



HighYield T7 mRNA Synthesis Kit (Ψ -UTP)

Synthesis of pseudouridine-modified (m)RNA

Cat. No.	Amount
RNT-106-S	15 reactions x 20 μ l
RNT-106-L	50 reactions x 20 μ l

For general laboratory use.

Shipping: shipped on gel packs

Storage Conditions: store at -20 °C

Additional Storage Conditions: avoid freeze/thaw cycles

Shelf Life: 12 months after date of delivery

Description:

HighYield T7 mRNA Synthesis Kit (Ψ -UTP) is designed to produce large amounts of pseudouridine-modified (m)RNA via *in vitro* transcription with T7 RNA polymerase. The resulting internally modified (m)RNA can subsequently be used for microinjection, transfection or *in vitro* translation experiments.

Pseudouridine modifications have been shown to increase (m)RNA stability and to reduce immunogenicity. A 5'-cap structure further increases translation efficiency. 5'-capping can be achieved by a) co-transcriptional capping with cap analogs (e.g. ARCA) or b) post-transcriptional capping with capping enzymes.

The kit contains sufficient reagents for **15 reactions (S-Pack) or 50 reactions (L-Pack) à 20 μ l (7.5 mM GTP, 7.5 mM Pseudo-UTP, 7.5 mM ATP, 7.5 mM CTP)**. An individual optimization of ARCA and Pseudo-UTP concentration can easily be achieved with the single nucleotide format.

A 20 μ l reaction yields about **100-130 μ g RNA after 30 min incubation (1 μ g T7 control template, 1.4 kb RNA transcript)**. Yields may however vary depending on the template (promotor design, sequence length, secondary structure formation).

Content:

HighYield T7 RNA Polymerase Mix

RNT-106-S: 2x 40 μ l incl. RNase inhibitor and 50 % glycerol (v/v)

RNT-106-L: 3x 40 μ l incl. RNase inhibitor and 50 % glycerol (v/v)

HighYield T7 Reaction Buffer

1x 200 μ l (10x), HEPES-based

ATP - Solution

1x 100 μ l (100 mM)

GTP - Solution

1x 100 μ l (100 mM)

CTP - Solution

1x 100 μ l (100 mM)

UTP - Solution

1x 100 μ l (100 mM)

Pseudo-UTP

RNT-106-S: 3x 10 μ l (100 mM)

RNT-106-L: 8x 10 μ l (100 mM)

T7 G-initiating control template (1.4 kbp)

1x 10 μ l (200 ng/ μ l), 1.4 kbp PCR fragment plus T7 class III phi6.5 promotor resulting in 1400 nt RNA transcript



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T7 A-initiating control template (1.4 kbp)

1x 10 μ l (200 ng/ μ l), 1.4 kbp PCR fragment plus T7 class II phi2.5 promoter (A-initiating) resulting in 1400 nt RNA transcript

PCR-grade water

1x 1.2 ml

DTT

1x 100 μ l (100 mM)

To be provided by user

T7 Promotor-containing DNA template
RNA purification tools
RNase-free DNase I

Important Notes (Read before starting)

Prevention of RNase contamination

Although a potent RNase Inhibitor is included, creating a RNase-free work environment and maintaining RNase-free solutions is critical for performing successful *in vitro* transcription reactions. We therefore recommend

- to perform all reactions in sterile, RNase-free tubes using sterile pipette tips.
- to wear gloves when handling samples containing RNA.
- to keep all components tightly sealed both during storage and reaction procedure.

Template requirements

- Template type:** Linearized plasmid DNA or PCR products containing a double-stranded G-initiating T7 class III phi6.5 promoter region upstream of the target sequence.

Minimum T7 promotor sequences:

T7 class III phi6.5 promoter (G-initiating)

5'-TAATACGACTCACTATAGNN...-3'

Bold: First base incorporated into RNA, NN: ideally CG

- Template quality:** DNA template quality directly influences yield and quality of transcription reaction. Linearized plasmid DNA needs to be fully digested and to be free of contaminating RNase, protein and salts. We recommend selecting restriction enzymes that generate blunt ends or 5'-overhangs and purification by phenol/chloro-form extraction. A PCR mixture can be used directly however, better yields will usually be obtained with purified PCR products (e.g. via silica-membrane based purification columns).

- mRNA production:** For the production of functional mRNA, the DNA template needs to encode the following structural features e.g. 3'-UTR, 5'-UTR, correctly orientated target sequence and poly(A)-tail. Alternatively, poly(A)-tailing can post-transcriptionally be performed with Poly(A) polymerase.

In vitro Transcription protocol

The general protocol is set up for 0.5 μ g - 1 μ g DNA template (refer to section 1.2 regarding template requirements), a final NTP concentration of 7.5 mM and 100% substitution of UTP by Pseudo-UTP, respectively.

Depending on the RNA sequence and final application, individual reaction optimization may improve product yield and biological function (e.g. variation Pseudo-UTP/UTP ratio, variation of template amount, variation of incubation time).

Component	Volume	Final conc.
PCR-grade water	X μ l	
HighYield T7 Reaction Buffer (10x)	2 μ l	1x
DTT (100 mM)	2 μ l	10 mM
GTP (100 mM)	1.5 μ l	7.5 mM
Pseudo-UTP (100 mM)	1.5 μ l	7.5 mM
CTP (100 mM)	1.5 μ l	7.5 mM
ATP (100 mM)	1.5 μ l	7.5 mM
Template DNA	X μ l	1 μ g
HighYield T7 RNA Polymerase Mix	2 μ l	
Total volume	20 μl	

- Place HighYield T7 RNA Polymerase Mix on ice.
- Thaw all remaining components at room temperature (RT), mix by vortexing and spin down briefly.
- Assemble all components at RT to a nuclease-free microtube (sterile pipette tips) in the following order:
 - Mix PCR-grade water, HighYield T7 Reaction Buffer and DTT by vortexing and spin down briefly.
 - Add nucleotide solutions and template DNA, vortex and spin down briefly.
 - Add HighYield T7 RNA Polymerase Mix vortex and spin down briefly.
- Incubate for 2h at 37°C in the dark (e.g. PCR cyclor). Individual optimization may increase product yield (0.5h-4h at 37°C).



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Please note: Reagents for the following steps are not provided within this kit.

DNA template removal

Depending on the down-stream application, removal of template DNA might be required. We recommend a salt-resistant, high efficiency DNAase such as Turbo™DNAse (ThermoFisher). Follow the manufacturer instructions.

Removal of 5'-triphosphate groups

5'-ends of *in vitro* phosphorylated RNAs carry a triphosphate group that is known to trigger RIG-1 mediated innate immune response in mammalian cells^[1,2]. Removal with phosphatases (e.g. CIP) before final purification is therefore recommended for RNA probes intended for transfection experiments. Please refer to the following references for more detailed information: [1],[2].

(m)RNA purification

Purification of (m)RNA is required prior to transfection or (m)RNA quantitation by absorbance measurement. Spin column purification will remove proteins, salts and unincorporated nucleotides. Please follow the manufacturer instructions and ensure that the columns match with product size and possess a sufficient binding capacity (e.g. RNA Clean & Concentrator™ columns (Zymo Research) or Monarch® RNA Cleanup kit (NEB)). Other RNA purification methods such as LiCl precipitation may work but have not been tested.

(m)RNA quantitation

RNA concentration can be determined by absorbance measurement at 260 nm (A_{260}) according to the Law-of-Lambert-Beer ($A_{260} = 1$ corresponds to 40 $\mu\text{g/ml}$ ssRNA).

Related Products:

Pseudo-UTP, #NU-1139

Selected References:

[1] Wienert *et al.* (2018) In vitro transcribed guide RNAs trigger an innate immune response via RIG-I pathway. *PLoS Biol.* **16** (7):e2005840.

[2] Kim *et al.* (2018) CRISPR RNAs trigger innate immune responses in human cells. *Genome Res.* **28** (3):367.