Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of FADD [K24R, K35R]

Enzyme description:- FADD 1-208 [K24R, K35R] = full length

Clone number:- DU23996

Source:- bacteria

Tag:- cleaved from N-terminal GST

Purification method:- GSH-Sepharose

Expression level:- 1 mg/L

Calculated molecular mass:-

Monoisotopic	23732
Average Mass	23745

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 5.68

Purity:- 90%

Enzyme storage buffer:-

50 mM HEPES pH 7.5, 150mM NaCl, 1mM DTT

Storage temperature:- -80ºC

Assay:-

Division of Signal Transduction Therapy

Clone Data Sheet

Protein name FADD [K24R, K35R]

Protein	FADD [K24R, K35R] 1-208 = full length
Synonyms	Fas-associated via death domain
Clone Number	DU23996
Species	human
Accession Number	Protein: Q13158 DNA: NM_003824
Tags	cleaved from N-terminal GST
Aminoacid sequence of the expressed protein	GPLGS**MDPFLVLLHSVSSSLSSSELTELRFLCLGRVGKRRLERVQSGLDLF SMLLEQNDLEPGHTELLRELLASLRRHDLLRRVDDFEAGAAAGAAPGEEDL CAAFNVICDNVGKDWRRLARQLKVSDTKIDSIEDRYPRNLTERVRESLRIW KNTEKENATVAHLVGALRSCQMNLVADLVQEVQQARDLQNRSGAMSPMSWN SDASTSEAS**
Native sequence	in bold
Protease cleavage	Prescission protease underlined
Cloning sites	BamH1 / Not1

DNA sequence of the insert

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ggatccATGGACCCGTTCCTGGTGCTGCTGCACTCGGTGTCGTCCAGCCT
GTCGAGCAGCGAGCTGACCGAGCTCAgGTTCCTATGCCTCGGGCGCGTGG
GCAAGCGCAgGCTGGAGCGCGTGCAGAGCGGCCTAGACCTCTTCTCCATG
CTGCTGGAGCAGAACGACCTGGAGCCCGGGCACACCGAGCTCCTGCGCGA
GCTGCTCGCCTCCCTGCGGCGCCACGACCTGCTGCGGCGCGTCGACGACT
TCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGT
GCAGCATTTAACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCT
GGCTCGTCAGCTCAAAGTCTCAGACACCAAGATCGACAGCATCGAGGACA
GATACCCCCGCAACCTGACAGAGCGTGTGCGGGAGTCACTGAGAATCTGG
AAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTGGTGGGGGCTCT
CAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAGC
AGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCATGG
AACTCAGACGCATCTACCTCCGAAGCGTCCTGAGCGGCCGC
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