Certificate of Analysis



Specified on product label.

pEF1α-DsRed-Monomer-N1 Vector

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Product Information

631978

pEF1α-DsRed-Monomer-N1 is a mammalian expression vector that constitutively expresses a protein of interest fused to the N-terminus of the red fluorescent protein DsRed-Monomer, even after stable integration of the vector into the host cell genome. Stable, constitutive expression of the fusion protein is driven by the human elongation factor 1 alpha (EF1α) promoter, allowing the monitoring of a variety of cellular processes (such as differentiation in primary or stem cells) without the transgene silencing associated with CMV promoters. The unmodified vector can be used to express DsRed-Monomer in mammalian cells.

Package Contents

1 tube of pEF1α-DsRed-Monomer-N1 Vector (20 μl/tube)

 $10 \, \mu g$

Storage Conditions

- Store plasmid at -20°C.
- Spin briefly to recover contents.
- Avoid repeated freeze/thaw cycles.

Shelf Life

1 year from date of receipt under proper storage conditions.

Storage Buffer

10 mM Tris-HCl (pH 8.0), 1 mM EDTA (pH 8.0)

Concentration

 $500 \text{ ng/}\mu\text{l}$

Shipping Conditions

Dry ice (-70°C)

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Certificate of Analysis

pEF1α-DsRed-Monomer-N1 Vector

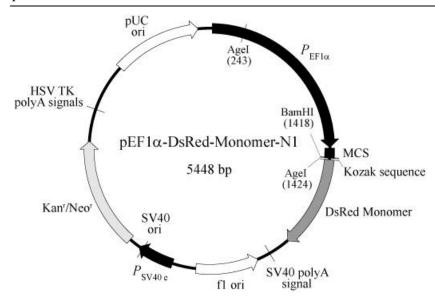


Figure 1. pEF1α-DsRed-Monomer-N1 vector map. Please note that the vector DNA provided by Clontech is methylated. If you wish to digest the vector with methylation-sensitive enzymes, you will first need to transform the vector into a dam⁻ host strain and purify fresh plasmid DNA.

	NheI											HindIII			EcoRI		
1346	ACG	CTA	GCG	CTA	CCG	GAC	TCA	GAT	CTC	GAG	CTC	AAG	CTT	CGA	ATT	CTG	
	Accl Kpnl Xmal								П					**	C444		
	Sall Acc65I			SmaI										Start of SRed-Monomer			
1394	CAG	TCG	ACG	GTA	CCG	CGG	GCC	CGG	GAT	CCA	CCG	GTC	GCC	ACC	ATG	GAC	AAC

Figure 2. pEF1α-DsRed-Monomer-N1 multiple cloning site (MCS).

Description

pEF1α-DsRed-Monomer-N1 is designed to express a protein of interest fused to the N-terminus of DsRed-Monomer, a monomeric mutant of the *Discosoma sp.* red fluorescent protein DsRed (1). The DsRed-Monomer coding sequence has been human-codon-optimized for high expression in mammalian cells (2). The excitation and emission maxima of native DsRed-Monomer are 557 nm and 585 nm, respectively. Expression of fusion proteins that retain the fluorescence properties of unmodified DsRed-Monomer can be monitored by flow cytometry and localized by fluorescence microscopy.

The multiple cloning site (MCS) in pEF1 α -DsRed-Monomer-N1 is positioned between the EF1 α promoter ($P_{\rm EF1}\alpha$) and the DsRed-Monomer coding sequence. Expression of the fusion protein is driven by the EF1 α promoter, which remains constitutively active even after stable integration of the vector into the host cell genome (3). A Kozak consensus sequence, located immediately upstream of the DsRed-Monomer gene, enhances the translational efficiency of DsRed-Monomer in eukaryotic systems (4), and SV40 polyadenylation signals direct proper processing of the 3' end of the DsRed-Monomer mRNA.

The vector backbone contains an SV40 origin for replication in mammalian cells expressing the SV40 large T antigen, a pUC origin of replication for propagation in *E. coli*, and an f1 origin for single-stranded DNA production. A neomycin-resistance cassette (Neo^r) allows stably transfected eukaryotic cells to be selected using G418 (5). This cassette consists of

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the SV40 early promoter ($P_{SV40 e}$), the Tn5 neomycin/kanamycin resistance gene, and polyadenylation signals from the herpes simplex virus thymidine kinase (HSV TK) gene. A bacterial promoter upstream of the cassette drives expression of the kanamycin resistance gene in $E.\ coli.$

Location of Features

- $P_{\text{EFI}\alpha}$ (human elongation factor 1 alpha promoter): 12–1346
- MCS (multiple cloning site): 1348–1422
- Kozak consensus sequence: 1429–1439
- DsRed-Monomer (human-codon-optimized): 1436–2110
- SV40 polyA signal: 2267–2301
- f1 origin of replication: 2364–2819 (complementary)
- $P_{\text{SV40 e}}$ (SV40 early promoter and enhancer sequences): 2993–3261
- SV40 origin of replication: 3160–3295
- Kan^r/Neo^r (kanamycin/neomycin resistance gene): 3344–4138
- HSV TK polyA signals: 4374–4392
- pUC origin of replication: 4723–5366

Additional Information

The gene of interest must be cloned into pEF1 α -DsRed-Monomer-N1 so that it is in-frame with the DsRed-Monomer coding sequence. The gene must contain a start codon (ATG), and lack in-frame stop codons.

Cells expressing DsRed-Monomer fusions can be detected by flow cytometry or fluorescence microscopy 12–16 hr after transfection. If required, stable transfectants can be selected using G418 (5). pEF1α-DsRed-Monomer-N1 can also be used as a cotransfection marker, as the unmodified vector will express DsRed-Monomer in mammalian cells.

Propagation in E. coli

- Suitable host strains: DH5α, HB101 and other general purpose strains. Single-stranded DNA production requires a host containing an F plasmid, such as the JM109 or XL1-Blue strains.
- Selectable marker: plasmid confers resistance to kanamycin (50 μg/ml) in E. coli hosts.
- E. coli replication origin: pUC
- Copy number: high

Excitation and Emission Maxima of DsRed-Monomer

Excitation: 557 nmEmission: 585 nm

References

- 1. Matz, M. V., et al. (1999) Nat. Biotechnol. 17(10):969–973.
- 2. Haas, J., et al. (1996) Curr. Biol. 6(3):315-324.
- 3. Wang, R. et al. (2008) Stem Cells Dev. 17(2):279–289.
- 4. Kozak, M. (1987) Nucleic Acids Res. 15(20):8125-8148.
- 5. Gorman, C. (1985) In *DNA Cloning: A Practical Approach, Vol. II*. Ed. D. M. Glover (IRL Press, Oxford, U.K.) pp. 143–190.

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Quality Control Data

Plasmid Identity & Purity

• Digestion with the indicated restriction enzymes produced fragments of the indicated sizes on a 0.8% agarose/EtBr gel:

Enzyme(s) Fragment(s)
BamHI 5.4 kb
AgeI 1.2 & 4.3 kb

• Vector identity was confirmed by sequencing.

• A_{260}/A_{280} : 1.8–2.0

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pEF1alpha-DsRed-Monomer-N1 Vector

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631978

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STATEMENT 44

The DsRed-Monomer and the Fruit Fluorescent Proteins are covered by one or more of the following U.S. Patents: 7,005,511; 7,157,566; 7,393,923 and 7,250,298.

STATEMENT 72

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