



## WDR1 (NM\_017491.5) - cDNA + Protein - 2024-05-15

ACTCCACTCC CGGCACGCCC GGTGCCGCCT TCCGGCTCCA GTCCCCGGGC -84

TCGGCCTCGG CGAGGTGTAA TTCGCAGCGC GGGCCGGCCC CGGAGGCTCT -34

CGGCGAGCGC GGC GCGGTAA CAAGTGGGCG AGGATGCCGT ACGAGATCAA 17

MetProT yrGluIleLy 6

GAGGTGTTT GCCAGCCTCC CGCAGGTGGA GAGGGGCGTC TCCAAGATCA 67 K7del

sLysValPhe AlaSerLeuP roGlnValGl uArgGlyVal SerLysIleI 23

TCGGCGGGGA CCCTAAGGGC AACAAATTTTC TGTACACCAA TGGAAAGTGC 117 D26N

leGlyGlyAs pProLysGly AsnAsnPheL euTyrThrAs nGlyLysCys 39

GTCATCCTAA GGAACATCGA CAACCCAGCC CTTGCTGACA TCTACACAGA 167

ValIleLeuA rgAsnIleAs pAsnProAla LeuAlaAspI leTyrThrGl 56

GCACGCCCAT CAGGTGGTGG TGGCCAAGTA TGCGCCCAGC GGATTCTACA 217

uHisAlaHis GlnValValV alAlaLysTy rAlaProSer GlyPheTyrI 73

TTGCCTCCGG AGATGTGTCT GGGAAGCTGA GGATCTGGGA TACCACGCAG 267

leAlaSerGl yAspValSer GlyLysLeuA rgIleTrpAs pThrThrGln 89

AAGGAGCACC TGTGAAGTA 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 GTCTTCCTCT GGGATAGTGG CTCTTCTGTG 417

lyArgGluLy sPheGlyAla ValPheLeuT rpAspSerGl ySerSerVal 139

GGCGAGATTA CAGGACACAA CAAAGTCATC AACAGCGTGG ACATCAAGCA 467 [H145Q](#)

GlyGluIleT hrGlyHisAs nLysValIle AsnSerValA spIleLysGl 156

GAGCCGGCCA TACCGGCTGG CCACGGGAAG CGATGATAAC TGC GCGGCAT 517

nSerArgPro TyrArgLeuA laThrGlySe rAspAspAsn CysAlaAlaP 173

TCTTTGAGGG ACCCCCATTC 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 CACCCATTG CTTTCTGCTT CTGGGGACAA 767

IleSerTrpS erProAspSe rThrHisLeu LeuSerAlaS erGlyAspLy 256

AACTTCCAAG ATTTGGGACG TCAGCGTGAA CTCCGTGGTC AGCACATTTC 817

sThrSerLys IleTrpAspV alSerValAs nSerValVal SerThrPheP 273

CCATGGGCTC CACGGTTCTG GACCAGCAGC TGGGCTGCCT 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 CATTTACTCT 1017

leGlnCysLe uThrValHis LysAsnGlyG lyLysSerTy rIleTyrSer 339

GGGAGCCACG ACGGACACAT TAATTACTGG 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 GGACTIONAGC GGACAAGGAG TTGTGAAACT 1217

TyrThrSerL euMetLeuAr gAspTyrSer GlyGlnGlyV alValLysLe 406

GGACGTTTAG CCAAAGTGCG TAGCCGTCGG CCCCAGGGGA TACCCGTGG 1267

uAspValGln ProLysCysV alAlaValGl yProGlyGly TyrAlaValV 423

TCG**TGTGCAT** TGGACAGATT GTCCTGCTGA AGGATCAGAG GAAGTGCTTC 1317 [V424M](#)

alValCysIl eGlyGlnIle ValLeuLeuL ysAspGlnAr gLysCysPhe 439

AGCATCGACA ACCCCGGCTA CGAGCCCGAA GTTGTGGCAG TGCACCCCGG 1367

SerIleAspA snProGlyTy rGluProGlu ValValAlaV alHisProGl 456

CGGGGACACG GTGGCAATTG GGGGTGTGGA CGGCAACGTC CGCCTGTATT 1417

yGlyAspThr ValAlaIleG lyGlyValAs pGlyAsnVal ArgLeuTyrS 473

CCATCCTGGG CACCACGCTG AAGGATGAGG GCAAGCTCCT AGAGGCCAAG 1467

erIleLeuGl yThrThrLeu LysAspGluG lyLysLeuLe uGluAlaLys 489

GGCCCCGTGA CCGACGTGGC CTACTCCAC GACGGCGCCT TCCTCGCGGT 1517

GlyProValT hrAspValAl aTyrSerHis AspGlyAlaP heLeuAlaVa 506

GTGCGACGCC AGCAAGGTGG TCACAGTGTT CAGCGTTGCT GACGGCTACT 1567

lCysAspAla SerLysValV alThrValPh eSerValAla AspGlyTyrS 523

CGGAGAACAA TGTTTTTTAT GGACACCATG CAAAAATCGT CTGCCTGGCC 1617

erGluAsnAs nValPheTyr GlyHisHisA laLysIleVa lCysLeuAla 539

TGGTCCCCAG ACAATGAACA CTTTGCCTCC GGTGGCATGG ACATGATGGT 1667

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 TGCCTCTGTC AAGGAGTGGG CAATCACCTA 1817  
LeuValThrT hrSerHisAs pAlaSerVal LysGluTrpT hrIleThrTy 606

CTGAGGAGCC CCACCCCCGC CTCTGGATGG ACCGAATCAG GGACTIONAGT \*46  
rStop

TTAACTGCAG CGGAACATGT CATTCTCTCTA TTTCTGTGAC GCGCCCCCAT \*96  
GCCCCACCC CACCACAAGA GGCAGGAGGG CCCAGTCATG ACCCTCGTCT \*146  
CTGCAGGGTG TCTGTACACG TTCTTCTGAA AGCTTTAGAC AGTAACAGTT \*196  
TGCACATGAA AAATAAAGCG AGCACCTAAA CAATGTGTGG AGCATAACTA \*246  
AAACCCACAG CCAACCAAAA CCTTGAGAAT GCGAAACATT CCAGAGGCAG \*296  
TAGCCTCCAA AGCACACAGA GCCCCTGGCC CCGCCGCGGC TCTCACTATC \*346  
TGTCAGGGGA GGTGTGTACAG 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 TTTCTTTTTT TTTTAATGTA TCTTAACTGT \*646  
TGCCTGTGAG TGTTTACAAA CTAGTGCATT GACGGCACCG TGTCCAAGTT \*696  
TTTAGAACCC TTGTTAGCCA GACCGAGGTG TCCTGGTCAC CGTTTCACCA \*746  
TCATGCTTTG ATGTTCCCCT GTCTTTCCCT CTTCTGCTCT CAAGAGCAAA \*796  
GGTTAATTTA AGGACAAAGA TGAAGTCACT GTAAACTAAT CTGTCATTGT \*846  
TTTTACCTTC CTTTTCTTTT TCAGTGCAGA AATTAAAAGT AAGTATAAAG \*896  
CACCGTGATT GGGAGTGTTT TTGCGTGTGT CGGAATCACT GGTAATGTT \*946

GGCTGAGAAC AATCCCTCCC CTTGCACTTG TGAAAACACT TTGAGCGCTT \*996

TAAGAGATTA GCCTGAGAAA TAATTAAATA TCTTTTCTCT TCA

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