Division of Signal Transduction Therapy

Standard Operation Procedure

GST-UCHL1

Enzyme description:-	GST-UCHL1
Clone number:-	DU15692
Source:-	BL21 Recombinant
Tag:-	N-terminal GST tag
Purification method:-	GSH sepharose
Expression level:-	6 mg/L

Calculated molecular mass:-

Monoisotopic	51615 Da
Average Mass	51646 Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:-	6.01
Purity:-	90%

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-UCHL1

Protein	GST-UCHL1
Synonyms	
Clone Number	DU15692
Species	Human
Accession Number	Protein: P09936 DNA: AAH00332.1
Tags	N-terminal GST tag
Amino acid sequence of expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFP NLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRYGV SRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDAL DVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAWPLQGWQATFGG GDHPPKSDLEVLFQGPLGS**MQLKPMEINPEMLNKVLSRLGVAGQWRFVDVLGL** **EEESLGSVPAPACALLLLFPLTAQHENFRKKQIEELKGQEVSPKVYFMKQTIG** **NSCGTIGLIHAVANNQDKLGFEDGSVLKQFLSETEKMSPEDRAKCFEKNEAIQ** **AAHDAVAQEGQCRVDDKVNFHFILFNNVDGHLYELDGRMPFPVNHGASSEDTL** **LKDAAKVCREFTEREQGEVRFSAVALCKAA**
Native sequence	in bold
Protease cleavage	Precission site underlined
Cloning sites	BamH1 / Not1

DNA sequence of insert

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GGATCCATGCAGCTCAAGCCGATGGAGATCAACCCCGAGATGCTGAACAAAGT
GCTGTCCCGGCTGGGGGTCGCCGGCCAGTGGCGCTTCGTGGACGTGCTGGGGC
TGGAAGAGGAGTCTCTGGGCTCGGTGCCAGCGCCTGCCTGCGCGCTGCTGCTG
CTGTTTCCCCTCACGGCCCAGCATGAGAACTTCAGGAAAAAGCAGATTGAAGA
GCTGAAGGGACAAGAAGTTAGTCCTAAAGTGTACTTCATGAAGCAGACCATTG
GGAATTCCTGTGGCACAATCGGACTTATTCACGCAGTGGCCAATAATCAAGAC
AAACTGGGATTTGAGGATGGATCAGTTCTGAAACAGTTTCTTTCTGAAACAGA
GAAAATGTCCCCTGAAGACAGAGCAAAATGCTTTGAAAAGAATGAGGCCATAC
AGGCAGCCCATGATGCCGTGGCACAGGAAGGCCAATGTCGGGTAGATGACAAG
GTGAATTTCCATTTTATTCTGTTTAACAACGTGGATGGCCACCTCTATGAACT
TGATGGACGAATGCCTTTTCCGGTGAACCATGGCGCCAGTTCAGAGGACACCC
TGCTGAAGGACGCTGCCAAGGTCTGCAGAGAATTCACCGAGCGTGAGCAAGGA
GAAGTCCGCTTCTCTGCCGTGGCTCTCTGCAAGGCAGCCTAAGCGGCCGC
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