



MEFV (NM_000243.3) - cDNA + Protein - 2025-04-02

CTACCAGAAG CCAGACAGCT GGCTCGAGCC TCTCCTGCTC AGCACCATGG 4 [chr16:g.3320350_3256171dup](#) [-12C>G](#)
Meta 2

CTAAGACCCC TAGTGACCAT CTGCTGTCCA CCCTGGAGGA GCTGGTGCCC 54 [L9L](#) [T12I](#)
laLysThrPr oSerAspHis LeuLeuSerT hrLeuGluGl uLeuValPro 18

TATGACTTCG AGAAGTTCAA GTTCAAGCTG CAGAACACCA GTGTGCAGAA 104 [Y19C](#) [K25R](#) [L28V](#) [Q34P](#) [K35R](#)
TyrAspPheG luLysPheLy sPheLysLeu GlnAsnThrs erValGlnLy 35

GGAGCACTCC AGGATCCCC CGGAGCCAGAT CCAGAGAGCC AGGCCGGTGA 154 [R39G](#) [R42W](#) [P50L](#)
sGluHisSer ArgIleProA rgSerGlnIl eGlnArgAla ArgProValL 52

AGATGGCCAC TCTGCTGGTC ACCTACTATG GGGAAAGAGTA CGCCGTGCAG 204 [A56S](#) [L57L](#) [G62W](#) [Y65Y](#) [V67E](#)
ysMetAlaTh rLeuLeuVal ThrTyrTyrG lyGluGluTy rAlaValGln 68

CTCACCCCTGC AGGTCCCTGCG GGCCATCAAC CAGCGCCTGC TGGCCGAGGA 254 [R75Q](#) [E84K](#)
LeuThrLeuG lnValLeuAr gAlaIleAsn GlnArgLeuL euAlaGluGl 85

GCTCCACAGG GCAGCCATTC AGGAATATTC CACACAAGAA AACGGCACAG 304 [H87R](#) [A89T](#) [Q97K](#) [Q97K](#) [Q97R](#) [N99N](#)
uLeuHisArg AlaAlaIleG lnGluTyrSe rThrGlnGlu AsnGlyThrA 102

ATGATTCCGC AGCGTCCAGC TCCCTGGGGG AGAACAAGCC CAGGAGCCTG 354 [D102D](#) [D103D](#) [S104C](#) [A105E](#) [S108R](#) [S108G](#) [L110P](#) [L110L](#) [G111R](#) [G111E](#) [G111G](#) [334_335insG](#) [P115T](#)

P115R R116S

spAspSerAl aAlaSerSer SerLeuGlyG luAsnLysPr oArgSerLeu 118

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LysThrProA spHisProGl uGlyAsnGlu GlyAsnGlyP roArgProTy 135

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R151S G152R

rGlyGlyGly AlaAlaSerL euArgCysSe rGlnProGlu AlaGlyArgG 152

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lyLeuSerAr gLysProLeu SerLysArgA rgGluLysAl aSerGluGly 168

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 yGlyAlaSer AlaAspLeuL ysGluGlyPr oGlyAsnPro GluHisSerV 302

TCACCGGAAG GCCACCAGAC ACGGCTGCGA GTCCCCCGCTG CCACGCCAG 954 [G304R](#) [P307P](#) [T309M](#) [P313H](#) [R314C](#) [R314H](#) [R314R](#) [A317T](#)
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 GluGlyAspP roValAspGl yThrCysVal ArgAspSerC ysSerPhePr 335

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 ProGlnProL euProGlnCy sLysArgHis LeuLysGlnV alGlnLeuLe 385

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 uPheCysGlu AspHisAspG luProIleCy sLeuIleCys SerLeuSerG 402

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lnGluHisGln nGlyHisArg ValArgProI leGluGluVal lAlaLeuGlu 418

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sserGlyGlu GluGlnArgS erTyrGlyGln uGluLysAla ValSerPheL 452

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ACACACCATG GATTTTCAGAG GAGGAAGTAC GGAGTCCGTTG CATAATCCGC *258 c.*245G>A
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