



WDR1 (NM_017491.5) - cDNA + Protein - 2026-06-15

ACTCCACTCC CGGCACGCC GGTGCCGCCT TCCGGCTCCA GTCCCCGGGC -84

TCGGCCTCGG CGAGGTGTAA TTCGCAGCGC GGGCCGGCCC CGGAGGCTCT -34

CGGCGAGCGC GGC GCGGTAA CAAGTGGCG AGGATGCCGT ACGAGATCAA 17

MetProT yrGluIleLy 6

GAGGTGTTT GCCAGCCTCC CGCAGGTGGA GAGGGGCGTC TCCAAGATCA 67 **K7del**

sLysValPhe AlaSerLeuP roGlnValGl uArgGlyVal SerLysIleI 23

TCGGCGGCCGA CCCTAAGGGC AACAAATTTTC TGTACACCAA TGGAAAGTGC 117 **D26N**

leGlyGlyAs pProLysGly AsnAsnPheL euTyrThrAs nGlyLysCys 39

GTCATCTTAA GGAACATCGA CAACCCAGCC CTTGCTGACA TCTACACAGA 167

ValIleLeuA rgAsnIleAs pAsnProAla LeuAlaAspI leTyrThrGl 56

GCACGCCCAT CAGGTGGTGG TGGCCAAGTA TGCGCCCAGC GGATTCTACA 217

uHisAlaHis GlnValValV alAlaLysTy rAlaProSer GlyPheTyrI 73

TTGCCCTCCGG AGATGTGTCT GGGAAAGCTGA GGATCTGGGA TACCACGCAG 267

leAlaSerGl yAspValSer GlyLysLeuA rgIleTrpAs pThrThrGln 89

AAGGAGCACC TGTTGAAGTA TGAGTACCAG CCTTTCGCTG GGAAGATCAA 317

LysGluHisL euLeuLysTy rGluTyrGln ProPheAlaG lyLysIleLy 106

AGACATTGCT TGGACTGAAG ACAGTAAGAG GATCGCCGTG GTCGGGGAAG 367 [G121R](#)
sAspIleAla TrpThrGluA spSerLysAr gIleAlaVal ValGlyGluG 123

GAAGGGAGAA GTTTGGAGCA GTCTTCTCTT GGGATAGTGG CTCTTCTGTG 417
lyArgGluLy sPheGlyAla ValPheLeuT rpAspSerGl ySerSerVal 139

GGCGAGATTA CAGGACA~~CAA~~ CAAAGTCATC AACAGCGTGG ACATCAAGCA 467 [H145Q](#)
GlyGluIleT hrGlyHisAs nLysValIle AsnSerValA spIleLysGl 156

GAGCCGGCCA TACCGGCTGG CCACGGGAAG CGATGATAAC TGC CGGCAT 517
nSerArgPro TyrArgLeuA laThrGlySe rAspAspAsn CysAlaAlaP 173

TCTTTGAGGG ACCCCATTC AAGTTCAAGT TCACAATTGG CGACCACAGC 567
hePheGluGl yProProPhe LysPheLysP heThrIleGl yAspHisSer 189

CGCTTTGTCA ACTGTGTGCG ATTCTCTCCT GATGGGAACA GATTTGCCAC 617
ArgPheValA snCysValAr gPheSerPro AspGlyAsnA rgPheAlaTh 206

AGCCAGTGCT GACGGCCAGA TATACATCTA TGACGGGAAG ACTGGGGAGA 667
rAlaSerAla AspGlyGlnI leTyrIleTy rAspGlyLys ThrGlyGluL 223

AGGTGTGCGC GCTGGGCGGA AGCAAGGCC CACGACGGTGG GATTTACGCA 717
ysValCysAl aLeuGlyGly SerLysAlaH isAspGlyGl yIleTyrAla 239

ATTAGTTGGA GTCCCGACAG CACCCATTTG CTTTCTGCTT CTGGGGACAA 767
IleSerTrpS erProAspSe rThrHisLeu LeuSerAlaS erGlyAspLy 256

AACTTCCAAG ATTTGGGACG TCAGCGTGAA CTCCGTGGTC AGCACATTC 817

sThrSerLys IleTrpAspV alSerValAs nSerValVal SerThrPheP 273

CCATGGGCTC CACGGTTCTG GACCAGCAGC TGGGCTGCC^T ATGGCAGAAG 867 [L286V](#)

roMetGlySe rThrValLeu AspGlnGlnL euGlyCysLe uTrpGlnLys 289

GACCACCTGC TCAGTGTCTC CCTGTCCGGG TACATCAACT ATCTGGACAG 917 [L293F](#)

AspHisLeuL euSerValSe rLeuSerGly TyrIleAsnT yrLeuAspAr 306

AAACAACCCC AGCAAGCCCC TGCACGTCAT CAAGGGTCAC AGTAAATCGA 967

gAsnAsnPro SerLysProL euHisValIl eLysGlyHis SerLysSerI 323

TCCAGTGTCT GACGGTGCAT AAAAACGGCG GCAAGTCCTA CATTACTCT 1017

leGlnCysLe uThrValHis LysAsnGlyG lyLysSerTy rIleTyrSer 339

GGGAGCCACG ACGGACACAT TAAT^TTACTGG GATTCAGAGA CGGGGGAGAA 1067

GlySerHisA spGlyHisIl eAsnTyrTrp AspSerGluT hrGlyGluAs 356

CGACTCCTTC GCTGGGAAAG GCCACACGAA CCAGGTGTCC AGGATGACCG 1117

nAspSerPhe AlaGlyLysG lyHisThrAs nGlnValSer ArgMetThrV 373

TGGATGAGTC GGGGCAGCTC ATCAGCTGCA GCATGGACGA CACCGTGCGG 1167

alAspGluSe rGlyGlnLeu IleSerCysS erMetAspAs pThrValArg 389

TACACCAGCC TCATGCTGCG GGACTACAGC GGACAAGGAG TTGTGAACT 1217

TyrThrSerL euMetLeuAr gAspTyrSer GlyGlnGlyV alValLysLe 406

GGACGTTTCCAG CCAAAGTGCG TAGCCGTCGG CCCCAGGGGA TACGCC^GTGG 1267 [V422M](#)

uAspValGln ProLysCysV alAlaValGl yProGlyGly TyrAlaValV 423

TCGTGTGCAT TGGACAGATT GTCCTGCTGA AGGATCAGAG GAAGTGCTTC 1317 V424M

alValCysIl eGlyGlnIle ValLeuLeuL ysAspGlnAr gLysCysPhe 439

AGCATCGACA ACCCCGGCTA CGAGCCCGAA GTTGTGGCAG TGCACCCCGG 1367

SerIleAspA snProGlyTy rGluProGlu ValValAlaV alHisProGl 456

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GlyProValT hrAspValAl aTyrSerHis AspGlyAlaP heLeuAlaVa 506

GTGCGACGCC AGCAAGGTGG TCACAGTGTT CAGCGTTGCT GACGGCTACT 1567

lCysAspAla SerLysValV alThrValPh eSerValAla AspGlyTyrS 523

CGGAGAACAA TGTTTTTTAT GGACACCATG CAAAATCGT CTGCCTGGCC 1617

erGluAsnAs nValPheTyr GlyHisHisA laLysIleVa lCysLeuAla 539

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TrpSerProA spAsnGluHi sPheAlaSer GlyGlyMetA spMetMetVa 556

GTATGTTTGG ACCCTGAGTG ACCCGGAAAC CAGAGTCAAG ATCCAAGATG 1717

lTyrValTrp ThrLeuSerA spProGluTh rArgValLys IleGlnAspA 573

CACACCGGCT GCACCATGTC AGCAGCCTGG CCTGGCTGGA CGAGCACACG 1767

laHisArgLe uHisHisVal SerSerLeuA laTrpLeuAs pGluHisThr 589

CTGGTCACGA CCTCCCATGA TGCCTCTGTCT AAGGAGTGG CAATCACCTA 1817 [A597V](#)

LeuValThrT hrSerHisAs pAlaSerVal LysGluTrpT hrIleThrTy 606

CTGAGGAGCC CCACCCCCGC CTCTGGATGG ACCGAATCAG GGACTAGAGT *46

rStop

TTAACTGCAG CGGAACATGT CATTCTCTA TTTCTGTGAC GCGCCCCCAT *96

GCCCCACCC CACCACAAGA GGCAGGAGGG CCCAGTCATG ACCCTCGTCT *146

CTGCAGGGTG TCTGTACACG TTCTTCTGAA AGCTTTAGAC AGTAACAGTT *196

TGCACATGAA AAATAAAGCG AGCACCTAAA CAATGTGTGG AGCATAACTA *246

AAACCCACAG CCCAACCAAA CCTTGAGAAT GCGAAACATT CCAGAGGCAG *296

TAGCCTCCAA AGCACACAGA GCCCCTGGCC CCGCCGCGGC TCTCACTATC *346

TGTCAGGGGA GGTGTACAG GTGAATGAGC CGGGGGGCTC ATGTTCCCTGC *396

CTGCAGAACA TTTCTGTACT AGTGAGAAGA GGAATATGC ATTGCAGTTC *446

AGCAAAGCCG GAATTCTGTG TTGAACAGAT GTCTGTCTCC CTAGTGTGTG *496

ACTCACACCT TGTGGCTGCC TTCAGAGCGC CACCTCCAGA TCAGATGGGG *546

ACACACAACC CCTGGATATG TTTCATTGTC AGATTTTGTG CTTGATTTTA *596

AGAATGGAAT TGTGGGTATC TTTCCTTTTT TTTTAAATGTA TCTTAACTGT *646

TGCCTGTCTAG TGTTTACAAA CTAGTGCCTT GACGGCACCG TGTTCCAAGTT *696

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TCATGCTTTG ATGTTCCCCT GTCTTTCCCCT CTTCTGCTCT CAAGAGCAAA *796

GGTTAATTTA AGGACAAAGA TGAAGTCACT GTAAACTAAT CTGTCATTGT *846

TTTTACCTTC CTTTTCTTTT TCAGTGCAGA AATTAAAAGT AAGTATAAAG *896

CACCGTGATT GGGAGTGTCT TTGCGTGTGT CGGAATCACT GGTAATGTT *946

GGCTGAGAAC AATCCCTCCC CTTGCACTTG TGAAAACACT TTGAGCGCTT *996

TAAGAGATTA GCCTGAGAAA TAATTAAATA TCTTTTCTCT TCA

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