

Division of Signal Transduction Therapy

Standard Operating Procedure

Preparation of M025 alpha [1 - 341]

Enzyme description:- MO25 alpha [1 – 341]

Clone number:- DU 2945

Source:- Recombinant

Expression system:- *E.coli*,

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Calculated molecular mass:-

Monoisotopic 66,650.38 daltons

Average Mass 66,693.16 daltons

[cysteines reduced, methionines have not been oxidised

Theoretical pI:- 6.09

Purity:- >80 %

Enzyme storage buffer:-

50 mM Tris-HCl pH 7.5, 150 mM NaCl, 270 mM sucrose, 0.1 mM EGTA,
0.1 % 2-mercaptoethanol, 0.03 % Brij-35, 1 mM benzamidine, 0.2 mM PMSF

Storage temperature:- -70 °C

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Clone Data Sheet

MO25 alpha [1 - 341]

Protein MO25 alpha [1 - 341]

Clone number DU 2945

Species Human

Accession number NM_016289.3

Tags N-terminal GST

Bacterially expressed protein
MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFEL
GLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNLGGCPKERAESMLE
GAVLDIYGVSRAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLN
GDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKY
LKSSKYIAWPLQGWQATFGGGDHPPKSDLEVLFQGPLGSMPFPFGKSH
KSPADIVKNLKE~~SMAVLEKQDISDKKAEKATEEVSKNLVAMKE~~ILYGT
NEKEPOTEAVAQLAQELYNSGLLSTLVADLQLIDFEGKKDVAQIFNNI
LRRQIGTRPTVEYICTQQNILFMLLKGYESPEIALNCGIMLRECIRH
EPLAKIILWSEQFYDFFRYVEMSTFDIASDAFATFKDLLTRHKLLSAE
FLEQHYDRFFSEYEKLLHSENYVTKRQSLKLLGE~~LLLDRHNFTIMTKY~~
~~ISKPENLKLMMNLLRDKSRNIQFEAFHVFKVFVANPNKTQPILDILLK~~
~~NQAKLIEFLSKFQNDRTEDEQFNDEKTYLVKQIRDLKRPAQQEA~~

Native sequence Amino acids M1 – A341 (end) of human MO25 alpha.

Residue M232 of fusion protein is equivalent to M1 of the native enzyme. The GST tag is located at residues 1 – 220.

Protease cleavage Prescission site (LEVLFQGP) at residues 221 – 228

Cloning sites *Bam*H1 sites of pGex6P-1

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Nucleotide sequence of insert

ggatccATGCCGTTCCGGAGTCTCACAAATCTCCAGCAGAC
ATTGTGAAGAATCTGAAGGAGAGCATGGCTGTTCTGAAAAGCAAGAC
ATTTCTGATAAAAAAGCAGAAAAGGCTACAGAAGAAGTTCCAAAAAT
CTGGTTGCCATGAAAGAAATTCTGTATGGCACAAATGAAAAAGAGCCT
CAGACAGAAGCAGTAGCTCAACTGCTCAAGAACTCTATAATAGTGGG
CTCCTTAGCACCCCTGGTAGCTGATTACAGCTCATTGACTTTGAGGGC
AAAAAAGACGTGGCTAAATTTCACAATATTCTCAGAAGACAAATT
GGTACGAGAACTCCTACTGTTGAATACATCTGCACCCAACAGAAATATT
TTGTTCATGTTATTGAAAGGGTATGAATCTCAGAAATAGCTCTAAAT
TGTGGAATAATGTTAAGAGAATGCATCAGACATGAACCACTTGCAAA
ATCATTGTTGCGAACAGTTTATGATTCTTCAGATATGTCGA
ATGTCAACATTGACATAGCTCAGATGCATTGCCACATTCAAGGAT
TTACTTACAAGACATAAATTGCTCAGTGCAGAATTGGAACAGCAT
TATGATAGATTTTCAGTGAATATGAGAACGTTACTTCATTCAAGAAAAT
TATGTGACAAAAAGACAGTCACTGAAGCTCTCGGTGAACTACTA
GATAGACACAACCTCACAAATTGACAAAATACATCAGTAAACCTGAG
AACCTCAAATTGATGAACCTGCTGCGAGACAAAAGTCGCAACATC
CAGTTGAGGCCTTCACGTTTAAGGTGTTGAGCCAATCTAAC
AAGACGCAGCCCATTCTAGACATCCTCCTCAAGAACCCAGGCCAAACTC
ATAGAGTTCTCAGCAAGTTCAGAACGACAGGACGGAGGATGAGCAG
TTAACGACGAGAACCTATTAGTTAACAGATCAGGGATTGAAG
AGACCAGCTCAGCAAGAAGCTtaaggatcc