

Division of Signal Transduction Therapy

Standard Operation Procedure

GST-USP6 [529-1406] C541S

Enzyme description:- GST-USP6 [529-1406] C541S

Clone number:- DU22196

Source:- Sf21 Recombinant

Tag:- N-terminal GST tag

Purification method:- GSH sepharose

Expression level:- 10 mg/L

Calculated molecular mass:-

Monoisotopic 125199 Da

Average Mass 125276 Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 6.73

Purity:- 90%

Enzyme storage buffer:-

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

Storage temperature:- -80°C

Assay:-

Ub-Rho110-Gly cleavage assay monitored by Ex/Em 485/535 nm

Assay buffer:-

40 mM Tris pH 7.5, 100 mM NaCl, 5 mM DTT, 0.01% Triton X-100, 0.005% Ovalbumin, 0.5 µM Ub-Rho110-Gly

Division of Signal Transduction Therapy

GST-USP6 [529-1406] C541S

<u>Protein</u>	GST-USP6 [529-1406] C541S
<u>Synonyms</u>	UBP6, HRP1, TRE2
<u>Clone Number</u>	DU22196
<u>Species</u>	Human
<u>Accession Number</u>	Protein: P35125 DNA: NM004505.2
<u>Tags</u>	N-terminal GST tag
<u>Amino acid sequence of expressed protein</u>	<p>MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFP NLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRYGV SRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDAL DVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLOGWQATFGG GDHPPKSDLEVLFOGPLGSKGATGLSNLGNTSFMNSSIQCVSNTQPLTQYFIS GRHLYELNRTNPIGMKGHMAKCYGDLVQELWSGTQKSVAPLKLRRTIKAYAPK FDGFQQQDSQELLAFLLDGLHEDLNRVHEKPYVELKDS DGRPDWEVAAEAWDN HLRRNRSIIVDLFHGQLRSQVKCKTCGHSVRFDPFNFLSLPLPMDSYMDEI TVIKLDGTTPVRYGLRLNMDEKYTGLKKQLRDL CGLNSEQILLAEVHDSNIKN FPQDNQKVQLSVSGFLCAFEIPVPSSPISASSPTQIDFSSSPSTNGMFTLTN GDLPKPIFIPNGMPNTVVPCGTEKNFTNGMVNGHMPSLPDSPFTGYIIAVHRK MMRTELYFLSPQENRPSLFGMPLIVPCTVHTRKLDLYDAVWIQVSWLARPLPP QEAS IHAQDRDNCMGYQYPFTLRVVQKDGNSCAWCPOYRFCRGCKIDCGEDRA FIGNAYIAVDWHPTALHLRYQTSQERVVDKHESVEQSRRQAEPINLDSCLRA FTSEEELGESEMYCSKCKTHCLATKKLDLWRLPPFLIIHLKRFQFVNDQWIK SQKIVRFLRESFDPSAFLVPRDPALCQHKPLTPQGDELSKPRILAREVKKVDA QSSAGKEDMLLSKSPSSLSANISSSPKGSPPSSSRKSGTSCPSSKNSSPSSPR TLGRSKGRLRLPQIGSKNKPSSSKKNLDASKENGAGQICELADALSRGHMRGG SQPELVTPQDHEVALANGFLYEHEACGNGCGDGYNSGQLGNHSEEDSTDDQRE DTHIKPIYNLYAISCHSGILSGGHYITYAKNPCKWYCYNDSSCEELHPDEID TDSAYILFYEQQIDYAOFLPKIDGKKMADTSSTDEDSesyEKYSMLQ</p>
<u>Native sequence</u>	in bold
<u>Protease cleavage</u>	Precision site underlined
<u>Cloning sites</u>	BamH1/Not1

DNA sequence of insert

GGATCCAAGGGAGCCACAGGTCTAAGCAACCTGGGAAACACATcctTTCATGAA
CTCAAGCATCCAGTGCCTTAGTAACACACAGCCACTGCACAGTATTTTATCT
CAGGGAGACATCTTTATGAACTCAACAGGACAAATCCCATTGGTATGAAGGG
CATATGGCTAAATGCTATGGTGATTTAGTGCAGGAACCTCTGGAGTGGAACTCA
GAAGAGTGTGGCCCATTAAGCTTCGGCGGACCATAGCAAAATATGCTCCCA
AGTTTGATGGGTTTCAGCAACAAGACTCCCAAGAACTTCTGGCTTTTCTCTTG
GATGGTCTTCATGAAGATCTCAACCGAGTCCATGAAAAGCCATATGTGGAAC
GAAGGACAGTGATGGCCGACCAGACTGGGAAGTAGCTGCAGAGGCCTGGGACA
ACCATCTAAGAAGAAATAGATCAATAATTGTGGATTTGTTCCATGGGCAGCTA
AGATCTCAAGTCAAATGCAAGACATGTGGGCATATAAGTGTCCGATTTGATCC
TTTCAATTTTTTGTCTTTGCCACTACCAATGGACAGTTACATGGACTTAGAAA
TAACAGTGATTAAGTTAGATGGTACTACCCCTGTACGGTATGGACTAAGACTG
AATATGGATGAAAAGTACACAGGTTTAAAAAACAGCTGAGGGATCTCTGTGG
ACTTAATTCAGAACAATCCTACTAGCAGAAGTACATGATTCCAACATAAAGA
ACTTTCCTCAGGATAACCAAAAAGTACAACCTCTCAGTGAGCGGATTTTTGTGT
GCATTTGAAATTCCTGTCCCTTCATCTCCAATTTAGCTTCTAGTCCAACACA
AATAGATTTCTCCTCTTACCATCTACAAATGGAATGTTACCCTAACTACCA
ATGGGGACCTACCCAAACCAATATTCATCCCAATGGAATGCCAAACACTGTT
GTGCCATGTGGAACGAGAAGAACTTACAAATGGAATGGTTAATGGTCACAT
GCCATCTCTCCTGACAGCCCTTTACAGGTTACATCATTCAGTCCACCGAA
AAATGATGAGGACAGAAGTATTTCTGTCACCTCAGGAGAATCGCCCAGC
CTCTTTGGAATGCCATTGATGTTCCATGCACTGTGCATACCCGGAAGAAAGA
CCTATATGATGCGGTTTGGATTCAAGTATCCTGGTTAGCAAGACCACTCCAC
CTCAGGAAGCTAGTATTCATGCCAGGATCGTGATAACTGTATGGGCTATCAA
TATCCATTCACCTACGAGTTGTGCAGAAAAGATGGGAACTCCTGTGCTTGGTG
CCCACAGTATAGATTTTGCAGAGGCTGTAATAATTGATTGTGGGGAAGACAGAG
CTTTCATTGGAATGCCTATATTGCTGTGGATTGGCACCCACAGCCCTTCAC
CTTCGCTATCAAACATCCAGGAAAGGGTTGTAGATAAGCATGAGAGTGTGGA
GCAGAGTCGGCGAGCGCAAGCCGAGCCATCAACCTGGACAGCTGTCTCCGTG
CTTTCACCAGTGAGGAAGAGCTAGGGGAAAAGTGAGATGTACTACTGTTCCAAG
TGTAAGACCCACTGCTTAGCAACAAGAAAGCTGGATCTCTGGAGGCTTCCACC
CTTCTGATTATTCACCTTAAGCGATTTCAATTTGTAATGATCAGTGGATAA
AATCACAGAAAAATTGTCAGATTTCTTCGGGAAAGTTTTGATCCGAGTGCTTTT
TTGGTACCACGAGACCCGGCCCTCTGCCAGCATAAACCACTCACACCCAGGG
GGATGAGCTCTCCAAGCCAGGATTTCTGGCAAGAGAGGTGAAGAAAAGTGGATG
CGCAGAGTTTCGGCTGGAAAAGAGGACATGCTCCTAAGCAAAAGCCATCTTCA
CTCAGCGCTAACATCAGCAGCAGCCAAAAGGTTCTCCTTCTTCATCAAGAAA
AAGTGGAAACCAGCTGTCCCTCCAGCAAAAACAGCAGCCCTAATAGCAGCCAC
GGACTTTGGGGAGGAGCAAAAGGAGGCTCCGGCTGCCCCAGATTGGCAGCAAA
AATAAGCCGTCAAGTAGTAAGAAGAACTTGGATGCCAGCAAAGAGAATGGGGC
TGGGCAGATCTGTGAGCTGGCTGACGCCTTGAGCCGAGGGCATATGCGGGGG
GCAGCCAACCAGAGCTGGTCACCTCAGGACCATGAGGTAGCTTTGGCCAAT
GGATTCCTTTATGAGCATGAAGCATGTGGCAATGGCTGTGGCGATGGCTACAG
CAATGGTCAGCTTGGAAACCACAGTGAAGAAGACAGCACTGATGACCAAAGAG
AAGACACTCATATTAAGCCTATTTATAATCTATATGCAATTTTCATGCCATTCA
GGAATTCTGAGTGGGGCCATTACATCACTTATGCCAAAACCCAAACTGCAA
GTGGTACTGTTATAATGACAGCAGCTGTGAGGAACCTCACCCCTGATGAAATTG
ACACCGACTCTGCCTACATTTCTTTCTATGAGCAGCAGGGGATAGACTACGCA
CAATTTCTGCCAAAGATTGATGGCAAAAAGATGGCAGACACAAGCAGTACGGA
TGAAGACTCTGAGTCTGATTACGAAAAGTACTCTATGTTACAGTAAGCGGCC
C