

LOCUS MinRW NFAT-GFP 9542 bp DNA circular

DEFINITION Ligation of MiTW NFAT-GFP (mutagenized to insert convenient sites) (

PacI/MfeI) (Ligation of MiTW (EcoRI/BglII) ( 7763 bp

ds-DNA circular 06-MAY-2012

ORGANISM

ApEinfo:methylated

:1

TRM lab

Fragment of MiTW, was cut with EcoRI at position 1429),

MSCV NFAT1(1-460) - eGFP (AvrII mutagenized by insertion CCTAGG pos

ition 1861)\* (BglII/MfeI) (This sequence has been entered manually.

Francesco Marangoni

Cropped from MSCV NFAT1(1-460) - eGFP (AvrII mut

agenized by insertion CCTAGG position 1861) to fragment (450-2595).

Fragment of MSCV NFAT1(1-460) - eGFP (AvrII mutagenized by insertion

CCTAGG position 1861)\*, was cut with BglII at position 4)

Fragment

of MiTW NFAT-GFP (mutagenized to insert convenient sites), was cut w

ith PacI at position 3446), MinW H2B-mRFP swappable\* (MfeI/PacI) (Li

gation of MinW (EcoRI/BglII) (This sequence has been entered manuall

y.

Francesco Marangoni

Fragment of MinW, was cut with EcoRI at posit

ion 1429), pHIV H2B-mRFP\* (BglII/MfeI) (This sequence has been enter

ed manually.

Francesco Marangoni

Amplify and cut BglII - MfeI

Cropp

ed from pHIV H2B-mRFP to fragment (4414-5528).

Fragment of pHIV H2B-

mRFP\*, was cut with BglII at position 3)

Cropped from MinW H2B-mRFP

swappable to fragment (7130-8243).

Fragment of MinW H2B-mRFP swappab

le\*, was cut with MfeI at position 4)

FEATURES Location/Qualifiers

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/gene="NFAT1(1-460)"

misc\_feature 6818..7706

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/note="(extended packaging signal)"

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dth 5 offset 0"

CDS complement(4511..5368)

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/gene="mRFP1"

misc\_feature 2006..2597

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121 gccgaccact accagcagaa cacccccatc ggcgacggcc ccgtgctgct gcccgacaac

181 cactacctga gcacccagtc cgccctgagc aaagacccca acgagaagcg cgatcacatg

241 gtcctgctgg agttcgtgac cgccgccggg atcactctcg gcatggacga gctgtacaag

301 taacaattcc gccccccccc cctaacgtta ctggccgaag ccgcttggaa taaggccggt

361 gtgcgtttgt ctatatgtta ttttccacca tattgccgtc ttttggcaat gtgagggccc

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481 gaatgcaagg tctgttgaat gtcgtgaagg aagcagttcc tctggaagct tcttgaagac

541 aaacaacgtc tgtagcgacc ctttgcaggc agcggaaccc cccacctggc gacaggtgcc

601 tctgcggcca aaagccacgt gtataagata cacctgcaaa ggcggcacaa ccccagtgcc

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