Division of Signal Tranduction Therapy

Standard Operating Procedure

Preparation of C15orf41 [1 – 281]

Enzyme description:-	C15orf41 [1 - 281]
Clone number:-	DU 49143
Source:-	Recombinant
Expression system:-	*E.coli*
Tag:-	N-terminal GST
Purification method:-	GSH Sepharose

Calculated molecular mass:-

Monoisotopic	59, 049.99 daltons
Average Mass	59, 088.11 daltons

[cysteines reduced, methionines have not been oxidised

Theoretical pI:-	6.00
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

Clone Data Sheet

C15orf41 [1 - 281]

Protein	C15orf41 [1 -281]
Clone number	DU 49143
Species	Human
Accession number	NM_001130010.2
Tags	N-terminal GST
Bacterially expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELG LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGA VLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSS KYIAWPLQGWQATFGGGDHPPKSDLEVLFQGPLGS**MILTKAQYDEIAQC** **LVSVPPTRQSLRKLKQRFPSQSQATLLSIFSQEYQKHIKRTHAKHHTSE** **AIESYYQRYLNGVVKNGAAPVLLDLANEVDYAPSLMARLILERFLQEHE** **ETPPSKSIINSMLRDPSQIPDGVLANQVYQCIVNDCCYGPLVDCIKHAI** **GHEHEVLLRDLLLEKNLSFLDEDQLRAKGYDKTPDFILQVPVAVEGHII** **HWIESKASFGDECSHHAYLHDQFWSYWNRFGPGLVIYWYGFIQELDCNR** **ERGILLKACFPTNIVTLCHSIA**
Native sequence	Amino acids M1 – A281 (end) of human C15orf41. 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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ggatccATGATACTGACCAAAGCTCAGTACGACGAGATAGCCCAGTGCC
TAGTGTCTGTGCCGCCTACCAGGCAGAGCCTGAGGAAGCTGAAGCAGAG
GTTTCCCAGTCAATCGCAGGCCACTCTGCTGAGCATCTTCTCCCAGGAG
TACCAGAAACACATTAAAAGAACACATGCCAAACATCATACTTCGGAAG
CAATTGAAAGTTATTACCAGAGGTACCTGAATGGAGTGGTGAAAAATGG
AGCTGCCCCAGTGCTCCTGGACCTGGCCAATGAGGTGGACTATGCGCCC
TCATTAATGGCTCGGCTTATACTGGAGAGGTTTCTACAGGAACACGAGG
AAACTCCACCCTCCAAGTCTATTATAAATAGTATGCTACGGGACCCTTC
TCAGATTCCAGATGGAGTTCTAGCAAATCAGGTCTATCAGTGCATTGTG
AACGACTGCTGTTACGGACCACTAGTGGACTGCATCAAGCATGCCATTG
GTCATGAGCATGAGGTCCTGCTGAGAGACTTGCTTCTAGAGAAAAACCT
GTCCTTCCTAGATGAAGATCAGCTTCGTGCAAAGGGTTATGACAAAACA
CCAGACTTCATTTTACAAGTACCAGTTGCTGTAGAAGGGCACATAATTC
ACTGGATTGAAAGCAAAGCCTCATTTGGTGATGAATGTAGCCACCACGC
CTACCTGCATGACCAGTTCTGGAGCTACTGGAATAGATTTGGGCCAGGC
TTAGTCATCTATTGGTATGGATTTATCCAGGAGCTGGACTGCAACCGGG
AAAGGGGCATCCTGCTCAAAGCCTGTTTCCCCACGAACATTGTCACCTT
ATGCCACAGCATAGCTtgagcggccgc
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