Taq HS DNA Polymerase (Glycerol-free)

QL101

Version 23.1

Product Description

Taq HS DNA polymerase is a hot-start Taq polymerase obtained by mixing Champagne Taq antibody with Taq DNA polymerase in an optimal ratio. Due to the unique thermo stability of Champagne Taq antibody, the activity of Taq HS DNA polymerase is still blocked at temperature up to 55°C, which minimizes non-specific amplification during the mixing and system heating. When the reaction is kept at 95°C for more than 30 sec, Champagene Taq antibody is completely inactivated and Taq enzyme activity is completely released, ensuring that the PCR system has extremely high amplification sensitivity and specificity. The activation of Taq HS DNA polymerase is not affected by pH, ionic strength, etc. It is applicable for various hot-start PCR and qPCR based on Taq DNA polymerase and can be used to amplify gene with low copy numbers from complex templates (genome and cDNA). It is the hot-start Taq enzyme of choice for PCR/qPCR molecular diagnostic reagents. Taq HS DNA polymerase has higher stability and detection rate. This product is a glycerol-free version of Taq HS DNA polymerase, which can be used for lyophilization.

Components

Components	QL101-01 1,000 U	QL101-02 5,000 U	QL101-03 50,000 U
Taq HS DNA polymerase (Glycerol-free) (5 U/μl)	200 μl	1 ml	10 × 1 ml

Storage

Store at -30 ~ -15°C and transport at ≤0°C.

Applications

It is applicable for amplification reactions of animal DNA, plant DNA, microbial DNA, etc.

Source

It is expressed from *E.coli* with the *Thermus aquaticus* DNA Polymerase gene.

Unit Definition

One unit (U) is defined as the amount of enzyme that incorporates 10 nmol of dNTPs into acid-insoluble material in 30 min at 74°C, with activated salmon sperm DNA as the template/primer.

Notes

For research use only. Not for use in diagnostic procedures.

Primer Design Guidance

1. It is recommended that the last base at the 3' end of the primer should be G or C.
2. Consecutive mismatches should be avoided in the last 8 bases at the 3' end of the primer.
3. Avoid hairpin structures at the 3' end of the primer.
4. Differences in the Tm value of the forward primer and the reverse primer should be no more than 1°C and the Tm value should be adjusted to 55 ~ 65°C (Primer Premier 5 is recommended to calculate the Tm value).
5. Extra additional primer sequences that are not matched with the template, should not be included when calculating the primer Tm value.
6. It is recommended that the GC content of the primer to be 40% - 60%.
7. The overall distribution of A, G, C, and T in the primer should be as even as possible. Avoid using regions with high GC or AT contents.
8. Avoid the presence of complementary sequences of 5 or more bases either within the primer or between two primers. Avoid the presence of complementary sequences of 3 or more bases at the 3' end of two primers.
9. Use the NCBI BLAST function to check the specificity of the primer to prevent nonspecific amplification.

Experiment Process

Reaction System

Components	Volume
ddH_2O	To 50 µl
10 × Taq HS Buffer (Mg^{2+} plus)[a]	5 µl
dNTP Mix (10 mM each)	1 µl (0.2 mM each)
Primer 1 (10 µM)	0.1 - 1 µM
Primer 2 (10 µM)	0.1 - 1 µM
DNA Template[b]	x µl
Taq HS DNA polymerase (5 U/µl)[c]	1 µl

a. For most PCR, the optimal final concentration of Mg^{2+} is 1.5 - 2 mM. The system already contains a final concentration of 2 mM Mg^{2+}. If necessary, the 25 mM $MgCl_2$ can be used to search for the optimal concentration of Mg^{2+} at intervals of 0.2 - 0.5 mM.

b. Optimal reaction concentration varies in different templates. In a 50 µl system, the recommended template usage is as follows:

Template Types	Amount
Human Genomic DNA	1 - 500 ng
E. coli Genomic DNA	1 - 100 ng
λDNA	0.1 - 10 ng
Plasmid DNA	0.1 - 10 ng

c. Adjust the amount of enzyme between 0.25 - 1 µl. Increasing the amount of enzyme can generally increase the amplification yield, but it may decrease the specificity. When using other concentrations of Taq HS DNA polymerase, just calculate the amount of enzyme according to the concentration.

▲ When the GC content of the DNA fragment is >60% and the optimized conditions cannot be amplified normally, it is recommended to use PCR Enhancer to optimize the PCR.

Reaction Program

Temperature	Time	Cycles
95°C	30 sec (Initial Denaturation)	
95°C	30 sec	30 - 35
55°C*	30 sec	
72°C	60 sec/kb	
72°C	7 min (Final Extension)	

* The annealing temperature needs to be adjusted according to the Tm value of the primer, generally set to be 3 ~ 5°C lower than the Tm value of the primer.