Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of GST-Fan1 (41-69) UBZ domain

Enzyme description:-	GST-Fan1 41-69 (UBZ-domain)
Clone number:-	DU20707
Source:-	BL21 recombinant
Tag:-	N-terminal GST
Purification method:-	GSH-Sepharose
Expression level:-	30mg/L

Calculated molecular mass:-

Monoisotopic	30447 Da
Average Mass	30466Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:-	6.00
Purity:-	90%

Enzyme storage buffer:-

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

Storage temperature:-	-80ºC

Assay:-

Division of Signal Transduction Therapy

Clone Data Sheet

GST-Fan1 41-69 (UBZ-domain)

Protein	Fan1 41-69 UBZ-domain monomer
Synonyms	Fanconi-associated nuclease 1; FANCD2/FANCI-associated nuclease 1; Myotubularin-related protein 15
Clone Number	DU20707
Species	Human
Accession Number	Protein: Q9Y2M0
Tags	N-terminal GST
Aminoacid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGL EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL DIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTH PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIA WPLQGWQATFGGGDHPPKSDLEVLFQGPLGSMAG**KLACPVCSKMVPRYDL** **NRHLDEMCANNDF**
Native sequence	in bold
Protease cleavage	Prescission protease site underlined
Cloning sites	BamHI / Not1
DNA sequence of the expression cassette	ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCCAC TCGACTTCTTTTGGAATATCTTGAAGAAAAATATGAAGAGCATTTGTATG AGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTTGAATTGGGTTTG GAGTTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAAATTAACACA GTCTATGGCCATCATACGTTATATAGCTGACAAGCACAACATGTTGGGTG GTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAAGGAGCGGTTTTG GATATTAGATACGGTGTTTCGAGAATTGCATATAGTAAAGACTTTGAAAC TCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTCG AAGATCGTTTATGTCATAAAACATATTTAAATGGTGATCATGTAACCCAT CCTGACTTCATGTTGTATGACGCTCTTGATGTTGTTTTATACATGGACCC AATGTGCCTGGATGCGTTCCCAAAATTAGTTTGTTTTAAAAAACGTATTG AAGCTATCCCACAAATTGATAAGTACTTGAAATCCAGCAAGTATATAGCA TGGCCTTTGCAGGGCTGGCAAGCCACGTTTGGTGGTGGCGACCATCCTCC AAAATCGGATCTGGAAGTTCTGTTCCAGGGGCCCCTGGGATCCATGGCCG GCAAACTTGCCTGCCCCGTTTGCAGTAAAATGGTGCCTAGATATGACTTA AACCGGCACCTTGATGAAATGTGTGCTAACAATGACTTCTGAGGCGCCGC GGCCGC