

## SolisFAST® Probe qPCR Mix (ROX), 5x

| Catalogue Number | Pack Size | 20 µl rxn |
|------------------|-----------|-----------|
| 28-02-0000S      | 0.2 ml    | 50        |
| 28-02-00001      | 1 ml      | 250       |
| 28-02-00001-5    | 5 x 1 ml  | 5 x 250   |
| 28-02-00020      | 20 ml     | 5000      |

### Shipping:

At room temperature

### Batch Number and Expiry Date:

See vial

### Storage and Stability:

- Routine storage at -20 °C until expiry date
- The mix can be stored at +4 °C for up to 6 months
- Stability at room temperature (15 - 25 °C) for 1 month
- Freeze-thaw stability: 30 cycles

**Store at -20 °C**

**Stability at room  
temperature  
1 MONTH**

### Reaction setup:

At room temperature

Manufactured by Solis BioDyne, in compliance with the ISO 9001 and ISO 13485 certified Quality Management System.

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### Step-by-step guidelines:

1. Thaw SolisFAST® Probe qPCR Mix, template DNA, primers, probe(s), and nuclease-free water. Mix each component by gentle vortexing or pipetting up and down, then centrifuge briefly.
2. Prepare a reaction mix. Add all required components except the template DNA.

| Component                              | Volume <sup>1</sup> | Final conc.                     |
|--|---------------------|---------------------------------|
| SolisFAST® Probe qPCR Mix (ROX) (5x)   | 4 µl                | 1x                              |
| Forward Primer(s) (10 µM) <sup>2</sup> | 0.8 µl              | 400 nM                          |
| Reverse Primer(s) (10 µM) <sup>2</sup> | 0.8 µl              | 400 nM                          |
| Probe(s) (10 µM) <sup>2</sup>          | 0.3 µl              | 150 nM                          |
| Template DNA (added at step 4)         | Variable            | cDNA: < 100 ng<br>gDNA: < 50 ng |
| Nuclease-free water                    | up to 20 µl         |                                 |
| <b>Total reaction volume</b>           | <b>20 µl</b>        |                                 |

<sup>1</sup> Scale all components proportionally according to sample number and reaction volumes. Make sure you use enough of each reagent for your reactions, plus 10% extra volume to accommodate pipetting errors.

<sup>2</sup> Optimal results may require titration of primer concentration between 200 and 600 nM and probe concentration between 100 and 200 nM. A final concentration of 400 nM each primer and 150 nM probe is suitable for most applications.

3. Mix the reaction mix thoroughly, then centrifuge briefly. Dispense appropriate volumes of mix into PCR wells.

4. Add template DNA to the PCR wells.

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### Product description:

- SolisFAST® Probe qPCR Mix (ROX) is a 5x-concentrated, ready-to-use solution optimized for fast, highly sensitive and reproducible probe-based qPCR assays.
- The mix contains all components necessary, except primers, probe(s), nuclease-free water, and DNA template.
- The mix is optimized for dual-labeled hydrolysis probes (e.g. TaqMan® probes) and is suitable for detection and quantitation of up to five targets simultaneously.

| Mix component                    | Description  |
|----------------------------------|--|
| <b>SolisFAST® DNA Polymerase</b> | <i>In silico</i> designed analogue of Taq DNA polymerase with enhanced stability at room temperature, fast hot-start and faster extension rates compared to the wild-type Taq DNA polymerase |
| <b>qPCR buffer</b>               | Includes 15 mM MgCl <sub>2</sub> (1x PCR solution 3 mM MgCl <sub>2</sub> ), dNTPs (dATP, dCTP, dGTP, dTTP), additives that maximize efficiency of PCR  |
| <b>Passive reference dye</b>     | ROX dye is an internal passive reference dye used to normalize the fluorescent reporter signal generated in qPCR   |

### Compatible real-time instruments:

The mix is compatible with low-ROX qPCR cyclers where ROX is used as a passive reference signal for normalization of fluorescent signal (see the compatibility table on page 7).

5. Seal the wells using the procedure recommended for the cycling instrument being used, and centrifuge the reactions briefly.
6. Program the thermal cycler using the cycling conditions recommended below.

| Step                                    | Temperature | Time   | Cycles |
|---|-------------|--------|--------|
| <b>Initial denaturation<sup>1</sup></b> | 95 °C       | 3 min  | 1      |
| Denaturation <sup>2</sup>               | 95 °C       | 5 sec  | 40     |
| Annealing/extension <sup>2</sup>        | 60 – 65 °C  | 20 sec |        |

<sup>1</sup> Incubation at 95 °C is crucial for the full activation of SolisFAST® DNA Polymerase and denaturation of template DNA. With low-complexity templates (e.g. cDNA) shorter initial denaturation time (30 sec-1 min) can be used. Complex templates, such as gDNA, require longer time to denature (2-3 min).

<sup>2</sup> The annealing/extension temperature depends on the melting temperature of the primers and DNA probe used. 5 sec denaturation and 20 sec annealing/extension are suitable for all qPCR cyclers listed on page 7.

7. Place the reactions into the qPCR cycler, and start the qPCR run.
8. After the reaction is completed, perform data analysis according to the instrument-specific instructions.

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## Recommendations for a successful qPCR experiment

Use dedicated software, such as Primer3 ([bioinfo.ut.ee/primer3](http://bioinfo.ut.ee/primer3)) or NCBI Primer-BLAST ([ncbi.nlm.nih.gov/tools/primer-blast](http://ncbi.nlm.nih.gov/tools/primer-blast)) to design target-specific primers and probes. Analyze your primers and probes for self-complementarity and stable secondary structures (e.g. hairpins) in their sequences. Avoid the 3'-self complementarity, because it increases the probability of primer-dimers formation. GC-content of primers and probe(s) should range from 35 - 65%.

In case of multiplexing, test the performance of primer-probe sets in individual assays before combining them in a multiplex assay.

Check the qPCR cycler's user manual for correct setup for multiplex analysis.

### Primers:

1. The optimal primer length is 20 - 30 bp targeting amplicons of 50 - 150 base pairs. Avoid runs of more than four consecutive G or C bases.
2. The optimal melting temperature ( $T_m$ ) of the primers is 60 - 64 °C. In order for both primers to bind efficiently,  $T_m$  of the two primers should not differ by more than 3 °C.

### Probe:

1. The length of the probes should be 9 - 40 bases. For the hydrolysis probes, it is usually up to 30 bases. The probe binding site should be in close proximity to the forward or reverse primer. However, the probe and primer binding sites should not overlap. Probe can bind to either strand of the target.

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5. To monitor possible contamination and primer-dimer formation, always include a no-template control (NTC), replacing the DNA template with nuclease-free water.

### Cycling:

The cycling conditions are compatible with qPCR instruments listed in the following compatibility table:

| Manufacturer       | Model                                       |
|--------------------|---|
| Applied Biosystems | 7500, 7500 Fast, 7900HT Fast                |
|                    | QuantStudio™ 3, 5, 6 Flex, 7 Flex, 12K Flex |
|                    | ViiA™ 7                                     |

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2. Melting temperature ( $T_m$ ) of the probe should be 6 - 8 °C higher than the  $T_m$  of the primers. In case the  $T_m$  of the probe is too low, less of the probe is bound to the target sequence. As a consequence, the product may be amplified, but the sensitivity will be compromised, because not all target sites are occupied by the probe, which results in reduced fluorescence signal and not a true representation of the target amount in the sample.

### Template

The integrity, purity and concentration of the DNA template should be suitable for the qPCR experiment.

1. The template needs to be purified of PCR inhibitors (e.g. EDTA).
2. The recommended final concentration of DNA template for the qPCR experiment is dependent upon the type of DNA used. For example, if you use cDNA as a template, qPCR efficiency would be largely dependent on the expression level of the target gene. Use up to 50 ng of complex (e.g. eukaryotic) DNA and up to 100 ng of cDNA in your reactions.
3. The final amount of cDNA sample in the qPCR reaction is up to one tenth of the final reaction volume. Overload of cDNA sample may inhibit your qPCR.
4. Perform and analyze your qPCR reactions in triplicates on a serially diluted template (e.g. 10-fold dilution series). Dilutions should be done in deionized water and should be prepared fresh before each experiment. Use the standard curve derived from the serial dilutions to assess qPCR efficiency and to determine the optimal template concentration for your qPCR assay.

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### Safety precautions:

Please refer to Safety Data Sheet for more information.

### Technical support:

Contact your sales representative for any questions or send an email to [support@solisbiodyne.com](mailto:support@solisbiodyne.com)

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