Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of His-Halo-SLX4 BTB domain dimer

Enzyme description:- SLX4 270-380 dimer = BTB domain dimer

Clone number:- DU45631

Source:- bacteria

Tag:- N-terminal His-Halo-

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

Expression level:- 0.5 mg/L

Calculated molecular mass:-

Monoisotopic	61091
Average Mass	61129

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 6.23

Purity:- 20% (contaminants are shorter fragments)

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-SLX4 BTB domain dimer

Protein	His-Halo-SLX4 (270-380) BTB domain dimer
Synonyms	BTBD12, FANCP, MUS312
Clone Number	DU45631
Species	human
Accession Number	DNA: NM_032444
Tags	N-terminal His-Halo-
Aminoacid sequence of the expressed protein	MHHHHHHMAEIGTGFPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYVWRNIIPHVAPTHRCIAPDLIGMGKSDKPDLGYFFDDHVRFMDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIAFMEFIRPIPTWDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEVEMDHYREPFLNPVDREPLWRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGVLIPPAEAARLAKSLPNCKAVDIGPGLNLLQEDNPDLIGSEIARWLSTLEISGENLYFQGGSM**LTLQQEFARVGASAHDDSLEEKGLFFCQICQKNLSAMNVTRREQHVNRCLDEAEKTLRPSVPQIPECPICGKPFLTLKSRTSHLKQCAVKMEVGPQLLLQAVRLQTAQPEGRSMLTLQQEFARVGASAHDDSLEEKGLFFCQICQKNLSAMNVTRREQHVNRCLDEAEKTLRPSVPQIPECPICGKPFLTLKSRTSHLKQCAVKMEVGPQLLLQAVRLQTAQPEGRS**
Native sequence	in bold
Protease cleavage	TEV protease site underlined

DNA sequence of the expression cassette	GGATCCATGTTGACCCTGCAGCAGGAGTTTGCACGGGTAGGAGCATCGGCACATGATGATAGCCTGGAGGAAAAGGGTTTGTTCTTCTGCCAGATTTGTCAAAAGAACCTCTCAGCCATGAACGTGACCCGAAGGGAACAGCATGTGAACAGGTGCTTGGATGAAGCTGAAAAGACACTAAGACCTTCTGTGCCTCAGATCCCTGAGTGCCCGATTTGTGGGAAACCGTTTCTTACCTTAAAGAGCAGAACCAGTCACTTGAAGCAGTGTGCTGTGAAGATGGAGGTTGGCCCCCAGCTCCTGCTTCAGGCTGTGCGGCTGCAGACAGCACAGCCTGAGGGTAGATCCATGTTGACCCTGCAGCAGGAGTTTGCACGGGTAGGAGCATCGGCACATGATGATAGCCTGGAGGAAAAGGGTTTGTTCTTCTGCCAGATTTGTCAAAAGAACCTCTCAGCCATGAACGTGACCCGAAGGGAACAGCATGTGAACAGGTGCTTGGATGAAGCTGAAAAGACACTAAGACCTTCTGTGCCTCAGATCCCTGAGTGCCCGATTTGTGGGAAACCGTTTCTTACCTTAAAGAGCAGAACCAGTCACTTGAAGCAGTGTGCTGTGAAGATGGAGGTTGGCCCCCAGCTCCTGCTTCAGGCTGTGCGGCTGCAGACAGCACAGCCTGAGGGTAGATCTTGACATCGAGTCGACGCTCGAGCGGCCGC
Restriction sites	BamH1 Not1