ELISABETH PHARMACON Ltd.
Rokycanova 4437/5
615 00 Brno-Zidenice, Czech Republic
Phone: +420 542 213 851
E-mail: info@elisabeth.cz
Web: www.elisabeth.cz
VAT: CZ26258412

EliZyme™ Super HRM MIX

Intended use:

For Research Use Only. Not for use in diagnostic procedures.

Storage:

Upon arrival store components at -20 °C. Avoid prolonged exposure to light. When stored under these conditions, the kit will retain full activity until the expiration date indicated on the kit label. Reagents may be stored at 4 °C up to 1 month.

Product description

The EliZyme™ Super HRM MIX is a combination of our highly pure Taq polymerase with dNTPs and $MgCl_2$. It uses the proprietary third-generation DNA-intercalating dye, which significantly reduces PCR inhibition. This new qPCR mastermix provides superior performance and accurately discriminates SNPs and quantifies methylation differences.

EliZyme™ Super HRM MIX relies on ultra-pure Taq polymerase, which is purified using a 12-step purification process that eliminates host DNA contamination and enhances reaction sensitivity and specificity.

Our high-throughput smart-screen technology has resulted in a buffer system that enables efficient amplification of GC-rich and AT-rich templates under both fast and standard cycling conditions. The EliZyme™ Super HRM MIX is highly sensitive and it can be utilized in in HRM analysis for detecting mutations, polymorphisms, and epigenetic variations in double-stranded DNA.

Content

	Ref. No.	Content	Size
EliZyme™ Super HRM MIX	EZ1501	1×0.5 ml mix	100 rxns
	EZ1505	2×1.25 ml mix	500 rxns
	EZ1514	1×7 ml mix	1400 rxns

Primers

Primers should have a predicted melting temperature of around 60 °C. The shorter the amplicon length, the faster the reaction can be cycled. The recommended amplicon length should be between 80 bp and 200 bp. Amplicon length should not exceed 400 bp.

Reaction setup

After thawing, briefly vortex the mix and shortly spin.

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Reagent	20 µl reaction	Final conc.
2X EliZyme™ SH Mix	5 µl	1×
Forward primer (10 µM)	0.8 µl	400 nM
Reverse primer (10 µM)	0.8 µl	400 nM
Template DNA	< 10 ng cDNA, 0.5-50 ng genomic DNA	Variable
PCR grade water	Up to 20 µl	

PCR cycling profile

Acquire data on the SYBR® Green or FAM channel.

Step	Temperature	Time	Cycles
Initial denaturation	95 °C	2 – 3 min*	1
Denaturation	95 °C	5 s	40
Annealing/Extension	60 – 65 °C**	20 – 30 s***	
HRM analysis****			

*2 min for cDNA, 3 min for genomic DNA.

** Do not use temperatures below 60 °C.

*** Do not exceed 30 s.

****Optional.

Manufacturer:

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Catalog number

Batch code


Use by (last day of month)


Upper limit of temperature


Manufacturer

Contains sufficient "N" tests