Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of His-USP21 [196-565]

Enzyme description:- His-USP21 [196-565]

Clone number:- DU22384

Source:- BL21 Recombinant

Tag:- N-terminal

Purification method:- N-terminal His_6 tag

Expression level:- 1.6 mg/L

Calculated molecular mass:-

Monoisotopic	42826 Da
Average Mass	42852 Da

[cycsteines reduced, methionines have not been oxidised]

Theoretical pI:- 9.15

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

His-USP21 [196-565]

Protein	His-USP21 [196-565]
Synonyms	
Clone Number	DU22384
Species	Human
Accession Number	Protein: Q9UK80 DNA: NM_001014443.2
Tags	N-terminal
Amino acid sequence of expressed protein	MHHHHHHVD**SDDKMAHHTLLLGSGHVGLRNLGNTCFLNAVLQCLSSTRPLRDF CLRRDFRQEVPGGGRAQELTEAFADVIGALWHPDSCEAVNPTRFRAVFQKYVP SFSGYSQQDAQEFLKLLMERLHLEINRRGRRAPPILANGPVPSPPRRGGALLE EPELSDDDRANLMWKRYLEREDSKIVDLFVGQLKSCLKCQACGYRSTTFEVFC DLSLPIPKKGFAGGKVSLRDCFNLFTKEEELESENAPVCDRCRQKTRSTKKLT VQRFPRILVLHLNRFSASRGSIKKSSVGVDFPLQRLSLGDFASDKAGSPVYQL YALCNHSGSVHYGHYTALCRCQTGWHVYNDSRVSPVSENQVASSEGYVLFYQL MQEPPRCL**
Native sequence	in bold
Protease cleavage	No protease site in this construct
Cloning sites	EcoR1/Sal1
DNA sequence of insert	GTCGACTCTGATGACAAGATGGCTCATCACACACTCCTTCTGGGCTCTGGTCA TGTTGGCCTTCGAAACCTGGGAAACACGTGCTTCCTGAATGCTGTGCTGCAGT GTCTGAGCAGCACTCGACCTCTTCGGGACTTCTGTCTGAGAAGGGACTTCCGG CAAGAGGTGCCTGGAGGAGGCCGAGCCCAAGAGCTCACTGAAGCCTTTGCAGA TGTGATTGGTGCCCTCTGGCACCCTGACTCCTGCGAAGCTGTGAATCCTACTC GATTCCGAGCTGTCTTCCAGAAATATGTTCCCTCCTTCTCTGGATACAGCCAG CAGGATGCCCAAGAGTTCCTGAAGCTCCTCATGGAGCGGCTACACCTTGAAAT CAACCGCCGAGGCCGCCGGGCTCCACCGATACTTGCCAATGGTCCAGTTCCCT CTCCACCCCGCCGAGGAGGGGCTCTGCTAGAAGAACCTGAGTTAAGTGATGAT GACCGAGCCAACCTAATGTGGAAACGTTACCTGGAGCGAGAGGACAGCAAGAT TGTGGACCTGTTTGTGGGCCAGTTGAAAAGTTGTCTCAAGTGCCAGGCCTGTG GGTATCGCTCCACGACCTTCGAGGTTTTTTGTGACCTGTCCCTGCCCATCCCC AAGAAAGGATTTGCTGGGGGCAAGGTGTCTCTGCGGGATTGTTTCAACCTTTT CACTAAGGAAGAAGAGCTAGAGTCGGAGAATGCCCCAGTGTGTGACCGATGTC GGCAGAAAACTCGAAGTACCAAAAAGTTGACAGTACAAAGATTCCCTCGAATC CTCGTGCTCCATCTGAATCGATTTTCTGCCTCCCGAGGCTCCATCAAAAAAAG TTCAGTAGGTGTAGACTTTCCACTGCAGCGACTGAGCCTAGGGGACTTTGCCA GTGACAAAGCCGGAAGTCCTGTATACCAGCTGTATGCCCTTTGCAACCACTCA GGCAGCGTCCACTATGGCCACTACACAGCCCTGTGCCGGTGCCAGACTGGTTG GCATGTCTACAATGACTCTCGTGTCTCCCCTGTCAGTGAAAACCAGGTGGCAT CCAGCGAGGGCTACGTGCTGTTCTACCAACTGATGCAGGAGCCACCCCGGTGC CTGTGAGCGGCCGC