

Assay:- Substrate for ERK and JNK

Division of Signal Transduction Therapy

CLONE DATA SHEET

EWS [2 - 656]

Protein EWS [2 - 656]

Clone number DU 1883

Species Human

Accession number NM_005243.3

Tags N-terminal GST

**Bacterially
expressed protein**

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFEL
GLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEIFSMLE
GAVLDIRYGVSRIAYS KDFETLKVDFLSKLPEMLKMFEDRLCHKTYLN
GDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKY
LKSSKYIAWPLQGWQATFGGGDHPKSDLEVLFGQPLGSPEF**ASTDYS**
TYSQAAAQQGYSAytaQPTQGYAQTtQAYGQOSYGTyGQPTDVSYtQA
QTTATyGQTAYATSYGQPPTGYTTPTAPQAYSQPVQGYGTGAYDttTA
TVTTTQASyAAQsAYGTQPAYPAYGQQPAATAPTRPDGNKPTETSQP
QSSTGGYNQPSLGYGQSNYSYPQVPGSYPMQPVtAPPsYPPTsYSSTQ
PTSYDQSSYSQONTyGQPSSyGQQSSyGQQSSyGQQPPTsYPPQtGSy
SQAPSQYSQQSSSyGQQSSFRQDHPSSMGVYGQESGGFSGPGENRSMS
GPDNRGRGRGGFDRGGMSRGGRGGRGGMGSAGERGGFNKPGGPMDEG
PDLDLGPPVDPDESDNSAIYVQGLNDSVTLDDLADFFKQCGVVKMNK
RTGQPMIHILDKETGKPKGDATVSyEDPPTAKAAVEWFDGKDFQGSK
LKVSLARKKPPMNSMRGGLPPREGRGMPPLRGPGGGPGGPGGPMGRM
GGRGGDRGGFPPRGPRGSRGNPSGGGNVQHRAGDWQCPNPGCGNQNFa
WRTECNQCKAPKPEGFLPPFPFPFGGDRGRGGPGGMRGGRGGLMDRGG
PGGMFRGGRGGDRGGFRGGRGMDRGGFGGRRGGPGGPPGPLMEQMGg
RRGGRGGPGKMDKGEHRQERRDRPY

Native sequence Amino acids A2 – Y656 of human EWS.
Residue A234 of the fusion protein is equivalent to A2 of the native protein. The GST tag is located at residues 1 – 220.

Protease cleavage PreScission (LEVLFQGP) residues 221 - 228

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Cloning sites

*Eco*R1 and *Sal*I sites of pGEX-6P-1

Nucleotide sequence of insert

gaattcGCGTCCACGGATTACAGTACCTATAGCCAAGCTGCAGCGCAG
CAGGGCTACAGTGCTTACACCGCCCAGCCCACTCAAGGATATGCACAG
ACCACCCAGGCATATGGGCAACAAAGCTATGGAACCTATGGACAGCCC
ACTGATGTCAGCTATACCCAGGCTCAGACCACTGCAACCTATGGGCAG
ACCGCCTATGCAACTTCTTATGGACAGCCTCCCACTGGTTATACTACT
CCAACTGCCCCCAGGCATACAGCCAGCCTGTCCAGGGGTATGGCACT
GGTGCTTATGATACCACCACTGCTACAGTCACCACCACCCAGGCCTCC
TATGCAGCTCAGTCTGCATATGGCACTCAGCCTGCTTATCCAGCCTAT
GGGCAGCAGCCAGCAGCCACTGCACCTACAAGACCGCAGGATGGAAAC
AAGCCCACTGAGACTAGTCAACCTCAATCTAGCACAGGGGGTTACAAC
CAGCCAGCCTAGGATATGGACAGAGTAACTACAGTTATCCCCAGGTA
CCTGGGAGCTACCCCATGCAGCCAGTCACTGCACCTCCATCTACCCT
CCTACCAGCTATTCTCTACACAGCCGACTAGTTATGATCAGAGCAGT
TACTCTCAGCAGAACACCTATGGGCAACCGAGCAGCTATGGACAGCAG
AGTAGCTATGGTCAACAAAGCAGCTATGGGCAGCAGCCTCCCACTAGT
TACCCACCCCAAAGCTGGATCCTACAGCCAAGCTCCAAGTCAATATAGC
CAACAGAGCAGCAGCTACGGGCAGCAGAGTTCATTCGGACAGGACCAC
CCCAGTAGCATGGGTGTTTATGGGCAGGAGTCTGGAGGATTTTCCGGA
CCAGGAGAGAACCGGAGCATGAGTGGCCCTGATAACCGGGGCAGGGGA
AGAGGGGGATTTGATCGTGGAGGCATGAGCAGAGGTGGGCGGGGAGGA
GGACGCGGTGGAATGGGCAGCGCTGGAGAGCGAGGTGGCTTCAATAAG
CCTGGTGGACCCATGGATGAAGGACCAGATCTTGATCTAGGCCCTCCT
GTAGATCCAGATGAAGACTCTGACAACAGTGCAATTTATGTACAAGGA
TTAAATGACAGTGTGACTCTAGATGATCTGGCAGACTTCTTTAAGCAG
TGTGGGGTTGTTAAGATGAACAAGAGAACTGGGCAACCCATGATCCAC
ATCTACCTGGACAAGGAAACAGGAAAGCCCAAAGGCGATGCCACAGTG
TCCTATGAAGACCCACCCACTGCCAAGGCTGCCGTGGAATGGTTTGAT
GGGAAAGATTTTCAAGGGAGCAAACCTTAAAGTCTCCCTTGCTCGGAAG
AAGCCTCCAATGAACAGTATGCGGGGTGGTCTGCCACCCCGTGAGGGC
AGAGGCATGCCACCACCACTCCGTGGAGGTCCAGGAGGCCAGGAGGT
CCTGGGGGACCCATGGGTGCGATGGGAGGCCGTGGAGGAGATAGAGGA
GGCTTCCCTCCAAGAGGACCCCGGGGTCCCGAGGGAACCCCTCTGGA
GGAGGAAACGTCCAGCACCGAGCTGGAGACTGGCAGTGTCCCAATCCG
GGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGAGTGCAACCAGTGT
AAGGCCCCAAAGCCTGAAGGCTTCCTCCCGCCACCCTTTCGCCCCCG
GGTGGTGATCGTGGCAGAGGTGGCCCTGGTGGCATGCGGGGAGGAAGA
GGTGGCCTCATGGATCGTGGTGGTCCCGGTGGAATGTTTCAGAGGTGGC
CGTGGTGGAGACAGAGGTGGCTTCGCTGGTGGCCGGGGCATGGACCGA
GGTGGCTTTGGTGGAGGAAGACGAGGTGGCCCTGGGGGGCCCCCTGGA
CCTTTGATGGAACAGATGGGAGGAAGAAGAGGAGGACGTGGAGGACCT
GGAAAAATGGATAAAGGCGAGCACCGTCAGGAGCGCAGAGATCGGCCC
TACtaggtcgac