



OptiTaq DNA Polymerase

Cat. No.	Size
E2600-01	200 units
E2600-04	500 units
E2600-02	1000 units
E2600-03	5000 units

Unit Definition: One unit is defined as the amount of enzyme required to catalyze the incorporation of 10 nmoles of dNTP into acid-insoluble material in 30 min at 74°C. The reaction conditions are: 50 mM Tris-HCl (pH 9.0 at 25°C), 50 mM NaCl, 5 mM MgCl₂, 200 µM each of dATP, dCTP, dGTP, dTTP (a mix of unlabeled and [³H]dTTP), 10 µg activated calf thymus DNA and 0.1 mg/ml BSA in a final volume of 50 µl.

Storage Conditions: Store at -20°C.

kb M 0.9 1.7 2.5 3.7 5.3 6.9 9.3 12 15 20

PCR amplification using EURx OptiTaq DNA

Polymerase. Lane M: molecular size marker-Perfect 1 kb DNA Ladder. Lanes 0.9 to 20 kb: PCR amplification reactions, using Pol Buffer B with 0.2 mM dNTPs and 1.25 U OptiTaq DNA Polymerase in 50 µl reaction volume. Mixture of stable thermophilic DNA polymerases capable of generating PCR products up to 20 kb with high fidelity; suitable for applications requiring high temperature synthesis of DNA.

Description:

- OptiTaq DNA Polymerase is a modified and optimized thermostable enzymes blend containing *Thermus aquaticus* DNA polymerase and *Pyrococcus sp.* DNA polymerase.
- Ultrapure, recombinant enzymes are used to prepare OptiTaq DNA Polymerase.
- The enzymes blend exhibits the 3'→5' proofreading activity, resulting in considerably higher PCR fidelity and processivity than possible with unmodified Taq DNA polymerase (1).
- Enables increased amplification product yield in comparison with Taq DNA polymerase over wide range of PCR products.
- Maintains the 5'→3' exonuclease activity.
- Adds extra A at the 3' ends.
- Suitable for multiplex PCR as it exhibits wider tolerance for Mg²⁺, salts concentration and pH (2,3).
- Improves PCR results with critical templates, such as containing GC-rich regions, palindromes or multiple repeats.
- OptiTaq DNA Polymerase is recommended for use in PCR and primer extension reactions at elevated temperatures to obtain a wide range of DNA products up to 20 kb.

Storage Buffer:

20 mM Tris-HCl (pH 8.0 at 22°C), 100 mM KCl, 0.5% Tween[™]20, 0.5% Igepal CA-630, 0.1 mM EDTA, 1 mM dithiothreitol, 50% glycerol.

10 x Reaction Buffers:

10 x Pol Buffer A (optimization buffer without $MgCl_2$): The buffer allows to optimize $MgCl_2$ concentration.

10 x Pol Buffer B (general application, up to 20 kb):

The buffer contains 15 mM $MgCl_2$ and is optimized for use with 0.2 mM of each dNTP.

10 x Pol Buffer C (coloured):

10 x Pol Buffer B enriched with two gel tracking dyes and a gel loading reagent. The buffer enables direct loading of PCR products onto an agarose gel.

Quality Control:

All preparations are assayed for contaminating endonuclease, 3'-exonuclease and nonspecific single- and double-stranded DNase activities. Typical preparations are greater than 95% pure, as judged by SDS polyacrylamide gel electrophoresis.

References:

- 1. Cline, J., Braham, J. and Hogrefe, H. (1996) Nucleic Acids Res. 24, 3546.
- 2. Chien, A., Edgar, D.B. and Trela, J.M. (1976) J. Bacteriol. 127, 1550.
- 3. Kaledin, A.S., Sliusarenko, A.G. and Gorodetskii, S.I. (1980) Biokhimiya 45, 644.

This product is developed, designed and sold exclusively for research purposes and *in vitro* use only.

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Preparation of PCR Reaction:

Component	Volume/reaction	Final concentration
10 x Pol Buffer A or	5 µl	1x
10 x Pol Buffer B or		
10 x Pol Buffer C		
25 mM MgCl₂	2-10 µl when using 10 x Pol Buffer A	1-5 mM
	0-7 μl when using 10 x Pol Buffer B or 10 x Pol Buffer C	1.5-5 mM
dNTP mix (5mM each)	2 µl	0.2 mM of each dNTP
Upstream primer	Variable	0.3-0.5 μM
Downstream primer	Variable	0.3-0.5 μM
OptiTaq DNA Polymerase, 5U/µl	0.25 µl	1.25 U
Template DNA	Variable	<0.5 µg/50 µl
Sterile double- distilled water	Variable	-
Total volume	50 µl	_

Notes:

- 1. Completely thaw and mix thoroughly all components of PCR reaction before use to avoid localized differences in salt concentration. It is especially important for magnesium solutions, because they form concentration gradient when frozen.
- 2. Prepare reaction mixes on ice. Mix well.
- 3. Place reactions in a thermal cycler that has been preheated to denaturation temperature.
- 4. Standard concentration of MgCl₂ in PCR reaction is 1.5 mM (as provided by the 1 x Pol Buffer B or the 1 x Pol Buffer C) when using 0.2 mM dNTP (each). In most cases this concentration will produce satisfactory results. However, in some cases, reaction may be improved by determining optimal concentration of MgCl₂.
- 5. The 10 x Pol Buffer C allows PCR reactions to be loaded directly onto an agarose gel without prior addition of a gel loading buffer. The buffer contains a gel loading reagent and two gel tracking dyes (a red dye and an yellow dye) that separate during electrophoresis. In a 1% agarose gel, the red dye migrates at the same rate as 600 bp DNA fragment and the yellow dye migrates faster than 20 bp. The dyes do not interfere with most downstream enzymatic applications, however it is recommended to purify PCR products prior enzymatic manipulation.
- 6. 1.25 U of OptiTaq DNA Polymerase is recommended concentration of the enzyme per 50 μ l amplification reaction. For most applications, enzyme will be in excess and will produce satisfactory results. In some cases it may be necessary to optimize the enzyme concentration.
- In most cases there is no need to add additives to the PCR reaction. For some difficult targets such as: GC-rich sequences, sequences with complex secondary structures additives such as DMSO can be included to improve amplification. Use DMSO in concentrations of 2-8%. The recommended starting DMSO concentration (if needed) is 3%.
- 8. As a general guide for how much template DNA to use, start with a minimum 10^4 copies of the target sequence to obtain a signal in 25-35 cycles (i.e. 1 μg of 1 kb ds DNA equals 9.1 x 10^{11} molecules, 1 μg of *E. coli* genomic DNA equals 2 x 10^8 molecules, 1 μg of human genomic DNA equals 3 x 10^5 molecules).
- 9. For long range PCR use: 50-500 ng of human genomic DNA, 0.1-10 ng of bacterial DNA, phage DNA or plasmid DNA.
- 10.Ensure that a template DNA is of sufficiently high quality. Use only high-molecular-weight DNA, when amplifying long PCR targets (over 20-50 kb, depending on the amplicon length).
- 11.Complex genomic DNA should be stored at 2-8°C. Avoid vortexing the genomic DNA.
- 12.Use only thin-walled 0.2 ml tubes performing long PCR amplification.

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Thermal Cycling Conditions for Products 0.1-10 kb

Step	Temperature	Time	Number of Cycles
Initial Denaturation	93-95°C	2-5 min	1
Denaturation	93-95°C	15-30 s	25-35
Annealing	50-68°C	30 s	
Extension	72°C or 68°C	1 min/1 kb	
Final Extension	72°C or 68°C	7 min	1
Cooling	4°C	Indefinite	1

Thermal Cycling Conditions for Products over 10 kb

Step	Temperature	Time	Number of Cycles
Initial Denaturation	92-94°C	2 min	1
Denaturation	92-94°C	10-15 s	10
Annealing	60-68°C	30 s	
Extension	68°C	1 min/1 kb	
Denaturation	92-94°C	10-15 s	15-25
Annealing	60-68°C	30 s	
Extension	68°C	1 min/1 kb +20 s in each additional cycle	
Final Extension	68°C	7 min	1
Cooling	4°C	Indefinite	1

Notes:

- 1. Annealing temperature should be optimized for each primer set based on the primer $T_{\rm m}.$ Optimal annealing temperatures may be above or below the estimated $T_{\rm m}.$ As a starting point, use an annealing temperature 5°C below $T_{\rm m}.$
- Typical primers for long PCR amplification have a length of 22-34 and should have annealing temperatures above 60°C to enhance reaction specificity.
- 3. When amplifying long PCR products keep denaturation steps as short as possible and denaturation temperature as low as possible (try not to exceed 2 min at 94°C during initial denaturation and 10-15 s at 94°C during cycle denaturation step). Sometimes fragments with high GC-content need higher denaturation temperatures, but keep in mind that the yield increases when denaturation temperature/duration is decreased.
- 4. For PCR products over 5 kb elongation temperature of 68°C is strongly recommended.
- 5. For PCR products over 10 kb elongation of extension step (+20 s in each additional cycle starting from 11th cycle) is strongly recommended due to loss of processivity of the enzymes blend.

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