

MEK1 ProtéGene™ Set

Catalog# P1030
Lot# 280821

Materials Provided:

1. pMEV-MEK1-WT (P1030a): 20 µg in 40 µl TE (pH7.5), 0.5 mg/ml.
2. pMEV-MEK1-DN (P1030b): 20 µg in 40 µl TE (pH7.5), 0.5 mg/ml.
3. pMEV-MEK1-CA (P1030c): 20 µg in 40 µl TE (pH7.5), 0.5 mg/ml.
4. pMEV-MEK1-K97R (P1030d): 20 µg in 40 µl TE (pH7.5), 0.5 mg/ml.
5. Product Information Sheets.

Note: Individual plasmids can be ordered separately. Also available is the kinase-deficient mutant pMEV-MEK1-K97R (Cat#P1030d). Some plasmids are shipped as lyophilized pellet.

Receiving and Storage:

If received in lyophilized form, add 40 µl sterile DI water to the vial, mix thoroughly by vortex and then collect the contents by centrifuging the vials briefly in a microcentrifuge. If received in liquid form, spin the vials briefly in a microcentrifuge to collect the contents. Store the products at 2-8°C if used immediately and store at -20°C for extended storage.

Expression Vector:

pMEV-2HA (a): Cat# P1001a.

Affinity Tag:

N-terminal 2 x HA, a 9-aa peptide derived from influenza virus (MGYPYDVPDYAYPDVPDYAGS...).

Prokaryotic Selection:

The kanamycin-resistance gene (aminoglycoside 3' phosphotransferase) expression cassette in the plasmids confers Kanamycin resistance to bacteria cells. Bacterial cells transformed with the plasmids should be maintained and grown in media containing 25-50 µg/ml Kanamycin (e.g. #LK-1100, Prepared LB Agar plates, Biomyx, San Diego, California).

Eukaryotic Selection:

The neomycin resistance gene, driven by SV40 early promoter, confers G418 resistance to eukaryotic cells. Stable mammalian cell lines can be selected with G418.

Description of MEK1 and Mutants

MEK1 and MEK2 are members of the dual specificity protein kinase family, which acts as a mitogen-activated protein (MAP) kinase kinase. MAP kinases, also known as extracellular signal-regulated kinases (ERKs), act as an integration point for multiple biochemical signals. MEK1 lies upstream of MAP kinases and stimulates the enzymatic activity of MAP kinases upon wide variety of extra- and intracellular signals. MEKs are involved in many cellular processes such as proliferation, differentiation, transcription regulation and development.

Several residues are essential for MEK to function: K97 for its catalytic activity, S218 and S222 for activation by upstream activators. The dominant negative mutant provided (P1030b) contains 3 point mutations (K97R; S218A; S222A) and can neither be phosphorylated by its activators nor phosphorylate its downstream effectors (ERKs). The constitutively active mutant (P1030c) contains 2 point mutations (S218E and S222E) and a deletion of amino acid residues 31-52.^(1, 6, 9) The resulting protein is ~400 times more active than recombinant MEK1 wild type expressed in *E. coli*, and is active without the need of being phosphorylated by its upstream activators.

Molecular Features of the Inserts:

Gene: *Homo sapiens* mitogen-activated protein kinase kinase 1

GenBank Reference Sequence: NM_002755

5'-Cloning Site: Bam HI

5'-Junction Sequence: 5'...tac gct gga tcc **ATG CCC AAG**...3'

3'-Cloning Site: Bam HI

3'-Junction Sequence: 5'...gcggatcccttgttgcaccac **TTA GAC GCC**...3'

hMEK1 Protein Sequence

(393 amino acid residues. Amino acid residues 31-52, K97, S218, S222 are in bold and underlined.)

MPKKKPTPIQLNPAPDGSAVNGETS**SAETNL****EAL****QKKL****EEL****DEQQ****RKR**
LEA**FLT****QKQKV****GEL****KDDDF****EK****I****SEL****GAG****NNGGV****VFK****VSH****KP****SGL****VMARK****L****I****H**
EIK**PAIRN****QI****REL****QVL****HECN****SPY****IVG****FY****GAF****YSD****GE****I****SICM****EHM****DGS****LQ**
VLK**KAGRI****PQE****ILGK****SIAV****IKGL****TLYRE****KHM****RDV****KPSN****ILVNSR****G**
LCDFG**VSG****QLID****S****MANS****FVG****TRSY****MSP****PERL****QGTH****YSV****QSDI****WMSGL****LSV****EMA**
VGRY**PIP****PPDA****KELEM****FGC****VEG****DAE****TPP****PR****TPG****PL****SSY****GMD****SRPP****MA**
I**FELLD****YIVN****NEPPP****KLPSGV****FSLF****QDF****VNK****CLIK****NPAE****DLK****QLMV****HAF**
KRS**DAE****EVD****FAG****WL****CSTI****GLN****QP****STP****THAAG**

hMEK1 Nucleotide Sequence

(1182bps. Nucleotides encoding aa32-51, K97, S218, S222 are in bold and underlined)

1 ATGCCAACAG AGAAAGCCGAC GCCCATCCAG CTGAACCCGG CCCCCGACGG
51 CTCCTGCAGT AAAGGCCGCA GCTCTCGGGA GACCAACTTG GAG**GCCTTG**
101 **AGAAGAGCT** **GGAGGAGCTA** **GAGCTTGATG** **ACGACAGCG** **AAAGCGCC**
151 **GAG****GCTTC** TTACCCAGAA GCAGAAGGT GGAGAACATGA AGGATGACGA
201 CTTTGAGATAA ATCAGTGAC TGGGGCTGGA CAATGGCGGT GTGGTTCTCA
251 AGGTCTCCCA CAAAGCTTCT GCGCTGGTCA TGCCCGAG**AA****G****CTAATT****CAT**
301 CTGGAGATCA AACCCGCAAT CGCGAACAG ATCATAAGG AGCTCGCAGG
351 TCTGCTATGAC CGACACTCTG CGTACAATCGT GGCGCTCTAT GGTGCGTTCT
401 ACACGGATGCG CGAGATCAGT ATCTGCATGG ACCACATGGA TGGAGGTTCT
451 CTGGATCAAG TCTTGAAGAA AGCTGGAAGA ATTCCCTGAAC AAATTTAGG
501 AAAAGTTAGG ATTCAGCTGAA TAAAAGGCTT GACATATCTG AGGGAGAAGC
551 CAAAGATCAT GCACAGAGAT CTCAGGCCCT CCAACATCTT AGTCAACTCC
601 CGTGGGGAGA TCAAGCTCTG TGACTTCTGGG GTCAAGGGGGC AGCTCATCGA
651 **TCC****CAT****GGC** AACT**TCC** TGGGGCACAAG GTCTCACATG TCGCCGAAAGA
701 GACTCAGGCG GACTCATTAC TCTGTGCACT GAGCACATCTG GAGCATGG
751 CTGTCCTCTG TAGAGATGGC GTTGGGGAGG TATCCCCTACCT CCCTCTCCAGA
801 TGCCAAGGAG CTGGAGCTGA TGTTGGGTG CCAGGTGGAA GGAGATGCGG
851 CTGAGACCCC ACCCAGCCCA AGGACCCCC GGAGGCCCTT TAGCTCATAC
901 GGAATGGACG CGCCGACCTC CATGGCAATT TTGGAGTTGT TGATTACAT
951 AGTCACCGAG CCTCTCTCAA AACTGCCAG TGGAGTGTTC AGCTGGTAAT
1001 TTCAAGATTG TTGGAATAAA TGCTTAATAA AAAACCCCGC AGAGAGAGCA
1051 GATTGAGAG AACTCATGGT TCATGCTTT ATCAAGAGAT CTGATGCTGA
1101 GGAAGTGGAT TTTCAGGGT GGCTCTGCTC CACCATCGGC CTTAACCGAC
1151 CCAGCACACC AACCCATGCT GCTGGCGTCT AA

Mutations:

pMEV-MEK1-WT (P1030a): No mutation

pMEV-MEK1-DN (P1030b): K97R; S218A; S222A

pMEV-MEK1-CA (P1030c): Δ32-51; S218E; S222E

pMEV-MEK1-K97R(P1030d): K97R

References:

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6. Mansour S. J. et al., 1994, *Science*, 265: 966-970
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