Taq HS DNA Polymerase

P132

Version 22.1

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℃, which minimizes non-specific amplification during the mixing and system heating. When the reaction is kept at 95℃ 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. This product has higher stability and detection rate.

Components

Components	P132-d1 500 U (5 U/μl)	P132-d2 1,000 U (5 U/μl)	P132-d3 5,000 U (5 U/μl)
10 × Taq HS Buffer (Mg^{2+} plus)	2 × 1 ml	4 ml	20 ml
dNTP Mix (10 mM each)	400 μl	800 μl	4 ml
Taq HS DNA polymerase (5 U/μl)	100 μl	200 μl	1 ml

Storage

Store at -30 ~ -15℃ and transport at ≤0℃.

Applications

This product is suitable for amplification of animal DNA, plant DNA, microbial DNA, etc.

Source

It is cloned from *Thermus aquaticus* and purified from *E.coli*.

Unit Definition

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

Notes

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

Experiment Process

Reaction system

ddH_2O	To 50 μl
10 × Taq HS Buffer (Mg^{2+} plus)[a]	5 μl
dNTP Mix (10 mM each)	1 μl
Primer1 (10 μM)	2 μl
Primer2 (10 μM)	2 μl
Template DNA[b]	x μl
Taq HS DNA polymerase (5 U/μl)[c]	1 μl

a. 1.5 - 2 mM of Mg^{2+} is optimal for most PCR amplification. The final concentration of Mg^{2+} in the above reaction system is 2 mM. If necessary, Mg^{2+} can be further optimized in 0.2 - 0.5 mM increments using 25 mM $MgCl_2$.

b. The optimal concentration for various templates is different. The recommended amount of DNA template for a 50 μl reaction is as follows:

Human Genomic DNA	1 - 500 ng
E. coil Genomic DNA	1 - 100 ng
λDNA	0.1 - 10 ng
Plasmid DNA	0.1 - 10 ng

c. Adjust the volume of enzyme between 0.25 μl and 1 μl. Increase the concentration of enzyme can generally improve the yield, but it could also cause decreased specificity. When using other concentrations of Taq HS DNA polymerase, calculate the volume of the enzyme according to the concentration.

▲Use PCR Enhancer (Vazyme #P021) to optimize PCR system when the GC content of target sequence is >60% and adjusting the reaction condition can't achieve normal amplification results.

Reaction program

95℃	30 sec (Initial-denaturation)	
95℃	30 sec	30 - 35 cycles
55℃*	30 sec	
72℃	60 sec/kb	
72℃	7 min (Final extension)	

*Annealing temperature is based on the Tm value of the primers and is generally 3 ~ 5℃ lower than the calculated Tm value.

Primer Design Guidance

1. It is recommend that the last base at the 3' end of 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℃ and the Tm value should be adjusted to 55℃ to 65℃ (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. Control 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 and 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 non-specific amplification.