Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of GST-USP21 [196-565]

Enzyme description:- GST-USP21

Clone number:- DU22385

Source:- BL21 Recombinant

Tag:- N-terminal GST

Purification method:- GSH sepharose

Expression level:- 1.5 mg/L

Calculated molecular mass:-

Monoisotopic	67,325 Da
Average Mass	67,366 Da

[cycsteines reduced, methionines have not been oxidised]

Theoretical pI:- 8.6

Purity:- 80%

Enzyme storage buffer:-

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

Storage temperature:- -80ºC

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-USP21 [196-565]

Protein	GST-USP21 [196-565]
Synonyms	
Clone Number	DU22385
Species	Human
Accession Number	Protein: Q9UK80 DNA: NM_001014443.2
Tags	N-terminal GST
Amino acid sequence of expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFP NLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRYGV SRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDAL DVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAWPLQGWQATFGG GDHPPKSD**SDDKMAHHTLLLGSGHVGLRNLGNTCFLNAVLQCLSSTRPLRDFC LRRDFRQEVPGGGRAQELTEAFADVIGALWHPDSCEAVNPTRFRAVFQKYVPS FSGYSQQDAQEFLKLLMERLHLEINRRGRRAPPILANGPVPSPPRRGGALLEE PELSDDDRANLMWKRYLEREDSKIVDLFVGQLKSCLKCQACGYRSTTFEVFCD LSLPIPKKGFAGGKVSLRDCFNLFTKEEELESENAPVCDRCRQKTRSTKKLTV QRFPRILVLHLNRFSASRGSIKKSSVGVDFPLQRLSLGDFASDKAGSPVYQLY ALCNHSGSVHYGHYTALCRCQTGWHVYNDSRVSPVSENQVASSEGYVLFYQLM QEPPRCL**
Native sequence	in bold
Protease cleavage	No cleavage sites in this construct
Cloning sites	Sal1 / Not1

DNA sequence of insert

TCTGATGACAAGATGGCTCATCACACACTCCTTCTGGGCTCTGGTCATGTTGG
CCTTCGAAACCTGGGAAACACGTGCTTCCTGAATGCTGTGCTGCAGTGTCTGA
GCAGCACTCGACCTCTTCGGGACTTCTGTCTGAGAAGGGACTTCCGGCAAGAG
GTGCCTGGAGGAGGCCGAGCCCAAGAGCTCACTGAAGCCTTTGCAGATGTGAT
TGGTGCCCTCTGGCACCCTGACTCCTGCGAAGCTGTGAATCCTACTCGATTCC
GAGCTGTCTTCCAGAAATATGTTCCCTCCTTCTCTGGATACAGCCAGCAGGAT
GCCCAAGAGTTCCTGAAGCTCCTCATGGAGCGGCTACACCTTGAAATCAACCG
CCGAGGCCGCCGGGCTCCACCGATACTTGCCAATGGTCCAGTTCCCTCTCCAC
CCCGCCGAGGAGGGGCTCTGCTAGAAGAACCTGAGTTAAGTGATGATGACCGA
GCCAACCTAATGTGGAAACGTTACCTGGAGCGAGAGGACAGCAAGATTGTGGA
CCTGTTTGTGGGCCAGTTGAAAAGTTGTCTCAAGTGCCAGGCCTGTGGGTATC
GCTCCACGACCTTCGAGGTTTTTTGTGACCTGTCCCTGCCCATCCCCAAGAAA
GGATTTGCTGGGGGCAAGGTGTCTCTGCGGGATTGTTTCAACCTTTTCACTAA
GGAAGAAGAGCTAGAGTCGGAGAATGCCCCAGTGTGTGACCGATGTCGGCAGA
AAACTCGAAGTACCAAAAAGTTGACAGTACAAAGATTCCCTCGAATCCTCGTG
CTCCATCTGAATCGATTTTCTGCCTCCCGAGGCTCCATCAAAAAAAGTTCAGT
AGGTGTAGACTTTCCACTGCAGCGACTGAGCCTAGGGGACTTTGCCAGTGACA
AAGCCGGAAGTCCTGTATACCAGCTGTATGCCCTTTGCAACCACTCAGGCAGC
GTCCACTATGGCCACTACACAGCCCTGTGCCGGTGCCAGACTGGTTGGCATGT
CTACAATGACTCTCGTGTCTCCCCTGTCAGTGAAAACCAGGTGGCATCCAGCG
AGGGCTACGTGCTGTTCTACCAACTGATGCAGGAGCCACCCCGGTGCCTGTGA
GCGGCCGC