

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of GST-USP10

Enzyme description:- USP10 1-798 S203P, V204L natural variant

Clone number:- DU15649

Source:- BL21 Recombinant

Tag:- N-terminal GST tag

Purification method:- GSH sepharose

Expression level:- 0.5 mg/L

Calculated molecular mass:-

Monoisotopic 114888 Da

Average Mass 114957 Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 5.37

Purity:- 30%

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

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Clone Data Sheet

GST-USP10

<u>Protein</u>	USP10 (1-798 S203P, V204L natural variant of USP10)
<u>Synonyms</u>	UBP10
<u>Clone Number</u>	DU15649
<u>Species</u>	Human
<u>Accession Number</u>	Acc No: AAH00263
<u>Tags</u>	N-terminal GST tag
<u>Amino acid sequence of expressed protein</u>	<p>MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFP NLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRYGV SRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDAL DVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLOGWQATFGG GDHPPKSDLEVLFOGPLGSPGIPGSTRAAAMALHSPQYIFGDFSPDEFNQFFV TPRSSVELPPYSGTVLCGTQAVDKLPDGOEYQRIEFGVDEVIEPSDTLPRTPS YSISSTLNPQAPEFILGCTASKITPDGITKEASYGSIDCQYPGSALALDGSSN VEAEVLENDGVSGGLGQREKRRKKRPPGYYSYKLDGGDDSI STEALVNGHAN SAVPNSVSAEDA EFMGDMPPPLTPRTCNSPQNSTDSVSDIVPDSFPFGALGSD TRTAGQPEGGPGADFGQSCFPAEAGRDTLSRTAGAQCVCVGTDTTENLGVANGQ ILESSGEGTATNGVELHTTESIDLDPKTESASPPADGTGSASGTLPVSQPKS WASLFHDSKPSSSSPVAYVETKYSPPAISPLVSEKQVEVKEGLVPVSEDPVAI KIAELLENVTLIHKPVSLQPRGLINKGNWCYINATLQALVACPPMYHLMKFI P LYSKVQRPCSTSPMIDSFVRLMNEFTNMPVPPKPRQALGDKIVRDIRPGA AFE PTYIYRLLTVNKSSLSEKGRQEDAE EYLGFI LNGLHEEMLNLKLLSPSNEKL TISNGPKNHSVNEEEQEEQEGSEDEWEQVGRNKT SVTRQADFVQTPITGIF GGHIRSVVYQSSKESATLQPF FTLQLDIQSDKIRTVQDALESLVARES VQGY TTKTKQVEEISRRVTLEKLPPVLVLHLKRFVYEKTGGCQKLIKNI EYPVDLEI SKELLSPGVKNKFNFKCHR TYRLFVAVYHHGNSATGGHYTTDFVQIGLNGWLR I DDQTVKVINQYQVVKPTAERTAYLLYRRVDLL</p>
<u>Native sequence</u>	in bold
<u>Protease cleavage</u>	Precision site underlined
<u>Cloning sites</u>	Not1 / Not1
<u>DNA sequence of insert</u>	<p>GCGGCCGCGATGGCCCTCCACAGCCCGCAGTATATTTTTGGAGATTTTAGCCC TGATGAATTCAATCAATTCTTTGTGACTCCTCGATCTTCAGTTGAGCTTCCTC CATACAGTGGAACAGTTCTGTGTGGCACACAGGCTGTGGATAAACTACCTGAT GGACAAGAATATCAGAGAATTGAGTTTGGTGTGCGATGAAGTCATTGAACCCAG TGACACTTTGCCGAGAACCCCGCTACAGTATTTCAAGCACACTGAACCCCTC AGGCCCTGAATTTATTCTCGGTTGTACAGCTTCCAAAATAACCCCTGATGGT ATCACTAAAGAAGCAAGCTATGGCTCCATCGACTGCCAGTACCCAGGCTCTGC CCTCGCTTTGGATGGAAGTTCTAATGTGGAGGCGGAAGTTTGGAAAAATGATG GTGTCTCAGGTGGTCTTGGACAAAGGGAGCGTAAAAAGAAGAAAAAGCGGCCA CCTGGATATTACAGCTATTTGAAAGATGGTGGCGATGATAGTATCTCCACAGA AGCCCTGGTCAATGGCCATGCCAATTCAGCAGTCCCGAACAGTGTGAGTGCAG AGGATGCAGAATTTATGGGTGACATGCCTCCGCCACTTACGCCCAGGACTTGT AACAGCCCCCAGA ACTCCACAGACTCTGTGAGTGCATTGTGCCTGACAGTCC TTCCCCGGAGCACTCGGCAGTGACACCAGGACTGCAGGGCAGCCAGAGGGGG</p>

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