



## HighFidelity ORANGE PCR Labeling Testkit

Preparation of AF594-, ATTO594- and TexasRed-labeled DNA probes by PCR

| Cat. No.       | Amount |
|----------------|--------|
| APP-101-ORANGE | 1 kit  |

**For general laboratory use.**

**Shipping:** shipped on gel packs

**Storage Conditions:** store at -20 °C

**Additional Storage Conditions:** avoid freeze/thaw cycles, store dark

**Shelf Life:** 12 months

### Spectroscopic Properties:

AF594:

$\lambda_{exc}$  590 nm,  $\lambda_{em}$  617 nm,  $\epsilon$  92.0 L mmol<sup>-1</sup> cm<sup>-1</sup> (Tris-HCl pH 7.5)

ATTO594:

$\lambda_{exc}$  602 nm,  $\lambda_{em}$  626 nm,  $\epsilon$  120.0 L mmol<sup>-1</sup> cm<sup>-1</sup> (Tris-HCl pH 7.5)

TexasRed:

$\lambda_{exc}$  583 nm,  $\lambda_{em}$  603 nm,  $\epsilon$  112.0 L mmol<sup>-1</sup> cm<sup>-1</sup> (Tris-HCl pH 7.5)

### Description:

HighFidelity ORANGE PCR Labeling Testkit is designed to produce randomly AF594-, ATTO594- and TexasRed-modified DNA probes by PCR to find the optimal label for the orange emission wavelength range. Such probes are ideally suited for Fluorescence *in situ* hybridization (FISH) and Northern Blot experiments. PCR-based labeling is superior to random-primed labeling with Klenow fragment if template amounts are limited or amplification of a specific DNA fragments is required. Amplification of probes up to 4kbp is feasible.

All labeled-dUTP are efficiently incorporated into DNA as substitute for its natural counterpart dTTP using an optimized reaction buffer and a High Fidelity Polymerase blend consisting of *Taq* polymerase and a proofreading enzyme. 50 % / 25 % labeled-dUTP substitution typically results in an optimal balance between reaction and labeling efficiency. Individual optimization of labeled-dUTP/dTTP ratio however, can easily be achieved with the single nucleotide format.

### Content:

#### High Fidelity Polymerase

in storage buffer with 50% glycerol (v/v)  
1x 40  $\mu$ l (100 units, 2.5 units/ $\mu$ l)

#### High Fidelity Labeling Buffer

1x 500  $\mu$ l (10x)

#### dATP - Solution

1x 20  $\mu$ l (100 mM)

#### dGTP - Solution

1x 20  $\mu$ l (100 mM)

#### dCTP - Solution

1x 20  $\mu$ l (100 mM)

#### dTTP - Solution

1x 20  $\mu$ l (100 mM)

#### dUTP-XX-AF594

1x 10  $\mu$ l (1 mM)

#### dUTP-XX-ATTO-594

1x 10  $\mu$ l (1 mM)

#### dUTP-TexasRed

1x 10  $\mu$ l (1 mM)

#### Lambda DNA

1x 20  $\mu$ l (100 ng/ $\mu$ l)

#### 500 bp forward primer

1x 20  $\mu$ l (10  $\mu$ M)



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### 500 bp reverse primer

1x 20  $\mu$ l (10  $\mu$ M)

### PCR-grade water

1x 1.2 ml

### To be provided by user

DNA template

Primer

DNA purification tools (optional)

### 1. Preparation of working solutions

#### 1.1 Preparation of 1 mM dATP/dCTP/dGTP working solution

- Thaw 100 mM dATP, 100 mM dCTP and 100 mM dGTP solutions on ice, vortex and spin-down briefly.
- Prepare a 1:100 dilution with PCR-grade water to achieve a final concentration of 1 mM (e.g. 2  $\mu$ l 100 mM dATP + 2  $\mu$ l 100 mM dCTP + 2  $\mu$ l 100 mM dGTP + 194  $\mu$ l PCR-grade water).
- 1 mM ATP/CTP/GTP working solution can be stored at -20°C. Prepare aliquots to avoid freeze/thaw cycles.

#### 1.2 Preparation of 1 mM dTTP working solution

- Thaw 100 mM dTTP solution on ice, vortex and spin-down briefly.
- Prepare a 1:100 dilution with PCR-grade water to achieve a final concentration of 1 mM (e.g. 2  $\mu$ l 100 mM dTTP + 198  $\mu$ l PCR-grade water).
- 1 mM dTTP working solution can be stored at -20 °C. Prepare aliquots to avoid freeze/thaw cycles.

### 3. Standard PCR Labeling protocol

The standard protocol is set-up for labeling of a 500 bp DNA fragment. An optimal balance between reaction and labeling efficiency is typically achieved with 50 % dUTP-XX-AF594 & dUTP-XX-594 or with 25 % dUTP-TexasRed substitution following the standard protocol below however, individual optimization might improve results for individual applications.

- Assemble the PCR on ice in the order stated below (DNase-free reaction tube).
- Vortex and spin-down briefly.
- Perform assay set-up and reaction under low-light conditions.

### 50 % substitution

| Component                                     | Volume     | Final concentration                                      |
|---|------------|--|
| PCR-grade water                               | X $\mu$ l  |  |
| High Fidelity Labeling Buffer (10x)           | 2 $\mu$ l  | 1x   |
| 1 mM dATP/dCTP/dGTP working solution (s. 1.1) | 2 $\mu$ l  | 100 $\mu$ M  |
| 1 mM dTTP working solution (s. 1.2)           | 1 $\mu$ l  | 50 $\mu$ M   |
| 1 mM labeled-dUTP                             | 1 $\mu$ l  | 50 $\mu$ M   |
| forward primer (10 $\mu$ M)                   | X $\mu$ l  | 0.1 - 1 $\mu$ M (e.g. 0.3 $\mu$ M 500 bp forward primer) |
| reverse primer (10 $\mu$ M)                   | X $\mu$ l  | 0.1 - 1 $\mu$ M (e.g. 0.3 $\mu$ M 500 bp reverse primer) |
| template DNA                                  | X $\mu$ l  | 1 - 10 ng genomic DNA (e.g. 1 ng Lambda DNA)             |
| High Fidelity Polymerase (2.5 units/ $\mu$ l) | 1 $\mu$ l  | 2.5 units  |
| Total volume                                  | 20 $\mu$ l |  |



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### 25 % substitution

| Component                                     | Volume | Final concentration                            |
|---|--------|--|
| PCR-grade water                               | X µl   |  |
| High Fidelity Labeling Buffer (10x)           | 2 µl   | 1x   |
| 1 mM dATP/dCTP/dGTP working solution (s. 1.1) | 2 µl   | 100 µM   |
| 1 mM dTTP working solution (s. 1.2)           | 1.5 µl | 50 µM  |
| 1 mM labeled-dUTP                             | 0.5 µl | 50 µM  |
| forward primer (10 µM)                        | X µl   | 0.1 - 1 µM (e.g. 0.3 µM 500 bp forward primer) |
| reverse primer (10 µM)                        | X µl   | 0.1 - 1 µM (e.g. 0.3 µM 500 bp reverse primer) |
| template DNA                                  | X µl   | 1 - 10 ng genomic DNA (e.g. 1 ng Lambda DNA)   |
| High Fidelity Polymerase (2.5 units/µl)       | 1 µl   | 2.5 units                                      |
| Total volume                                  | 20 µl  |  |

### 4. Probe purification:

Probe purification is not required for most hybridization experiments. If a downstream application requires purification (e.g. concentration determination by absorbance measurement) we recommend silica-membrane or gel filtration-based purification.

### Related Products:

Aminoallyl-dUTP-XX-AF594, #NU-803-XX-AF594  
 Aminoallyl-dUTP-XX-ATTO-594, #NU-803-XX-594  
 Aminoallyl-dUTP-Texas Red, #NU-803-TXR

### Recommended cycling conditions

| Cycle step               | Temperature | Time   | Cycles |
|--------------------------|-------------|--------|--------|
| Initial denaturation     | 95°C        | 2 min  | 1x     |
| Denaturation             | 95°C        | 20 sec | 30x    |
| Annealing <sup>1)</sup>  | 58°C        | 30 sec |        |
| Elongation <sup>2)</sup> | 68°C        | 60 sec |        |
| Final Elongation         | 68°C        | 2 min  | 1x     |

<sup>1)</sup>The annealing temperature depends on the melting temperature of primers used.

<sup>2)</sup>The elongation time depends on the length of fragments to be amplified. A time of 2 min/kbp is recommended. Elongation at 72°C works as well.

For optimal amplification results and high incorporation rates an individual optimization of the recommended PCR assay and cycling conditions may be necessary for each new primer-template pair.