

miRNASelect™ pEP-hsa-mir-941 Expression Vector

CATALOG NUMBER: MIR-941

STORAGE: -80°C

QUANTITY: 100 µL of bacterial glycerol stock

Background

MicroRNAs (miRNAs) are 18–24 nucleotide RNA molecules that regulate the stability or translational efficiency of target mRNAs. These regulatory RNAs function by acting as sequence-specific guides which recruit a large protein complex known as the RNA-induced silencing complex (RISC) to target mRNAs which are subsequently silenced. Diverse functions have been attributed to miRNAs including the regulation of cellular differentiation, proliferation, and apoptosis. Moreover, significant evidence has accumulated implicating a fundamental role for miRNAs in the development of cancer.

miRNAs are initially transcribed as long precursor transcripts known as primary microRNAs (pri-miRNAs). Within these transcripts, the mature miRNA sequences are found in ~60–80 nucleotide hairpin structures. Mature miRNAs are generated from pri-miRNAs by sequential processing (Fig. 1). Pri-miRNAs are initially recognized in the nucleus by the microprocessor complex which includes as core components the RNase-III enzyme Drosha and its obligate partner DGCR8. This complex excises the hairpin structure containing the mature miRNA sequence. The liberated hairpins, referred to as precursor miRNAs (pre-miRNAs), are recognized by the nuclear export factor exportin 5 which transports them to the cytoplasm. There, the RNase-III enzyme Dicer performs a second cleavage to generate a double-stranded 18–24 nucleotide RNA molecule. The RISC then associates with this RNA duplex and unwinds it. Generally, only one strand is stably incorporated into the RISC; the other is discarded and rapidly degraded. miRNAs guide the RISC to target messages that are subsequently cleaved or translationally silenced.



Figure 1. miRNA Biogenesis and function

Synthetic miRNA molecules based on predicted mature miRNA sequence are sometimes used. Despite their optimized design criteria, synthetic miRNAs underscore the importance of primary miRNA in its native expressed form. The primary miRNA contains critical biological components involved in mature miRNA expression and cellular processing, and is often processed into several mature miRNA molecules.

Cell Biolabs' microRNA precursor vectors express each individual human miRNA precursor in its native context while preserving putative hairpin structures to ensure biologically relevant interactions with endogenous processing machinery and regulatory partners, and that leads to properly cleaved microRNAs.

Each individual miRNA precursor is cloned between BamHI and Nhe I sites (Figure 2).

The pEP-mir vectors contain the following features:

- **miRNA precursor** – 100 bp stem loop precursor in its native context flanked by a human intron sequence to preserve the putative hairpin structure and proper endogenous processing
- **EF-1 α Promoter** - ensures a high level of expression in mammalian cells
- **Puromycin resistance marker** - to monitor cells positive for expression and stable selection
- **SV40 polyadenylation signal** - enables efficient termination of transcription
- **pUC origin** - for high copy replication and maintenance of the plasmid in *E. coli*
- **Ampicillin resistance gene** - for selection in *E. coli*

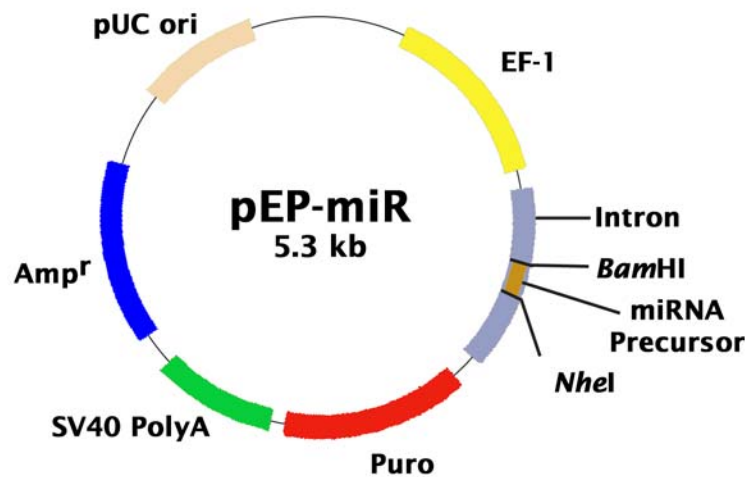


Figure 2. Schematic representation of pEP-miR expression vector.

miRNA precursor sequence:

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1  tcgaggatcc  ctttaagtct  tctgaggagc  atggacctgc  tagactgcaa  gctgctgcat
61  tctgaggagc  agggacctgc  taaactgcaa  gctgccgcag  gcggagattt  ttgcctgttt
121 ggtttatattt  gttaccactg  agtccccagc  tctgagaaca  gagcgaggca  tgtgatcgat
181 gcatcgtaac  tgttgagcaa  atgaatgctg  agctgtgatg  gcaccgacgt  gtccggggag
241 aggacgcacc  cggctgtgtg  gacatgtgcc  cagggcccag  gacagcgcca  cggaagagga
301 cacacccggc  tgtgtggaca  tgtgccagg  gcccgggaca  gcgccacgga  agaggacgca
361 cccggctgtg  tgcacatgtg  cccaggggcc  gggacagcgc  cacggaagag  gacgcacccg
421 gctgtgtgca  catgtgcca  gggcccggga  cagcgccacg  gaagaggacg  caccggctg

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481 tgtgcacatg tgcccagggc ccgggacagc gccacggaag aggacgcacc cggctgtgtg
541 gacatgtgcc cagggcccg gacagcgcca cggaagagga cgcacaggac agcgccacgg
601 aagaggacgc acccggtgt gtgcacatgt gccaggggcc cgggacagcg ccacggaaga
661 ggacgcaccc ggctgtgtgc acatgtgccc agggcccggg acagcgccat ggaagaggac
721 gcacccggct gtgtgcacat gtgcccaggg cccgggacag cgccacggaa gaggacgcac
781 ccggctgtgt gcacatgtgc ccagggcccg ggacagcgcc acggaagagg atgcacccgg
841 ctgtgtggac atgtgcccag ggcccgggac agcgccacgg aagaggacgc acccggtgt
901 gtggacatgt gccaggggcc cgggacagcg ccacggaaga ggacgcaccc ggctgtgtgg
961 acatgtgccc agggcccggg acagcgccac ggaagaggac gcacaggaca gcgccacgga
1021 agaggacgca cccggctgtg tggcagggga ggttcccaag agcaggctca gggctctggg
1081 gtctgagtga gggctctcca gccaggctag ctcga

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Methods

- 1) Bacterial culture: the microRNA precursor construct is provided as bacterial glycerol stock. Individual colonies can be obtained by culturing in an LB-ampicillin plate.
- 2) Plasmid isolation: we recommend EndoFree Plasmid Kits (QIAGEN).
- 3) Transfection into target cells: we recommend Lipofectamine 2000 (Invitrogen).
- 4) Stable selection: 48 hrs post-transfection, select stable clones in 1-10 µg/mL Puromycin-containing medium.

References

1. microRNA sequences listed in Sanger's miRBase (<http://microrna.sanger.ac.uk/sequences/>).
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3. Johnson, S. M., H. Grosshans, J. Shingara, M. Byrom, R. Jarvis, A. Cheng, E. Labourier, K. L. Reinert, D. Brown and F. J. Slack (2005) *Cell* **120**: 635-47.
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