Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of His-Halo-Mud1 UBA domain tetramer

Enzyme description:- Mud1 291-332 = UBA domain tetramer

Clone number:- DU23893

Source:- bacteria

Tag:- N-terminal His-Halo-

Purification method:- Ni^{++}-Sepharose

Expression level:- 10 mg/L

Calculated molecular mass:-

Monoisotopic 54415
Average Mass 54446
[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 4.58

Purity:- 90%

Enzyme storage buffer:-

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

Storage temperature:- -80ºC

Assay:-

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Clone Data Sheet

Protein name His-Halo-Mud1 UBA domain tetramer

Protein	His-Halo-Mud1 UBA 291-332 = UBA domain tetramer
Synonyms	
Clone Number	DU23893
Species	Schizosaccharomyces pombe
Accession Number	Protein: Q10256, NP_001018195.1 DNA:NM_001018619.1
Tags	N-terminal His-Halo-
Aminoacid sequence of the expressed protein	MGSSHHHHHHENLYFQMAEIGTGFPFDPHYVEVLGERMHYVDVGPRDGTP VLFLHGNPTSSYVWRNIIPHVAPTHRCIAPDLIGMGKSDKPDLGYFFDDH VRFMDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIAFMEFIRP IPTWDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEV EMDHYREPFLNPVDREPLWRFPNELPIAGEPANIVALVEEYMDWLHQSPV PKLLFWGTPGVLIPPAEAARLAKSLPNCKAVDIGPGLNLLQEDNPDLIGS EIARWLSTLEISG**GSGGGPTDPGLNSKIAQLVSMGFDPLEAAQALDAANG** **DLDVAASFLLGGGRSGGGPTDPGLNSKIAQLVSMGFDPLEAAQALDAANG** **DLDVAASFLLGGGRSGGGPTDPGLNSKIAQLVSMGFDPLEAAQALDAANG** **DLDVAASFLLGGGRSPTDPGLNSKIAQLVSMGFDPLEAAQALDAANGDLD** **VAASFLL**
Native sequence	in bold
Protease cleavage	TEV site does not work
DNA sequence of the expression cassette	ATGGGCAGCAGCCATCATCATCATCATCACGAAAACCTGTATTTTCAGAT GGCAGAAATCGGTACTGGCTTTCCATTCGACCCCCATTATGTGGAAGTCC TGGGCGAGCGCATGCACTACGTCGATGTTGGTCCGCGCGATGGCACCCCT GTGCTGTTCCTGCACGGTAACCCGACCTCCTCCTACGTGTGGCGCAACAT CATCCCGCATGTTGCACCGACCCATCGCTGCATTGCTCCAGACCTGATCG GTATGGGCAAATCCGACAAACCAGACCTGGGTTATTTCTTCGACGACCAC GTCCGCTTCATGGATGCCTTCATCGAAGCCCTGGGTCTGGAAGAGGTCGT CCTGGTCATTCACGACTGGGGCTCCGCTCTGGGTTTCCACTGGGCCAAGC GCAATCCAGAGCGCGTCAAAGGTATTGCATTTATGGAGTTCATCCGCCCT ATCCCGACCTGGGACGAATGGCCAGAATTTGCCCGCGAGACCTTCCAGGC CTTCCGCACCACCGACGTCGGCCGCAAGCTGATCATCGATCAGAACGTTT TTATCGAGGGTACGCTGCCGATGGGTGTCGTCCGCCCGCTGACTGAAGTC GAGATGGACCATTACCGCGAGCCGTTCCTGAATCCTGTTGACCGCGAGCC ACTGTGGCGCTTCCCAAACGAGCTGCCAATCGCCGGTGAGCCAGCGAACA TCGTCGCGCTGGTCGAAGAATACATGGACTGGCTGCACCAGTCCCCTGTC CCGAAGCTGCTGTTCTGGGGCACCCCAGGCGTTCTGATCCCACCGGCCGA AGCCGCTCGCCTGGCCAAAAGCCTGCCTAACTGCAAGGCTGTGGACATCG GCCCGGGTCTGAATCTGCTGCAAGAAGACAACCCGGACCTGATCGGCAGC GAGATCGCGCGCTGGCTGTCGACGCTCGAGATTTCCGGCGGATCCGGCGG AGGCCCCACTGACCCCGGTTTGAACTCCAAAATTGCACAGCTAGTCAGTA TGGGATTTGATCCATTAGAGGCTGCGCAGGCGTTAGACGCTGCGAATGGA GATTTAGATGTAGCTGCTTCTTTTCTCCTTGGCGGAGGCAGATCCGGCGG AGGCCCCACTGACCCCGGTTTGAACTCCAAAATTGCACAGCTAGTCAGTA

TGGGATTTGATCCATTAGAGGCTGCGCAGGCGTTAGACGCTGCGAATGGA
GATTTAGATGTAGCTGCTTCTTTTCTCCTTGGCGGAGGCAGATCCGGCGG
AGGCCCCACTGACCCCGGTTTGAACTCCAAAATTGCACAGCTAGTCAGTA
TGGGATTTGATCCATTAGAGGCTGCGCAGGCGTTAGACGCTGCGAATGGA
GATTTAGATGTAGCTGCTTCTTTTCTCCTTGGCGGAGGCAGATCCCCCAC
TGACCCCGGTTTGAACTCCAAAATTGCACAGCTAGTCAGTATGGGATTTG
ATCCATTAGAGGCTGCGCAGGCGTTAGACGCTGCGAATGGAGATTTAGAT
GTAGCTGCTTCTTTTCTCCTTTAAGCGGCCGC