

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of His-Halo-SQSTM UBA domain trimer

<u>Enzyme description:-</u>	SQSTM 389-439 trimer = UBA domain trimer
<u>Clone number:-</u>	DU23894
<u>Source:-</u>	bacteria
<u>Tag:-</u>	N-terminal His-Halo-
<u>Purification method:-</u>	Ni ⁺⁺ -Sephrose
<u>Expression level:-</u>	5 mg/L
<u>Calculated molecular mass:-</u>	
Monoisotopic	53052
Average Mass	53020
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	5.10
<u>Purity:-</u>	90%
<u>Enzyme storage buffer:-</u>	
50 mM HEPES pH 7.5, 10% glycerol, 150mM NaCl, 1mM DTT	
<u>Storage temperature:-</u>	-80°C
<u>Assay:-</u>	

Division of Signal Transduction Therapy

Clone Data Sheet

Protein name His-Halo-SQSTM UBA domain trimer

<u>Protein</u>	His-Halo-SQSTM UBA 389-439 = UBA domain trimer
<u>Synonyms</u>	ORCA, OSIL, EBIAP, p62
<u>Clone Number</u>	DU23894
<u>Species</u>	human
<u>Accession Number</u>	Protein: Q13501
<u>Tags</u>	N-terminal His-Halo-
Aminoacid sequence of the expressed protein	MGSSHHHHHHENLYFQMAEIGTGFPDPHYVEVLGERMHYVDVGPDRDGTPLFLHGNPTSSYVWRNIIPHVAPTHRCIAPDLIGMKSDKPDLYFFDDHVRFMDFIEALGLEEVVLIHDWGSALGFHWAKRNPERVKGIAFMFIRPIPTWDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEVEMDHYREPFLNPVDREPLWRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLIPPAEAARLAKSLPNCKAVDIGPGLNLLQEDNPDIGSEIARWLSTLEISGGSGGGEADPRLIESLSQMLSMGFSDEGGWLT RLLOTKNYDIGAALDTIQYSKHGGGRSGGGEADPRLIESLSQMLSMGFSDEGGWLT RLLOTKNYDIGAALDTIQYSKHGGGRSEADPRLIESLSQMLSMGFSDEGGWLT RLLOTKNYDIGAALDTIQYSKH
Native sequence	in bold
Protease cleavage	TEV site does not work
<u>DNA sequence of the expression cassette</u>	ATGGGCAGCAGCCATCATCATCATCACGAAAACCTGTATTTTCAGatggcagaaatcggactggtcttccattcgacccccattatgtggaagtcc tgggcgagcgcgatgcactacgtcgcgatggttggtccgcgcgatggcaccctgtgctgttccctgcacggtaacccgacctcctcctacgtgtggcgcaacatcatcccgcgatgttgaccgaccatcgcctgcattgctccagacctgatcgtatgggcaaaccgacaaaccagacctgggttatttcttcgacgaccacgtccgcttcatggatgccttcatcgaagccctgggtctggaagaggcgtcctggctattcagactggggctccgctctgggtttccactgggccaagcgcaatccagagcgcgtcaaaggtattgcatttatggagttcatccgccctatcccgacctgggacgaatggccagaatttggccgcgagaccttccaggccttccgcaccaccgacgtcggccgcaagctgatcgcgatcagaacgttttatcgcagggtagcctgcccgatgggtgtcgtccgcccgtgactgaagtcgagatggaccattaccgcgagccgttccctgaatcctggtgaccgcgagccactgtggcgcttcccaaaccgagctgccaatcgccgggtgagccagcgaacatcgtcgcgctggtcgaagaatacatggactggctgaccagctcccctgtccgaagctgctgttctggggcaccaccaggcgttctgatcccaccggccgaagccgctcgcctggccaaaagcctgcctaactgcaaggctgtggacatcggcccggctgcaatctgctgcaagaagacaaccggacctgatcggcagcgagatcgcgcgctggctgtcgcgacgctcgagatttccggcGGATCCGGCGGAGGCGAGGCTGACCCGGGCTGATTGAGTCCCTCTCCAGATGCTGTCCA TGGGCTTCTCTGATGAAGGCGGCTGGCTCACCAGGCTCCTGCAGACCAAGAACTATGACATCGGAGCGGCTCTGGACACCATCCAGTATTCAAAGCATGCGGAGGCAGATCCGGCGGAGGCGAGGCTGACCCGGGCTGATTGAGTCCCTCTCCAGATGCTGTCCATGGGCTTCTCTGATGAAGGCGGCTGGCTCACC

AGGTCCTGCAGACCAAGAACTATGACATCGGAGCGGCTCTGGACACCAT
CCAGTATTCAAAGCATGGCGGAGGCAGATCCGAGGCTGACCCGGGCTGA
TTGAGTCCCTCTCCAGATGCTGTCCATGGGCTTCTCTGATGAAGGCGGC
TGGCTCACCAGGCTCCTGCAGACCAAGAACTATGACATCGGAGCGGCTCT
GGACACCATCCAGTATTCAAAGCATTGAGCGGCCGC