

Division of Signal Transduction Therapy

Standard Operating Procedure

Preparation of C15orf41 L178Q [1 - 281]

Enzyme description:- C15orf41 L178Q [1 – 281]

Clone number:- DU 24444

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal MBP

Purification method:- Amylose Resin

Calculated molecular mass:-

Monoisotopic 76, 600.74 daltons

Average Mass 76, 649.02 daltons

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 5.35

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, 0.2 mM PMSF, 1 mM Benzamidine.

Storage temperature:- -70

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Clone Data Sheet

C15orf41 L178Q [1 – 281]

Protein C15orf41 L178Q [1 – 281]

Clone number DU 24444

Species Human

Accession number NM_001130010.2

Tags N-terminal MBP

Bacterially expressed protein

MMKIEEGKLVIIWINGDKGYNGLAEVGGKFEKDTGIKVTVEHPDKLEEK
FPQVAATGDGPDIIFWAHDRFGGYAQSGLLAEITPDKAFQDKLYPFTW
DAVRYNGKLIAYPIAVEALSLIYNKDLLPNPPKTWEEIPALDKELKAK
GKSALMFNLQEPYFTWPLIAADGGYAFKYENGYDIKDVGVNDNAGAKA
GLTFLVDLIIKNKHMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTS
KVNYGVTVLPFTFKGQPSKPFVGVLSAGINAASPNKELAKEFLENYLLT
DEGLEAVNKDKPLGAVALKSYEEELVKDPRIAATMENAQKGEIMPNIIP
QMSAFWYAVRTAVINAASGRQTVDEALKDAQTNSSSNNNNNNNNNNLG
DDDDKVPEFLEVLFGQPLGSMILTKAQYDEIAQCLVSVPPTRQSLRKL
KQRFPSQSQATLLSIFSQEYQKHIKRTHAKHHTSEAIESYYQRYLNGV
VKNGAAPVLLDLANEVDYAPSLMARLILERFLQEHEETPPSKSIINSM
LRDPSQIPDGVLANQVYQCIVNDCCYGPLVDCIKHAIGHEHEVLLRDL
LLEKNQSFLEDEDQLRAKGYDKTPDFILQVPVAVEGHIHWIESKASFG
DECSSHAYLHDQFWSYWNRFPGPLVIYWYGFIQELDCNRERGIILLKAC
FPTNIVTLCHSIA

Native sequence Amino acids M1 – A281 (end) of human C15orf41.
Residue M405 of the fusion protein is equivalent to M1 of the native enzyme. The GST tag is located at residues 1 – 393

The protein has an L178Q mutation.
Residue L178 is equivalent to Q582 of the fusion protein.

Protease cleavage PreScission (LEVLFQGP) residues 394 - 401

Cloning sites *Bam*H1 and *Not*1 site of pMEX6P-1

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**Nucleotide
sequence of
insert**

ggatccATGATACTGACCAAAGCTCAGTACGACGAGATAGCCCAGTGC
CTAGTGTCTGTGCCGCTACCAGGCAGAGCCTGAGGAAGCTGAAGCAG
AGGTTTCCCAGTCAATCGCAGGCCACTCTGCTGAGCATCTTCTCCCAG
GAGTACCAGAAACACATTTAAAAGAACACATGCCAAACATCATACTTCG
GAAGCAATTGAAAGTTATTACCAGAGGTACCTGAATGGAGTGGTGAAA
AATGGAGCTGCCCCAGTGCTCCTGGACCTGGCCAATGAGGTGGACTAT
GCGCCCTCATTAATGGCTCGGCTTATACTGGAGAGGTTTCTACAGGAA
CACGAGGAAACTCCACCCTCCAAGTCTATTATAAATAGTATGCTACGG
GACCCTTCTCAGATTCCAGATGGAGTTC TAGCAAATCAGGTCTATCAG
TGCATTGTGAACGACTGCTGTTACGGACCACTAGTGGACTGCATCAAG
CATGCCATTGGTCATGAGCATGAGGTCTGCTGAGAGACTTGCTTCTA
GAGAAAACCaGTCCTTCCTAGATGAAGATCAGCTTCGTGCAAAGGGT
TATGACAAAACACCAGACTTCATTTTACAAGTACCAGTTGCTGTAGAA
GGGCACATAATTC ACTGGATTGAAAGCAAAGCCTCATT TGGTGATGAA
TG TAGCCACCACGCCTACCTGCATGACCAGTTC TGGAGCTACTGGAAT
AGATTTGGCCAGGCTTAGTCATCTATTGGTATGGATTTATCCAGGAG
CTGGACTGCAACCGGGAAAGGGGCATCCTGCTCAAAGCCTGTTTCCCC
ACGAACATTGTCACCTTATGCCACAGCATAGCTtgagcggccgc