WDR1 (NM_017491.5) - cDNA + Protein - 2024-12-30

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ACTCCACTCC CGGCACGCCC GGTGCCGCCT TCCGGCTCCA GTCCCCGGGC -84

TCGGCCTCGG CGAGGTGTAA TTCGCAGCGC GGGCCGGCCC CGGAGGCTCT -34

CGGCGAGCGC GGCGCGGTAA CAAGTGGGCG AGGATGCCGT ACGAGATCAA 17
                                    MetProT yrGluIleLy 6


GAAGGTGTTC GCCAGCCTCC CGCAGGTGGA GAGGGGCGTC TCCAAGATCA 67    K7del
sLysValPhe AlaSerLeuP roGlnValGl uArgGlyVal SerLysIleI 23


TCGGCGGCGA CCCTAAGGGC AACAATTTTC 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 TGTTGAAGTA TGAGTACCAG CCTTTCGCTG GGAAGATCAA 317
LysGluHisL euLeuLysTy rGluTyrGln ProPheAlaG lyLysIleLy 106
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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 TGCGCGGCAT 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 AGCAAGGCCC ACGACGGTGG GATTTACGCA 717
ysValCysAl aLeuGlyGly SerLysAlaH isAspGlyGl yIleTyrAla 239

ATTAGTTGGA GTCCCGACAG CACCCATTTG CTTTCTGCTT CTGGGGACAA 767
IleSerTrpS erProAspSe rThrHisLeu LeuSerAlaS erGlyAspLy 256
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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 GGACTACAGC GGACAAGGAG TTGTGAAACT 1217
TyrThrSerL euMetLeuAr gAspTyrSer GlyGlnGlyV alValLysLe 406

GGACGTTCAG CCAAAGTGCG TAGCCGTCGG CCCCGGGGGA TACGCCGTGG 1267  V422M
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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

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 CTACTCCCAC 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
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CACACCGGCT GCACCATGTC AGCAGCCTGG CCTGGCTGGA CGAGCACACG 1767
laHisArgLe uHisHisVal SerSerLeuA laTrpLeuAs pGluHisThr 589

CTGGTCACGA CCTCCCATGA TGCCTCTGTC AAGGAGTGGA CAATCACCTA 1817 A597V
LeuValThrT hrSerHisAs pAlaSerVal LysGluTrpT hrIleThrTy 606

CTGAGGAGCC CCACCCCCGC CTCTGGATGG ACCGAATCAG GGACTAGAGT *46
rStop


TTAACTGCAG CGGAACATGT CATTTCTCTA TTTCTGTGAC GCGCCCCCAT *96
GCCCCCACCC 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 GGTTGTACAG GTGAATGAGC CGGGGGGCTC ATGTTCCTGC *396
CTGCAGAACA TTTCTGTACT AGTGAGAAGA GGGAATATGC ATTGCAGTTC *446
AGCAAAGCCG GAATTCTGTG TTGAACAGAT GTCTGTCTCC CTAGTGTGTG *496
ACTCACACCT TGTGGCTGCC TTCAGAGCGC CACCTCCAGA TCAGATGGGG *546
ACACACAACC CCTGGATATG TTTCATTGTC AGATTTTGTG CTTGATTTTA *596
AGAATGGAAT TGTGGGTATC TTTCCTTTTT TTTTAATGTA TCTTAACTGT *646
TGCCTGTCAG TGTTTACAAA CTAGTGCGTT 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 GGTAAATGTT *946
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GGCTGAGAAC AATCCCTCCC CTTGCACTTG TGAAAACACT TTGAGCGCTT *996
TAAGAGATTA GCCTGAGAAA TAATTAAATA TCTTTTCTCT TCA
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