

Division of Signal Transduction Therapy

Standard Operating Procedure

Preparation of MO25 beta [5 - 337]

Enzyme description:- MO25 beta [5 – 337]

Clone number:- DU 38053

Source:- Recombinant

Expression system:- *E.coli*,

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Calculated molecular mass:-

Monoisotopic 65, 595.26 daltons

Average Mass 65, 637.32daltons

[cysteines reduced, methionines have not been oxidised

Theoretical pI:- 6.43

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 beta [5 - 337]

<u>Protein</u>	MO25 beta [5 - 337]
<u>Clone number</u>	DU 38053
<u>Species</u>	Human
<u>Accession number</u>	NM_030925.2
<u>Tags</u>	N-terminal GST
<u>Bacterially expressed protein</u>	MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFEL GLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNLGGCPKERAESMLE GAVLDIYGVSRAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLN GDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKY LKSSKYIAWPLQGWQATFGGGDHPPKSDLEVLFQGPLGSMLPLFSKSH KNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEK EPPTTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRR QIGTRSPTEVYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPL AKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVLVADFLE QNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDHRHNFAIMTKYISK PENLKLMNNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP KLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLKKTAP
<u>Native sequence</u>	Amino acids P5 – P337 (end) of human MO25 beta. Residue P234 of fusion protein is equivalent to P5 of the native enzyme. The GST tag is located at residues 1 – 220.
<u>Protease cleavage</u>	Prescission site (<u>LEVLFQGP</u>) at residues 221 – 228
<u>Cloning sites</u>	<i>Bam</i> H1 and <i>Not</i> 1 sites of pGex6P-1

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Nucleotide sequence of insert

ggatccatgttgCCTTGTTAGTAAATCACACAAAAATCCAGCAGAA
ATTGTGAAAATCCTGAAAGACAATTGCCATTGGAAAAGCAAGAC
AAAAAGACAGACAAGGCTTCAGAAGAAGTGTCTAAATCACTGCAAGCA
ATGAAAGAAATTCTGTGTGGTACAAACGAGAAAGAACCCCCGACAGAA
GCAGTGGCTCAGCTAGCACAAGAACTCTACAGCAGTGGCTGCTGGTG
ACACTGATAGCTGACCTGCAGCTGATAGACTTGGAGGGAAAAAGAT
GTGACCCAGATATTAAACAACATCTTGAGAAGACAGATAGGCACTCGG
AGTCCTACTGTGGAGTATATTAGTGTCTCATCCTCATATCCTGTTATG
CTCCTCAAAGGATATGAAGCCCCACAGATTGCCTTACGTTGTGGATT
ATGCTGAGAGAATGTATTGACATGAACCACCTGCCAAATCATCCTC
TTTCTAATCAATTCAAGAGATTCTTAAGTACGTGGAGTTGTCAACA
TTTGATATTGCTTCAGATGCCTTGCTACTTCAAGGATTACTAAC
AGACATAAAAGTGTGGTAGCAGACTTCTAGAACAAAATTACGACACT
ATTTTGAAAGACTATGAGAAATTGCTTCAGTCTGAGAATTATGTTACT
AAGAGACAGTCTTAAAGCTGCTAGGGGAGCTGATCCTGGACCGTCAC
AACTTGCATCATGACAAAGTATATCAGCAAGCCGAGAACCTGAAA
CTCATGATGAACCTCCTCGGGATAAAAGTCCAACATCCAGTTGAA
GCCTTCATGTTTAAGGTGTTGTGGCCAGTCCTCACAAACACAG
CCTATTGTGGAGATCCTGTTAAAAAATCAGCCAAACTCATTGAGTT
CTGAGCAGCTCCAAAAGAAAGGACGGATGATGAGCAGTTCGCTGAC
GAGAAGAACTACTTGATTAAACAGATCCGAGACTTGAAGAAAACGGCC
CCTttagcgccgcg