator™ Solution	10 µL	20 µL
Total volume	55 µL	110 µL

4. Proceed to “Seal the reaction plate” on page 20.

Vortex, then centrifuge the reaction plate

1. Inspect the reaction plate to confirm that all edges, corners, and spaces between the rows and columns of the wells are completely sealed.
2. Firmly attach the plate to the vortexer.
3. Vortex the plate for 20 minutes (96-well plate) or 30 minutes (384-well plate), using the settings indicated.

IMPORTANT! Do not vortex beyond the specified time.

Vortexer	Plate type	Speed or setting
Thermo Scientific™ Digital Vortex Mixer	96-well	1,800 rpm
	384-well	2,000 rpm
Digital Vortex-Genie™ 2	96-well	1,800 rpm
	384-well	2,000 rpm
Eppendorf™ MixMate™	96-well	1,800 rpm
	384-well	2,600 rpm
IKA™ MS 3 Digital Orbital Shaker	96-well or 384-well	1,800 rpm (Mode B)
IKA™ Vortex 3	96-well or 384-well	Setting 5 ^[1]
Taitec MicroMixer E-36	96-well or 384-well	Maximum
Union Scientific™ Vertical Shaker ^[2]	96-well or 384-well	Setting 100

^[1] Use the maximum setting that does not cause the vortexer to become unstable.

^[2] If needed, add additional plates to meet the mass requirements.

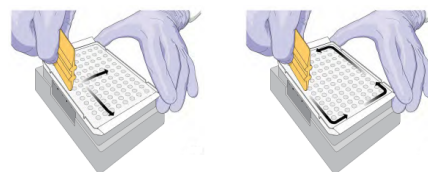
4. Centrifuge the plate at 1,000 × g in a swinging-bucket centrifuge for 2 minutes.
5. Immediately proceed to capillary electrophoresis.

STOPPING POINT If you cannot run capillary electrophoresis immediately, store the reaction plate as described (see “Guidelines for storing the reaction plate” on page 21).

Seal the reaction plate

IMPORTANT! Apply firm pressure to the adhesive film during application to allow a tight, leak-proof seal during vortexing.

1. Place the reaction plate on a MicroAmp™ Splash-Free 96-Well Base, then wipe off any liquid on the surface of the plate.
2. Remove a single adhesive film from the box. While holding the film backing-side up, bend both tabs upward.
3. In one swift movement, peel back the white backing from the center sealing surface. Do not touch the center sealing surface.
4. While holding the film by the tabs, lower the film onto the reaction plate (adhesive side facing the plate). Make sure that the film completely covers all wells of the reaction plate.
5. While applying firm downward pressure, move the applicator slowly across the film, both horizontally and vertically.
6. Repeat step 5 five times. While applying pressure, run the edge of the applicator along all four sides of the outer border of the film.
7. Inspect the reaction plate to confirm that all wells are sealed.
The plate is properly sealed when an imprint of each well is visible on the surface of the film.
8. Proceed to “Vortex, then centrifuge the reaction plate” on page 19.



Guidelines for storing the reaction plate

Sequencing reactions purified with the BigDye XTerminator™ Purification Kit are stable at room temperature for up to 48 hours.

Store reaction plates covered with adhesive film, septa, or heat seal film at room temperature for up to 48 hours.

Note: After removing the reaction plate from storage, centrifuge the plate at $1,000 \times g$ in a swinging-bucket rotor for 2 minutes, then proceed to run capillary electrophoresis.

Purify the sequencing reactions with ethanol/EDTA precipitation

The following protocol takes approximately 90 minutes.

Note: This method helps produce a clean signal, but it can cause subtle loss of small molecular weight fragments.

IMPORTANT! Absolute ethanol absorbs water from the atmosphere, which gradually decreases its concentration and can affect sequencing results. Store appropriately and replace frequently.

1. Prepare a 125 mM EDTA solution from 0.5 M EDTA, pH 8.0.
2. Prepare 70% ethanol using absolute ethanol.

IMPORTANT!

- Prepare a fresh 70% ethanol solution each day. Discard any unused solution at the end of the day.
- Do NOT pre-mix 125 mM EDTA solution and absolute ethanol. Premixing can cause precipitation of the EDTA.

3. Briefly centrifuge the sequencing plate in a swinging bucket centrifuge at $1,000 \times g$ for 5–10 seconds.
4. Remove the MicroAmp™ Clear Adhesive Film from the plate.
5. Add the following in order:

Component	Volume	
Sequencing reaction (starting volume)	10 μ L	20 μ L
125 mM EDTA solution	2.5 μ L	5 μ L
Absolute ethanol	30 μ L	60 μ L
Total volume	42.5 μ L/well	85 μ L/well

IMPORTANT! Dispense EDTA directly into the sample in each well. If droplets are visible on the wall of the well, briefly centrifuge the plate to ensure that the EDTA mixes with the sequencing reactions.

6. Seal the plate with MicroAmp™ Clear Adhesive Film.
7. Vortex the plate for 2–3 seconds, then centrifuge at $1,000 \times g$ for 5–10 seconds.
8. Incubate the plate at room temperature for 15 minutes.

IMPORTANT! Timing of this step is critical.

9. Centrifuge the plate in a swinging bucket centrifuge at $1,870 \times g$ for 45 minutes at 4°C .

IMPORTANT! Proceed to the next step immediately. If there is a delay between steps, centrifuge the plate for an extra 2 minutes, then proceed to the next step immediately.

10. Slowly remove the MicroAmp™ Clear Adhesive Film to prevent disruption of the pellet. Place 4 layers of absorbent paper into the centrifuge, then carefully invert the plate onto the paper without dislodging the pellet. Centrifuge at $185 \times g$ for 1 minute.

Do not tip out the liquid first. Do not tap the plate to help with liquid removal.

11. Add 70% ethanol to each well.

Starting reaction volume	Volume 70% ethanol
10 μL	30 μL
20 μL	60 μL

12. Seal the plate with MicroAmp™ Clear Adhesive Film, then centrifuge at $1,870 \times g$ for 15 minutes at 4°C .

IMPORTANT! Proceed to the next step immediately. If there is a delay between steps, centrifuge the plate for an extra 2 minutes, then proceed to the next step immediately.

13. Slowly remove the MicroAmp™ Clear Adhesive Film to prevent disruption of the pellet. Place 4 layers of absorbent paper into the centrifuge, then carefully invert the plate onto the paper towel without dislodging the pellet. Centrifuge at $185 \times g$ for 1 minute.

Note: Do not tip out the liquid first. Do not tap the plate to help with liquid removal.

14. Allow the plate to air dry, face up and protected from light, for 5–10 minutes at room temperature.

Note: Alternatively, seal the plate with MicroAmp™ Clear Adhesive Film, then store protected from light at 4°C for CE preparation or -20°C until use.



Perform capillary electrophoresis

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Capillary electrophoresis guidelines

- We recommend that you verify the quality of the spectral calibration before proceeding. To generate a new spectral calibration, use the appropriate sequencing standard for your instrument.
- Existing mobility files can be used with their respective platforms.
- Resuspend purified and dried sequencing reactions in 10 µL of Hi-Di™ Formamide. Do not heat samples to resuspend. Run samples as soon as possible after resuspension.

Note: It is not necessary to resuspend samples purified with the BigDye XTerminator™ Purification Kit.

- Standard heat seal consumables can only be used for the 3730x/ DNA Analyzer.
- Select the correct mobility file for your instrument, polymer, and dye chemistry.
- You need to use the BDx run modules if you used the BigDye XTerminator™ Purification Kit for sequencing reaction clean up.
- Check **At PCR Stop** in the **Basecalling** tab when analyzing PCR products with the following applications or instruments. Do not select this setting when performing *de novo* or plasmid sequencing.
 - SeqStudio™ Flex Series Genetic Analyzer
 - SeqStudio™ Genetic Analyzer
 - Sequence Quality Check application in InnoviGene™ Suite
 - Sequencing Analysis Software
 - Quality Check (QC) software on the Thermo Fisher™ Connect Platform
 - SeqScape™ Software
 - Variant Reporter™ Software

Calibration guidelines

Sequencing standards provide a sample for multi-color spectral correction for the dye emission overlap of the BigDye™ Terminators.

Spectral calibrations for the BigDye™ Terminator v1.1 are not compatible with BigDye™ Terminator v3.1.

Perform new spectral calibrations after you install a capillary array or move capillaries in the detection areas.

See your specific instrument user guide for more information on calibration.

Sequencing standards

Instrument	Dye set	Standards for spectral calibration ^[1]	Cat. no.
SeqStudio™ Genetic Analyzer	E	3500/Flex Series Sequencing Standard, BigDye™ Terminator v1.1	4404314
SeqStudio™ Flex Series Genetic Analyzer			
3500/3500xL Genetic Analyzer			
3730/3730xL DNA Analyzer		3730/3730xL DNA Analyzer Sequencing Standards, BigDye™ Terminator v1.1	4336799

^[1] See the sequencing standard product insert for instructions about performing spectral calibrations.

Electrophoresis on the 3500/3500xL Genetic Analyzer

IMPORTANT! Use BDX run modules only if you prepare samples with the BigDye XTerminator™ Purification Kit. Use non-BDX run modules for samples purified with other methods.

Note: You need to specify the mobility file in the analysis settings.

Item	Module name	Polymer	Capillary length	Mobility files
Dye set E (BigDye™ Terminator v1.1)	RapidSeq36_POP4	POP-4™	36-cm	KB_3500_POP4_BDTv1.mob
	RapidSeq36_POP4xL	POP-4™	36-cm	
	BDxRapidSeq36_POP4	POP-4™	36-cm	
	BDxRapidSeq36_POP4xL	POP-4™	36-cm	
	RapidSeq36_POP6	POP-6™	36-cm	KB_3500_POP6_BDTv1.mob
	RapidSeq36_POP6xL	POP-6™	36-cm	
	BDxRapidSeq36_POP6	POP-6™	36-cm	
	BDxRapidSeq36_POP6xL	POP-6™	36-cm	

(continued)

Item	Module name	Polymer	Capillary length	Mobility files
Dye set E (BigDye™ Terminator v1.1)	MicroSeq50_POP6	POP-6™	50-cm	KB_3500_POP6_BDTv1.mob
	MicroSeq50_POP6xl	POP-6™	50-cm	
	StdSeq50_POP6	POP-6™	50-cm	
	StdSeq50_POP6xl	POP-6™	50-cm	
	BDxStdSeq50_POP6	POP-6™	50-cm	
	BDxStdSeq50_POP6xl	POP-6™	50-cm	
	RapidSeq50_POP6	POP-6™	50-cm	
	RapidSeq50_POP6xl	POP-6™	50-cm	
	BDxRapidSeq50_POP6	POP-6™	50-cm	
	BDxRapidSeq50_POP6xl	POP-6™	50-cm	
	FastSeq50_POP6	POP-6™	50-cm	
	FastSeq50_POP6xl	POP-6™	50-cm	
	BDxFastSeq50_POP6	POP-6™	50-cm	
	BDxFastSeq50_POP6xl	POP-6™	50-cm	
	RapidSeq36_POP7	POP-7™	36-cm	KB_3500_POP7_BDTv1.mob
	RapidSeq36_POP7xl	POP-7™	36-cm	
	BDxRapidSeq36_POP7	POP-7™	36-cm	
	BDxRapidSeq36_POP7xl	POP-7™	36-cm	
	FastSeq36_POP7	POP-7™	36-cm	
	FastSeq36_POP7xl	POP-7™	36-cm	
	BDxFastSeq36_POP7	POP-7™	36-cm	
	BDxFastSeq36_POP7xl	POP-7™	36-cm	
	MicroSeq50_POP7	POP-7™	50-cm	
	MicroSeq50_POP7xl	POP-7™	50-cm	
	StdSeq50_POP7	POP-7™	50-cm	
	StdSeq50_POP7xl	POP-7™	50-cm	
	BDxStdSeq50_POP7	POP-7™	50-cm	
	BDxStdSeq50_POP7xl	POP-7™	50-cm	

(continued)

Item	Module name	Polymer	Capillary length	Mobility files
Dye set E (BigDye™ Terminator v1.1)	RapidSeq50_POP7	POP-7™	50-cm	KB_3500_POP7_BDTv1.mob
	RapidSeq50_POP7xl	POP-7™	50-cm	
	BDxRapidSeq50_POP7	POP-7™	50-cm	
	BDxRapidSeq50_POP7xl	POP-7™	50-cm	
	FastSeq50_POP7	POP-7™	50-cm	
	FastSeq50_POP7xl	POP-7™	50-cm	
	BDxFastSeq50_POP7	POP-7™	50-cm	
	BDxFastSeq50_POP7xl	POP-7™	50-cm	
	ShortReadSeq50_POP7	POP-7™	50-cm	
	ShortReadSeq50_POP7xl	POP-7™	50-cm	
	BDxShortReadSeq50_POP7	POP-7™	50-cm	
	BDxShortReadSeq50_POP7xl	POP-7™	50-cm	

Performing electrophoresis

For information about performing sample electrophoresis on the 3500/3500xL Genetic Analyzer, see *3500/3500xL Genetic Analyzer with 3500 Series Data Collection Software v3.3 User Guide* Pub. No. [100079380](#)).

Electrophoresis on the 3730/3730xl DNA Analyzer

IMPORTANT! Use BDx run modules only if you prepare samples with the BigDye XTerminator™ Purification Kit. Use non-BDx run modules for samples purified with other methods.

Note: You need to specify the mobility file in the analysis settings.

Item	Module name	Polymer	Capillary length	Mobility files
Dye set E (BigDye™ Terminator v1.1)	StdSeq36_POP6	POP-6™	36-cm	KB_3730_POP6_BDTv1.mob
	BDX_StdSeq36_POP6	POP-6™	36-cm	
	RapidSeq36_POP6	POP-6™	36-cm	
	BDX_RapidSeq36_POP6	POP-6™	36-cm	
	LongSeq50_POP6	POP-6™	50-cm	

(continued)

Item	Module name	Polymer	Capillary length	Mobility files
Dye set E (BigDye™ Terminator v1.1)	BDX_LongSeq50_POP6	POP-6™	50-cm	KB_3730_POP6_BDTv1.mob
	StdSeq36_POP7	POP-7™	36-cm	KB_3730_POP7_BDTv1.mob
	BDX_StdSeq36_POP7	POP-7™	36-cm	
	TargetSeq36_POP7	POP-7™	36-cm	
	BDX_TargetSeq36_POP7	POP-7™	36-cm	
	RapidSeq36_POP7	POP-7™	36-cm	
	BDX_RapidSeq36_POP7	POP-7™	36-cm	
	FastSeq36_POP7	POP-7™	36-cm	
	BDX_FastSeq36_POP7	POP-7™	36-cm	
	FastSeq50_POP7	POP-7™	50-cm	
	BDX_FastSeq50_POP7	POP-7™	50-cm	
	LongSeq50_POP7	POP-7™	50-cm	
	BDX_LongSeq50_POP7	POP-7™	50-cm	
	XLRSeq50_POP7	POP-7™	50-cm	
	BDX_XLRSeq50_POP7	POP-7™	50-cm	

Performing electrophoresis

For information about performing sample electrophoresis on the 3730xl DNA Analyzer, see:

- *3730xl DNA Analyzer with 3730xl Data Collection Software 5 User Guide* (Pub. No. [100077621](#))
- *Applied Biosystems™ 3730/3730xl DNA Analyzer Maintenance and Troubleshooting Guide* (Pub. No. [4359473](#))

Electrophoresis on the SeqStudio™ Genetic Analyzer

IMPORTANT! Use BDX run modules only if you prepare samples with the BigDye XTerminator™ Purification Kit. Use non-BDX run modules for samples purified with other methods.

Note: The mobility information is automatically selected based on the dye set that is used to collect the data.

Item	Module name	Polymer	Capillary length	Mobility files
Dye set E (BigDye™ Terminator v1.1)	ShortSeq	N/A (Cartridge)	N/A (Cartridge)	Automatic per dye set designation
	ShortSeq_BDX	N/A (Cartridge)	N/A (Cartridge)	
	MediumSeq	N/A (Cartridge)	N/A (Cartridge)	
	MediumSeq_BDX	N/A (Cartridge)	N/A (Cartridge)	
	LongSeq	N/A (Cartridge)	N/A (Cartridge)	
	LongSeq_BDX	N/A (Cartridge)	N/A (Cartridge)	

Electrophoresis on the SeqStudio™ Flex Series Genetic Analyzer

IMPORTANT! Use BDX run modules only if you prepare samples with the BigDye XTerminator™ Purification Kit. Use non-BDX run modules for samples purified with other methods.

Note: The mobility information is automatically selected based on the dye set that is used to collect the data.

Item	Module name	Polymer	Capillary length	Mobility files
Dye set E (BigDye™ Terminator v1.1)	RapidSeq36_POP7	POP-7™	36-cm	Automatic per dye set designation
	RapidSeq36_POP7xl	POP-7™	36-cm	
	BDxRapidSeq36_POP7	POP-7™	36-cm	
	BDxRapidSeq36_POP7xl	POP-7™	36-cm	
	FastSeq36_POP7	POP-7™	36-cm	
	FastSeq36_POP7xl	POP-7™	36-cm	
	BDxFastSeq36_POP7	POP-7™	36-cm	
	BDxFastSeq36_POP7xl	POP-7™	36-cm	

(continued)

Item	Module name	Polymer	Capillary length	Mobility files
Dye set E (BigDye™ Terminator v1.1)	RapidSeq36_POP6	POP-6™	36-cm	Automatic per dye set designation
	RapidSeq36_POP6xl	POP-6™	36-cm	
	BDxRapidSeq36_POP6	POP-6™	36-cm	
	BDxRapidSeq36_POP6xl	POP-6™	36-cm	
	RapidSeq36_POP4	POP-4™	36-cm	
	RapidSeq36_POP4xl	POP-4™	36-cm	
	BDxRapidSeq36_POP4	POP-4™	36-cm	
	BDxRapidSeq36_POP4xl	POP-4™	36-cm	
	ShortReadSeq50_POP7	POP-7™	50-cm	
	ShortReadSeq50_POP7xl	POP-7™	50-cm	
	BDxShortReadSeq50_POP7	POP-7™	50-cm	
	BDxShortReadSeq50_POP7xl	POP-7™	50-cm	
	RapidSeq50_POP7	POP-7™	50-cm	
	RapidSeq50_POP7xl	POP-7™	50-cm	
	BDxRapidSeq50_POP7	POP-7™	50-cm	
	BDxRapidSeq50_POP7xl	POP-7™	50-cm	
	FastSeq50_POP7	POP-7™	50-cm	
	FastSeq50_POP7xl	POP-7™	50-cm	
	BDxFastSeq50_POP7	POP-7™	50-cm	
	BDxFastSeq50_POP7xl	POP-7™	50-cm	
	StdSeq50_POP7	POP-7™	50-cm	
	StdSeq50_POP7xl	POP-7™	50-cm	
	BDxStdSeq50_POP7	POP-7™	50-cm	
	BDxStdSeq50_POP7xl	POP-7™	50-cm	
	RapidSeq50_POP6	POP-6™	50-cm	
	RapidSeq50_POP6xl	POP-6™	50-cm	
	BDxRapidSeq50_POP6	POP-6™	50-cm	
	BDxRapidSeq50_POP6xl	POP-6™	50-cm	

(continued)

Item	Module name	Polymer	Capillary length	Mobility files
Dye set E (BigDye™ Terminator v1.1)	FastSeq50_POP6	POP-6™	50-cm	Automatic per dye set designation
	FastSeq50_POP6xl	POP-6™	50-cm	
	BDxFastSeq50_POP6	POP-6™	50-cm	
	BDxFastSeq50_POP6xl	POP-6™	50-cm	
	StdSeq50_POP6	POP-6™	50-cm	
	StdSeq50_POP6xl	POP-6™	50-cm	
	BDxStdSeq50_POP6	POP-6™	50-cm	
	BDxStdSeq50_POP6xl	POP-6™	50-cm	
	MicroSeqID50_POP6	POP-6™	50-cm	
	MicroSeqID50_POP6xl	POP-6™	50-cm	



Troubleshooting Sanger sequencing data

Troubleshooting poor Sanger sequencing quality

Common sources of noise	How to recognize the source	Page Number
No signal	Little to no raw signal.	33
Low signal intensity	The raw signal is below the recommended minimum relative fluorescence units (RFU).	35
Mixed sequence throughout	Mixed sequence content throughout the length of the trace.	37
Mixed sequence up to or after a point	Mixed sequence content starting at a specific point.	38
Poor mobility correction	Peaks overlapped and unevenly spaced	39
Dye blobs	Large broad peak normally seen at 85–90 bp or 125–130 bp.	40
Signal saturation	The raw signal exceeds the recommended maximum RFU. Note: Excessive raw signal causes pull-up peaks in the analyzed data, which can incorrectly be identified as mixed bases.	41

For more information on Sanger sequencing symptoms and troubleshooting, see the *DNA Sequencing by Capillary Electrophoresis Chemistry Guide Second Edition* (Pub. No. [4305080](#)).

Recommended raw signal ranges

Different capillary electrophoresis instruments have different recommended fluorescence ranges and levels at which signal is saturated. Optimal data quality depends on maintaining signal levels within the appropriate range for your instrument.

Relative fluorescent units (RFU) are the standard measurement used in fluorescent detection systems with charged coupled device (CCD) technology. When dye-labeled fragments pass through the detection window, they are excited by a laser, emitting photons that are captured by the CCD. Fragments with higher RFU values indicate stronger signal intensity and better dye-labeled amplification compared to those with lower RFU values.

To support reliable results, ensure that the raw fluorescent signals remain in the suggested upper and lower signal ranges specified for your instrument model. The troubleshooting sections that follow will help you identify and resolve issues related to raw fluorescent signals that fall outside these recommended ranges.

Instrument	Recommended raw signal range (Sequencing)	Fluorescence saturation
SeqStudio™ Genetic Analyzer	500–10,000 RFU	32,000 RFU
SeqStudio™ Flex Series Genetic Analyzer	500–10,000 RFU	32,000 RFU
3500/3500xL Genetic Analyzer	500–10,000 RFU	32,000 RFU
3730xl DNA Analyzer	500–10,000 RFU	32,000 RFU

Signal is in range. Peak heights are 2,000 RFU on average.

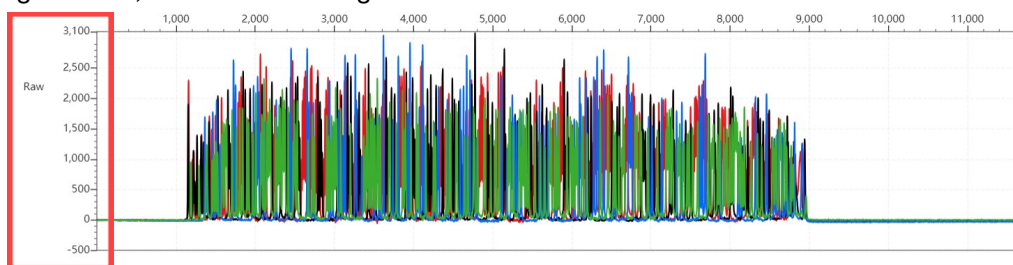


Figure 1 Expected result

The use of controls

The use of controls is recommended to simplify troubleshooting.

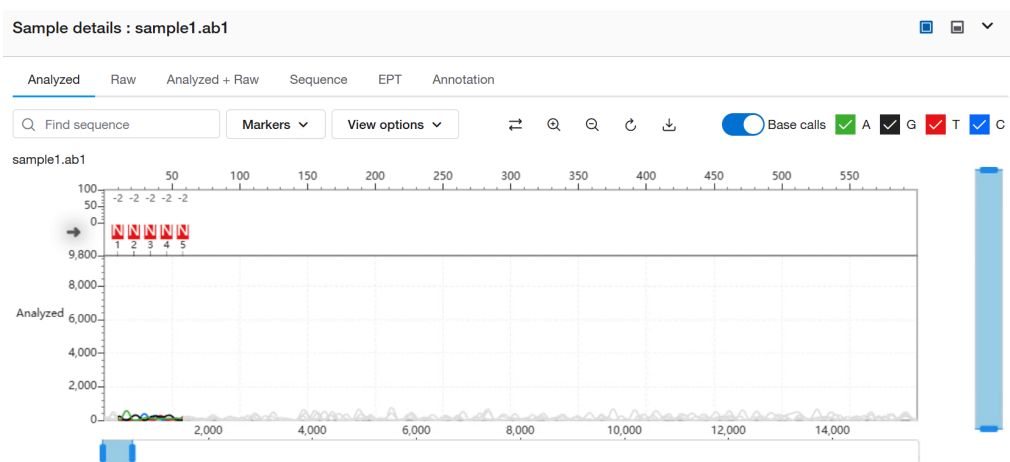
- pREF-BDT™ Control DNA—Results can help you determine whether failed reactions are caused by poor template quality or sequencing reaction failure. See “Control template” on page 10.
- Big Dye Terminator Sequencing standards—Results can help you distinguish between chemistry problems and instrument problems.
- Use of Hi-Di™ Formamide only injection (*Optional*)—Results can help distinguish sample problems and instrument problems related to contamination.

No signal

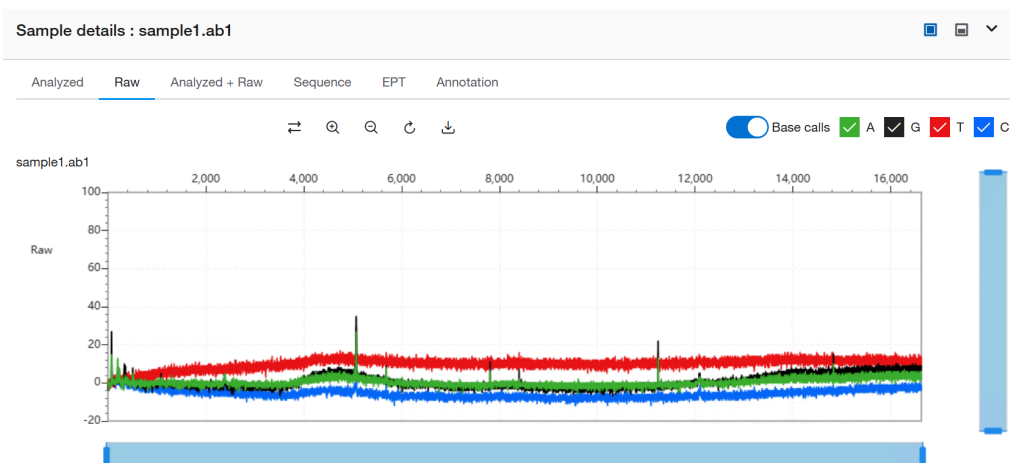
Lack of signal can be determined by looking at the scale of signal produced in the raw data view. Signal should be above the minimum recommended RFU. See “Recommended raw signal ranges” on page 31. Lack of signal can be caused by many factors. These include problems in the sequencing reaction (template quantity/quality), thermal cycler malfunction (plate failure), and capillary electrophoresis failure (failing laser, air bubbles in lines, etc.).

Example of no signal due to hardware failure or a failed reaction

Analyzed data view



Raw data view



No signal: possible causes and recommended actions

Possible cause	Recommended action
Insufficient template	Quantify the DNA template.
	Increase the amount of DNA in the sequencing reactions. See “Template quantity” on page 13.
Inhibitory contaminant in the template	Clean up the template. See Chapter 2, “Prepare templates”.
Insufficient primer	Quantify the primer and increase the amount of primer in the sequencing reactions if needed.
Primer has no annealing site	Use a primer that is complementary to the template.
Poor primer design or incorrect primer sequence	Review the primer design and if needed redesign the primer.
Missing reagent	Repeat the reactions, carefully following the protocol. Use pREF-BDT™ Control DNA to confirm reagent workflow performance.
Old or mishandled reagents	Use fresh reagents.
Thermal cycler malfunction	Test the thermal cycler according to the instructions provided by the manufacturer. Then, repeat the reactions.
Thermal cycling conditions incorrect	Calibrate the thermal cycler regularly.
	Use the correct thermal cycling parameters.
	Use the correct tubes or plates for your thermal cycler.
	Set the ramp rate to 1°C/second.
Extension products lost during reaction cleanup	Use the correct centrifuge speeds and times for the precipitation procedures and the centrifugation column or centrifugation plate procedures.
	Check that the ethanol concentration is correct for the precipitation protocols.
Extension products not resuspended	Carefully resuspend the sample pellet in Hi-Di™ Formamide.
Electrokinetic injection failure	Run the Sequencing standard to confirm the performance of the instrument and consumables.
	Confirm the BDX run module is being used for BigDye XTerminator™-purified samples.
	Confirm the correct volume is in the well.
	Confirm that the sample plate does not have a bubble at the bottom of the well. Briefly centrifuge to remove bubble.

Low signal

Low signal intensity can be caused by many factors including thermal cycler malfunction (in the case of an entire plate failure) and insufficient sequencing template quantity/quality.

Examples of low signal intensity

The examples below show severely low signal traces.

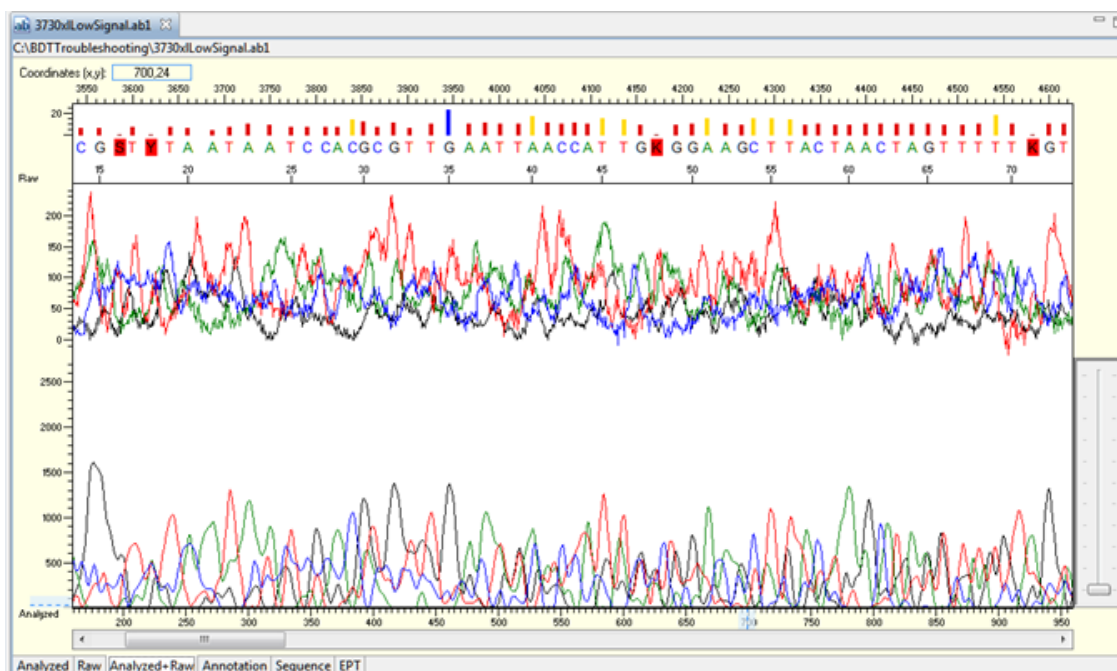


Figure 2 Severely low signal intensity

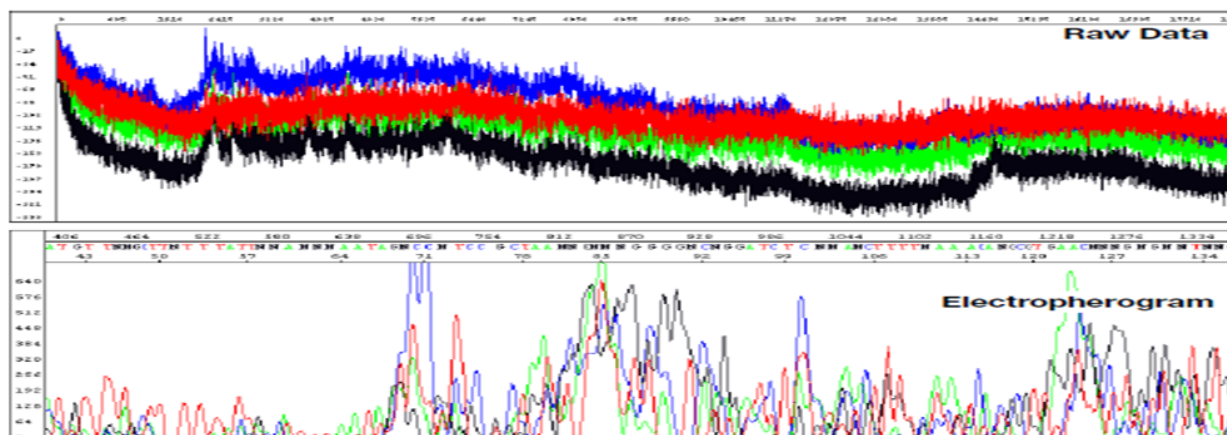


Figure 3 Severely low signal intensity due to hardware failure or a failed reaction

More severe signal issues are often related to poor injection, failed reaction, or a blocked or broken capillary.

Low signal possible causes and recommended actions

If sequencing signal is weak, verify that DNA quality, PCR purification, and sequencing reaction purification were performed correctly.

To increase signal strength, adjust one or more of the following parameters:

- Increase the injection time or the injection voltage (re-inject the sample).
- Increase the amount of primer or template in the cycle sequencing reaction.

Possible cause	Recommended action
Insufficient DNA in the sequencing reactions	Increase DNA quantity in the sequencing reactions. See “Template quantity” on page 13.
	Load or inject more of the resuspended sequencing reactions by changing the run module and increasing the injection time. See the appropriate instrument user guide for more information.
Poor primer quality or quantity	Prepare a fresh working stock of primer or order new primer. Use 0.32 μM in the final reaction.
Degraded template	Prepare fresh DNA and repeat the reactions.
Poor PCR cleanup	Purify PCR products before use. See “DNA template amplification with PCR” on page 11.
Old or mishandled reagents	Use fresh reagents.
Thermal cycling conditions incorrect	Calibrate the thermal cycler regularly.
	Use the correct thermal cycling parameters.
	Use the correct tubes or plates for your thermal cycler.
	Set the ramp rate to 1°C/second.
Insufficient Ready Reaction Mix in the reactions	The sequencing chemistry was diluted. For recommended procedures, see “Prepare the reactions” on page 14.

Mixed sequence throughout the electropherogram

Example of mixed sequence throughout

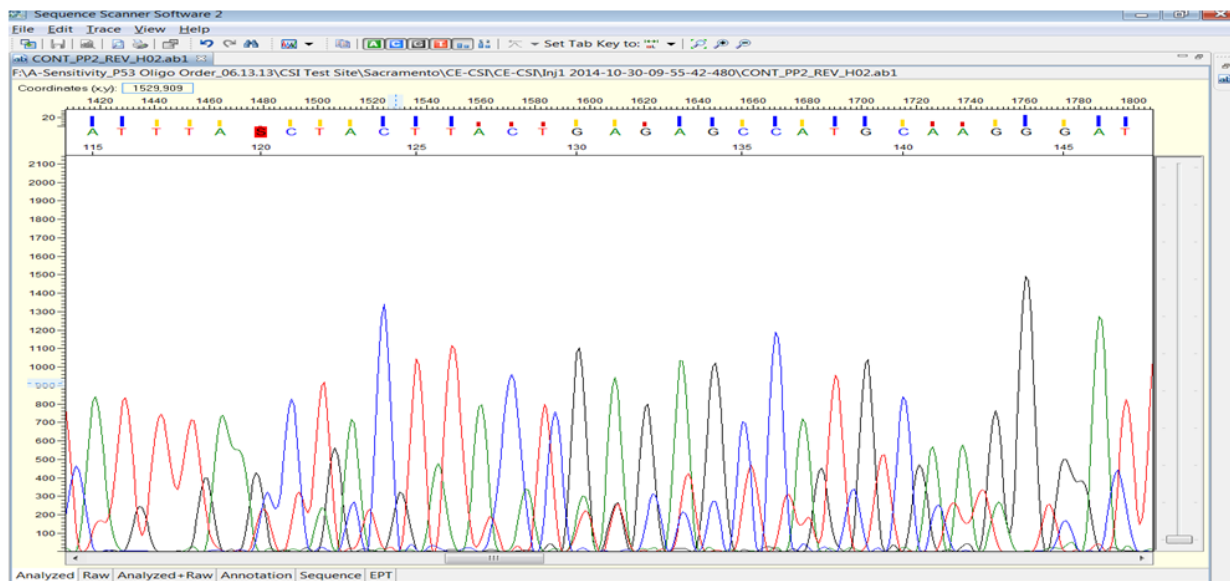


Figure 4 Secondary sequence contamination caused by well-to-well contamination of one sample into another

Mixed sequence throughout possible causes and recommended actions

Possible cause	Recommended action
Inhibitory contaminant in the template	Clean up the template.
Multiple templates in the sequencing reaction	Examine the template on an agarose gel to be sure that only one template is present.
Multiple priming sites	Verify that the primer has only one priming site. If needed, redesign the primer. See Appendix B, "Select sequencing primers".
Multiple primers when sequencing PCR products	Purify the PCR template to remove excess primers before sequencing.
Primer with N-1 contamination	Use an HPLC-purified primer.
High signal saturating the detector	Use less DNA in the sequencing reactions. See "Template quantity" on page 13. Reduce the amount loaded or injected from the resuspended sequencing reactions by lowering the injection time or injection voltage in the run module. See the appropriate instrument user guide for more information.

(continued)

Possible cause	Recommended action
Incorrect run module	Use a default run module.
Incorrect instrument settings	Use the correct instrument settings for BigDye™ Terminator chemistry.

Mixed sequence up to or after a certain point

Example of mixed sequence after a point



Figure 5 Example of mixed sequence content following a heterozygous insertion or deletion. Mixed sequence content is seen in both forward and reverse traces.

Mixed sequence up to or after a certain point possible causes and recommended actions

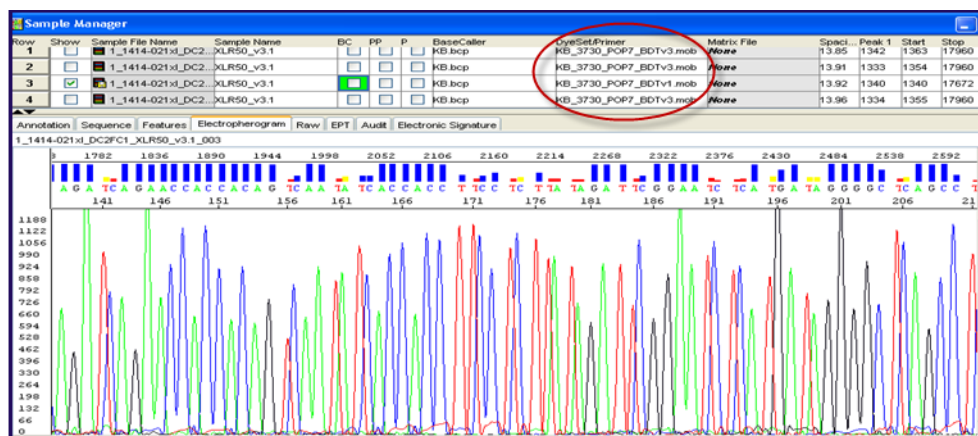
Possible cause	Recommended action
Mixed plasmid separation	Be sure that you have only one template.
Multiple PCR products	
Primer-dimer contamination in PCR sequencing	Optimize your PCR amplification.
	Be sure that there is no sequence complementarity between the two PCR primers.

(continued)

Possible cause	Recommended action
Primer-dimer contamination in PCR sequencing	Be sure that your sequencing primer does not overlap the sequences of the PCR primers. Use a Hot Start technique, such as with AmpliTaq Gold™ DNA Polymerase.
Slippage after repeat region in template	Try an alternative sequencing chemistry. Use an anchored primer. Some customers have gotten past poly(A) regions using a mixture of oligo dT18 primers with either a C, A, or G as the 3' terminal dinucleotide or 2-base anchors. See the <i>DNA Sequencing by Capillary Electrophoresis Chemistry Guide Second Edition</i> (Pub. No. 4305080) for more information.
Heterozygous insertion or deletion mutation (HIM)	Obtain forward and reverse sequence data and assemble using one of the following software platforms: - SeqScape™ Software SeqScape™ Software lists HIMs in the Mutations Report. Clicking the Base Change in the Mutations Report to view the mutation in the Project view. - Variant Reporter™ Software available on the Thermo Fisher™ Connect Platform Variant Reporter™ Software lists HIMs in the Project Summary Report.

Poor mobility correction

Example of poor mobility correction



Example electropherogram with the wrong mobility file selected.

Poor mobility correction possible causes and recommended actions

Possible cause	Recommended action
Incorrect dye set/primer (mobility) file	Use the correct dye set/primer file.
Incorrect Peak 1 location for data analysis	Select a new Peak 1 location.

Dye blobs

Dye blobs are caused by unincorporated dye terminators remaining in solution after purification of the cycle sequencing reactions. Unincorporated dye terminators from the BigDye™ Terminator v3.1 Cycle Sequencing Kit and BigDye™ Direct Cycle Sequencing Kit are most commonly seen to co-migrate with the ~ 85–90 bp labeled fragments. In more severe instances, these blobs can also be detected at ~ 60–65 bp and within 125–140 bp regions. Dye blobs are typically seen as broad “C” or “T” peaks, but can also show up as “G” blobs. Dye blobs are more common when first testing new sequencing purification methods.

Example of dye blobs

Figure 6 shows severe dye blobs in the 60–65bp, 85–100bp, and 125–140bp regions. Although the sequence quality appears high, the blobs obscure nearly 40 bp of the 100 bases displayed. This would make the sequence unsuitable for variant detection.

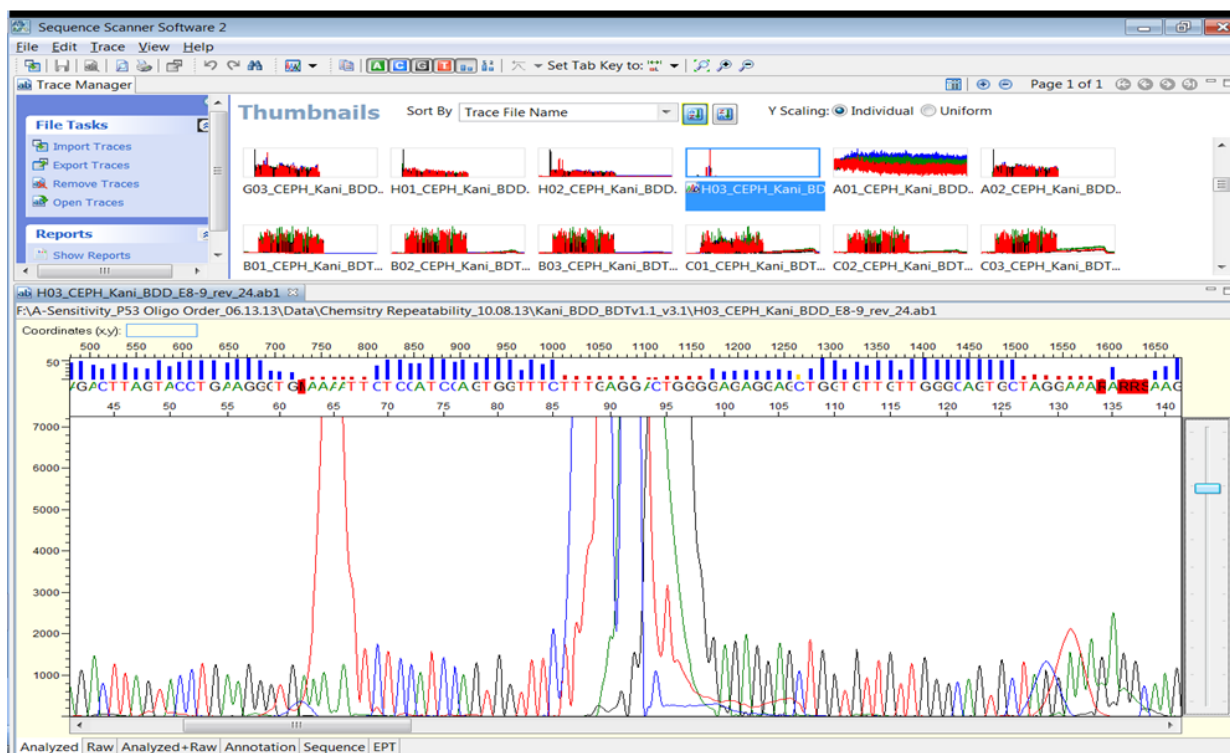


Figure 6 Severe dye blobs in the 60–65bp and 125–140bp regions

Dye blobs: possible causes and recommended actions

Possible cause	Recommended action
Sample bypassed the purification material when using spin columns/spin plates for sequencing clean-up.	Ensure transfer of the sample to the center of the purification material without the pipet tip touching the purification material. Sample dispensed along the walls of the clean-up column may bypass the purification material. Use a single channel pipette and/or position the tip directly above the spin column/plate while dispensing at low speed.
Ethanol concentration is too high during ethanol precipitation. This leads to unincorporated dye terminators and salts precipitating with the sequencing product.	Repeat procedure with correct ethanol concentration.
Incorrect ratio of BigDye XTerminator™ reagents.	Mix the BigDye XTerminator™ Solution by inversion 10 times or until the solution is homogeneous before dispensing. Use wide bore tips when pipetting BigDye XTerminator™ Solution. If you pre-mix the SAM/BigDye XTerminator™ Solution, ensure that the solution is well mixed before each sample well dispense step to maintain the appropriate ratio of reagents.
Insufficient mixing during the vortexing step when using the BigDye XTerminator™ Purification Kit.	Verify that the plate is firmly attached to the vortexer. Follow the protocol for vortexing. See <i>BigDye XTerminator™ Purification Kit Quick Reference</i> (Pub. No. 4383427) for recommended vortexers.

Signal saturation

High sample signal causes saturation of the sensor on the instrument. Signal saturation causes pull-up spectral peaks that cannot be corrected by spectral calibration. Extreme signal saturation will appear as mixed sequence.

Examples of signal saturation

The following figure shows examples of signal saturation. The red line indicates the maximum raw signal recommended.

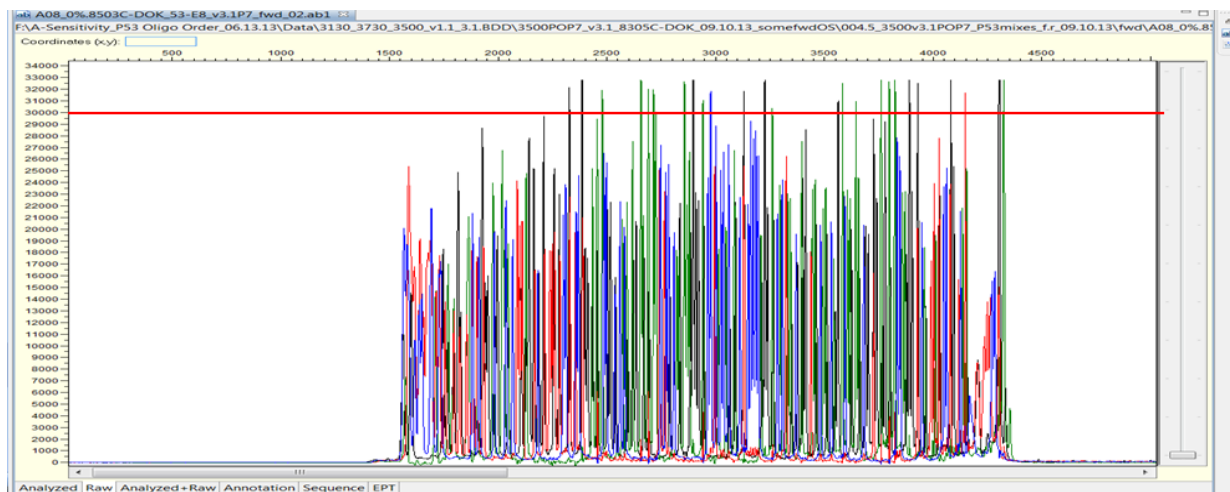
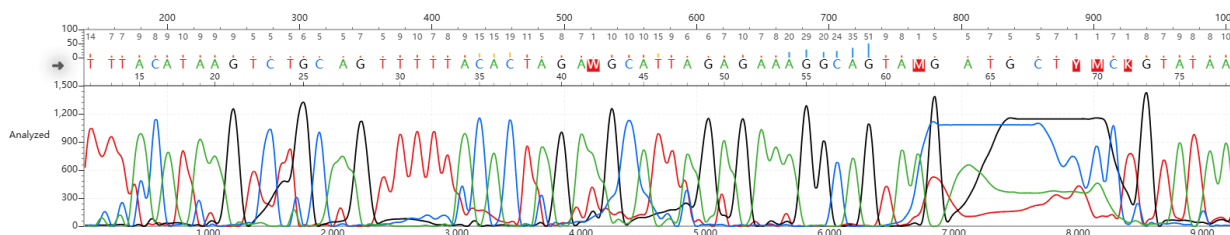


Figure 7 Signal saturation – Raw data view of minor signal saturation on a 3500 Genetic Analyzer

Example of extreme signal saturation

Mixed sequence in the **Analyzed** view. Mixed sequence can be due to extreme signal saturation caused by pull-up peaks. A quick review of the raw data can help diagnose a scenario such as this; the raw data view of the analyzed sample shown here is shown in the top panel in Figure 7.



Signal saturation: possible causes and recommended actions

Possible cause	Recommended action
Too much template was used in the sequencing reaction resulting in too much sequencing product.	If the sample has been on instrument <24 hours, reduce injection time in run module, then re-inject the sample.
	If the sample is purified with the BigDye XTerminator™ Purification Kit and has been on instrument <24 hours, carefully remove 10 µL of sample off the BigDye XTerminator™ solution in the plate, then add 10 µL of 0.1 mM EDTA to dilute the sample. Re-inject the sample using a standard run module (non-BigDye XTerminator™ module). Decrease the injection voltage and injection time to match the BDX run module.

(continued)

Possible cause	Recommended action
Too much template was used in the sequencing reaction resulting in too much sequencing product.	Repeat the sequencing reaction using less template.
Water was used as the injection solution.	Use Hi-Di™ Formamide or a 0.1 mM EDTA with UltraPure™ DNase/RNase-Free Distilled Water injection solution for samples. Note: Using water as an injection solution causes highly variable quantities of DNA to be injected, because there is no competition for the charged DNA/salts.



Select sequencing primers

Primer considerations

The following factors can have a significant effect on the quality of the sequencing data obtained in dye terminator cycle sequencing reactions with this kit:

- Choice of sequencing primer sequence
- Approach to primer purification

These decisions are particularly important when sequencing is done on capillary electrophoresis systems where signal strength is critical. Some of the guidelines provided below are based on information that is general knowledge, while others are based on practical experience gained by our scientists.

Primer guidelines

The method of primer purification and choice of M13-tailed or non-tailed sequencing primers can have a significant effect on the ease of reaction set up and the quality of the sequencing data that is obtained in dye terminator cycle sequencing reactions.

- Use HPLC-purification for all primers to minimize cycle sequencing noise and enable longer sequencing reads.
- Use M13 sequencing primers to simplify the sequencing workflow when sequencing multiple PCR products and to decrease the loss of valuable 5' unresolvable bases. With M13 sequencing primers, you make single forward and reverse reaction mixes, instead of multiple, primer-specific reaction mixes.

Note: The M13 forward or reverse sequence must be incorporated at the 5' end of the PCR primer to use the M13 sequencing primers.

Direction	Sequence	Notes
Forward M13	TGT AAA ACG ACG GCC AGT	Included in the kit.
Reverse M13	CAG GAA ACA GCT ATG ACC	Not included in the kit.

Optimize primer selection

Follow these guidelines to optimize primer selection:

- Primers should be at least 18 bases long to:
 - Ensure good hybridization
 - Minimize the chance of having a secondary hybridization site on the target DNA

- Avoid primers with secondary structure or that can hybridize to form dimers.
Several computer programs for primer selection are available. These programs help identify potential secondary structure problems and determine if a secondary hybridization site exists on the target DNA.
- Avoid runs of an identical nucleotide, especially guanine, where runs of four or more Gs should be avoided.
- Keep the G–C content in the 30–80% range.
- For cycle sequencing, primers with melting temperatures (T_m) above 45°C produce better results than primers with lower T_m s.
- For primers with a G–C content <50%, it may be necessary to extend the primer sequence beyond 18 bases to keep the $T_m > 45^\circ\text{C}$.

Primer Designer™ Tool

Primer Designer™ Tool is a free online tool to search for the appropriate PCR/Sanger primer pair from a database of >650,000 pre-designed primer pairs for resequencing the human exome.

Go to <http://www.thermofisher.com/primerdesigner> for more information, including a direct link to purchase the designed primers online.

Primers ordered through the tool are free of known SNPs and primer-dimers, highly target-specific, and used under universal PCR conditions. Primers can be ordered unmodified, M13-tailed, HPLC-purified or desalted. The primers are checked by mass spectrometry and strict bioinformatics metrics, with bench verification showing a >95% success rate.



pREF-BDT™ Control DNA

The 1,000 bp pREF-BDT™ Control DNA reference sequence includes the –21 M13 forward primer.

TGTAACGACGGCCAGT (–21 M13 forward primer)				
GAATTGTAAT	ACGACTCACT	ATAGGGCGAA	TTCGAGCTCG	40
GTACCCGGGG	ATCCTCTAGA	GTCGACCTGC	AGGCATGCAA	80
GCTTGAGTAT	TCTATAGTGT	CACCTAAATA	GCTTGGCGTA	120
ATCATGGTCA	TAGCTGTTTC	CTGTGTGAAA	TTGTTATCCG	160
CTCACAATTC	CACACAACAT	ACGAGCCGGA	AGCATAAAGT	200
GTAAAGCCTG	GGGTGCCTAA	TGAGTGAGCT	AACTCACATT	240
AATTGCGTTG	CGCTCACTGC	CCGCTTTCCA	GTCGGGAAAC	280
CTGTCGTGCC	AGCTGCATTA	ATGAATCGGC	CAACGCGCGG	320
GGAGAGGCGG	TTTGCGTATT	GGGCGCTCTT	CCGCTTCCTC	360
GCTCACTGAC	TCGCTGCGCT	CGGTCGTTCG	GCTGCGGCGA	400
GCGGTATCAG	CTCACTCAAA	GGCGGTAATA	CGGTTATCCA	440
CAGAATCAGG	GGATAACGCA	GGAAAGAACA	TGTGAGCAAA	480
AGGCCAGCAA	AAGGCCAGGA	ACCGTAAAAA	GGCCGCGTTG	520
CTGGCGTTTT	TCCATAGGCT	CCGCCCCCCT	GACGAGCATC	560
ACAAAAATCG	ACGCTCAAGT	CAGAGGTGGC	GAAACCCGAC	600
AGGACTATAA	AGATACCAGG	CGTTTCCCCC	TGGAAGCTCC	640
CTCGTGCGCT	CTCCTGTTCC	GACCCTGCCG	CTTACCGGAT	680
ACCTGTCCGC	CTTTCTCCCT	TCGGGAAGCG	TGGCGCTTTC	720
TCATAGCTCA	CGCTGTAGGT	ATCTCAGTTC	GGTGTAGGTC	760
GTTCGCTCCA	AGCTGGGCTG	TGTGCACGAA	CCCCCGTTC	800
AGCCCGACCG	CTGCGCCTTA	TCCGGTAACT	ATCGTCTTGA	840
GTCCAACCCG	GTAAGACACG	ACTTATCGCC	ACTGGCAGCA	880
GCCACTGGTA	ACAGGATTAG	CAGAGCGAGG	TATGTAGGCG	920



(continued)

TGTAACGACGGCCAGT (–21 M13 forward primer)				
GTGCTACAGA	GTTCTTGAAG	TGGTGGCCTA	ACTACGGCTA	960
CACTAGAAGG	ACAGTATTTG	GTATCTGCGC	TCTGCTGAAG	1000



Safety



WARNING! GENERAL SAFETY. Using this product in a manner not specified in the user documentation may result in personal injury or damage to the instrument or device. Ensure that anyone using this product has received instructions in general safety practices for laboratories and the safety information provided in this document.

- Before using an instrument or device, read and understand the safety information provided in the user documentation provided by the manufacturer of the instrument or device.
- Before handling chemicals, read and understand all applicable Safety Data Sheets (SDSs) and use appropriate personal protective equipment (gloves, gowns, eye protection, and so on). To obtain SDSs, visit [thermofisher.com/support](https://www.thermofisher.com/support).

Chemical safety



WARNING! GENERAL CHEMICAL HANDLING. To minimize hazards, ensure laboratory personnel read and practice the general safety guidelines for chemical usage, storage, and waste provided below. Consult the relevant SDS for specific precautions and instructions:

- Read and understand the Safety Data Sheets (SDSs) provided by the chemical manufacturer before you store, handle, or work with any chemicals or hazardous materials. To obtain SDSs, see the "Documentation and Support" section in this document.
- Minimize contact with chemicals. Wear appropriate personal protective equipment when handling chemicals (for example, safety glasses, gloves, or protective clothing).
- Minimize the inhalation of chemicals. Do not leave chemical containers open. Use only with sufficient ventilation (for example, fume hood).
- Check regularly for chemical leaks or spills. If a leak or spill occurs, follow the manufacturer cleanup procedures as recommended in the SDS.
- Handle chemical wastes in a fume hood.
- Ensure use of primary and secondary waste containers. (A primary waste container holds the immediate waste. A secondary container contains spills or leaks from the primary container. Both containers must be compatible with the waste material and meet federal, state, and local requirements for container storage.)
- After emptying a waste container, seal it with the cap provided.
- Characterize (by analysis if needed) the waste generated by the particular applications, reagents, and substrates used in your laboratory.
- Ensure that the waste is stored, transferred, transported, and disposed of according to all local, state/provincial, and/or national regulations.
- **IMPORTANT!** Radioactive or biohazardous materials may require special handling, and disposal limitations may apply.



WARNING! HAZARDOUS WASTE (from instruments). Waste produced by the instrument is potentially hazardous. Follow the guidelines noted in the preceding General Chemical Handling warning.



WARNING! 4L Reagent and Waste Bottle Safety. Four-liter reagent and waste bottles can crack and leak. Each 4-liter bottle should be secured in a low-density polyethylene safety container with the cover fastened and the handles locked in the upright position.

Biological hazard safety



WARNING! Potential Biohazard. Depending on the samples used on this instrument, the surface may be considered a biohazard. Use appropriate decontamination methods when working with biohazards.



WARNING! BIOHAZARD. Biological samples such as tissues, body fluids, infectious agents, and blood of humans and other animals have the potential to transmit infectious diseases. Conduct all work in properly equipped facilities with the appropriate safety equipment (for example, physical containment devices). Safety equipment can also include items for personal protection, such as gloves, coats, gowns, shoe covers, boots, respirators, face shields, safety glasses, or goggles. Individuals should be trained according to applicable regulatory and company/institution requirements before working with potentially biohazardous materials. Follow all applicable local, state/provincial, and/or national regulations. The following references provide general guidelines when handling biological samples in laboratory environment.

- U.S. Department of Health and Human Services, *Biosafety in Microbiological and Biomedical Laboratories (BMBL)*, 6th Edition, HHS Publication No. (CDC) 300859, Revised June 2020
[cdc.gov/labs/bmbi](https://www.cdc.gov/labs/bmbi)
- Laboratory biosafety manual, fourth edition. Geneva: World Health Organization; 2020 (Laboratory biosafety manual, fourth edition and associated monographs)
[who.int/publications/i/item/9789240011311](https://www.who.int/publications/i/item/9789240011311)



Documentation and support

Related documentation

Document	Publication number	Description
<i>DNA Sequencing by Capillary Electrophoresis Chemistry Guide Second Edition</i>	4305080	This chemistry guide is designed to familiarize you with Applied Biosystems™ genetic analyzers for automated DNA sequencing by capillary electrophoresis, to provide useful tips for ensuring that you obtain high-quality data, and to help troubleshoot common problems.
<i>Troubleshooting Sanger sequencing data User Bulletin</i>	MAN0014435	This document provides guidance for the review of your data and troubleshooting tips for improving sequencing data quality.
<i>BigDye XTerminator™ Purification Kit User Guide</i>	4374408	Describes protocols for BigDye XTerminator™ purification
<i>SeqStudio™ Genetic Analyzer Instrument and Software User Guide</i>	MAN0018646	This manual provides instructions for the set-up, operation, and maintenance of the SeqStudio™ Genetic Analyzer. It also provides the instructions for setting up the Data Collection software for a run and contains additional information for instrument troubleshooting.
<i>SeqStudio™ Flex Series Genetic Analyzer with Instrument Software v1.2 User Guide</i>	100104689	This manual provides instructions for the set-up and operation of the SeqStudio™ Flex Series Genetic Analyzer. It provides the instructions for setting up the Data Collection software, autoanalysis, monitoring and viewing data for a run.
<i>3500/3500xL Genetic Analyzer with 3500 Series Data Collection Software v3.1 User Guide</i>	100031809	This manual provides instructions for the set-up, operation, maintenance and troubleshooting of the 3500/3500xL Genetic Analyzer. It also provides the instructions for setting up the Data Collection software, analysis, monitoring and viewing data for a run.
<i>User Guide: Applied Biosystems™ 3730/3730xl DNA Analyzer</i>	4331468	This manual provides instructions for the set-up and operation of the 3730/3730xl DNA Analyzer. It provides the instructions for setting up the Data Collection software, autoanalysis, monitoring and viewing data for a run

Portable document format (PDF) versions of this guide and the documents listed above are available at thermofisher.com.

Customer and technical support

Visit thermofisher.com/support for the latest service and support information.

- Worldwide contact telephone numbers
- Product support information
 - Product FAQs
 - Software, patches, and updates
 - Training for many applications and instruments
- Order and web support
- Product documentation
 - User guides, manuals, and protocols
 - Certificates of Analysis
 - Safety Data Sheets (SDSs; also known as MSDSs)

Note: For SDSs for reagents and chemicals from other manufacturers, contact the manufacturer.

Limited product warranty

Life Technologies Corporation and its affiliates warrant their products as set forth in the Life Technologies' General Terms and Conditions of Sale at www.thermofisher.com/us/en/home/global/terms-and-conditions.html. If you have questions, contact Life Technologies at www.thermofisher.com/support.

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