

## *Division of Signal Transduction Therapy*

### **Standard Operation Procedure**

#### **Preparation of FADD [K35R]**

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

**Clone number:-** DU23998

**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:-** 90%

**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 [K35R]**

**Protein** FADD [K35R] 1-208 = full length  
**Synonyms** Fas-associated via death domain  
**Clone Number** DU23998  
**Species** human  
**Accession Number** Protein: Q13158 DNA: NM\_003824  
**Tags** cleaved from N-terminal GST  
Aminoacid sequence of the expressed protein **GPLGSMDPFLVLLHSVSSSLSSSELTELKFLCLGRVGRRLERVOGSLDLF**  
**SMLLEQNDLEPGHTELLRELLASLRRHDLRRVDDFEAGAAAGAAPGEEDL**  
**CAAFNVICDNVVKDWRRLARQLKVS****DTKIDSI****EDRYPRNLTERVRESLRIW**  
**KNTEKENATVAHLV****GALRSCQMNLVADLVQEVQ****QARDLQNRSGAMSPMSWN**  
**SDASTSEAS**  
Native sequence in bold  
Protease cleavage Precission protease underlined  
Cloning sites BamH1 / Not1

**DNA sequence of the insert** GGATCCATGGACCCGTTCCCTGGTGCTGCTGCACTCGGTGTCGTCAGCCT  
GTCGAGCAGCGAGCTGACCGAGCTCAAGTTCCTATGCCTCGGGCGCGTGG  
GCAAGCGCAGGCTGGAGCGCGTGCAGAGCGGCCTAGACCTCTTCTCCATG  
CTGCTGGAGCAGAACGACCTGGAGCCCGGGCACACCGAGCTCCTGCGCGA  
GCTGCTCGCCTCCCTGCGGGGCCACGACCTGCTGCGGGCGCTCGACGACT  
TCGAGGCGGGGGCGGGCGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGT  
GCAGCATTTAACGTCAATATGTGATAATGTGGGGAAAGATTGGAGAAGGCT  
GGCTCGTCAGCTCAAAGTCTCAGACACCAAGATCGACAGCATCGAGGACA  
GATACCCCGCAACCTGACAGAGCGTGTGCGGGAGTCACTGAGAATCTGG  
AAGAACACAGAGAAGGAGAACGCAACAGTGGCCACCTGGTGGGGGCTCT  
CAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTTCAGC  
AGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCATGG  
AACTCAGACGCATCTACCTCCGAAGCGTCCTGAGCGGCCGC