

Description

MyTaq[™] Red Mix is a ready-to-use 2x mix for fast, highly-specific PCR. The advanced formulation of MyTaq Red Mix exhibits more robust amplification than other commonly used polymerases, delivering very high yield over a wide range of PCR templates, and making it the ideal choice for most routine assays. MyTaq Red Mix contain all the reagents (including stabilizers) necessary for trouble-free PCR reaction set up. The product is supplied conveniently all in one tube, reducing the number of pipetting steps and facilitating increased efficiency, throughput and reproducibility.

The specially designed MyTaq Red formulation does not interfere with the PCR and allows users to load samples directly onto a gel after the PCR without the need to add loading buffer.

MyTaq Red Mix only requires the addition of template, primers and water, reducing the risk of pipetting errors and contamination as well as shortening the set-up time.

Components

	200 Reactions	1000 Reactions
MyTaq Red Mix, 2x	4 x 1.25ml	20 x 1.25ml

Standard MyTaq Red Mix Protocol

The following protocol is for a standard $50 \mu l$ reaction and can be used as a starting point for reaction optimization.

PCR reaction set-up:

All reactions must be set-up on ice.

Template	200ng
Primers (20μM each)	1µl
MyTaq Red Mix, 2x	25µl
Water (ddH ₂ O)	up to 50µl

PCR cycling conditions:

We suggest these conditions in the first instance:

Step	Temperature	Time	Cycles
Initial denaturation	95°C	1min	1
Denaturation	95°C	15s	
Annealing*	User determined	15s	25-35
Extension*	72°C	10s	

* These parameters may require optimization, please refer to the Important Considerations and PCR Optimization section if needed.

Important Considerations and Optimization

The optimal conditions will vary from reaction to reaction and are dependent on the template/primers used.

Primers: Forward and reverse primers are generally used at the final concentration of $0.2-0.6\mu$ M each. As a starting point we recommend using 0.4μ M as a final concentration (*i.e.* 20pmol of each primer per 50 μ l reaction volume). Too high a primer concentration can reduce the specificity of priming, resulting in non-specific products.

When designing primers we recommend using primer-design software such as Primer3 (http://frodo.wi.mit.edu/primer3) or visual OMP^{TM} (http://dnasoftware.com) with monovalent and divalent cation concentrations of 10mM and 3mM respectively. Primers should have a melting temperature (Tm) of approximately $60^{\circ}C$

Template: The amount of template in the reaction depends mainly on the type of DNA used. For templates with low structural complexity, such as plasmid DNA, we recommend using 50pg-10ng DNA per 50μ l reaction volume. For eukaryotic genomic DNA, we recommend a starting amount of 200ng DNA per 50μ l reaction, this can be varied between 5ng-500ng. It is important to avoid using template resuspended in EDTA-containing solutions (*e.g.* TE buffer) since EDTA chelates free Mg²⁺.

Initial denaturation: An initial denaturation step of 1min at 95°C is recommended for non-complex templates such as plasmid DNA or cDNA. For more complex templates such as eukaryotic genomic DNA, longer initial denaturation times of up to 3mins are required in order to facilitate complete melting of the DNA.

Denaturation: Our protocol recommends a 15s cycling denaturation step at 95°C which is also suited to GC-rich templates, however for low GC content (40-45%) templates, the denaturation time can be decreased down to 5s.

Annealing temperature and time: The optimal annealing temperature is dependent upon the primer sequences and is usually 2-5°C below the lower Tm of the pair. We recommend running a temperature gradient to determine the optimal annealing temperature, alternatively 55°C can be used as a starting point. Depending on the reaction the annealing time can also be reduced to 5s.

Extension temperature and time: The extension step should be performed at 72°C. The extension time depends on the length of the amplicon and the complexity of the template. For low complexity template such as plasmid DNA, an extension time of 10s is sufficient for amplicons under 1kb or up to 5kb. For amplification of fragments over 1kb from high complexity template, such as eukaryotic genomic DNA, longer extension times are recommended. In order to find the fastest optimal condition, we suggest incrementing the extension time successively up to 30s/kb.

Troubleshooting Guide

Problem	Possible Cause	Recommendation	
No PCR product	Missing component	- Check reaction set-up and volumes used	
	Defective component	- Check the aspect and the concentrations of all components as well as the storage condi- tions. If necessary test each component individually in controlled reactions	
	Cycling conditions not optimal	 Decrease the annealing temperature Run a temperature gradient to determine the optimal annealing temperature Increase the extension time, especially if amplifying a long target Increase the number of cycles 	
	Difficult template	- Increase the denaturation time	
Smearing or Non-Specific products	Excessive cycling	- Decrease the number of cycles	
	Extension time too long	- Decrease the extension time	
	Annealing temperature too low	- Increase the annealing temperature	
	Primer concentration too high	- Decrease primer concentration	
	Extension during set-up	- Make sure all reactions are set-up on ice. Run reaction as quickly as possible	
	Contamination	 Replace each component in order to find the possible source of contamination Setup the PCR and analyze the PCR product in separated areas 	

Technical Support

If the troubleshooting guide does not solve the difficulty you are experiencing, please contact your local distributor or our Technical Support with details of reaction set-up, cycling conditions and relevant data.

Email: tech@bioline.com

Associated Products

Product Name	Pack Size	Cat No
Agarose	500g	BIO-41025
Agarose tablets	300g	BIO-41027
HyperLadder™ 1kb	200 Lanes	BIO-33025
SureClean Plus	1 x 5ml	BIO-37047

TRADEMARKS

1. MyTaq and HyperLadder are Trademarks of Bioline Reagents Ltd

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