

Product datasheet for **SC128121**

FGD4 (NM_139241) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	FGD4 (NM_139241) Human Untagged Clone
Tag:	Tag Free
Symbol:	FGD4
Synonyms:	CMT4H; FRABP; ZFYVE6
Mammalian Cell Selection:	None
Vector:	<u>pCMV6-XL4</u>
E. coli Selection:	Ampicillin (100 ug/mL)



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Fully Sequenced ORF: >OriGene ORF within SC128121 sequence for NM_139241 edited (data generated by NextGen Sequencing)

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ATGGAGGAAATTAACCTGCCTCTGCTTCTTGTGTCTCAAAAGAAAAACCCAGTAAGGTA
TCAGATCTCATCAGTCGCTTTGAAGGAGGCAGCTCATTATCAAATTATAGTGATTGAAG
AAAGAGTCTGCTGTGAACCTAAATGCTCCTAGAACCCAGGAAGGCATGGATTGACAACC
ACACCTCAACAAAACTCCTCTCCCAGCACTTGCCACAGAGGCAGGGAATGATACAGAT
AAGACTCAGGGTGCACAGACTTGTGTGGCCAACGGTGTAAATGGCAGCACAAAACCATG
GAATGTGAGGAGGAGAAAGCTGCCACTCTTAGCTCAGATACTTCTATTCAAGCTTCTGAA
CCCTTGCTTGATATGCACATAGTGAATGGAGAAAGAGATGAAACTGCCACAGCTCCTGCA
TCACCCACAACAGACAGCTGTGATGGAATGCTTCTGACAGTAGCTACAGGACTCCAGGC
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GAGACTAATGAGCAAAAACCTTCAAAAATAGCCAATGAACTTTTGCTTACTGAAAGAGCT
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AACCGAGGCTCGTTTCCAGCAGAGATGGTGAATAAAATCTTTTCTAATATTTTCATCAATA
AATGCCTTCCATAGTAAATTCCTCTTGCCAGAGCTGGAGAAACGAATGCAAGAATGGGAA
ACTACTCTAGAATTGGAGACATCCTTCAGAAATTGGCACCATTCTTAAGATGTATGGA
GAATATGTGAAAGGATTTGATAATGCAATGGAATTGGTAAAAACATGACAGAACGTATT
CCCCAGTTCAAATCAGTGGTTGAAGAAATTCAGAAACAGAAAACTGTGGGAGCTTAAC
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GACTATCTAAGGAAATTCCTCTGATTCCTGGACTGGAATGATGCTAAAAATCACTT
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AATGAACCTAATAAAAGAAGGACAGATCCTCAAACTAGCTGCTCGAAACACTTCAGCACAA
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CATTGTCGAGCATGTGGATATGTGGTTTGTGGAAATGCTCCGACTACAAAGCTCAACTT
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TCTGGAACAGTGTGGTGTGCAGCTTCTTCACTATATGGAGAAGTCAAAACCTTGGCAG
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GGTGAGACACCAGGTGGTCCAAATGAGCATCCAGCCACCTTGGATGATCATCCTGAACCT
AAGAAAAAATCAGAATGCTGA

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Clone variation with respect to NM_139241.2
 374 c=>t;1305 g=>a;1518 g=>a

5' Read Nucleotide Sequence:

>OriGene 5' read for NM_139241 unedited
 GGGGTTNCATTTGTATACGACTCACTATAGGCGGCCGGAATTCGCACGAGGCAGGGGA
 GCCTGTGCTGGGTGAGATTATCTGCAATGGACCGGGTAAATGGGAGGCTTGCTTTGGCTC
 GCTGGAAGAACAAATGAAGGGAGTTTTACTTCAACCATTTGTGACTTCTGGCCAAGAGGA
 ATAAATTCAGCTTTTATAAGGCAGCAGTACCTGTCCAAAGATCGCTTTAGTTCCACCTTG
 CTCCACAAGCAGCACAACCACACTGGTTGGTGAGAATGTATCTGAAGAAGAGGCTCAGGG
 AATAAATGGGAACAGGCCAGCAAAACACTCAGCTGCAAGTCCAAAGCCACAAGTGCCTCC
 AAAGCCATTACACTGCAGAATTCACCTTCGTCCAATATACACCAAACCCCAAGGCATAA
 AGCTTTACCTAGTGCAAAACCAAGGATGGAGGAAATTAACCTGCCTCTGCTTCTTGTTGT
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 ATTATCAAATTATAGTGATTTGAAGAAAGAGTCTGCTGTGAACCTAAATGCTCCTAGAAC
 CCCAGGAAGGCATGGATTGACAACCACACCTCAACAAAACTCCTCTCCAGCACTTGCC
 ACAGAGGCAGGGAATGATACAGATAAGACTCAGGGTGACAGACTTGTGTGGCCAAACGG
 TGTAATGGCAGCACAACCAAGATGGAATGTGAGGAGGAGAAAGTGCCACTCTTAGCTC
 AGAACTTCTATTCAAGCTTCTGAACCTTGCTTGATATGCACATAGTGAATGGAGAAAGA
 GATGAAACTGCCACAGCTCCTGCATCACCCACACAGACAGCTGTGATGGAAATGCTTCTG
 ACAGTAGCTACAGGACTTCCAGCTAC

3' Read Nucleotide Sequence:

>OriGene 3' genomic read for NM_139241 unedited
 GGGGCGGTTGTACATCTCAAAAAAGGTTTAATTTGNATAAAAAGCATAAGTTAAATAGTA
 AACTTAGTGTGAGATTTTAAATCACAAGTACAAAAGAGTGAAGAGCAGCCTTCATGACAAG
 GAATCATGTGACCAGCCCCACCCCAACATAGGTTATCATATGTGGATTTTGTTCATT
 CCGACAAAGGAAAAGGCCATACAGTTATCTTAAGTGTTCAATTATATAGAGACCTTATTT
 AACCATGCTCGATTATCTTACGGAAAAGAAAAACATGACGATAAATGTGGTTTCCACATA
 TCCTAGTTCTGTAAAAAGTCAAGTGTCTCATAAAGTTTGGGTTTTGGTGAATGTTTGT
 ACATGCTGATGTTAACTACTGCAATAATTATAGGATTGTTAACGGGTAATAACCTGTAT
 GACTTTGACTGTCCCACTGACCAATATGCACCTTAATCTTACAATAATCAAGACTGACGC
 ATTAAGTGAACCTCATCTTATATTAATAGAACCTCTCTAGAGAGGCACTGTTTTAAATA
 GGCCCTGACACAAAAAATGGGCCTTTAAAAGTACTGTTTCGAATTCACAAATTAGTGCCA
 TGCCACATAAATTACCAATTTTTGTAAAAATATCAATCCCCTCCAATGCCAAATCGCAAA
 ACCTAAATCACCCGAAACATTTTCTTACATTTTCAAGAACATTGCTCAGTTCCACGGTACAC
 CTGGCTTTTCATATTTAAAAATCAATTAGGGATTAAATGTGGACCCTTACCCATGTCTAAC
 ATATATATTTAACTCCACATAAACCAAAATTGCTATTTCTTAAGTACATTCTTAAGCAGT
 CTTATTTGCAACACCATTATATTCCTTTCTTTTTCAGTCGCGAAATACTAC

Restriction Sites:

NotI-NotI

ACCN:

NM_139241

Insert Size:

4500 bp

OTI Disclaimer:

Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).

Components:

The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).

Reconstitution Method:

1. Centrifuge at 5,000xg for 5min.
2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.
3. Close the tube and incubate for 10 minutes at room temperature.
4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.
5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.

RefSeq: [NM_139241.1](#), [NP_640334.1](#)

RefSeq Size: 2931 bp

RefSeq ORF: 2301 bp

Locus ID: 121512

UniProt ID: [Q96M96](#)

Cytogenetics: 12p11.21

Domains: RhoGEF, FYVE, PH

Gene Summary: This gene encodes a protein that is involved in the regulation of the actin cytoskeleton and cell shape. This protein contains an actin filament-binding domain, which together with its Dbl homology domain and one of its pleckstrin homology domains, can form microspikes. This protein can activate MAPK8 independently of the actin filament-binding domain, and it is also involved in the activation of CDC42 via the exchange of bound GDP for free GTP. The activation of CDC42 also enables this protein to play a role in mediating the cellular invasion of *Cryptosporidium parvum*, an intracellular parasite that infects the gastrointestinal tract. Mutations in this gene can cause Charcot-Marie-Tooth disease type 4H (CMT4H), a disorder of the peripheral nervous system. Multiple alternatively spliced transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Jan 2015]

Transcript Variant: This variant (3) has an alternate 5' terminal exon, which results in a different 5' UTR and translation initiation at a downstream AUG start codon, compared to variant 1. The resulting isoform (3) has a shorter N-terminus, compared to isoform 1.

Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.