

Product datasheet for **RG220074**

DNAH2 (NM_020877) Human Tagged ORF Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	DNAH2 (NM_020877) Human Tagged ORF Clone
Tag:	TurboGFP
Symbol:	DNAH2
Synonyms:	DNAHC2; DNHD3
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-AC-GFP (PS100010)
E. coli Selection:	Ampicillin (100 ug/mL)
ORF Nucleotide Sequence:	>RG220074 representing NM_020877 Red=Cloning site Blue=ORF Green=Tags(s)

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGATCGCC**

ATGTCCAGCAAAGCTGAGAAGAAGCAGCGATTGAGTGGCCGAGGAAGCTCCCAGGCAAGCTGGTCAGGGC
GGGCCACTCGGGCTGCTGTGGCCACACAGGAGCAGGGGAATGCCCGGCTGTCAGTGAGCCAGAGCTGCA
GGCTGAGCTCCCCAAGGAGGAGCCTGAGCCACGGTTGGAGGGACCTCAAGCACAGAGTGAAGAATCAGTG
GAGCCCGAGGCAGATGTGAAGCCCTCTCCTTTCCCGAGCTGCGCTGACAGGACTGGCGGATGCAGTGT
GGACACAGGAGCATGATGCCATTCTGGAACACTTTGCCAGGACCCTACAGAATCCATCCTCACCATCTT
CATTGACCCTTGTGGGCTGAAGCTAGAGCTGGGCATGCCTGTACAGACCAGAACAGCTTGTCTAC
TTCATTGCGCAAGCACCAGTTCCCATCACCTGGGAGAACTTCGAGGCAACTGTGCAGTTTGGGACGGTGC
GGGGCCCCATATCCCGGCCCTGCTTCGGCTGCTCGGTGGAGTCTTTGCCCTCAGATCTTTGCAAACAC
AGGCTGGCCTGAGAGCATTAGAAATCATTTTGCTTCTCATCTGCACAAGTTCTTGGCCTGCCTGACAGAC
ACTCGGTACAAACTGGAGGGGCACACGGTCCTCTACATCCCTGCAGAGGCCATGAACATGAAGCCTGAGA
TGGTGATAAAGGACAAAGAGCTGGTGCAACGGCTAGAGACCTCCATGATCCACTGGACCCGGCAGATAAA
GGAGATGCTCAGTGCCCAGGAGACTGTGGAGACAGGAGAAAAATTAGGTCCTCTGGAGGAGATTGAGTTC
TGCGCAACCGATGCATGGACCTGTCTGGCATCAGTAAGCAGCTGGTGAAGAAGGGAGTGAAGCAGTTG
AATCCATCCTGCACCTTGCCAAGTCGTCTACTTGGCGCCCTTTATGAAACTGGCAGCAGATCCAGGA
TGGCTCTCGTCAAGCACAGTCAAACCTGACCTTTTTGTCAATCCTGAAGGAACCTTACCAGGAGTTGGCT
TTCATGAAGCCCAAGGACATCTCTAGCAAGCTCCCTAAGCTGATCAGTCTCATCCGCATCATCTGGGTCA
ACTCTCCCACTACAACACTCGGGAGAGACTGACCTCGCTCTCCGAAAGGTATGTGACTGTCAGTATCA
CTTCGCCCCGCTGGGAAGATGGCAAGCAGGGTCCCCTTCTTGGTCTTTGGTGCCAGGGGCCACAGATA
ACACGGAACTTGCTGGAGATTGAGGACATCTTTCATAAAAATCTGCACACGCTGCGAGCCGTTCCGGGG
GTATCCTGGATGTCAAGAACACCTGTTGGCATGAAGACTACAATAAGTTCCGTGCCGGAATCAAGGACCT
GGAGGTGATGACCCAGAACCTGATCACCTCAGCCTTCGAGTTGGTGCGGGACGTGCCGACGGCGTCTT



CTGCTGGACACCTTCCACAGGCTTGCCCTCCCGGAGGCTATCAAGCGGACTTATGACAAGAAGGCGGTGG
 ATCTCTACATGCTGTTCAATAGCGAGCTGGCCCTGGTGAACCGTGAACGGAAACAAGAAATGGCCAGACCT
 GGAGCCCTACGTGGCCAGTATTCGGAAAGGCGCGCTGGGTGCACATCCTCCGGCGTCGCATCGACAGA
 GTCATGACCTGCCTTGTGGTGCATTTCTGCCCGTATTGGGACTGGAAAGGAGAGTGTGCACACCT
 ATCAGCAGATGGTCCAGGCCATTGATGAGCTGGTTCGAAAAACCTTCCAAGAGTGGACATCAAGTCTGGA
 CAAGGATTGCATTCGGCGGTTGGATACCCATTGCTGCGAATCAGCCAGGAGAAGGCGGGCATCTGGAT
 GTCAACTTTGACAAGTCCCTTCTGATTCTTTGCGGAAATTGACTACTGGGAGGCGCTGTTGTGAGA
 CGCCCCATTACGTGGTGAACGTAGCTGAGCGAGCCGAGGACCTGCGCATTCTGCGTGAAAAATCTGCTACT
 CGTTGCTAGAGACTACAATAGGATTATTGCCATGCTGTCCCAGATGAGCAGGCCCTATTCAAAGAGCGT
 ATTCGGCTCCTGGATAAGAAGATCCACCCGGGACTCAAGAAACTGCACTGGGCCTTGAAGGGGGCCAGTG
 CCTTCTTCATCACGGAGTGCCGTATACATGCCAGCAAGGTGCAGATGATTGTGAATGAGTTCAAGGCATC
 CACTCTGACCATTGGCTGGCGAGCCCAAGAGATGTCAGAGAAGCTGTGGTACGCATTAGTGCCAAACGG
 GTATACAGGGACCTGGAATTTGAAGAGGACCAAGAGAGCATCGGGCAGCTGTACAGCAGAAATTGATGA
 ACCTGCACCAGGATGTGGTGACCATCATGACCAACTCCTATGAGGTCTTCAAGAATGATGGTCTGAGAT
 TCAGCAGCAGTGGATGCTGTACATGATTGGCTGGACCGCATGATGGAGGATGCCCTGCGCTGAATGTG
 AAGTGGTCACTGCTAGAACTATCCAAGGCTATCAACGGGGATGGAAGACCAGCCAAACCCACTCTTCC
 AAGTCTTGTCAATTTGAAGAATGATCTGCAAGGAAGTGTGGCACAGGTGGAATTTCAACCCACTCTGCA
 GACTTTGGCAGGTGTGGTCAATGACATTGGCAACCACCTTTTTCCACCATCTCTGTCTTCTGCCACCTC
 CCTGACATTTCCACCAAGCGCAAGTTACATCGTGAACCCATCCAACAGTTGTGGAGCAAGATGAGGACA
 TCAAGAAGATCCAGACCCAAATCAGCAGCGGCATGACTAACAACGCAAGCCTGCTGCAGAACTACCTCAA
 GACCTGGGACATGTACCGGGAGATCTGGGAGATCAACAAGGACTCCTTCAATTCATCGCTACCAGCGCCTC
 AACCTCCTGTCTTCTTTTGTGCGGACATTGCCCGCTACACGGAAGTTGCTAATAACGTGCAGAAGG
 AGGACAGTACCAACATCCAGTTTGTGCTGTGGACTGTTTCGCACCTCAAGTTCTCCCTGGTGCAGCA
 CTGCAATGAATGGCAGAACCAAGTTGCGGACTCTGCTCAGGGAGATGGCTGTGGGCGCCTCTGGAGCTG
 CACACCTACCTGAAGGAGAACGCAGAGAAAAATCAGCCGCCCTCCGCAGACACTGGAGGAACTGGGGTCA
 GCTTGCAGCTCGTGGATGCCCTGAAGCAGGACTTGGCCAACGTGGAGACTCAGATCCCTCCCATACACGA
 GCAATTTGCCATTCTTGAAGTACGAGGTGCCAGTGCAGGACAGTGTCTGGAGATGCTGGACAGTCTC
 AACGGGGAGTGGTTGTCTTCAACAAACTCTGCTGGACAGTAAGCAAATGCTGAAGAAACACAAGGAGA
 AATTCAAGACAGGCTGATCCACTCGGCAGATGACTTCAAGAAGAAAGCACATACACTTCTGGAAGATTT
 CGAATTCAAAGGCCATTTACCAGCAACGTGGGATACATGTCTGCCTTAGACCAGATTACACAAGTCCGG
 GCCATGCTGATGGCCATCGGGAAAGAGGAAAATAGTCTCCGAGCCAACCTGGGCATCTTCAAGATCGAGC
 AGCCACCTCCAAGGACCTTCAAGACCTGGAGAAGGAGCTCGATGCCCTCCAGCAAAATCTGGGAGATCGC
 ACGAGACTGGGAGGAGAACTGGAATGAGTGAAGACTGGCCGGTTCTGTATCCTGCAGACGGAAACCATG
 GAGACCACGGCCACGGGCTGTTTCGTGCGCTCACAAAATTAGCCAAAGAGTATAAGGACCAGAACTGGG
 AAATTTGAAACCCTCGCTCAAAAATAGAGCAGTTCAAGAGGACCATGCCTCTCATCTCAGACCTGCG
 GAACCTGCCCTTAGAGAGAGGCACTGGGACCAGTCCGGGATGAGATCCAGCGGGAGTTTGTACAGGAA
 TCTGAAAGCTTCACTTGGAGCAGATTGTGGAGCTTGGATGGATCAGCATGTGGAGAAAATGGGGAGA
 TCTCTGCTCAGCAACTAAAGAGCTGGCTATAGAAGTGGCTTTACAAAACATTGCCAAGACCTGGGATG
 GACTCAGCTCGACATAGTACCCTACAAGGATAAGGGCCATCATCGGCTCAGAGGTACAGAAGAAGTATTC
 CAGGCACTGGAAGATAAACCAGGTAGCTCTGTCTACCATGAAGGCATCACGCTTTGTCAAGGCCTTTGAGA
 AGGATGTGGACCACTGGGAACGCTGCCTCTCCCTCATTTTGGAGGTTATTGAGATGATTCTCACAGTGCA
 GCGTCAGTGGATGTACTTAGAGAATATCTTCTAGGAGAAGACATCCGCAAGCAGCTGCCAATGAATCG
 ACCTTATTTGACCAGGTCAACAGCAACTGGAAAGCCATCATGGACAGGATGAACAAGGACAACAATGCTC
 TCCGGAGACCCATCACCCAGGCTCCTGGACACATTGATAGAAATGAATACAATCTGGAAGATATTCA
 GAAATCTCTGGATATGTATTTAGAGACCAAGCGACATATTTCCCGGCTTCTACTTCTTGTCCAATGAT
 GACCTGCTGGAGATTCTGGCCAGTCCCGAAACCCAGAGGCTGTGCAGCCACACCTCAAAAAATGCTTTG
 ACAACATCAAGTTGCTGAGAATCCAGAAGTTGGAGGGCCAGCAGCAAATGGGAAGCTGTGGGATGTT
 CTCGGGCGACGGCGAGTACATTGACTTCTCCACTCAGTATTTTTAGAAGGCCCTGTGGAGTCTGGCTT
 GCGGATGTGGAACAGACCATGAGGGTGACCTGCGGGACCTTCTCCGGAACCTGCCACCTGGCCCTCAGGA
 AGTTCTCAACAAGAGGGACAAATGGGTGAAGGAGTGGGCTGGCCAGGTGGTGTCACTGCCAGTGCAGAT
 CCAGTGGACGGCTGATGTACCAAGTGCCTGCTGACAGCGAAGGAGCGGGCAGACAAGAAAAATCCTCAAG
 GTCATGAAGAAGAACCAGGTGTCAATCTGAATAAGTATTCAGAAGCCATCAGGGGGAACCTTGACCAAGA

TCATGCGGCTTAAAATTGTGGCTCTGGTGACGATAGAAATTCATGCCCGGGATGTGTTGGAGAAGCTTTA
 CAAGAGTGGCCTCATGGATGTCAATTCCTTTGACTGGCTCAGCCAACCTTCGGTTCTACTGGGAGAAGGAT
 CTTGATGACTGTGTGATCCGCCAGACCAACACGCAATTCAGTATAAATTAGAGTACTGGGTAACCTCGG
 GCCGGCTCGTCATACCCCCCTGACGGACAGGTGTTACATGACACTGACCACGGCATTGCACCTGCACCG
 AGGGGGCTCCCCAAAGGCCCTGCAGGCACAGGCAAGACCAGACCGTCAAGGACCTGGGCAAGGCCCTG
 GGCATATATGTCATTGTGGTCAACTGCTCTGAGGGCCTGGACTACAAGTCCATGGGCCGAATGTACTCAG
 GTCTGGCCACAGATCCTGTGCATCCTGTGCCCTGGCTGCCGGCCTCACCCATTTCCATTTTGTATGGC
 TTTGAAATAAATCTGGTGTGGTCTGTGGGATCTTCATTACCATGAATCCTGGCTATGCTGGCCGCACAG
 AGCTTCCCAGAAAATCTTAAATCCATGTTCCGCCAATTGCCATGGTGGTGCCTGACTCCACCCTCATTGC
 AGAAATCATTCTCTTTGGAGAGGGCTTTGGCAACTGCAAGATTCTGGCCAAGAAGGTGTACACACTCTAC
 TCACTGGCTGTGCAGCAGCTGTCCAGACAGGACCACTATGACTTTGGCCTGCGTGCCTCACCTCCCTTC
 TGCGCTATGCTGGCAAGAAGCGCCCTACAGCCGGATCTGACTGATGAAGAGGTTCTGCTGCTCAAT
 GAGAGATATGAACATCGCAAGCTCACTCAGTTGATGCACCCCTGTTCAATGCCATCGTCAAGATCTG
 TTTCCCAACATTGAGCTGCCTGTCAATTGACTATGGCAAGCTGCGGGAGACCGTTGAGCAGGAGATTGAG
 ACATGGGCTGCAAAGCAGCCGTTACCCCTACCAAGGTTTTCCAGTTGTATGAAACCAAGAAGCTCCCG
 CCACTCCACCATGATCGTGGGCTGCACGGGCAGCGGCAAGACTGCCTCATGGCGCATTCTACAGGCCCTC
 CTGTCTCTCTGTGCCGCGCCGAGACCCTAATTCAACATTGTTAGAGAGTTCCCTTTGAACCCCAAGG
 CATTGTCCCTAGGGGAAGTGTATGGGGAATATGACCTCAGCACCATGAATGGACAGATGGCATCTTGTG
 CAGTGTGATGCGGACGGCATGTGCAGATGAGAAACCCGACGAGAAGTGGATCCTGTTTCGATGGCCCCGTG
 GACACACTGTGGATCGAGAACAATGAACTCCGTCATGGACGATAACAAGGTGTTGACCCTCATCAACGGCG
 AGCGCATCGCGATGCCGAGCAGGTGTCTCTCTGTTTGAAGTGGAGGACCTGGCAATGGCCTCTCCGGC
 CACTGTATCCCGCTGCGGGATGGTCTACTGACTACGCTGACCTGGGCTGGAAGCCCTATGTTTCAGTCA
 TGGCTGGAGAAGAGGCCAAAGGCTGAGGTGGAGCCCTTCAACGCATGTTGAAAAGCTCATCAACAAGA
 TGCTGGCCTTTAAGAAGGACAATGCAAGGAGCTGGTGGCCCTGCCCGAGTACAGCGGTATCACCTCCCT
 CTGCAAGCTGACTCTGCCCTGGCCACGCCAGAGAATGGGGTGAACCCAGCTGACGGCGAGAAGTATGTC
 ACCATGGTAGAGATGACATTTGTGTTCCAGCATGATCTGGTCTGTGTGCTCTGTGGATGAGGAGGGCC
 GGAAGAGGATCGACAGCTACCTCCGAGAGATCGAGGGCTCCTTTCCCAATAAGGACACGGTATATGAGTA
 TTTTGTGGACCCCAAAATACGGAGTTGGACATCATTGAGGACAAGCTCCCTAAGAGTTGGCGCTACCT
 CCAAACGCCCTTCTATAAGATCATGGTGGCCACCGTCGACACTGTTGCTACAACCTACCTGGTGAGCA
 GCTTGGTGGCCAACCAGAATCCATTCTGCTGGTGGGTCGCTGGGACTGGGAAGACCTCCATCGCCCA
 GAGCGTTCGAGTCCCTGCCCTCCAGCCAGTGGTGGTCTCGTTGTCAACATGTCGCGACAGACCACA
 TCCAATAACGTGCAGAGCATCATTGAGAGCAGGGTTGAGAAGCGAACCAAGGGTGTCTACGTGCCATTG
 GGGGCAAAAGCATGATCACCTTTATGGATGACCTAAATATGCCCGCTAAGGACATGTTTGGGTCCCAGCC
 ACCCTGGAGCTGATCCGCCTCTGGATTGACTATGGCTTCTGGTATGACCGTACGAAGCAGACCATCAAG
 TACATTCGAGAAATGTTCTGATGGTGGCATGGGCCCCCTGGGGTGGACGGACTGTCATCTCCCAA
 GGCTACGGAGTCGCTTCAACATTATCAACATGACCTTCCCACAAAGTCCCAGATCATCCGCATATTCGG
 CACCATGATCAATCAGAAGCTTCCAGGACTTTGAGGAAGAGGTGAAGCCCATTGGGAACGTGGTGACAGAG
 GCCACCCTGGACATGTACAACACCGTGGTACAGCGCTTCTGCCACGCCACCAAGATGCATTACCTCT
 TCAACCTTCGAGACATCTCCAAGGTGTTCCAGGGCATGCTTAGAGCCAACAAGGACTTCCATGATACCAA
 GTCCAGCATCACACGGCTCTGGATCCATGAATGTTTCAGAGTCTTCTGACCGGCTGGTTGATGCGGCA
 GACACAGAAGCCTTCATGGGCATCATAAGCGACAAGCTCGGCTCCTTCTTTGACCTCACATTTTCATCATC
 TCTGTCCAGCAAGCGTCTCTATCTTTGGGATTTCTGAAGGAGCCCAAGGTGTATGAAGACCTCAC
 GGATCTGACAGTGTGAAGACAGTCATGGAGACAGCTCTAAATGAGTATAACCTGTCACCCTCTGCTGTG
 CCCATGCAGTGTGCTCTTCCGAGAGGCTATTGAACACATCACACGGATCGTGGGGTCTTTGGACAGC
 CTCGGGGCAACATGCTCCTGGTGGTATCGGGGGCAGCGGACGCCAGAGTCTGGCCCGCTGGCTTCATC
 CATCTGCGACTACACCACCTCCAGATCGAGGTCACCAAAACATTATCGGAAGCAGGAGTCCGAGATGAT
 ATCAAGCGTCTGTATCGCCAGGCTGGGGTGGAGCTCAAGACCACGTCCTTCATTTTTGTGGACCCCAA
 TAGCTGATGAGTCTTCTAGAGGACATCAACAACATCCTCAGCTCAGGGCAGGTGCCAAATCTCTACAA
 GCCTGATGAATTTGAAGAGATCCAGTCGCATATCATAGACCAGGCCCGGGTGGAGCAGGTGCCTGAGTCA
 TCGGACAGCCTCTTCGCCTACCTCATTGAACGCGTGCAGAACAACCTGCACATCGTCTGCTCAGCC
 CCATGGGGATCCCTCAGGAAGTGGATCCGCCAGTACCCAGCCTTGGTGAAGTGCACAACCATCAACTG

GTTCTCAGAGTGGCCCAAGAGGCCCTGCTCGAGGTGGCTGAGAAGTGCCTCATAGGAGTAGACCTGGGA
 ACTCAGGAGAATATCCACAGGAAGGTGGCCAGATCTTTGTCACTATGCACTGGTCAGTAGCTCAGTATT
 CCCAGAAGATGCTGTTGGAAGTGCAGGAGACACAATATGTACACCCACCAAATACCTGGAAGTCCCTGTC
 TGGATATAAGAAGTTGCTGGGAGAAAAACGGCAGGAGCTGCTGGCCAAAGCCAATAAACTGCGGACAGGC
 TTGTTCAAGATCGACGAAACTAGGAAAAGGTGCAAGTATGTCGTTGGAGCTGGAGGATGCCAAGAAGA
 AGGTGGCTGAGTCCAGAAGCAGTGTGAGGAGTACCTGGTCATCATTGTGCAGCAGAAGCGGGAGGCAGA
 TGAGCAGCAGAAGGCCGTAAACAGCCAACAGTGAAGAAGATTGCAAGTGGAGAAATCAAGTGTGAGGACTG
 GCTGACAATGCCAGAAAAGATCTAGAAGAGGCACTGCCCGCCCTGGAAGAGGCCATGCGGGCCCTGGAGT
 CTCTGAACAAGAAGGATATAGGAGAGATCAAGTCTTATGGACGGCCCAAGTGGAGATAGTGT
 GCAGGCAGTTATGATTCTTCAGGCAACAGGCCACATGGGCAGAGGCCAAGAGGCAGCTAGGGGAACAG
 AACTTCATCAAGTCACTGATCAACTTTGATAAAGACAATATCTCAGATAAGGTTCTGAAGAAGATTGGGG
 CCTACTGCGCCAGCCTGACTTCCAGCCTGATATCATCGCCCGCTCCTGCTGCCAAGTCCCTCTG
 CATGTGGTGGCGCCATGGAGCTGTATGGCGGCTATATCGGGTGGTGGAGCCCAAGCGAATCCGAATG
 AACGCTGCCTGGCTCAGCTTCGGGAGAAGCAAGCCGCTCGCTGAGGCCAGGAGAAGCTGCGGGAGG
 TAGCTGAGAACTGGAGATGCTAAAGAAACAGTATGATGAGAAGCTGGCAGAGAAGGAGGAGCTTCGCAA
 GAAGTCTGAAGAGATGGAGCTGAAGCTGGAGCGAGCTGGGATGCTCGTGTGCGGGTTGGCTGGCGAGAAG
 GCCAGATGGGAGGAGACAGTCCAGGGCCTGGAGGAGGACCTGGGCTACCTGGTGGGGACTGTCTCTGG
 CAGCTGCCTTCTGTCTACATGGGACCCTTCTGACCAACTACCGGGATGAGATTGTCAACCAAATCTG
 GATCGGGAAGATCTGGGAGCTTCAGGTTCTTGTCCCTTCTTCGCCATCGATAAATCTGTGCAAT
 CCTACCAAAGTCCGGGACTGGAACATCCAAGGGTTGCCCTCAGACGCCTTCTCCACTGAGAATGGCATCA
 TCGTCACCCGAGGCAACAGGTGGGCACTGATGATCGACCTCAGGCCAGGCCCTGAAATGGATTAAGAA
 CATGGAAGGAGGCCAGGGCCTGAAGATCATCGACTGCAGATGAGCGATTACCTGCGAATCTAGAACAC
 GCCATTCACTTTGGATACCCGGTCTACTTCAGAACGTGCAGGAATATCTGGACCCACACTGAACCCCA
 TGCTCAACAAATCTGTAGCCGAATCGGTGGTGGCTGTTGATGCGCATTGGCGATAAAGGAGGTGGAATA
 TAATACCAATTTCCGTTTCTACATCACCACCAAGCTCTCAACCCCACTACAGCCAGAGACCTCAGCC
 AAGACCACCATCGTCAACTTTGCTGTTAAAGAACAGGGCCTGGAGGCCAGCTGCTGGGCATTGTGGTGC
 GGAAGGAGCGCCTGAGCTGGAGGAGCAGAAGGACTCACTGGTCAACATCGCGGCTGGTAAAAGGAA
 GCTCAAGGAGCTGGAGGATGAGATCCTGCGGCTGCTGAATGAGGCCACCGGCTCCTGCTGGATGATGTG
 CAGCTGGTGAACACGCTGCATACCTCCAAGATCACAGCCACAGAGGTGACTGAGCAGCTGGAGACCAGT
 AGACCACAGAGATCAACTGACTTGGCGGGGAGGCTTACCGCCATGCGCCAGCGGGCATCAATCCT
 GTTCTTGTGCTCAATGATATGGGCTGCATCGACCCATGTACCAGTTCTCACTGGATGCCTACATCAGC
 CTCTTTATTCTCAGCATTGACAAAAGCCACCGCAGCAATAAGCTGGAGGACCGCATTGACTACCTGAATG
 ACTACCACACCTACGCTGTCTACAGGTACACCTGCCGTACCCTTTTGAACGCCACAACTACTATTCAG
 TTTTATATGTGTGCCAAAATCTTGAGACTTCTGGCAAGCTCAACATGGATGAATACAATCTTTTCTA
 CGTGGGGTGTGGTCTTGGATCGGGAGGGCCAAATGGACAATCCATGTAGTAGCTGGCTTGAGATGCCT
 ACTGGGATAACATCACAGAGCTAGACAACTGACCAACTCCACGGACTCATGAATCCTTTGAGCAGTA
 CCCTCGTACTGGCACCTGTGGTATACCAATGCTGCCCGGAGAAGGCGATGCTGCCAGGTGAGTGGGAA
 AATGCCTGCAATGAAATGCAACGGATGCTGATCGTTGCTCCCTGCGCCAGGACCGCTGGCCTTCTGCG
 TGACCTCCTTATCATCACCAACCTTGGCTCCCGCTTATCGAGCCGCTGTGCTGAATATGAAGTCGGT
 GCTGGAGGATTCAACCCACAGTCCCCTCCTGTTTATCCTGTCCCCTGGTGTGGACCCACAGTGCC
 CTGCTGACAGTGGCAGAGCAGATGGGCATGGCCAGCGCTTCCACGCCCTGTCCCTGGGCCAGGGCCAGG
 CCCCCATCGTGTGCTCGGCTCCTCCGAGAGGGTGTGACTCAGGGACACTGGGTGTTCTGGCAAATGCCA
 CCTGTCACTGTCTGGATGCCTAATCTGGACAAGCTGGTGGAGCAGCTGCAGGTGGAGGATCCTCATCCA
 TCCTTCCGCTCTGGCTCAGCTCCATCCCCACCCAGACTTCCCTATCTCAATCTTGAGGTGAGCATCA
 AGATGACCACAGAGCCACCAAAGGGCCTAAAGGCCAATGACACGTCTTACCAACTGATGTCAGAACC
 ACAGTTTTCCCGCTGCTCCAACCTGCCAAATATAAGAAGCTGCTGTTTTCACTGTCTTCTTCCACTCT
 GTGTTACTTGAACGCAAAAAGTTCTGCACTTGGCTGGAACATCATCTATGGCTTCAATGACTCCGACT
 TTGAGGTGTGAGAAAATTTGCTGAGCCTTATCTCGATGAGTACGAGGAGACACCTTGGGACGCACTTAA
 GTACCTCATTGCCGCATCAACTATGGTGGACATGTCACAGATGACTGGGACCGGCGCTGCTGACCACC
 TACATCAATGATTATTTCTGTGACCAGTCTATCAACTCCCTTCCACCGGTTGTGAGCACTGGAGACTT
 ATTTATCCCCAAGGATGGCAGCCTCGCTTCTTACAAGGAATACATCAGCTTATTGCCTGGCATGGACCC
 CCCTGAGGCCCTTGGCCAGCACCCCAATGCTGATGTGGCTCTCAGATCACTGAGGCACAAAACCTTTT

GATACTTTGCTTTCCTTGAACCTCAGATTACACCCACCAGGGCTGGAGGCCAGACCCGGGAAGAGAAGG
 TCCTTGAGTTGGCCGCTGATGTGAAGCAGAAGATCCCTGAAATGATCGACTATGAGGGGACTCAAAAAC
 GCTAGCTCTCGACCCCTCCCCCTCAATGTGGTCTTCTCGAGGAGATCCAGAGATACAACACACTGATG
 CAGACCATCCTGTTCTACTGACAGACCTAGAGAAAGGCATCCAGGGTCTCATCGTCATGTCTACAAGCC
 TGGAAGAGATTTCAATTGCATCTTTGATGCCATGTTCTCCGCTCTGGGAAAGGCATACCCCTCACA
 AAAGCCATTGGCTGCCTGGACCCGGGACTTGGCCATGCGTGTGGAGCAGTTTGAGCTGTGGGCCAGCCGG
 GCCCGCTCTGTGATCTTCTGGTTGCTGGTTTACCTTTCCACTGGCTTCCCTCACTGCTGTGCTGC
 AGTCTTACAGTCGCCAAAACAACGTTTTCAGTGGACAGCCTCTCCTGGGAGTTTATCGTTTCCACTTGGA
 TGACAGCAACCTAGTGTATCCCCCAAGGATGGTGTCTGGGTCCGGGGCCTGTACCTGGAAGGTGCTGGC
 TGGGACCGGAAGAACTCTGCTTGGTGGAGGCAGAGCCCATGCAGCTTGTCTGCCTCATGCCACGATCC
 ACTTCCGGCTGCAGAGAGCCGCAAGAAGAGCGCAAGGGCATGTACTCTGCCCTGCTATTACTATCC
 CAACCGGGCAGGCAGCTCAGACCGAGCCTCTTTGTATCGGCATTGACCTGCGGTCTGGGGCCATGACA
 CCTGATCATTGGATCAAGAGGGGACTGCTCTACTCATGAGCCTGGACAG

AGCGGACCGACGCGTACGCGGCCGCTCGAG - GFP Tag - GTTTAA

Protein Sequence:

>RG220074 representing NM_020877

Red=Cloning site Green=Tags(s)

MSSKAEEKQRLSGRGSSQASWSGRATRAAVATQEQGNAPAVSEPELQAELPKEEPEPRLEGPOAQSEESV
 EPEADVPLFLSRAAL TGLADAVWTQEHDAILEHFAQDPTESIL TIFIDPCFGLKLELGMVQVTQNLVY
 FIRQAPVPITWENFEATVQFGTVRGPYIPALLRLLGGVFAPQIFANTGWPE SIRNHFASHLHKFLACLTD
 TRYKLEGHTVLYIPAEAMNMKPEMVIKDKELVQRLETSMIHWTRQIKEMLSAQETVETGENLGPLLEEIEF
 WRNRCMDL SGISKQLVKKGVKHVESILHLAKSSYLAPFMKLAQQIQDGSRAQSNLTFLSILKEPYQELA
 FMKPKDISSKLPKLI SLIRI IWVNSPHYNTRERL TSLFRKVCDCQYHFARWEDGKQGPLPCFFGAQGPQI
 TRNLEIEDIFHKNLHTLRAVRGGILDVKNCTWHEDYNKFRAGIKDLEVMQNLITSAFELVRDVPHGVL
 LLDTFHLASREAIKRTYDKKAVDL YMLFNSELALVNRERKWPDL EYVAQYSGKARVWHILRRRIDR
 VMTCLAGAHFLPRIGTGKESVHTYQQMVQAI DELVRKTFQEWTS SLDKDCIRRLDTPLLRISQEKAGMLD
 VNFDKSLLILFAEIDYWERLLFETPHYVVNVAERAEDLRILRENLLL VARDYNRI IAMLSPDEQALFKER
 IRLLDKIHPLGLKHLHWALKGASAFFITECRIHASKVQMI VNEFKASTLTIGWRAQEMSEKLLVRI SGKR
 VYRDLEFEEDQREHRAAVQQKLMNLHQDVVTIMTNSYEVFKNDGPEIQQQWMLYMI RLDRLMMDALRLNV
 KWSLLELSKAI NGDGKTSNPLFQVLVILKNDLQGSVAQVEFSPTLQTLAGVVNDIGNHFLSTISVFC
 PDILT KRKLHREPIQT VVEQDEDIKKIQTQISSGMTNNASLLQNYLKTWDMYREIWEINKDSFIHRYQRL
 NPPVSSFVADIARYTEVANNVQKEETVTNIQFVLLDCSHLKFSLVQHCNEWQNKFATLLREMAAGRLEL
 HTYLKENAEKISRPPQTL EELGVSLLVDALKHDLANVETQIPPIHEQFAILEKYEVPVEDSVLEMLDSL
 NGEWVVFQQTLLDSKQMLKKHKEKFKTGLIHSADDFKKAHTLLEDFEFKGHFTSNVGYMSALDQITQVR
 AMLMAMREEENSLRANLGI FKIEQPPSKDLQNL EKELDALQIWEIARDWEENWNEWKTGRFLILQTE
 ETTAHGLFRRLTKLAKEYKDRNWEI IETTRSKIEQFKRTMPLISDLRNPALRERHWDQVRDEIQREFDQE
 SESFTLEQIVELGMDQHVEKIGEISASATKELAEI VALQNI AKTWDVTQLDIVPYKDKGHRLRGTEEVF
 QALEDNQVALSTMKASRFVKA FEKDVVDHWRCLSLILEVIEMILTVQRQWMYLENIFLGEDIRKQLPNES
 TLFDQVNSNWKAIMDRMKN DNNALRSTHHPGLD TL IEMNTILEDIQKSLDMYLETKRHIFPRFYFLSND
 DLLEILGQSRNPEAVQPHLKKCFDNIKLLRIQKVG GPSSKWEAVGMFSGDGEYIDFLHVSFLEGPVESWL
 GDVEQTMRVTLRDL LRNCHLALRKFLNKRDKWKEWAGQVVITASQIQWADVTKCLLTAKERADKKILK
 VMKKNQVSI LNKYSEAIRGNLTKIMRLKIVALVTIEIHARDVLEKLYKSGLMDVNSFDWLSQLRFYWEKD
 LDDCVIRQNTNTQFQYNYEYLGN SGRLVITPLTDRCYMTLTTALHLHRGGSPKGPAGTGKTETVKDLGKAL
 GIYVIVNCSEGLDYKSMGRMYSLAQTGA WCFDEFNRINIEVL SVVAHQILCILSALAAGLTHFHFDG
 FEINLVWSCGIFITMNPYAGRTEL PENLKSFRPIAMVVPDSTLIAEILFGEFGNCKILAKKVVYTL
 SLAVQQLSRQDHYDFGLRALTSL LRYAGKRRRLQPDLTDEEVL LLSMRDMNIAKLTSVDAPL FNAIVQDL
 FPNIELPVIDYGLRETVEQEIRDMGLQSTPFTLTKVFQLYETKNSRHSTMI VGTGSGKTASWRILQAS
 LSSLCRAGDPNFNIVREFPLNPKALSLGEL YGEYDLSTNEWTDGILSSVMRTACADEKPDEKWLFDGPV
 DTLWIENMNSVMDDNKVLT LINGERIAMPEQV SLLFEVEDLAMASPATVSRGMVYTDYADLGWKPYPVQS
 WLEKRPKAEVEPLQRMFEKLINKMLAFKKNCKELVPLPEYSGITSLCKLYSALATPENGVPADGENYV
 TMVEMTFVFSMIWSVCASVDEEGRKRIDSYLREIEGSFPNKD TVVEYFVDPKIRSWTSFEDKLPKSWRYP

PNAPFYKIMVPTVDTVRYNYLVSSLVANQNPILLVGPVGTGKTSIAQSVLQSLPSSQWSVLVVNMSAQT
 SNNVQSIIESRVEKRTKGVYVPPFGGKSMITFMDDLNPAPKDMFGSQPPELIRLWIDYGFWDRTKQTIK
 YIREMFLMAAMGPPGGRTVISPRLSRFNIINMTFPTKSQIIRIFGTMINQKLQDFEVEVKPIGNVTE
 ATLDMYNTVVQRFLPTPTKMHYLFNLRDISKVFQGLRANKDFHDTKSSITRLWIHECFRVFSDRLVDA
 DTEAFMGIISDKLGSFFDLTFHHLCPKSRPPIFGDFLKEPKVYEDLTDLVTKVMETALNEYNLSPSVV
 PMQLVLFREAIEHITRIVRVIGQPRGNMMLLVGIGGSGRQSLARLASSICDYTFQIEVTKHYRQKQFRDD
 IKRLYRQAGVELKTTSFIFVDTQIADESFLIEDINNILSSGEVFNLYKPDFEVEIQSHIIDQARVEQVPE
 SDSL FAYLIERVQNLHIVLCLSPMGDPFRNWIRQYPALVNCTTINWFSEWPQEALLEVAEKCLIGVDLG
 TQENIHRKVAQIFVTMHWSVAQYSQKMLLELRRHNYVTPTKYLELLSGYKLLGKQRQELLAQANKLRTG
 LFKIDETREKVQVMSLELEDAKKKVAEFQKQCEEYLVIIIVQKREADEQQKAVTANSEKIAVEEIKCQAL
 ADNAQKDEEALPALEEAMRALESNKKDIGEIKSYGRPPAQVEIVMQAVMILRGNEPTWAEAKRQLGEQ
 NFIKSLINFDKDNISDKVLKIGAYCAQPDFQPDIGRVSAAKSLCMWVRAMELYGRLYRVVPEKIRIM
 NAALAQREKQAALAEAEQKLEVAEKLEMLKKQYDEKLAQKEELRKKSEEMELKLERAGMLVSLGAGEK
 ARWEETVQGLEEDLGYLVGDCLLAAFLSYMGPFLTNYRDEIVNQIWIWIKIWEVQVPCSPSFAIDNFLCN
 PTKVRDWNIQGLPSDAFSTENGIIVTRGNRWALMIDPQAQALKWIKNMEGGQGLKIIDLQMSDYLRILEH
 ATHFGYPVLLQNVQEYLDPTLNPLNKSVARIGGRLLMRIGDKEVEYNTNFRFYITTKLSNPHYSPE
 TSKTTIVNFAVKEQGLEAQLLGIVVRKERPELEEQKDSLVINIAAGKRKLKELEDEILRLLNEATGSLDDV
 QLVNLTHTSKITATEVTEQLETSETTEINTDLAREAYRPAQRASILFFVLNDMGCIDPMYQFSLDAYIS
 LFIILSIDKSHRSNKLEDRIDYLDNYHTYAVYRYTCRTEFERHKLKLSFHMCAKILETSGLKNMDEYNFFL
 RGGVLDREGQMDNCPSSWLADAYWDNITELDKLTFNHGLMNSFEQYPRDWHLWYTNAPEKAMLPGEWE
 NACNEMQRMLIVRSLRQDRVAFVTSFIIITNLGSRFIEPPVLMKSVLEDSTPRSPVILSPGVDPTSA
 LLQLAEHMGMAQRFHALSLGQGQAPIAARLLREGVTQGHVWFLANCHLSLWMPNLDKLEQVQVEDPH
 SFRLWLSIPHPDFPISILQVSIKMTTEPPKGLKANMTRLYQLMSEPQFSRCSKPAKYKLLFLSLCFFHS
 VLLERKKFLQGWNIYGFNDSDFEVSLENLLSLYLDEYEETPWDALKYLIAGINYGGHVTDDWDRRLTT
 YINDYFCDQSLSTPFHRLSALEYFIPKDGSLASYKEYISLLPGMDPPEAFGQHPNADVASQITEAQLF
 DTLLSLQPQITPTRAGGQTRREEKVLAAADVKQKIPEMIDYEGTQKLLALDPSPLNVLLQEIQRYNTLM
 QTILFSLTDLEKGIQGLIVMSTSLLEEIFNCIFDAHVPLWGKAYPSQKPLAAWTRDLAMRVEQFELWASR
 ARPPVIFWLSGTFPTGFLTAVLQSSARQNNVSDSLSWEFIVSTVDDSNLVYPPKDGWVVRGLYLEGAG
 WDRKNSCLVEAEPMLVCLMPTIHFRAESRKKSAKGMYSKPCYYPNAGSSDRASFVIGIDLRSAMT
 PDHWIKRGTALLMSLDS

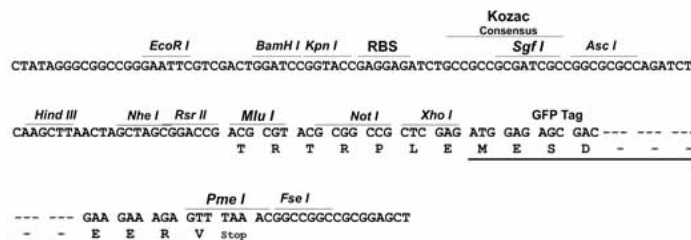
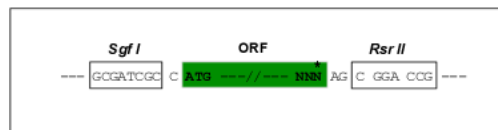
SGPTRRRLE - GFP Tag - V

Restriction Sites:

SgfI-RsrII

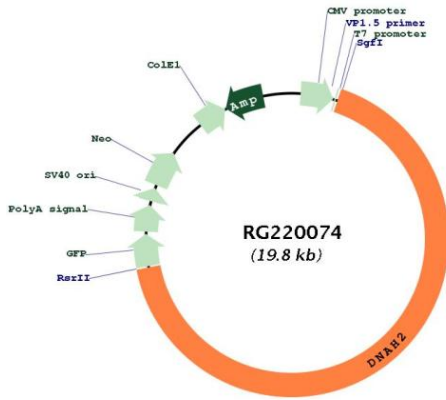
Cloning Scheme:

Cloning sites used for ORF Shuttling:



ACCN:	NM_020877
ORF Size:	13281 bp
OTI Disclaimer:	<p>Due to the inherent nature of this plasmid, standard methods to replicate additional amounts of DNA in E. coli are highly likely to result in mutations and/or rearrangements. Therefore, OriGene does not guarantee the capability to replicate this plasmid DNA. Additional amounts of DNA can be purchased from OriGene with batch-specific, full-sequence verification at a reduced cost. Please contact our customer care team at custsupport@origene.com or by calling 301.340.3188 option 3 for pricing and delivery.</p> <p>The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing variants is recommended prior to use. More info</p>
OTI Annotation:	This clone was engineered to express the complete ORF with an expression tag. Expression varies depending on the nature of the gene.
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:	<ol style="list-style-type: none"> 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_020877.2 , NP_065928.2
RefSeq Size:	13505 bp
RefSeq ORF:	13284 bp
Locus ID:	146754
UniProt ID:	Q9P225
Cytogenetics:	17p13.1
Protein Pathways:	Huntington's disease
Gene Summary:	<p>Dyneins are microtubule-associated motor protein complexes composed of several heavy, light, and intermediate chains. The axonemal dyneins, found in cilia and flagella, are components of the outer and inner dynein arms attached to the peripheral microtubule doublets. DNAH2 is an axonemal inner arm dynein heavy chain (Chapelin et al., 1997 [PubMed 9256245]).[supplied by OMIM, Mar 2008]</p>

Product images:



Circular map for RG220074