

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of GST-UBE2Z

Enzyme description:- GST-UBE2Z 1-354 (full length)

Clone number:- DU11585

Source:- human recombinant

Tag:- N-terminal GST-tag

Purification method:- GSH-Sepharose

Expression system:- *E.coli*

Calculated molecular mass:-

Monoisotopic 64992 Da

Average Mass 65032 Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 7.8

Purity:- 80%

Enzyme storage buffer:-

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

Storage temperature:- -80°C

Assay:-

Loading with Ubiquitin and UBE1 in the presence of Mg-ATP

Loading buffer: 50mM HEPES pH 7.5

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Clone Data Sheet

GST-UBE2Z

Protein GST-UBE2Z (1-354)
Synonyms USE1
Clone Number DU11585
Species Human
Accession Number Protein: Q9H832 DNA: NM_023079.3
Tags N-terminal GST-tag

Aminoacid sequence of the expressed protein
MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGL
EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLEGAVL
DIRYGVSRIAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLNGDHVTH
PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIA
WPLQGWQATFGGGDHPPKSDLEVLFOGPLGSM**AESPTEEAATAGAGAAGP**
GASSVAGVVGVS**SGSGGGFGPPFLPDVWAAAAAAGGAGGPGSGLAPLPGLP**
PSAAAHGAALLSHWDPTLSSDWDGERTAPQCLLR**IKRDIMSIYKEPPPGM**
FVVPD**TVDMTKIHALITGPFDT****PYEGGFFLVFRCPPDYPIHPPRVKLM**
TGNNTVRFNPNFYRNGKVCLSILGTWTGPAWSPAQSISSVLISIQSLMTE
NPYHNEPGFEQERHPGDSKNYNECIRHETIRVAVCDMMEGKCPCPEPLRG
VMEKSFLEYDYFYEVACKDRLHLOGQTMQDPFGEKRGHFDYQSLLMRLGL
IRQKVLERLHNENAEMSDSDSSSSSGTETDLHGSLRV

Native sequence in bold
Protease cleavage Precission protease site underlined
Cloning sites BamH1 / NotI

DNA sequence of insert
GGATCCATGGCGGAGAGTCCGACTGAGGAGGCGGCAACGGCGGGCGCCGG
GGCGGCGGGCCCCGGGGCGAGCAGCGTTGCTGGTGTGTTGGCGTTAGCG
GCAGCGGCGGCGGGTTTCGGGCCGCCTTTCCTGCCGGATGTGTGGGCGGCG
GCGGCGGCAGCGGGCGGGGCCGGGGGCCGGGGAGCGGCCTGGCTCCGCT
GCCCCGGCTCCCGCCCTCAGCCGCTGCCACGGGGCCGCGCTGCTTAGCC
ACTGGGACCCACGCTCAGCTCCGACTGGGACGGCGAGCGCACCGCGCCG
CAGTGTCTACTCCGGATCAAGCGGGATATCATGTCCATTTATAAGGAGCC
TCCTCCAGGAATGTTTCGTTGTACCTGATACTGTTGACATGACTAAGATTC
ATGCATTGATCACAGGCCCATTTGACACTCCTTATGAAGGGGGTTTCTTC
CTGTTTCGTGTTTCGGTGTCCGCCCGACTATCCCATCCACCCACCTCGGGT
CAAACTGATGACAACGGGCAATAACACAGTGAGGTTTAACCCCAACTTCT
ACCGCAATGGGAAAGTCTGCTTGAGTATTCTAGGTACATGGACTGGACCT
GCCTGGAGCCCAGCCAGAGCATCTCCTCAGTGCTCATCTCTATCCAGTC
CCTGATGACTGAGAACCCCTATCACAATGAGCCCGGCTTTGAACAGGAGA
GACATCCAGGAGACAGCAAAAACTATAATGAATGTATCCGGCCACGAGACC
ATCAGAGTTGCAGTCTGTGACATGATGGAAGGAAAGTGTCCCTGTCCCTGA
ACCCCTACGAGGGGTGATGGAGAAGTCCTTTCTGGAGTATTACGACTTCT
ATGAGGTGGCCTGCAAAGATCGCCTGCACTTCAAGGCCAAACTATGCAG
GACCTTTTGGAGAGAAGCGGGCCACTTTGACTACCAGTCCCTCTTGAT
GCGCCTGGGACTGATACGTCAGAAAGTCTGGAGAGGCTCCATAATGAGA
ATGCAGAAATGGACTCTGATAGCAGTTCATCTGGGACAGAGACAGACCTT
CATGGGAGCCTGAGGGTTTAGGCGGCCG

Sequence difference compared with NM_023079.3 CDS: c846t (silent)

