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PRODUCT: pDsRed-Monomer-Hyg-C1 Vector

CATALOG No. 632495

LOT NUMBER

Specified on product label.

STORAGE CONDITIONS

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

PLASMID STORAGE BUFFER

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

SHELF LIFE

1 year from date of receipt under proper storage conditions.

SHIPPING CONDITIONS

Blue ice (4°C) or dry ice (-70°C)

DESCRIPTION

pDsRed-Monomer-Hyg-C1 encodes DsRed-Monomer, a monomeric mutant of the *Discosoma* sp. red fluorescent protein DsRed. pDsRed-Monomer-Hyg-C1 is designed for studies in mammalian systems. This vector allows expression of a protein of interest as a C-terminal fusion to DsRed-Monomer. The vector contains a hygromycin resistance gene for the selection of stable transfectants. pDsRed-Monomer-Hyg-C1 can also be used as a cotransfection marker since the unmodified vector constitutively expresses DsRed-Monomer. The fluorescent protein coding sequence in this construct has been human codon-optimized for efficient expression and enhanced brightness in mammalian cells.

CONCENTRATION: 500 ng/ μl

PLASMID SIZE: 5.7 kb

CLONING SITES: *Acc I, Apa I, Asp718 I, BamH I, Hind III, Kpn I, Sac I, Sal I, Sma I, Xho I, Xma I*

ANTIBIOTIC RESISTANCE

- Ampicillin (100 $\mu\text{g}/\text{ml}$ for propagation in *E. coli* cells)
- Hygromycin (500 $\mu\text{g}/\text{ml}$ for selection in mammalian cells)

PACKAGE CONTENTS

- 20 μg pDsRed-Monomer-Hyg-C1 Vector

OTHER

- pDsRed-Monomer-Hyg-C1 Vector Information Packet (PT3842-5)

FOR RESEARCH USE ONLY

QUALITY CONTROL DATA

See back of page.



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(PA842693)

QUALITY CONTROL DATA

- Digestion with the indicated restriction enzymes produced fragments of the indicated sizes on an agarose/EtBr gel:

Enzyme(s)	Fragment(s)*
<i>Age</i> I	5.7 kb
<i>EcoR</i> I	1.5 & 4.2 kb

- The presence of the correct fluorescent protein variant was confirmed by sequencing.
- Plasmid purity was analyzed by OD A_{260}/A_{280} measurement and found to be ≥ 1.8

* **Note:** Fragment sizes are estimates; the apparent sum of all fragment sizes for a given digest may not equal the actual size of the plasmid due to number rounding.

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