Division of Signal Tranduction Therapy

Standard Operating Procedure

Preparation of RILPL1 [1 - 403]

Enzyme description:- RILPL1 [1 - 403]

Clone number:- DU 26562

Source:- Recombinant

Expression system:- *E.coli*

Tag:- C-terminal GST

Purification method:- GSH-Sepharose

Calculated molecular mass:-
Monoisotopic 74, 197.83 daltons
Average Mass 74, 244.47 daltons
[cysteines reduced, methionines have not been oxidised

Theoretical pI:- 5.29

Purity:- >75 %

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

RILPL1 [1 - 403]

Protein	RILPL1 [1 - 403]
Clone number	DU 26562
Species	Human
Accession number	NM_178314.4
Tags	C-terminal GST
Bacterially expressed protein	**MEEERGSALAAESALEKNVAELTVMDVYDIASLVGHEFERVIDQHGCEA IARLMPKVVRVLEILEVLVSRHHVAPELDELRLELDRLRLERMDRIEKE RKHQKELELVEDVWRGEAQDLLSQIAQLQEENKQLMTNLSHKDVNFSEE EFQKHEGMSERERQVMKKLKEVVDKQRDEIRAKDRELGLKNEDVEALQQ QQTRLMKINHDLRHRVTVVEAQGKALIEQKVELEADLQTKEQEMGSLRA ELGKLRERLQGEHSQNGEEEPETEPVGEESISDAEKVAMDLKDPNRPRF TLQELRDVLHERNELKSKVFLLQEELAYYKSEEMEEENRIPQPPPIAHP RTSPQPESGIKRLFSFFSRDKKRLANTQRNVHIQESFGQWANTHRDDGY TEQGQEALQHL**AAALEVLFQGPLSRMSPILGYWKIKGLVQPTRLLLEYL EEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSMAIIR YIADKHNMLGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDF LSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLD AFPKLVCFKKRIEAIPQIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSD
Native sequence	Amino acids M1 – L403 (end) of human RILPL1. Residue M1 of the fusion protein is equivalent to M1 of the native enzyme. The GST tag is located at residues 418 – 637.
Protease cleavage	PreScission (LEVLFQGP) residues 407 - 414
Cloning sites	*Eco*R1 and *Not*1 sites of pEX-GST

Nucleotide Sequence Of Insert

gaattcATGGAGGAGGAGCGGGGGTCGGCGCTGGCGGCCGAGTCGGCGC
TGGAGAAGAACGTGGCCGAGCTGACCGTCATGGACGTGTACGACATCGC
GTCGCTTGTGGGCCACGAGTTCGAGCGGGTCATTGACCAGCACGGCTGC
GAGGCCATCGCGCGCCTCATGCCCAAGGTCGTGCGCGTCCTGGAGATCC
TGGAGGTGCTGGTCAGCCGCCACCACGTCGCGCCCGAGCTGGACGAGCT
GCGCCTGGAGCTGGACCGCCTGCGCCTGGAGAGGATGGACCGCATCGAG
AAGGAGCGCAAGCACCAGAAGGAGCTGGAGCTGGTGGAGGATGTGTGGC
GAGGGGAGGCGCAGGACCTCCTCTCCCAGATCGCCCAGCTGCAGGAGGA
GAACAAGCAGCTCATGACCAACCTCTCCCACAAGGATGTCAACTTCTCA
GAGGAGGAGTTCCAGAAGCATGAAGGCATGTCAGAGCGGGAGCGACAGG
TGATGAAGAAGCTGAAGGAGGTGGTGGACAAACAACGCGACGAGATCCG
CGCCAAGGACAGGGAGCTGGGCCTGAAAAATGAGGACGTTGAGGCTTTA
CAGCAGCAGCAGACACGGCTGATGAAGATCAACCATGACCTTCGGCACC
GGGTCACGGTGGTGGAGGCCCAGGGGAAAGCCCTGATCGAACAGAAGGT
GGAGCTGGAGGCAGACCTGCAGACCAAGGAGCAGGAGATGGGCAGCCTG
CGAGCAGAGCTGGGGAAGTTGCGAGAGAGGCTGCAGGGGGAGCACAGCC
AGAATGGGGAGGAGGAGCCTGAGACGGAGCCGGTGGGAGAGGAGAGCAT
CTCCGACGCAGAGAAGGTGGCCATGGATCTCAAGGACCCCAACCGCCCC
CGGTTCACCCTGCAGGAGCTGCGGGACGTGCTGCACGAGAGGAACGAGC
TCAAGTCCAAGGTGTTCTTGCTGCAGGAGGAGCTGGCTTACTATAAGAG
TGAAGAAATGGAAGAGGAAAACCGAATACCCCAACCCCCACCCATCGCC
CACCCGAGGACGTCCCCCCAGCCGGAGTCGGGCATCAAGCGACTGTTTA
GCTTCTTCTCCCGAGATAAGAAGCGCCTGGCCAACACACAGAGAAACGT
GCACATCCAGGAGTCCTTTGGACAGTGGGCAAACACCCACCGCGATGAC
GGTTACACAGAGCAAGGACAGGAAGCCCTGCAGCATCTGgcggccgca