

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of FADD [K110R]

Enzyme description:- FADD 1-208 [K110R] = full length

Clone number:- DU23999

Source:- bacteria

Tag:- cleaved from N-terminal GST

Purification method:- GSH-Sepharose

Expression level:- 1 mg/L

Calculated molecular mass:-

Monoisotopic	23704
Average Mass	23717
[cysteines reduced, methionines have not been oxidised]	

Theoretical pI:- 5.68

Purity:- 70%

Enzyme storage buffer:-

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

Storage temperature:- -80°C

Assay:-

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Clone Data Sheet

Protein name FADD [K110R]

<u>Protein</u>	FADD [K110R] 1-208 = full length
<u>Synonyms</u>	Fas-associated via death domain
<u>Clone Number</u>	DU23999
<u>Species</u>	human
<u>Accession Number</u>	Protein: Q13158 DNA: NM_003824
<u>Tags</u>	cleaved from N-terminal GST
Aminoacid sequence of the expressed protein	<u>GPLGSMDPFLVLLHSVSSSLSSSELTELKFLCLGRVGRKRLERVQSGLDLF</u> <u>SMLLEQNDLEPGHTELLRELLASLRRHDLRRVDDFEAGAAAGAAPGEEDL</u> <u>CAAFNVICDNVGRDWRRLARQLKVSDTKIDSIEDRYPRNLTERVRESLRIW</u> <u>KNTEKENATVAHLVGALRSCQMNLVADLVQEVQQARDLQNRSGAMSPMSWN</u> <u>SDASTSEAS</u>
Native sequence	in bold
Protease cleavage	Prescission protease underlined
Cloning sites	BamH1 / Not1

<u>DNA sequence of the insert</u>	GGATCCATGGACCCGTTCTGCTGCTGCACTCGGTGTCGTCCAGCCT GTCGAGCAGCGAGCTGACCGAGCTCAAGTTCCTATGCCTCGGGCGCGTGG GCAAGCGCAAGCTGGAGCGCGTGCAGAGCGGCCTAGACCTCTTCTCCATG CTGCTGGAGCAGAACGACCTGGAGCCCGGGCACACCGAGCTCCTGCGCGA GCTGCTCGCCTCCCTGCGGCGCCACGACCTGCTGCGGCGCGTCGACGACT TCGAGGCGGGGCGGCGGCCGGGCGCGCCTGGGGAAGAAGACCTGTGT GCAGCATTTAACGTCATATGTGATAATGTGGGGA ^a AGATTGGAGAAGGCT GGCTCGTCAGCTCAAAGTCTCAGACACCAAGATCGACAGCATCGAGGACA GATACCCCGCAACCTGACAGAGCGTGTGCGGGAGTCACTGAGAATCTGG AAGAACACAGAGAAGGAGAACGCAACAGTGGCCACCTGGTGGGGGCTCT CAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTTCAGC AGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCATGG AACTCAGACGCATCTACCTCCGAAGCGTCCTGAGCGGCCGC
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