Division of Signal Tranduction Therapy

Standard Operating Procedure

Preparation of RILPL2 [1 - 211]

Enzyme description:-	RILPL2 [1 - 211]
Clone number:-	DU 27541
Source:-	Recombinant
Expression system:-	*E.coli*
Tag:-	N-terminal GST
Purification method:-	GSH-Sepharose

Calculated molecular mass:-

Monoisotopic	50, 778.03 daltons
Average Mass	50, 810.34 daltons

[cysteines reduced, methionines have not been oxidised

Theoretical pI:-	5.22
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

RILPL2 [1 - 211]

Protein RILPL2 [1 - 211]

Clone number DU 27541

Species Human

Accession number NM_145058.2

Tags N-terminal GST

Bacterially expressed protein

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELG
LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGA
VLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH
VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSS
KYIAWPLQGWQATFGGGDHPPKSDLEVLFQGPLGS**MEEPPVREEEEEEG**
EEDEERDEVGPEGALGKSPFQLTAEDVYDISYLLGRELMALGSDPRVTQ
LQFKVVRVLEMLEALVNEGSLALEELKMERDHLRKEVEGLRRQSPPASG
EVNLGPNKMVVDLTDPNRPRFTLQELRDVLQERNKLKSQLLVVQEELQC
YKSGLIPPREGPGGRREKDAVVTSAKNAGRNKEEKTIIKKLFFFRSGKQ
T

Native sequence Amino acids M1 – T211 (end) of human RILPL2.
Residue M232 of the fusion protein is equivalent to M1 of the native enzyme. The GST tag is located at residues 1 – 220.

Protease cleavage PreScission (LEVLFQGP) residues 221 – 228

Cloning sites *Bam*H1 and *Not*1 sites of pGEX6P-1

Nucleotide Sequence Of Insert

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ggatccATGGAGGAGCCCCCTGTGCGAGAAGAGGAAGAGGAGGAGGGAG
AGGAGGACGAGGAGAGGGACGAGGTTGGGCCCGAGGGGGCGCTGGGCAA
GAGCCCCTTCCAGCTGACCGCCGAGGACGTGTATGACATCTCCTACCTG
TTGGGCCGCGAGCTTATGGCCCTGGGCAGCGACCCCCGGGTGACGCAGC
TGCAGTTCAAAGTCGTCCGCGTCCTGGAGATGCTGGAGGCGCTGGTGAA
TGAGGGCAGCCTGGCGCTGGAGGAGCTGAAGATGGAGAGGGACCACCTC
AGGAAGGAGGTGGAGGGGCTGCGGAGACAGAGCCCTCCGGCCAGCGGGG
AGGTGAACCTGGGCCCAAACAAAATGGTGGTTGACCTGACAGATCCCAA
CCGACCCCGCTTCACTCTGCAGGAGCTAAGGGATGTGCTGCAGGAACGC
AACAAACTCAAGTCGCAGCTCCTGGTGGTGCAGGAAGAGCTGCAGTGCT
ACAAGAGTGGCCTGATTCCACCAAGAGAAGGCCCAGGAGGAAGAAGAGA
AAAAGATGCTGTGGTTACTAGTGCCAAAAATGCTGGCAGGAACAAGGAG
GAGAAGACAATCATAAAAAAGCTGTTCTTTTTTCGATCGGGGAAACAGA
CCtaggcggccgc
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