PerfectStart™ *Taq* DNA Polymerase

Please read the manual carefully before use

Cat. No. AP401

Store at: -20°C for two years

Concentration: 2.5 units/μl

Description:

PerfectStart™ *Taq* DNA Polymerase is a hot-start DNA polymerase that utilizes three monoclonal antibodies to efficiently bind to the enzyme, effectively blocking its activity and preventing non-specific amplification at low temperatures. As the denaturation step progresses, the antibodies are inactivated and *Taq* DNA Polymerase is activated, which can effectively enhance the amplification efficiency and improve the amplification sensitivity and specificity. The amplified product has an "A" base at the 3' end and can be directly cloned into the *pEASY*®-T vectors.

- Compared with *TransStart*® *Taq* DNA Polymerase and *TransStart*® *TopTaq* DNA Polymerase, *PerfectStart*™ *Taq* DNA Polymerase has higher amplification efficiency, specificity and sensitivity.
- Room-temperature reaction setup reduces non-specific amplification.
- Different from chemical modification, long denaturing step is not needed, which can avoid damaging the DNA template and reducing the activity of DNA Polymerase.
- The reaction solution is specifically designed for molecular diagnosis, and the amplification length is no more than 1 kb.

Highlights

- Hot start and high specificity.
- High sensitivity.
- High amplification efficiency.
- Low *E. coli* genomic DNA residue.

Application

- Low copy number templates.
- Complex templates.
- GC/AT-rich templates.
- Real-time Quantitative PCR (qPCR).
- Multiplex PCR.
- Single nucleotide polymorphisms (SNPs)

Unit definition

One unit of *PerfectStart*™ *Taq* DNA Polymerase incorporates 10 nmol of deoxyribonucleotide into acid-precipitable material in 30 minutes at 74°C using activated salmon sperm DNA as the template/primer.

Quality Control

The purity by SDS-PAGE detection is more than 99%; No activity of exogenous nuclease is detected; Host-free residual DNA detected by PCR method; Effective amplification of single-copy genes from human genome.

Storage Buffer

20 mM Tris-HCl (pH 8.0), 0.1 mM EDTA, 1 mM DTT, 100 mM KCl, 50% Glycerol, Stabilizers.

10×*PerfectStart*™ Taq Buffer (With Mg^{2+})

200 mM Tris-HCl (pH 9.0), 200 mM $(NH_4)_2SO_4$, 20 mM $MgSO_4$, 10% Glycerol, others.

GC Enhancer

For complex templates or GC/AT-rich templates. GC Enhancer can be added to the reaction system.

Kit Contents

Component	AP401-01/11	AP401-02/12	AP401-03/13
PerfectStart™ *Taq* DNA Polymerase	250 U×1	500 U×1	500 U×6
10×*PerfectStart*™ *Taq* Buffer	1.2 ml×1	1.2 ml×2	1.2 ml×12
2.5 mM dNTPs	-/800 µl×1	-/800 µl×2	-/1.2 ml×8
6×DNA Loading Buffer	500 µl×1	1 ml×1	1 ml×2
10×GC Enhancer	200 µl×1	400 µl×1	1 ml×1

Recommended PCR System and Conditions (taking 50 µl reaction system as an example)

Component	Volume	Final Concentration
Template DNA	Variable	as required
Forward Primer (10 µM)	1 µl	0.2 µM
Reverse Primer (10 µM)	1 µl	0.2 µM
10×*PerfectStart*™ *Taq* Buffer	5 µl	1×
2.5 mM dNTPs	4 µl	0.2 mM
PerfectStart™ *Taq* DNA Polymerase	0.5-1 µl	1.25-2.5 units
Nuclease-free Water	Variable	-
Total volume	50 µl	-

94°C	2-5 min	
94°C	30 sec	30-35 cycles
50-60°C	30 sec	
72°C	1-2 kb/min	
72°C	5-10 min	

Recommended Multiplex PCR System and Conditions (taking 50 µl reaction system as an example)

Component	Volume	Final Concentration
Template	Variable	as required
Multiplex PCR Primer Mix	Variable	0.2 µM/Each Primer
10×*PerfectStart*® *Taq* Buffer	5 µl	1×
2.5 mM dNTPs	4 µl	0.2 mM
PerfectStart® *Taq* DNA Polymerase	1 µl	2.5 units
Nuclease-free Water	Variable	-
Total volume	50 µl	-

94℃	2-5 min	
94℃	30 sec	30-35 cycles
50-60℃	45 sec	
65℃	1-2 min	
65℃	5 min	

Note

• The final concentration of $MgSO_4$ is sufficient for most targets and amplification. For optimal results, the concentration of $MgSO_4$ can be increased by 1-3 mM.

• Ensure that each pair of primers is designed correctly and can amplify fragment; the primer mix needs to be pre-mixed, if there are more multiples, the concentration of the primer stock solution can be increased. The recommended final concentration of each primer is 0.2 μM, which can be adjusted in the range of 0.05-0.4 μM according to the brightness of the bands. The target fragment should not be too long, no more than 500 bp in length is recommended.

• If there is a little precipitation after 10×*PerfectStart*® Taq Buffer is thawed, please dissolve it in a 37℃ water bath and mix it for use.

For research use only, not for clinical diagnosis.

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