

Division of Signal Transduction Therapy

Standard Operating Procedure

Preparation of Moesin [400 - 577]

Enzyme description:- Moesin [400 - 577]

Clone number:- DU 27094

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Calculated molecular mass:-

Monoisotopic 47, 265.78 daltons

Average Mass 47, 295.86 daltons

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 5.39

Purity:- >80 %

Enzyme storage buffer:-

50 mM Tris-HCl pH 7.5, 270 mM Sucrose, 150 mM NaCl, 0.1 mM EGTA,
0.1 % 2-mercaptoethanol, 0.02 % Brij-35, 1 mM benzamidine, 0.2 mM PMSF

Storage temperature:- -70 °C

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Clone Data Sheet

Moesin [400 - 577]

<u>Protein</u>	Moesin [400 - 577]
<u>Clone number</u>	DU 10763
<u>Species</u>	Human
<u>Accession number</u>	NM_0024442
<u>Tags</u>	N-terminal GST
<u>Bacterially expressed protein</u>	<p>MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELG LEFPNLPHYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLEGA VLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSS KYIAWPLQGWQATFGGGDHPKSDLEVLFOGPLGSKEALLQASRDQKKT QEQLALEMAELTARISQLEMARQKKESEAVEWQQAQMVEDLEKTRAE LKTAMSTPHVAEPAENEQDEQDENGAEASADLRADAMAKDRSEEERTTE AEKNERVQKHLKALTSELANARDESKKTANDMIHAENMRLGRDKYKTLR QIRQGNTKQRIDEFESM</p>
<u>Native sequence</u>	<p>Amino acids K400 – M577 (end) of human Moesin. Residue K232 of the fusion protein is equivalent to K400 of the native enzyme. The GST tag is located at residues 1 – 220.</p>
<u>Protease cleavage</u>	PreScission (<u>LEVLFQGP</u>) residues 221 - 228
<u>Cloning sites</u>	<i>Bam</i> H1 and <i>Not</i> 1 sites of pGEX6P

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**Nucleotide
Sequence
of Insert**

ggatccAAGGAGGCCTTGCTGCAGGCCTCCCGGGACCAGAAAAAGA
CTCAGGAACAGCTGGCCTTGGAAATGGCAGAGCTGACAGCTCGAAT
CTCCCAGCTGGAGATGGCCCGACAGAAGAAGGAGAGTGAGGCTGTG
GAGTGGCAGCAGAAGGCCAGATGGTACAGGAAGACTTGGAGAAGA
CCCGTGCTGAGCTGAAGACTGCCATGAGTACACCTCATGTGGCAGA
GCCTGCTGAGAATGAGCAGGATGAGCAGGATGAGAATGGGGCAGAG
GCTAGTGCTGACCTACGGGCTGATGCTATGGCCAAGGACCGCAGTG
AGGAGGAACGTACCACTGAGGCAGAGAAGAATGAGCGTGTGCAGAA
GCACCTGAAGGCCCTCACTTCGGAGCTGGCCAATGCCAGAGATGAG
TCCAAGAAGACTGCCAATGACATGATCCATGCTGAGAACATGCGAC
TGGGCCGAGACAAATACAAGACCCTGCGCCAGATCCGGCAGGGCAA
CACCAAGCAGCGCATTGACGAATTTGAGTCTATGtaagcggccgc

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