

CLUSTAL O(1.2.4) multiple sequence alignment

NM_001309975.1	GGCACCTTCGGGGAAATAAGATCGTCAACTTTTTTAAGGATTGTGGAGGACATTTATCGTC	60
NM_000492.4	-----	0
NM_001009781.1	-----TGGAA-GCAAATGACATC	17
NM_001309975.1	CCATTGTGTCTGACTTTCCTCGGGAGCTGCGCGGGTGGGGGACGCACACCAATGTGATC	120
NM_000492.4	-----GTAGTAGGTCTTTGGCATT	19
NM_001009781.1	ACAGCAGGTCAGAGAAAAAGGGCGAGCGGCAGGCAGAGAGAAGAGTAGGGCTTTTGGCACT	77
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NM_001309975.1	GGGGCTCAGAGACCCTCAGGTGCAGAGAAACAAAGCTGGCGTGCTCTTAGGATGCAGAA	180
NM_000492.4	AGGAGCTTGAGCCAGACGGCCCTAGCA-GGGACCCAGCGCCGAGAGACCATGCAGAG	78
NM_001009781.1	AGGAGCTCTTGTCGGCCTGCCCGGCAGGGACCTCGGTGCCCCAGAGACCATGCAGAG	137
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NM_001309975.1	GTCACCGGTGGAAGATGCGAACTTCCTCTCCAGATTTGTCTTTTGGTGGATTACACCACT	240
NM_000492.4	GTCGCCTCTGGAAGGCCAGCGTTGTCTCCAACTTTTTTTCAGCTGGACCAGACCAAT	138
NM_001009781.1	GTCGCCTCTGGAAGGCCAGCGTCGTCTCCAACTTTTTTTCAGCTGGACCAGACCAAT	197
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NM_001309975.1	GTTGAGGAAAGGTTTCACTAAAAAGTTAGAGCTGACCGACGTGTACAAGGCTCCTTCTTT	300
NM_000492.4	TTTGAGGAAAGGATACAGACAGCGCTTGAATTGTGAGACATATACCAAATCCCTTCTGT	198
NM_001009781.1	TTTGAAGAAAGGATACAGACAGCGCTTGAATTGTGAGACATATACCATATCTCTTCTTC	257
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NM_001309975.1	TGACCTGGCAGACACCTCTCCGAGAGACTCGAAAGGGAATGGGACAAAGAGGTGGTGTT	360
NM_000492.4	TGATTCTGCTGACAATCTATCTGAAAAATTGGAAGAGAATGGGATAGAGAGCTGGCTTC	258
NM_001009781.1	TGATTCTGCTGACAATCTATCTGAAAAATTGGAAGAGAATGGGACAGAGAACTGGCTTC	317
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NM_001309975.1	AGCCAAAGGCAGGCCCAAGCTCCTGAAAGCACTGGCCCGATGCTTCTTCTCCCGTTTGC	420
NM_000492.4	AAAG---AAAAATCCTAAACTCATTAAATGCCCTTCGGCGATGTTTTTCTGGAGATTTAT	315
NM_001009781.1	AAAG---AAAAATCCCAAACCTCATTAAATGCCCTTCGACGATGCTTTTTCTGGAGATTTAT	374
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NM_001309975.1	CTTCTTCGGTGTCTCCTCTACCTCGGGGAGGCGTCCAAGACTGTGCAGCCTCAGCTTTC	480
NM_000492.4	GTTCTATGGAATCTTTTTATATTAGGGGAAGTCACCAAAGCAGTACAGCCTCTCTTACT	375
NM_001009781.1	GTTCTATGGAATCATATTATATTAGGGGAAGTCACCAAAGCAGTCCAGCCTCTCTTACT	434
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NM_001309975.1	AGGTGCGCATCATTGCTTCTTCGACCCCTTCATGCTGCGGAGCGAAGTCAGGGATACTA	540
NM_000492.4	GGGAAGAATCATAGCTTCTATGACCCGATAACAAGGAGGAACGCTCTATCGCGATTTA	435
NM_001009781.1	GGGAAGAATCATAGCTTCTATGACCCAGATAACAAGGTGGAACGCTCCATTGCCATTTA	494
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NM_001309975.1	TTTGCCCTGGGGCTCGGCCTCCTGTTACCGCTCGCTTCATCCTGCTGCAGCCGCAAT	600
NM_000492.4	TCTAGGCATAGGCTTATGCCTTCTCTTTATTGTGAGGACACTGCTCCTACACCCAGCCAT	495
NM_001009781.1	CTTAGGCATAGGCCTATGCCTTCTCTTTATCGTGAGGACGCTGCTCCTGCACCCAGCCAT	554
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NM_001309975.1	CTATGGCCTGCATCACCTTGGCATGCAGATTCGATTGCTCTTTTCAGCCTCATATACAA	660
NM_000492.4	TTTTGGCCTTCATCACATTGGAATGCAGATGAGAATAGCTATGTTTAGTTTGATTATATA	555
NM_001009781.1	TTTTGGTCTCCATCACATTGGAATGCAGATGAGAATAGCTATGTTTAGTTTGATTATATA	614
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NM_001309975.1	AAAGACACTTAAGTTGTCCAGTAAGGTTTTGGACAAGATCAGCACCGGGCAACTCGTCAG	720
NM_000492.4	GAAGACTTTAAAGCTGTCAAGCCGTGTTCTAGATAAAATAAGTATTGGACAACCTGTTAG	615
NM_001009781.1	AAAGACTTTGAAGCTATCAAGCCGTGTTCTGGATAAAATAAGTATTGGACAACCTGTTAG	674
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NM_001309975.1	TCTGATGTCTGCCACCTCAACAAGCTGGATGAGAGCCTGGGTCTAGCGCACTTTGTGTG	780
NM_000492.4	TCTCCTTTCCAACAACCTGAACAAATTTGATGAAGGACTTGCACTTGGCACATTTTCGTGTG	675
NM_001009781.1	TCTCCTTTCCAACAACCTGAACAAATTTGATGAAGGACTTGCACTTGGCACATTTTCGTGTG	734
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NM_001309975.1	GATCACACCTCTGCAGTGTATATTGTGTACTGGTTTGATCTGGGAGCTGATTGAGGTGAA	840

NM_000492.4	GATCGCTCCTTTGCAAGTGGCACTCCTCATGGGGCTAATCTGGGAGTTGTTACAGGCGTC	735
NM_001009781.1	GATTGCTCCTCTGCAAGTGACGCTGCTGATGGGGCTGCTCTGGGACTTGTTGCAGGCCCTT	794
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NM_001309975.1	CGGCTTCTGTGCCCTGGCATCTCTGACCTTCTTGGCATTCTCCAAGCTTGGCTCTCCCT	900
NM_000492.4	TGCCTTCTGTGGACTTGTTTCTGATAGTCCTTGCCCTTTTTCAGGCTGGGCTAGGGAG	795
NM_001009781.1	CACCTTCTGTGGGCTTGCTTTCCTCGTAGTCCTGCCTTCTTCAAGCCGGTTAGGGAA	854
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NM_001309975.1	GAAGATGGGCCCTCCCCGGGCACAGCGTGCTGGGCTGATAAACCGACGTCTGGCTCTTAC	960
NM_000492.4	AATGATGATGAAGTACAGAGATCAGAGAGCTGGGAAGATCAGTGAAAGACTTGTTGATTAC	855
NM_001009781.1	AATGATGATGAAGTACAGAGATCAGAGAGCTGGAAAGATCAATGAAAGACTGGTGATAAC	914
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NM_001309975.1	TTCTGAGATTGTGGAGAACATTCACCTCCGTGAAGGCGTATGGCTGGGAGGAAGTGATGGA	1020
NM_000492.4	CTCAGAAATGATTGAAAATATCCAATCTGTTAAGGCATACTGCTGGGAAGAAGCAATGGA	915
NM_001009781.1	CTCAGAAATGATTGAAAATATCCAATCAGTTAAGGCATACTGCTGGGAAGAAGCAATGGA	974
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NM_001309975.1	AACTATTATCAAAAACATTAGACAGGATGAAATGACTCTCACCAGGAAGATCGGCTCTCT	1080
NM_000492.4	AAAAATGATTGAAAACCTAAGACAAACAGAACTGAAACTGACTCGGAAGGCAGCCTATGT	975
NM_001009781.1	AAAAATCATTGAAAACCTAAGACAAACAGAACTGAAACTTACCCGGAAGGCAGCCTATGT	1034
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NM_001309975.1	GCGGTATTTCTACAGTGCCTCATACTTTTTCTCCGCCATACTGGTTATTGTATCCGCCAT	1140
NM_000492.4	GAGATACTTCAATAGCTCAGCCTTCTTCTTCTCAGGGTTCTTTGTGGTGTTTTTATCTGT	1035
NM_001009781.1	GAGATACCTCAATAGCTCAGCCTTCTTCTTCTCAGGGTTCTTTGTGGTATTTTTATCTGT	1094
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NM_001309975.1	TGTGCCTCATGCACTCAGTAACGGCATTATATTGCGGCGAATCTTCACCACGGCGTCATA	1200
NM_000492.4	GCTTCCTCATGCACTAATCAAAGGAATCATCTCCGGAATAATTCAACCACATCTCATT	1095
NM_001009781.1	GCTTCCTTATGCACTGCTCAAAGGAATCATCTTCGAAAAATATTCAACCATCTCATT	1154
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NM_001309975.1	CTGCGTAGTGTTACGTATGACGCTCACCCGCCAGCTGCCAGGCTCCATCCAGATGTGGTA	1260
NM_000492.4	CTGCATTGTTCTGCGCATGGCGGTCACTCGGCAATTTCCCTGGGCTGTACAAACATGGTA	1155
NM_001009781.1	CTGCATTGTTTTGCGCATGGCAGTTACTCGGCAGTTCCCTGGGCAGTACAAACTTGGTA	1214
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NM_001309975.1	CGACACGTTGGCATTGGTCAAAAGATCGAGGATTTCTGCTGAAGGAAGAATACAAAGT	1320
NM_000492.4	TGACTCTCTTGGAGCAATAAACAAAATACAGGATTTCTTACAAAAGCAAGAATATAAGAC	1215
NM_001009781.1	TGATTCTCTTGGAGCAATAAATAAAATACAGGATTTCTTACAAAAGCAAGAATATAAGAC	1274
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NM_001309975.1	AATGGATTATAGCCTGACCACAGTTGACTAGAGCTAATCAATGTTTCATCATCCTGGGA	1380
NM_000492.4	ATTGGAATATAACTTAACGACTACAGAAGTAGTGATGGAGAATGTAACAGCCTTCTGGGA	1275
NM_001009781.1	ATTGGAATATAACTTAACAACTACAGATGTAGTGATGGAGAATGTAACAGCCTTCTGGGA	1334
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NM_001309975.1	TGAGGGGATTGTTGAGCTCTTTGAGAAGATCAAGCGGGAAACAAAGCCAATGGACAACCT	1440
NM_000492.4	GGAGGGATTGAGGAATTATTTGAGAAAGCAAAACAAAACAATAACAATAGAAAAACTTC	1335
NM_001009781.1	GGAGGGATTAGTAAATTATTTGAGAAAGCAAAAGAAAATAATAACAATAGAAAAATTTCT	1394
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NM_001309975.1	TACCGGTGATGACGGACTGTTCTTCACTAACTTGTA-----CGTCACCCCTGTCCTCAA	1494
NM_000492.4	TAATGGTGATGACAGCCTCTTCTTCACTAATTTCTCACTTCTTGGTACTCCTGTCCTGAA	1395
NM_001009781.1	TAATTGTGATACAGCCTCTTCTTCACTAATTTCTCACTTCTTGGTACTCCTGTCCTGAA	1451
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NM_001309975.1	AAACATCAACCTACGCTTAGAGGAAGGCATGATGCTGGCAGTGGCTGGATCTACCGGATC	1554
NM_000492.4	AGATATTAATTTCAAGATAGAAAGAGGACAGTTGTTGGCGGTTGCTGGATCCACTGGAGC	1455
NM_001009781.1	AGATATCAGTTTCAAGATAGAAAGAGGACAGTTGTTGGCAGTTGCTGGATCTACGGGAGC	1511
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NM_001309975.1	AGGAAAGAGTTCCTGCTTATGATGATCCTGGGGGAGTTGGTGCCATCAGAGGGTAAAAT	1614
NM_000492.4	AGGCAAGACTTCACCTTCTAATGGTGATTATGGGAGAAGTGGAGCCTTCAGAGGGTAAAAT	1515
NM_001009781.1	AGGCAAGACTTCACCTTCTCATGATGATTATGGGAGAATTGGAACCTTCGAGGGTAAAAT	1571
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NM_001309975.1	TCCTCGGAGCAACCTGTATCACCATGTGCTACAGCACCTCAACGGCAGGCGCCAGTCGGT	2514
NM_000492.4	GCCTCGCATCAGCGTGATCAGCACTGGCCCCACGCTTCAGGCACGAAGGAGGCAGTCTGT	2376
NM_001009781.1	GCCTCGGAGCAATGCAGTCAACAGTGGCCCCACATTTCTGGGAGGGAGGAGGCAGTCAGT	2432
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NM_001309975.1	CCTGGCGTTTCATCACCAACGCTCAGGGCC-AG----GAGCGCAGAGAGCAGATGCAGTC	2568
NM_000492.4	CCTGAACCTGATGACA--CACTCAGTTAACCAAGGTCAGAACATTCACCGAAAGACAAC	2433
NM_001009781.1	TCTGAACCTTATGACCTGCTCCTCAGTGAACCAAGGTCAGAGCATTTCATCGAAAGACAGC	2492
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NM_001309975.1	TTCCTTCAGAAAAAAGCTGTCCATCACCCCGCAGTGTAACCTGGCATCCGAGCTGGACAT	2628
NM_000492.4	AGCATCCACACGAAAAAGTGCTACTGGCCCCCTCAGGCA--AACTTGACTGAACTGGATAT	2490
NM_001009781.1	GACATCCACACGAAAAATGCTACTGGCTCCTCAGGCA--AGCTTAGCCGAAATAGATAT	2549
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NM_001309975.1	CTACGCCCGACGCTTGTCCAAGGACAGTGTTTTTGCATCAGTGAGGAAGTGGATGAAGA	2688
NM_000492.4	ATATTCAAGAAGGTTATCTCAAGAACTGGCTTGGAATAAGTGAAGAAATTAACGAAGA	2550
NM_001009781.1	ATATTCAAGACGGTTATCTCAAGATACTGGCTTGGAATAAGTGAAGAAATTAATGAAGA	2609
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NM_001309975.1	AGACATGGAAGAATGCTTTGCAGATGACCGTGAGGACATCTTCGAAACTACCTCATGGAG	2748
NM_000492.4	AGACTTAAAGGAGTGCTTTTTTGTGATGATATGGAGAGCATACCAGCAGTGACTACATGGAA	2610
NM_001009781.1	AGATTTAAGGGATTGCTTTTTTGTGATGATGTGGAGAACATACCAGCAGTGACTACCTGGAA	2669
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NM_001309975.1	TACTTATCTTCGATATGTTTCCACCAACAGAAGTTTGATCTATGTCTTGATTTTCATTTT	2808
NM_000492.4	CACATACCTTCGATATATTACTGTCCACAAGAGCTTAATTTTTGTGCTAATTTGGTGCTT	2670
NM_001009781.1	TACATACCTTCGATATATTACTGTCCACAAGAGCTTAATGTTTGTGCTAATTTGGTGCTT	2729
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NM_001309975.1	GATTGTCTTTGCCATTGAGGTTGCCGTTGTGTCTATTGGGATTTTCTCATTACTTCTGA	2868
NM_000492.4	AGTAATTTTTCTGGCAGAGGTGGCTGCTTCTTTGGTTGTGCTGTGGCTCCTTGGAACAC	2730
NM_001009781.1	AGTTGTGTTTCTGGTTGAGGTGGCTGCTTCTTTGGTTGTGTTGTGCTGTTTCCGAAAAT	2789
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NM_001309975.1	GATATGGAGGGATGGCGCCAACCCTAACTCCCCCAACTACATCGATGAGCAGCACCCGAA	2928
NM_000492.4	TCCTCTTCAAGACA-----AAGGGAATAG	2754
NM_001009781.1	ACTTTTGCAAGACA-----AAGGAAATAG	2813
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NM_001309975.1	CGCCTCTTCGACTCCTGTCCACCTTGCAGTGCATAGTCACACCAACCAGCGCCTACTACAT	2988
NM_000492.4	TACTCATAGTAGAAATAACAGCTATGCAGTGATTATCACCAGCACCAGTTCGTATTATGT	2814
NM_001009781.1	TACTAAGAATGCAAGTAACAGTTATGCAGTGATCATCACCAGCACCAGCTCGTATTATAT	2873
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NM_001309975.1	CATCTACATATTCTTTGCTCACTCAGATAGCATACTGGCCCTTGGAGTCTTTAGGGGTCT	3048
NM_000492.4	GTTTTACATTTACGTGGGAGTAGCCGACACTTTGCTTGCTATGGGATTCTTCAGAGGTCT	2874
NM_001009781.1	TTTTTACATTTATGTGGGAGTAGCTGACACTTTGCTTGCTCTAGGACTCTTCAGAGGTTT	2933
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NM_001309975.1	CCCTTTAGTCCACACGTTGCTCACTGTGTCTAAAAGACTTCACGAACAGATGCTTAGCTC	3108
NM_000492.4	ACCACTGGTGCATACTCTAATCACAGTGTCGAAAATTTACACCACAAAATGTTACATTC	2934
NM_001009781.1	ACCACTGGTGCATACTCTAATCACAGTGTCAAAACTTTACACCACAAAATGCTACAGTC	2993
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NM_001309975.1	TGTGCTACGGGCCCTATGTCTGTTCTCAACACCATGAAAACAGGCCGATAATGAACAG	3168
NM_000492.4	TGTTCTTCAAGCACCTATGTCAACCCTCAACACGTTGAAAAGCAGGTGGGATTCTTAATAG	2994
NM_001009781.1	TGTTCTTCAAGCCCTATGTCAACCCTCAACACGTTGAAAACAGGTGGAATTCTTAATAG	3053
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NM_001309975.1	ATTCATAAAGACATGGCCGTCATTGATGACATGCTACCACTAGTGCTTTTTGACCTCAT	3228
NM_000492.4	ATTCTCCAAAGATATAGCAATTTTGGATGACCTTCTGCCTCTTACCATATTTGACTTCAT	3054
NM_001009781.1	ATTCTCCAAAGATATAGCAGTTTGGATGATCTTCTGCCTCTTACCATATTTGACTTCAT	3113
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NM_001309975.1	ACAGTTAACTTTACTCGTCATCGGATGCATCTTCACGGTGTCCATCATGAGACCATACAT	3288
NM_000492.4	CCAGTTGTTATTAATTGTGATTGGAGCTATAGCAGTTGTGCGAGTTTTACAACCCTACAT	3114
NM_001009781.1	TCAGTTGTTATTAATTGTGATTGGAGCTGTGGTGGTCTCCGTTTTACAACCCTACAT	3173

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NM_001309975.1	CTTCATATCTGCAATCCCCTGGCTGTGATCTTTGTGGTCATGAGGAAGTACTTCTTACG	3348
NM_000492.4	CTTTGTTGCAACAGTGCCAGTGATAGTGGCTTTTATTATGTTGAGAGCATATTTCTCCA	3174
NM_001009781.1	CTTCCTAGCTACAGTGCCAGTGATAGCGGCTTTTATTCTCTTGAGAGGCTACTTCTCCA	3233
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NM_001309975.1	AACCTGACAGCAGCTCAAACAAGTACAGGCTGAAGCCGCTAGTCCCCTCTTCTCTCACCT	3408
NM_000492.4	AACCTCACAGCAACTCAAACAAGTGAATCTGAAGGCAGGAGTCCAATTTTCACTCATCT	3234
NM_001009781.1	CACCTCCCAGCAACTCAAGCAGCTGGAATCTGAAGGCAGGAGTCCAATTTTCACTCATCT	3293
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NM_001309975.1	CATCATCTCGCTGAAGGGTTTATGGACAATCCGAGCCTTTGGACGTCAGACTTACTTTCGA	3468
NM_000492.4	TGTTACAAGCTTAAAGGACTATGGACACTTCGTGCCTTCGGACGGCAGCCTTACTTTGA	3294
NM_001009781.1	TGTTACAAGCTTAAAGGACTATGGACACTTCGTGCCTTTGGACGGCAGCCTTACTTTGA	3353
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NM_001309975.1	GACGCTCTTCCACAAAGCTCTGAACACCCACACAGCCACCTGGTTCCACTACCTGTCCAC	3528
NM_000492.4	AACCTGTTCACAAAGCTCTGAATTTACATACTGCCAACTGGTTCTTGTACCTGTCAAC	3354
NM_001009781.1	AACCTTATTCCACAAAGCTCTGAATTTACATACTGCCAACTGGTTTGTATCTGTCAAC	3413
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NM_001309975.1	GCTGAGATGGTTCCTGTTCCGCTGCGACGTCATCTTTGTGCTGTTCTTCACCGCGCTGC	3588
NM_000492.4	ACTGCGCTGGTTCCAAATGAGAATAGAAATGATTTTGTGCTCTTCTTATTGCTGTTAC	3414
NM_001009781.1	ACTGCGCTGGTTCCAAATGAGAATAGAAATGATTTTGTGCTTTCTTATTGCTGTTAC	3473
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NM_001309975.1	CTTCATTGCTGTCGGAACCAACCAGGACAGACCAGGTGAGATCGGTATCATTGTGGCCCT	3648
NM_000492.4	CTTCATTTCCATTTTAAACAACAGGAGAAGGAGAAGGAAGAGTTGGTATTATCTGACTTT	3474
NM_001009781.1	CTTCATTTCCATTTTAAACAACAGGTGAAGGAGAAGGAAGAGTTGGGATTATTCTAATTT	3533
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NM_001309975.1	AGCCATGCTGATCCTGGGCACCTTCCAATGGGCTATCATCACCAGTATCAATGTGGACGG	3708
NM_000492.4	AGCCATGAATATCATGAGTACATTGCAAGTGGGCTGTAAACTCCAGCATAGATGTGGATAG	3534
NM_001009781.1	AGCCATGAATATCATGGGTACATTGCAAGTGGGCTGTAAACTCTAGCATAGATGTGGATAG	3593
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NM_001309975.1	TCTGATGCGTTCGGTGGATCGGGTGTTCAAATTCATCGACTTGGCATCGGAAGAGACGCT	3768
NM_000492.4	CTTGATGCGATCTGTGAGCCGAGTCTTTAAGTTCATTGACATGCCAACAGAAG--GTAA	3591
NM_001009781.1	CTTGATGCGATCTGTGAGCCGAGTCTTTAAGTTTATTGATATGCCAACAGAAGATGGTAA	3653
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NM_001309975.1	CCAGGGAAAATCTGGAGGGGAAAGGAGGC-----CCCGACC-----TGGT	3807
NM_000492.4	ACCTACCAAGTCAACCAAAACCATACAAGAATGGCCAACCTCTCGAAAGTTATGATTATTGA	3651
NM_001009781.1	ACCTAACAAATTCATTACAGACCATCAAAGATAGTCAACCCTCAAAAGTTATGATCATCGA	3713
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NM_001309975.1	CATCAACAACCTCAGTACTCACAGCTACTGGCCTAACCGGGGCCAGCTGGAAGTGCAGGG	3867
NM_000492.4	GAATTCACACGTGAAGAAAGATGACATCTGGCCCTCAGGGGGCCAAATGACTGTCAAAGA	3711
NM_001009781.1	GAATCAACATGTAAAGAAAGATGACATCTGGCCCTCAGGAGGCCAAATGACTGTCAAAGA	3773
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NM_001309975.1	CCTGACTGTTAAATACACGGAGGCTGGGCGCGCCGTGCTCAACGACATCTCCTTCTCTGT	3927
NM_000492.4	TCTCACAGCAAAATACACAGAAGGTGGAAATGCCATATTAGAGAACATTTCTTCTCAAT	3771
NM_001009781.1	CCTCACAGCAAAGTACATAGACGGAGGGAATGCCATACTAGAGAACATATCCTTCTCAAT	3833
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NM_001309975.1	GGATGGTGGGCAGAGCGTGGGCCTGCTGGGTGGAACAGGTTCTGGGAAGAGCACCCTGCT	3987
NM_000492.4	AAGTCCTGGCCAGAGGGTGGGCCTCTTGGGAAGAACTGGATCAGGGAAGAGTACTTTGTT	3831
NM_001009781.1	AAGTCCCGGCCAGAGGGTGGGCCTCTTGGGAAGAACTGGATCAGGGAAGAGCACTTTGTT	3893
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NM_001309975.1	GTCCGCTCTGCTGGGCCTCAACTACACGGAAGGGGAAATGTTTATTGACGGGGTTTCTTC	4047
NM_000492.4	ATCAGCTTTTTTGAGACTACTGAACACTGAAGGAGAAATCCAGATCGATGGTGTGCTTG	3891
NM_001009781.1	ACTGGCTTTTTTGAGACTGCTGAATACCAAGGAGAAATCCAAATAGATGGTGTGCTTG	3953
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NM_001309975.1	CAGCTCCATGCCGCTGCAAGCATGGAGGAAAGCCTTCGGAGTGGTGCCGCAGAAAGCTT	4107
NM_000492.4	GGATTCAATAACTTTGCAACAGTGGAGGAAAGCCTTTGGAGTGATACCACAGAAAGTATT	3951

NM_001009781.1	GGATTCAATTACTTTGCAACAATGGAGGAAGGCCTTTGGAGTCATACCACAGAAAGTATT ** ** * ***** ***** ***** * ** ***** **	4013
NM_001309975.1	TATTCTGACTGGAACCTTCCGGATGAACCTGGACCCGTACGGGCGCTACAGTGACGATGA	4167
NM_000492.4	TATTTTTCTGGAACATTTAGAAAAAACTTGGATCCCTATGAACAGTGGAGTGATCAAGA	4011
NM_001009781.1	CATCTTTTCTGGAACATTTAGAAAAAACTTGGATCCCTATGAACAGTGGAGTGATCAAGA ** * ***** ** * * *** ** ** * * * * * ***** ** *	4073
NM_001309975.1	GCTGTGGCGGGTGGCCGAGGAGGTTGGCTTGAAGTCAGTAATCGAGCAGTTCACAGACAA	4227
NM_000492.4	AATATGGAAAGTTGCAGATGAGGTTGGGCTCAGATCTGTGATAGAACAGTTTCCTGGGAA	4071
NM_001009781.1	AATATGGAAAGTTGCAGATGAGGTCGGACTCAGATCTGTGATAGAGCAGTTTCCTGGGAA * *** ** ** * ***** ** * * ** ** * * * ***** ** * **	4133
NM_001309975.1	GCTGGACTTTGAGCTTAAGGACGGAGGCAGTGTGCTGAGCAATGGGCACAAACAGCTGAT	4287
NM_000492.4	GCTTGACTTTGTCTTGTGGATGGGGGCTGTGTCTTAAGCCATGGCCACAAGCAGTTGAT	4131
NM_001009781.1	GCTTGATTTTGTCTTGTGGATGGGGGTTGTGTTCTAAGCCACGGCCACAAGCAGTTGAT *** ** ***** ** * ** *	4193
NM_001309975.1	GTGTCTCGCCGCTCCATCCTCAGCAAGGCCCGCATTCTGCTGCTGGACGAGCCGTCCTC	4347
NM_000492.4	GTGCTTGCTAGATCTGTTCTCAGTAAGGCGAAGATCTTGCTGCTTGATGAACCCAGTGC	4191
NM_001009781.1	GTGCTTGCCAGATCTGTTCTCAGTAAAGCAAAGATCTTGCTGCTTGATGAACCCAGTGC *** * ** *	4253
NM_001309975.1	CTACCTGGACCCCATAACTGCAGGTCCTGAGAAAGACGCTGAAGCAGTCGTTTTCTGG	4407
NM_000492.4	TCATTTGGATCCAGTAACATACCAAATAATTAGAAGAACTCTAAAACAAGCATTTGCTGA	4251
NM_001009781.1	TCATTTGGATCCAATAACATACCAGATCATTGGAAGAACCTAAAACAAGCATTTGCTGA * ***** ** ***** ** * * * * * * * * * * * * * * * *	4313
NM_001309975.1	CTGCACCGTCATCCTATCAGAACACAAAGTGGAGCCGCTGCTGGAGTGCCAGTCATTCTT	4467
NM_000492.4	TTGCACAGTAATTTCTCTGTGAACACAGGATAGAAGCAATGCTGGAATGCCAACAAATTTT	4311
NM_001009781.1	TTGCACAGTAATCCTCTCTGAACACAGGATAGAAGCAATGTTGGAATGTCAACGATTTT ***** ** *	4373
NM_001309975.1	GATGATAGAGAAGAGCTCTGTAAAAAGCTACGACTCCATTGAGAGCTCATGAACGAGAT	4527
NM_000492.4	GGTCATAGAAGAGAAACAAAGTGCGGCAGTACGATTCCATCCAGAACTGCTGAACGAGAG	4371
NM_001009781.1	GGTCATAGAGGAAAAACAAGTGCGGCAGTATGATTCCATCCAGAGGATGCTGAGCGAGAA * * ***** *	4433
NM_001309975.1	GAGCCACCTGAAGCAGGCCATCAGCCCCGCCGACCGGCTCCACCTCTTCCCCACACCCCA	4587
NM_000492.4	GAGCCTCTTCCGGCAAGCCATCAGCCCCCTCCGACAGGGTGAAGCTCTTCCCCACCGGAA	4431
NM_001009781.1	GAGCCTCTTCCGGCAGGCCATCAGCCCCGAGACCGGCTGAAGCTCTTGCCCCACCGGAA ***** *	4493
NM_001309975.1	CCGCCTGAACTCCATCAAGAGGCCTCAGCCGCAGACCACCAAGATCTCTCCCTGCCGGA	4647
NM_000492.4	CTCAAGCAAGTGCAAGTCTAAGCCCC-----AGATTGCTGCTCTGAAAGA	4476
NM_001009781.1	CTCGAGCAGGCAGAGGTCTCGGGCCA-----ACATCGCCGCTCTGAAGGA *	4538
NM_001309975.1	AGAAGCCGAGGATGAAATCCAGGACACGCGGCTTTAAGCAGCCAGCTCCACACCAACACA	4707
NM_000492.4	GGAGACAGAAGAAGAGGTGCAAGATACAAGGCTTTAGAGAGCAGCATAAATGTTGACATG	4536
NM_001009781.1	GGAGACAGAGGAAGAGGTGCAAGAAACAAAGCTGTAGAGAGCGGAACAAGTGTGCTG ** *	4598
NM_001309975.1	CAAAACCAAGACTTTGATCAAGTGATCGGATGATAATAAGTCCTCG-----	4753
NM_000492.4	GGACATTTGCTCATGGAATTGGAGCTCGTGGACAGTCACCTCATGGAATTGGAGCTCGT	4596
NM_001009781.1	GGACGTCCACACGTGGGAGCTGAAGGAA----- * * * * *	4626
NM_001309975.1	-----TTGTCTGAGTTAGCGGTAAAGA-----GCAA	4779
NM_000492.4	GGAACAGTTACCTCTGCCTCAGAAAAACAAGGATGAATTAAGTTTTTTTTT-----AAAA	4650
NM_001009781.1	-----AAAGTTTCTGCCTCAGAAAAACAAGGAGGAATGATTTTTTTTTTTGAAAAAGAA ***** * * * * * * * * * *	4680
NM_001309975.1	AAGGATCCTTGGCATTGAGCTGCTGTAGAAGCGGATTT--GTATTG-----AATCAA	4829
NM_000492.4	AAGAAACATTTGGTAAGGGGAATTGAGGACACTGATATGGGTCTTGATAAATGGCTTCCT	4710
NM_001009781.1	GGAAAAATTGGGGTAAGAGGAATTAAGGACACTCCTGTGGGTCCGGATCCATGGCTTCCT * * * * * * * * * * * * * * * *	4740
NM_001309975.1	CTTAAAGAGAAT--TTAGAAGAGCAAAGGCAACAAACAGACATTTATTTTTACATTTT	4887

NM_000492.4	GGCAATAGTCAAATTTGTGTGAAAGGTACTTCAAATCCTTGAAGATTTACCACTTGTGTTT	4770
NM_001009781.1	GGCAGTGGTCAAATTTGTGTGACAGGTACTTCAAATCCTTGAAGATTTACCACTTG----- * * ** * * * * * * * * * * *	4795
NM_001309975.1	TTAAGTAAAGCTACACATTTAAAT-AGTATATTGTTTAA-GAGATATAAAGACGTTTTTG	4945
NM_000492.4	TGCAAGCCAGATTTTCTGAAAACCCTTGCCATGTGCTAGTAATTGGAAAGGCAGCTCTA	4830
NM_001009781.1	-----	4795
NM_001309975.1	TTTTACAGATGACACCCTGCAAAGGATTCT-----TCTACCCCTTTAAAAACGAGTTT	4998
NM_000492.4	AATGTCAATCAGCCTAGTTGATCAGCTTATTGTCTAGTGAAACTCGTTAATTTGTAGTGT	4890
NM_001009781.1	-----	4795
NM_001309975.1	TCCTGAG-AGAAGCGCAGTTCCTTCACTGTGAG-----AAATAAAAATAACCTGAACAC	5051
NM_000492.4	TGGAGAAGAACTGAAATCATACTTCTTAGGGTTATGATTAAGTAATGATAACTGGAAACT	4950
NM_001009781.1	-----	4795
NM_001309975.1	CCCGTCTAAATATTAGCATCTCAAATT-TCTCAGTTATCTCAGAATCTCAGTTTTTAAA	5110
NM_000492.4	TCAGCGGTTTATATAAGCTTGTATTCTTTTTCTCTCTCTCCCATGATG-TTTAGAAA	5009
NM_001009781.1	-----	4795
NM_001309975.1	CTCATTTTCAATTCAAATGGACTGCTAAGCATTCTAACTT-----CGTATCAATGC	5163
NM_000492.4	-----CACAACTATATTGTTTGCTAAGCATTCCAATCTCATTTCCAAGCAAGTA	5061
NM_001009781.1	-----	4795
NM_001309975.1	TCCATCTCCCCTCATGATCAAACCGACTGTGCCTGAACTTAA-----	5205
NM_000492.4	TTAGAA-TACCACAGGAACCACAAGACTGCACATCAAATATGCCCCATTCAACATCTAG	5120
NM_001009781.1	-----	4795
NM_001309975.1	----TGATT-----GGTTCTGATTATTGCTTT----TTTATCTGGCAC	5240
NM_000492.4	TGAGCAGTCAGGAAAGAGAACTTCCAGATCCTGGAAATCAGGGTTAGTATTGTCCAGGTC	5180
NM_001009781.1	-----	4795
NM_001309975.1	TGCATCCAGCCTAAATCGGATCTTTCAGACCTGC-----TCTGAAGACCTTGAGA	5290
NM_000492.4	TACCAAAAATC-----TCAATATTTAGATAATCACAATACATCCCTTACCTGGGAAAGG	5235
NM_001009781.1	-----	4795
NM_001309975.1	GCAATAATATTCAAGGAGAGGCAGCCAGCATGGTACGAAACACCTGGAAGTTAGG----C	5346
NM_000492.4	GCTGTTATAATCTTTCACAGGGG-ACAGGATGGTTCCCTTGATGAAGAAGTTGATATGCC	5294
NM_001009781.1	-----	4795
NM_001309975.1	TAGGAAGCCTTGTCATGATGTCACGATCTGT-----TGTTGAGT-----AAGAGACAA	5393
NM_000492.4	TTTTCCCAACTCCAGAAAGTGACAAGCTCACAGACCTTTGAACTAGAGTTTAGCTGGAAG	5354
NM_001009781.1	-----	4795
NM_001309975.1	TCGATATGAGTAGATGTGCAGCAGGAAGGGCTCGTCTGTAATGAACCAATCAGAGTTG--	5451
NM_000492.4	AGTATGTTAGTGCAAATTTGTCACAGGACAGCCCTTCTTTCCACAGAAGCTCCAGGTAGAG	5414
NM_001009781.1	-----	4795
NM_001309975.1	----TG-----AAAGTGAAGTGTGGGTGGAAATGCTTCATGTCATT-----	5488
NM_000492.4	GGTGTGTAAGTAGATAGGCCATGGGCACTGTGGGTAGACACACATGAAGTCCAAGCATT	5474
NM_001009781.1	-----	4795
NM_001309975.1	-----CTTTGTAAGTAGCAGGTTTCAAACACACAACCTAGATCATAGATTCTCCAAC	5539
NM_000492.4	AGATGTATAGGTTGATGGTGGTATGTTTTCAGGCTAGATGTATGTACTTCATGCTGTCTA	5534
NM_001009781.1	-----	4795

NM_001309975.1	TTCAACTA-----TATTTG---CCCAGAAAAACCAAGCGTGGTTCGGTCTTTTCTAT	5588
NM_000492.4	CACTAAGAGAGAATGAGAGACACACTGAAGAAGCACCAATCATGAATTAGTTTTATATGC	5594
NM_001009781.1	-----	4795
NM_001309975.1	TTCTCCCGTGTGTTGTCTGGAAAAACATGCATGACCTAGTGGAGAT-----	5635
NM_000492.4	TTCTGTTTTATAATTTTGTGAAGCAAAATTTTTCTCTAGGAAATATTTATTTTAATAAT	5654
NM_001009781.1	-----	4795
NM_001309975.1	-----CAACTTGAACCTCTTTTATTT	5656
NM_000492.4	GTTTCAAACATATATAACAATGCTGTATTTTAAAAGAATGATTATGAATTACATTTGTAT	5714
NM_001009781.1	-----	4795
NM_001309975.1	ATTTTATTTTCTATCTTTGATTTCTTCACTAGCTTTACATTTCCAAAGTGCA-----	5708
NM_000492.4	AAAATAATTTTATATTTGAAATATTGACTTTTTATGGCACTAGTATTTCTATGAAATAT	5774
NM_001009781.1	-----	4795
NM_001309975.1	-----	5708
NM_000492.4	TATGTTAAAACTGGGACAGGGGAGAACCTAGGGTGATATTAACCAGGGGCCATGAATCAC	5834
NM_001009781.1	-----	4795
NM_001309975.1	-----	5708
NM_000492.4	CTTTTGGTCTGGAGGGAAGCCTTGGGGCTGATGCAGTTGTTGCCACAGCTGTATGATTC	5894
NM_001009781.1	-----	4795
NM_001309975.1	-----	5708
NM_000492.4	CCAGCCAGCACAGCCTCTTAGATGCAGTTCTGAAGAAGATGGTACCACCAGTCTGACTGT	5954
NM_001009781.1	-----	4795
NM_001309975.1	-----	5708
NM_000492.4	TTCCATCAAGGGTACACTGCCTTCTCAACTCCAAACTGACTCTTAAGAAGACTGCATTAT	6014
NM_001009781.1	-----	4795
NM_001309975.1	-----	5708
NM_000492.4	ATTTATTACTGTAAGAAAATATCACTTGTCAATAAAATCCATACATTTGTGTGAAA	6070
NM_001009781.1	-----	4795