

Division of Signal Transduction Therapy

Clone Data Sheet

FGR [1 - 529]

Protein FGR [1 - 529]

Clone number DU 61009

Species Human

Accession number NM_001042729.1

Tags N-terminal GST

Baculovirus expressed protein

MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNK
KFELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKE
RAEISMLEGAVLDIRYGVSR IAYS KDFETLKVDFLSKLPEMLKM
FEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKL
VCFKKRIEAIPOIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSD
LEVL FQG PLGSMGCVFCKKLEPVATAKEDAGLEGDFRSYGAADH
YGPDP TKARPASSFAHIPNYSNFSSQAINPGFLDSGTIRGVSGI
GVTLFIALYDYEARTEDDLTF TKGEKFHILNNTTEGDWWEARSLS
SGKTGCIPSNYVAPVDSIQAEWYFGKIGRKDAERQLLSPGNPQ
GAFLIRESETTKGAYSLSIRDWDQTRGDHV KHYKIRKLDMGGYY
ITTRVQFNSVQELVQH YMEVNDGLCNLLIAPCTIMKPQTLGLAK
DAWEISRSSITLERRLGTGCFGDVWLGTWNGSTKVAVKTLKPGT
MSPKAFLEEAQVMKLLRHDKLVQLYAVVSEEP IYIVTEFMCHGS
LLDFLKNPEGQDLRLPQLVDMAAQVAEGMAYMERMNYIHRDLRA
ANILVGERLACKIADFGLARLIKDDEYNPCQGSKFPIKWTAPEA
ALFGRFTIKSDVWSFGILLTELITKGRI PYPGMNKREVLEQVEQ
GYHMPCPPGCPASLYEAMEQ TWRLDPEERPTFEYLOSFLDYFT
SAEPQYQPGDQT

Native sequence Amino acids M1 – T529 (end residue) of human FGR.
Residue M232 of the fusion protein is equivalent to M1 of the
native enzyme. The GST tag is located at residues 1 - 220.

Protease cleavage PreScission (LEVL FQGP) residues 221 - 228

Cloning sites *Bgl*II and *Not*I to *Bam*H1 and *Not*I sites of pFastBac Dual.

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**Nucleotide
sequence of insert**

agatctATGGGCTGTGTGTTCTGCAAGAAATTGGAGCCGGTGGCC
ACGGCCAAGGAGGATGCTGGCCTGGAAGGGGACTTCAGAAGCTAC
GGGGCAGCAGACCACTATGGGCCTGACCCACTAAGGCCGGCCT
GCATCCTCATTGCCCCACATCCCCAACTACAGCAACTTCTCCTCT
CAGGCCATCAACCTGGCTTCCTTGATAGTGGCACCATCAGGGGT
GTGTCAGGGATTGGGGTGACCCTGTTTCATTGCCCTGTATGACTAT
GAGGCTCGAACTGAGGATGACCTCACCTTCACCAAGGGCGAGAAG
TTCCACATCCTGAACAATACTGAAGGTGACTGGTGGGAGGCTCGG
TCTCTCAGCTCCGGAAAACTGGCTGCATTCCAGCAACTACGTG
GCCCCGTGACTCAATCCAAGCTGAAGAGTGGTACTTTGGAAAG
ATTGGGAGAAAGGATGCAGAGAGGCAGCTGCTTTCACCAGGCAAC
CCCCAGGGGGCCTTCTCATTTCGGGAAAGCGAGACCACCAAAGGT
GCCTACTCCCTGTCCATCCGGGACTGGGATCAGACCAGAGGCGAT
CATGTGAAGCATTACAAGATCCGCAAACCTGGACATGGGCGGCTAC
TACATCACACACGGGTTTCAGTTCAACTCGGTGCAGGAGCTGGTG
CAGCACTACATGGAGGTGAATGACGGGCTGTGCAACCTGCTCATC
GCGCCCTGCACCATCATGAAGCCGCAGACGCTGGGCCTGGCCAAG
GACGCCTGGGAGATCAGCCGCAGCTCCATCACGCTGGAGCGCCGG
CTGGGCACCGGCTGCTTCGGGGATGTGTGGCTGGGCACGTGGAAC
GGCAGCACTAAGGTGGCGGTGAAGACGCTGAAGCCGGGCACCATG
TCCCCGAAGGCCTTCCTGGAGGAGGCGCAGGTCATGAAGCTGCTG
CGGCACGACAAGCTGGTGCAGCTGTACGCCGTGGTGTGCGGAGGAG
CCCATCTACATCGTGACCGAGTTCATGTGTACGGCAGCTTGCTG
GATTTTCTCAAGAACCCAGAGGGCCAGGATTTGAGGCTGCCCCAA
TTGGTGGACATGGCAGCCCAGGTAGCTGAGGGCATGGCCTACATG
GAACGCATGAACTACATTCACCGCGACCTGAGGGCAGCCAACATC
CTGGTTGGGAGCGGCTGGCGTGCAAGATCGCAGACTTTGGCTTG
GCGCGTCTCATCAAGGACGATGAGTACAACCCCTGCCAAGGTTCC
AAGTTCCCATCAAGTGGACAGCCCCAGAAGCTGCCCTCTTTGGC
AGATTCACCATCAAGTCAGACGTGTGGTCCTTTGGGATCCTGCTC
ACTGAGCTCATCACCAAGGGCCGAATCCCCTACCCAGGCATGAAT
AAACGGGAAGTGTGGAACAGGTGGAGCAGGGCTACCACATGCCG
TGCCCTCCAGGCTGCCCAGCATCCCTGTACGAGGCCATGGAACAG
ACCTGGCGTCTGGACCCGGAGGAGAGGCCCTACCTTCGAGTACCTG
CAGTCCTTCCTGGAGGACTACTTCACCTCCGCTGAACCACAGTAC
CAGCCCGGGGATCAGACAtagcggccgc