Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of GST-FLAG-FAF1

Enzyme description:- GST-FLAG-FAF1 1-650 (full length)

Clone number:- DU20777

Source:- BL21 recombinant

Tag:- N-terminal GST

Purification method:- GSH-Sepharose

Expression level:- 1.2mg/L

Calculated molecular mass:-

Monoisotopic 102533 Da
Average Mass 102596 Da
[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 4.84

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-FLAG-FAF1

Protein	FAF1
Synonyms	hFAF1; CGI-03; HFAF1s; UBXD12; UBXN3A
Clone Number	DU20777
Species	Human
Accession Number	Protein: Q9UNN5
Tags	N-terminal GST
Aminoacid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGL EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL DIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTH PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIA WPLQGWQATFGGGDHPPKSDENLYFQGGSPEFPGRRMDYKDDDDK**MASNM** **DREMILADFQACTGIENIDEAITLLEQNNWDLVAAINGVIPQENGILQSE** **YGGETIPGPAFNPASHPASAPTSSSSSAFRPVMPSRQIVERQPRMLDFRV** **EYRDRNVDVVLEDTCTVGEIKQILENELQIPVSKMLLKGWKTGDVEDSTV** **LKSLHLPKNNSLYVLTPDLPPPSSSSHAGALQESLNQNFMLIITHREVQR** **EYNLNFSGSSTIQEVKRNVYDLTSIPVRHQLWEGWPTSATDDSMCLAESG** **LSYPCHRLTVGRRSSPAQTREQSEEQITDVHMVSDSDGDDFEDATEFGVD** **DGEVFGMASSALRKSPMMPENAENEGDALLQFTAEFSSRYGDCHPVFFIG** **SLEAAFQEAFYVKARDRKLLAIYLHHDESVLTNVFCSQMLCAESIVSYLS** **QNFITWAWDLTKDSNRARFLTMCNRHFGSVVAQTIRTQKTDQFPLFLIIM** **GKRSSNEVLNVIQGNTTVDELMMRLMAAMEIFTAQQQEDIKDEDEREARE** **NVKREQDEAYRLSLEADRAKREAHEREMAEQFRLEQIRKEQEEEREAIRL** **SLEQALPPEPKEENAEPVSKLRIRTPSGEFLERRFLASNKLQIVFDFVAS** **KGFPWDEYKLLSTFPRRDVTQLDPNKSLLEVKLFPQETLFLEAKE**
Native sequence	in bold
Protease cleavage	TEV protease site underlined
Cloning sites	Sal1I / Not1
DNA sequence of insert	GTCGACga**ATGGACTACAAGGACGACGATGACAAG**ATGGCGTCCAACATG GACCGGGAGATGATCCTGGCGGATTTTCAGGCATGTACTGGCATTGAAAA CATTGACGAAGCTATTACATTGCTTGAACAAAATAATTGGGACTTAGTGG CAGCTATCAATGGTGTAATACCACAGGAAAATGGCATTCTACAAAGTGAA TATGGAGGTGAGACCATACCAGGACCTGCATTTAATCCAGCAAGTCATCC AGCTTCAGCTCCTACTTCCTCTTCTTCTTCAGCGTTTCGACCTGTAATGC CATCCAGGCAGATTGTAGAAAGGCAACCTCGGATGCTGGACTTCAGGGTT GAATACAGAGACAGAAATGTTGATGTGGTACTTGAAGACACCTGTACTGT TGGAGAGATTAAACAGATTCTAGAAAATGAACTTCAGATACCTGTGTCCA AAATGCTGTTAAAAGGCTGGAAGACGGGAGATGTGGAAGACAGTACGGTC CTAAAATCTCTACACTTGCCAAAAAACAACAGTCTTTATGTCCTTACACC

AGATTTGCCACCACCTTCATCATCTAGTCATGCTGGTGCCCTGCAGGAGT
CATTAAATCAAAACTTCATGCTGATCATCACCCACCGAGAAGTCCAGCGG
GAGTACAACCTGAACTTCTCAGGAAGCAGTACTATTCAAGAGGTAAAGAG
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TGGAGCAGATTCGCAAAGAACAAGAAGAGGAACGTGAGGCCATCCGGCTG
TCCTTAGAGCAAGCCCTGCCTCCTGAGCCAAAGGAAGAAAATGCTGAGCC
TGTGAGCAAACTGCGGATCCGGACCCCCAGTGGCGAGTTCTTGGAGCGGC
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AAAGGATTTCCATGGGATGAGTACAAGTTACTGAGCACCTTTCCTAGGAG
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TCCCTCAAGAAACCCTTTTCCTTGAAGCAAAAGAGTAAGCGGCCGC