

MRC PPU Reagents and Services

Standard Operating Procedure

Preparation of LC3C [1 – 148]

Enzyme description:- LC3C [1 – 148]

Clone number:- DU 61997

Source:- Recombinant

Expression system:- *E.coli*,

Tag:- N-terminal GST

Purification method:- GSH-Agarose

Calculated molecular mass:-

Monoisotopic 43, 647.35 daltons
Average Mass 43, 675.74 daltons
[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 6.63

Purity:- >80 %

Enzyme storage buffer:-

50 mM Tris-HCl pH 7.5, 150 mM NaCl, 270 mM sucrose,
0.1 % 2-mercaptoethanol, 1 mM benzamidine, 0.2 mM PMSF

Storage temperature:- -70 °C

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Clone Data Sheet

LC3C [1 - 148]

Protein LC3C [1 - 148]

Clone number DU 61997

Species Human

Accession number NM_001004343.2

Tags N-terminal GST

Bacterially expressed protein MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFEL
GLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNLGGCPKERAIEISMLE
GAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLN
GDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPIQIDKY
LKSSKYIAWPLQGQATFGGGDHPPKSDLEVLFGQPLGSMPPPKIPS
VRPFKQRKSLAIRQEEVAGIRAKFPNKIPVVVERYPRETFLPPLDKTK
FLVPQELTMTQFLSIIRSRMVLRATEAFYLLVNNKSLVSMSTMAEIIY
RDYKDEDGFVYMTYASQETFGCLESAAPRDGSSLEDRPCNPL

Native sequence Amino acids M1 – L148 (end) of human LC3C.
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 - 229

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

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Full Nucleotide Sequence

ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCC
ACTCGACTTCTTTTGGGAATATCTTGAAGAAAAATATGAAGAGCATTTG
TATGAGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTTGAATTG
GGTTTGGAGTTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAAA
TTAACACAGTCTATGGCCATCATACTTATATAGCTGACAAGCACAAAC
ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAA
GGAGCGGTTTTGGATATTAGATACGGTGTTTCGAGAATTGCATATAGT
AAAGACTTTGAACTCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAA
ATGCTGAAAATGTTCTGAAGATCGTTTATGTCATAAAACATATTTAAAT
GGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGAT
GTTGTTTTTATACATGGACCCAATGTGCCTGGATGCGTTCCCAAAATTA
GTTTGTTTTTAAAAAACGTATTGAAGCTATCCCACAAATTGATAAGTAC
TTGAAATCCAGCAAGTATATAGCATGGCCTTTGCAGGGCTGGCAAGCC
ACGTTTGGTGGTGGCGACCATCCTCCAAAATCGGATCTGGAAGTTCTG
TTCCAGGGGGCCCCTGGGATCCATGCCGCCTCCACAGAAAATCCCAAGC
GTCAGACCCCTTCAAGCAGAGGAAAAGCTTGGCAATCAGACAAGAGGAA
GTTGCTGGAATCCGGGGCAAAGTTCCCCAACAAAATCCCGGTGGTAGTG
GAGCGCTACCCCAGGGAGACGTTCCCTGCCCCCGCTGGACAAAACCAAG
TTCCTGGTCCCGCAGGAGCTGACCATGACCCAGTTCCTCAGCATCATC
CGGAGCCGCATGGTCCTGAGAGCCACGGAAGCCTTTTACTTGCTGGTG
ACAACAAGAGCCTGGTCAGCATGAGCGCAACCATGGCAGAGATCTAC
AGAGACTACAAGGATGAGGATGGCTTCGTGTACATGACCTACGCCTCC
CAGGAGACATTTGGCTGCCTGGAGTCAGCAGCCCCCAGGGATGGGAGC
AGCCTTGAGGACAGACCCTGCAATCCTCTCtag