

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of UBR5

Enzyme description:- UBR5 2411-2798 (end)

Clone number:- DU45326

Source:- BL21 recombinant

Tag:- N-terminal GST

Purification method:- GSH-Sepharose

Expression level:- 0.8mg/L

Calculated molecular mass:-

Monoisotopic 70562 Da

Average Mass 70606 Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 5.64

Purity:- 90%

Enzyme storage buffer:-

50mM HEPES pH 7.5, 150mM NaCl, 10% glycerol, 1mM DTT

Storage temperature:- -80°C

Assay:-

Division of Signal Transduction Therapy

Clone Data Sheet

UBR5 2411-2798

<u>Protein</u>	UBR5 2411-2798
<u>Synonyms</u>	HYD, EDD1
<u>Clone Number</u>	DU45326
<u>Species</u>	Human
<u>Accession Number</u>	Protein: O95071
<u>Tags</u>	N-terminal GST
Aminoacid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGL EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL DIRYGVSRIAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLNGDHVTH PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIA WPLQGWQATFGGGDHPPKSDLEVL <u>FQGPLGS</u> AFASKITGMLLELSPAQLL LLLASEDSLRRARVDEAMELI IAHGREN <u>GADS</u> ILDLGLVDSSEKVVQENRK RHGSSRSVVMDLDDTDDGDDNAPLFYQPGKRGFYTPRPGKNTPEARLNCF RNIGRILGLCLLQNELCPI TLNRHVIKVLLGRKVNWHDFAFFDPVMYESL RQLILASQSSDADAVFSAMDFAIDLCKEEGGQVELIPNGVNI PVTPQ NVYEYVRKYAEHRMLVVAEQPLHAMRKGLLDVLPKNSLEDLTAEDFRLLV NGCGEVNVQMLISFTSFNDESGENAEKLLQFKRWFWSIVEKMSMTERQDL VYFWTSSPSLPASEEGFQPMPSITIRPPDDQHLPTANTCISRLYVPLYSS KQILKQKLLLAIKTKNFGFV
Native sequence	in bold
Protease site	Precission Protease site underlined
Cloning sites	BamH1/NotI

**DNA sequence of
the expression
cassette**

ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCCAC
TCGACTTCTTTTGGAAATATCTTGAAGAAAAATATGAAGAGCATTGTATG
AGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTTGAATTGGGTTTG
GAGTTTCCAATCTTCCTTATTATATTGATGGTGATGTTAAATTAACACA
GTCTATGGCCATCATACTTATATAGCTGACAAGCACAACATGTTGGGTG
GTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAAGGAGCGGTTTTG
GATATTAGATACGGTGTTCGAGAATTGCATATAGTAAAGACTTTGAAAC
TCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTTCG
AAGATCGTTTATGTCATAAAACATATTTAAATGGTGATCATGTAACCCAT
CCTGACTTCATGTTGTATGACGCTCTTGATGTTGTTTTATACATGGACCC
AATGTGCCTGGATGCGTTCCCAAATTAGTTTGTTTTTAAAAACGTATTG
AAGCTATCCACAAATTGATAAGTACTTGAAATCCAGCAAGTATATAGCA
TGGCCTTTCAGGGCTGGCAAGCCACGTTTGGTGGTGGCGACCATCCTCC
AAAATCGGATCTGGAAGTTCTGTTCCAGGGGCCCTGGGATCCGCATTTG
CAAGTAAAATCACTGGCATGTTGTTGGAATTATCCCCAGCTCAGCTGCTT
CTCCTTCTAGCAAGTGAGGATCTCTGAGAGCAAGAGTGGATGAGGCCAT
GGAATCATTATTGCACATGGACGGGAAAAATGGAGCTGATAGTATCCTGG
ATCTTGGATTAGTAGACTCCTCAGAAAAGGTACAGCAGGAAAACCGAAAG
CGCCATGGCTCTAGTCGAAGTGTAGTAGATATGGATTTAGATGATACAGA
TGATGGTGATGACAATGCCCTTGTGTTTTACCAACCTGGGAAAAGAGGAT
TTTATACTCCAAGGCCTGGCAAGAACACAGAAGCAAGGTTGAATTGTTTC
AGAAACATTGGCAGGATTCTTGGACTATGTCTGTTACAGAATGAACTATG
TCCTATCACATTGAATAGACATGTAATTAAGTATTGCTTGGTAGAAAAG
TCAATTGGCATGATTTTGCTTTTTTTGATCCTGTAATGTATGAGAGTTTG
CGGCAACTAATCCTCGCGTCTCAGAGTTCAGATGCTGATGCTGTTTTCTC
AGCAATGGATTTGGCATTGCAATTGACCTGTGTAAGAAGAAGGTGGAG
GACAGGTTGAACTCATTCTAATGGTGTAATAATACCAGTCACTCCACAG
AATGTATATGAGTATGTGCGGAAATACGCAGAACACAGAATGTTGGTAGT
TGCAGAACAGCCCTTACATGCAATGAGGAAAAGGTCTACTAGATGTGCTTC
CAAAAATTCATTAGAAGATTTAACGGCAGAAGATTTTAGGCTTTTGGTA
AATGGCTGCGGTGAAGTCAATGTGCAAATGCTGATCAGTTTTACCTCTTT
CAATGATGAATCAGGAGAAAATGCTGAGAAGCTTCTGCAGTTC AAGCGTT
GGTCTGGTCAATAGTAGAGAAGATGAGCATGACAGAACGACAAGATCTT
GTTTACTTTTTGGACATCAAGCCCATCACTGCCAGCCAGTGAAGAAGGATT
CCAGCCTATGCCCTCAATCACATAAGACCACCAGATGACCAACATCTTC
CTACTGCAAATACTTGCATTTCTCGACTTTACGTCCCACTCTATTCTCT
AAACAGATTCTCAAACAGAAAATTGTTACTCGCCATTAAGACCAAGAATTT
TGGTTTTGTGTAG