Division of Signal Transduction Therapy

Standard Operation Procedure

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

Enzyme description:-	GST-Fan1 41-69 (UBZ-domain dimer)
Clone number:-	DU20727
Source:-	BL21 recombinant
Tag:-	N-terminal GST
Purification method:-	GSH-Sepharose
Expression level:-	70mg/L

Calculated molecular mass:-

Monoisotopic	34267 Da
Average Mass	34288Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:-	6.17
Purity:-	90%

Enzyme storage buffer:-

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

Storage temperature:-	-80°C

Assay:-

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Clone Data Sheet

GST-Fan1 41-69 (UBZ-domain dimer)

Protein	Fan1 41-69 UBZ-domain dimer
Synonyms	Fanconi-associated nuclease 1; FANCD2/FANCI-associated nuclease 1; Myotubularin-related protein 15
Clone Number	DU20727
Species	Human
Accession Number	Protein: Q9Y2M0
Tags	N-terminal GST
Aminoacid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGL EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL DIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTH PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIA WPLQGWQATFGGGDHPPKSDLEVLFQGPLGSMAG**KLACPVCSKMVPRYDL** **NRHLDEMCANNDF**GGGGGGGG**KLACPVCSKMVPRYDLNRHLDEMCANNDF**
Native sequence	in bold
Protease cleavage	Prescission protease site underlined
Cloning sites	*NaeI*/*SfoI*
DNA sequence of the expression cassette	ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCCAC TCGACTTCTTTTGGAATATCTTGAAGAAAAATATGAAGAGCATTTGTATG AGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTTGAATTGGGTTTG GAGTTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAAATTAACACA GTCTATGGCCATCATACGTTATATAGCTGACAAGCACAACATGTTGGGTG GTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAAGGAGCGGTTTTG GATATTAGATACGGTGTTTCGAGAATTGCATATAGTAAAGACTTTGAAAC TCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTCG AAGATCGTTTATGTCATAAAACATATTTAAATGGTGATCATGTAACCCAT CCTGACTTCATGTTGTATGACGCTCTTGATGTTGTTTTATACATGGACCC AATGTGCCTGGATGCGTTCCCAAAATTAGTTTGTTTTAAAAAACGTATTG AAGCTATCCCACAAATTGATAAGTACTTGAAATCCAGCAAGTATATAGCA TGGCCTTTGCAGGGCTGGCAAGCCACGTTTGGTGGTGGCGACCATCCTCC AAAATCGGATCTGGAAGTTCTGTTCCAGGGGCCCCTGGGATCCATGGCC*G* *GCAAACTTGCCTGCCCCGTTTGCAGTAAAATGGTGCCTAGATATGACTTA* *AACCGGCACCTTGATGAAATGTGTGCTAACAATGACTTCGGTGGAGGTGG* *AGGTGGAGGC*GGCAAACTTGCCTGCCCCGTTTGCAGTAAAATGGTGCCTA GATATGACTTAAACCGGCACCTTGATGAAATGTGTGCTAACAATGACTTC TGAGGCGCCGCGGCCGC