

*Division of Signal Transduction Therapy*

**Standard Operating Procedure**

**Preparation of eIF4E [2 - 217]**

**Protein description:-** eIF4E [2 - 217]

**Clone number:-** DU 1129

**Source:-** Recombinant

**Expression system:-** *E.coli*

**Tag:-** N-terminal GST

**Purification method:-** GSH Sepharose

**Expression level:-** 5 mg/L

**Calculated molecular mass:-** 51, 757 daltons

**Purity:-** > 95 %

**Enzyme storage buffer:-**

50 mM Tris-HCl pH 7.5, 50 % glycerol, 150 mM NaCl, 0.1 mM EGTA,  
0.1 % 2-mercaptoethanol, 0.02 % Brij-35, 0.2 mM PMSF, 1 mM Benzamidine.

**Storage temperature:-** -20 °C

**Assay:-** Substrate for MNK2 alpha

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**CLONE DATA SHEET**

**eIF4E [2 – 217]**

<b><u>Protein</u></b>	eIF4E [2 - 217]
<b><u>Clone number</u></b>	DU 1129
<b><u>Species</u></b>	Human
<b><u>Accession number</u></b>	NM_001968
<b><u>Tags</u></b>	N-terminal GST
<b><u>Bacterially expressed protein</u></b>	MSPILGYWKIKGLVQPTRLLEYLEEKYEHLRYERDEGDKWRNKKFEL GLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLE GAVLDIRYGVSRIAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLN GDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKY LKSSKYIAWPLQGQATFGGGDHPKSDLEVLFGQPLGSATVEPETTP TPNPPTTEEEKTESNQEVANPEHYIKHPLQNRWALWFFKNDKSKTWQA NLRLISKFDTVEDFWALYNHIQLSSNLMPGCDYSLFKDGI EPMWEDEK NKRGGRWLITLKNQQRSDLDLRFWLETLLCLIGESFDDYSDDVCGAVV NVRAGDKIAIWTTECENREAVTHIGRVYKERLGLPPKIVIGYQSHAD TATKSGSTTKNRFVV
<b><u>Native sequence</u></b>	Amino acids A2 – V217 (end) of human eIF4E. Residue A232 of the fusion protein is equivalent to A2 of the native protein. The GST tag is located at residues 1 – 220
<b><u>Protease cleavage</u></b>	PreScission ( <u>LEVLFQGPL</u> ) residues 221 - 229
<b><u>Cloning sites</u></b>	<i>Bam</i> HI and <i>Eco</i> RI sites of pGEX 6P-1

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**Nucleotide  
sequence of insert**

GGATCCGCGACTGTCGAACCGGAAACCACCCCTACTCCTAA  
TCCCCGACTACAGAAGAGGAGAAAACGGAATCTAATCAGG  
AGGTTGCTAACCCAGAACACTATATTAACATCCCCTACAG  
AACAGATGGGCACTCTGGTTTTTTAAAAATGATAAAAGCAA  
AACTTGGCAAGCAAACCTGCGGCTGATCTCCAAGTTTGATA  
CTGTTGAAGACTTTTGGGCTCTGTACAACCATATCCAGTTG  
TCTAGTAATTTAATGCCTGGCTGTGACTACTCACTTTTTTAA  
GGATGGTATTGAGCCTATGTGGGAAGATGAGAAAAACAAAC  
GGGAGGACGATGGCTAATTACATTGAACAAACAGCAGAGA  
CGAAGTGACCTCGATCGCTTTTGGCTAGAGACACTTCTGTG  
CCTTATTGGAGAATCTTTTGATGACTACAGTGATGATGTAT  
GTGGCGCTGTTGTTAATGTTAGAGCTAAAGGTGATAAGATA  
GCAATATGGACTACTGAATGTGAAAACAGAGAAGCTGTTAC  
ACATATAGGGAGGGTATAACAAGGAAAGTTAGGACTTCCTC  
CAAAGATAGTGATTGGTTATCAGTCCCACGCAGACACAGCT  
ACTAAGAGCGGCTCCACCACTAAAAATAGGTTTGTGTTa  
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