

MRCPPU Reagents and Services

Standard Operating Procedure

Preparation of FAM83H [1 - 1179]

Enzyme description:- FAM83H [1 – 1179]

Clone number:- DU 28403

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Agarose

Calculated molecular mass:-

Monoisotopic 153, 859.59 daltons

Average Mass 153, 955.46 daltons

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 6.35

Purity:- >80 %

Enzyme storage buffer:-

50 mM Tris-HCl pH 7.5, 150 mM NaCl, 270 mM sucrose, 0.1 mM EGTA,
0.1 % 2-mercaptoethanol

Storage temperature:- -70 °C

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Clone Data Sheet

FAM83H [2 - 1179]

Protein FAM83H [1 - 1179]

Clone number DU 28403

Species Human

Accession number NM_198488.3

Tags N-terminal GST

**Bacterially
expressed protein**

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGL
EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL
DIRYGVSRIAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLNGDHVTH
PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIA
WPLQGWQATFGGGDHPKSDLEVLVLFQGPLGSMARRSQSSSQGDNPLAPGY
LPPHYKEYYRLAVDALAEGGSEAYSRLFATEGAPDFLCPEELEHVSRLR
PPQYVTREPPEGSLLDMDGSSGTYWPNVDQAVPELDLWPLTFGFQG
TEVTTLVQPPPPDPSIKDEARRMIRSAQQVVAVVMDMFTDVLLESEVLE
AAARRVPVYILLDEMNAQHFLDMADKCRVNLHHVDFLRVRTVAGPTYICR
TGKSFKGHVKEKFLLDCAVMSGYSFMWSFEKIHRSLAHVFQGELVSS
FDEEFRILFAQSEPLVPSAAALARMDAYALAPYAGAGPLVGVPGVGAFTP
FSFPKRAHLLFPPPREEGLGFPSFLDPDRHFLSAFRREEPPRMPGGALEP
HAGLRPLSRLEAEAGPAGELAGARGFFQARHLEMDAFKRHSFATEGAGA
VENFAAARQVSRQTFLSHGDDFRFQTSHFHRDQLYQQQYQWDPQLTPARP
QGLFEKLRGGRAFADPDDFTLGAGPRFPELGPDPGHQRLDYVPSSASREV
RHGSDPAFAPGPRGLEPSGAPRPNLTQRFPCQAAARPGPDPAPEAPER
GGPEGRAGLRWRLASYSLGCHGEDGGDDGLPAPMEAEAYEDDVLPAGGR
APAGDLLPSAFRVPAAFPTKVPVPGPGSGGNGPEREGPEEPGLAKQDSFR
SRLNPLVQRSSRLRSSLIFSTSQAEAGAAGAAAATEKVQLLHKEQTVSETL
GPGGEAVRSAASTKVAELLEKYKGPARDPGGGAGAITVASHSKAVVSQAW
REEVAAPGAVGGERRSLESCLLDLDRSFAQQLHQEAERQPGAASLTAAQL
LDTLGRSGSDRLPSRFLSAQSHSTSPQGLDSPLPLEGSGAHQVLHNESKG
SPTSAYPERKGSPTPGFSTRRGSPTTGFIQKGSPTSAYPERRGSPVPPV
PERRSSPVPPVPERRGSLTLTISGESPKAGPAEEGPGSPMEVLRKGSRLR
RQLLSPKGERRMEDEGGFPVPQENGQPE SPRRLSLGQGDSTEAAATEERP
RARLSSATANALYSSNLRDDTKAILEQISAHGQKHRVAPAPSPGPTHNSP
ELGRPPAAGVLAPDMSDKDKCSAIFRSDSLGTQGRLSRTLPAEERDRL
LRRMESMRKEKRVYSRFEVFCCKEEASSPGAGEGPAEEGTRDSKVGKFFV
KILGTFKSKK

Native sequence Amino acids M1 – K1179 (end) of human FAM83H.
Residue M232 of fusion protein is equivalent to M1 of the native
enzyme. The GST tag is located at residues 1 – 220.

Protease cleavage Precission site (LEVLVFGP) at residues 221 – 228

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Cloning sites

*Bam*H1 and *Sal*I sites of pGex6P-1

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Nucleotide sequence of insert

ggatccGCCACCATGGAGCAGAAGCTGATCTCTGAAGAGGACTTGCCG
TTCCCGTTTGGGAAGTCTCACAAATCTCCAGCAGACATTGTGAAGAAT
CTGAAGGAGAGCATGGCTGTTCTGGAAAAGCAAGACATTTCTGATAAA
AAAGCAGAAAAGGCTACAGAAGAAGTTTCCAAAAATCTGGTTGCCATG
AAAGAAATTCTGTATGGCACAAATGAAAAAGAGCCTCAGACAGAAGCA
GTAGCTCAACTTGCTCAAGAACTCTATAATAGTGGGCTCCTTAGCACC
CTGGTAGCTGATTTACAGCTCATTGACTTTGAGGGCAAAAAGACGTG
GCTCAAATTTTCAACAATATTCTCAGAAGACAAATTGGTACGAGAACT
CCTACTGTTGAATACATCTGCACCCAACAGAATATTTTGTTCATGTTA
TTGAAAGGGTATGAATCTCCAGAAATAGCTCTAAATTGTGGAATAATG
TTAAGAGAATGCATCAGACATGAACCACTTGCAAAAATCATTTTGTGG
TCGGAACAGTTTTATGATTTCTTCAGATATGTGCAAAATGTCAACATTT
GACATAGCTTCAGATGCATTTGCCACATTCAAGGATTTACTTACAAGA
CATAAATTGCTCAGTGCAGAATTTTTGGAACAGCATTATGATAGATTT
TTCAGTGAATATGAGAAGTTACTTCATTCAGAAAATTATGTGACAAAA
AGACAGTCACTGAAGCTTCTCGGTGAACTACTACTAGATAGACACAAC
TTCACAATTATGACAAAATACATCAGTAAACCTGAGAACCTCAAATTA
ATGATGAACCTGCTGCGAGACAAAAGTCGCAACATCCAGTTTGAGGCC
TTTCACGTTTTTAAGGTGTTTGTAGCCAATCCTAACAAGACGCAGCCC
ATCCTAGACATCCTCCTCAAGAACCAGGCCAAACTCATAGAGTTCCTC
AGCAAGTTTCAGAACGACAGGACGGAGGATGAGCAGTTTAAACGACGAG
AAGACCTATTTAGTTAAACAGATCAGGGATTTGAAGAGACCAGCTCAG
CAAGAAGCTtaaggatcc