

5'
3'

ACAGTGC GCGTGC GCTTAT CCTGTCCC AGGTGTCC AGCTTT GTGCCTG ATTGATG TAATCCC GGTGCG GTTCGG TGCAGT TTTT
TGTCA CGCGC AC CGGA ATAGG ACAGGG TCCAC AGGTGC AAAACAC GGGACTA AACTAC ATTAGGG CCGAC GCGCAG CCACG CGTCA AAAA

85

DCTN1 >

CAGTCAGGGCTGGACTGCGGGAAAAAGAGGGTTCACTCGACCCAGAACGCCTCTGGGCCTCTGGGCCGAAGGGTTCTGGGCGGTCC
GTCAGTCCC GACCTG AC GCGCCT TTTTCT CCAAGT GAGCTGG GTCTT GCGGAG ACCCGG AGACCC GGCTTCC CAAGAC CC GCGCAG G

170

DCTN1 >

TGGAAGGGTCTGGCGGCGAGTCGGGCAGCCACGAGGGCGGGGAGGGCGGGGCCGGCCCCGAGGGTCTTGGGCGTCGGTCGTCG
ACCTTCCC AGACCG CCGCTC AGCCCG TCGGGT GCTCCC GCGCCCT CCCGCCCC GGCCGGGG CGTCCC AGAACC CGCAGC CAGCAG C

255

DCTN1 >

GTGGGGTCGGAGCTGGGCGCGGAGCCCTCACAGTGCAGGTACGGAGGCGGACTCTGCCAACCGTCTGCTCCGCGGCCCCCTA
CACCCAGCCTCGACCCGCGCCTCGGGGAGTGTACAGTCCATGCCTCCGCGCTGAGACGGTTGGCAGACGAGGCGGCCGGGGGAT

340

DCTN1 >

CGTGTTCTGTGAGGTTGCCGGCGGTGGGCTGGGGACCGAGCCCGGTGTGCGGGGCGGGGACTGGCAGGGGTGGGCGCTTGTGCGGG
GCACAAGCACTCCAACGGCCGCCACCCGACCCCTGGCTCGGGCCACACGCCCCGCCCTGACCGTCCCCACCCGCGAACAGCCCC

425

DCTN1 >

TCCGGGGGCTCCGCCTGAGCGTTTGCCCCGAGGGCCGGTCTGACCCACCTCAGCTCTTCAGCCTAGCATTGTTCTCCTGGGATCAG
AGGCCCCCGAGGCGGACTCGCAAACGGGGCTCCGGCCAGACTGGGTGGAGTCGAGAAGTCGGATCGTAACAAGAGGACCCCTAGTC

510

DCTN1 >

AGTGACTGCGCCTTAGAGTTCCTCCAGAACTGCAAGGGTCTCCCCTCCGTTCTGCGAGCGTCTGAGGCGCCCCTGAATCCATAC
TCACTGACGCGGAATCTCAAGGAGGTCTTGACGTTCCAGAGGGGAGGCAAGGACGCTCGCAGACTCCGCGGGGACTTAGGTATG

595

DCTN1 >

TGAGCTACAGGTTTCTGTGGGCACATGGTTGAGAAATTCGTCTCAAACGGGGAGAAAAATCGTAAAGGACTCACAGCATGGGAG
ACTCGATGTCCAAAGGACACCCGTGTACCAACTCTTTAAGCAGAGTTTGCCCTCTTTTTAGCATTTCCTGAGTGTGCTACCCCTC

680

DCTN1 >

TCTGGATATGACTTGTGTGTGATCCTACTCCTGGGGTCCGCCTTAGCTGGCAAGATGATCCTTGAGGTCATCTTGCGCATCCC
AGACCTATACTGAACACACACACTAGGATGAGGACCCAGGCGGAATCGACCGTTCTACTAGGAACTCCAGTAGAACGCGTAGGG

765

DCTN1 >

TTGTCTTTAGACAGAACCACAGCTAAATCACACAGATAAGGATCTCTGCTGTTTCAGAGGCAGGGATTTGAAAACCTTACCGTCAT
AACAGAAATCTGTCTTGGTGTGATTTAGTGTGTCTATTCTAGAGACGACAAAGTCTCCGTCCCTAAACTTTTGAATGGCAGTA

850

DCTN1 >

TTATTGCAGTGAGGAGAGCAGCAAACCCATGTTGACCACTGGCTACTCAGGTATACTTAAGGTACCGAGAGGCGAAGAGCTAGGA
AATAACGTCACCTCCTCTCGTCGTTTTGGGTACAACCTGGTGACCGATGAGTCCATATGAATTCCATGGCTCTCCGCTTCTCGATCCT

935

DCTN1 >

GGTAGAGATTGACATCCTTTACTTAATGTACTGCCAAAGCCTAAGCTATGAGATGTTAAAAGAGATAATGATAACTTTATTTTTA
CCATCTCTAACTGTAGGAAATGAATTACATGACGGTTTTCGGATTTCGATACTCTACAATTTTTCTCTATTACTATTGAAATAAAAAAT

1020

DCTN1 >

AAAAAGGCATTTTGTTCGAAAAGCTGTTGGAAAATTCGTGGTTAAACTTTACTACAGAATATTGCAGAGCCTTTAATATGCTAA
TTTTTCCGTAAAAACAAAAGCTTTTCGACAACCTTTTAAGCACCAATTTGAAATGATGTCTTATAACGTCTCGGAAATTATACGATT

1105

DCTN1 >

TAATATTTACCATGAATCTCCAACCTGGGGGTATGGTATGTAGAATTTTGGAAAATTTTACTAGGATATACTGTTATTCTTGGGTGA
ATTATAAATGGTACTTAGAGGTTGACCCCATACCATACATCTTAAAACCTTTTAAAATGATCCTATATGACAATAAGAACCCTACT
DCTN1

1190

TGCCTCTGGCTAACATGTGGGAACCGTTTGGGAATTGGAGTTCCAGAATTAGAAATTCAGGATTTAGAAGGGGCAGTATGGGTCA
ACGGAGACCGATTGTACACCCTTGGCAAACCTTAACCTCAAGGTCTTAATCTTTAAGTCTTAAATCTTCCCCGTCATACCCAGT
DCTN1

1275

GTGCGCTTTGAGTTTTAATGGCGTGACATGTAATGCGATCTCGTTACAGTACAGATTCTGATTGGTTCTGCATTTCTAACAAGT
CACGCGAAAACCTCAAAATTACCGCACGTGTACATTACGCTAGAGCAATGTCATGTCTAAGACTAACCAAGACGTAAAGATTGTTCA
DCTN1

1360

TCCAGGTGATGCTAATGCTGCTGGCCCATGGAACACAATCTGAGTAGCAAAAAGTATAGATCACTGGATTGAAAAGTTAGAGACCA
AGGGTCCACTACGATTACGACGACCGGGTACCTTGTGTTAGACTCATCGTTTTTCATATCTAGTGACCTAACTTTCAATCTCTGGT
DCTN1

1445

TGTTTTCCAGAACAGATGTGCTGCCTTGAGAGAGTCACTTTATCTGTCCAGGCCTATAAGGTAGGAGTCTGGACTACAAGATCTC
ACAAAAGGTCTTGTCTACACGACGGAACCTCTCTCAGTGAAATAGACAGGTCCGGATATTCCATCCTCAGACCTGATGTTCTAGAG
DCTN1

1530

AAATATTTCTTTCAGATTTAAAATCTGTGAGTCTAGTCGAGTTATCCCTGTAGTGTGAAATCTATCTGAAAATTTCTTGCCAA
TTTATAAAGAAAGTCTAAATTTTAAAGACACTCAGATCAGCTCAATAGGGACATCACAACTTAAGATAGACTTTATAAGAACGGTT
DCTN1

1615

TTTGGCAAATTTTGCAGCTTGGCTTGAACATTTAAAATAATGGGCAATTATCTGCATATAGGGCATCCCATTTTATTCTTGGAAAT
AAACCGTTTTAAAACGTCGAACCGAACTTGTAAATTTTATTACCCGTTAATAGACGTATATCCCGTAGGGTAAAATAAGAACCTTA
DCTN1

1700

AGCTCAAGAAGGAAGTTCTTCATGTTGCTGAAATACATCTCTGCAACTTCCATGCTGTTGGTCCTAGATTATCTCTTAAACAATCA
TCGAGTTCTTCTTCAAGAAGTACAACGACTTTATGTAGAGACGTTGAAGGTACGACAACCAGGATCTAATAGAGAATTGTTAGT
DCTN1

1785

AACAGGAAAGAAGTGTTACCCGTCTTCTAAAATGTTGACTCCAAGTATTAGATGACAGCTGTGCCTACTATGATTTTTCTAAGC
TTGTCTTTTCTTCACAATGGGCAGAAGGATTTTACAACCTGAGGTTTATAATCTACTGTGACACGGATGATACTAAAAAGATTCTG
DCTN1

1870

GGAATTGTATTTAATTCTTCCATTATGTTTAAAGAAATCCCTTTCTTAAATTTGCTTTGTTCTCTGTGGAGTGTAGTGGGGCTTT
CCTTAACATAAATTAAGAAGGTAATACAAATCTTTAGGGAAAAGAATTTAAACAGAAAACAAGAGACACCTCACATCACCCCGAAA
DCTN1

1955

GGCTGGACTTTGAAGGATGGGTGTGGCTTGAAGACTAGAAAAGTATCTTAAAGCAGTTGACACTGGTGCAGAGATGGGACTGCAT
CCGACCTGAAAACCTTCTACCCACACCGAACGTTCTGATCTTTTTCATAGAATTCGTCAACTGTGACCACGTCTCTACCCTGACGTA
DCTN1

2040

CTGTTGAATCCAGGATTGTTTGAATTATAGTAAGAAATGAGATTATCAGTGAAAAGATGTCGGGCAGATGGGTGTAGGGACAAAGCA
GACAACCTTAGGTCTTAACAAACTAATATCATTCTTTACTCTAATAGTCACTTTCTACAGCCCGTCTACCCACATCCCTGTTTCGT
DCTN1

2125

GTATTTTAGCAGATGTATGTGCTTTACTGTGATGTATAAGGTGGTTGGAACCTAGGGAAGGAGGGGGAGACGGAGCTGGATAGGCT
CATAAAATCGTCTACATACACGAAATGACACTACATATTCCACCAACCTTGATCCCTTCTCCCCCTCTGCCTCGACCTATCCGA
DCTN1

2210

TCACATAGCAATATTAGACAATTTAGGTTGATAATAATAATGCCTTATATTTTATGTATGACACTTTACAGAAGCTTTTCACAGGCA
AGTGTATCGTTATAATCTGTTAAATCCAACCTATTATTATTACGGAATATAAATACATACTGTGAAATGTCTTGAAAAGTGTCCGT

2295

DCTN1

TGATTTCAATTTGATCTAATATTCCTACGAGGTAGGCAGAGCAGCTGTTATGCTGTTTTGTTAGATGATGCACCAAAGAGGGTAAAT
ACTAAAGTAAACTAGATTATAAGGATGCTCCATCCGTCTCGTCGACAATACGACAAAAACATCTACTACGTGGTTTTCTCCCATTTA

2380

DCTN1

GATTTGCCTTAATTTTCAAAGCTATTACATGGCAGACTGAAGTAGTGATAGTGATAATGGAGGAGAAAAGGAAAAGATGCAGGAGGC
CTAAACGGGAATTTAAAAGTTTCGATAATGTACCGTCTGACTTCATCACTATCACTATTACCTCCTCTTTCTTTCTACGTCTCTCCG

2465

DCTN1

AGTACTAAGGACGAATTGATAAGTGGGGCCTGACTGACCATGAGGGTACAAAGGAGAAGAAGTTGTTAGGGAGGAGTCAAAGTAG
TCATGATTCCTGCTTAACTATTACCCCGGACTGACTGGTACTCCCATGTTTCTCTTCTTCAACAATCCCTCCTCAGTTTTCATC

2550

DCTN1

TTGGGTGAATCATAATACCATTGAGAACTGCCACTCTAGGTTTTACTCTGCCAGCTCTATCATTGCTAGCAGCTGCTTGGAGTTA
AACCCACTTAGTATTATGGTAACTCTTGACGGTGAGATCCAAAATGAGACGGTCGAGATAGTAACGATCGTCGACGAACCTCAAT

2635

DCTN1

TAGGTTGAAAGGGATTATAGATGATTCACAGGTTGCTTGGCCTGTCTACAGCTACTAGGTGATACTGGGGGCACTTGGGCTATCT
ATCCAACCTTTCCCTAATATCTACTAAGGGTCCAACGAACCGGACAGATGTCGATGATCCACTATGACCCCGTGAACCCGATAGA

2720

DCTN1

GTCCCATACCAAGGAAAATAGGAACTCGGTCCTCAGTGTCCCCTGAAGATGTAAGAGCTGGAATATTGCCAGATTCATATCTATA
CAGGGTATGGTTCCCTTTTATCCTTGAGCCAGGAGTCAAGGGGACTTCTACATTCTCGACCTTATAACGGTCTAAGTATAGATAT

2805

DCTN1

TTAAGGTCCTTGCCATCCTGGAGACTCTGACTTTGGCTTTGTATCATTTTCTTTTGGAGATTCAGGCTGATGTTAGTTGAATGTG
AATTCAGGAACGGTAGGACCTCTGAGACTGAAACCGAAACATAGTAAAAGGAAAACCTAAGTCCGACTACAATCAACTTACAC

2890

DCTN1

ATCAAGGGACAGGTTAGCTATTTAGTCTGGCCTCCCAAGGGCTTCACTACAGCAGAGCATGGGCCCTTGCTGCCCAAATCCTT
TAGTTCCCTGTCCAATCGATAAATCAGACCGGAGGGGTTCCCGAAGTGATGTCGTCTCGTACCCGGGAACGACGGGGTTTAGGAA

2975

DCTN1

CCTAATGCTGTTTCCAGGAGATTTGCACCTCACCTAGAGCTGTCTCTGTGGTTCTTTTACCCTGAAAGTATACAGGATTGAGAT
GGATTACGACAAAAGGTCCTCTAAACGTGGAGTGGATCTCGACAGAGACACCAAGAAAATGGGACTTTTCATATGTCTCTAACTCTA

3060

DCTN1

TTAGTGTCACTACCAAATTCATAGGACCTAGGGCTGTTTCTGCACTTTTAGTTTTCTTAGGCTTCTGTCTGGAGTGGAAAAGAGCC
AATCACAGTGATGGTTTTAAGGTATCCTGGATCCCGACAAGGACGTGAAAATCAAAGAATCCGAAGACAGACCTCACCTTTCTCGG

3145

DCTN1

ATGTTTACTGAGGGTTAGGGGAGAGATGTGTGTGTGCGTACATATGTGCACATAAGTGGTGATTTCCCAAGTGGTGGTGGTCTTC
TACAAATGACTCCCAATCCCTCTCTACACACACACGCATGTATACACGTGTATTACCACCTAAAGGGGTCACCACCACCAGAAG

3230

DCTN1

AAGAGTGGAGCTACTCTCAGGGAAAAGCTGTCAGAGCCAGTTTATATCCTGAGTGTGATGTTGGTACAGGCATCTATTCAACATTG
TTCTCACCTCGATGAGAGTCCCTTTTCGACAGTCTCGGTCAAATATAGGACTCACACTACAACCATGTCCGTAGATAAGTTGTAAC

3315

DCTN1

AATACCTTCTCTTTGCAAAGCCCTACGCCGAGTGCTTAGATACTGAGATGGATACAATCCTCTGTCTCTGGAGGAATTCATAGTAG
TTATGGAAGAGAAAACGTTTCGGGATGCGGCTCACGAATCTATGACTCTACCTATGTTAGGAGACAGGACCTCCTTAAGTATCATC
DCTN1

3400

AGTAAGAGATGATATTTTAAATAGAATGTGGTATTGAAATGGAGATATGTCTCAAGTGCTCTGTGAGCACAGAGGAGGGAATGAT
TCATTCTCTACTATAAAAATTTATCTTACACCATAAATTTACCTCTATACAGAGTTCACGAGACACTCGTGTCTCTCCCTTACTA
DCTN1

3485

TAGCTCCACATGGAGAAGCCAGGAGAGTCTTTAGGAAAAGAGGTGAGAATTGGGCTGAGCCTTGAAGGATGAGGAGGAAGAATTGT
ATCGAGGTGTACCTCTTCGGTCTCTCAGAAATCCTTTCTCCACTCTTAACCCGACTCGGAACTTCTACTCTCTCTCTTAACA
DCTN1

3570

CCTGGTGACATTTGTAACATTTGCAGATGCATAAAGGGAAAGGCAGATAGATCCAAGTGGCTGGAATAAAAAGAGAACTTTGGTGA
GGACCACTGTAAACATTGTAAACGTCTACGTATTTCCCTTTCCGTCTATCTAGGTTTACCGACCTTATTTTCTCTTGAAACCACT
DCTN1

3655

TTGATGCGACCGGATTCATAATGAAGCCATGTTGTTTTATTTGTTTTGTTTGTAGAGATGGGGTATCACTATGCTGCCAGGC
AACTACGCTGGCCTAAGTATTACTTCGGTACAACAAAATAAAAACAAAACAACAAATCTCTACCCCATAGTGATACGACGGGTCGG
DCTN1

3740

TGGAGTGCAGTGGCTATTCACAGACAAGATCATCACGCACTACAGCCTTGAACCTCTGGCCTCAAGTGATCCCCCTCAGCCTCCT
ACCTCACGTACCGATAAGTGTCTGTTCTAGTAGTGCGTGATGTCGGAACCTTGAGGACCGGAGTTCCTAGGGGGAGTCGGAGGA
DCTN1

3825

GAGTATAGGTGGGTCTGCAGGCTGCTGTGCCAGTTTGAGGCCAGTTTTTTGTTTTGTTTTGTTTTGAGATACAGTCTTGCTCTG
CTCATATCCACCCAGACGTCCGACGACACGGTCAAACCTCCGGTCAAAAAACAAAACAAAACAAAACCTCTATGTCAGAACGAGAC
DCTN1

3910

TCAACCAGGCTGGAGTGTGGTGGTGAGATTTTGGCTCACTGCAACCTCCTGAGTAGTTGGGACTATAGCTACTACAGGTGGGACT
AGTTGGTCCGACCTCACACCACCACTCTAAAACCGAGTGACGTTGGAGGACTCATCAACCTGATATCGATGATGTCCACCCTGA
DCTN1

3995

ACTTAGCCTCCTGAGTAACTGGTACTATAGGCATGCACCACCACACCCAGCTAATTTTTGTATTTTTAGTAGAGACAGGCTT
TGAATCGGAGGACTCATTGACCATGATATCCGTACGTGGTGGTGGTGGGTCGATTAAAAACATAAAAAATCATCTCTGTCCGAA
DCTN1

4080

TCACCATGTTGTCCAGGCTGATCTCAAACCTCCTGGCCTCAAGTGATCTGCCCGCCTTGGGCTCTCAGAGTGCTAGGATTACAGGT
AGTGGTACAACAGGTCCGACTAGAGTTTGAGGACCGGAGTTCCTAGACGGGCGGAACCCGAGAGTCTCACGATCCTAATGTCCA
DCTN1

4165

GTAGCCACTGTGCTTGGTCAAGGCCAGGTTGTTAATGGCCTGTAGTGCAAGTGCTAAAAAGATTTTCATTTTGTGGGCAGAGAAGCC
CATCGGTGACACGAACCAAGTTCCGGTCCAACAATTACCGGACATCACGTACGATTTTTCTAAAGTAAAAACACCCGTCTCTTCGG
DCTN1

4250

ACTGGAGACTTTTAGGCAGGAAGATGACATGATTGTATTTGGGAAGCTAAATGTGGAAATTGAAGGGGGAGAACCTGGTTCAGG
TGACCTCTGAAAAATCCGTCTTCTACTGTACTAACATAAAAACCTTCGATTTACACCTTTAACTTCCCCCTCTTGGAACCAAGTCC
DCTN1

4335

GACATCGGGAGACTCTTGTAATATCATAGACATGGTTTAGGGCTGAGCTAAGGATTAGGTCAGTGGGGATAGAGAGGACAGGATG
CTGTAGCCCTCTGAGAACATTATAGTATCTGTACCAAATCCCGACTCGATTCTAATCCAGTCACCCCTATCTCTCTCTGTCTTAC
DCTN1

4420

AATCTGAGAGAGACTGGAGAAACAGAATTAACCAGACATAATGACTAAATTGGTTGTTGAGAACAAGAGAGGGGAGTTGTTGCGGA
TTAGACTCTCTCTGACCTCTTTGTCTTAATTGGTCTGTATTACTGATTTAACCAACAACCTCTTGTCTCTCCCTCAACAACGCCT
DCTN1

4505

TGACTCAGTTTTCTATTTTGAGTGGATGGTGGTGCCAATAGCAAAGAGAGAATATAGAAGAAGAACTTTTTTTGTTTGTGTTGTT
ACTGAGTCAAAAAGATAAAAACCTCACCTACCACCACGGTTATCGTTTTCTCTCTTATATCTTCTTCTTGAAAAAAAACAAACAAACAA
DCTN1

4590

TTTGGTGGGGGAGATACCAAGTGTGTTTTGGGTCAATTTGAACTTGAGGGCTCTGTGGCAGTTAGCAGACAGTGAGATATGAGTC
AAACCACCCCTCTATGGTTCACACAAAACCCAGTATAAATTGAACTCCCGAGACACCGTCAATCGTCTGTCACTCTATACTCAG
DCTN1

4675

TGAAGTTCAGAAGAGTTTCTGTCTAGGGGCAGTAAGTATGAGTGGTAGTTGAAAGTTGTGGGAATGGTTGAGGTCTCCAGCCACG
ACTTCAAGTCTTCTCAAAGACAGATCCCCGTCAATTCATACTCACCATCAACTTCAACACCCCTTACCAACTCCAGAGGGTTCGGTGC
DCTN1

4760

CTTACAGAAGGCTGAAAATAATGACAGAGGAGATGAGAAGGATTGACGTGCAAGGGTAGGAGAGAATGTTGCCAGGAAGCTAGG
GAATGTCTTCCGACTTTTATTACTGTCTCCTCTACTCTTCTAACTGCACGTTCCCATCCTCTCTTACAACGGGTCTTTCGATCC
DCTN1

4845

AAAGGAGAAAATTCAGGAAAAGGATTGACAATCTCAGTTGCTACAGGGAGATCAAGTTAGGATGAGCTTGGGAAATGCACCTTG
TTTCTCTTTTAAAGTCTTTTCTAACTGTTAGAGTCAACGATGTCCCTCTAGTTCAATCCTACTCGAACCCCTTACGTGGAAC
DCTN1

4930

AGGTTGTGTAGGACATTGGGGTCACCAGGGCTCTTTTAAAGTGTGAGCAGCTTCAGTGGAGTGGTAGGGATGGAGCCAGATAGCA
TCCAACACATCCTGTAACCCCAAGTGGTCCCGAGAAAATTTCACTCTCGTGAAGTCACTCACCATCCCTACCTCGGTCTATCGT
DCTN1

5015

ATGGATCGAGAAGTAGATGGGAAGTGAAGATAGAGAATGTGTAICTCACTTTGAGTAGTTCAGCAGAGAAAAGGAAGAAACAGAAT
TACCTAGCTCTTCATCTACCCTTCACTTCTATCTCTTACACATGAGTGAAACTCATCAAGTCGTCTCTTTCTTCTTATGTCTTA
DCTN1

5100

GGTGGCAGCTTGTGGAAGAGGTAGCAGGGACTTGTTCCTAGAATGGAAGTCTTGTATTGGGTTTTCTGATGCCATGTAAGA
CCACCGTCGAACACCTTCTCCATCGTCCCTGAACA AAAAGGATCTTACCTTCAGAACA AATACCCAAAAGACTACGGTACATTCT
DCTN1

5185

TCCAGTAGACAGGGTGCAATGAAGACACAAGAGAAAAGACGATTGCTAAATCAAGTCCTCAGAGGAGAGGGGAAGGGGTGGGCC
AGGTCATCTGTCCACGTTACTTCTGTGTTCTCTTTTCTGCTAACGATTTAGTTTCAGGAGTCTCCTCTCCCTTCCCAACCCGGG
DCTN1

5270

TGAAAAGAAGGGGATACCATTTTCTTTAAAGAGGAATGTTGGAAGAAAAGGAAGGAATTTAGGAAGAAAAGAGATAATGACATATGC
ACTTTTCTTCCCTATGGTAAAAGAAAATTTCTCCTTACAACCTTCTTTCTTCTTAAATCCTTCTTTCTCTATTACTGTATACG
DCTN1

5355

ATGCAGATATATCTAAATTTTCAAAGAAATCTTACCTAATAGGGCCAGTTTTCTTTTTTCAGCAAGGTTATCTGCTGAGAGGTGG
TACGTCTATATAGATTTAAAAGTTTCTTTAAGAATGGATTATCCCGGTCAAAGAAAAGTTCGTTCCAATAGACGACTCTCCACC
DCTN1

5440

GAATGCTGGTGTGGCTTGGGTGGGAGTAAGGACTTGAAAATGTAAAGGAAGCTTGAAAATAACTGTTAAGAGGAAAAGAGGAAGAC
CTTACGACCACAACCGAACCCACCCTCATTCTGAACTTTTACATTTCTTTCGAACTTTATTGACAATTTCTCTTTCTCTTCTG
DCTN1

5525

AGTGGAACTGAAATAAGCTCCAAGAGTGTGAGTACCCTCTGAACTGAAATCCTACACTATAAGCCTCCCCTTCATCTTTCTCAT
5610
TCACCTTGACTTTATTTCGAGGTTCTCACAACTCATGGGAGACTTGACTTTAGGATGTGATATTCGGAGGGGAAGTAGAAAGAGTA
DCTN1 >

AATAATAATGGCTGACATTTATTGAGTGCTTTATACAAGGCACTGTTCTAAGTGCTTTTCAGGCATTCTCATGTGATTTTTACAA
5695
TTATTATTACCGACTGTAAATAACTCACGAAATATGTTCCGTGACAAGATTACGAAAAGTCCGTAAGAGTACACTAAAAATGTT
DCTN1 >

CAATCCTGTTAGAAAAGTTATTGTTATTATCCCTTTCTTCCAGAAGAGGAAATTGAGGCATAGAGGATTAGTAGCGCTTGATTTG
5780
GTTAGGACAATCTTTCAATAACAATAATAGGGAAAAGAAGGTCTTCTCCTTTAACTCCGTATCTCCTAATCATCGCGAACATAAAC
DCTN1 >

ATGAATCTCTTACGTCTGCAGAAATGGATTCCCTTTTCTGAGGCATCAGAGAAGACAGAAATTTAATCCCAACTCCCGGTTTCTG
5865
TACTTAGAGAATGCAGACGTCTTTACCTAAGGAAAAGGACTCCGTAGTCTCTTCTGTCTTTAAATTAGGGTTGAGGGCCAAAGAC
DCTN1 >

AACCTTGAGAGCCTAGAGTCTAGGGTTGCTAAGGAGGGAATCTTACCATGCCAGTTTGTGGGCATGATGGTGGCATGGAGGGGGC
5950
TTGGAATCTCGGATCTCAGATCCCAACGATTCCCTCCCTTAGAATGGTACGGTCAAACACCCGTACTIONACCACCGTACCTCCCCCG
DCTN1 >

AGGACAGTGGGATCACTGTTGCTGTCAGCTTTTGACAACACTACATAGGGAAACTCGGATATTCTTGAGTGATTTTTCCAGCATCCT
6035
TCCTGTCACCCTAGTGACAACGACAGTCGAAAACACTGTTGATGTATCCCTTTGAGCCTATAAGAACTCACTAAAAAGGTCGTAGGA
DCTN1 >

GACTAGAAAAGACAAGTGACCGATAGTGATTTGTCAGGTATTGTGGGCTGAGATTGTGTCATCTGAGAGGTGAATAAGAAGAGAGA
6120
CTGATCTTTCTGTTCACTGGCTATCACTAAACAGTCCATAACACCCGACTCTAACACAGTAGACTCTCCACTTATTCTTCTCTCT
DCTN1 >

CCTTGTCCTGTTCCCTATCACCTAGAAAAGGAGAATTTTTCTTGGCAGAGAGACAGGCAGATCTAAAACCTTATATAATAACAT
6205
GGAACAGGGACAAGGATAGTGGATCTTTTTCTCTTAAAAAAGAACCGTCTCTCTGTCCGTCTAGATTTTTGGAATATATTATTGTA
DCTN1 >

AATGATTATTAACCTCACCTTATGTGTTTTCTCAGTTTGTGTGACAGATACAATTTGTAGGTAAGCTGTATACCTGACTTGAGTGA
6290
TTACTAATAATTGAGTGGAATACACAAAAGAGTCAAACACACTGTCTATGTTAAACATCCATTCGACATATGGACTGAACTCACT
DCTN1 >

AAGGAGAGAGTGATGGGATGGCGTGGATGGAAGAGAAACGGACTTACCTTTTCTGCTGCAGCCACTGAAGCATCATCTCTGTGT
6375
TTCCTCTCTCACTACCCTACCGCACCTACCTTCTCTTTGCTGAAATGGA AAAAGGACGACGTCGGTGACTTCGTAGTAGAGACACA
DCTN1 >

CCTTCCTTTTGAAGTTGCCATGGATACGCCTTTGCATGGTGGTTTGAAGGAGATTGATTTCCATTATGATCAGATGATGACGTGGG
6460
GGAAGGAAAACCTCAACGGTACCTATGCGGAAAACGTACCACCAAACCTCTCTAACTAAAGGTAATACTAGTCTACTACTGCACCC
DCTN1 >

TTTAAAAAGAGAAAAGGATGGAATGCTCTGCTTTTGGGGAGTGGCCGGCGAGCTGCCAAAAGGCAGAGCCCAGTACAGCCGATAG
6545
AAATTTTTCTCTTTTCTTACCTTACGAGACGAAAACCCCTCACCGGCCGCTCGACGGGTTTTCCGTCTCGGGTCATGTGCGCTATC
DCTN1 >

GGCTGTGGCTTTGTTGGCTGCTTTGGCTTTTGTGAAATGGTGCATCTCTCTCTTTAGAGCGCAGGCTCAGGGTTCC
6630
CCGACACCGAAAACAACCGACGAAAACCGAAAACGACTTCAACACTTTACCACGTAGAGAGAGAAATCTCGCGTCCGAGTCCCAAGG
DCTN1 >

CTGTCTACAGGGTCCTAGTGCCAGGAACTTGCTGGTTGATTCAGGGGGAGGAATCAGCAGGAACTTCGAACAGCCTAAGTAGGAC
GACAGATGTCCAGGATCACGGTCTTGAACGACCAACTAAGTCCCCCTCCTTAGTCGTCTTGAAGCTTGTGCGATTTCATCTCG
DCTN1

6715

TTCTGATACCACTGAGAGGATTGAGGTTCTTGAGTGCAGGGCTGAGTGCCTCTTGCCTTCTTGCAGAAGTTCTATATTGAAGAT
AAGACTATGGTGACTCTCCTAACTCCAAGAACTCACGTCCCGACTCACGGAGAACGGAAGAAGCTCTTCAAGGATATAAATTCTA
DCTN1

6800

AAGTGAAGCATATAGCATAGCTTTTCTTCTTGAAGTCTGGGCCCTTGGAGGTGGGCCTGGAAGTCACTGGATATTTTC
TTCACCTTCGTATATCGTATCGAAAAGAAGAACTGAAAATCTCCAGACCCGGGAACCTCCACCCGGACCTTCAGTGACCTATAAAG
DCTN1

6885

TGGGGAAAGGGGACATTTTGAAGTGGAGTAGAGCTGCATTCAGAGTGGGAGTGGGTTTGTAGACGTTTTTTTAGGGTAATGAGGA
ACCCCTTTCCCTGTAAAACCTCTACCTCATCTCGACGTAAGTCTCACCTCACCCAAACATCTGCAAAAAAATCCATTACTCCT
DCTN1

6970

GCTGGAGAAGGGAAGGAAGTCCGTTGAGTGTGTAGGCCTTATCTATGAAATCCGCAAGGCAGATACTGAGTAGGACCTAGGAACA
CGACCTCTTCCCTTCTTCCAGGCAACTCACACATCCGGAATAGATACTTTAGGCGTTCGGTCTATGACTCATCCTGGATCCTTGT
DCTN1

7055

AAAAGCTCTGTGTACGTTGTCTTCTGGGGTCTGTGAATATCTGGAATCCAGCTTTCCAAGCTTCCAGTCTCCAGCCTCCATTT
TTTTCGAGACACATGCAACAGAAGACCCAGGACACTTATAGACCTTAGGTGCAAAAGGTTGCAAGGTCAGAGGGTCGGAGGTAAA
DCTN1

7140

ACCACTCAGTAAGCAGACCTTTTCTTCTGACTCCTGAAGGACTTAGGTCCACGTTTATCTCTTCTTACTAGTGCTTTCAGAG
TGGTGAGTCATTCGTCTGGAAAAGGAAAGACTGAGGACTTCTGAATCCAGGTGCAAAATAGAGAAGGAATGATCACGAAAGTCTC
DCTN1

7225

ATGTATAGTTTTGCCTTGCTGTCAGACTGCCTGGGTTTCAGACAAGCTCCTCTAGGAGTGGGAAAAGCAGGGAAAAGCAGACAGTTG
TACATATCAAAACGGAACGACAGTCTGACGGACCCAAAGTCTGTTGAGGAGATCCTCACCTTTTCGTCCCTTTTCGTCTGTCAAC
DCTN1

7310

GGTTAGCCCAGGATCAAGGTTTGATAAGGTGAGACAAGAGGAGATCAAGGTATCAAAGGATGCTGGGGTGCCAGTAAAAACAAGG
CCAATCGGGTCTAGTTCCAAACTATTCCACTCTGTTCTCCTCTAGTTCCATAGTTTCTTACGACCCACGGTCAATTTTTGTTCC
DCTN1

7395

TAGAAATGGTTCAGACAGGGGAGAAATGGTAGAGGTGGAAAAGAGGCTTTTCTCCTCACTTTCTCCTTTTTTCATTCTCCAAAAT
ATCTTTACCAAGTCTGTCCCTCTTTACCATCTCCACCTTTTCTCCGAAAAGGAGGAGTGAAAAGAGGAAAAAGTAAGAGGTTTTA
DCTN1

7480

CTTATTTTCTATAATTTCTGAAATTTCTCTAAGACTATTGGCAGACACAGAGATTATTATTTATCAGACACAGAGATTTTTC
GAATAAAAGGATATTAAAGGACTTTAAAGAGATTCTGATAACCGTCTGTGTCTCTAATAATAAATAGTCTGTGTCTCTAAAAAGG
DCTN1

7565

CCTCCTCTCTTCTCATTCTTAGATATTTTAGTGGTATTTAATATCATTGGAGAGGAAAATGGATTAGAAATCCAAGAGGTGTC
GGAGGAGAGAAGAGTAAAAAGATCTATAAAATCACCATAAATTATAGTAACCTCTCCTTTTACCTAATCTTTAGGTTCTCCACAG
DCTN1

7650

TGTCTCCTCCCTGGCTGGGGTAACATTAACCCAGGATTGTCCTATGGGATATGGGCCTGGGCCCGGTAATGCTGTGGAAGGAGCA
ACAGAGGAGGGACCGACCCATTGTAATTGGGTCTAACAGGATACCCTATACCCGGACCCGGGCCATTACGACACCTTCTCTCGT
DCTN1

7735

CCTACCTGTAGAGATATTCAGATGTGCCCTCTGCCATTTTTTGGCTATGAGACTTGGGCAAGTCATTTGACTTCTGAGACATAG
GGATGGACATCTCTATAAGTCTACACGGGGGAGACGGTAAAAAACCGATACTCTGAACCCGTTTCAGTAAACTGAAGACTCTGTATC
DCTN1

7820

TTCTGTCATCTGTGGAATGGAGAGAATGGAATCTGTTTTGGCTACATCACAGGTTCATTTTTGAAGGAGATAGTGAAGTACATGT
AAGACAGTAGACACCTTACCTCTCTTACCTTAGACAAAACCGATGTAGTGTCCAAGTAAAAACTTCTCTATCACTTCATGTACA
DCTN1

7905

ATTCGTGTATGCAATTAAGTTTTCCCAGAGAAGGCCCTAAGAACAGGACGCATTTTCTCTCTCCTAACATGTTGTTTCTCCTCC
TAAGCACATACGTTAATTCAAAGGGGTCTCTTCCGGGATTCTTGTCTGCGTAAAAGAGAGAGGATTGTACAACAAAGAGGGAGG
DCTN1

7990

CATTTTTTTCAGTTCTGTTAATGTTTCAATTATTACATTTCTCATGCTTGAAAACCTCTGAGTGTATTTATTCATTTACTTATTC
GTAAAAAAGTCAAGACAATTACAAAGTTAATAATGTAAAGAGTACGAACTTTTGAGGACTCACATAAATAAGTAAATGAATAAG
DCTN1

8075

ATGCATTCATTGACCCATCTATTTATCCTTGCAGCATTTGAGTTCCTACTGTGCGCAAGTCATCGTGGATATTCCTTAAAATAA
TACGTAAGTAACTGGGTAGATAAATAGGAACGTCGTAAACTCAAGGATGACACGCGTTTCAGTAGCACCTATAAGGGAAATTTTATT
DCTN1

8160

TGAATGAAGATGATATCTACCATTTGTTGAGCACACAGACATTGTGCTAAACGCTTTACTTAAATCTTATTTAATCTTCAAATG
ACTTACTTCTACTATAGATGGTAAACAACCTCGTGTGTCTGTAACACGATTTGCGAAATGAATTTAGAATAAATTAGAAGTTTTAC
DCTN1

8245

TCCCTGTGAGGTAACATTATTTCTTCTTTTTGCAGTTGAGGTAACCGGGACTCAGGAAGTTAAATATCTTGCTCAGAGGAGAAC
AGGGACACTCCATTGTAATAAAGAAGGAAAAACGTCAACTCCATTGGCCCTGAGTCTTCAATTTATAGAACGAGTCTCCTCTTG
DCTN1

8330

CAAAGGTATATTCAGGTCTGTCTCCAGAGCCCATGTAGGCCTGCTGCCTCTTTCCTCATGTTTGATCTATTACAAGGCCTTCTCA
GTTTCCATATAAGTCCAGACAGAGGTCTCGGGTACATCCGGACGACGGAGAAAGGAGTACAAACTAGATAATGTTCCGGAAGAGT
DCTN1

8415

GGGCTTTTTTGGTACTGTCTCTGAACTGGCCTCTTCTTCTCCTCCTGATCCTGGTTCAAACCTTCTTACCCTGTGTCAAATGT
CCCGAAAAAACCATGACAGAGACTTGACC GGAGAAAGAAGAGGAGGACTAGGACCAAGTTTGGAAAGGAATGGGACACAGTTTACA
DCTN1

8500

TGCAGCAGCCTCCTTGCTGTTATTCCTGTCTTTGCCAGGTTGCTCCTGCCTGCACTCCATCCTGCAGGTGTCATCAGTTTGATCT
ACGTCGTCGGAGGAACGACAATAAGGACAGAAACGGTCCAACGAGGACGGACGTGAGGTAGGACGTCCACAGTAGTCAAAC TAGA
DCTN1

8585

TCCTAAAATAGTTTTCACTATGCAGTCTCCTGCTCAGGAACAAGACTGCCTTCTGTTATTATTGGATCAAGTCCTTCTCTGTCT
AGGATTTTATCAAAGTGATACGTCAGAGGACGAGTCTTGTCTGACGGAAGGACAATAATAACCTAGTTCAGGAAGAGACAGA
DCTN1

8670

GCCTGATGTTAAACTCCGTGCCTACCCACAGTTACCTCCCAGTATGTTGCAATGTTATTCAATAAATGTTTATTCAATAAATATT
CGGACTACAATTTGAGGCACGGATGGGTGTCAATGGAGGGTCAACAACGTTACAATAAGTTATTTACAATAAAGTTATTTATAA
DCTN1

8755

TGACCATGAGCTACTTACTGGCTATTGGATCATAAAGAGGAAAAGGTGTGGGCTATGCTTCAAAGGCTTATAGTTTGATAGAAT
ACTGGTACTCGATGAATGACCGATAACCTAGTATTTCTCCTTTTCCACACCCGATACGAAGTTTTCCGAATATCAAACCTATCTTA
DCTN1

8840

AACCATCTACAATTCGTTACTTCAGCTAAGCTAGGGTTCTTTACTATTTCGCTAGTCAAGCAAAGTTATTTCTGCCTCTGTTTCATA
TTGGTAGATGTTAAGCAATGAAGTCGATTCGATCCCAAGAAATGATAAGCGATCAGTTTCGTTTTCAATAAAGACGGAGACAAGTAT
DCTN1

8925

CTGTGTTTACAAGTTACAGGGCTTTGTAGGCCTTTCCACATATTTTTATTTTTATTTATTTATTTATTTTTTTTTTTTTTTTGGAGA
GACACAAGTGTTCATGTCCCGAAACATCCGGAAAGGTGTATAAAAAATAAAAAATAAAATAAATAAATAAAAAAAAAAAAAAACTCT
DCTN1

9010

CGGAGTCTCGCTCTGTCGCCAGGCGGGACTGCGGACTGCAGTGGCGCAATCTCGGCTCACTGCAAGCTCCGCTTCCCGGGTTCA
GCCTCAGAGCGAGACAGCGGGTCCGCCCTGACGCCTGACGTCAACCGCTTAGAGCCGAGTGACGTTTCGAGGCGAAGGGCCCAAGT
DCTN1

9095

CGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCGCCCGCCACCGCGCCCGGCTAATTTTTTTTTGTATTTTA
GCGGTAAGAGGACGGAGTCGGAGGGCTCATCGACCCTGATGTCCGCGGGCGGTGGCGCGGGCCGATTAAAAAAAAACATAAAAAAT
DCTN1

9180

GTAGAGACAGGGTTTACCTTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCATGATCCACCCGCCTCGGCCTCCCAAAGTGCT
CATCTCTGTCCCAAAGTGGAAACAATCGGTCTACCAGAGCTAGAGGACTGGAGTACTAGGTGGGCGGAGCCGGAGGGTTTACGA
DCTN1

9265

GGGATTACAGGCGTGAGCCACCGCGCCCGGCCTCCACATATTTTTAAAAATCCCATAAATCAAGGCATGCTTAGGTACTCCCTT
CCCTAATGTCCGCACTCGGTGGCGCGGGCCGGAGGTGTATAAAAAATTTAAGGGTATTAAGTTCCGTACGAATCCATGAGGGAA
DCTN1

9350

TCTTTCTAGCTCACCTCTCCTGTCTATAATTTCTTATATTTATTGTGTAGATGTATATAACATTTAGTATCATGTCAGGTAAT
AGAAAAGATCGAGTGGAGAGAGGACAGATATTAAGAATATAAAATAACACATCTACATATATGGTAAATCATAGTACAGTCCATTA
DCTN1

9435

TCTTTGCAGTTCTATAATTTCTGTACTTTTTACAAGGTGCTTTTTTTTTTTTTTTTTTTGAGTCTCAGTCTGTCGCCCTGGCTGGA
AGAAACGTCAAGATATTAAGACATGAAAAATGTTCCACGAAAAAAAAAAAAAAAAAACTCAGAGTCAGACAGCGGGACCGACCT
DCTN1

9520

GTGCAGTGGTGCACCTTGGCTCACTGCAACCTTACCTCCCGGCTTCAAGCGATTCTCATGCCTATAGTCTCTCAAGTAGCTAG
CACGTCACCACGCTGGAACCGAGTGACGTTGGAAGTGGAGGGCCGAAGTTTCGCTAAGAGTACGGATATCAGAGAGTTCATCGATC
DCTN1

9605

GATTATAGGTATGCGCCACCACACCCAGCTCATTTTTGTATTTTTAGTAGAGATAGGGTTTACCATGTCAGCCAGGCTGGTCTT
CTAATATCCATACGCGGTGGTGTGGGTCGAGTAAAAACATAAAAAATCATCTCTATCCCAAAGTGGTACAGTCGGTCCGACCAGAA
DCTN1

9690

GAACTCCTGGTCTCAAGTGAGCCACCGGCCTCAGCCTCTCAAAGTGTGGGATTACAGGCATGAGCCACCACACCTGGCCTACAA
CTTGAGGACCAGAGTTCACCTCGGTGGCCGGAGTCGGAGAGTTTTACAACCTAATGTCCGTACTCGGTGGTGTGGACCGGATGTT
DCTN1

9775

GGTACCTGTATATGCTTTAGCTTTTTTGAACCTCATGATACTGACGTAGATATGGCAGATATTATTTTCATTTATAGGAAAATA
CCATGGACATATACGAAATCGAAAAAATTTGGAGTACTATGACTGCATCTATACCGTCTATAATAAAAGTAAAGTATCCTTTTTAT
DCTN1

9860

AACAGATTCGAAGAAATAGGGGACTATTGATACCTATGTGGTTAGTGAGTTGTGAGGCTATTTTTAGATCTGAGCTCTTTTGAA
TTGTCTAAGGTTCTTTAATCCCTGATAACTATGGATACCAATCACTCAACACTCCGATAAAAAATCTAGACTCGAGAAAACTT
DCTN1

9945

TTTTTTAAGGCAGTGTGGCCTACAGGAAGAGCAGGGCCTTGGAAAGCCTAGATATGTCTGTGGTAATGGTGAGGGGTAGTAGAAAAG

AAAAAATTCGGTCACACCGGATGTCCTTCTCGTCCCGGAACCTTCGGATCTATACAGACACCATTACCACTCCCCATCATCTTTC

DCTN1 >

CACAGAGGGCTCTGGGTCAGGTTGTTTCCAGTTTTGGCTCTACTCCTCACAGTCTGTGTGTCTTCAGGGAAGTTGCTCAGTTCTC

GTGTCTCCCAGACCCAGTCCAACAAAGGTCAAACCGAGATGAGGAGTGTGACACACAGAAAGTCCCTTCAACGAGTCAAGAG

DCTN1 >

AAAGACTCAGTTGCCTTGTGAGCATCATCCCTGGCCAACCTCTCAATGGGGTTATTGTAATGTCTATATATGATGACATTGTTCT

TTTCTGAGTCAACGGAAACAGTCGTAGTAGGGACCGTTGGAGAGTTACCCCAATAACATTACAGATATATACTACTGTAACAAGA

DCTN1 >

TAGCTAACTTTTATTTAGCACTTATTAATAACCAGGCGGTGTCCTGGATGCTTTGTTTGGATTATCTCAGCTAATCCTCACGATA

ATCGATTGAAAATAAATCGTGAATAATTTATGGTCCGCCACAGGACCTACGAAACAAACCTAATAGAGTCGATTAGGAGTGCTAT

DCTN1 >

CCTCTCTGAGATATGTTCTTTGTTACTTCCCTATGACGGATGAGGAAATTGAGGCATAGAGATGTTAAGTAACTAGACCAAGTTT

GGAGAGACTCTATACAAGAAACAATGAAGGGATACTGCCTACTCCTTTAACTCCGTATCTCTACAATTCATTGATCTGGTTCAAA

DCTN1 >

ATGTAGCTACCAAGTGATAAAAGCCAGGAAAGTAGCCTGAGTCTAGAACCAGTACTCAACCATGGTTCTATAAAATGTCTTTTTTT

TACATCGATGGTTCACTATTTTCGGTCTTTTCATCGGACTCAGATCTTGGTTCATGAGTTGGTACCAAGATATTTTACAGAAAAAAA

DCTN1 >

AAGGTGTCCTATAGACTGTAAAGTGCTCCGAACATGTGAGGTCCAGGCTGCAAGGATGTGCCTGGCCCTGCCACCTGTGTAATG

TTCCACAGGATATCTGACATTTACAGAGGCTTGTACACTCCAGGTCCGACGTTCTTACACGGACCGGGACGGGTGGACACATTAC

DCTN1 >

GCGAATAGGGAAAGGAGGGGGCGACATGGAGATTTTGCAGGGAGGAGAGAGATTATTTCTAGGGGGTCTGGCCAGGACTGAAGA

CGCTTATCCCTTTCTCCCCGCTGTACCTCTAAAACGTCCCTCCTCTCTAATAAAGGATCCCCCAGACCGGTCTGACTTCT

DCTN1 >

TTTGGAAATTGTGTTTTGGGGCCATATTTCTGAATGTTGGCTGTCATTCTCCTGTTGGGCTACCTGGCCTATCTTAAGAGGGTAGA

AAACCTTAACACAAAACCCCGGTATAAAGACTTACAACCGACAGTAAGAGGACAACCCGATGGACCGGATAGAATTCTCCCATCT

DCTN1 >

GCGGGGTAAAGTCACTGTTCTGCCAGTGAAGTAAGCCAGTGCAGAAAAGACAGGCGTCCCTAGGCCCAAGGGAACTAGATCCAT

CGCCCCATTTCAAGTGACAAGACGGTCACTTCATTTCGGGTACGTCCTTTCTGTCCGCAGGGATCCGGGTTCCCTTGATCTAGGTA

DCTN1 >

ACCATACTCAGTGGAGCCATAGGTCAGACCCCAGGCCAACCTTGTTGGCTGTGTAGGGGCAGGGACCCTGGTCTTTTGGTTTCTA

TGGTATGAGTCACCTCGGTATCCAGTCTGGGGTCCGGTTGGAACAACCGACACATCCCCGTCCCTGGGACCAGAAAACCAAAGAT

DCTN1 >

GCCCATGATAGATGGGCCAGTGAATGAAAGCAGTGTGGTAACATAGTCCCTTGGAGACCTCTCATTAGAATGCATAATCTCATT

CGGGTACTATCTACCCGGTCACTTACTTTTCGTACACCAATTGTATCAGGGAACCTCTGGAGAGTAATCTTACGTATTAGAGTAAT

DCTN1 >

AATTAACAATTCTAATTATAAAAGTAATACATGGTTACTGAAGAATTTTTGTGAAATACAAAAGCGTAGAAAATAAACCATTTT

TTAATTTGTTAAGATTAATATTTTTCATTATGTACCAATGACTTCTTAAAAACACTTTATGTTTTTCGCATCTTTTATTTGGTAAAG

DCTN1 >

ATTGGGTCTGAGATGCTAGGAGGCCAAGGCCAAGAGTACAAGGGGCAGATGACTGAGGTGGACTGGGCCTTGTGCTACAAGAAGAA
11,135
TAACCCAGACTCTACGATCCTCCGTTCCGGTTCTCATGTTCCCCGCTACTGACTCCACCTGACCCGGAACACGATGTTCTTCTT
DCTN1 >

AGAAGGGCTCTCTGCTTTTACTACTGCCTTTAGTAATCCAGTTGAGTCTGATACTCTTGTGTTTTACAACCTGGCCCCCTTATAA
11,220
TCTTCCCGAGAGACGAAAACCTGATGACGGAAATCATTAGGTCAACTCAGACTATGAGAACACAAAATGTTGGACCGGGGAATATT
DCTN1 >

CAACCATAAAGGGTGAAGGGTACTATGGCAACCTTTGCCAGCCTTGTGGGAGGGGGCTAGGGTACTTGGCTTGCCTTTGCTATGT
11,305
GTTGGTATTTCCCACTTCCCACTGATACC GTTGGAAACGGTCGGAACACCTCCCCCGATCCCATGAACCGAACGAAACGATACA
DCTN1 >

GTGTGAAGTTGCCTTCATTACTGCCCTTCTCTTGTGCTGCCTCCTGGGCAGGGCCTGCCTCCTCTGGCTCAGTGTGAGATTGAAATC
11,390
CACACTTCAACGGAAAGTAATGACGGGAAGAGAACGACGGAGGACCCGTCCCGGACGGAGGAGACCGAGTCACTCTAACTTTAG
DCTN1 >

CAGGCCCTACTCACATGAATTTGGACCCTGAGTCCAGAGTTTAGAGAGGGGAGGGAGAGAGAAGAGCACCAGAAAAGGTAGATGAG
11,475
GTCCGGGATGAGTGTACTTAAACCTGGGACTCAGGTCTCAAATCTCTCCCTCCCTCTCTCTTCTCGTGGTCTTTCCATCTACTC
DCTN1 >

AGACCCTATTTTTGGCTGTGTGGAGGCTCTAGGCAGCTGATCGCTTTGAAAGTGTCACTTGATGCTTATGGGCCTGCTGAGGCCTT
11,560
TCTGGGAATAAAACCGACACACCTCCGAGATCCGTCGACTAGCGAAACTTCACAGTGAACCTACGAATACCCGGACGACTCCGGAA
DCTN1 >

ACATCCTGGGGGAGAGGGGAACAGTGATGGTGAGTGGGTACAGACTAGGAGGACGTGTCAAGACTGCTTCCAGCCCTAGGACAGT
11,645
TGTAGGACCCCTCTCCCTTGTCACTACCACTCACCCATGTCTGATCCTCCTGCACAGTCTGACGAAGGTCGGGATCCTGTCA
DCTN1 >

GTATTCAAGAGTTGAGTGTGCTGAGGGTCTGTGGCGTATGCCAGCCCTTAGTTTCTGGCCACGTGAAGCAGGGGGGCACTAGGAC
11,730
CATAAGTTCTCAACTCACGACTCCAGACACCGCATACGGGTGCGGAATCAAAGACCGGGTGCCTTCGTCCCCCGTGATCCTG
DCTN1 >

CCAGAGGCTAGCACGGTTCCTGACAAGTCTAGAGCAGCACTAGCGCAGAGTGAGACTCATCAGCTGGCAAGCAGGATTCTGTGTC
11,815
GGTCTCCGATCGTGCCAAGGACTGTTTCAGATCTCGTCGTGATCGCGTCTCACTCTGAGTAGTCGACCGTTCGTCTAAGACACAG
DCTN1 >

DCTN1-226 >

TCTGGGTTTCAGGAATCCTCAGGCAGCAGAGGGGACTTGCTCCTCAGCCCCATCACTGCCCCACCCCTACCCGTGTAGGCCACC
11,900
AGACCCAAGTCTTAGGAGTCCGTCTCCCTGAACGAGGAGTCGGGGGTAGTGACGGGGGTGGGGATGGGCACATCCGGTGG
DCTN1 >

DCTN1-226 >

GAGTGAGGCCCATGGACTGGGGAGGGCTGTGCCTGACGACTCCTGTGTCCCTCTATGAGGGCCAGCGCCCTGACCCCTCTGCCT
11,985
CTCACTCCGGGTACCTGACCCCTCCCGACACGGACTGCTGAGGACACAGGGAGATACTCCCGGTCGCGGGACTGGGAGGACGGA
DCTN1 >

DCTN1-226 >

AGGTTTCTACCTTTTCTCTCTGTCTTTGGCCAGCTGGGGGAGGGGGTAGAGGCCGGGTGAGCAACATGGCACAGAGCAAGAGGGCA
TCCAAAGATGGAAAAGAGAGACAGAAACC GGTCGACCCCTCCCCATCTCCGGCCCACTCGTTGTACCGTGTCTCGTTCTCCGT

12,070

DCTN1

DCTN1-226

1 5
M A Q S K R H
ENSE00003766163
DCTN1-226

CGTGTTACAGCCGGGTAAGTGGCCCTAATCTGGGATGGCCCTGGAGGGCTGCTGGGGAAGGCCTGGCTGCCTGTGGACATCATTGC
GCACATGTCGGCCATTACCCGGGATTAGACCTACCCGGGACCTCCCGACGACCCCTTCCGGACCGACGGACACCTGTAGTAACG

12,155

DCTN1

DCTN1-226

10
V Y S R
ENSE00003766163

DCTN1-226

TGTGGGGGCTGGGGAGATAGGCTGGAGCTCAGCTGAGGGCACTCAGACTGTGTTTTCTAAGGAGCCCTCGAAGCCCTGGTGGTGT
ACACCCCGACCCCTCTATCCGACCTCGAGTCGACTCCCGTGAGTCTGACACAAAAGATTCTCGGGAGCTTCGGGACCACCACA

12,240

DCTN1

DCTN1-226

DCTN1-226

AAGGCTGGACAGGCTTCCCTTTACAGAGTTGATCCCTAAATGGGGACTAGCAAGGCCTGACCTCTGACTCTAATTGGCCCTCATA
TTCCGACCTGTCCGAAGGGAAATGTCTCAACTAGGGATTTACCCTGATCGTTCCGGACTGGAGACTGAGATTAACCCGGGAGTAT

12,325

DCTN1

DCTN1-226

DCTN1-226

CCAGGGGCTCCTGAGGGGGTCCAGACTATCCTGGGGACTCAGAATGGGGATGATGGCTCAGAGAGGTCTTACAGTGAAGCCTTTC
GGTCCCCGAGGACTCCCCCAGGTCTGATAGGACCCCTGAGTCTTACCCTACTACCGAGTCTCTCCAGAATGTCACTTCGGAAAG

12,410

DCTN1

DCTN1-226

DCTN1-226

TTAAGAGCTGCTTTGTTATTTGTTACTTGCTTTCTTTCTTCTGAGATAGAATCTGTAGCTACTGTTGTGGCCCCCTGGTTCTG
AATTCTCGACGAAACAATAACAATGAACGAAAGAAAGAGAAGACTCTATCTTAGACATCGATGACAACACCCGGGGGACCAAGAC

12,495

DCTN1

DCTN1-226

DCTN1-226

AGAGGCTTATTGGGGTTGGAAAGTGGGGGAGTCTCTGACTTTGGGTTTCAGCCTTTTATATCACTGGCAATTCTTTTATTGTCAG
TCTCCGAATAACCCCAACCTTTCACCCCTCAGAGACTGAAACCCAAGTCGGAAAATATAGTGACCGTTAAGGAAAATAACAGTC

12,580

DCTN1

DCTN1-226

DCTN1-226

GTCCATGAGAGCCATCCTGCTGTTCCAGGTGTGATTTGGGGTCTCGGAGCCTCTGGGAACCTACATCCTCACCTTCCTGGATGAGC
CAGGTACTCTCGGTAGGACGACAAGGTCCACACTAAACCCAGGACCTCGGAGACCCCTTGATGTAGGAGTGGAAAGGACCTACTCG

12,665

DCTN1

DCTN1-226

DCTN1-226

TGTTTGGGGAAGGGAATTAGGCAGTGATAGGCTGGGAGGTGTCCTGGCTCTTCCCTGGCTCTGCCAGGGCTCCCTTCTGAAGCTA
ACAAAACCCCTTCCCTTAATCCGTCACTATCCGACCCCTCCACAGGACCGAGAAGGGACCGAGACGGTCCCAGGGGAAGACTTCGAT

12,750

DCTN1

DCTN1-226

DCTN1-226

TTATAAATGAGAGTATCAGAAGGGTCTCCCATAGAGTCTTTAGGATGATGGTATCACTTCATCATGCCTCATTTCATCTGTTTGCT
AATATTTACTCTCATAGTCTTCCCAGAGGGTATCTCAGAAATCCTACTACCATAGTGAAGTAGTACGGAGTAAGTAGACAAACGA

12,835

DCTN1

DCTN1-226

DCTN1-226

GCAAGGCCCTGGTTCATGGAGTTGCTGTTGCTAAAAATGACCTAAGTGTGATTTTCTTCTAAACCATGGGCCTATTTGGGACCT
CGTTCCGGGGACCAAGTACCTCAACGACAACGATTTTTACTGGATTACACTAAAAGAAGATTTGGTACCCGGATAAACCCCTGGA

12,920

DCTN1

DCTN1-226

DCTN1-226

AATTTTCTATTGTGTTTCAGTCATCATGGGTGTGCCGAAGCTAAGAGCTGCCAAGGACAGTGTCTTAGTCTGTTGTTTTGCCTTG
TTAAAAGATAACACAAGTCAGTAGTACCCACACGGCTTCGATTCTCGACGGGTTCTGTGTACAGAATCAGACAACAAAACGGAAC

13,005

DCTN1

DCTN1-226

DCTN1-226

CCCATCTGTGGAGTGATAAACCATTCATTTGGACCACTGAGCAGAGTCTTGGGGACAGAGCGAGGGGTAGATCCACCCAATTTAC
GGGTAGACACCTCACTATTTGGTAAGTAAACCTGGTGACTCGTCTCAGAACCCTGTCTCGCTCCCCATCTAGGTGGGTAAATG

13,090

DCTN1

DCTN1-226

DCTN1-226

TTGGCCTGTGTTTTCTTTTTATAGCAACATAGCATGGAGAAGAATCTCCAGAGCTTGGGGATAGAGAGTTGACCAAACAAGACT
AACCGGACACAAAAGGAAAAATATCGTTGTATCGTACCTCTTCTTAGAGGTCTCGAACCCCTATCTCTCAACTGGTTTTGTTCTGA

13,175

DCTN1

DCTN1-226

DCTN1-226

CAGGCCAGGTAGAAAGGGGAGTTGAATGGTTGAATGGGCTGTGGTGAAGCATCTGGGGTTTCATGGTGGGTTTGTGGATGGGGGTG
GTCCGGTCCATCTTCCCCTCAACTTACCAACTTACCCGACACCACTTCGTAGACCCCAAAGTACCACCCAAACACCTACCCCCAC

13,260

DCTN1

DCTN1-226

DCTN1-226

GGAGGAGTCAGATCAGGAAGGAGAGGTGGTGACTTAAGGGTCTGGAAGGAGGCACAATTGTGTGCCTCTGAAAGGGTGAGGCCTA
CCTCCTCAGTCTAGTCCTTCCCTCACCACCTGAATTCCCAGACCTTCTCCGTGTTAACACACGGAGACTTCCCACTCCGGAT

13,345

DCTN1

DCTN1-226

DCTN1-226

AGAAAACCATTTGAAACACAGAGGAGACAAGTGACAGTGGAAAGGGGAAACAGGATTCTGTAGGATCACCCACTGAATTGCCTGTC
TCTTTTGGTAAACTTTGTGTCTCCTCTGTTCACTGTCACCTTCCCCTTTGTCTAAGACATCCTAGTGGGTGACTTAACGGACAG

13,430

DCTN1

DCTN1-226

DCTN1-226

PCR Forward
GCCTGGTCTAAACTGAGTTATTTGC

TTCCAGCTCAGACTCCTGAGTCAGGGCATTGGGTTGTGGGGAGCCTGGTCTAAACTGAGTTATTTGCTTGATCTTATTTCCCCT
AAGGGTCGAGTCTGAGGACTCAGTCCCCTAACCCAACACCCCTCGGACCAGATTTGACTCAATAAACGAACTAGAATAAAGGGGA

13,515

DCTN1

DCTN1-226

DCTN1-226

CCTGAGAAGAGAATTAAGGAGACAGTGCTCCTGAGAAAAGCAGCCATGTGGTGACATTCACAGACTGGTCAATGAATTCTGATTTG
GGACTCTTCTCTTAATTCCTCTGTACGAGGACTCTTTCGTGCGGTACACCACTGTAAGTGTCTGACCAGTTACTTAAGACTAAAC

13,600

DCTN1

DCTN1-226

DCTN1-226

TTATAAAAAATATAAACTTAAAAATTCTAGCAGATTCCAGAGGAATTTGGAGAAATCTTAGAATATCATTGGCATTITTTTCAAAG
AATATTTTTTATATTTGAATTTTTAAGATCGTCTAAGGTCTCCTTAAACCTCTTTAGAATCTTATAGTAACCGTAAAAAAGTTTC

13,685

DCTN1

DCTN1-226

DCTN1-226

GGGAATTTGGGGGTCCACCCAATTCTGTAATGGGGTTTAAAGAAAATGACTCTGGTTGTTTTTCAGTCCAGCATCTTGGCTGAGG
CCCTTAAACCCCAAGGTGGGTTAAGACATTTACCCCAAATCTTTTACTGAGACCAACAAAAAGTCAGGTCGTAGAACCAGACTCC

13,770

DCTN1

DCTN1-226

DCTN1-226

CATTTCTTATACATAAGAATGCCACCTTTGATCTGAGGCCTCTAACTGTCTGTGTTTACCTGTGTCTTTTCAGACGCCACGGGCA
GTAAAGAATATGTATTCTTACGGTGGAAACTAGACTCCGGAGATTGACAGACACAAATGGACACAGAAAAGTCTGCGGGTTCGCCGT

13,855

DCTN1

DCTN1-226

T P S G
ENSE00003632144

DCTN1-226

Sanger Sequencing

TCCCGTGTAGAGGTGATTGG

GCAGGATGAGTGC GGAGGCAAGCGCCCCGGCCTCTGCGGGTGGGCTCCCGTGTAGAGGTGATTGGAAAAAGGCCACCGAGGGCACTGT
CGTCTACTCACGCCTCCGTTTCGCGGGCCGGAGACGCCACCCGAGGGCACATCTCCACTAACCTTTTCCGGTGGCTCCGTGACA

13,940

DCTN1

DCTN1-226

S R M S A E A S A R P L V G S R V E V I G K G H R G T V

ENSE00003632144

DCTN1-226

gRNA Protospacer

CAAATGGGTAGGCGTGATTCT

GGCCTATGTTGGAGCCACACTGTTTGGCACTGGCAAATGGGTA GCGGTGATTCTGGATGAAGCAAAGGGCAAAAATGATGGAAGT
CCGGATACAACCTCGGTGTGACAAACGGTGACCGTTTACCCAT CGCACTAAGACCTACTTCGTTTCCCGTTTTTACTACCTTGA

14,025

DCTN1

DCTN1-226

A Y V G A T L F A T G K W V G V I L D E A K G K N D G T

ENSE00003632144

DCTN1-226

Donor Template WT -> SNV

Protospacer Sequence

PAM

SNV

GTGTGACAAACGGTGACCGTTTACCCAT CGCACTAAGACCTACTTCGTTTCCCGTTTTTACTACCTTGA

Donor Template WT -> SNV

GTTCAAGGCAGGAAGTACTTCACTTGTGATGAAGGGCATGGCATCTTTGTGCGCCAGTCCCAGGTATTCACGCCCTTCTTTTGTG
CAAGTTCCGTCCTTCATGAAGTGAACACTACTTCCCGTACCGTAGAAACACGCGGTCCAGGGTCCATAAGTGCGGGAAGAAAAACAC

14,110

DCTN1

DCTN1-226

V Q G R K Y F T C D E G H G I F V R Q S Q

ENSE00003632144

DCTN1-226

Donor Template WT -> SNV

CAAGTTCCGTCCTTCATGAAGTGAACACTA

Donor Template WT -> SNV

TCTGTGCATGTGTGCACATGTCTGTGCGCATGTGCAGCTGATGTGTTGGTACTTCGTTTTCTGAGCATGGGCATAAGCCTCTGGT
AGACACGTACACACGTGTACAGACAGCGTACACGTCGACTACACAACCATGAAGCAAAAAGGACTCGTACCCGTATTTCGGAGACCA

14,195

DCTN1

DCTN1-226

DCTN1-226

TGGGAGAGTGGAAAGGTAGTGGGGGAGGGAAGATTGAAGATGCATCCTTAGGGAAAGCTGCCCTGTACTCTTGGTTTGTCTGGAGCC
ACCTTCTCACCTTCCATCACCCCTCCCTTCTAACTTCTACGTAGGAATCCCTTCGACGGGACATGAGAACCAAACGAACCTCGG

14,280

DCTN1

DCTN1-226

DCTN1-226

TGGGGAGGGGCCCATATTACAGCCGTCCTTGATCTGGCTATATTGAAACTATTGATCTGGCTATATTGAATCTGGCCTCAGATCC
ACCCCTCCCCGGGTATAATGTCGGCAGGAACTAGACCGATATAACTTTGATAACTAGACCGATATAACTTAGACCGGAGTCTAGG

14,365

DCTN1

DCTN1-226

ENSE...

DCTN1-226

AGGTATTTGAAGATGGAGCAGATACTACTTCCCCAGAGACACCTGATTCTTCTGCTTCAAAAAGTCTCAAAAAGAGGTAACAACCA
TCCATAAACTTCTACCTCGTCTATGATGAAGGGGTCTCTGTGGACTAAGAAGACGAAGTTTTTCAGGAGTTTTCTCCATTGTTGGT

14,450

DCTN1

DCTN1-226

95 V F E D G A D T T S P E T P D S S A S K V L K R 115

ENSE00000762538

DCTN1-226

CTTCTACCTCGTCTATGATGAAGGG
PCR Reverse

CCCACTTAAAGTTGCCTCCCCATAGCCAGGAGGAGTCCCCAGGACTTCTCCTCATAACATGGGGCCACAGTAGATCCTAAGATTT
GGGTGAATTTCAACGGAGGGGTATCGGTCTCCTCAGGGGTCTGAAGAGGAGTATTGTACCCCGGTGTCATCTAGGATTCTAAA

14,535

DCTN1

DCTN1-226

DCTN1-226

TTTTCCGTCACTACCATATTCCCTTATTATATCTCCCCCTACCTCTCTATACAAGTACACACTTTGTTTCTGTTTGTCTTTCTACA
AAAAGGCAGTGATGGTATAAGGGAATAATATAGAGGGGGATGGAGAGATATGTTTCATGTGTGAAACAAAGACAAACGAAAGATGT

14,620

DCTN1

DCTN1-226

DCTN1-226

GAGGGAAGTATGATACAAGTCAAAAGACTAGCAAACTGGTGAGTGATTTGGGGGTGGGAATGGGGAATAATAAAGGGAGGGGAAGGA
CTCCCTTGACTATGTTGACGTTTCTGATCGTTTACCCTCACTAAACCCACCCTTACCCTTATTATTTCCCTCCCTTCCCT

14,705

DCTN1

DCTN1-226

120 E G T D T T A K T S K L 130

ENSE00003786741

DCTN1-226

GAAAGAGGAGGGATACCCAGTGCTAGGCAGGTAGAAGTAGTGGTGGTCTGATTTGCCTTCTAGTCTCTCCAACCTCCCTAAGA
CTTTCTCCTCCCTATGGGTACAGATCCGTCCATCTTCATCATCCACTCAGACTAAACGGAAGATCAGAGAGGTTGAAGGGATTCT

14,790

DCTN1

DCTN1-226

DCTN1-226

AGGAGGCTTTCTGGGGATTAATTGCTGTGTTAGAGTTACAGTAAAGATGGTAGAAGGGAAAACTCATAGGCTCCAGAAAGTTCAG
TCCTCCGAAAGACCCCTAATTAACGACACAATCTCAATGTCAATTTCTACCATCTTCCCTTTTTGAGTATCCGAGGTCTTCAAGTC

14,875

DCTN1

DCTN1-226

DCTN1-226

GGTCAAATGAGATTGAGCTGAGGGTGATAGGAAGGACAGGTCTGGCCCTAGTAGTGTAGCCAACCTTCTACCTTTTTGGTACCCAA
CCAGTTTACTCTAACTCGACTCCCACTATCCTTCTGTCCAGACCGGGATCATCACATCGGTTGAAGGATGGAAAAACCATGGGTT

14,960

DCTN1

DCTN1-226

DCTN1-226

AGATGCCAACATCTAAAGGGTCTGAGGGTAAGGTTAAGGTAGAAGATAGAGGAAGAAGCAATCTCCTATTCACAAGTGAATGGCA
TCTACGGTTGTAGATTTCCAGACTCCCAATTCATCTTCTATCTCCTTCTTCGTTAGAGGATAAGTGTTCACCTTACCGT

15,045

DCTN1

DCTN1-226

DCTN1-226

AGGAGCCGGGCCCTCTGCCTCCTGTTTTAAGCTGGATGCAGAGAGTGCTTCTAGTTCTTCTCTGCTACTCTGTGCAGGATGTGT
TCCTCGGCCCGGGAGACGGAGGACAAAATTCGACCTACGTCTCTCACGAAGGATCAAGAAGAGACGATGAGACACGTCTTACACA

15,130

DCTN1

DCTN1-226

DCTN1-226

GTGAGGTGGGGCTGCAGACTCTGCAGCTTCTCTGGGCCAAGGTGTGAACATCCTGGAAGCTGATCTTTGAGGGGCTACTCATCTC
CACTCCACCCCGACGTCTGAGACGTGGAAGAGACCCGGTTCCACACTTGTAGGACCTTCGACTAGAAACTCCCCGATGAGTAGAG

15,215

DCTN1

DCTN1-226

DCTN1-226

ACCCTGACTCCCCCTACCCGCGTCTAACCTGTGTAAGCCCGAGTTGGTCTTAACACCTATGCCAGGACATCTGTTCTCTAACT
TGGGACTGAGGGGGGATGGGCGCAGATTGGACACATTCGGGCTCAACCAGAATTGTGGATACGGGTCCTGTAGACAAGAGATTGA

15,300

DCTN1

DCTN1-226

DCTN1-226

CTGCCCTTTCTACTCCTCATGCAGCGGGGACTGAAGCCTAAGAAGGTGGTGTGTTTACTATTTGTGCCTGGGTGGATGGGGGCC
GACGGGAAAGGATGAGGAGTACGTGCCCCCTGACTTCGGATTCTTCCACCACACAAATGATAAACACGGACCCACCTACCCCGG

15,385

DCTN1

DCTN1-226

135
R G L K P K K

ENSE00001408363

DCTN1-226

ATGAGCCCCTTCCCCAGCTGTCCTGCATGTCCCTGGGCTGCTGCATGCATGTGTGTGTGACCTTGGGCTGGGATGGCCAGAGGAA
TACTCGGGGAAGGGGTTCGACAGGACGTACAGGGACCCGACGACGTACGTACACACACACTGGAACCCGACCCTACCGGTCTCCTT

15,470

DCTN1

DCTN1-226

DCTN1-226

ATGGTGGCCTTGGCTTTTCAGAGTTCCCTTTGAAGGGTGCAAGAACATCAGGCTCAGTGTCCATACCCAGGTAGCACTCATTAGGGA
TACCACCGGAACCGAAAAGTCTCAAGGAAACTTCCCACGTTCTTGTAGTCCGAGTCACAGGTATGGGTCCATCGTGAGTAATCCCT

15,555

DCTN1

DCTN1-226

DCTN1-226

TGATTCTCTCTGCCCCAGGACTCCAAGTCAAAGATTCCCCAATCAAAAACATAAGCATTGACTGTAAATAGCAGCAGTGTGAA
ACTAAGAGAGACGGGGTCCCTGAGGTTTCAGTTTCTAAGGGTTAGTTTTTGTATTCGTAAACTGACATTTATCGTCGTCACACTT

15,640

DCTN1

DCTN1-226

DCTN1-226

ATAGATCATTACTGGGTTACAGTGTGTTCTCACTTAGCCCCGAGCTTGGACGACTGTGGAAGGATAGACTGGGGGAATGGGGCTG
TATCTAGTAAATGACCCAATGTCACACAAGAGTGAATCGGGCTCGAACCTGCTGACACCTTCTATCTGACCCCTTACCCCGAC

15,725

DCTN1

DCTN1-226

DCTN1-226

AGGAAGGTACCAAGTGAGGGGGTTTTGCAGGAAGATGGGAGGTCAGGGAACAGAGCCTAGGAAGAAGTCCCAAGTTGGAAAAC
TCCTTCCATGGTTCACTCCCCAAAACGTCCTTCTACCCTCCAGTCCCTTGTCTCGGATCCTTCTTGTGACAGGGTTCAACCTTTTG

15,810

DCTN1

DCTN1-226

DCTN1-226

CTAAGAGCCTTCATGTGCCTGCCTGTGGATGGGCACAGCCATAAATATCCCCACACCCCACTCTGCCCATCAGTCTGTCCC
GATTCTCGGAAGTACACGGACGGACACCTACCCGTGTCGGTATTTATAGGGGTGTGGGGTGTGAGACGGGGTAGTCAGACAGGG

15,895

DCTN1

DCTN1-226

DCTN1-226

TGTCTCCTTCTCTGGTGGTGTGCCTGAGGCCTACCTCCTACCCCTTGCAGCCTTTCATCAACCATCATTGGAGTGGGGCTCAAT
ACAGAGGAAGGAGACCACACGGACTCCGGATGGAGGATGGGGAACGTCGGAAAGTAGTTGGTAGTAACCTCACCCCGAGTTA

15,980

DCTN1

DCTN1-226

DCTN1-226

CATGTCACGTCCCCTCCCCTTCCCACCATAGACTCTTTAAACTCTTAGATCACTGCCATGACCACTTCTCAAACCAGCCCCTGC
GTACAGTGCAGGGGAGGGGAAGGGTGGTATCTGAGAAATTTGAGAATCTAGTGACGGTACTGGTGAAGGAGTTTGGTCGGGGACG

16,065

DCTN1

DCTN1-226

DCTN1-226

CTTGGGCCTCTGCCCAAGCTGTTTTTGACCTGCATGTGCCTGTCTGGCCTGTATGTACTGTGCTGTATGTACAATTCTGTGATTT
GAACCCGGAGACGGGTTCGACAAAAAAGTGGACGTACACGGACAGACCCGGACATACATGACACGACATACATGTTAAGACACTAAA

16,150

DCTN1

DCTN1-226

DCTN1-226

CCTTGTGCGTCAGCCTATCTCAGGCCATTCTGACATTGCATGGAGAGCTGCTGGATTGGGGCTGTGGGAGGGAAGAGGAAAACATC
GGAACAGCAGTCGGATAGAGTCCGGTAAGACTGTAACGTACCTCTCGACGACCTAACCCCGACACCCTCCCTTCTCCTTTTGTAG

16,235

DCTN1

DCTN1-226

DCTN1-226

TCCTTTTCCAGGGGGAAACCAGCTCCTGGTTGGTGATGGGTCTTTGGAGTCTTGCCATGGTAGAGACCACATGCTGGTACTTGC
AGGAAAAGGTCCCCCTTTGGTCGAGGACCAACCACTACCCAGGAAACCTCAGAACGGTACCATCTCTGGTGTACGACCATGAACG

16,320

DCTN1

DCTN1-226

DCTN1-226

TTTGGTAGGGAATGGGGATATAAGGAAAAATAATGCTGTGAAGGATCCTGGGCCATTTTCAGAGTCATAGAACTTGGCTTTGTCC
AAACCATCCCTTACCCCTATATTCTTTTATTACGACACTTCTTAGGACCCGGGTAAAGTCTCAGTATCTTTGAACCGAAACAGG

16,405

DCTN1

DCTN1-226

DCTN1-226

TTTGATTATTGTCTCCTGGTTGGGGCTTCCATTTACCTCAGGCCTTGAATAGAGAAGAGCATGAAACTATGGTCTGATATTTAT
AAACTAATAACAGAGGACCAACCCCGAAGGTAAAGTGGAGTCCGGAACCTTATCTCTTCTCGTACTTTGATACCAGACTATAAATA

16,490

DCTN1

DCTN1-226

DCTN1-226

GGAGTTCTGGCCCCAGCCTGGTCTGACCCTGGGCTGGGGCCTGAGCAATGCCCAAATCCAGGGGCTTTGGCAGCTGCCTGGGGAA
CCTCAAGACCGGGGTCGGACCAGACTGGGACCCGACCCCGGACTCGTTACGGGTTTAGGTCCCCGAAACCGTGCACGGACCCCTT

16,575

DCTN1

DCTN1-226

DCTN1-226

ATGTGAAAAAGCCAGCCTAGGCCACCCATGCTGCCCCTTCTGCACTCACGTTGGAAAAGTGTCAATCAGACAGTTGAGTGCCCCCA
TACACTTTTTTCGGGTCGGATCCGGTGGGTACGACGGGAAGACGTGAGTGCAACCTTTTACAGTTAGTCTGTCAACTCACGGGGGT

16,660

DCTN1

DCTN1-226

DCTN1-226

CCCCGGAGCACCCAGTCTTCCCTCTCCAGTAGTTATTTTTCAAAGCAGAGGGGCCCTGCTCTCACCCATGTGGATCAGGGAGCTG
GGGGCCTCGTGGGGTCAGAAGGAGAGGTCATCAATAAAAAAGTTTCGTCTCCCGGGGACGAGAGTGGGTACACCTAGTCCCTCGAC

16,745

DCTN1

DCTN1-226

DCTN1-226

GTTCCAGAGCAAAAGAATATGCTTTGAAGGGGAAGGCAGAAGAAAACCTCAGATGTCTCTGCAAAGTGCCTAGTTCTTTTTGGAAA
CAAGGTCTCGTTTTCTTATACGAAACTTCCCCTTCCGTCTTCTTTGAGTCTACAGAGACGTTTCACGGATCAAGAAAAACCTTT

16,830

DCTN1

DCTN1-226

DCTN1-226

CCCTTTAGAGACAGGCTTTAACCTGTCTACAACCAGGGGATGGTTGGAGAGGAGCCCAACAGTCATTAGAGCTGCTGCTACCCAG
GGGAAATCTCTGTCCGAAATTGGACAGATGTTGGTCCCCTACCAACCTCTCCTCGGGTTGTCAGTAATCTCGACGACGATGGGTC

16,915

DCTN1

DCTN1-226

DCTN1-226

ATGCGTGTTCGCGAGGGTTTCGTAGTCACTGTGTGTGCTCCTCAGAGCTGAAGCCTGTTGCTGGAGGGGCACTCTAGATGTGTGT
TACGCACAAGGCGTCCCAAAGCATCAGTGACACACACGAGGAGTCTCGACTTCGGACAACGACCTCCCCGTGAGATCTACACACA

17,000

DCTN1

DCTN1-226

DCTN1-226

GCCAGATGAGAGACTGTAAGGGTGTGGCCAGGTTGTATAAGAGACAGAAGTGGAGTTAATGGGGCTGTGGGTAGGTGGGTGGCGG
CGGTCTACTCTCTGACATTCCACACAACGGTCCAACATATTCTCTGTCTTCACTCAATTACCCCGACACCCATCCACCCACCGCC

17,085

DCTN1

DCTN1-226

DCTN1-226

GGGCAGAATGTGAGTATGATGAGAGAGACTGCTGGAGCAGAGAGGCCATGTGTCCCTCCCCAGTGATGCCCTGGCCCCATAGAAT
CCCGTCTTACACTCATACTACTCTCTGACGACCTCGTCTCTCCGGTACACAGGGAGGGGTCACTACGGGACCGGGTATCTTA

17,170

DCTN1

DCTN1-226

DCTN1-226

GCCATTTCTGGGATAGCCCCTGGCCCAAGTTTTTTGGAGCACGCTCTTGGGGGTGGGCAAGGGAGGGGAAGAGAGGAGCCAAAACCT
CGGTAAAGACCCTATCGGGGACCGGGTCAAAAAACCTCGTGCGAGAACCACCCCGTTCCTCCCTTCTCTCCTCGGTTTTGGA

17,255

DCTN1

DCTN1-226

DCTN1-226

GTTCTTTGGAGAAAGAAGCAGGACAAGCTCTGCGCATGACTGTTCATGAGGAGGAGGAGCCAGCAAAGCCCTAGATGGTTGCTAGG
CAAGAAAACCTCTTTCTTCGTCTGTTTCGAGACGCGTACTGACAGTACTCCTCCTCCTCGGTCGTTTCGGGATCTACCAACGATCC

17,340

DCTN1

DCTN1-226

DCTN1-226

TGACTGAGGAGCAGTGGCTCCACCCCATGGAGCAGAGGAGGGTGGGTGCATGACGTCAGGTGGAGCTGGTGCTGCGGCCACTGA
ACTGACTCCTCGTCAACGAGGTGGGGGTACCTCGTCTCCTCCCACCCACGTAAGTGCAGTCCACCTCGACCACGACGCCGGTGACT

17,425

DCTN1

DCTN1-226

DCTN1-226

GGCTGCCATCAGCCTAAGCTGGTGAACCTGGGCCAGGCACCGCTCCGGTGCCTGCCGGAGCCTGGCGATCCAGCTGCACGTCTGCG
CCGACGGTAGTCGGATTCGACCACTTGACCCGGTCCGTGGCGAGGCCACGGACGGCCTCGGACCGCTAGGTTCGACGTGCAGACGC

17,510

DCTN1

DCTN1-226

DCTN1-226

GGGGCCTCTGTGTCAGAGCGGGCGCCGTTTGCAGGCTGGGAAGCTGCCGCACCGGGAGGCTGAGACTGCATTGTTGGGATTTGAT
CCCCGGAGACACAGTCTCGCCGCCGGCAAACGTCCGACCTTCGACGGCGTGGCCCTCCGACTCTGACGTAACAACCCTAAACTA

17,595

DCTN1

DCTN1-226

DCTN1-226

GCACTAATCTCCTGTCTCCGCCGCCCTTTCCCTCTGTTTCGGTCTCTTGCCTCCCTCCCTTCGTCTGTCTTCTCCTCCGTGTGTTTG
CGTGATTAGAGGACAGAGGCGGGGAAAGGGAGACAAGCCAGAGAACGGGAGGGAGGGAAAGCAGACAGGAAGGAGGCACACAAAC

17,680

DCTN1

DCTN1-226

DCTN1-226

TCTATCCTCCTCTGTCCCTCCTCTTTCCCTCTCCTTGCTTTCTTTGGTTTTCTGCAATGATGAGACAGGCACCGACAGCCCGAAAG
AGATAGGAGGAGACAGGGAGGAGAAAGGAGAGGAACGAAAGAAACCAAAAGACGTTACTACTCTGTCCGTGGCTGTCCGGCTTTTC

17,765

DCTN1

DCTN1-226

DCTN1-226

140
A P T A R K
ENSE00002453672

GTACTCTTGCTTGGCTCTCGTCCTGCTGCTGGGTTGCCAGGGCAATGGTGGCAGCAGGCTGCTGGGGTGGGGGTGGGGGCTGATTG
CATGAGAACGAACGAGAGCAGGACGACGACCCAACGGTCCCCTTACCACCGTCGTCCGACGACCCACCCCCACCCCCGACTAAC

17,850

DCTN1

DCTN1-226

DCTN1-226

ACTTCATCTGTCTACCTGGTCGGGGAGGCGGGTGAGGACGAAGGTGGGTTAGGGAGAGGTGTGTGTCACCACTATGCCCCACACC
TGAAGTAGACAGATGGACCAGCCCCTCCGCCCACTCCTGCTTCCACCCAATCCCTCTCCACACACAGTGGTGATACGGGGTGTGG

17,935

DCTN1

DCTN1-226

DCTN1-226

CTGGGCATTTGCTTACTGCCTTGCCTGCTTTTGGCTCTGCCTGTGTTCCAGGCCTTAACACCCAGTGGCCTCACAGGCTTGGGCT
GACCCGTAAACGAATGACGGAACGGACGAAAACCGAGACGGACACAAGGTCCGGAATTGTGGGTACCCGGAGTGTCCGAACCCGA

18,020

DCTN1

DCTN1-226

DCTN1-226

TCAGGCAGCCTCTACCGCATACCGGATCTGGGAGGGTTTCTGTGGTAGAACCTAGGGAAGCAGGCCAGGTATCTCAGTGCCTC
AGTCCGTCGGAGATGGCGTATGGCCTAGACCCTCCCAAAGGACACCATCTTGGATCCCTTCGTCCGGGTCCATAGAGTCACGGAG

18,105

DCTN1

DCTN1-226

DCTN1-226

TAGCAGGCCTGCCTGCCTCACCCAACCTTTGCTAGAATACCTCTTGGTTGTTCTCCAGTATCCCCAATCCCCAGGATTTGTAT
ATCGTCCGGACGGACGGAGTGGGTTGGAAACGATCTTATGGAGAACCAACAAGAGGGTTCATAGGGGGTTAGGGGTCTTAAACATA

18,190

DCTN1

DCTN1-226

DCTN1-226

CAGGGCACTTTACCAGGGTGGGATGGGGAACCTAGAATAGTCTTTGACCCACAGCTGTGGAAGCTTAGCCCAGGGTAGAAGAGGT
GTCCCGTGAAATGGTCCACCCCTACCCCTTGGATCTTATCAGAAACTGGGTGTCGACACCTTCGAATCGGGTCCCATCTTCTCCA

18,275

DCTN1

DCTN1-226

DCTN1-226

GGGAATTGGCCTCAGTGTATGCTGGAAATAGGGCCCAAGCCAAATCTTGTCTTGGCTAGAGCAGTGAGATACTGGGTAGCAAGAA
CCCTTAACCGGAGTCACATACGACCTTTATCCCGGGTTCGGTTTAGAACAGAACCAGTCTCGTCACTCTATGACCCATCGTTCTT

18,360

DCTN1

DCTN1-226

DCTN1-226

CACTATTTGGAAATTGGAGTTAATTGTCCACTTACCATTTTGCAGTAACCTGAAGGGGCTGTAGTTTCTCTGTGCTGCTGCCCAC
GTGATAAACCTTTAACCTCAATTAACAGGTGAATGGTAAAACGTCATTGGACTTCCCCGACATCAAAGAGACACGACGACGGGTG

18,445

DCTN1

DCTN1-226

DCTN1-226

CCCCACCTCCTTTTCTACAGCTGGGTGGGGTTACTTTTGTGAGCTCTGGGCTTCTGCTAATGCAATATTCATGGTCCTGACACCT
GGGGTGGAGGAAAGGATGTCGACCCACCCCAATGAAACGACTCGAGACCCGAAGACGATTACGTTATAAGTACCAGGACTGTGGA

18,530

DCTN1

DCTN1-226

DCTN1-226

GAGCCCTCTTCCCTAGTGATCGGGACTGCTGCAGGATCTGGTTCTGGGGAAGGGGGTTGGGGGAGGGAGGACAGCAGCATTGTTC
CTCGGGAGAAGGGATCACTAGCCCTGACGACGTCTTAGACCAAGACCCCTTCCCCCAACCCCTCCCTCCTGTCGTCGTAACAAG

18,615

DCTN1

DCTN1-226

DCTN1-226

TACCCTAGGGACCTGATCTCCCATTTCTGGGCTTAGATTACGCTCGTCCATGTTGGGGTTTCTAGGGAGTTCTGTGTAGAGTCTAGC
ATGGGATCCCTGGACTAGAGGGTAAAGACCCGAATCTAATGCGAGCAGTGTACCCCAAAGATCCCTCAAGACACATCTCAGATCG

18,700

DCTN1

DCTN1-226

DCTN1-226

ACTTGAAGGAAGAGGGCTGACCTGGGAAAAGTCCTTGGGAGTGGTGGCTGGGCGGGGCTCTGGCTCTGGACTGGAGTTGGAGAGAT
TGAACCTTCTTCTCCGACTGGACCCCTTTCAGGAACCCCTCACCACCGACCCGCCCCGGAGACCGAGACCTGACCTCAACCTCTCTA

18,785

DCTN1

DCTN1-226

DCTN1-226

CGTTAGCAGGAGGACTGGTCTCATGGGACCTTCTCACTAGCTGCTTCTTGTCTATGGCTCAGCCTAGAGATGGACTTCTGGGA
GCAATCGTCCTCCTGACCAGAGTACCCTGGAAGAGTGATCGACGAAGGAACAAGATACCGAGTCGGATCTCTACCTGAAGACCCCT

18,870

DCTN1

DCTN1-226

DCTN1-226

TTTCTGGGGTGTCTGAAGGGGTGAGGCCTGCAAGGATTGGACAAAAGTGGGAGCAGGAACCAAGGGGAACAGGAATTCTGGGTTC
AAAGACCCACAGACTTCCCCTCCGGACGTTCTAACCTGTTTTACCCCTCGTCCTTGGTTCCCTTGTCTTAAGACCCAAAG

18,955

DCTN1

DCTN1-226

DCTN1-226

CTGAAGTAGGAATACAGTGATTCACTGAAGGGGAGAAGGGGATGGGATGGGGGGGAGGGTGGCTAACTGTAGCCCCATTCTCTGTTA
GACTTCATCCTTATGTCACATAAGTGACTTCCCTCTTCCCTACCTACCCCCCTCCACCGATTGACATCGGGGTAAGGACAAT

19,040

DCTN1

DCTN1-226

DCTN1-226

TTTCTTCTGCTCTCATTGCTGTCCCTTTTGTCTCTGTCTTTCTGCCATTGTCCTTTCTTTCTGACTACTTCTCTTCTGGCTCC
AAAGAAGACGAGAGTAACGACAGGGAAAACGAGAGACAGAAAAGACGGTAACAGGAAAAGAAAGGACTGATGAAGAGAAGACCGAGG

19,125

DCTN1

DCTN1-226

DCTN1-226

TGTTGCCTGTCCAGACCACAACCTCGGCGACCCAAAGGTGAGAAAACAGGCCCTGTGTGAGCCACTGCTGAGTGTACACACACGTT
ACAACGGACAGGTCTGGTGTGAGCCGCTGGGTTCCACTCTTTGTCCGGGGACACACTCGGTGACGACTCACATGTGTGTGCAA

19,210

DCTN1

DCTN1-226

145 T T T R R P K 150
ENSE00003693700

DCTN1-226

TCAGGCATGTGGATGTATGAGGGCACGTGTATGAGCAAGTGAAAGTTCGTCATAGTGTATCCTGGGTTCTCTTCAGAGGAAAAGGG
AGTCCGTACACCTACATACTCCCGTGCACATACTCGTTCACTTTCAAGCAGTATCACATAGGACCCAAGAGAAGTCTCCTTTCCC

19,295

DCTN1

DCTN1-226

DCTN1-226

TGGGGGTTTCGCAAGTGCTGGCAGGCACCTCCTGGGGAAAATGGCTTTTGGCTTTTAGGAGGTTGTCTAAGCCAGTAGCTTGAATGC
ACCCCAAGCGTCACGACCGTCCGTGGAGGACCCCTTTTACCGAAAACCGAAAATCCTCCAACAGATTTCGGTCATCGAACTTACG

19,380

DCTN1

DCTN1-226

DCTN1-226

AAAAGAGAAATGAATGGGGTTGTGGTGGTTAATCAAAGCAGGCTTTCTTGAACAAGGGGAATTTTGACCAGTTTTGATGGGAGGGA
TTTTCTCTTTACTTACCCCAACACCAATTAAGTTTTCGTCCGAAAGAACTTGTTCCTTAAAACCTGGTCAAAACTACCCCTCCCT

19,465

DCTN1

DCTN1-226

DCTN1-226

TTGGAAGAAAGATGAACTTGGCCATGTAAAATGTCAGGGGATAAGGAGGTGAGTGTGTCTGTGACAGGCCTTGGGTGGGGATGTC
AACCTTCTTTCTACTTGAACCGGTACATTTTACAGTCCCTATTCTCCACTCACACAGACACTGTCCGGAACCCACCCCTACAG

19,550

DCTN1

DCTN1-226

DCTN1-226

TGAGGATTGCACATGATCTCTGAGTGTTCAGCCCACTGGGAGACCTTGGGGCTCAGCACTTTGAGCACATTGGCAGGCCTGTCTGC
ACTCCTAACGTGTACTAGAGACTCACAGTCGGGTGACCTCTGGAACCCCGAGTCGTGAAACTCGTGTAACCGTCCGGACAGACG

19,635

DCTN1

DCTN1-226

DCTN1-226

TCCAGGGCTTGAACCTTCAGGTCAGCTCCTCTGCCACCTTCTCCCTGCCACAGGGGCATGGATAGTGTGGCCAGATCGGGGG
AGGTCCCGAACCTGAAGTCCAGTCGAGGAGACGGGTGGAAGAGGGGACGGGGTGTCCCCGTACCTATCACAACGGTCTAGCCCCC

19,720

DCTN1

DCTN1-226

DCTN1-226

AGATGACGAAGAGTTGTTTCAAGGGGGAGTCTAGGGGTACAACCTTTCACCTTGGCCCTTTTACCTGCAGGGTCTCTGAAATAGA
TCTACTGCTTCTCAACAAAGTTCCCCCTCAGATCCCCATGTTGAAAGTGAACCGGGAAAATGGACGTCCCAGGAGACTTTATCT

19,805

DCTN1

DCTN1-226

DCTN1-226

CTGAGAGAGGGAGATTTCAGCTTGACTCCCAAAGAGGGCTTAGCAGGGGTAGAGAGCCTGGCACCCCCACTTTTGGCCCAACCTTC
GACTCTCTCCCTCTAAGTCGAACTGAGGGTTTCTCCCGAATCGTCCCCATCTCTCGGACCGTGGGGGTGAAAACCGGGTTGGAAG

19,890

DCTN1

DCTN1-226

DCTN1-226

TGTGGAAATTAGATTGTACTTTTTCCGTCTAGGGGTGGAGGGCATAGACCTGGAGCAAGGATGGGACTGAGAGTATAATGGAGTT
ACACCTTTAATCTAACATGAAAAAGGCAGATCCCCACCTCCCGTATCTGGACCTCGTTCCCTACCCTGACTCTCATATTACCTCAA

19,975

DCTN1

DCTN1-226

DCTN1-226

GCTAGAATGATCACAAGTGGGTCATAGATGGGGTTCTAGGGAATAACGGATTCTGCTCTTAAGGGTAGTGCCAGAGCTAGGAGG
CGATCTTACTAGTGTTCACCCAGTATCTACCCCCAAGATCCCTTATTGCCTAAGACGAGAATTCCCATCACGGTCTCGATCCTCC

20,060

DCTN1

DCTN1-226

DCTN1-226

AATGTGGAGTCAGTGCCAAGCGAGGAGCCTTATAATCTTATGTCTTTCTTTATCTTTTCCCTCCCTCTCTCCTCTGCCTCCATCC
TTACACCTCAGTCACGGTTCGCTCCTCGGAATATTAGAATACAGAAAGAGAATAGAAAAGGAGGGAGAGAGGAGACGGAGGTAGG

20,145

DCTN1

DCTN1-226

DCTN1-226

TCCCCCTGTCCTTTGTCACATCTCTCTCTGCCTCTCTGTATCATTTTTCTTGTCCCCTTCATTCTTCTTTTCTCACTGTGCTTT
AGGGGGACAGGAAACAGTGATAGAGAGAGACGGAGAGACATAGTAAAAGGAACAGGGGAAGTAAGAAGAAAAGAGTGACACGAAA
DCTN1 >

DCTN1-226 >
----- >
DCTN1-226 >

GATACTCTCTTTCTGCTTTTTCCCTTTTCTGTCTCCTTCCCTTGCCATATTCTCATATTCTGTTTCTGTTTCTTACTACCCCT
CTATGAGAGAAAAGACGAAAAAGGGAAAAAGACAGAGGAAGGGAAACGGTATAAGAGTATAAGACAAAAGACAAGGAGAATGATGGGGA
DCTN1 >

DCTN1-226 >
----- >
DCTN1-226 >

ATCCTCTGCTTTCTTTCTGGTCTGCCTCTACCCTTTCTGAATAGCCCACGCGCCCAGCCAGTACTGGGGTGGCTGGGGCCAGTAG
TAGGAGACGAAAGAAAGACCAGACGGAGATGGGAAAGACTTATCGGGTGC GCGGGTCGGTCATGACCCCACCGACCCCGGTCATC
DCTN1 >

DCTN1-226 >
----- >
DCTN1-226 >
P T R P A S T G V A G A S S
ENSE00003509714 >
DCTN1-226 >

CTCCCTGGGCCCCCTCTGGCTCAGCGTCAGCAGGTGAGCTGAGCAGCAGTGAGCCCAGCACCCCGGCTCAGACTCCGCTGGCAGCA
GAGGGACCCGGGGAGACCGAGTCGCAGTCGTCCACTCGACTCGTCTGTCACTCGGGTCGTGGGGCCGAGTCTGAGGGCAGCCGTCGT
DCTN1 >

DCTN1-226 >
----- >
DCTN1-226 >
S L G P S G S A S A G E L S S S E P S T P A Q T P L A A
ENSE00003509714 >
DCTN1-226 >

CCCATCATCCCCACGCCGGTCCTCACCTCTCCTGGAGCAGTCCCCCGCTTCTTCCCCATCCAAGGTAAGGCCTGGGGTAGGGG
GGGTAGTAGGGGTGCGGCCAGGAGTGGAGAGGACCTCGTCAAGGGGGCGAAGGAAGGGGTAGGTTCCATTCCGGACCCCATCCCC
DCTN1 >

DCTN1-226 >
----- >
DCTN1-226 >
P I I P T P V L T S P G A V P P L P S P S K
ENSE00003509714 >
DCTN1-226 >

TAAAGGAGAATCAAGACACCCAGAGGCTTGTGGCTACCCGCTGTGTCTTAAAAATTTCTTGGGGTTGGCAAAGACCTAGAACTTG
ATTTCTCTTAGTTCTGTGGGTCTCCGAACACCGATGGGCGACACAGAACTTTTAAAGGACCCCAACCGTTTCTGGATCTTGAAC
DCTN1 >

DCTN1-226 >
----- >
DCTN1-226 >

GATCAGAAAAGGGTGAGGACATAGCCTATGGATATCTTGTACTGACTGAGCCATCCTTTCTTTCTTGCCTTATGCCATACTTT
CTAGTCTTTCCCACTCCTGTATCGGATACCTATAGAACGATGACTGACTCGGTAGGAAAGGAAAGAACGGGAATACGGTATGAAA
DCTN1 >

DCTN1-226 >
----- >
DCTN1-226 >

CCCCATATATACTGTGCTACGGTTTCCTCTCAGATGTTCTTATGCCACTGACTGTTGGCCACCCTGGGGCTGGGTGATGTTTGCA
GGGGTATATATGACACGATGCCAAAGGAGAGTCTACAAGAATACGGTGACTGACAACCGGTGGGACCCCGACCCACTACAAACGT

20,825

DCTN1

DCTN1-226

DCTN1-226

CACTTTCTTGTGTTCTTTGCGCCAGCTCAGTGTGGTGGAGAGGAGGAGTGGGCTGTGCACAGACCGTGAGGCCTCTCCTTTGCA
GTGAAAGAACACAAGAAACGCGGTTCGAGTCACAACCACCTCTCCTCCTCACCCGACACGTGTCTGGCACTCCGGAGAGGAAACGT

20,910

DCTN1

DCTN1-226

DCTN1-226

GGAGGAGGAGGGACTAAGGGCTCAGGTGCGGGACCTGGAGGAGAACTAGAGACCCTGAGACTGAAACGGGCAGAAAGACAAAGCA
CCTCCTCCTCCCTGATTCCCGAGTCCACGCCCTGGACCTCCTCTTTGATCTCTGGGACTCTGACTTTGCCCGTCTTCTGTTTCGT

20,995

DCTN1

DCTN1-226

DCTN1-226

E E E G L R A Q V R D L E E L E T L R L K R A E D K A
ENSE00003589987

DCTN1-226

AAGCTAAAAGAGCTGGAGAAACACAAAATCCAGCTGGAGCAGGTGCAGGAATGGAAGAGCAAAATGCAGGAGCAGCAGGCCGACC
TTCGATTTTCTCGACCTCTTTGTGTTTTAGGTCGACCTCGTCCACGTCTTACCTTCTCGTTTTACGTCCTCGTCCGGCTGG

21,080

DCTN1

DCTN1-226

DCTN1-226

K L K E L E K H K I Q L E Q V Q E W K S K M Q E Q Q A D
ENSE00003589987

DCTN1-226

TGCAGCGGCGCCTCAAGGAGGGCAGAAAAGGTTTACTCTGGATGAAGGGGGTGGCTGGGGCAGCCTGAGACCTAAGGAAGCATGC
ACGTCCGCCGCGGAGTTCTCCTCCGCTCTTTCCAACTGAGACCTACTTCCCCACCGACCCCGTCGGACTCTGGATTCTTCGTACG

21,165

DCTN1

DCTN1-226

DCTN1-226

L Q R R L K E A R K
ENSE00003589987

DCTN1-226

TGGAAACTAGACTGGAGCTGGAGCCTGGAACATACTGTGAGAAAGGCCTGGGGCATCTCTGTGCTGGTACCCCTCCACCTCCA
ACCTTTGATCTGACCTCGACCTCGGACCTTGTATGACACTCTTTCGGACCCCGTAGAGACACGACCATGGGGGAGGGTGGAGGT

21,250

DCTN1

DCTN1-226

DCTN1-226

CTTCTTCTCAGGAAGCCAAGGAGGGCGCTGGAGGCAAAGGAACGCTATATGGAGGAGATGGCTGATACTGCTGATGCCATTGAGA
GAAGAAGGAGTCTTTCGGTTCTCCGCGACCTCCGTTTCTTTCGGATATACCTCCTCTACCGACTATGACGACTACGGTAACTCT

21,335

DCTN1

DCTN1-226

DCTN1-226

E A K E A L E A K E R Y M E E M A D T A D A I E
ENSE00003655193

DCTN1-226

TGGCCACTTTGGACAAGGAGATGGCTGAAGAGCGGGCTGAGTCCCTGCAGCAGGAGGTGGAGGGCACTGAAGGAGCGGGTGGACGA
ACCGGTGAAACCTGTTCTCTACCGACTTCTCGCCGACTCAGGGACGTCGTCCTCCACCTCCGTGACTTCTCGCCACCTGCT

21,420

DCTN1

DCTN1-226

M A T L D K E M A E E R A E S L Q Q E V E A L K E R V D E

ENSE00003655193

DCTN1-226

GCTCACTACTGACTTAGAGATCCTCAAGGCTGAGATTGAAGAGAAGGGTAAGGGGGCCACAGCTGCTGGGGGCCAAACGGTCAGG
CGAGTGATGACTGAATCTCTAGGAGTTCGACTCTAACTTCTCTTCCATTCCCGGGTGTGCGACGACCCCGGTTTGCCAGTCC

21,505

DCTN1

DCTN1-226

L T T D L E I L K A E I E E K

ENSE00003655193

DCTN1-226

TGAGAACCATGCCTGAAAGTGTTAATGATCTTCTCCAGGCTCAGATGGCGCTGCATCCAGTTATCAGCTCAAGCAGCTTGAGGAG
ACTCTTGGTACGGACTTTCACAATTACTAGAAGAGGTCCGAGTCTACCGCGACGTAGGTCAATAGTCGAGTTCGTGAACTCCTC

21,590

DCTN1

DCTN1-226

G S D G A A S S Y Q L K Q L E E

ENSE00003581273

DCTN1-226

CAGAATGCCCGCCTGAAGGATGCCCTGGTGAGGTAGGGTCTTCAGTGCTTGCCCTCTGATGCTTACTCTTGTGTCTCCAAATGTGT
GTCTTACGGGCGGACTTCTACGGGACCACTCCATCCAGAAGTCACGAACGGAGACTACGAATGAGAACACAGAGGTTTACACA

21,675

DCTN1

DCTN1-226

Q N A R L K D A L V R

ENSE00003581273

DCTN1-226

TAGAGCACCCATCGCCAGAGACTCTGACACGTGCTTTCCTCCTTCTGCCTTCTCACATCCCTGCAGGATGCGGGATCTTCTTC
ATCTCGTGGGTAGCGGTCTCTGAGACTGTGCACGAAAGGAGGAAGACGGAAGGAGTGTAGGGACGTCCTACGCCCTAGAAAGAAG

21,760

DCTN1

DCTN1-226

M R D L S S

ENSE00003673000

DCTN1-226

CTCAGAGAAGCAGGAGCATGTGAAGCTCCAGAAGCTCATGGAAGAAGAACCAAGAGCTGGAAGTTGTGAGGCAACAGCGGGAG
GAGTCTCTTCGTCTCGTACACTTCGAGGTCTTCGAGTACCTTTCTTCTTGGTTCTCGACCTTCAACACTCCGTTGTGCGCCCTC

21,845

DCTN1

DCTN1-226

S E K Q E H V K L Q K L M E K K N Q E L E V V R Q Q R E

ENSE00003673000

DCTN1-226

CGTCTGCAGGAGGAGCTAAGCCAGGCAGAGAGCACCATTGATGAGCTCAAGGAGCAGGTCTGGGGAGCCCAGCCCTCACCCAGA
GCAGACGTCCTCCTCGATTCGGTCCGTCTCTCGTGGAATACTACTCGAGTTTCTCGTCCAGACCCCTCGGGTTCGGGGAGTGGGTCT

21,930

DCTN1

DCTN1-226

R L Q E E L S Q A E S T I D E L K E Q

ENSE00003673000

DCTN1-226

ATCCCCACCTGACTCTCCTATCAGTTGATGCCTCCTCTTTCTAGGTACCTTCCAGCAGCCCTTCTCCCTATCCTCCCCGTAACA
TAGGGGGTGGACTGAGAGGATAGTCAACTACGGAGGAGAAAGATCCATGGAAGGTCGTCGGGAAGAGGGATAGGAGGGGCATTGT

22,015

DCTN1

DCTN1-226

DCTN1-226

CAGGTGGATGCTGCTCTGGGTGCTGAGGAGATGGTGGAGATGCTGACAGATCGGAACCTGAATCTGGAAGAGAAAAGTGCGCGAGT
GTCCACCTACGACGAGACCCACGACTCCTCTACCACCTCTACGACTGTCTAGCCTTGGACTTAGACCTTCTCTTTTACGCGCTCA

22,100

DCTN1

DCTN1-226

V D A A L G A E E M V E M L T D R N L N L E E K V R E

ENSE00003486002

DCTN1-226

TGAGGGAGACTGTGGGAGACTTGGTAAGAGAAGAGCAGACCCCTGACATCTGACTTGGACCTGCTGAGAAAAAGATTGACATGTG
ACTCCCTCTGACACCCCTCTGAACCATTCTCTTCTCGTCTGGGGACTGTAGACTGAACCTGGACGACTCTTTTTTCTAACTGTACAC

22,185

DCTN1

DCTN1-226

L R E T V G D L

ENSE00003486002

DCTN1-226

ACCCTTGGCCTTTGAGCAGGGTGTGCGGTGAGGGACCCAGCCTGGGCTTGTACCCTGACCCTGCCTTTTTTTTTTTTTTTTTTTT
TGGGAACCGGAAACTCGTCCCACACGCCACTCCCTGGGTTCGGACCCGAACGATGGGACTGGGACGGAAAAAAAAAAAAAAAAAAAA

22,270

DCTN1

DCTN1-226

DCTN1-226

TCTGAGATGGAATCTCGCTCTGTTGCCAGGCTGGAGCGCAGTGGCGCAATAATCTCGGCTCACTGCAACCTCCGCCTCCAGGTT
AGACTCTACCTTAGAGCGAGACAACGGTCCGACCTCGCGTACC CGGTTATTAGAGCCGAGTGACGTTGGAGGCGGAGGGTCCAA

22,355

DCTN1

DCTN1-226

DCTN1-226

CAAGCGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGTACTACAGGCATGCGCCACCATACCCAGCTAATTTTTGTATTTTTAGT
GTTTCGCTAAGAGGACGGAGTCGGAGGGCTCATCGACCATGATGTCCGTACGCGGTGGTATGGGTTCGATTAAAAACATAAAAAATCA

22,440

DCTN1

DCTN1-226

DCTN1-226

AGAGATGGGGTTTTACCCATGTTGGCCAGCATGATCTCGATCTCGACCTCATGATCCGCCTGCTTTGACCTCCCAAAGTGCTGGGA
TCTCTACCCCAAAGTGGTACAACCGGTCGTA TAGAGCTAGAGCTGGAGTACTAGGCGGACGAAACTGGAGGGTTTCACGACCCT

22,525

DCTN1

DCTN1-226

DCTN1-226

TTACAGGTGTGAACCACCGCCGCTGGCCGACCCTGCCTTTCTTTAGCCCAAACATATGGTGTGGTGTCTAGGAAGCGATGAATGA
AATGTCCACACTTGGTGGCGGGCAGCCGGCTGGGACGGAAAGAAATCGGGTTTGATACCACACCACAGGATCCTTCGCTACTTACT

22,610

DCTN1

DCTN1-226

465
E A M N E
ENSE00003658047

DCTN1-226

GATGAACGATGAGCTGCAGGAGAATGCACGTGAGACAGAACTGGAGCTGCGGGAGCAGCTGGACATGGCAGGCGCGGGTTTCGT
CTACTTGCTACTCGACGTCCTCTTACGTGCACTCTGTCTTGACCTCGACGCCCTCGTTCGACCTGTACCGTCCGCGCGCCCAAGCA

22,695

DCTN1

DCTN1-226

470 M N D E L Q 475 E N A R E T 480 E L E R E Q L D M A G A R V R 495
ENSE00003658047

DCTN1-226

GAGGCCCAAGAGCGTGTGGAGGCAGCCAGGAGACGGTTGCAGACTACCAGCAGACCATCAAGAAGTACCGCCAGCTGACCGCCC
CTCCGGGTCTTCGCACACCTCCGTCGGGTCCCTCTGCCAACGTCTGATGGTTCGCTGGTAGTTCTTCATGGCGGTTCGACTGGCGGG

22,780

DCTN1

DCTN1-226

500 E A Q K R V E 505 A Q E T 510 V A D Y Q 515 Q T I K K 520 Y R Q L T A 525
ENSE00003658047

DCTN1-226

ATCTACAGGTACATGCCCACTGTTTGTCTCTGCCACCATCACCCAGGGCTTCCTTATGACCCAGCTGTGCTTCACTGTCTCT
TAGATGTCCATGTACGGGTGACAAACGAGAGACGGGTGGTAGTGGGGTCCC GAAGGAATACTGGGTGCACACGAAGTGACAGAGA

22,865

DCTN1

DCTN1-226

H L Q
ENSE0000...

DCTN1-226

CCTCCTAGGATGTGAATCGGGAACTGACAAACCAGCAGGAAGCATCTGTGGAGAGGCAACAGCAGCCACCTCCAGAGACCTTTGA
GGAGGATCCTACACTTAGCCCTTGACTGTTTGGTTCGTCTTCGTAGACACCTCTCCGTTGTCGTCGGTGGAGGTCTCTGGAAACT

22,950

DCTN1

DCTN1-226

530 D V N R E L T N Q Q 535 E A S V E R Q Q Q P P P E T F D 550
ENSE00003543635

DCTN1-226

CTTCAAAATCAAGTTTGGCTGAGACTAAGGCCCATGCCAAGGTCAGGAAAAGTGTGTGGGTCTGAGGGAGCCCTGCCTGGGATGAAC
GAAGTTTTAGTTCAAACGACTCTGATTCCGGGTACGGTTCAGTCTTTTACACACCCAGACTCCCTCGGGACGGACCTACTTGG

23,035

DCTN1

DCTN1-226

555 K I K F 560 A E T K A H A K 565

ENSE00003543635

DCTN1-226

TGGTATGGGGTCTGGGCTTCAGATTCTGGGGGAAGGGGTGCTTTGTGTGGTGGTTTTGAAGACTCTGGCCTGGGCTTGCCCTAG
ACCATACCCAGACCCGAAGTCTAAGGACCCCTTCCCCACGAAACACACCACCAAACCTTCTGAGACCCGGACCCGAACGGGATC

23,120

DCTN1

DCTN1-226

DCTN1-226

AAGCAAGGGATCTACTGGAGCAAGGCATGGGAATTTTGGGGCTCTTTCAGCTCTGGCTAAGAGTCTCCTCCTGTTACCTCAC
TTCGTTCCCTAGATGACCTCGTTCCGTACCCTTAAACCCCGAGAAAAGTCGAGACCGATTCTCAGGAGGGAGGGACAAGTGGAGTG

23,205

DCTN1

DCTN1-226

DCTN1-226

AGGCAATTGAGATGGAATTGAGGCAGATGGAGGTGGCCAGGCCAATCGACACATGTCCCTGCTGACAGCCTTCATGCCTGACAG
TCCGTTAACTCTACCTTAACTCCGTCTACCTCCACCGGGTCCGGTTAGCTGTGTACAGGGACGACTGTCGGAAGTACGGACTGTC

23,290

DCTN1

DCTN1-226

570 A I E M E L R Q M E V A 575 Q A N R H M S L L T A 590 F M P D 595 S

ENSE00000762527

DCTN1-226

CTTCCTTCGGCCAGGTGGGGACCATGACTGCGTTCTGGTGTCTGTTGCTCATGCCTCGTCTCATTTGCAAGGTATGGCCAATCAAT
GAAGGAAGCCGGTCCACCCCTGGTACTGACGCAAGACCACGACAACGAGTACGGAGCAGAGTAAACGTTCCATACCGGTTAGTTA

23,375

DCTN1

DCTN1-226

600 F L R P G G D H D 605 V L V L L M P R L I C K 615

ENSE00000762527

DCTN1-226

CACATGTTCCACAGAAATCTAGTGAACCTTGCCATGAACCAGGCATTGAAGATGCTGAGTGAAGACAACAGAGTCTCTGCCACAA
GTGTACAAGGTGTCTTTAGATCACTTGAACGGTACTTGGTCCGTAACCTTCTACGACTCACTTCTGTTGTCTCAGAGACGGGTGTT

23,460

DCTN1

DCTN1-226

DCTN1-226

AGAGTTTATGGTATAGTGGAGGAACACAGCAAAGTCACCGATTAATATATATTACAAATGGTGTGTTTTCAAGGAGAGATAGGTT
TCTCAAATACCATATCACCTCCTTGTGTCGTTTCAGTGGCTAATTATATATAATGTTTACCACACAAAAGTTCTCTCTATCCAA

23,545

DCTN1

DCTN1-226

DCTN1-226

CTGTGAGAGAGCACAATTAGAGATTTGATTTAGAGGTGAGCAGGGTGTGACTGAGGGAATAACATTGTCTGAGGGCCAGGAGGTG
GACACTCTCTCGTGTTAATCTCTAAACTAAATCTCCACTCGTCCCACACTGACTCCCTTATTGTAACAGACTCCCGGTCTCTCCAC

23,630

DCTN1

DCTN1-226

DCTN1-226

CCTAGGGGTTAACCTTGGGGATGATGGGCAGGATAGCATTCTAGGTGGAGAGATAGCAGGAGTGGCAGCTTTAAGTCAGGAAAGA
GGATCCCCAATTGGAACCCCTACTACCCGTCTATCGTAAGATCCACCTCTCTATCGTCCTCACCGTCGAAATTCAGTCCTTTCT

23,715

DCTN1

DCTN1-226

DCTN1-226

CCTTGATTCCACCGGTCCCCTACTACCCCTTTTCAATTTTACATCCTGACTCCTCACAACCTCCAGTAATCACATCACTACCCCTTTCCC
GGAACCTAAGGTGGCCAGGGTATGGGAAAGTAAAAGTGTAGGACTGAGGAGTGTGGAGGTCATTAGTGTAGTGATGGGAAAGGG

23,800

DCTN1

DCTN1-226

DCTN1-226

CATGCAAGATTCCCCACCCAGGTAAGAGCTATTTCTGCTTTCTCTCCCATGTGTGTCCATGCTCCCCACATAGTTAAGCTCTGAG
GTACGTTCTAAGGGGTGGGTCCATTCTCGATAAAGACGAAAGAGAGGGTACACACAGGTACGAGGGGTGTATCAATTCGAGACTC

23,885

DCTN1

DCTN1-226

DCTN1-226

TACTATATTCCTGAGTCTCTGTTCTCCATCCTCTGCTCTGAGGCCAGGTTCTGGTGCTTTTTCCACAGGCAGAGCTGATCCG
ATGATATAAGGACTCAGAGACAAGAGGTAGGAGACGAGACTCCGGGTCCAAGGACCACGAAAAAGGGTGTCCGTCTCGACTAGGC

23,970

DCTN1

DCTN1-226

DCTN1-226

620
A E L I R
ENSE00001261323

GAAGCAGGCCCCAGGAGAAGTTTGAACCTAAGTGAGAACTGTTTCAGAGCGGCCTGGGCTGCGAGGAGCTGCTGGGGAGCAACTCAGC
CTTCGTCCGGGTCTCTTCAAACCTTGATTCACCTTTGACAAGTCTCGCCGGACCCGACGCTCCTCGACGACCCCTCGTTGAGTCG

24,055

DCTN1

DCTN1-226

DCTN1-226

625 630 635 640 645 650
K Q A Q E K F E L S E N C S E R P G L R G A A G E Q L S

ENSE00001261323

DCTN1-226

TTTGCTGCTGGACTGGTGTACTCGCTGAGCCTGCTGCAGGCCACGCTACACCGCTATGAGCAGTAAGTGACTCCTGACTCCCTCA
AAACGACGACCTGACCACATGAGCGACTCGGACGACGTCCGGTGCATGTGGCGATACTCGTCATTCACTGAGGACTGAGGGAGT

24,140

DCTN1

DCTN1-226

DCTN1-226

655 660 665 670
F A A G L V Y S L S L L Q A T L H R Y E H

ENSE00001261323

CCCCAGGGTGGGGGTCCAGGATTGGCCAGAAGTGGAGATTGCCTGGCAGACTCTAGCCTCACAGTGCCTTCTCTGGTCTCTAGTG
GGGGTCCCACCCCCAGGTCTTAACCGGTCTTGACTCTAACGGACCGTCTGAGATCGGAGTGTACACGGGAAGAGACCAGAGATCAC

24,225

DCTN1

DCTN1-226

DCTN1-226

CCCTCTCTCAGTGCAGTGTGGATGTGTATAAGAAAGTGGGCAGCCTGTACCCTGAGATGAGTGCCCATGAGCGCTCCTTGGATTT
GGGAGAGAGTACAGTACACCTACACATATTCTTTACCCGTCGGACATGGGACTCTACTCACGGGTACTCGCGAGGAACCTAAA

24,310

DCTN1

DCTN1-226

A L S Q C S V D V Y K K V G S L Y P E M S A H E R S L D F

ENSE00003666120

DCTN1-226

CCTCATTGAACTGCTGCACAAGGATCAGCTGGATGAGACTGTCAATGTGGAGCCTCTACCAAGGCCATCAAGTACTATCAGGTG
GGAGTAACCTTGACGACGTGTTCTAGTCGACCTACTCTGACAGTTACACCTCGGAGAGTGGTTCCGGTAGTTTCATGATAGTCCAC

24,395

DCTN1

DCTN1-226

L I E L L H K D Q L D E T V N V E P L T K A I K Y Y Q

ENSE00003666120

DCTN1-226

TGGGGCAAGAATTTGGGCTTGGGGCAGGAGGCAGGGAAGCTTTCACTTGATGGGGGCTCTTACTAATATATTCAAGGTTGTATGT
ACCCCGTTCTTAAACCCGAACCCCGTCCCTCCGTCCTTCCGAAAGTGAAGTACCCCGAGAATGATTATATAAGTTCCAACATACA

24,480

DCTN1

DCTN1-226

DCTN1-226

CCCATGCTTGCTGCTTGAGGCCTGGTTTGCTCTTAGATGAACTCTCCATATGATGCAGCTGCTTGAGGGCTTTGGATTCTCTTGT
GGGTACGAACGACGAACTCCGGACCAAACGAGAATCTACTTGAGAGGTATACTACGTCGACGAACTCCCGAAACCTAAGAGAACA

24,565

DCTN1

DCTN1-226

DCTN1-226

ACCTCCAGAGACCCATGATGACCAGGGCTCAAACCTACAGTTTGGGAAGAACTCCCCACCCGCTCCAGGGCTAAAAAGTTGTCTGT
TGGAGGTCTCTGGGTACTACTGGTCCCGAGTTTGTATGTCAAACCTTCTTGAGGGGTGGGCGAGGTCCCGGATTTTCAACAGACA

24,650

DCTN1

DCTN1-226

DCTN1-226

CTGTTATCTCTCCTCAGCATCTGTACAGCATCCACCTTGCCGAACAGCCTGAGGACTGTACTATGCAGCTGGCTGACCACATTAA
GACAATAGAGAGGAGTTCGTAGACATGTCGTAGGTGGAACGGCTTGTGCGACTCCTGACATGATACGTCGACCGACTGGTGTAAATT

24,735

DCTN1

DCTN1-226

H L Y S I H L A E Q P E D C T M Q L A D H I K

ENSE00003625068

DCTN1-226

GGTGAAGTATCTGGGCCAGTGATTGAGCCCCCGTGGAGATCAGAAATGGAGGGGCATCAGGTCAAGAGATCAGGCACCCAAGAAGT
CCACTTCATAGACCCGGTCACTAACTCGGGGGCACCTCTAGTCTTTACCTCCCCTAGTCCAGTTCTCTAGTCCGTGGGTTCTTCA

24,820

DCTN1

DCTN1-226

DCTN1-226

GTCACATAAGACTAGGGCAGAGTTACCAAAGCCATATCAGGGAAACTAGAGGACCTACTTATGTATGGGGGTCAGCAGAGGATGG
CAGTGTATTCTGATCCCCTCAATGGTTTCGGTATAGTCCCTTTGATCTCCTGGATGAATACATACCCCCAGTCGTCTCCTACC

24,905

DCTN1

DCTN1-226

DCTN1-226

GGACTTCTTAGAGATGTTGATAAGGCAGAAGGGCTCCTGCTGGGGGCTGATGATTGCATGCTTCTATCCTCACAGTTCACGCAGA
CCTGAAGAATCTCTACAACCTATTCCGTCTTCCCGAGGACGACCCCGACTACTAACGTACGAAGATAGGAGTGTCAAGTGCCTCT

24,990

DCTN1

DCTN1-226

F T Q
ENSE0000350...

DCTN1-226

GTGCTCTGGACTGCATGAGTGTGGAGGTAGGACGGCTGCGTGCCTTCTTGCAGGTGAGAACACATCTAGATCTGTGTGAGCTCCT
CACGAGACCTGACGTACTCACACCTCCATCCTGCCGACGCACGGAAGAACGTCCACTCTTGTGTAGATCTAGACACACTCGAGGA

25,075

DCTN1

DCTN1-226

755 760 765 770
S A L D C M S V E V G R L R A F L Q

ENSE00003503948

DCTN1-226

CTTCTTTCTTAGTCCTCACTTCTTACTCCGAGCCTTAATGCTAACTTGGTTCTCCATCCATTTTCTTTTTCTGAGTAGGGTGG
GAAGAAAGAATCAGGAGTGAAGGAATGAGGCTCGGAATTACGATTGAACCAAGAGGTAGGTAAAAGAAAAAGGACTCATCCCACC

25,160

DCTN1

DCTN1-226

G G
ENSE...

DCTN1-226

GCAGGAGGCTACAGATATTGCCCTCCTGCTCCGGGATCTGGAACTTCATGCAGTGACATCCGCCAGTTCTGCAAGAAGATCCGA
CGTCTCCGATGTCTATAACGGGAGGACGAGGCCCTAGACCTTTGAAGTACGTCACTGTAGGCGGTCAAGACGTTCTTCTAGGCT

25,245

DCTN1

DCTN1-226

775 780 785 790 795 800
Q E A T D I A L L L R D L E T S C S D I R Q F C K K I R

ENSE00003507126

DCTN1-226

AGGCGAATGCCAGGGACAGATGCTCCTGGGATCCCAGCTGCACTGGCCTTTGGACCACAGGTTTAAGGCTGCAACTGGGGAAGGG
TCCGCTTACGGTCCCTGTCTACGAGGACCCTAGGGTGCACGTGACCGGAAACCTGGTGTCCAAATTCCGACGTTGACCCCTTCCC

25,330

DCTN1

DCTN1-226

805 810 815 820
R R M P G T D A P G I P A A L A F G P Q

ENSE00003507126

DCTN1-226

AAGGAAACTGAGTAGAAACATGAAGGGTATAGCACTTGAAGATCTGGATCTGGTTAGGGGACAAAAATGGTTTTGGGGTAGCTGG
TTCTTTGACTCATCTTTGTACTTCCCATATCGTGAACCTTCTAGACCTAGACCAATCCCCTGTTTTTACCAAAACCCCATCGACC

25,415

DCTN1

DCTN1-226

DCTN1-226

AAACTGTGGTGCTGAACCCAGGGTTGACTCCTGACTCTGGCCTGGCACACAGGTATCTGACACGCTCCTAGACTGCAGGAAACAC
TTTGACACCACGACTTGGGTCCCAACTGAGGACTGAGACCGGACCGTGTGTCCATAGACTGTGCGAGGATCTGACGTCTTTTGTG

25,500

DCTN1

DCTN1-226

DCTN1-226

825 830
V S D T L L D C R K H
ENSE00001199788

TTGACGTGGGTCGTGGCTGTGCTGCAGGAGGTGGCAGCTGCTGCTGCCAGCTCATTGCCCACTGGCAGAGAATGAGGGGCTAC
AACTGCACCCAGCACCGACACGACGTCCTCCACCGTCGACGACGACGGGTGCGAGTAACGGGGTGACCGTCTCTTACTCCCCGATG

25,585

DCTN1

DCTN1-226

DCTN1-226

835 840 845 850 855 860
L T W V V A V L Q E V A A A A Q L I A P L A E N E G L
ENSE00001199788

TTGTGGCTGCTCTGGAGGAACTGGCTTTCAAAGCAAGCGAGCAGGTGGGCCTGGATGGCTGGGTAGAAGGTGTGGGGAGAGTTAG
AACACCGACGAGACCTCCTTGACCGAAAGTTTCGTTTCGCTCGTCCACCCGGACCTACCGACCCATCTTCCACACCCCTCTCAATC

25,670

DCTN1

DCTN1-226

DCTN1-226

865 870 875
L V A A L E E L A F K A S E Q
ENSE00001199788

TGACCAGTGTGGGGCTTTTACTTCTGCCCTTGGCTCCTGCAGATCTATGGGACCCCTCCAGCAGCCCTATGAGTGTCTGCGCC
ACTGGTCACACCCCGAAAAATGAAGACGGGAACCGAGGACGTCTAGATACCCTGGGGGAGGTCGTGCGGGGATACTCACAGACGCGG

25,755

DCTN1

DCTN1-226

DCTN1-226

880 885 890
I Y G T P S S S P Y E C L R
ENSE00003598271

AGTCATGCAACATCCTCATCAGTACCATGAACAAGCTGGCCACAGCCATGCAGGAGGGGGAGTATGATGCAGAGCGGCCCCCCAG
TCAGTACGTTGTAGGAGTAGTCATGGTACTTGTTCGACCGGTGTCGGTACGTCTCCCCCTCATACTACGTCTCGCCGGGGGGTC

25,840

DCTN1

DCTN1-226

DCTN1-226

895 900 905 910 915
Q S C N I L I S T M N K L A T A M Q E G E Y D A E R P P S
ENSE00003598271

CAAGGTAGGTGGAGATTTCTTGGAGAAAGTTGCAGAGGCCTGTAGGAGTAAGACTTGCAGAGCTACTGCTAGTTGTGGGAGGACG
GTTCCATCCACCTCTAAAGGAACCTCTTCAACGTCTCCGGACATCCTCATTCTGAACGTCTCGATGACGATCAACACCCCTCCTGC

25,925

DCTN1

DCTN1-226

920
K

EN...

DCTN1-226

GGGAGACAGGAGGAAGGCATCTGGAGAGCACCATCCTGCCTAGAAGGCAGGGTTTTCCCTGTAACCTGGATCTCTCTGTAAAGGAGC
CCCTCTGTCTCCTTCCGTAGACCTCTCGTGGTAGGACGGATCTTCCGTCCCAAAGGGACATTGACCTAGAGAGACATTCTCTCG

26,010

DCTN1

DCTN1-226

DCTN1-226

ACAGTGATGATCTCTTCTCTCCACCCTCACTTTCTCACCCCTACCGACCATTCTTAGCCTCCACCGGTTGAACTGCGGGCTGC
TGTCACTACTAGAGAAGAGAGGTGGGAGTGAAAGAGTGGGGGATGGCTGGTAAGGAATCGGAGGTGGCCAACCTTGACGCCCCGACG

26,095

DCTN1

DCTN1-226

925
P P P V E L R A A
ENSE00003562831

DCTN1-226

TGCCCTTCGTGCAGAGATCACAGATGCTGAAGGCCTGGGTTTGAAGCTCGAAGATCGAGAGACAGTTATTAAGGAGTTGAAGAAG
ACGGGAAGCACGTCTCTAGTGTCTACGACTTCCGGACCCAAACTTCGAGCTTCTAGCTCTCTGTCAATAATTCTCAACTTCTTC

26,180

DCTN1

DCTN1-226

930 A L R A E 935 I T D A E 940 L G L K 945 E D R E 950 T V I K E 955 L K K

ENSE00003562831

DCTN1-226

TCACTCAAGATTAAGGTGAGGGTAGTGTAGGCTCAGGATCTGGGGGCCAGGAAATTGGTAGGACTCAGGAAAGCAGTGAGTGTG
AGTGAGTTCTAATTCCACTCCCATCACATCCGAGTCTTAGACCCCCGGTCTTTAACCATCCTGAGTCTTTTCGTCACTCACAAC

26,265

DCTN1

DCTN1-226

960
S L K I K

ENSE00003562831

DCTN1-226

GGGATCGGGACCAAGACGGCTTGGGAGTTAAGGGGAGAAAGTGGGGCCTGCAATCAATGGGAGCTGTGGTGAGCCCTCAGGGAAAC
CCCTAGCCCTGGTTCTGCCGAACCTCAATTCCCTCTTACCCCCGACGTTAGTTACCCTCGACACCACTCGGGAGTCCCTTGG

26,350

DCTN1

DCTN1-226

DCTN1-226

TACTATCTCATGGTCTAGCCCCAGTTTCCAGGGACTGTGGGGAGGATGTCAGGGATCTAGAAGTTCTGTCTTGTCCAGGGAGA
ATGATAGAGTACCAGATCGGGGGTCAAAGGTCCCTGACACCCCTCCTACAGTCCCTAGATCTTCAAGACAGGAACAGGTCCCTCT

26,435

DCTN1

DCTN1-226

G E
ENSE...

DCTN1-226

GGAGCTAAGTGAGGCCAATGTGCGGCTGAGCCTCCTGGAGAAGAAGTTGGACAGTGCTGCCAAGGATGCAGATGAGCGCATCGAG
CCTCGATTCACTCCGGTTACACGCCGACTCGGAGGACCTCTTCTTCAACCTGTACAGACGGTTCCTACGTCTACTCGCGTAGCTC

26,520

DCTN1

DCTN1-226

965 970 975 980 985 990
E L S E A N V R L S L L E K K L D S A A K D A D E R I E

ENSE00003625419

DCTN1-226

AAAGTCCAGACTCGGCTGGAGGAGACCCAGGCCTGCTGCGAAAGAAGGAGAAGTCAGGCACCTTTCCCTGGGGCCTTGCTTCCTC
TTTCAGGTCTGAGCCGACCTCCTCTGGGTCCGTGACGACGCTTTCTTCTTCAAGTCCGTGAAAGGGACCCCGGAACGAAGGAG

26,605

DCTN1

DCTN1-226

995 1000 1005 1010
K V Q T R L E E T Q A L L R K K E K

ENSE00003625419

DCTN1-226

TAATCCTCCCACTGCTGGAGCTCTCTGCCTCCTAACCCATACCCCTACTCAGGTTCTCTTATAGTGAGACTCCCCATTTTCTTTA
ATTAGGAGGGTGACGACCTCGAGAGACGGAGGATTGGGTATGGGGATGAGTCCAAGAGAATATCACTCTGAGGGGTAAAAGAAAT

26,690

DCTN1

DCTN1-226

DCTN1-226

CCCACTGCCAACCCCACTTGCATCACCCAGCCTAAGCCTGTGCTGCTCTGCCCTGGCTTCTCACTGGCAGGGCTATTCCAAGGAC
GGGTGACGGTTGGGGTAACGTAGTGGGGTCGGATTTCGGACACGACGAGACGGGACCGAAGAGTGACCGTCCCGATAAGGTTCTCTG

26,775

DCTN1

DCTN1-226

DCTN1-226

CTCTCAGGACTGAATAGTCAAGGAGTGCTTTAGAGAAGGGACACTGCCAAAGCCCAGATTCTCTTTCACAGAGAGTTTGAGGAGA
GAGAGTCTGACTTATCAGTTCCTCACGAAATCTCTTCCCTGTGACGGTTTCGGGTCTAAGAGAAAGTGCTCTCAAACCTCCTCT

26,860

DCTN1

DCTN1-226

E F E E

ENSE00003468565

DCTN1-226

CAATGGATGCACTCCAGGCTGACATCGACCAGCTGGAGGCGAGAGAAGGCAGAACTAAAGCAGCGTCTGAACAGCCAGTCCAACG
GTTACCTACGTGAGGTCCGACTGTAGCTGGTTCGACCTCCGTCTCTCCGTCTTGATTTCGTCGCAGACTTGTGGTTCAGGTTTGC

26,945

DCTN1

DCTN1-226

1015 1020 1025 1030 1035 1040
T M D A L Q A D I D Q L E A E L K Q R L N S Q S K R

ENSE00003468565

DCTN1-226

CACGATTGAGGGACTCCGGGGCCCTCCTCCTTCAGGCATTGCTACTCTGGTCTCTGGCATTGCTGGTGGTGAGTACTGTGGAATA
GTGCTAACTCCCTGAGGCCCGGGAGGAGGAAGTCCGTAACGATGAGACCAGAGACCGTAACGACCACCACTCATGACACCTTAT

27,030

DCTN1

DCTN1-226

1045 1050 1055 1060 1065
T I E G L R G P P P S G I A T L V S G I A G

ENSE00003468565

DCTN1-226

GGCAGCACTAGCACAGAGGAGATTGTCTTCTCTCCTGTCTTGGCCTCATTTTTGACCTCTGCCCCACCCCTTACCCCGGGTA
CCGTCGTGATCGTGTCTCTCTAACAGAAGAGAGGACAGGAACCGGAGTAAAACTGGAGACGGGGTGGGGGGAATGGGGGCCCAT

27,115

DCTN1

DCTN1-226

DCTN1-226

TTCAGCCAGGAACATGCTTACACAGTTTCACTCTGTGCCAGTTTTACCAAGTTTTCCCTTCCGCTGAAGATGTGTGCTGAGTTT
AAGTCGGTCTTGTACGAATGTGTCAAAGTGAGACACGGTCAAAGTGGTTCAAAGGGGAAGGCGACTTCTACACACGACTCAA

27,200

DCTN1

DCTN1-226

DCTN1-226

CTCTGGGCAAAGGAGGGCATTACTAAATTGTTAATGAGGCTCAGAATAATGATGACAGTTGGTCTCTAGTAGATGTCCTTTCTGG
GAGACCCGTTTCTCCCGTAATGATTTAAACAATTACTCCGAGTCTTATTACTACTGTCAACCAGAGATCATCTACAGGAAAGACC

27,285

DCTN1

DCTN1-226

DCTN1-226

CTCTGTAATCTGACCTTTCTGCCAGCCCTATATCCCAGAGGGTTGTCAGCCAGCAGCAGGCTGGGCTGACTCTCCTGGGGCATC
GAGACATTAGACTGGAAAGACGGGTCGGGATATAGGGTCTCCAACAGTCGGTCGTCCGACCCGACTGAGAGGACCCCGTAG

27,370

DCTN1

DCTN1-226

DCTN1-226

CAGCCCTGCCGATACCTGCTCTTGATTGCTTCTCTGCTTGGACACTGTGTTTTCTCACTGAGTTCATGTGGCTTCATTTTATGA
GTCGGGACGGGCTATGGACGAGAACTAACGAAGAGACGAACCTGTGACACAAAAGAGTGACTCAAGTACACCGAAGTAAAACT

27,455

DCTN1

DCTN1-226

DCTN1-226

TGTGGTCATATCTTCCACTGCTGAATTATCCCAGTTTCACTTGGGGCTTGTGTTTTGACCTTTGTCTAGTCACTCAGTATAGTCA
ACACCAGTATAGAAGGTGACGACTTAATAGGGTCAAAGTGAACCCGAACACAAAACACTGGAAACAGATCAGTGAGTCATATCAGT

27,540

DCTN1

DCTN1-226

DCTN1-226

GGGCTCCTCACCTAGAGTTTTTCTGGTTACCAGTTCTAGCCTCCCCAGTTACCTGACTCAGGAGGTGGCTGCTGCTGCTTTGTT
CCCGAGGAGTGGATCTCAAAGACCAATGGTCAAGATCGGAGGGGTCAATGGACTGAGTCCTCCACCGACGACGACAGAAACAA

27,625

DCTN1

DCTN1-226

DCTN1-226

CTCCTCTGCCCTATAGTTTGTGTTTGTACTCTCCAGTTTCTCACTTAACCTTCTCACCTCCAGAAGACAGGCTTTTTGCCCTGG
GAGGAGACGGGATATCAAAACAAAACAAATGAGAGGTCAAAGAGTGAATTGGAAGAGTGGAGGTCTTCTGTCCGAAAAACGGGACC

27,710

DCTN1

DCTN1-226

DCTN1-226

AATTAACCCCTTAGGGCCTCCAGACTTTCCAGCTGCTCCTGAGTCTTGTGACCTGACCTCACCTACATAGAGTCTTTGACAAAG
TTAATTTGGGAATCCCGGAGGTCTGAAAGGGTGCAGCAGGACTCAGAACAGTCGACTGGAGTGGATGTATCTCAGAAACTGTTTC

27,795

DCTN1

DCTN1-226

DCTN1-226

TCTCTGTTACTGACACCCCTTGATCTTGGGAGGTGACCAAGTACCTTCTTGACTTTAGGCTCTTGTGGTACAGACAGCTCTGTGT
AGAGACAATGACTGTGGGGAAGTGAACCCCTCCACTGGTTCATGGAAGAAGTCAAATCCGAGAACACCATGTCTGTGCGAGACACA

27,880

DCTN1

DCTN1-226

DCTN1-226

TCTTTGGAGAGAGTTTCCAGGATTACTACTTTGTGTTGTTTTAGCACTCTTGAAACAAACATTAGCACTCTTTAAACAAACATA
AGAAACCTCTCTCAAAGGTCTAATGATGAAACACAACAAAAATCGTGAGAAGTTTGTGTAATCGTGAGAAATTTGTTTGTAT

27,965

DCTN1

DCTN1-226

DCTN1-226

GTTCTGAATTTATGAAACTTCCACCAAAAAAGAGGTCTTTTGCCTCAGAGCAATGGGGAATCCTTAGGAGCAAGGGAGTGTGT
CAAGACTTAAATACTTTGAAGGGTGGTTTTTCTTCCAGAAAACGGAGTCTCGTTACCCCTTAGGAATCCTCGTTCCTCACACA

28,050

DCTN1

DCTN1-226

DCTN1-226

TTGCATCCCCAACTTAAGCTTTGCTGCTGGTGAGCACTAAGGGTGCAGACATATTGGGGTCTCTGGAGCATTCTCCGTGCCCTTC
AACGTAGGGGTTGAATTCGAAACGACGACCACTCGTGATTCCCACGTCTGTATAACCCAGAGACCTCGTAAGAGGCACGGGAAG

28,135

DCTN1

DCTN1-226

DCTN1-226

TTGGAGATGGCATCTGAGACAGGGAGGCAGGAACAGCCTCATGTTCCAAGTACTTTGTACAGTGCACACTCTCTTTGCCACTGTT
AACCTCTACCGTAGACTCTGTCCCTCCGTCTTGTGCGAGTACAAGGTTTCATGAAACATGTCACGTGTGAGAGAAACGGTGACAA

28,220

DCTN1

DCTN1-226

DCTN1-226

CTTCACACATTGTACCCTGTCTTGTGGCCTCACTCCTGTTTTGGTGTCTTTCTTTAACACTTATCTGCTCGTCCCCAAAGATAGGT
GAAGTGTGTAACATGGGACAGAACACCCGGAGTGAGGACAAACCACAGAAAGAAATTGTGAATAGACGAGCAGGGGTTTCTATCCA

28,305

DCTN1

DCTN1-226

DCTN1-226

GGCAGAGAGTCTTGTTAGAGAAAAGTATGATGATTAGGAAAAGGGTTTTCTGCAGGTTGTGTCCAGGATTCTCTGGTGTGTCCC
CCGTCTCTCAGAACAATCTCTTTCATACTACTAATCCTTTTCCAAAAGGACGTCCAACACAGGTCTTAAGGAGACCACACAGGG

28,390

DCTN1

DCTN1-226

DCTN1-226

CGTAACCCCCAAATCACCTAACTCCTCTCTCCTCTTTTCTGCTCCCCCATGGGCTATCCCAGACACAGAAGAAGCAGCAGCGAGG
GCATTGGGGGTTTAGTGGATTGAGGAGAGAGGAGAAAAGGACGAGGGGGTACCCGATAGGGCTCGTGTCTTCTTGTCTCGTCTCC

28,475

DCTN1

DCTN1-226

DCTN1-226

E E Q Q R
ENSE00002484288

TAGAGACCCACTCTGGCCGGGGTTACCAGGCTGGTGGGAGTTGGAGCTAAGGGAGCAGGGTGGAGGGGGAAGCCAGGACTGGAG
ATCTCTGGGTGAGACCGGCCCCCAATGGTCCGACCACCCTCAACCTCGATTCCCTCGTCCCACCTCCCCCTTCGGTCTGACCTC

28,560

DCTN1

DCTN1-226

DCTN1-226

ATGGGTGATGGGGGGATGAGGAAAAGGGGAAGAGTAGGAATGGAGCCCAATTTTCAACCCTTTCCACTTGGGGCTGATGAGATTTT
TACCCACTACCCCCCTACTCCTTTCCCTTCTCATCCTTACCTCGGGTTAAAAGTTGGGAAAAGGTGAACCCCGACTACTCTAAAA

28,645

DCTN1

DCTN1-226

DCTN1-226

TTATGGTCCCCACAGGAGCCATCCCTGGGCAGGCTCCAGGGTCTGTGCCAGGCCAGGGCTGGTGAAGGACTCACCACTGCTGCT
AATACCAGGGGTGTCTCGGTAGGGACCCGTCCGAGGTCCCAGACACGGTCCGGGTCCCAGCCACTTCTGAGTGGTGACGACGA

28,730

DCTN1

DCTN1-226

DCTN1-226

G A I P G Q A P G S V P G P G L V K D S P L L L
ENSE00003498466

TCAGCAGATCTCTGCCATGAGGCTGCACATCTCCAGCTCCAGCATGAGAACAGCATCCTCAAGGTGAGGGAGCCACGGGGAGGA
AGTCGTCTAGAGACGGTACTCCGACGTGTAGAGGGTCCGAGGTCTGACTCTTGTCTGAGGAGTCCACTCCCTCGGTGCCCTCCT

28,815

DCTN1

DCTN1-226

DCTN1-226

1095 Q Q I S A M R L H I S Q L Q H E N S I L K
ENSE00003498466

CTGGGATGGGAGATGGAGCATATTTGCCCCATTGATGATAGATGACAGGGGCTCCTAGCACCTCTTACCACTATCCTTCTTTTT
GACCCCTACCCTCTACCTCGTATAAACGGGGTAACACTACTATCTACTGTCCCCGGAGGATCGTGGAGAATGGTGATAGGAAGAAAAA 28,900

DCTN1

DCTN1-226

DCTN1-226

TCATCCACAGGGAGCCCAGATGAAGGCATCCTTGGCATCCCTGCCCCCTCTGCATGTTGCAAAGCTATCCCATGAGGGCCCTGGC
AGTAGGTGTCCCTCGGGTCTACTTCCGTAGGAACCGTAGGGACGGGGGAGACGTACAACGTTTCGATAGGGTACTCCCGGGACCG 28,985

DCTN1

DCTN1-226

G A Q M K A S L A S L P P L H V A K L S H E G P G

ENSE00003488537

DCTN1-226

AGTGAGTTACCAGCTGGAGCGCTGTATCGTAAGACCAGCCAGCTGCTGGAGACATTGAATCAATTGAGCACACACACGCACGCTAG
TCACTCAATGGTCGACCTCGCGACATAGCATTCTGGTCGGTCGACGACCTCTGTAACCTAGTTAACTCGTGTGTGTGCGTGCATC 29,070

DCTN1

DCTN1-226

S E L P A G A L Y R K T S Q L L E T L N Q L S T H T H V

ENSE00003488537

DCTN1-226

TAGACATCACTCGCACCAGCCCTGGTATGTACCTGCCAACCCCAAGATGAATAAACTGCCCCCTCCACTTGGCCCCAGGGATTT
ATCTGTAGTGAGCGTGGTCGGGACCATAACATGGACGGTTGGGGTTCTACTTATTTTGACGGGGGAGGTGAACCGGGTCCCTAAA 29,155

DCTN1

DCTN1-226

V D I T R T S P

ENSE00003488537

DCTN1-226

AGCCCCTGCTCAGGTGGTTCCCCACCACAGAAGCTCTTCCAGCAGTGTCTTTGGCTTCACTGTTCAGTTTGTGTTGATTCACC
TCGGGGACGAGTCCACCAAGGGGGTGGTGTCTTCGAGAAGGGTCGTCAACAAGAAACCGAAGTGACAAGTCAAACAACCTAAGTGG 29,240

DCTN1

DCTN1-226

DCTN1-226

CACTCTCTCTCAAGTACTTGTCTCTGTTAGAGAGTCTTATACCTGCACCCCTAACCCCTTAATCCAGTAGAACTGCCTGCCTGCGCC
GTGAGAGAGAGTTCATGAACAAGACAATCTCTCAGAATATGGACGTGGGGATTGGGAATTAGGTCATCTTGACGGACGGACGCGG 29,325

DCTN1

DCTN1-226

DCTN1-226

TTGGTGGGCCTCACCAAGCTTTCTCTCCCCACAGCTGCCAAGAGCCCGTCGGCCCAACTTATGGAGCAAGTGGCTCAGCTTAAGTC
AACCACCCGGAGTGGTCGAAAGAGAGGGGTGTGACGCTTCTCGGGCAGCCGGGTTGAATACCTCGTTACCGAGTCAATTCAG 29,410

DCTN1

DCTN1-226

A A K S P S A Q L M E Q V A Q L K S

ENSE00003490713

DCTN1-226

CCTGAGTGACACCGTTCGAGAAGCTCAAGGTCAGCTCAGTTTGGCCAGGCAGAGCTCACTTTCACAGCATAAACTGGTGGAGCCAGGC
GGACTCACTGTGGCAGCTCTTCGAGTTCAGTTCGAGTCAAACGGTCCGTCTCGAGTGAAGTGTCTGATTTGACCACCTCGGTCCG

29,495

DCTN1

DCTN1-226

1195 1200
L S D T V E K L K

ENSE00003490713

DCTN1-226

ACTTGTGGAGTTCTCTGAGCCCAGCCCTGTGCTAGACAGCAATTGGGGAGGAGATGGAAGGGAAGGCAGGGTTCTTGCCTTGG
TGAACACCTCAAGGAGACTCGGGTCGGGACACGATCTGTCTGTTAACCCCTCCTCTACCTTCCCTTCCGTCCAAGAACGGAACCT

29,580

DCTN1

DCTN1-226

DCTN1-226

AGCTCACTGTCTCAGTGCAAACAGAAGACAGATTCTCATAACAAAATGGATAAGCTAGGGTAATCTTTAGAGTGACTGGTTCAGG
TCGAGTGACAGAGTACGTTTTGTCTTCTGTCTAAGAGTATTGTTTTACCTATTCGATCCATTAGAAATCTCACTGACCAAGTCC

29,665

DCTN1

DCTN1-226

DCTN1-226

CTTTAGCTTCCATCAGCGCTGAGATCATTGTGGGGTAGAACGGTTGGGCATGGCTTCCCAAGAGCGGTAGAATGTGAGTTGGGCC
GAAATCGAAGGTAGTCGCGACTCTAGTAACACCCCATCTTGCCAACCCGTACCGAAGGGTTCTCGCCATCTTACACTCAACCCGG

29,750

DCTN1

DCTN1-226

DCTN1-226

TTACAGGATGAGGACTTGCAAAGTAAGGAGGAGTGCTGGTGTGGGGATGGGGTTGGAGATGAGAGCAAAAGTATGTTGATATAGA
AATGTCTACTCCTGAACGTTTCATTCCTCCTCACGACCACCCCTACCCCAACCTCTACTCTCGTTTTTCATACAACCTATATCT

29,835

DCTN1

DCTN1-226

DCTN1-226

GGACTAAGTCCCTGCCCCCTGGTATTAGTGTCTCTGTGAAACCACGTGGTCTTGTGCTAGCCTGTGGGGGTCCCATAAATGAAC
CCTGATTCAGGGACGGGGGGACCATAATCACAGAGACACTTTGGTGCACCAGAACACGATCGGACACCCCAAGGGTATTTACTTG

29,920

DCTN1

DCTN1-226

DCTN1-226

CCTTGTCTTCTCTCCCTTCCCTAGGATGAGGTCCTCAAGGAGACAGTATCTCAGCGCCCTGGAGCCACAGTACCCACTGACTT
GGAACAGAAGGAGAGGGGAAGGGATCTACTCCAGGAGTTCTCTGTCTATAGAGTCGCGGGACCTCGGTGTCTATGGGTGACTGAA

30,005

DCTN1

DCTN1-226

1205 1210 1215 1220
D E V L K E T V S Q R P G A T V P T D F

ENSE00003683337

DCTN1-226

TGCCACCTTCCCTTCATCAGCCTTCTCAGGGTGAGGGGGAGCATGGGGTGGAGGATGGGACAGTGTGGAGAGCTCAGGCGGGCC
ACGGTGGAAGGGAAGTAGTCGGAAGGAGTCCCACTCCCCCTCGTACCCACCTCTACCCTGTACACCTCTCGAGTCCGCCCGG

30,090

DCTN1

DCTN1-226

1225 1230
A T F P S S A F L R

ENSE00003683337

DCTN1-226

CCCCTCTCTCCAGAATTGGAGGAGGCCTTTGGAGTCTCAGGTCTAACAACTGCATACCTTGGGTTATCTGGCCAAATTTTACTT
GGGGAGAGGAGGTCTTAACCTCCTCCGGAACCTCAGAGTCCAGATTGTTGACGTATGGAACCCAATAGACCGGTTTAAATGAA

30,175

DCTN1

DCTN1-226

DCTN1-226

ACAAGTAACTCAGAAGTGCTTACAGTGCTTTGAAATTCGAATATTTTAGCACCTAAACACCTTCCGTGACTTTTGACACCAGGAG
TGTTTCATTGAGTCTTACGAATGTCACGAACTTTAAGGTTATAAAATCGTGGATTTGTGGAAGGCACTGAAAACCTGTGGTCTC

30,260

DCTN1

DCTN1-226

DCTN1-226

GGCCTCAAACTCCCTTGTGAGATTATGTATCCCATTTCTTATTTGAAAAATGTGGTCACAATAGCCAGGATCTCAGAAGCCCT
CCGGAGTTTTGAGGGAACAGTCTAATACATAGGGGTAAGAATAAACTTTTTACACCAGTGTTATCGGGTCTTAGAGTCTTCGGGA

30,345

DCTN1

DCTN1-226

DCTN1-226

AGTCACCCAGGAGCTGCCTTGGTCTCAGTGCTCAGGGACCCCTTCAGTGGCCACAGCTCAAGTGAGCCCTGACCTGGAGTCTT
TCAGTGGGTCTCGACGGAACAGAGTACAGAGTCCCTGGGGAAGTACCAGGTTGTCGAGTTCACTCGGGGACTGGACCTCAGAA

30,430

DCTN1

DCTN1-226

DCTN1-226

TTTCTCCTCATCAACCACCAGGCCAAGGAGGAGCAGCAGGATGACACAGTCTACATGGGCAAAGTGACCTTCTCATGTGCGGCTG
AAAGAGGAGTAGTTGGTGGTCCGGTTCTCCTCGTCTGCTACTGTGTCAGATGTACCCGTTTCACTGGAAGAGTACACGCCGAC

30,515

DCTN1

DCTN1-226

1235 1240 1245 1250
A K E E Q Q D D T V Y M G K V T F S C A A

ENSE00003911922

DCTN1-226

GTTTTGGACAGCGACACCGGCTGGTGTGACCCAGGAGCAGCTGCACCAGCTTCACAGTCGCCTCATCTCCTAAGCACTCCTTTTC
CAAAACCTGTGCTGTGGCCGACCACGACTGGGTCTCGTGCAGCTGGTTCGAAAGTGTGAGGAGTAGAGGATTCTGTGAGGAAAG

30,600

DCTN1

DCTN1-226

1255 1260 1265 1270 1275
G F G Q R H R L V L T Q E Q L H Q L H S R L I S

ENSE00003911922

DCTN1-226

CCCTGCTGTCCCCTTCGACCCCTCAGCCCTCTGGTGCCGCTCTGCCCGATGCACAGCCACCTCAGCCAGCCCCCAGGTAGAAACGT
GGGACGACAGGGGAAGCTGGGAGTCGGGAGACCACGGCGAGACGGGCTACGTGTTCGGTGGAGTCGGTTCGGGGGTCCATCTTTGCA

30,685

DCTN1

DCTN1-226

GGGTTAAGCTCTTCCTGCCCGTTTCAGCTTCACTCCCACCCTTTTCAGCGTCCTGCCCTTCACCTTGACCCGGGTTCCCCCACTC
CCCAATTCGAGAAGGACGGGGCAAGTCGAAGTGAGGGTGGGAAAGTCGCAGGACGGGGAAAGTGGAAGTGGGCCCAAGGGGGTGAG

30,770

DCTN1

DCTN1-226

CCATTCCCTGGCCTCTGCCATAATTTGTTGTTCAACTGCTCCCTCCTTCCTGAGGGGCCTCAGGGCTTGTGGGGGGTAGGCTGAG
GGTAAGGGACCGGAGACGGTATTAACAACAAGTTGACGAGGGAGGAAGGACTCCCCGGAGTCCCGAACACCCCCCATCCGACTC

30,855

DCTN1

DCTN1-226

ACCCACCAACAAAGGTTAAGTGAGGTCCCCTTGATTGAGGACTTCACCCCTTGATTAAGCAACTTCTGCTTCAGTGC
TGGGGTGGTGGTTTCCAATTCCTCCAGGGGAACCTAAGTCTGAAAGTGGGGAACTAATTTTCGTTGAAGACGAAGTCACG











































3'

30,934

5'

DCTN1

DCTN1-226

Feature	Location	Size			Type
✓ DCTN1	1 .. 30,934	30,934 bp			gene
/note	= gene ENSG00000204843 Protein coding				
DCTN1-203	1 .. 30,931	30,931 bp			prim_transcript
/note	= primary transcript ENST00000409240				
DCTN1-212	52 .. 14,052	14,001 bp			prim_transcript
/note	= primary transcript ENST00000440727				
DCTN1-AS1-204	184 .. 6591	6408 bp			prim_transcript
/note	= primary transcript ENST00000426715 lncRNA				
DCTN1-210	221 .. 30,932	30,712 bp			prim_transcript
/note	= primary transcript ENST00000434055 Nonsense mediated decay				
DCTN1-228	222 .. 30,933	30,712 bp			prim_transcript
/note	= primary transcript ENST00000680606				
DCTN1-206	223 .. 30,930	30,708 bp			prim_transcript
/note	= primary transcript ENST00000409868				
DCTN1-208	245 .. 14,656	14,412 bp			prim_transcript
/note	= primary transcript ENST00000417090				
DCTN1-211	288 .. 14,395	14,108 bp			prim_transcript
/note	= primary transcript ENST00000437375				
DCTN1-209	308 .. 14,088	13,781 bp			prim_transcript
/note	= primary transcript ENST00000421392				
DCTN1-AS1-203	661 .. 6592	5932 bp			prim_transcript
/note	= primary transcript ENST00000418990 lncRNA				
DCTN1-AS1-201	808 .. 6564	5757 bp			prim_transcript
/note	= primary transcript ENST00000412957 lncRNA				
DCTN1-AS1-205	1423 .. 6595	5173 bp			prim_transcript
/note	= primary transcript ENST00000427343 lncRNA				
DCTN1-AS1-208	1436 .. 6395	4960 bp			prim_transcript
/note	= primary transcript ENST00000664792 lncRNA				
DCTN1-208	1461 .. 14,656	13,196 bp			CDS
▶ 4 segments	= 405 bp				
/note	= coding sequence ENSP00000402509				
/translation	= MCCLERVTLVQAYK,,TPSGSRMSAEASARPLRVGSRVEVIGKGHRGTVAAYVGATLFATGKWVGVILDEAKGKNDGTVQGRKYFTCDEGHGIFVRQSQ,,IQVFEDGADTTSPETPDSSASKVLKR,,EGDTTAKTSKL 135 amino acids = 14.4 kDa				
DCTN1-AS1-207	1771 .. 6614	4844 bp			prim_transcript
/note	= primary transcript ENST00000664266 lncRNA				
DCTN1-AS1	1794 .. 6614	4821 bp			gene
/note	= gene ENSG00000237737 lncRNA				
DCTN1-AS1-206	1794 .. 6370	4577 bp			prim_transcript
/note	= primary transcript ENST00000437991 lncRNA				
DCTN1-AS1-202	3910 .. 6602	2693 bp			prim_transcript
/note	= primary transcript ENST00000416630 lncRNA				
DCTN1-213	6647 .. 13,901	7255 bp			prim_transcript
/note	= primary transcript ENST00000449655				

Feature	Location	Size	Type
DCTN1-215	11,531 .. 20,445	8915 bp	prim_transcript
/note	= primary transcript ENST00000458655		
DCTN1-215	11,536 .. 20,445	8910 bp	CDS
▶ 8 segments	= 560 bp		
/note	= coding sequence ENSP00000414315		
/translation	= MLMGLLRPYILGERGTVM,,TPSGSRMSAEASARPLRVGSRVEVIGKGRGTVA YV GATL FATGKWWGVILDEAKGKNDGTVQGRKYFTCDEGHGIFVRQSQ,,IQVFEDGADTTSPETPDSSASKVLKR,,EGTDTTAKTSKL,,RGLKPKK,,APTARK,,TTTRRPK,,PTRPASTGVAGASSSLGPGSGSASAGELSSS		
186 amino acids	= 19.5 kDa		
DCTN1-201	11,733 .. 30,934	19,202 bp	prim_transcript
/note	= primary transcript ENST00000361874		
DCTN1-202	11,733 .. 30,934	19,202 bp	prim_transcript
/note	= primary transcript ENST00000394003		
DCTN1-214	11,743 .. 15,347	3605 bp	prim_transcript
/note	= primary transcript ENST00000454119		
DCTN1-226	11,777 .. 30,933	19,157 bp	prim_transcript
/note	= primary transcript ENST00000628224		
DCTN1-205	11,789 .. 30,589	18,801 bp	prim_transcript
/note	= primary transcript ENST00000409567		
DCTN1-207	11,805 .. 14,088	2284 bp	prim_transcript
/note	= primary transcript ENST00000413111		
DCTN1-201	12,051 .. 30,589	18,539 bp	CDS
▶ 31 segments	= 3822 bp		
/note	= coding sequence ENSP00000354791		
/translation	= MAQSKRHVYSR,,TPSGSRMSAEASARPLRVGSRVEVIGKGRGTVA YV GATL FATGKWWGVILDEAKGKNDGTVQGRKYFTCDEGHGIFVRQSQ,,IQVFEDGADTTSPETPDSSASKVLKR,,EGTDTTAKTSKL,,RGLKPKK,,APTARK,,TTTRRPK,,PTRPASTGVAGASSSLGPGSGSASAGELSSS		
EPSTPAQTPLAAPIIPTPVLTSPGAVPPLPSPSK,,EEEGLRAQVRDLEEKLET LRLKRAEDKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRR			
LKEARK,,EAKEALEAKERYMEEMADTDAIEMATLDKEMAEERAESLQVEVALKERVDELTTDLEILKAEIEEK,,GSDGAASSYQLKQLEEQN			
ARLKDALVR,,MRDLSSEKQEHVKLQKLMKKNQLEVVRRQERERLEELSQAESTIDELKEQ,,VDAALGA EEMVEMLTDRNLNLEEKVREL			
ETVGD,,EAMNEMNDELQENARETELELREQLDMAGARVREARQKRV EAAQETVADYQQTICKYRQLTAHLQ,,DVNRELTNQQEASVERQQ			
PPPETFDFKIKFAETKAHAK,,AIEMELRQMEVAQANRHMSLLTAFMPDSFLRPGGDHDCVLLVLLMPLRLICK,,AELIRKQAQEFELSENCSERP			
GLRGAAGEQLSFAAGLVYSLLLQATLHRYEH,,ALSQCSVDVYKKGSLYPMSAHERSLDFLIELLHKDQLETVNVEPLTKAIKYYQ,,HLYSIH			
LAEQPEDCTMQ LADHIK,,FTQSALDCMSVEVGR LRAFLQ,,GGQEATDIALLLRDLETSCSDIRQFCKKIRRRMPGTDA PGIPAAALAFGPQ,,VSD			
TLLDCRKHHTVAVLQEVAAAAQLIAPLAENEGLLVAALEELAFKASEQ,,IYGT PSSSPYECLRQSCNIIISTMNKLATAMQEGEYDAERPP			
SK,,PPPVELRAAALRAEITDAEGLGLKLEDRETVIKELKKS LKIK,,GEELSEANVRLSLEKLDLSAAKDADERIEKVQTRLEETQALLRKKEK,,EF			
EETMDALQADIDQLEAEKALQRLNSQSKRTIEGLRGP PPSGIATLVSGIAG,,GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHE			
NSYKGAQMKA SLA SLPPLVKA KLSHEGPGSELPA GALYRKTSQ LLETLNQLSTHTHVVDITRTSP,,AAKSPSAQLMEQVAQLKSLSDTVEKLG			
,,DEV LKETVSQRPGATVPTDFATFPSSAFLR,,AKEEQDDTVYMGKVTFSCAAGFGQRHRLVLTQEQ LHLQ LHSRLIS*			
DCTN1-202	12,051 .. 30,589	18,539 bp	CDS
▶ 31 segments	= 3816 bp		
/note	= coding sequence ENSP00000377571		
/translation	= MAQSKRHVYSR,,TPSGSRMSAEASARPLRVGSRVEVIGKGRGTVA YV GATL FATGKWWGVILDEAKGKNDGTVQGRKYFTCDEGHGIFVRQSQ,,IQVFEDGADTTSPETPDSSASKVLKR,,EGTDTTAKTSKL,,APTARK,,TTTRRPK,,PTRPASTGVAGASSSLGPGSGSASAGELSSS		
EPSTPAQTPLAAPIIPTPVLTSPGAVPPLPSPSK,,EEEGLRAQVRDLEEKLET LRLKRAEDKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRR			
LKEARK,,EAKEALEAKERYMEEMADTDAIEMATLDKEMAEERAESLQVEVALKERVDELTTDLEILKAEIEEK,,GSDGAASSYQLKQLEEQN			
ARLKDALVR,,MRDLSSEKQEHVKLQKLMKKNQLEVVRRQERERLEELSQAESTIDELKEQ,,VDAALGA EEMVEMLTDRNLNLEEKVREL			
ETVGD,,EAMNEMNDELQENARETELELREQLDMAGARVREARQKRV EAAQETVADYQQTICKYRQLTAHLQ,,DVNRELTNQQEASVERQQ			
PPPETFDFKIKFAETKAHAK,,AIEMELRQMEVAQANRHMSLLTAFMPDSFLRPGGDHDCVLLVLLMPLRLICK,,AELIRKQAQEFELSENCSERP			
GLRGAAGEQLSFAAGLVYSLLLQATLHRYEH,,ALSQCSVDVYKKGSLYPMSAHERSLDFLIELLHKDQLETVNVEPLTKAIKYYQ,,HLYSIH			
LAEQPEDCTMQ LADHIK,,FTQSALDCMSVEVGR LRAFLQ,,GGQEATDIALLLRDLETSCSDIRQFCKKIRRRMPGTDA PGIPAAALAFGPQ,,VSD			
TLLDCRKHHTVAVLQEVAAAAQLIAPLAENEGLLVAALEELAFKASEQ,,IYGT PSSSPYECLRQSCNIIISTMNKLATAMQEGEYDAERPP			
SK,,PPPVELRAAALRAEITDAEGLGLKLEDRETVIKELKKS LKIK,,GEELSEANVRLSLEKLDLSAAKDADERIEKVQTRLEETQALLRKKEK,,EF			
EETMDALQADIDQLEAEKALQRLNSQSKRTIEGLRGP PPSGIATLVSGIAG,,EEQQR,,GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHE			
NSYKGAQMKA SLA SLPPLVKA KLSHEGPGSELPA GALYRKTSQ LLETLNQLSTHTHVVDITRTSP,,AAKSPSAQLMEQVAQLKSLSDTVEKLG			
,,DEV LKETVSQRPGATVPTDFATFPSSAFLR,,AKEEQDDTVYMGKVTFSCAAGFGQRHRLVLTQEQ LHLQ LHSRLIS*			

DCTN1-205

12,051 .. 30,589

18,539 bp

CDS

28 segments = 3762 bp

/note = coding sequence ENSP00000386843

/translation = MAQSKRHVYSR,,TPSGSRMSAEASARPLRVGSRVEVIGKGRGTVAYV GATLFATGKWWGVILDEAKGKNDGTVQGRKYFTCDEGHGIFVRQ SQ,,IQVFEDGADTTSPETPDSSASKVLKR,,EGDTTAKTSKL,,PTRPASTGVAGASSLGPSPGSASAGELSSSEPSTPAQTPLAAPIIPTPVLTSPGAVPPLPSPSK,,EEEGLRAQVRDLEEKLET LRLKRAEDKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLEARK,,EAKEALEAKERYMEEMADTADAIEMATLDKEMAEERAESLQQEVEALKERVDELTTDLEILKAEIEEK,,GSDGAASSYQLKQLEEQNARLKDALVR,,MRDLSSEKQEHVKLQKLMMEKKNQEELEVVRQQRERLQEELSQAESTIDELKEQ,,VDAALGAEEMVEMLDRNLNLEEKVRELRETVGDL,,EAMNEMNDELQENARETELELREQLDMAGARVREARQKRVEAAQETVADYQQTICKYRQLTAHLQ,,DVNRELTNQQEASVERQQPPPETFDKFKIFAETKAHAK,,AIEMELRQMEVAQANRHMSLLTAFMPDSFLRPGGDHDCV LLLLMPRLICK,,AELIRKQAQEKFELSENCSERPGLRGAAGEQLSFAAGLVYSL SLLQATLHRYEH,,ALSQCSVDVYKKGSLYPMSAHERSLDFLIELLHKDQLDET VNV EPLTKAIKYYQ,,HLYSIHLAEQPEDCTMQLADHIK,,FTQSALDCMSVEVGR LRAFLQ,,GGQEATDIALLLRDLETSCSDIRQFCKKIRRRMPGTDAPGIPAALAFGPQ,,VSDTLDCRKHLLTWWVAVLQEVAAAAQLIAPLAENEGLLVAALEELAFKASEQ,,YGT PSSSPYECLRQSCNLISTMKNKLATAMQEGEYDAERPPSK,,PPPVELRAAALRAEITDAEGLGLKLEDRETVIKELKSLKIK,,GEELSEANVRLSLEKLD SAAKADADERIEKVQTRLEETQALLRKEK,,EFEETMDALQADIDQLEAEKAL KQRLNSQSKRTIEGLRGGPPSGIATLVSGIAG,,GAIPGQAPGSVPGPGLVKD SP LLLQ Q ISAMRLHISQLQHENSILK,,GAQMKA SLA SLPLHV A KLSHEGPGSELPA GALYRKT SQ LLETLNQLSTHTHVVDITRTSP,,AAKSPSAQLMEQVAQLKSLSDTVEK LK,,DEVLKETVSQRPGATVPTDFATFPSSAFLR,,AKEEQDDTVYMGKVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS*

DCTN1-226

12,051 .. 30,589

18,539 bp

CDS

32 segments = 3837 bp

/note = coding sequence ENSP00000487279

/translation = MAQSKRHVYSR,,TPSGSRMSAEASARPLRVGSRVEVIGKGRGTVAYV GATLFATGKWWGVILDEAKGKNDGTVQGRKYFTCDEGHGIFVRQ SQ,,IQVFEDGADTTSPETPDSSASKVLKR,,EGDTTAKTSKL,,RGLKPKK,,APTARK,,TTTRRPK,,PTRPASTGVAGASSLGPSPGSASAGELSSS EPSTPAQTPLAAPIIPTPVLTSPGAVPPLPSPSK,,EEEGLRAQVRDLEEKLET LRLKRAEDKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRR LKEARK,,EAKEALEAKERYMEEMADTADAIEMATLDKEMAEERAESLQQEVEALKERVDELTTDLEILKAEIEEK,,GSDGAASSYQLKQLEEQNARLKDALVR,,MRDLSSEKQEHVKLQKLMMEKKNQEELEVVRQQRERLQEELSQAESTIDELKEQ,,VDAALGAEEMVEMLDRNLNLEEKVRELRETVGDL,,EAMNEMNDELQENARETELELREQLDMAGARVREARQKRVEAAQETVADYQQTICKYRQLTAHLQ,,DVNRELTNQQEASVERQQPPPETFDKFKIFAETKAHAK,,AIEMELRQMEVAQANRHMSLLTAFMPDSFLRPGGDHDCV LLLLMPRLICK,,AELIRKQAQEKFELSENCSERPGLRGAAGEQLSFAAGLVYSL SLLQATLHRYEH,,ALSQCSVDVYKKGSLYPMSAHERSLDFLIELLHKDQLDET VNV EPLTKAIKYYQ,,HLYSIHLAEQPEDCTMQLADHIK,,FTQSALDCMSVEVGR LRAFLQ,,GGQEATDIALLLRDLETSCSDIRQFCKKIRRRMPGTDAPGIPAALAFGPQ,,VSDTLDCRKHLLTWWVAVLQEVAAAAQLIAPLAENEGLLVAALEELAFKASEQ,,YGT PSSSPYECLRQSCNLISTMKNKLATAMQEGEYDAERPPSK,,PPPVELRAAALRAEITDAEGLGLKLEDRETVIKELKSLKIK,,GEELSEANVRLSLEKLD SAAKADADERIEKVQTRLEETQALLRKEK,,EFEETMDALQADIDQLEAEKAL KQRLNSQSKRTIEGLRGGPPSGIATLVSGIAG,,EEQQR,,GAIPGQAPGSVPGPGLVKD SP LLLQ Q ISAMRLHI S Q LLETLNQLSTHTHVVDITRTSP,,AAKSPSAQLMEQVAQLKSLSDTVEK LK,,DEVLKETVSQRPGATVPTDFATFPSSAFLR,,AKEEQDDTVYMGKVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS*

DCTN1-203

13,861 .. 30,589

16,729 bp

CDS

27 segments = 3711 bp

/note = coding sequence ENSP00000386406

/translation = MSAEASARPLRVGSRVEVIGKGRGTVAYV GATLFATGKWWGVILDEAKGKNDGTVQGRKYFTCDEGHGIFVRQSQ,,IQVFEDGADTTSPETPDSSASKVLKR,,EGDTTAKTSKL,,RGLKPKK,,APTARK,,TTTRRPK,,PTRPASTGVAGASSLGPSPGSASAGELSSSEPSTPAQTPLAAPIIPTPVLTSPGAVPPLPSPSK,,EEEGLRAQVRDLEEKLET LRLKRAEDKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLEARK,,EAKEALEAKERYMEEMADTADAIEMATLDKEMAEERAESLQQEVEALKERVDELTTDLEILKAEIEEK,,GSDGAASSYQLKQLEEQNARLKDALVR,,MRDLSSEKQEHVKLQKLMMEKKNQEELEVVRQQRERLQEELSQAESTIDELKEQ,,VDAALGAEEMVEMLDRNLNLEEKVRELRETVGDL,,EAMNEMNDELQENARETELELREQLDMAGARVREARQKRVEAAQETVADYQQTICKYRQLTAHLQ,,DVNRELTNQQEASVERQQPPPETFDKFKIFAETKAHAK,,AIEMELRQMEVAQANRHMSLLTAFMPDSFLRPGGDHDCV LLLLMPRLICK,,AELIRKQAQEKFELSENCSERPGLRGAAGEQLSFAAGLVYSL SLLQATLHRYEH,,ALSQCSVDVYKKGSLYPMSAHERSLDFLIELLHKDQLDET VNV EPLTKAIKYYQ,,HLYSIHLAEQPEDCTMQLADHIK,,FTQSALDCMSVEVGR LRAFLQ,,GGQEATDIALLLRDLETSCSDIRQFCKKIRRRMPGTDAPGIPAALAFGPQ,,VSDTLDCRKHLLTWWVAVLQEVAAAAQLIAPLAENEGLLVAALEELAFKASEQ,,YGT PSSSPYECLRQSCNLISTMKNKLATAMQEGEYDAERPPSK,,PPPVELRAAALRAEITDAEGLGLKLEDRETVIKELKSLK IK,,GEELSEANVRLSLEKLD SAAKADADERIEKVQTRLEETQALLRKEK,,EFEETMDALQADIDQLEAEKAL KQRLNSQSKRTIEGLRGGPPSGIATLVSGIAG,,GAIPGQAPGSVPGPGLVKD SP LLLQ Q ISAMRLHISQLQHENSILK,,GAQMKA SLA SLPLHV A KLSHEGPGSELPA GALYRKT SQ LLETLNQLSTHTHVVDITRTSP,,AAKSPSAQLMEQVAQLKSLSDTVEK LK,,DEVLKETVSQRPGATVPTDFATFPSSAFLR,,AKEEQDDTVYMGKVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS*

DCTN1-206

13,861 .. 30,589

16,729 bp

CDS

30 segments = 3771 bp

/note = coding sequence ENSP00000387327

/translation = MSAEASARPLRVGSRVEVIGKGRGTVAYV GATLFATGKWWGVILDEAKGKNDGTVQGRKYFTCDEGHGIFVRQSQ,,IQVFEDGADTTSPETPDSSASKVLKR,,EGDTTAKTSKL,,RGLKPKK,,APTARK,,TTTRRPK,,PTRPASTGVAGASSLGPSPGSASAGELSSSEPSTPAQTPLAAPIIPTPV LTSPGAVPPLPSPSK,,EEEGLRAQVRDLEEKLET LRLKRAEDKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLEARK,,EAKEALEAKERY MEEMADTADAIEMATLDKEMAEERAESLQQEVEALKERVDELTTDLEILKAEIEEK,,GSDGAASSYQLKQLEEQNARLKDALVR,,MRDLSSEKQEHVKLQKLMMEKKNQEELEVVRQQRERLQEELSQAESTIDELKEQ,,VDAALGAEEMVEMLDRNLNLEEKVRELRETVGDL,,EAMNEMNDELQENARETELELREQLDMAGARVREARQKRVEAAQETVADYQQTICKYRQLTAHLQ,,DVNRELTNQQEASVERQQPPPETFDKFKIFAETKAHAK,,AIEMELRQMEVAQANRHMSLLTAFMPDSFLRPGGDHDCV LLLLMPRLICK,,AELIRKQAQEKFELSENCSERPGLRGAAGEQLSFAAGLVYSL SLLQATLHRYEH,,ALSQCSVDVYKKGSLYPMSAHERSLDFLIELLHKDQLDET VNV EPLTKAIKYYQ,,HLYSIHLAEQPEDCTMQLADHIK,,FTQSALDCMSVEVGR LRAFLQ,,GGQEATDIALLLRDLETSCSDIRQFCKKIRRRMPGTDAPGIPAALAFGPQ,,VSDTLDCRKHLLTWWVAVLQEVAAAAQLIAPLAENEGLLVAALEELAFKASEQ,,YGT PSSSPYECLRQSCNLISTMKNKLATAMQEGEYDAERPPSK,,PPPVELRAAALRAEITDAEGLGLKLEDRETVIKELKSLK IK,,GEELSEANVRLSLEKLD SAAKADADERIEKVQTRLEETQALLRKEK,,EFEETMDALQADIDQLEAEKAL KQRLNSQSKRTIEGLRGGPPSGIATLVSGIAG,,GAIPGQAPGSVPGPGLVKD SP LLLQ Q ISAMRLHISQLQHENSILK,,GAQMKA SLA SLPLHV A KLSHEGPGSELPA GALYRKT SQ LLETLNQLSTHTHVVDITRTSP,,AAKSPSAQLMEQVAQLKSLSDTVEK LK,,DEVLKETVSQRPGATVPTDFATFPSSAFLR,,AKEEQDDTVYMGKVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS*

Feature	Location	Size	Type
DCTN1-204	17,736 .. 30,589	12,854 bp	CDS
▶ 26 segments = 3420 bp			
/note	= coding sequence ENSP00000387270		
/translation	= MMRQAPTARK,,TTTRRPK,,PTRPASTGVAGASSSLGPGSGSASAGELSSSEPSTPAQTPLAAPIIPTPVLTPSGAVPPLPSPSK,,EEGLRAQVRD LEEKLETLRKRAEDKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLEARK,,EAKAELEAKERYMEEMADTADAIEMATLDKEMAERA ESLQQEVEALKERVDELTTDLLEILKAEIEEK,,GSDGAASSYQLKQLEEQNARLKDALVR,,MRDLSSEKQEHVKLQKLMKKNQLELVVRQQR RLQEELSQAESTIDELKEQ,,VDAALGAEEMVEMLTDRNLNLEEKVRELRETVGDL,,EAMNEMNDELQENARETELELREQLDMAGARVREAQK RVEAAQETVADYQQTICKYRQLTAHLQ,,DVNRELTNQEQASVERQQQPPPETFDFKIKFAETKAHAK,,AIEMELRQMEVAQANRHMSLLTAF MPDSFLRPGGDHDCVLLVLLMPRLICK,,AELIRKQAQEKFELSENCSERPGLRGAAGEQLSFAAGLVYSLSLQLATLHRYEH,,ALSQCSVDVYK VGSLYPEMSAHERSLDFIELLHKDQLDDEVNVEPLTKAIKYYQ,,HLYSIHLAEQPEDCTMQLADHIK,,FTQSALDCMSVEVGRRAFLQ,,GGQE ATDIALLLRDLETSCSDIRQFCKKIRRRMPGTDAPGIPAAALAFGPQ,,VSDTLDCRKHHTWVAVLQEVAAAAAQLIAPLAENEGLLVALEELA FKASEQ,,IYGTSSSPYECLRQSCNLISTMNKLATAMQEGEYDAERPPSK,,PPPVELRAAALRAEITDAEGLGKLEDRETVIKELKSKLKIK,,GE ELSEANVRLSLEKLDKSAKADADERIEKVQTRLEETQALLRKKEK,,EFEETMDALQADIDQLEAEKALQRLNSQSKRTIEGLRGGPPSGIATL VSGIAG,,GAIPGQAPGSPVPGPLVKDPSPLLQQISAMRLHISQLQHENSILK,,GAQMKA SLASLPLPHVAKLSHEGPGSELPA GALYRKTSQLL EITVQHTHTHTVVDITRSPKDAKSPSAQLMEQVAQLKLSLSDTVEKLK,,DEV LKETVSQRPGATVPTDFATFPSSAFLR,,AKEEQDDTVYMGK VTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS*		
DCTN1-227	17,736 .. 30,589	12,854 bp	CDS
▶ 27 segments = 3435 bp			
/note	= coding sequence ENSP00000487724		
/translation	= MMRQAPTARK,,TTTRRPK,,PTRPASTGVAGASSSLGPGSGSASAGELSSSEPSTPAQTPLAAPIIPTPVLTPSGAVPPLPSPSK,,EEGLRAQVRD LEEKLETLRKRAEDKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLEARK,,EAKAELEAKERYMEEMADTADAIEMATLDKEMAERA ESLQQEVEALKERVDELTTDLLEILKAEIEEK,,GSDGAASSYQLKQLEEQNARLKDALVR,,MRDLSSEKQEHVKLQKLMKKNQLELVVRQQR RLQEELSQAESTIDELKEQ,,VDAALGAEEMVEMLTDRNLNLEEKVRELRETVGDL,,EAMNEMNDELQENARETELELREQLDMAGARVREAQK RVEAAQETVADYQQTICKYRQLTAHLQ,,DVNRELTNQEQASVERQQQPPPETFDFKIKFAETKAHAK,,AIEMELRQMEVAQANRHMSLLTAF MPDSFLRPGGDHDCVLLVLLMPRLICK,,AELIRKQAQEKFELSENCSERPGLRGAAGEQLSFAAGLVYSLSLQLATLHRYEH,,ALSQCSVDVYK VGSLYPEMSAHERSLDFIELLHKDQLDDEVNVEPLTKAIKYYQ,,HLYSIHLAEQPEDCTMQLADHIK,,FTQSALDCMSVEVGRRAFLQ,,GGQE ATDIALLLRDLETSCSDIRQFCKKIRRRMPGTDAPGIPAAALAFGPQ,,VSDTLDCRKHHTWVAVLQEVAAAAAQLIAPLAENEGLLVALEELA FKASEQ,,IYGTSSSPYECLRQSCNLISTMNKLATAMQEGEYDAERPPSK,,PPPVELRAAALRAEITDAEGLGKLEDRETVIKELKSKLKIK,,GE ELSEANVRLSLEKLDKSAKADADERIEKVQTRLEETQALLRKKEK,,EFEETMDALQADIDQLEAEKALQRLNSQSKRTIEGLRGGPPSGIATL VSGIAG,,GAIPGQAPGSPVPGPLVKDPSPLLQQISAMRLHISQLQHENSILK,,GAQMKA SLASLPLPHVAKLSHEGPGSELPA GALYRKTSQLL EITVQHTHTHTVVDITRSPKDAKSPSAQLMEQVAQLKLSLSDTVEKLK,,DEV LKETVSQRPGATVPTDFATFPSSAFLR,,AKEEQDDTVYMGK VTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS*		
DCTN1-217	18,706 .. 21,082	2377 bp	prim_transcript
/note	= primary transcript ENST00000463583 protein_coding_CDS_not_defined		
DCTN1-216	18,873 .. 20,413	1541 bp	prim_transcript
/note	= primary transcript ENST00000462813 Retained intron		
DCTN1-218	20,046 .. 30,929	10,884 bp	prim_transcript
/note	= primary transcript ENST00000466110 Retained intron		
DCTN1-219	20,193 .. 21,109	917 bp	prim_transcript
/note	= primary transcript ENST00000470351 Retained intron		
DCTN1-225	22,693 .. 30,933	8241 bp	prim_transcript
/note	= primary transcript ENST00000497666 protein_coding_CDS_not_defined		
DCTN1-223	24,075 .. 26,116	2042 bp	prim_transcript
/note	= primary transcript ENST00000495643 protein_coding_CDS_not_defined		
DCTN1-224	25,894 .. 26,631	738 bp	prim_transcript
/note	= primary transcript ENST00000495895 Retained intron		
DCTN1-221	27,187 .. 30,933	3747 bp	prim_transcript
/note	= primary transcript ENST00000491465 Retained intron		
DCTN1-220	28,711 ..180,484	151,774 bp	gene
/note	= gene ENSG00000264324 Protein coding		
DCTN1-220	28,711 ..180,484	151,774 bp	prim_transcript
/note	= primary transcript ENST00000451608 Nonsense mediated decay		
DCTN1-222	29,159 .. 30,037	879 bp	prim_transcript
/note	= primary transcript ENST00000492717 Retained intron		

Primer	Length	Binding Sites	T _m	Date Added
✓ PCR Forward /sequence = GCCTGGTCTAAACTGAGTTATTTGC 44% GC / 7663.0 Da	25-mer	13,474 .. 13,498	58°C	Jan 20, 2023
✓ Sanger Sequencing /sequence = TCCCGTGTAGAGGTGATTGG 55% GC / 6204.1 Da	20-mer	13,900 .. 13,919	58°C	Jan 20, 2023
✓ Donor Template WT -> SNV /sequence = ATCACAAAGTGAAGTACTTCCTGCCTTGAACAGTTCCATCATTTTTGCCCCTTTGCTTCATCCAGAATCACGCTTACCCATTTGCCAGTGGC 45% GC / 578.9 Da	100-mer	13,956 .. 14,055	75°C	Jan 20, 2023
✓ gRNA Protospacer /sequence = CAAATGGGTAGGCGTGATTC 50% GC / 6197.1 Da	20-mer	13,974 .. 13,993	56°C	Jan 20, 2023
✓ PCR Reverse /sequence = GGGAAGTAGTATCTGCTCCATCTTC 48% GC / 7648.0 Da	25-mer	14,374 .. 14,398	58°C	Jan 20, 2023