

MRC PPU Reagents and Services

Clone Data Sheet

CLK2 D327A [138 - 499]

Protein CLK2 D327A [138 - 499]

Clone number DU 31001

Species Human

Accession number NM_001294338.2

Tags N-terminal GST

Baculovirus expressed protein

MSPILGYWKIKGLVQPTRLLEYLEEKYEHLIERDEGDKW
RNKKFELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNML
GGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFL
SKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLY
MDPMCLDAFPKLVCFKKRIEAI PQIDKYLKSSKYIAWPLQG
WQATFGGGDHPPKSDLEVLFQGPLGS**RRAKSVEDDAEGHLI**
YHVGDWLQERYEIVSTLGE**GT****FGRVVQCVDHRRGGARVALK**
I IKNVEKYKEAARLEINVLEKINEKDPDNKNLCVQMFDFD
YHGHMCISFELLGLSTFD**FL****KDNNYLPYP****PI****HQVRHMAFQLC**
QAVKFLHDNKLTH**TD****LKPENILFVNSDYELTYNLEKKRDER**
SVKSTAVRVV**AF****GSATFDHEHHSTIVSTRHYRAPEVILEL**
GWSQPCDVWSIGCII**FE****YYVGF****TL****FQTHDNREHLAMMERIL**
GPIPSRMIRKTRKQKYFYRGRLDWDENTSAGRYVRENCKPL
RRYLTSEAEHHQLFDLIESMLEYEP**AK****RLTLGEALQHPFF**
ARLRAEPPNKLWDSSRDISR

Native sequence Amino acids R138 – R499 (end) of human CLK2.
Residue R232 of the fusion protein is equivalent to R138 of the native enzyme. The GST tag is located at residues 1 – 220.

The enzyme has a D327**A** mutation.
Residue D327 is equivalent to **A421** of the fusion protein.

Protease cleavage PreScission (LEVLFQGP) residues 221 - 228

Cloning sites *Bam*H1 and *Not*I sites of pFastBAC GST

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Nucleotide
Sequence of insert

ggatcccGGAGAGCCAAGAGTGTAGAGGACGACGCTGAGGGCCACCTC
ATCTACCACGTCGGGGACTGGCTACAAGAGCGATATGAAATCGTTAGC
ACCTTAGGAGAGGGGACCTTCGGCCGAGTTGTACAATGTGTTGACCAT
CGCAGGGGTGGGGCTCGAGTTGCCCTGAAGATCATTAAAGAATGTGGAG
AAGTACAAGGAAGCAGCTCGACTTGAGATCAACGTGCTAGAGAAAATC
AATGAGAAAGACCCTGACAACAAGAACCTCTGTGTCCAGATGTTTGAC
TGGTTTGACTACCATGGCCACATGTGTATCTCCTTTGAGCTTCTGGGC
CTTAGCACCTTCGATTTCTCAAAGACAACAACCTACCTGCCCTACCCC
ATCCACCAAGTGCGCCACATGGCCTTCCAGCTGTGCCAGGCTGTCAAG
TTCTCCATGATAACAAGCTGACACATACAGACCTCAAGCCTGAAAAT
ATTCTGTTTGTGAATTCAGACTATGAGCTCACCTACAACCTAGAGAAG
AAGCGAGATGAGCGCAGTGTGAAGAGCACAGCTGTGCGGGTGGTAGCC
TTTGGCAGTGCCACCTTTGACCATGAGCACCATAGCACCATTGTCTCC
ACTCGCCATTACCGAGCACCAGAAGTCATCCTTGAGTTGGGCTGGTCA
CAGCCTTGTGATGTGTGGAGTATAGGCTGCATCATCTTTGAATACTAT
GTGGGATTCACCCTCTTCCAGACCCATGACAACAGAGAGCATCTAGCC
ATGATGGAAAGGATCTTGGGTCCATCCCTTCCCGGATGATCCGAAAG
ACAAGAAAGCAGAAATATTTTTACCGGGTTCGCCTGGATTGGGATGAG
AACACATCAGCTGGGCGCTATGTTTCGTGAGAACTGCAAACCGCTGCGG
CGGTATCTGACCTCAGAGGCAGAGGAACACCACCAGCTCTTCGATCTG
ATTGAAAGCATGCTAGAGTATGAACCAGCTAAGCGGCTGACCTTGGGT
GAAGCCCTTCAGCATCCTTTCTTCGCCCCGCTTCGGGCTGAGCCGCC
AACAAGTTGTGGGACTCCAGTCGGGATATCAGTCGGTgagcggccgc