Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of GST-FAT10

Enzyme description:- GST-FAT10 (1-165 = full length mature)

Clone number:- DU21924

Source:- human recombinant

Tag:- N-terminal GST-tag

Purification method:- GSH-Sepharose

Expression system:- E.coli

Calculated molecular mass:-

Monoisotopic 45122 Da
Average Mass 45150 Da
[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 8.07

Purity:- 90%

Enzyme storage buffer:-

50mM HEPES pH 8.2, 150mM NaCl, 20% glycerol, 1mM TCEP

Storage temperature:- -80ºC

Assay:-

Division of Signal Transduction Therapy

Clone Data Sheet

GST-FAT10

Protein	GST-FAT10 1-165 (full length)
Synonyms	
Clone Number	DU21924
Species	Human
Accession Number	Protein: O15205 Gene: NM_006398
Tags	N-terminal GST-tag
Aminoacid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEF PNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRY GVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLY DALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAWPLQGWQA TFGGGDHPPKSDENLYFQGGS**MAPNASCLCVHVRSEEWDLMTFDANPYDSVK** **KIKEHVRSKTKVPVQDQVLLLGSKILKPRRSLSSYGIDKEKTIHLTLKVVKP** **SDEELPLFLVESGDEAKRHLLQVRRSSSVAQVKAMIETKTGIIPETQIVTCN** **GKRLEDGKMMADYGIRKGNLLFLACYCIGG**
Native sequence	FAT10 in bold
Protease site	TEV- Protease site underlined
Cloning sites	BamH1 / Not1
DNA sequence of cassette	ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCCACTC GACTTCTTTTGGAATATCTTGAAGAAAAATATGAAGAGCATTTGTATGAGCG CGATGAAGGTGATAAATGGCGAAACAAAAAGTTTGAATTGGGTTTGGAGTTT CCCAATCTTCCTTATTATATTGATGGTGATGTTAAATTAACACAGTCTATGG CCATCATACGTTATATAGCTGACAAGCACAACATGTTGGGTGGTTGTCCAAA AGAGCGTGCAGAGATTTCAATGCTTGAAGGAGCGGTTTTGGATATTAGATAC GGTGTTTCGAGAATTGCATATAGTAAAGACTTTGAAACTCTCAAAGTTGATT TTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTCGAAGATCGTTTATGTCA TAAAACATATTTAAATGGTGATCATGTAACCCATCCTGACTTCATGTTGTAT GACGCTCTTGATGTTGTTTTATACATGGACCCAATGTGCCTGGATGCGTTCC CAAAATTAGTTTGTTTTAAAAAACGTATTGAAGCTATCCCACAAATTGATAA GTACTTGAAATCCAGCAAGTATATAGCATGGCCTTTGCAGGGCTGGCAAGCC ACGTTTGGTGGTGGCGACCATCCTCCAAAATCGGATGAAAACCTGTATTTTC AGGGCGGATCCATGGCTCCCAATGCTTCCTGCCTCTGTGTGCATGTCCGTTC CGAGGAATGGGATTTAATGACCTTTGATGCCAACCCATATGACAGCGTGAAA AAAATCAAAGAACATGTCCGGTCTAAGACCAAGGTTCCTGTGCAGGACCAGG TTCTTTTGCTGGGCTCCAAGATCTTAAAGCCACGGAGAAGCCTCTCATCTTA TGGCATTGACAAAGAGAAGACCATCCACCTTACCCTGAAAGTGGTGAAGCCC AGTGATGAGGAGCTGCCCTTGTTTCTTGTGGAGTCAGGTGATGAGGCAAAGA GGCACCTCCTCCAGGTGCGAAGGTCCAGCTCAGTGGCACAAGTGAAAGCAAT GATCGAGACTAAGACGGGTATAATCCCTGAGACCCAGATTGTGACTTGCAAT GGAAAGAGACTGGAAGATGGGAAGATGATGGCAGATTACGGCATCAGAAAGG GCAACTTACTCTTCCTGGCATGTTATTGTATTGGAGGGTGAGCGGCCGC