

Product datasheet for SC308361

FAM83A (NM_207006) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	FAM83A (NM_207006) Human Untagged Clone
Tag:	Tag Free
Symbol:	FAM83A
Synonyms:	BJ-TSA-9
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC308361 representing NM_207006. Blue=Insert sequence Red=Cloning site Green=Tag(s)

GCTCGTTTGTAGTGAACCGTCAGAATTTTGTAAATACGACTACTATAGGGCGCCGGGAATTCGTGACTG
GATCCGGTACCGAGGAGATCTGCCGCC**GCGATCGCC**
ATGAGCCGGTCAAGGCACCTGGGCAAAATCCGGAAGCGTCTGGAAGATGTCAAGAGCCAGTGGTCCGG
CCAGCCAGGGCTGACTTTAGTGACAACGAGAGTGCCCGGCTGGCCACGGACGCCCTCTGGATGGGGT
TCTGAAGCCTACTGGCGGTGCTCAGCCAGGAAGGCGAGGTGGACTTCTGTCTCGGTGGAGGCCAG
TACATCCAGGCCAGGCCAGGGAGCCCCGTGTCCCCAGACACCCTGGGAGGGCGGAAGCAGGCCCT
AAGGGACTGGACTCCAGTCCCTACAGTCCGGCACCTACTTCCCTGTGGCCTCAGAGGGCAGCGAGCCG
GCCCTACTGCACAGCTGGCCTCAGCTGAGAAGCCCTACCTGAAGGAAAAATCCAGCGCCACTGTGTAC
TTCCAGACCGTCAAGCACAACAACATCAGAGACCTCGTCCGCCGCTGCATCACCCGGACTAGCCAGGTC
CTGGTCATCCTGATGGATGTGTTACGGATGTGGAGATCTTCTGTGACATTCTAGAGGCAGCCAACAAG
CGTGGGGTGTTCGTTTGTGTGCTCCTGGACCAGGGAGGTGGAAGCTCTTCCAGGAGATGTGTGACAAA
GTCCAGATCTCTGACAGTCACTCAAGAACATTTCCATCCGGAGTGTGGAAGGAGAGATACTGTGCC
AAGTCAGGCAGGAAATTCGCTGGCCAAATCCGGGAGAAGTTCATCATCTCGGACTGGAGATTTGCTCTG
TCTGGATCTTACAGCTTACCTGGCTCTGCGGACACGTGCACCGGAACATCCTCTCCAAGTTCACAGGC
CAGGCGGTGGAGCTGTTTGACGAGGAGTCCGCCACCTTACGCCCTCTCCAAGCCTGTGATGGGCTG
AAGTCCCCGGCTGGTCCGCCCGTCCCGCCGGAGCAGCCCGGCAATGGCCGCTTAGCAGCAGC
AGTGGCTCCGCCAGTGACCGCACGTCTCCAACCCCTTACGCGCCGCTCGGCAGGCAGCCACCCGTT
CCTGAAAGTAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAACTTTGGTTCTGATGGCTTTCTGA

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC

Restriction Sites: SgfI-MluI



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Plasmid Map:	□
ACCN:	NM_207006
Insert Size:	1104 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).
OTI Annotation:	This TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.
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:	<ol style="list-style-type: none">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_207006.2
RefSeq Size:	3701 bp
RefSeq ORF:	1104 bp
Locus ID:	84985
UniProt ID:	Q86UY5
Cytogenetics:	8q24.13
MW:	40.6 kDa
Gene Summary:	<p>Probable proto-oncogene that functions in the epidermal growth factor receptor/EGFR signaling pathway. Activates both RAS/MAPK and PI3K/AKT/TOR signaling cascades downstream of EGFR. Required for the RAS/MAPK signaling cascade activation upon EGFR stimulation, it also activates both signaling cascades independently of EGFR activation. [UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (2) uses an alternate 3' exon structure resulting in different 3' UTR and 3' coding regions, compared to variant 1. It encodes isoform b, which has a shorter and distinct C-terminus, compared to isoform a. 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.</p>