



HotStart Taq DNA polymerase

Hotstart Taq DNA Polymerase (5 U/ μ l)	100 μ l
10 \times reaction Buffer (Mg2+ Plus)	1ml X 2ea

For research use only

Cat No: YT1701

Size: 500 U

Store at -20°C for 2 years

Description

HotStart Taq DNA Polymerase is a highly thermostable recombinant DNA polymerase derived from the thermophile, *Thermus aquaticus*, and is a hotstart Taq DNA Polymerase by specific anti-Taq monoclonal antibody.

HotStart Taq DNA polymerase catalyzes the 5'→3' synthesis of DNA but has no detectable 3'→5' proofreading exonuclease activity, and possesses low 5'→3' exonuclease activity, which results in a 3'-dA overhang on the PCR product.

Especially, this enzyme can be applied to multiplex PCR, allele specific PCR, SNP analysis and real-time PCR by fluorescent intercalating dye like SYBR Green and TaqMan Probe.

Storage Buffer

20mM Tris-HCl (pH8.0), 100mM KCl, 1mM DTT, 0.1% Nonidet P-40, 0.1% Tween® 20 and 50% (v/v) glycerol

10X Reaction Buffer

100mM Tris-HCl (pH8.8), 500mM KCl and 1% Triton® X-100 , 15mM MgCl_2

1. Add the following components to a thin-walled PCR tube::

Reagent	Quantity for 20 μ l volume
Nuclease-Free Water	X μ l
10x Reaction Buffer	2.0 μ l
10mM dNTP Mixture	2.0 μ l
25mM MgCl_2	0.4 ~ 2.0 μ l ¹
Forward primer(10 μ M)	0.25 ~ 2.0 μ l
Reverse primer (10 μ M)	0.25 ~ 2.0 μ l
Template DNA	X μ l
HotStart Taq DNA Polymerase (5 U/ μ l)	0.2 μ l
Total	20 μ l

- Recommendation for template DNA concentration in a 20 μ l reaction volume

- 1) Human genomic DNA: 0.1 ng ~ 1 μ g
- 2) Bacterial genomic DNA: 0.1 ng ~ 100 ng
- 3) Plasmid DNA: 0.01 ng ~ 5 ng

2. PCR Cycles

Step	Temperature	Duration
Initial Denaturation	95 $^{\circ}\text{C}$	10 minutes
25-40 Cycles	95 $^{\circ}\text{C}$	15-30 seconds
	55-65 $^{\circ}\text{C}$	15-30 seconds
	72 $^{\circ}\text{C}$	30 sec per kb of product length
Final Extension	72 $^{\circ}\text{C}$	5 minutes
Hold	12 $^{\circ}\text{C}$	∞

¹ -additional volume (μ l) of MgCl_2 per 20 μ l reaction

Final MgCl_2 conc.c reaction (mM)	1.5	2	2.5	3	3.5	4
Volume of 25 mM MgCl_2	0	0.4	0.8	1.2	1.6	2