

Division of Signal Transduction Therapy

Standard Operating Procedure

Preparation of KLF2 [2 - 355]

Enzyme description:- KLF2 [2 – 355]

Clone number:- DU 3100

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Calculated molecular mass:-

Monoisotopic 64, 055.35 daltons

Average Mass 64, 096.51 daltons

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 8.12

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, 0.2 mM PMSF, 1 mM Benzamidine.

Storage temperature:- -70

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Clone Data Sheet

KLF2 [2 – 355]

Protein KLF2 [2 – 355]

Clone number DU 3100

Species Human

Accession number NM_016270.3

Tags N-terminal GST

Bacterially expressed protein

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFEL
GLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLE
GAVLDIRYGVSR IAYS KDFETLKVDFLSKLPEMLKMFEDRLCHKTYLN
GDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKY
LKSSKYIAWPLQGWQATFGGGDHPKSDLEVLFGQPLGS**ALSEPILPS**
FSTFASPCRERGLQERWPRAEPESGGTDDDLNSVLDLFI L SMGLDGLGA
EAAPEPPPPPPPAFYYPEPGAPPYSAPAGGLVSELLRPELDAPP**GP**
ALHGRFLLAPPGRLVKAEPPEADGGGGYG CAPGLTRGPRGLKREGAPG
PAASC MRGPGGRPPPPDPPLSPDGPARLPAPGPRASFPPFGGPGF
GAPGPGLHYAPPAPPAFGLFDDAAAAAALGLAPPAARGLLTPPASPL
ELLEAKPKRGRRSWPRKRTATH TCSYAGCGKTYTKSSHLKAHLRHTTG
EKP YHCNWDGCGWKFARSD ELTRHYRKHTGHRPFQCHLCDRAFSRSDH
LALHMKRHM

Native sequence Amino acids A2 – M355 (end) of human KLF2.
Residue A232 of the fusion protein is equivalent to A2 of the native enzyme. The GST tag is located at residues 1 – 220.

The protein has the following amino acid substitution:

L – **P**, where L104, is residue **P334** is the fusion protein.

This change is a defined snp.

Protease cleavage PreScission (LEVLFQGP) residues 221 – 228

Cloning sites *Bam*H1 and *Eco*R1 site of pGEX6P-1

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Nucleotide Sequence Of Insert

ggatccGCGCTGAGTGAACCCATCCTGCCGTCCTTCTCCACTTTCGCCAGCCCGTGCCGCGAGCG
CGGCCTGCAGGAGCGCTGGCCGCGCGCCGAACCCGAGTCCGGCGGCACCGACGACGACCTCAACA
GCGTGCTGGACTTCATCCTGTCCATGGGGCTGGATGGCCTGGGCGCCGAGGCCGCCCGGAGCCG
CCGCCGCCGCCCCGCGCCTGCGTTCATTACCCGAACCCGGCGCGCCCCGCCCTACAGCGC
CCCCGCGGGTGGCCTGGTGTCTGAGCTGCTGCGACCCGAGCTGGATGCGCCGCCGGGGCCCGCAC
TGCACGGCCGCTTCTGCTGGCGCCCGCCGGCCGCTGGTCAAGGCCGAGCCCCCTGAAGCGGAC
GGCGGCGGCGGCTACGGCTGCGCCCCCGGGCTGACCCGTGGACCGCGCGGCCCTCAAGCGCGAGGG
CGCCCCGGGCCCCGGCGGCTTCGTGCATGCGAGGTCCCGGGGGCCGCCCCCGCCGCCGCCGACA
CACCGCCGCTCAGCCCCGACGGCCCCGCGCGCCTGCCCGCGCCCGGTCCGCGCGCCTCCTTCCCG
CCGCCTTTCGGTGGCCCTGGTTTCGGCGCGCCCGGGCCCGGCCTGCATTACGCGCCGCCTGCGCC
CCCAGCCTTCGGTCTCTTCGACGACGCGGCCGCGCCGCGGCAGCCCTGGGCCTGGCGCCCCCG
CCGCCCGGGTCTCCTCACGCCGCTGCGTCCCCGCTGGAGCTGCTGGAGGCCAAGCCAAAGCGC
GGCCGCCGCTCTTGGCCCCGCAAACGCACCGCCACTCACACCTGCAGCTACGCGGGCTGCGGCAA
GACCTACACCAAGAGTTCGCATCTGAAGGCGCATCTGCGCACGCACACAGGTGAGAAGCCCTACC
ACTGCAACTGGGACGGCTGCGGCTGGAAGTTTGC GCGCTCAGACGAGCTCACGCGCCACTACCGA
AAGCACACGGGCCACCGGCCATTCAGTGCCATCTGTGCGATCGTGCCTTCTCGCGCTCCGATCA
CCTGGCGCTGCACATGAAACGGCACATGtaggaattc