HS Taq DNA Polymerase

（M011）

Product Description

HS Taq DNA Polymerase is a **chemically modified Taq DNA Polymerase** that is fully inactive at room temperature. Its activity is only released after heating at 95 °C, effectively preventing non-specific amplification and primer-dimer formation during reaction setup and ramp-up.

Compared with antibody-based hot-start Taq enzymes, HS Taq DNA Polymerase provides **more complete inactivation** and higher stringency. Compared with other chemically modified hot-start Taq enzymes, it requires only **5 minutes for activation** and is fully compatible with standard PCR protocols.

Paired with an optimized buffer system, HS Taq DNA Polymerase minimizes non-specific amplification and primer dimers, delivering exceptional sensitivity and specificity. It is ideal for amplifying low-copy genes from complex templates.

二、Components

Product Name	Cat. No.	Volume
HS Taq DNA Polymerase	M011	5 U/μL，250 U

Definition of Activity Unit

One unit (U) is defined as the amount of enzyme that incorporates **10 nmol of total nucleotides** into acid-insoluble material within **30 minutes at 74 °C** using activated salmon sperm DNA as the template/primer.

Storage Conditions

Storage: **-30 ~ -15 °C**

Shipping: ≤ 0 °C (ice pack)

Avoid repeated freeze-thaw cycles.

Applications

This product is widely used for DNA amplification from animals, plants, microorganisms, and other sources.

Recommended Uses

Featuring 5′→3′ exonuclease activity, high specificity, and high sensitivity, this hot-start enzyme is suitable for:

1. Quantitative real-time PCR (qPCR)
2. cDNA library construction

3. Mutant analysis and construction
4. Genetic disease diagnosis
5. Forensic identification

Primer Design Guidelines

1. The 3′-terminal base of primers is preferably **G or C**.
2. Avoid consecutive mismatches in the last 8 bases at the 3′ end.
3. Avoid hairpin structures at the 3′ end.
4. Tm values of forward and reverse primers should differ by ≤ 1 °C; optimal Tm: **55 ~ 65 °C** (calculated using Primer Premier 5 recommended).
5. Non-complementary overhangs should **not** be included in Tm calculation.
6. GC content: **40% ~ 60%**.
7. Uniform distribution of A, G, C, T; avoid GC- or AT-rich regions.
8. Avoid complementary sequences of ≥ 5 bases within a primer or between primers; avoid ≥ 3 complementary bases at the 3′ ends of primer pairs.
9. Verify primer specificity using **NCBI BLAST** to prevent non-specific amplification.

1. Reaction System (Recommended to prepare on ice)

Component	20 μL Reaction	50 μL Reaction	Final Concentration
10 × Taq Buffer	2 μL	5 μL	1 ×
Primer 1 (10 μM)	0.4 μL	1 μL	0.2 μM each
Primer 2 (10 μM)	0.4 μL	1 μL	0.2 μM each
dNTP Mix (10 mM each)	0.4 μL	1 μL	0.2 μM each
Template DNA	x μg	x μg	/
HS Taq DNA Polymerase（5 U/ μL）	0.4 μL	1 μL	0.1 U/μL
Nuclease-free Water	To 20 μL	To 50 μL	/

Note：Mix thoroughly before use.

1）Recommended template amounts (50 μL reaction): Mammalian genomic DNA: 0.1 ~ 1 μg; *E. coli* genomic DNA: 10 ~ 100 ng; Plasmid DNA: 0.1 ~ 10 ng

2）Enzyme volume can be adjusted from **0.25 ~ 1 μL**. Higher volume usually improves yield but may reduce specificity.

3）Optimal final Mg^{2+} concentration: **1.5 ~ 2 mM**. Titrate with 25 mM $MgCl_2$ at 0.2 ~ 0.5 mM increments if needed.

2. PCR Protocol

Step	Temperature	Time	Cycles
Initial denaturation	95℃	5 min	1
Denaturation	95℃	30 sec	30~35
Annealing	55℃	30 sec	
Extension	72℃	30 s / kb	
Final extension	72℃	10 min	1

Notes：

1）Extend initial denaturation to **10 min** for complex templates.

2）Annealing temperature: adjust based on primer Tm; typically **2 ~ 5 °C below Tm**.

3）Extension time: 30 sec / kb recommended; **60 sec / kb** for gene cloning to maximize yield.