

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of His-UCHL1

<u>Enzyme description:-</u>	His-UCHL1
<u>Clone number:-</u>	DU15693
<u>Source:-</u>	BL21 Recombinant
<u>Tag:-</u>	N-terminal His ₆ -tag
<u>Purification method:-</u>	Ni ⁺⁺ -Sephrose
<u>Expression level:-</u>	6 mg/L

Calculated molecular mass:-

Monoisotopic	27251 Da
Average Mass	27267 Da
[cysteines reduced, methionines have not been oxidised]	

Theoretical pI:- 5.92

Purity:- 95%

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

Clone Data Sheet

His-UCHL1

<u>Protein</u>	His-UCHL1
<u>Synonyms</u>	
<u>Clone Number</u>	DU15693
<u>Species</u>	Human
<u>Accession Number</u>	Protein: P09936 DNA: AAH00332.1
<u>Tags</u>	N-terminal His ₆ -tag
<u>Amino acid sequence of expressed protein</u>	MGSSHHHHHHSSGLEVL<u>FQGP</u>GSMQLKPMEINPEMLNKVLSRLGVAGQWR FVDVLGLEEESLGSVPAPACALLLLFPLTAQHENFRKKQIEELKGQEVSP KVYFMKQTI GNSCGTIGLIHAVANNQDKLGFEDGSVLKQFLSETEKMSPE DRAKCFEKNEAIQAAHDAVAQEGQCRVDDKVNHFHILFNNVDGHLIELDG RMPFPVNHGASSEDLLKDAAKVCREFTEREQGEVRFSAVALCKAA
<u>Native sequence</u>	in bold
<u>Protease cleavage</u>	Precision site underlined
<u>Cloning sites</u>	BamH1 / Not1
<u>DNA sequence of insert</u>	GGATCCATGCAGCTCAAGCCGATGGAGATCAACCCCGAGATGCTGAACAA AGTGCTGTCCCGGCTGGGGGTCGCCGGCCAGTGGCGCTTCGTGGACGTGC TGGGGCTGGAAGAGGAGTCTCTGGGCTCGGTGCCAGCGCCTGCCTGCCGG CTGCTGCTGCTGTTTTCCCTCACGGCCAGCATGAGAAGTTCAGGAAAAA GCAGATTGAAGAGCTGAAGGGACAAGAAGTTAGTCCTAAAGTGTACTTCA TGAAGCAGACCATTTGGGAATTCCTGTGGCACAATCGGACTTATTCACGCA GTGGCCAATAATCAAGACAAACTGGGATTTGAGGATGGATCAGTTCTGAA ACAGTTTCTTTCTGAAACAGAGAAAATGTCCCCTGAAGACAGAGCAAAAT GCTTTGAAAAGAATGAGGCCATACAGGCAGCCCATGATGCCGTGGCACAG GAAGGCCAATGTCGGGTAGATGACAAGGTGAATTTCCATTTTATTCTGTT TAACAACGTGGATGGCCACCTCTATGAACTTGATGGACGAATGCCTTTTC CGGTGAACCATGGCGCCAGTTCAGAGGACACCCTGCTGAAGGACGCTGCC AAGTCTGCAGAGAATTCACCGAGCGTGAGCAAGGAGAAGTCCGCTTCTC TGCCGTGGCTCTCTGCAAGGCAGCCTAAGCGGCCGC