

Product datasheet for **SC308479**

FREM2 (NM_207361) Human Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: FREM2 (NM_207361) Human Untagged Clone
Tag: Tag Free
Symbol: FREM2
Synonyms: CRYPTOP; FRASRS2
Mammalian Cell Selection: Neomycin
Vector: PCMV6-Neo
E. coli Selection: Ampicillin (100 ug/mL)

Fully Sequenced ORF: >OriGene ORF sequence for NM_207361 edited
 ATGCACTCAGCCGGGACTCCCGGGTTATCCTCGCGCCGGACAGGCAACTCCACCAGCTTT
 CAACCAGGACCGCCACCGCCCGCCCGGCTGCTGCTGCTGCTGCTTCTCCTGTCACTG
 GTAAGCCGCGTCCCGGCACAGCCCGCTGCCTTCGGCAGGGCGTTGCTGTCCCTGGTCTC
 GCGGGGGTGCAGGGTCCCTGCTGAGGAGGCCATAGTGCTGGCGAACCGCGACTCCGG
 GTGCCCTTCGGCCGTGAAGTCTGGCTGGATCCCCTGCATGACCTGGTGTGCAGGTGCAG
 CCCGGGGACCGTGCAGCGTTTCGGTACTAGACAACGACGCACTGGCCAGCGACCGGGC
 CGCCTGAGTCCCAAGCGCTTCCCGTGCAGCTTTGGCCCTGGCGAGGTGCGCTACTCTCAC
 CTGGGCGCGCAGCCCGTCTCGGGACCGCGTCCGGCTGCAGCTGCGCTATGACGCGCC
 GGAGGGGAGTAGTGCTACCACTGGTACTGGAGGTGGAGGTGGTCTTACCCAGCTGGAG
 GTTGTGACTCGGAACTTGCTCTGGTCTGGAAGAGCTGCTGGGGACCAGCAATGCCCTG
 GACGCGCGGAGCCTGGAGTTCGCCTTCCAGCCGAGACAGAGGAGTGCCGCGTGGGCATC
 CTGTCCGCTTGGGCGCGCTGCCTCGCTATGGAGAACTCCTCCACTACCCGAGGTCCCT
 GGAGGAGCCAGAGAGGGAGGCGCCCGGAGACTCTCCTGATGGACTGCAAAGCTTCCAG
 GAACTAGGCGTGCCTATCGCCACACAGCCGCGCAGTCGCTCACCACAGGGACTGGATA
 CCCATGGTGGTGGAGTGCCTTACGAGGGGCTCCTGTGGGCAGCCCTGCTTTGAAACGC
 GAGCACTTCCAGGTTCTGGTGGAGATCCGAGGAGGGGCGGAGAACTGCACCCAAGCCC
 AGTTTCGTGGCCATGATGATGATGGAGGTGGACCAGTTTGTACTGACGGCCCTGACCCCA
 GACATGCTGGCAGCCGAGGATGCTGAGTCTCCTCTGACCTGTTGATCTTCAACCTTACT
 TCTCCATTCCAGCCTGGCCAGGGCTACTTGGTGAGCACCAGATGATCGCAGCCTGCCCTT
 TCCTCCTTCACTCAGAGGATCTGCGGCTCCTGAAGATTGCCTACCAGCCCCCTTCTGAA
 GACTCTGACCAGGAGCGCCTCTTTGAACTGGAATTGGAGGTAGTGGATCTAGAAGGAGCA
 GCTTCAGACCCTTTTGCCTTCATGGTAGTGGTGAAGCCCATGAACACAATGGCTCCGGTG
 GTCACCCGGAATACCGGTCTTATTCTCTATGAGGGTCAGTCTCGGCCCTCACAGGCCCT
 GCAGGCAGTGGTCCGAAAACCTGGTTCATCAGCGATGAGGATGACCTAGAAGCAGTGGCG
 CTAGAGGTGGTGGCTGGGCTCCGGCATGGTCACCTTGTCATTCTGGGTGCTTCCAGTGGC
 AGCTCTGCTCCCAAGAGCTTACAGTGGCTGAGCTGGCAGCCGGCCAGGTGGTCTACCAG



[View online »](#)

CATGATGACAGAGACGGCTCGCTGAGCGACAACCTGGTGCCTTCGCATGGTGGATGGAGGA
 GGCAGGCACCAGGTACAGTTTCTGTTCCCCATCACCTTAGTGCCTGTGGATGACCAGCCA
 CCTGTTCTCAATGCCAACACGGGGCTGACACTGGCAGAGGGTGAACAGTGGCCATCCTG
 CCCCTTCCCTGAGTGCAACTGACATGGATTAGATGATTCTCTGCTGCTTTTTGTGCTG
 GAGTACCCTTCTAACTACGGGGCATCTGCTTCCGCCAACTCACCTCCCCATGAG
 AAGCAGAACTTCTCAGAGGCCTTTGGAGGAAGGAGGGGGCATTATGAGCGAACAGTG
 ACAGAGTGGCAGCAGCAGGACATAACAGAGGGCAGGCTGTTCTATAGACACTCTGGGCC
 CATAGTCTGGGCCAGTACAGACCAGTTCACATTTAGAGTCCAGGATAACCATGACCCT
 CCTAATCAGTCCGGGCTACAGCGGTTTGTGATTGATCCATCCTGTGGATCGCCTCCCT
 CCGGAGCTGGGCAGTGGCTGTCCCTTCGTATGGTGGTACAGGAATCCCAGCTCACACCA
 CTGAGGAAGAAGTGGCTGCGCTACACTGACCTGGACACAGATGACCGAGAACTACGTTAC
 ACAGTGACTCAGTCCCCACAGACACAGACGAAAATCACCTGCCAGCCCCACTGGGTACC
 TTGGTCTTGACTGACAACCCCTCAGTCGTGGTGACCCATTTACCCAAGCCAGATCAAC
 CATCATAAAATTGCTTACAGACCCCGGGTCAAGAAGTGGGCGTGGCTACTCGAGTGGCC
 CAGTTCAGTTCAGGTGGAAGCCGAGCTGGGAATGTGGCTCCAGGTACCTTTACCTT
 TACTTGATCCCCGTGGACAACCAGCCACCTGAGATCCTCAACACCGGCTTCACTATTCAG
 GAGAAGGGTCACCACATCCTGAGTGAGACAGAGTTGCACGTGAATGATGTAGACACTGAT
 GTTGCCCATATCTCTTCACTCTCACTCAGGCACCCAAACATGGCCACATGAGAGTGTCT
 GGACAGATCCTGCATGTAGGGGCTCTTCCACTTGGAGGACATAAAACAGGGCCGAGTT
 TCCTATGCCCATAAATGGGGACAAGTCCCTGACTGATAGCTGCTCCTTGGAAAGTCACTGAC
 AGACATCATGTGGTGCCCATCACTCTCAGAGTAAATGTCCGGCCAGTGGATGATGAAGTG
 CCCATACTGAGCCATCCTACTGGCACTCTGGAGTCTATCTAGATGTCTTAGAAAATGGG
 GCTACTGAAATCACTGCCAATGTTATTAAGGGGACCAATGAGGAAACTGATGACTTGATG
 TTGACTTTCCTCTTGGAAAGATCCACCTTTGTATGGGGAAATCTTGGTCAATGGCATTCCA
 GCAGAGCAGTTTACTCAAAGGGACATCTTGGAGGGCTCTGTTGTATATACCCACACCAGT
 GGTGAGATAGGCCTATTGCCTAAAGCGGATTCTTTAACCTGAGTCTGTCAGATATGTCT
 CAAGAATGGAGAATTGGTGGCAATACTATCCAAGGAGTACTATATGGGTGACCATCCTG
 CCTGTTGATAGCCAGGCCCCAGAAAATCTTGTAGGTGAACAGTTGATAGTAAATGGAAGGT
 GATAAAAGTGTATAACATCAGTGCATATAAGTGTGAAGATGTCGACTCCCTGAATGAT
 GACATCTTGTGCACTATAGTTATTCAGCCTACTCAGGTTATGTTGAAAACATTTCTCCA
 GCACCAGGCTCTGAGAAATCAAGAGCAGGGATTGCCATAAGTGCCTTCACTTGAAGAT
 CTCAGGCAGGGCCACATAAACTATGTCCAGAGTGTCCATAAAGGGGTGGAACCTGTGGAG
 GACCGATTTGATTTTCGTTGTTCTGATGGCATTAACTTTTCAGAGAGACAGTTCTTCCCC
 ATTGTAATCATTCCCACCAATGATGAACAGCCAGAGATGTTTATGAGAGAATTTATGGTG
 ATGGAAGGCATGAGTCTGGTAATTGATACACCCATTCTCAATGCTGCTGATGCTGATGTT
 CCCCTGGATGATTTAACTTTCACTATTACCCAATTCCTCACTCATGGTCACATCATGAAT
 CAGCTGATAAATGGCACGGTTTTGGTCGAAAGCTTACCTTGGATCAGATCATAGAGAGT
 TCCAGCATTATTTATGAGCATGATGACTCCGAGACCCAGGAAGACAGTTTTTGTGATTA
 CTAACAGATGGGAAGCACTCTGTGGAAAAGACGGTCTCATTATAGTTATCCCTGTTGAT
 GATGAGACGCCCCAGAATGACTATCAATAATGGACTAGAAAATAGAAATGGGGATACCAAG
 ATTATCAACAACAAAATATTAATGGCAACAGATTTAGATTGAGAAGACAAATCTTTGGTT
 TATATTATTCGTTATGGGCCAGGACATGGCTTATTACAGAGACGAAAACCTACTGGTGCC
 TTTGAAAATATCACACTGGGCATGAATTTTACCCAGGATGAAGTAGACAGAAACTTAATT
 CAGTATGTCCATTTGGGGCAAGAGGGCATTGGGACCTAATTAATTTGATGTGACTGAT
 GGAATAAATCCCCTCATAGATCGTTACTTTTATGTGTCCATCGGGAGCATTGACATTGTC
 TTCCCTGATGTGATAAGTAAGGGAGTGTCTTGAAGAAGGTGGCAAAGTCACTCTTACA
 ACAGACCTACTAAGCACTAGTGACTTGAACAGTCTGATGAAAACCTGGTTTTTACCATC
 ACCAGGGCTCCCATGCGAGGTACCTGGAATGCACGGATCAGCCTGGTGTGTCCATCAGC
 TCTTTCACCTCAGCTGCAACTGGCTGGAAAACAAAATCTACTACATCCACACAGCTGATGAT
 GAAGTGAAAATGGACAGTTTTGAGTTTTCAAGTACCCGATGGACGTAACCTGTCTTTGCG
 ACATTCGATATCTCCATTAGCGATGTGGACAATAAAAAGCCAGTGGTCACCATCCACAAG
 CTGTTGTCAGTGAAAGTAAAACAAGCTGATTACTCCTTTTGGAGCTCACTGTGCAAGAC

AGAGATACTCCTGACAAGCTCCTGAAATTCACATACACCCAGGTGCCTATTCATGGCCAT
 CTCCTATTCAACAATACCAGACCTGTCATGGTTTTACCAAGCAAGACTTGAATGAAAC
 TTAATCAGCTACAACATGATGGCACTGAGTCAAGTGAAGATAGCTTCTCCTTCACAGTG
 ACTGATGGCACCACATACAGACTTCTATGTTTTCTGATACGGTGTGGTGAACAAGGAGA
 CCCCAAGTGATGAAGATCCAGGTCTTGGCTGTTGACAACAGTGTCCCAAAATCGCAGTG
 AATAAGGGGGCCTCTACACTTCGCACTTAGCCACTGGCCACTTGGGGTTCATGATCACA
 AGCAAAATATTGAAAGTGGAGGACAGAGACAGCTTACACATTTCTCTTAGATTTATCGTG
 ACAGAGGCCCTCAACATGGATATCTTCTCAACCTGGACAAGGCAACCACAGCATCACT
 CAGTTCACACAAGCTGACATTGATGACATGAAAATATGCTATGTCTTAAGAGAAGGGCT
 AATGCCACAAGTGATATGTTCTATTTTGCAGTTGAAGATGGTGGTGGAAACAAGTTAACG
 TACCAGAAATTTCTGCTGAATTGGGCATGGATCTCCTTTGAAAAGGAATATTACCTGGTC
 AATGAGGACTCCAAATTTCTAGATGTTGTTCTTAAACGTAGAGTTACTTGGGAGAACT
 TCTTTTAAAGTATTGGCACAAGAGACAGAAGTGCAGAAAAGACAAAGACTTCAAGGGC
 AAAGCACAGAAAAGTGCAGTTCAACCCAGGCCAGACCAGGGCCACATGGCGAGTGGG
 ATCCTGAGTGATGGGGAGCATGAGCAGTCTGAAACCTTTAGGTGGTACTCTCAGAGCCC
 GTGCTGGCTGCCTTGGAAATTCACACAGTCGCCACTGTTGAGATCGTTGATCCAGGAGAT
 GAGCCAATGTGTTTATCCCCAGTCCAAATACTCCGTTGAAGAAGATGTTGGTGGAGCTG
 TTCATTCACATCAGGAGGAGCGGAGATGTGAGCCAGGAGTTGATGGTGGTCTGTTATACC
 CAACAAGGAACAGCAACTGGAAGTGTGCCGACTTCCGTTGTCTTACTCTGATTACATA
 TCCAGGCCGTGAGGACCACACAGTGTGTCCGCTTTGACAAGATGAACGGGAGAAAAGT
 TGTCCGATAGTCATAATTGATGACTCTTGTACGAGGAGGAGGAAACCTTCCATGTCCT
 CTGAGCATGCCATGGGGGAAGAATCGGATCAGAGTTCCAGGGGCTCAAGTTACAATC
 GTTCTGTGACAAAAGATGATGAACCCATCTTTACTTCGGTGATGTGGAATACTCTGTGGAT
 GAGAGTCTGGCTATGTGGAAGTGCAGGTGTGGAGAACGGGCACACTGACCTGTCCAAGTCT
 TCTAGTGTACAGTGAGGTCTCGGAAAACAGATCCTCCCTCTGCAGATGTGGAACAGAC
 TATGTGGGCATCAGCCGTAATTTAGATTTTGCACCTGGAGTCAACATGCAGCCTGTTCTG
 GTTGTCTTCTGGATGACCTTGGACAACCCAGCGCTGGAGGGAATTGAGAAATTTGAACTG
 GTGCTTCGCATGCCTATGAACGCAGCCCTTGGCGAGCCAGCAAAGCCACAGTGTCCATA
 AATGACTCTGTCTCCGATTTGCCTAAGATGCAATTCAAAGAACGAATATATACTGGCAGC
 GAAAGTGATGGGCAGATAGTTACAATGATCCATAGGACTGGGGATGTCCAGTACAGATCT
 TCAGTGAGATGCTACACCCGGCAGGGGTCTGCACAGGTGATGATGGACTTTGAAGAACGC
 CCAAACACTGATACCTCCATCATCACATTCCTCCCTGGTGAGACAGAAAAGCCCTGCATT
 CTTGAGCTGATGGACGATGTGCTCTATGAGGAGGTAGAGGAGCTCCGCCTGGTACTCGGC
 ACTCCACAAGCAACTCTCCCTTTGGGGCTGCAGTTGGTGAACAAAATGAAACTCTCATA
 AGGATCCGAGATGATGCTGATAAGACTGTTATTAATTTGGAGAAACCAATTTAGTGTC
 ACTGAACCCAAAGAACCTGGAGAGTCCGTTGTTAAGAATTCAGTGATTCGCCAAGGA
 GACACTTCAAAGTTCATTGTGAGAGTCCACACCAAGGATGGCTCGGCCACCTCTGGA
 GAAGACTACCACCTGTGTCAGAAGAAATGAGTTTAAAGGAAGGGGAAACCCAGCACGTG
 GTTGAATCGAAGTTACCTTTGACGGGGTGAGAGAGATGAGAGAGGCCTTCACTGTTTAC
 CTAACCTGATGAAAATATGATAGCAGAGATGCAGTTGACGAAAAGCCATTGTGTACATA
 GAAGAAATGAGCAGCATGGCAGATGTCATTTTCTTCTGTCCTCAAATTTGATCCCTG
 TTGATGTATGACGACACTTCAAAGCTAAGGAGAGTGTGAACCCATGTCTGGCTATCCT
 GTCATCTGTATCACAGCTTGCAACCCAAATATTCAGACTACGATAAACAGGCTCTATC
 TGTGCAAGTGAGAACATCAATGACACTTTGACGCGGTACCGGTGGCTGATTAGTGCACCT
 GCGGGCCCTGACGGTGTGACCAGCCCTATGAGAGAAGTGGACTTCGACACCTTTTTTACG
 TCATCAAAGATGGTCACACTGGACTCCATATACTTTGAGCCTGGCTCCCGGTACAGTGC
 GCAGCTCGTGTGTAACACCAATGGGGATGAAGGCCTGGAGCTCATGAGCCCTATTGTA
 ACCATCAGCAGAGAAGAAGGTCTTTGTCAGCCCGTGTACCTGGGGTGTGGAGCAGAG
 CCGTTCTCAGCTAAATTCGCTACACAGGCCCTGAGGATGCAGACTACACAAACCTTATC
 AAGCTCACTGTCACAATGCCACACATAGATGGCATGCTCCCGTGATCTCCACTAGAGAG
 CTTTCAAATTTGAGCTCACCTCAGCCCTGATGGCACAAGAGTTGGAACCCACAAGTGC
 TCCAACCTCCTGGATTATACTGAAGTGAAGACTCATTATGGTTTCTTACTGATGCTACC

```

AAAAATCCAGAAATAATTGGAGAGACATATCCTTACCAGTACAGCTTGTCCATCAGAGGT
TCCACTACCTTGGCGTTCTACCGGAACCTGAACCTAGAGGCTGTTTATGGGAGTTTCGTT
AGCTACTATGACATGTCAGAACTCCTTGCTGACTGTGGTGGCACCATTGGAACAGATGGA
C::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AGGTCCTA
AACCTAGTGCAGTCTATGTGACCCTTCGAGTCCCTCTGTATGTTTCTACGTGTTCCAT
TCCCCCGTGGGGTAGGAGGCTGGCAGCATTGTTGACTTGAAGTCAGAGCTTCGTCTAACT
TTTGTGTACGACACCGCCATCTGTGGAATGATGGAATTGGCAGCCCCCAGAGGCTGAA
CTTCAAGGTTCTCTATCCAACCAGCATGCGCATCGGTGATGAGGGCGCTTGGCCGTG
CACTTCAAGACAGAGGCTCAGTTCCATGGCTTATTTGTGTGTACATCCCGCATCCTTT
ACAAGCTCAGTGATCATGTCAGCTGATCATCCAGGCTGACATTTCCCTCCGCCTCATA
AGGAGTGAACCAACCTATAAACCAGCCAGTACAGCAGTGGAGCTTTGTCTCTGACTTTGCC
GTACGTGACTACTCAGGGACCTATACTGTGAAGCTGGTGCATGCACTGCCCATCACAT
CAGGAATACCGCTGCCAGTCACCTGCAACCCAGAGAACCTGTACCTTTGACCTTGAC
ATCCGATTCCAACAGGTCACTGATCCAGTGGCTGCTGAGTTTAGCTTGAACCCAAATG
TACCTGCTCTCTAAGAAGAGTCTCTGGTGTCTGATGGATCCATGGGATTCGGGCAAGAG
AGTGATGTTGCTTTTGCAGAAGGTGATATAATTTATGGTCGTGCATGGTGGATCCTGTC
CAGAATCTGGGTGACTCCTTTTACTGCAGCATTGAGAAGGTGTTTCTATGCACTGGAGCT
GATGGCTATGTTCCCAAGTATAGTCCAATGAATGCAGAATATGGCTGCTTAGCCGACTCT
CCTTCACTCTTATATAGATTTAAAATTGTGGACAAAGCTCAGCCAGAGACACAAGCGACC
AGTTTTGGAAATGTCCTATTTAATGCCAAACTAGCAGTGGATGACCCTGAAGCCATTCTC
TTAGTGAATCAGCCTGGATCTGATGGATTTAAAGTCGACTCAACACCACTCTTTCAGGTC
GCTCTAGGCCGAGAATGGTATATACATACGATCTATACAGTGAGATCGAAAGACAATGCC
AATCGAGGTATTGGCAAAGAAGTGTGGAGTACCATTCTCTGGTGAAGCAAGGAAAGCCC
CAATCCACCACCAAGAGCCGGAAGAAGAGAGAGATCAGGAGCACACCCTCACTGGCATGG
GAGATTGGTGTGAAAACAGTCGAGGAACAACATCCAGCACATTGCCCTGGACCGCACC
AAGAGGCAGATCCCCATGGGAGAGCACCTCCAGATGGCATCCTCCCCTGGGAGCTCAAC
AGCCCCAGCTCTGCAGTCAAGCTGGTCACTGTGGTGGGAGGCACACGGTAGGGTACTC
ACCATCTGCCTCACTGTGATGTCAGTGTGATGTGCAGGGGCAAGGAAAGTTTCAGGGGG
AAGGATGCCCCGAAAGGCTCCAGCAGCAGTGAAGCCATGGTGCCCCACAGAGCCATCAC
AATGACAGCTCAGAAGTTTGA
    
```

- Restriction Sites:** Please inquire
- ACCN:** NM_207361
- Insert Size:** 14000 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 clone has been fully sequenced and found three SNPs within the protein associated with this reference, NM_207361.3, and only one SNP changes amino acid.
- 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_207361.3](#), [NP_997244.3](#)

RefSeq Size: 9510 bp

RefSeq ORF: 9510 bp

Locus ID: 341640

UniProt ID: [Q5SZK8](#)

Cytogenetics: 13q13.3

Protein Families: Transmembrane

Gene Summary: This gene encodes an integral membrane protein containing numerous CSPG (chondroitin sulfate proteoglycan element) repeats and Calx-beta domains. The encoded protein localizes to the basement membrane, forming a ternary complex that plays a role in epidermal-dermal interactions. This protein is important for the integrity of skin and renal epithelia. Mutations in this gene are associated with Fraser syndrome. [provided by RefSeq, Apr 2014]