

gi | 226053125 | ref | NM_001146184.1 | -----GCAAGAGTCTGGCCAGCTGCGGCAAGGAGAGGTTTGGGAGGCGGGAGATGTCCACCCCTGGCTGTGGTGGCCCGCCGGCCGGCCGGCCCA 91
gi | 114679299 | ref | XM_001141226.1 | -----ACTTCAGGGCATTAGACAAGTTGCCACAGTCCCAGTTCGCCAAGTTAGTCCAGCTAACTCCTCGAGTAGGTCCTGTGAAAGCCCAAGGGG---TCATGCTTG--TAACGTGTGTGAGGCCAACTTTGTG 133
gi | 58331165 | ref | NM_008817.2 |
gi | 73947372 | ref | XM_533574.2 |
gi | 50872144 | ref | NM_001002887.1 | TTGGAGCAGAGGATCGGCACATGTCCACCCCTGGCTGCTGGCCCTCCCGAGCGCCTGGGGCCGTGTGGGGCCACTAGAAGTTCACAGGCTGCGCAAGTGTGCGAGCTGTGAGCCCGGGCAGGGGGGTTCCTTGAAGTCCGGTGAAGCTGTGCT 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 226053125 | ref | NM_001146184.1 | TGAGGGTGGCT-AGGCGGCTGTTCGTGCCGAGGCTGCCGAGCACAGGTTGAGCTTTGCTTCTGATCTTCGCTCTTCCTGGAGA-CGACTGGCGAGAGGAAGAGGACTAGGTCCAAACGCTAGGTGGCTGGGTCCAGGTCCCTG 239
gi | 114679299 | ref | XM_001141226.1 | CGTTGTGTTGCC-TATTTACTGGGCACTCCCATATCCCAAAAGCATTGTGATGCCCTCTGGTAAAGGTGGCTCCACTGCTGCCCTGGTCTTCAACTTCTG---GGACATGTGTAATCTCCTTACGATC-----TACAGGTCCCTG 269
gi | 58331165 | ref | NM_008817.2 |
gi | 73947372 | ref | XM_533574.2 |
gi | 50872144 | ref | NM_001002887.1 | CTTCTCTTCTCGAGGTGATCGGCAGGAGGCAAGAGGCACTAGGTCCAAACGCTCAGGTGTCTGTGTCCAGGTCCCCTGGCAATTTTACTGTTCCCTGTGCAATAGCTACTTGTTCAGAAAGTCCGGAGGGAAGCCGTGTTCCACCAAGTCCCTG 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 226053125 | ref | NM_001146184.1 | AGTACTGACGGTCAAGGCCTGCCGCTCTTCTGTGACTCATGTTTGGTTCTCCAGTCAAAAATTTTACTTAGAGAAATGCTGCTCCAAAGCACTTGTCTGCCACCAAACTAAGAAAGTCTGGGCCCAAACTGTATGAGCTAGA 389
gi | 114679299 | ref | XM_001141226.1 | AGTACTGACGGTCAAGGCCTGCCGCTCTTCTGTGACTCATGTTTGGTTCTCCAGTCAAAAATTTTACTTAGAGAAATGCTGCTCCAAAGCACTTGTCTGCCACCAAACTAAGAAAGTCTGGGCCCAAACTGTATGAGCTAGA 419
gi | 58331165 | ref | NM_008817.2 | -----AGACGCTGGGGAGTCAGGAGTCCGGGAGGAC--GAGCATCGGA---GGAGAGCGGAG 54
gi | 73947372 | ref | XM_533574.2 | -----ATGCTGCTCCAAAGTACTTGTCTGCCACCAAAAGGAGTCTGGGTTCCAGATGTATGAGCTAGA 71
gi | 50872144 | ref | NM_001002887.1 | AGCACTGACTGCC-CCCGCTGCTGCTGCCCTGTTGGCCCATGTTGGTTCTCCAGTCAAAAATTTTCTTACAGACATGCTGCTCCCAAGTCCCTGTGAGAGAGT---GGGCCCAAACTGTATGAGCTAGA 446
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 226053125 | ref | NM_001146184.1 | CAGTGACTTGACTAAGGAGCCGGATGTCATCATAGGAGAAAGTCCAACTGACTCTGAGTTTTTTCATCAGAGGTTTGGAACTAATCTATGTGAAATTTGTTGGGCTCGGAAGACC---CTGATCAAACTCCGAAACCTCT--GCCTC 534
gi | 114679299 | ref | XM_001141226.1 | CAGTGACTTGACTAAGGAGCCGGATGTCATCATAGGAGAAAGTCCAACTGACTCTGAGTTTTTTCATCAGAGGTTTGGAACTAATCTATGTGAAATTTGTTGGGCTCGGAAGACC---CTGATCAAACTCCGAAACCTCT--GCCTC 564
gi | 58331165 | ref | NM_008817.2 | AGATGCTCCACCCCTGGG---CTGGTGGCCCGCCGG---GGCCCGGTTCAAGTGGGTGCACTAGACTGCCAGCCCTGGTCCGGGTGTGTGCTGAGAGTGTGTGCTCCGGAGCCCTACTTCTTATCTTATCCTTTTGGAGAC 197
gi | 73947372 | ref | XM_533574.2 | CAGTGACTTGACTAAGGAGCCGGATGTCATCATAGGAGAAAGTCCAACTGACTCTGAGTTTTTTCATCAGAGGTTTGGAAATTTGTTGGGCTCGGAAGACC---CTGATCAAACTCCGAAACCTCT--GCCTC 216
gi | 50872144 | ref | NM_001002887.1 | CAGTGACTTGACTGAG---CCGACGCAATCCCAAGGAGGCGCCACTGACTCTGAGTTCTTTTCATCAGAGGTTTGGAAATTTCTCTACTGTGAAATTTGTTGGGCTCGGAAGACC---CTTCTCAAACTCCGAAACCTCT--GCCTC 588
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 226053125 | ref | NM_001146184.1 | GATTGGTTGACGCCGGA---GATCC---GCACCAAGGAGG--AGATCATCGAGCTCTTGGTCTTGAAGCAGTACCTGACCATCATCCCTGAAAAGCTCAAGCC-TTGGGTGCGAGCAAAAAGCCGGAGAACTGTGAGAACTCGTCA 674
gi | 114679299 | ref | XM_001141226.1 | GATTGGTTGACGCCGGA---GATCC---ACACCAAGGAGG--AGATCATCGAGCTCTTGGTCTTGAAGCAGTACCTGACCATCATCCCTGAAAAGCTCAAGCC-TTGGGTGCGAGCAAAAAGCCGGAGAACTGTGAGAACTCGTCA 704
gi | 58331165 | ref | NM_008817.2 | AACTGGCAAGAGGAGACTAGTCTCCAACAGCTAGGTGGCTGGTCCAGGCCAGGCCCTCCAGCAAGGGGAGATCAGTTGATCATCCCTGAAAAGCTCAAGCC-TTGGGTGCGAGCAAAAAGCCGGAGAACTGTGAGAACTCGTCA 343
gi | 73947372 | ref | XM_533574.2 | GATTGGTTGACGCCGGA---GATCC---GCACTAAGGAGG--AGATTAATGAGCTCTTGGTCTTGAAGCAATACCTGACCATCCCTGAAAAGCTCAAGCC-TTGGGTGCGAGCAAAAAGCCGGAGAACTGTGAGAACTAGTTAC 356
gi | 50872144 | ref | NM_001002887.1 | GATTGGTTGACGCCGGA---GATCC---GCACCAAGGAGG--AGATTAATGAGCTCTTGGTCTTGAAGCAGTACCTGACCATCCCTGAAAAGCTCAAGCC-TTGGGTGCGAGCAAAAAGCCGGAGAACTGTGAGAACTCGTTC 728
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



gi | 226053125 | ref | NM_001146184.1 | TCTGCTGGAGAAATACAAAGGAGATGTACCAACCAAGAGACGACAAACAGTGACGTGACCGCAGCAGACATGACCCGGAAAGAGAGAGTCTCACCACTCAGTCCATTCTTT---CAGTGACCCGGACTGGGACCGGAG 821
gi | 114679299 | ref | XM_001141226.1 | TCTGCTGGAGAAATACAAAGGAGATGTACCAACCAAGAGACGACAAACAGTGACGTGACCGCAGCAGACATGACCCGGAAAGAGAGAGTCTCACCACTCAGTCCATTCTTT---CAGTGACCCGGACTGGGACCGGAG 851
gi | 58331165 | ref | NM_008817.2 | TCCGTTGGAGAGTTTCAAG--ATGTACCATCACGAGACGACCAACAGTGACATGAAACAGTACCGCAGCAGACATGAGCCGAAAGTGGGAGAGAAAGCCCACTCAGTCTCATGTCTTGTGGCAGTGGAGCCGAG 490
gi | 73947372 | ref | XM_533574.2 | TCTCTGAAAATTAAGGGATGTATGAGCCAGGAGACGACAAACAGTGACCTCCACAGTGAAGACGATGACCCGAAAGGAGAGAGTCCCAACCAAGCTCCGCTCTTCTTTCTACTGGGACCCGGAGAGGGAGCCGAG 506
gi | 50872144 | ref | NM_001002887.1 | TCTCTGAAAATTAAGGGATGTATGAGCCGAGGACGACAAACAGTGACCTCCACAGTGAAGACGATGACCCGAAAGGAGAGAGTCCCAACCAAGCTCCGCTCTTCTTTCTACTGGGACCCGGAGAGGGAGCCGAG 875
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900



gi | 226053125 | ref | NM_001146184.1 | GGGCCAGAGCAGAGACATGGAGCCAAGACCGCTGGTCCCACACCGAAGCCCAAGAGCAGGATGCTCCGCGGGATCTTTCCCTTCTGTGTGGTGGCAAAACAAGCTTTGAAATGGACAGAGGGACGA---CAGGGACTCC---AG 965
gi | 114679299 | ref | XM_001141226.1 | GGGCCAGAGCAGAGACATGGAGCCAAGACCGCTGGTCCCACACCGAAGCCCAAGAGCAGGATGCTCCGCGGGATCTTTCCCTTCTGTGTGGTGGCAAAACAAGCTTTGAAATGGACAGAGATGACGA---CAGGGACTCC---AG 995
gi | 58331165 | ref | NM_008817.2 | GGGCCAGAGCAGAGACATGGAGCCTCGAGACCGCTGGCCATACACCAGGAATCCCAGAAAGCAGGCTGCTCAAAGGGATCTTTCTTTCTGTGTGTGCAAGACCAATTTTGGATGGACAGAGATGATGA---CAGAGCTTCC---AT 634
gi | 73947372 | ref | XM_533574.2 | AGCCAGAAAGCAGAGACCTGGAGTCTCGAGACCGCTGGCCATATACCAGGAATCCCAGAAAGCAGACTTCTCAAAGGGATCTTTCCCTTCTGTGTGGTGGCAAAACAAGCTTTGCGATGGAAAGAGAGTGCAAAAGTGGGATCTGTGAT 656
gi | 50872144 | ref | NM_001002887.1 | TGGCCGGAGCCGGGACATGGAGTCAAGGACCGCTGGCCGCTCCGGAGCCCCAGGAGCAGGTTTCAAGAGGGGATCTCCCTTCTGTGTGGTGGCAAGCA---GGAAAGAGAGCAGAGCCAGGGACTCCCTGTCT 1016
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050



gi | 226053125 | ref | NM_001146184.1 | GGCTTATGAGTCCCGATCTCAGGATGCTGAATCATACCAAAATGTGTGGACCTCGCTGAGGACAGGAAAACCTCACAAACAATCCAGGACAACTGGAAAACTACAGGAAGCTGCTCCCTCG---TGCAGCTTGTCTGAAGACGATGG 1112
gi | 114679299 | ref | XM_001141226.1 | GGCTTATGAGTCCCGATCTCAGGATGCTGAATCATACCAAAATGTGTGGACCTCGCTGAGGACAGGAAAACCTCACAAACAATCCAGGACAACTGGAAAACTACAGGAAGCTGCTCCCTCG---TGCAGCTTGTCTGAAGACGATGG 1142
gi | 58331165 | ref | NM_008817.2 | GGATTTATGAGTCTCGATCCAGGATGCCGAGTCAACCAAGATTTGTGGAACTCAAAGAGGACAAAGAGCTCAGAACTCCAATTCAGGACAACTGGAGAAAACAGAAAGCTGCTCGTGGGATCCAGCTTGCAGGATGCAAT 784
gi | 73947372 | ref | XM_533574.2 | GGATTTATGAGTCAAGATCCAGGATGCTGTGTATACCAAGACCTTGTGAACCTGACTGAGGACAGGAAGCCTCAGAAACCGATTGAGGACAACTGGAGAACTATAGGAAAATGCTCTCTCTTG--- 781
gi | 50872144 | ref | NM_001002887.1 | GGATTTGAGTCCAGATCTGAGGAGCGGTGTGTATCCAGGATATGTGTGGCCCTCACTGAGGATCGAAGCCCCAGAACCCGATTGAGGACAACTGGAGAACTACCGCAAGCTGCTCTACTGGGGGTTCCAGCTTGCAGGACGATGG 1166
.....1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....1170.....1180.....1190.....1200



gi | 226053125 | ref | NM_001146184.1 | CCACCTCCACATGACGAGGCCACTCATCAAGATCCAAAGAAAGTGCTACCCAAAGCACCAGTCCAGGCTCAAAAATATGCTGAGGCCAAAAAATCAACCCACCCGGCGGGGATTTGTGAAGATGAATCTTCCCACGGATGATAAT 1262
gi | 114679299 | ref | XM_001141226.1 | CCACCTCCACATGACGAGGCCACTCATCAAGATCCAAAGAAAGTGCTACCCAAAGCACCAGTCCAGGCTCAAAAATATGCTGAGGCCAAAAAATCAACCCACCCGGCGGGGATTTGTGAAGATGAATCTTCCCACGGATGATAAT 1292
gi | 58331165 | ref | NM_008817.2 | ACACCTCTCACATGACAAAGGCCACTCATCGAGGTTCCAAAGAAAGTCCCTACCCAAAGCACCAGGCTCAAAAATATGCTGAGGCCAAAAAATCAACCCACCCGGCGGGGATTTGTGAAGATGAATCTTCCCACGGATGATAAT 934
gi | 73947372 | ref | XM_533574.2 | -----GGCTGAAAACCACTGAAACCAAAAAGTTGCCATCCGGGGGGGATTTGTGAAGATGAATCTTCCCACGGATGATAAT 863
gi | 50872144 | ref | NM_001002887.1 | CCACCTCACATGACCCAGGCCACTCGGCAAGGTCAAAGAAAGTGCTACCCAAAGCACCAGGCTCAAAAATATGCTGAGGCCAAAAAATCAACCCACCCGGCGGGGATTTGTGAAGATGAATCTTCCCACGGATGATAAT 1316
.....1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350



gi | 226053125 | ref | NM_001146184.1 | GGAAAAATTCATCAAGGATGTGTCAGCAGTCCAAAACGGGAAGACAAAGGGAGTCAAGCCAGCGGTCAACA---GAGATTCGCCAGAAATGTGAGATGATAAATGGAAGGACATTTCAATGAAACAAGAGGGAGTCAAGTCCAGCAGCG 1409
gi | 114679299 | ref | XM_001141226.1 | GGAAAAATTCATCAAGGATGTGTCAGCAGTCCAAAACGGGAAGACAAAGGGAGTCAAGCCAGCGGTCAACA---GAGATTCGCCAGAAATGTGAGATGATAAATGGAAGGACATTTCAATGAAACAAGAGGGAGTCAAGTCCAGCAGCG 1439
gi | 58331165 | ref | NM_008817.2 | GGAAAAATTCATCAAGGATGTGGCTCGCAACCCCAAAATCCGGAAGACAAAGGGAGTGAACAGGCGTCTCCTCCAAAGTTCCCCAG---GCCTAATGATAAATGGAAGGACATTTCAATGAAACAAGAGGGAGTCAAGTCCAGCAGCG 1081
gi | 73947372 | ref | XM_533574.2 | GGAAAAATTCATCAAGGATTTTCACTAATCCAAAACGGGAAGGGCCAGAGAAATCTAACCAGTCCGTCACA---GAGGTTCCCCAGAAAGGTTTCAATGAAACAAGAGGGAGTCAAGTCCAGCAGCG 1010
gi | 50872144 | ref | NM_001002887.1 | GGAGAAGTTCATCAAGGACGTGCCAGCTCCAGGTCGGGGGGGCAAGGAGTCAAGTGAAGCGGCA---CCGGCTCTCCCGGAGGGGGGGGCACTGGAAGAGAGCATCGTTCCAGGAGGGAGGGGGGAGCTCCAGAGAG 1463
.....1360.....1370.....1380.....1390.....1400.....1410.....1420.....1430.....1440.....1450.....1460.....1470.....1480.....1490.....1500



gi | 226053125 | ref | NM_001146184.1 | GGTTTATGAAAGGAAATGCAATTTAGGGGAGG---CTTTAGGTTTAAATCAACCCCTTGTTCAGAAAAGAGGTTCTTGAAGAAAGAGGGCTATCATTTTGACAAGATGGGAAGGGCTCGATTCCAGATCAAAAAGCTGTCCCAGGAA 1556
gi | 114679299 | ref | XM_001141226.1 | GGTTTATGAAAGGAAATGCAATTTAGGGGAGG---CTTTAGGTTTAAATCAACCCCTTGTTCAGAAAAGAGGTTCTTGAAGAAAGAGGGCTATCATTTTGACAAGATGGGAAGGGCTCGATTCCAGATCAAAAAGCTGTCCCAGGAA 1586
gi | 58331165 | ref | NM_008817.2 | GGGTTATGAAAGGAGCGCAATTTAGGGGCGG---CTTCCGGTTCAACCCAGCCTTGGCTTCCAGAAAGAGAGCTCTTGAAGAAAGAGGGCTTACCAATTTGATTTGATGAGCGGGGATGGGCCATGAGCATAAAAAGCTGTGAGGGAA 1228
gi | 73947372 | ref | XM_533574.2 | GGGCTATGAAAGGAAATGCTTTTGGGGAGG---CTTTAATATGAATTCGAGTCTTGTTCAGAAAAGAGAGTCTTGAAGAAAGAGGGCTATCAGTTTGACAAGATGGGAAGGGTTCAGTTTATGAGCAAAAAGCTATGCGGGAA 1157
gi | 50872144 | ref | NM_001002887.1 | GGGCCCAAGGGGGGCGCTTTGGGGGAGGAGGCTTCACTGCTGTGGTTCAGACCTTGGTTCCAAAAGAGGCTCTTGGAGAAAGAGGGCTTCCACTTCGACCGGGAAGGGAGGGCCAGTGCATCCAGGGGGGGGGCAAGGAA 1613
.....1510.....1520.....1530.....1540.....1550.....1560.....1570.....1580.....1590.....1600.....1610.....1620.....1630.....1640.....1650



gi | 226053125 | ref | NM_001146184.1 | GAAGCCCTTTGAAATGTGGTGTGAGATGAGAAAAACCATGAGCGTGAGCAGCCTGAGCAGCCTCAGCTCCCCCTCCTTTACCGAGTCAAGCCAAATGATTTGGGGCAATGCCATATGTATGTGATGAGTGTGGGAGGTGGTTCAAGTGT 1706
gi | 114679299 | ref | XM_001141226.1 | GAAGCCCTTTGAAATGTGGTGTGAGATGAGAAAAACCATGAGCATGAGCAGCCTGAGCAGCCTCAGCTCCCCCTCCTTTACCGAGTCAAGCCAAATGATTTGGGGCAATGCCATATGTATGTGATGAGTGTGGGAGGTGGTTCAAGTGT 1736
gi | 58331165 | ref | NM_008817.2 | GAAGCCCTTTGAGTGTGGTGTGAGATGAGAAAGCAGCTATGAGCATGGGCAACCTGAAACAGCC-----CTTCCCTTCTGAGTCCGAGTCAAGCCAAATGATTTGGGGCAATGCCATATGTATGTGATGAGTGTGGGAGGTGGTTCAAGTGT 1369
gi | 73947372 | ref | XM_533574.2 | GAGA CTTTTTGAATGTG---TGAATGAGAAAAACCATGAGTATGAGCAGCCTTATGTCAC---CCTCCTTCAAGAGTCCAGCCAAATTTGATTTGGGGCAATGCCATATGTATGTGATGAGTGTGGGAGGTGGTTCAAGTGT 1295
gi | 50872144 | ref | NM_001002887.1 | AAGGCCCTTTCAGTGTGGAGGCGGAGCCGAGGCGCCAGGCGCCAGGCGGAGTCCAGCAGCTGAGCGCTCCGCCCCGGCCCCGTCGACCGCTCCAGCTTCCGGGGCAATGCCATATGTATGTGATGAGTGTGGGAGGTGGTTCCGCGGT 1763
.....1660.....1670.....1680.....1690.....1700.....1710.....1720.....1730.....1740.....1750.....1760.....1770.....1780.....1790.....1800



gi | 226053125 | ref | NM_001146184.1 | CATCTCAGAAATTTGTTGAGCACCAGATCATGCATAGAGAGAGAACCTCTATGAGTATGGTGGTCTTTATCCACAGTGTGGCTGTCACTGAAAGTTGAGAAAAGTCAAGGTTGGAGGGAAAAGCTTTTGAATGTAAGGACGTGGAGAGAC 1856
gi | 114679299 | ref | XM_001141226.1 | CATCTCAGAAATTTGTTGAGCACCAGATCATGCATAGAGAGAGAACCTCTATGAGTATGGTGGTCTTTATCCACAGTGTGGCTGTCACTGAAAGTTGAGAAAAGTCAAGGTTGGAGGGAAAAGCTTTTGAATGTAAGGACGTGGAGAGAC 1886
gi | 58331165 | ref | NM_008817.2 | CATCTCTGAGTTTGTGAGCACCAGATCATGCACACTAGGAGAGAACCTCTATGAAATATGGAGAGCTTTTATTATAGTGTGGCTGTCAATGAGGTGCAAAAAGGTCAGGGTGGGGGAAAAGCTTTTGAATGTAAGGAAATGTGGAGAAA 1519
gi | 73947372 | ref | XM_533574.2 | GATTTTCAGAAATTTGTGCGAACATCAGATCATGCATACTAGAGAGAGAACCTCTATGAGTACGGTGAACTCGTTTATTATAGTGTGGCTGTCACTGAGGTTGAGAAAAGTCAAGGTTGGGGGAAAAGCTTTTGAATGTAAGGAGTGTGGGAAA 1445
gi | 50872144 | ref | NM_001002887.1 | CATTTCAGATTTTGTGGAGCACCAGATCATGCACCCGGGAGAGCCTGTACAGATATGGGAGTCTTTCATCCACAGTGTCAAGCTGAGTGGCCAGAGCAGGCCCCAGGGTGCAGGGGCTCTGAGGGTCCGA----- 1901



gi | 226053125 | ref | NM_001146184.1 | CTTCAATAAGAGTCCCGCTTGGCTGAAATCGGAAGATTATGCTAGAGGTTATCTTGTGAAATGTAAGAAATCAGGAAATGTGAGGAAAGCTTTCATGCTAGCCCCCTTTAGTGGCTTCAAGAAAATATATGGCAAAGCAAAATCTA 2006
gi | 114679299 | ref | XM_001141226.1 | CTTCAATAAGAGTCCCGCTTGGCTGAAATCGGAAGATTATGCTAGAGGTTATCTTGTGAAATGTAAGAAATCAGGAAATGTGAGGAAAGCTTTCATGCTAGCCCCCTTTAGTGGCTTCAAGAAAATATATGGCAAAGCAAAATCTA 2036
gi | 58331165 | ref | NM_008817.2 | CTTCAATAAGAGTCCCGCTTGGCTGAAATCGGAAGATTATGCTAGAGGTTATCTTGTGAAATGTAAGAAATCAGGAAATGTGAGGAAAGCTTTCATGCTAGCCCCCTTTAGTGGCTTCAAGAAAATATATGGCAAAGCAAAATCTA 1669
gi | 73947372 | ref | XM_533574.2 | CTTCAATAAGAGTCCCGCTTGGCTGAAATCGGAAGATTATGCTAGAGGTTATCTTGTGAAATGTAAGAAATCAGGAAATGTGAGGAAAGCTTTCATGCTAGCCCCCTTTAGTGGCTTCAAGAAAATATATGGCAAAGCAAAATCTA 1595
gi | 50872144 | ref | NM_001002887.1 | -----GCCCCTGGCTGGCCGAGCATCGGGGGGCCAGGCCAAGAGCACCCTCCGGGGCAGTGGGAGCAGGAGCAGGACGAGCCCTTCTGCCCCAGCCCCCTTTCAGTGGCTTCAAGAAATGTAAGGCAAGGCAAGTTCTA 2042



gi | 226053125 | ref | NM_001146184.1 | CGAGTGCAGGGTGTGTAAGGAAACCTTCCCTCATAGTTCTGCCCCGATTGAGCACCAGAAAATCCACCTTTGGGG-----ATGACAAAGATAAATGAGCGTGAACATGAACGTGA----- 2114
gi | 114679299 | ref | XM_001141226.1 | CGAGTGCAGGGTGTGTAAGGAAACCTTCCCTCATAGTTCTGCCCCGATTGAGCACCAGAAAATCCACCTTTGGGG-----ATGACAAAGATAAATGAGCGTGAACATGAACGTGA----- 2144
gi | 58331165 | ref | NM_008817.2 | TGAGTGC AAGGTGTGCAAGGAGACCTTTCTGCAAGTTCCCGCTGATTGAGCACCAGAAAATCCATGGTAGAGGCCAATCAGATAGCAGAGATAAATGAGCGTGAACCCGAACTGTGATCTGTACCTGCACTGCAAGAGGCAGCGTGA 1819
gi | 73947372 | ref | XM_533574.2 | TGAAATGTAAGGTGTGTAAGGAAACCTTCCCTCATAGTTCTGCCCCGATTGAGCACCAGAAAATCCACCTTTGGGG-----ATGACAAAGATAAATGAGCGTGA----- 1690
gi | 50872144 | ref | NM_001002887.1 | CGAGTGC AAGGTGTGCAAGGAGACCTTTCTTGCAGCTCCGGCCCTGATTGAGCACCAGAAAATCCACAGCCACC-----AGGACAGGGAGAAAGGAGGTAG----- 2138



gi | 226053125 | ref | NM_001146184.1 | -----ACGTGAAAGTGTGAGCGCGGGGAAACCTTTAGGCCAGCCCGACCTTAAATGAGTTTCAAGAAAATGTAATGGTAAAAGAGAAAATGTAAGAAATGTAAGGTTGTTGGGGAGACTTTCTTCAATAGCTCATCCCTGAA 2246
gi | 114679299 | ref | XM_001141226.1 | -----ACGTGAAAGTGTGAGCGCGGGGAAACCTTTAGGCCAGCCCGACCTTAAATGAGTTTCAAGAAAATGTAATGGTAAAAGAGAAAATGTAAGAAATGTAAGGTTGTTGGGGAGACTTTCTTCAATAGCTCATCCCTGAA 2276
gi | 58331165 | ref | NM_008817.2 | GCGCGAAAGTGTGAGCGCGGGGAGCTGAGGCTTGGGAAACCTTTTGAACCTTGTCAAACTTCAATGAGTTTCCGAAATGTAAGAAATGTAAGGTTGTTGGGGAGACTTTCTTCAATAGCTCATCCCTGAA 1799
gi | 73947372 | ref | XM_533574.2 | -----GGGAAACCTTTTGAACCTT-----CCTTAAATGAGTTTCAAGAAAATGTAATGGTAAAAGAGAAAATGTAAGAAATGTAAGGTTGTTGGGGAGACTTTCTTCAATAGCTCATCCCTGAA 1979
gi | 50872144 | ref | NM_001002887.1 | -----TACGGGCCCTGTGAGGCCACCCCAATGCTCGGAGAGTTGAGAGGGCTTGGGAAAGAGAAAAGCTTTCAGTGCAGAGTCTGTGGGAGACTTCCACCAAGTGCAGCCCTGCG 2255



gi | 226053125 | ref | NM_001146184.1 | AGAACATCAGAAAATCCATACCTAGAGGGGAAACCCATTTGAAAACCAAGGGTAAAGTGTGTGAGGAAACCTTTATCCTGGTCACTCCCTTAAAAGCGTCAAGAAAATTAACAATAAGGAGAAAGCTCTGTGACTTTACAGATGGCCGGGATGC 2396
gi | 114679299 | ref | XM_001141226.1 | AGAACATCAGAAAATCCATACCTAGAGGGGAAACCCATTTGAAAACCAAGGGTAAAGTGTGTGAGGAAACCTTTATCCTGGTCACTCCCTTAAAAGCGTCAAGAAAATTAACAATAAGGAGAAAGCTCTGTGACTTTACAGATGGCCGGGATGC 2426
gi | 58331165 | ref | NM_008817.2 | GGAGCATCAGAAAATCCATACCTAGAGGGGAAACCCATTTGAAAACCAAGGGTAAAGTGTGTGAGGAAACCTTTATCCTGGTCACTCCCTTAAAAGCGTCAAGAAAATTAACAATAAGGAGAAAGCTCTGTGACTTTACAGATGGCCGGGATGC 2116
gi | 73947372 | ref | XM_533574.2 | AGAACATCAGAAAATCCATACCTAGAGGGGAAACCCATTTGAAAACCAAGGGTAAAGTGTGTGAGGAAACCTTTATCCTGGTCACTCCCTTAAAAGCGTCAAGAAAATTAACAATAAGGAGAAAGCTCTGTGACTTTACAGATGGCCGGGATGC 1949
gi | 50872144 | ref | NM_001002887.1 | GGAGCACCAGAAAGCCACGGCCGAGGGAGCCCTGTGAGGCAAGGGCCAGAGCTTCCAGGAGACCTTCACTTCTGAGGAGCCCTGAAAGAGGCGCCAGAAAGCTTCTAAAAGAGAAAGCTTCAAGCTTTAGAGAGGGCCGGGATGC 2405



gi | 226053125 | ref | NM_001146184.1 | CTTCAATGCAAAGCTCAGAGCTCAGTGTGAGCATCAGAAAATTCATTCTCGAAAGAACCTCTTTGAAAGGCAGAGGGTATGAGAAAATCTGTCTATTCAATGTTGGGCCATTCACTGAATCTCAGAAAGTCACTATAACAAGACCTCTTGAAG 2546
gi | 114679299 | ref | XM_001141226.1 | CTTCAATGCAAAGCTCAGAGCTCAGTGTGAGCATCAGAAAATTCATTCTCGAAAGAACCTCTTTGAAAGGCAGAGGGTATGAGAAAATCTGTCTATTCAATGTTGGGCCATTCACTGAATCTCAGAAAGTCACTATAACAAGACCTCTTGAAG 2576
gi | 58331165 | ref | NM_008817.2 | ACTGATGGGAAACTCAGACTCCAGCAGGATCAGAAAACCGTTCCCGAAGGAACTCTTTGAGGCAAGAGATTGAGAAAACCTTCTGTT-----GAAATCTCAGAAAGTCACTATAACAAGACCTCTGAAA 2248
gi | 73947372 | ref | XM_533574.2 | CTTTGGCAAAGCTCAGACTCAGTGTGAGCATCAGAAAATTCATTCTCGAAAGAACCTTATGAAAGCCAGGGGTGAGAGAGTCTGTCTATTCAATGTTGGGCCATTCACTGAATCTCAGAAAGTCACTATAACAAGACCTCTGAAA 2099
gi | 50872144 | ref | NM_001002887.1 | CTTTGGGCGGAGCTCAGACTTCTGAGCACCAGAAAATTCATTCTCGGAAAGCTACTTCCAGAGCCGGGGTATGAGAAAGCCGTGTCTCCACAGCATGTCCATGCCCCCTCTCAGAAAGTCAACAGATCACCAGGCCGCCAGGGA 2555



gi | 226053125 | ref | NM_001146184.1 | TGTATGAGGACGAAAAGCGTTCCACCAATTAGCTCTAACCCCTATGAAAACGAGAAGATTCCCACTAAGGAAAATGCTATGAGGCAAAATCATATGAGAGGTCTGTTATTATAGCTTAGCCTCTGTGGAAGCTCAGAAAAGT---CACAG 2693
gi | 114679299 | ref | XM_001141226.1 | TGTATGAGGACGAAAAGCGTTCCACCAATTAGCTCTAACCCCTATGAAAACGAGAAGATTCCCACTAAGGAAAATGCTATGAGGCAAAATCATATGAGAGGTCTGTTATTATAGCTTAGCCTCTGTGGAAGCTCAGAAAAGT---CACAG 2723
gi | 58331165 | ref | NM_008817.2 | CAAAGCAGATCACAAGCCGTTCCACCAATGCTGTAACCCCTAATGACAAGCTGAAAATCCCACTATGAAAATGGCTCCAGGGCAAAATCCATATGAGAGGTCTGTTATTATAGCTTAGCCTCTGTGGAAGCTCAGAAAAGT---CATGG 2395
gi | 73947372 | ref | XM_533574.2 | TGAGGAGGATGAGAAGCCGTTCCACCAATTAGCTCTAACCCCTATGACAATCAGAAGATTCCCACTAAAAGAAAATGCCTGTGAGGGAAAACCTACGAGAGGTCTGTTATTATAGCTTAGCCTTTGCTAAAAGCTCAGAAAAGTTGTCTACAG 2249
gi | 50872144 | ref | NM_001002887.1 | TGAGGACGAAAGAGAGCAATTACTCCAGTAGCAGCCCCGAAATGATGGCCAGGAGGCC-----GGGGCTACGAGAGGAGCCGCTACGAGAGGGCCATCCTCCACAGCCTGGCCCGCTTCGGGCTCCCGTGGC-----CTCAG 2690
.....2710.....2720.....2730.....2740.....2750.....2760.....2770.....2780.....2790.....2800.....2810.....2820.....2830.....2840.....2850



gi | 226053125 | ref | NM_001146184.1 | TGTAGCAGGGCCAGTAAA CCAAAAATAATGGCAGAGCTACCAATTAGAGCTTCGATGCTATCAACCATCAGAGAGTTGCTCTGGAGGGAAACACCTCTGAAGGAAAGGAAATACAGTAGGCTGTGTTATCCATAGCTTAGTGGCTTCCAA 2843
gi | 114679299 | ref | XM_001141226.1 | TGTAGCAGGGCCAGTAAA CCAAAAATAATGGCAGAGCTACCAATTAGAGCTTCGATGCTATCAACCATCAGAGAGTTGCTCTGGAGGGAAACACCTCTGAAGGAAAGGAAATACAGTAGGCTGTGTTATCCATAGCTTAGTGGCTTCCAA 2873
gi | 58331165 | ref | NM_008817.2 | TGGACTGGGTTTCACTAAA CCAAGA CCAATGGCAGAGTCTAGCACCCAGAGCTCAAGCAGCATTTA CTA CCCCAGAGCACTCTGGAGGCCAACACCTATGAAGGAAAAGAAATCAAGGACTCTATCATCCATAGCTTAGCAGCTCCCTCG 2545
gi | 73947372 | ref | XM_533574.2 | TGCAGTGGGGCCAGTAAA CCAAGCTGATTCAGAAATCTGCCACTCAGACCTCAGGTGTTATTGAAATCAGAAAATCCATGCTGGAGAGAA---TTCTGAAGGAAAGAAATATGAACATCTGTTATCCATAGCTTAGTCTGTTTCAA 2396
gi | 50872144 | ref | NM_001002887.1 | GGAAAGCAGGGG--AGCCCTCCACATACC-TCTCAGGCTTGTGACCCGCA CAGAAACCCCAACCTGGGAGAGCCCTTATGCTGGAGGCAG-----GCACAGCTTTTTTCAAGGACTCAGTCTTCTA CCGCGCATCGGCCCTGCG 2828
.....2860.....2870.....2880.....2890.....2900.....2910.....2920.....2930.....2940.....2950.....2960.....2970.....2980.....2990.....3000



gi | 226053125 | ref | NM_001146184.1 | ACCCTCCAAAGAGTCAAAATGAAATGAAATTTGGTGGAACTAATGAGAAGGGAGAACTCCCTCAATTTATATCTCAGACCTTAATGATAAGCGACAGAAGATTCTGTCAGAGAGAACCCCTTGTGAAGGGGGCAGTAAGAAATCGCAACTATGA 2993
gi | 114679299 | ref | XM_001141226.1 | ACCCTCCAAAGAGTCAAAATGAAATGAAATTTGGTGGAACTAATGAGAAGGGAGAACTCCCTCAATTTATATCTCAGACCTTAATGATAAGCGACAGAAGATTCTGTCAGAGAGAACCCCTTGTGAAGGGGGCAGTAAGAAATCGCAACTATGA 3023
gi | 58331165 | ref | NM_008817.2 | ACCCTCTGAAAAGTCAATAGCAAAATGACCAATTTCAATGATGAGGGGGGAGAACTCCCTCAATTTATATCTCAGACCTTAATGATAAGCGAGAAAGATTCTGTCAGAGAGAACCCCTTGTGAAGGGGGCAGTAAGAAATCGCAACTATGA 2692
gi | 73947372 | ref | XM_533574.2 | ACCCTCCAAAATTTGCAAGTGGAAAACGAACTGCTTCAA TGTGATGAGAAGGGAGAACTCCCTCACTTCTCCTCTCAATCTCTGTGATAAGCAA CAGAAAATCTCCTGCCAGAGAGACCCCTTATGAAGGGGGTAAAGATTA---ACAACAAA 2543
gi | 50872144 | ref | NM_001002887.1 | TCCCTCTGACCACCTTGTGGGGAAAGCCCGAGCGGGTGGCAGAGAGACGGCGAAAGCCCTCCGGCCAGCTCAGAT---GGCCGACGACCAAGAGGCACTGTCAGAGAGAAAGAACTTGAAGGCGCAAGAAATTA CCA-GCCCTCCATGA 2974
.....3010.....3020.....3030.....3040.....3050.....3060.....3070.....3080.....3090.....3100.....3110.....3120.....3130.....3140.....3150



gi | 226053125 | ref | NM_001146184.1 | AGACTCTGTCTATCAGAGTGTATTCGGTCCAAA CCTCAGAAAAGTGTCTCTGGAGGGATCTGGTGTGTTAAGAGGATGGCGAAATCTCTGTTCCAGCTCAAATGCTCGTGAATCCAGAGAGGCTCTGCTAAAAAGAAATACAT 3143
gi | 114679299 | ref | XM_001141226.1 | AGACTCTGTCTATCAGAGTGTATTCGGTCCAAA CCTCAGAAAAGTGTCTCTGGAGGGATCTGGTGTGTTAAGAGGATGGCGAAATCTCTGTTCCAGCTCAAATGCTCGTGAATCCAGAGAGGCTCTGCTAAAAAGAAATACAT 3173
gi | 58331165 | ref | NM_008817.2 | -----CACACAAAATGATCCCGTCTGAGCTCC---AAGTCTTTCTGGAGAG---TCCCATGACTCTAAGCAGGATGTCTCGTTTTCAAGTCTCCAGCTCAAATGCTCGTGAATCCAGAGAGGCTCTGCTAAAAAGAAATACAT 2827
gi | 73947372 | ref | XM_533574.2 | GGACTCTGTCTATCAGAGTGTATTCGGTCCAAA CCTCAGAAAAGTGTCTCTGGAGGGATCTGGTGTGTTAAGAGGATGGCGAAATCTCTGTTCCAGCTCAAATGCTCGTGAATCCAGAGAGGCTCTGCTAAAAAGAAATACAT 2675
gi | 50872144 | ref | NM_001002887.1 | -----TGCACTCCCTGCAATTT---TGGTGTGCTCAAACATTTGCCCGAGAGAGATTTTTCGAAATGTCTAGAAATGTGGAGGTTCTTTGTCCTGACTCTGAGCTGGCTGAACCCAGAAAGTCCCAACAGGAAGAGCTTTT 3113
.....3160.....3170.....3180.....3190.....3200.....3210.....3220.....3230.....3240.....3250.....3260.....3270.....3280.....3290.....3300



gi | 226053125 | ref | NM_001146184.1 | TGAGCATAGGAGCAATGAGACCTCTGTAAATCCTCTCTGCTTTTGGTGAACAA---ACATTTGCCCTCGAGGGATGCTCTATGAATGTCCAGGAGTGTGGGGAGTCTTTGCTCATAGCTCTGACCTCACTGAGCACCAGAAATTC 3290
gi | 114679299 | ref | XM_001141226.1 | TGAGCATAGGAGCAATGAGACCTCTGTAAATCCTCTCTGCTTTTGGTGAACAA---ACATTTGCCCTCGAGGGATGCTCTATGAATGTCCAGGAGTGTGGGGAGTCTTTGCTCATAGCTCTGACCTCACTGAGCACCAGAAATTC 3320
gi | 58331165 | ref | NM_008817.2 | TGAGCCCAGGAACAAAGAGACCTCTGTTATCCACTCCCTACCTTTTGGTGAAGTTCTGCAAGGTCAACGTAAGGCAAGTTCTTATGAGTGTCCAGAAATGCGGGGAGGCTTTGCTGTAAGTCTGAGCTCACTTGAAGCACCAGAAATTC 2977
gi | 73947372 | ref | XM_533574.2 | CGAGCATAGGAACCTATGAGACCTCTGTAAATCCTCTCCCTACGTTTTGGTGAACCTCAAACATTTGCCCTAGAGAGAAATCTATGAATGTCCAGAGTGTGGAGAAATCCCTTTGTTGCTATCTCCGACTCACTGAGCTCAGAAATTC 2825
gi | 50872144 | ref | NM_001002887.1 | TGGAAATAAAACCTACCTACGCTCTGCTTCCAGCCTGTCTCTCACTGACCCCTCAGACCAAGCTACCAAGCCAGTCAAGTGCAGATGAGTTATCCCAAGGAGCACTCAGACCGTTATGCTGAGGTAGG---AGC-TCAGACCAAGTTA 3260
.....3310.....3320.....3330.....3340.....3350.....3360.....3370.....3380.....3390.....3400.....3410.....3420.....3430.....3440.....3450



gi | 226053125 | ref | NM_001146184.1 | TGATAGGAGAGCCCTCTGGAAGCAGAAAATATGAAATGGTCTGTCTATTCGACGCTTGGCCCTACTGACC---CTCAAA CAAAGTTACGCCCAAGAGC-----AGTATGCTAAAGAGCAAGCGCGGAA CAAATGT 3417
gi | 114679299 | ref | XM_001141226.1 | TGATAGAGAGAAAGCCCTCTGGAAGCAGAAAATATGAAATGGTCTGTCTATTCGACGCTTGGCCCTACTGACC---CTCAAA CAAAGTTACGCCCAAGAGC-----AGTATGCTAAAGAGCAAGCGCTGGAA CAAATGT 3447
gi | 58331165 | ref | NM_008817.2 | TGATAGAGAGAAAGCCTCTGGAAGCCGACATTATGAGCCCTCTGCTATCCGACGCTTGGCCCAAGTACC---CTCAGACCAAGTTATGCCCAAGAAC-----GTTTCTCAAGAAAGTGTGG---TAAATT 3101
gi | 73947372 | ref | XM_533574.2 | CAGATAGAAAGAGCCCTCTGGAAGCAGAAAATATGAAATGGTCTGTCTATTCGACGCTTGGCCCTACTGACC---CTCAAA CAAAGTTACGCCCAAGAGC-----AGTATGCTAAAGAGCAAGCTGCA CAA CAAATGT 2973
gi | 50872144 | ref | NM_001002887.1 | TGCT---GAGAGCCAGCTCAGACCAAGTTACCCGTAGAGCCAGCTCAGACCAAG---TTACGCCCAAGAACAGCTCAGACCAAGTTACCTGAGGCAC-----CAGCTGAGGCTAGTTATCTGAGGAAACAGCTCAGACCAAGTTG 3396
.....3460.....3470.....3480.....3490.....3500.....3510.....3520.....3530.....3540.....3550.....3560.....3570.....3580.....3590.....3600



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gi|58331165|ref|NM_008817.2|
gi|73947372|ref|XM_533574.2|
gi|50872144|ref|NM_001002887.1|

GAGAGGAATCCTGCTCTTGGTGGGTCAGGCAATTCGATGCCCTTTTGG--TGTGGAACAAGGCTTCATTCTATAGCT-CTGCCCTTAATGAGCATAATGAGACTTCATAGGGAAGATGATTTACT-GGAGCAG-----AGCCAGATGGCTGAGG 4099
GAGAGGAATCCTGCTCTTGGTGGGTCAGGCAATTCGATGCCCTTTTGG--TGTGGAACAAGGCTTCATTCTATAGCT-CTGCCCTTAATGAGCATAATGAGACTTCATAGGGAAGATGATTTACT-GGAGCAG-----AGCCAGATGGCTGAGG 4129
GAAAGGAATCCTGCTGCTTGGTGGGTCAGGCAATTCGATGCCCTTTTGG--TGTGGAACAAGGCTTCATTCTATAGCT-CTGCCCTTAATGAGCATAATGAGACTTCATAGGGAAGATGATTTACT-GGAGCAG-----AGCCAGATGGCTGAGG 4095
CAGAAGAATCCTCC--TGCAGGAAATCTCTTCAATGCCATGTG--TGTGGAACAAGGCTTCATTCTATAGCT-CTGCCCTTAATGAGCATAATGAGACTTCATAGGGAAGATGATTTACT-GGAGCAG-----GGCCAGAGAGGTGAGG 3658
AAGAACCAGCTCAGACCAAGTTGACCGAAGAACAGCTCAGACCAAGTTATACCCAAGAACAGCTCAGACCAAGTTGACCGAAGAACAGCTCAGACCAAGTTATACCCAAGAACAGCTCAGACCAAGTTGACCGAAGAACAGCTCAG 4441



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gi|50872144|ref|NM_001002887.1|

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AAGCTATCATTCCAGGCTTAGCCCTCAGTGAATTCAGAGAAAGTCAAGCCGAAGAGAGAGACTTTTGAATGTGCAGTCTGTGGGAATCTTTGGTCA-ACCCAGCAGAACTGCGAGATCAGTAACT--GTTCAAGAAATGAGCCCTAT 4245
AAGCTATCATTCCAGGCTTAGCCCTCAGTGAATTCAGAGAAAGTCAAGCCGAAGAGAGAGACTTTTGAATGTGCAGTCTGTGGGAATCTTTGGTCA-ACCCAGCAGAACTGCGAGATCAGTAACT--GTTCAAGAAATGAGCCCTAT 4275
AGATTTTCAATCAAGGCTAGCCCTCAGTGAATTCAGAGAAAGTCAAGCCGAAGAGAGAGACTTTTGAATGTGCAGTCTGTGGGAATCTTTGGTCA-ACCCAGCAGAACTGCGAGATCAGTAACT--GTTCAAGAAATGAGCCCTAT 4244
ATGCAGTCAATCCAGGCTTAGCCCTCAGTGAATTCAGAGAAAGTCAAGCCGAAGAGAGAGAGACTTTTGAATGTGCAGTCTGTGGGAATCTTTGGTCA-ATCCAGCAGAACTGCGAGATCAGTAACT--GTTCAAGAAATGAGCCCTAT 3807
CCAGTTAACCAGAAAGACAGCTCAGACCAAGTTATACCCAAGAACAGCTCAGACCAAGTTGACCGAAGAACAGCTCAGACCAAGTTATACCCAAGAACAGCTCAGACCAAGTTAACCAGAAACAGCTCAGACCAAGTTAACCAGAA 4590



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gi|58331165|ref|NM_008817.2|
gi|73947372|ref|XM_533574.2|
gi|50872144|ref|NM_001002887.1|

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GAGTACG---GGTCTCTATACTCACAATCATTCTTACTGAGCCCTCAAGGAGCTATACCATTCTATGAATGCAAGGATTTGGTAAAGTCC---TTTATTATAGCACAGTCTCTCAATAACAT--AAGGAGTTCATCTGGAAGA 4388
GAGTACG---GGTCTCTATACTCACAATCATTCTTACTGAGCCCTCAAGGAGCTATACCATTCTATGAATGCAAGGATTTGGTAAAGTCC---TTTATTATAGCACAGTCTCTCAATAACAT--AAGGAGTTCATCTGGAAGA 4418
GAGTATG---GGCCCTCCTACAACCACCTCCTTTCTCAGAGCCCTCAGGAAGCACAATCCGAATGCAAGGATTTGGTAAAGTCC---TTCTAGACAGACTGCTCAATCGCTGAGCCG--ATGGTGGTTTCAATCCAGGCG 4387
GATTATG---GGGCTCTTTTGTTCACCTCATTCTTACTGAGCCCTCAAGGAGAGATACCATTCTATGAATGCAAGGATTTGGTAAAGTCC---TTTATTATAGCACAGTCTCTCAATAACAT--CAGAAGTTCATCTGGAAGA 3950
GAACCCAGCTCAGACCAAGTTAACCAGAAAGACAGCTCAGACCAAGTTATACCCAAGAACAGCTCAGACCAAGTTGACCGAAGAACAGCTCAGACCAAGTTAACCAGAAACAGCTCAGACCAAGTTAACCAGAAACAGCTCAG 4740



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gi|58331165|ref|NM_008817.2|
gi|73947372|ref|XM_533574.2|
gi|50872144|ref|NM_001002887.1|

**
AG--AAGAAGAAGATGAAGCAGCAGCAGCTGCAGCAGCAGCAGC--CCAGGA--AGTTGAAGCCAATGTCATGTTCCAAAGTATTTGAGGATTGAG--GGCTAAACCTAGAGGCTGCTGAGCCAGAAAGTGAGGCTGCCAGGCC 4529
AG--AAGAAGAAGATGAAGCAGCAGCAGCTGCAGCAGCAGCAGC--CCAGGA--AGTTGAAGCCAATGTCATGTTCCAAAGTATTTGAGGATTGAG--GGCTAAACCTAGAGGCTGCTGAGCCAGAAAGTGAGGCTGCCAGGCC 4559
AG--AAGTGGGTCAGAAAATGATAGCTGCCATGC-----CCAAGA--GGTGAAGCCAATGTCATGTTCCAAAGTATTTGAGGATTGAG--GGGTCAAATGCAAGGCTGCTGAGCCAGAAAGTGAGGCTGCCAGGCC 4519
AG--AGGAAGAAGAAAGAGC-----CCAAGA--GGTGAAGCCAATGTCATGTTCCAAAGTATTTGAGGATTGAG--GGATCAAATGTAAGGCTGCTGAGCCAGAAAGTGAGGCTGCCAGGCC 4067
AGTTACGCCAAGAACAGGCTCAGACCAAGTTAACCAGAAAGACAGCTCAGACCAAGTTAACCAGAAAGACAGGCTCAGACCAAGTTAACCAGAAAGACAGGCTCAGACCAAGTTAACCAGAAAGACAGGCTCAGACCAAGTTAACCAGAA 4889



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gi|58331165|ref|NM_008817.2|
gi|73947372|ref|XM_533574.2|
gi|50872144|ref|NM_001002887.1|

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AGAAGTGGAGGCTCTGAGCCAGAAAGTGGAGGCTCTGAGCCAAACGGAGGAGGCTGAA--GGGCCAGAT--GGAGAGGCTGCAGAGCCATTGGAGAGGCTGGACAGCCAAATGGAGAGGCC--GAGCAGCCAAATGGGGATGCTGAT--G 4672
AGAAGTGGAGGCTCTGAGCCAGAAAGTGGAGGCTCTGAGCCAAACGGAGGAGGCTGAA--GGGCCAGAT--GGAGAGGCTGCAGAGCCATTGGAGAGGCTGGACAGCCAAATGGAGAGGCC--GAGCAGCCAAATGGGGATGCTGAT--G 4702
CAGGTGGAGGCTCAGCAGCCTAGGTGGAGGCTCAGCAGCCTAATGGAGAGGCTGAA--GGGCCAGAT--GGAGAGGCTGCAGAGCCATTGGAGAGGCTGGACAGCCAAATGGAGAGGCC--GAGCAGCCAAATGGGGATGCTGAT--G 4662
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ACCGGCTCAGACCAAGTTAACCAGAAAGACAGCTCAGACCAAGTTAACCAGAAAGACAGGCTCAGACCAAGTTAACCAGAAAGACAGGCTCAGACCAAGTTAACCAGAAAGACAGGCTCAGACCAAGTTAACCAGAAAGACAGGCTCAG 5033



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gi|73947372|ref|XM_533574.2|
gi|50872144|ref|NM_001002887.1|

AGCCAGATGGTGCAGGATTTGAAGAACCCAGAAGAAGAGC--TGAAGAGCCAGAGGGGAA-----AAGTGAAGAGCCAG--AGG--GAGATGCCAGCAGGCTGAC--GGTGTGGGAAT--TGAAGAACCCAGAAGA--AGGTGAAGAT 4803
AGCCAGATGGTGCAGGATTTGAAGAACCCAGAAGAAGAGC--TGAAGAGCCAGAGGGGAA-----AAGTGAAGAGCCAG--AGG--GAGATGCCAGCAGGCTGAC--GGTGTGGGAAT--TGAAGAACCCAGAAGA--AGGTGAAGAT 4833
AGCCAGAAGCAGCAGGATTTGAAGAACCCAGAAGAAGAGC--TGAAGAGCCAGAGGGGAA-----ACGTGAAAGAGCCAG--AGG--GAGATGCCAGATGAGCCGAT--GGTGTGGGAAT--TGAAGAACCCAGAAGAAGGAGGAT 4796
AACCAGATGGTGCAGGATTTGAAGAACCCAGAAGAAGAGC--TGAAGAGCCAGAGGGGAA-----AGGTGAAGAGCCAG--AGG--GAGATGCCAGATGAGCCGAT--GGGTCAGGAT--CCAAGAACCCAGAAGAAGGAGGAT 4344
GACCAAGTACCCAGGAAAC--GGTCTCAGACCAAGTTAACCAGAAAGACAGCTCAGACCAAGTTAACCAGAAAGACAGGCTCAGACCAAGTTAACCAGAAAGACAGGCTCAGACCAAGTTAACCAGAAAGACAGGCTCAGACCAAGTTAACCAGAA 5181



gi | 226053125 | ref | NM_001146184.1 | CAAGAG--ATTTCAGGTAGAAGAACCATACTATGACT---GCCATGAATGCACAGAAACCTTCACCTT-CCAGCACAGCATTGAGTAAACCTGAAAACTCATGCCAGCATGATCATATTTGAGCCTGCAAAATGCCCTTTGGGGAGTGCT 4945
 gi | 114679299 | ref | XM_001141226.1 | CAAGAG--ATTTCAGGTAGAAGAACCATACTATGACT---GCCATGAATGCACAGAAACCTTCACCTT-CCAGCACAGCATTGGTGAACACCTGAAAACTCATGCCAGCATGATCATATTTGAGCCTGCAAAATGCCCTTTGGGGAGTGCT 4975
 gi | 58331165 | ref | NM_008817.2 | CAAGAG--ATTTCAGGTAGAAGAACCATACTACTCAACT---GTATGAATGCCAGAAACCTTCAGCTT-CCAGCTCAGCCTTTGGGGAGCATTCTGAAAAAGTCCAGCCGAGTGTGATCATCTTGGAGCCGGCAATGCTCCTGGAGGATGCT 4938
 gi | 73947372 | ref | XM_533574.2 | CAAGAG--ATTTCAGGTAGAAGAACCGTACTATGACT---GTAGGGAATGTGGAGAAACCTTCACCTT-CCAACTCAGCCTATGGTGAACACCTGAAAAACCCATGCCAGGTGATAATATTTGAGCCTGGAAATGCTATGGGGAAAGCT 4486
 gi | 50872144 | ref | NM_001002887.1 | GAGGAAACAGCTCAGACCAAGATCAAGGGAAACGAGCTCAGATCAGATAAGCGAAAGAACAGCTCAGACCAAGATAAGCGAAGAACAGCTCAGACCAAGTATAGCCAGG-AAACAGCTCAGA--CCAGATATGCCGA-GGAAACAGCC 5327



gi | 226053125 | ref | NM_001146184.1 | CAGGCTA--CATCG-AACGTGCCAGCACCAGCACAGGTGGTCCCAAACAAGCTGAT--GAGAAGTACTTCAAATGTGACGCTGTGGGGAGCTCTTCAATG--ACCGCTGTCCCTGCCAGACACCAGAA--ACCCCACTGGC--- 5082
 gi | 114679299 | ref | XM_001141226.1 | CAGGCTA--CATCG-AACGTGCCAGCACCAGCACAGGTGGTCCCAAACAAGCTGAT--GAGAAGTACTTCAAATGTGACGCTGTGGGGAGCTCTTCAATG--ACCGCTGTCCCTGCCAGACACCAGAA--ACCCCACTGGC--- 5112
 gi | 58331165 | ref | NM_008817.2 | CTGGCTA--CATTG-AACGGGCCAGCACCAGTGCAGGTGGTCCGGAGCAGAGCAGC--GACAAGTACTTCAAATGTGATGTGTGGGGCAACTCTTCAACG--ACCGCTGTCCCTGCCAGACACCAGAA--TCTCACACTGGT--- 5075
 gi | 73947372 | ref | XM_533574.2 | CACACTA--CACTG-AACTAGCCAGCACCAGCACTAGTGAACAATGATAGGGCAGAT--GACAAGTACTTCAAATGTGATGTGTGGGGAGCTTTTCAAGT--ATCGCTGTCCCTGTGACACCAGAA--ACTCATACTGTTGTG 4627
 gi | 50872144 | ref | NM_001002887.1 | CAGACCAATTATCTGAGCAACAGC-TCAGACCAAGT-ATGCCGAGGAAACGCCCAAGCAAGTATTCTGAGGAAACAGCTCAGACCAAGTATGCTGGGAAACAGCTCAGACCAAGTATGCCAGGAAACAGCTCAGACCAAGT-AT 5474



gi | 226053125 | ref | NM_001146184.1 | ---TGAGGGCATGGGTAAAGTTAGAA-----AACCTTCA-CCTAGGACTTGACCCCTTACCAAACCCACA--GAGAAT-CCAAACCA--ATCCATGA-----TAATGTGAGTGGGAGACTTAACTTGTGTGTTACA--CAC 5204
 gi | 114679299 | ref | XM_001141226.1 | ---TGAGGGCATGGGTAAAGTTAGAA-----AACCTTCA-CCTAGGACTTGACCCCTTACCAAACCCACA--GAGAAT-CCAAACCA--ATCCATGA-----TAATGTGAGTGGGAGACTTAACTTGTGTGTTACA--CAC 5234
 gi | 58331165 | ref | NM_008817.2 | ---TGAGTAACCAAGGTGAAGAAAAGAAAGCAAAAGCCAAACCTTCTTCCCAACCCAGACCCCTTAAATAACACAAAGAGAGC-CTAAACCA--ACCCA-----TAATGTCTATAAGAAA-TTCACTCTGTAT-ACA--TAC 5206
 gi | 73947372 | ref | XM_533574.2 | CTTCTCAGAGCCCTGCTCTACTTTCAGAAAGCTCTCCAAAAGAAAGGGAAGAAATCCAGTCAAGTCCCTGCCGCCCTGGAGCAT--GGAACTGTGATCTTCAG--GGATGTGGCCATGATCTTCAACCAAGAACAGTGGCAGTGC 4771
 gi | 50872144 | ref | NM_001002887.1 | GGTGAGAGAACCCCTGAGACTAGTTTATGCTGAACTAGTACGCTAGTAACTAGTAACTCCGACTAGTTACCGTGAACCCAGCTGAGTCCGGTTACTTTGAAACCCAGCTCAGTCTAGTTATATCTGAAACCGC 5624



gi | 226053125 | ref | NM_001146184.1 | CTGACTTAACATC-----TCTAAACTCAGATTGAAAAGAGA-----CCGA-----ATGTGCAGATTCCA-CAGTCTTAAGCTTTCCCTTCCAGATGTCAGTGTCTGCA---TGTGGGAAAGCCATAGCACACATCT 5321
 gi | 114679299 | ref | XM_001141226.1 | CTGACTTAACATC-----TCTAAACTCAGATTGAAAAGAGA-----CCGA-----ATGTGCAGATTCCA-CAGTCTTAAGCTTTCCCTTCCAGATGTCAGTGTCTGCA---TGTGGGAAAGCCATAGCACACATCT 5351
 gi | 58331165 | ref | NM_008817.2 | CGGACTTCAATCAAAAG-ACCTTCACTCTCATATCCAGACTGAAAAGAAAGAAAGCATTGCA-----ACGAGGGGACTCTTTTTCAGTTTAACTGTTTCCCTATGGAACTCAGTGTAT--A-----TTTGGGAAAGCTAGAGTGAATCT 5341
 gi | 73947372 | ref | XM_533574.2 | TGGAGCTTCCGCCAGAAAGCACTTATCAGGATGTGATGCTGGGAAACTATGGGCACCTGGCATCTTTGGGGCATTGTGTTCTTCAAACCCAGTGTATCCAGCTTAGAGCAAGGAGCAGCCCTTGTCTAAGGAGAGC-GCATCCCT 4920
 gi | 50872144 | ref | NM_001002887.1 | TGAGACCAATTTATCTGACCCACCAAGCTCAGTCAAGTTTGTGATGAAACCAAG--CTGAGGC--TAGTTATGCTGA-TCTAGCAGTGTGATCAGTTATGCTGAACACAGCTGAGACAGC-TATGCTGACCTGCGAGCTCAGATCA 5767



gi | 226053125 | ref | NM_001146184.1 | -TACC--TT-----TCCAAGTAA--TCAGATTGAG--AAAAACCTA---TGAGTATTCCAGACTACAGAGTTTGCCTAACTCAACTGTA--AATGACAC---TTGTGTAACGTATATATAGTGTTCATGAGGTGTATATAAATA- 5447
 gi | 114679299 | ref | XM_001141226.1 | -TACC--TT-----TCCAAGTAA--TCAGATTGAG--AAAAACCTA---TGAGTATTCCAGACTACAAAGTTTGCCTAACTCAACTGTA--AATGACAC---TTGTGTAACGTATATATAGTGTTCATGAGGTGTATATAAATA- 5477
 gi | 58331165 | ref | NM_008817.2 | ACATC--TTCCATTTCACTAAGTAA--CTAGATTGAGGGAAAACCTAG--TGACAAATCCAGACCCAGAGGTTCCCCAGCTCAGTGTAT--AATGATACCCCTTTCATACCTCTATACATAATGATCTCCCTGATATATAAATGA- 5481
 gi | 73947372 | ref | XM_533574.2 | CCAGC--TCCC-----CAGCGAGGCAAGTGTGGAATCAGTGGGAGCCCGCA---TCTCCAAGGTGAGCAGGAGGAGCTACCGCTTGTGTTGAA--GACATTTCCA--AAGCCAGGCATCTATAGAGCCCTTCCCGGGGAAAGCAAGGAA 5058
 gi | 50872144 | ref | NM_001002887.1 | GCTATGATGAACCAACAGCTGACACTAGTTATGCTGAGCTAGCAGCTCAGATCAGTTATCTGAAACAGCAGATCAGACTAGTTATGCTGAGCTAGCAGCTCAGACCAAGTATCTGAAAC-CACTAGCTCAGACCAAGTATGCTGAGCTA 5916



gi | 226053125 | ref | NM_001146184.1 | GCAAATTATGACAGAA--CAGTGATCACATATATTTGG--ATTTA---TATGATATACAGTT-ACAGTTTACTCTGCAGAGGTAC--CTTACCTGGTAT--TCTTTGAAATTTTTTTTTTTTGGAGGAGGAAAG-----AGAGCAACA 5578
 gi | 114679299 | ref | XM_001141226.1 | GCAAATTATGACAGAA--CAGTGATCACATATATTTGG--ATTTA---TATGATATACAGTT-ACAGTTTACTCTGCAGAGGTAC--CTTACCTGGTAT--TCTTTGAA--TTTTTTTTTTTTTGGAGGAGGAAAG-----AGAGCAACA 5607
 gi | 58331165 | ref | NM_008817.2 | GCAAAAT-----CAGTGAT-ACATATATTTGG--ATTTAG--TGTGTATAGAAATTTACAGTTTACTCTGCAGAGGTAC--CTTACCTGGTAT--TCTTTGAA--TTTTTTTTTTTTTGGAGGAGGAAAG-----AGAGCAACA 5595
 gi | 73947372 | ref | XM_533574.2 | GTGGTCCAAAGGGGTT-CCAGGACAGAAAGGATTTTGGAACTGAGGACAGGCACTGAGG--GCAGCAGAAATCTGGCCCTCAGGCTGCCCTCAGAC--TCATGCAAAAAATCTCCCTAGAAAGAAAAGCCAT-----GAATCTACG 5199
 gi | 50872144 | ref | NM_001002887.1 | ACAAGTGACACTAGTTCTCCAGCAACAGCTCCAAATGAAAGGAGTGGGGAACTCTTCCCAAGTTGAGACCTTGGCAGACATCAGAAATCTATGCCCAGAGAAATCCATGATGGGAAAGCTGTTTGGAGACCTGTG 6066



gi		226053125		ref		NM_001146184.1		AATTGTATTATTTTAAAGTGTCTTAGATCCTGAGAAAGATTTATTGTGCATTAATTGA-----ACCCGTCAAT--ATCTTTTGAAGTAAT---TGTTTTGTTTCTTACC-CTTAAATAGTCTTGTGAAGCTGT--AGCCAT	5709
gi		114679299		ref		XM_001141226.1		AATTGTATTATTTTAAAGTGTCTTAGATCCTGAGAAAGATTTATTGTGCATTAATTGA-----ACCCGTCAAT--ATCTTTTGAAGTAAT---TGTTTTGTTTCTTACC-CTTAAATAGTCTTGTGAAGCTGT--AGCCAT	5738
gi		58331165		ref		NM_008817.2		ATTTAGCATATATTGTAAATAATTG---CCATGCAGAAAGCTTTTCTGTGCATCAATTGA-----ACCCCATAGT--ATCCTTTCCAGTAAATGGA--GTGTTCTGCCCTACCTCTTAGATAGTCTTGTGAAGGTGT--GGTGT	5728
gi		73947372		ref		XM_533574.2		GCCGTGAGGAGATCCCTGACTTTCTGCCACCACGATGACAACATCACAGATCACTCTCAAGGAAAGAAAGACCCCAAAAAG--AGATATTCAATGGAATAAC-ACGGCACTAGGCTCTGAGACAAGGTCGCAAGAATCC--AAAGGG	5344
gi		50872144		ref		NM_001002887.1		ATGCAAGGACCTGGGCTGATGGGT--TCCGGAAGAAAGACTGGAAAGAGCAAGG--GGAGCCGAGGAGCCCGAAACCTCCATCTATGGCTGTAAGGACTGTGGGTGGGCTTCCGTGACCGCGGGAACCTCCGGGACCAAGAAAGT	6212



gi		226053125		ref		NM_001146184.1		GATAGATAACATGGCTTTTACTCCTTACTGTTTGAAGATAAAGT---ACTTTAGCTTCTTTTGCAGCCATTTCACTGCGCCAACACTT---TGGAACCTAATAC-TGTG-TAAGGCTTTACAATA--TACGGAATGGCTTTTGTG	5848
gi		114679299		ref		XM_001141226.1		GATAGATAACATGGCTTTTACTCCTTACTGTTTGAAGATAAAGT---ACTTTAGCTTCTTTTGCAGCCATTTCACTGCGCCAACACTT---TGGAACCTAATAC-TGTG-TAAGGCTTTACAATA--TACGGAATGGCTTTTGTG	5877
gi		58331165		ref		NM_008817.2		GAAAGATCGTGTGCTTTTGAATCCTGGCTGTGTGGAA--ACAGGC---ATTTTAGCTTCT---ACGCCATTTGGTGTGACATCCACCCAGCCG---TTGAGACTGAT--TGTG-TAACCTTTACAATA--TATGGATTG-TCTGTG	5859
gi		73947372		ref		XM_533574.2		CGAAG--GCACA-CTTTAAATGTAAAGAAATGTGGAACAACTTC---AACAGACCTCCACCTATTGAGCTGAGCGGATCCACACAGGAGGAAACCCACAGATGCTATGAGTGTGGGAGGACTTCCGGCACAGCTCCTTCTT	5486
gi		50872144		ref		NM_001002887.1		CCACGGCCGGGAGTACTGGTGGACAGCCGTGAGTACAGCACCCTCCGGTGCATGCGCCTGTGACCGAGTACCCAAAAGATTGCTCCGGAGGAGCTACTGAGTCCCGGCTTCCGGAAGTGGTCTGTGCACAGCTCGTTCT	6362



gi		226053125		ref		NM_001146184.1		ACCCAG--ATTGATGGTTGCCACA TGTATGTTTGTGAA--GTGGTTCTCATGCAAAAAATTACACACTT-----TGTGTTCTGGGTTT---TTTTTTTTTAAACCACTCAATA TGTGTTGATGATAGTGA-ATTGA	5977
gi		114679299		ref		XM_001141226.1		ACCCAG--ATTGATGGTTGCCACA TGTATGTTTGTGAA--GTGGTTCTCAT-----TGTGTTCTGGGTTT---TTTTTTTTTAAACCACTCAATA TGTGTTGATGATAGTGA-ATTGA	5988
gi		58331165		ref		NM_008817.2		ACCCAA--ATCAACCCATCCCTACAT-TTATATACTTACA---GTGGTTTTCTGCAAAAAAAAAAATGTTACA TTTAGGTGTTCTTTAAAGGTTTTGTTTTCTAAACCACTCATCTGTGTTGTA--TAGTGA-ATTC	5999
gi		73947372		ref		XM_533574.2		CCTCACGCATATAGAATTCACTGGAGAGAGCCCTCAAGTGTAAAGAGTGTGGGAAAGCCCTTCAACAGCAGCTCCACA TTAGCCAGCCACACAGGA-CACACAGGGGAGAAAGCCCTTCCAGATGTGAGGAGTGGGGA-AAACA	5634
gi		50872144		ref		NM_001002887.1		TTTTGAGCACCAGAAAGTCCACGAGCAGGACCAGTTCTACGGCCACAGGGGTTATG--AGCCCTTCTGACAGCCCTGATTGTCAGCCCGCGGCGGCCAGGGCCCGCCAGAAAGCCCGCCGGTGGGCCGAGTGCAGGTA	6510



gi		226053125		ref		NM_001146184.1		T-----AAAACCCGAAGCTTTTCCCT-----GTAAATCTTA-----CATCTTGCCCTTTAAAGAAATGGGTTACAACCATCA---CTAGATCAGTAGTGCCATAATGAA--GGTTGAGAAC-----CGTAGGA-----GAG	6088
gi		114679299		ref		XM_001141226.1		T-----AAAACCCGAAGCTTTTCCCT-----GTAAATCTTA-----CATCTTGCCCTTTAAAGAAATGGGTTACAACCATCA---CTAGATCAGTAGTGCCATAATGAA--GGTTGAGAAC-----CGTAGGA-----GAG	6099
gi		58331165		ref		NM_008817.2		T-----GAAACCTGAAAGCTTTTCCCT-----GTAAATCTTAA-----TGTCTTGGCTTTAAAGAGTGGGTGACAACCATCG---CTAGATCAGTAGTGCCATAATGAAAGTTGGGAAAC-----CACAGGA-----GAG	6112
gi		73947372		ref		XM_533574.2		TTCAAGCAGAGCA CCAAGCTTTCTCTCACCCGGAGGGTGCCACTGAGAGGAGCCCTACCAGTGCAGTGTGAGAA--ATCA---TTTGGCCGCAGTCTTCTTAAACAGAGCACAAGAGAAATCCACACAGGA-----GAC	5769
gi		50872144		ref		NM_001002887.1		TGCGGGCAGGACTTCTATCCATGCTCGTCCCTCAGCGGAGCAGCGCCCGGGGCCATGCGCGCAGGGGCTACCGGATCAGGGCCAGGGGGGCGGGCCGGCGGGGGCCGGCCGGCCAGGAGCCGCAAGAAACCCGGGCGAGGAG	6660



gi		226053125		ref		NM_001146184.1		--GCTCTCATGCTGTAATAATGTTGCAAGGCTAAATAACCTTTCTCACTTCCCTTTGTGCGCTTCCCTGCTTAAGTGAACAAGTACAAATGTC---TTGGGTCCCCGTGTCAGCATCAGCTT-----ATGCT-GCCACAAGTCACT	6223
gi		114679299		ref		XM_001141226.1		--GCTCTCATGCTGTAATAATGTTGCAAGGCTAAATAACCTTTCTCACTTCCCTTTGTGCGCTTCCCTGCTTAAGTGAACAAGTACAAATGTC---TTGGGTCCCCGTGTCAGCATCAGCTT-----ATGCT-GCCACAAGTCACT	6234
gi		58331165		ref		NM_008817.2		--GCTCTTACATTTGTAATAATGAAACCAAACTGACAACTTTCTTAGTGTG---TGTGCTTCCCTGCTTAAGTGAACAAGTGGCAGCGTCCG---TTGAGTCACTGTGTGGTGTGTAATT-----GTGCTGCCACAAGTCACT	6246
gi		73947372		ref		XM_533574.2		AAGCCATATCATTGCAAAAGTGTGTGGAAAGCCTTTAGATGCAACTCGCATCTTTCTGAGCACCAGAGGATCCACCAGGAGGAAAAAATCCTAC---CGGTGTGAGCAGTGTGGAA-----CGTACT---TCCGAAACGGC	5898
gi		50872144		ref		NM_001002887.1		CAGCCCTACAGTGTGAGACTCGCGGAGTCTTCCCGACGAGGCCGATCCAGGAGCAGATGCGTGTGACAGGAGGCGGAGCCCTACGACTAGGGGCGCCCTTCTGTGACAGCTTTTCTTCCAGGAGCCGCGCAAGGGAG	6810



gi		226053125		ref		NM_001146184.1		TGCAACC-TAGGTCGCCAGGAGCTAGTATCCTTAGATC-TTTCTATCGGTA-ACHTAATTCTCTGTTATTTAT-CTGACCCCTAACTCCATGCTAACTTG-CATTAAAAAAAAAAAAAA-----	6341
gi		114679299		ref		XM_001141226.1		TGCAACC-TAGGTCGCCAGGAGCTAGTATCCTTAGATC-TTTCTATCGGTA-ACHTAATTCTCTGTTATTTAT-CTGACCCCTAACTCCATGCTAACTTG-CATTAAAAAAAAAAAAAA-----	6353
gi		58331165		ref		NM_008817.2		GTCTCCG-TGGGTGCCAGGAGCTAGATACTTTAGATC-TTTGTCTCCAGACTTAATTCCTCT-GTCTCTAT-GTGTCTGC-AACCCCAAGTCTATCGCA-TTTTAAAGAAAAGCAAAACACACACACACATACACACACAC	6390
gi		73947372		ref		XM_533574.2		TCCACCTGTGCGAACACAGAGGGTGCACAGCGGGGC-CCCCAGAGCAATGCCGAGTGTGGAGAGCTTAC-C-GCCCGAGGGTGCCTTCTGAAGCA-CCAAAAGAGCCACAGAGA-----	6017
gi		50872144		ref		NM_001002887.1		TGGCCCTTCTATGAGTCAAGGACTCGGCAAGTCTTCTTCCAGCACCATCTCTCAAAAGCACCAGAAAGCTGCACCTGCAAGGAGGAGGGCGGGCCGGCCGAGGGCCAGGAGGCGCAAGTCTCTGTCCTCC	6960



gi | 226053125 | ref | NM_001146184.1 | -----TTC TTTA CAGTCAA---CCCAAGCTTA---ACATGGACTCAGGTTCCCGAGCAGCCTTAATTGTTTGTAAACATCTGTTCCCTTCTTTTTCAGCTCTCCCTAGAGTATTTCTGAGTGT-----GTGTTCACTAACT-T 6470
gi | 114679299 | ref | XM_001141226.1 | -----TTC TTTA CAGTCAA---CCCAAGCTTA---ACATGGACTCAGGTTCCCGAGCAGCCTTAATTGTTTGTAAACATCTGTTCCCTTCTTTTTCAGCTCTCCCTAGAGTATTTCTGAGTGT-----GTGTTCACTAACT-T 6482
gi | 58331165 | ref | NM_008817.2 | CAAAAGCTTTCTTTTATAGTTAA---TCCCTAGCTTACTTAAACATGGACTCAGGTTCCCGAGCAGCCTTAAGTTTGTAAACATCTGTTCCCTTCTTTTTCAGCTCTCCCTAGAGTATTTCTGAGTGT-----GTGTTCACTAACT-T 6534
gi | 73947372 | ref | XM_533574.2 | -----GAAGCATACTTA---CCGGTGTGAGGGATGTGGAAAGCCCTTCCGGTGCAGGTCAAGATTCAAGAGACATCAAGAGGATGCATGCCGGAAGCAAGCCATAATGTGCCCTGAGTGTGGGAAAGCCTTACCGACAGCTC-C 6153
gi | 50872144 | ref | NM_001002887.1 | CGGGAAGTCTCTGCCATCCAGGGCTCCAAACGTG---GAGGGGG---CTGAGCCCGAGGTGGAGGGCCCGAGCCCGAGGTGGAGGGCCCGAGCCCGAGGTGGAGGGCCCGAA---CCCTCGGGGAGGCGGAGGGCCCGAGGTGGAGGGCCCG 7106
.....7210.....7220.....7230.....7240.....7250.....7260.....7270.....7280.....7290.....7300.....7310.....7320.....7330.....7340.....7350



gi | 226053125 | ref | NM_001146184.1 | AGTATTC TTTTA-ATTACAAA-TTGACC---TCACAGCTTGAGGTTTCTTGTCCTAATCTGTGGAATACCTG-T--GCTCCTTTGCTTCCCTCCCTCCCTCGCATATAACTATATAAGAAATTTTTTTTGGCCTTGAGTTGGCTGGAA 6612
gi | 114679299 | ref | XM_001141226.1 | AGTATTC TTTTA-ATTACAAA-TTGACC---TCACAGCTTGAGGTTTCTTGTCCTAATCTGTGGAATACCTG-T--GCTCCTTTGCTTCCCTCCCTCCCTCGCATATAACTATATAAGAAATTTTTTTTGGCCTTGAGTTGGCTGGAA 6624
gi | 58331165 | ref | NM_008817.2 | CATGTCA CCTGATGTCAAAA-CTGACT---TCCCAGCTTGAGATTTTTCTGCTCCGATAC-ACGGACTGGGTG-C--GCTCCTTTACTTCCCTCCCT----- 6624
gi | 73947372 | ref | XM_533574.2 | ACCCTTAAACAATCACTGCAAAAATTCACA---GCACAGAGAACTGTACCCCTTCCCAAAATGTGAGACGGCCTT-CAGGCACTCTCTGCTCCCTGTGTCCACCAGAAACCAATGCTGGAAAGGGAACAGTGA----- 6282
gi | 50872144 | ref | NM_001002887.1 | GGAGCCGAGCCGCGAGCCGAGCAGCCACCCAGCCAGCCAGCCGACATGGACCCGACAGCCGAGCCGCGCCGCGGCTCCGAGGACCCGAGGAGCCGCGCAAGAACCCGAGGGCCGACGACGAGCCGAGCCGCGGCGGCA 7256
.....7360.....7370.....7380.....7390.....7400.....7410.....7420.....7430.....7440.....7450.....7460.....7470.....7480.....7490.....7500



gi | 226053125 | ref | NM_001146184.1 | AAAAAATATAAAATTTAAAAATTTAAAAAAGATTGCAAAATGTAAGTGTAAGATCATTTGAAACAGCAAATTAAGTACCCACTGGGGGAAATGTGTCTGAATCTTACTTCTGGAATCTGCAGGATTAGGGCTTGGAAGTATGT 6762
gi | 114679299 | ref | XM_001141226.1 | AAAAAATATAAAATTTAAAAATTTAAAAAAGATTGCAAAATGTAAGTGTAAGATCATTTGAAACAGCAAATTAAGTACCCACTGGGGGAAATGTGTCTGAATCTTACTTCTGGAATCTGCAGGATTAGGGCTTGGAAGTATGT 6774
gi | 58331165 | ref | NM_008817.2 | ----- 6624
gi | 73947372 | ref | XM_533574.2 | ----- 6282
gi | 50872144 | ref | NM_001002887.1 | CGAGGACCCCGAGGAGGGGCGAGGAGCAAGATCCAGGTGGAGGAGCCCTACTACGACTGCGGGCAGTGGGGGAGACCCTCCCTCGGGCGCCGCTACCGGAGCACCCTGACGGCGCAGCCAGCCCTCGTCACTCCCTGGAAGCCCG 7406
.....7510.....7520.....7530.....7540.....7550.....7560.....7570.....7580.....7590.....7600.....7610.....7620.....7630.....7640.....7650



gi | 226053125 | ref | NM_001146184.1 | CAAAGATGCAAGGAGTGTCAAAGTTTGGAAAGATTGTAGACTGAGAGCAAGAGCAGAAATGAGTGAGTCAAAGAAAGGAGTCCATAATATACCCAGATCTAGGAGGGGAGAGGAGACAGACAGAAAGAAAACCCAGAGGCAAGAACT 6912
gi | 114679299 | ref | XM_001141226.1 | CAAAGATGCAAGGAGTGTCAAAGTTTGGAAAGATTGTAGACTGAGAGCAAGAGCAGAAATGAGTGAGTCAAAGAAAGGAGTCCATAATATACCCAGATCTAGGAGGGGAGAGGAGACAGACAGAAAGAAAACCCAGAGGCAAGAACT 6924
gi | 58331165 | ref | NM_008817.2 | ----- 6624
gi | 73947372 | ref | XM_533574.2 | ----- 6282
gi | 50872144 | ref | NM_001002887.1 | CGGCCCTCTACGGCCAGGGCCCGGGTGGCCCAAGGGCCGCGCCGAGCCGAGCTTTCAAGTGGCAGCGTGTGGGGCAGCTCTTCAAGCAGCCGCTGTCCCTGGCCAGGCACCAGAACCCCAACCCGCTG--AGGCCCGGGGGCG 7554
.....7660.....7670.....7680.....7690.....7700.....7710.....7720.....7730.....7740.....7750.....7760.....7770.....7780.....7790.....7800



gi | 226053125 | ref | NM_001146184.1 | GTAGAAGCCAGGTTTCTGAGAAATGAATTGACCGGGGTGTCTGAGCAGTTTGGAAAAGGAGTTTGTATGTTATGGTGTAGGTGAGGGCTGGCTGCATAGGAAAGGACTGAGGTGGAAAGGACATCGGGAAAGCTGAGGGGCAGTGAGG 7062
gi | 114679299 | ref | XM_001141226.1 | GTAGAAGCCAGGTTTCTGAGAAATGAATTGACCGGGGTGTCTGAGCAGTTTGGAAAAGGAGTTTGTATGTTATGGTGTAGGTGAGGGCTGGCTGCATAGGAAAGGACTGAGGTGGAAAGGACATCGGGAAAGCTGAGGGGCAGTGAGG 7074
gi | 58331165 | ref | NM_008817.2 | ----- 6624
gi | 73947372 | ref | XM_533574.2 | ----- 6282
gi | 50872144 | ref | NM_001002887.1 | CCTTGGGACCCGACCTCTCAACCACCTCACCAGACCCACTGCGACCCCGGACTGCACTCACCCGACCTGGAATTTCAGACACCCGGCCCGGACAGCCCAAGCCAGTGAAGTCCGGCGGGCGGGGCTCCAATGGGACCCCG 7704
.....7810.....7820.....7830.....7840.....7850.....7860.....7870.....7880.....7890.....7900.....7910.....7920.....7930.....7940.....7950



gi | 226053125 | ref | NM_001146184.1 | TTTACTACATGGGAAAAGGACTCTTGAACGAGAAATCAGTGTGATGTGGGGTGAACCTTGTGGGTACATTACTTGGTGTAAACATTTGTGGCAGTGGTACCCCTTTTTCAGAAAACAACCTTGC-TGTAAATCAGGGTGTCCGTTCCAA 7211
gi | 114679299 | ref | XM_001141226.1 | TTTACTACATGGGAAAAGGACTCTTGAACGAGAAATCAGTGTGATGTGGGGTGAACCTTGTGGGTACATTACTTGGTGTAAACATTTGTGGCAGTGGTACCCCTTTTTCAGAAAACAACCTTGC-TGTAAATCAGGGTGTCCGTTCCAA 7223
gi | 58331165 | ref | NM_008817.2 | ----- 6624
gi | 73947372 | ref | XM_533574.2 | ----- 6282
gi | 50872144 | ref | NM_001002887.1 | CCGGCCCTTCAACCAACACCAACCGGACCCACCAGCTGGCCGCACTGACCCAGCGGCCGCGGATTTCAGACTCTCGGCCCAAGGTTGAGATGTTGCAAGCTCCCTTGTCCAGCACACAGGTAACCTCGGGCACACAGGGCACTCGG 7854
.....7960.....7970.....7980.....7990.....8000.....8010.....8020.....8030.....8040.....8050.....8060.....8070.....8080.....8090.....8100



gi|226053125|ref|NM_001146184.1| CTTT CAGCTA GTGAAAAGGTAGTAA CAAATGGTAAAC AAGAGAAATGATTGTTTAAACCTATCTGTGGA CACTTAATGCAA CTGTTTAAAAATGATAATCACGAGTTATGTAGCAA CTTGAAATATATTTACAGAACATTAA GTGGAGAA 7361
gi|114679299|ref|XM_001141226.1| CTTT CAGCTA GTGAAAAGGTAGTAA CAAATGGTAAAC AAGAGAAATGATTGTTTAAACCTATCTGTGGA CACTTAATGCAA CTGTTTAAAAATGATAATCACGAGTTATGTAGCAA CTTGAAATATATTTACAGAACATTAA GTGGAGAA 7373
gi|58331165|ref|NM_008817.2| 6624
gi|73947372|ref|XM_533574.2| 6282
gi|50872144|ref|NM_001002887.1| CCGCCCGCCG CCGGGGCTTCGCGGCTGCAGAGAGCGCCCGTCTGTGACAGCCCGGGA CCTCCGCGCACTGCC TCCCGAGCTGTGCACAGAAACA GCCAGCACAGTGAACTGGACTGAGTGTGC CGCTCACTGGCCGCTTACCCTGCAG 8003
.....8110.....8120.....8130.....8140.....8150.....8160.....8170.....8180.....8190.....8200.....8210.....8220.....8230.....8240.....8250



gi|226053125|ref|NM_001146184.1| ACGAGGACACGAAAGTATATTTATACACAGTTAACTCAACAGTTCA TTTATATGCGTTCATTTAACAGTTCA TTTAAA CAGTTCATTA TAACTGTTTAAAAATATATATGCTTATAGT CAAAAGCTGTTGTGGTGTGTGTGTGTA 7511
gi|114679299|ref|XM_001141226.1| ACGAGGACACGAAAGTATATTTATACACAGTTAACTCAACAGTTCA TTTATATGCGTTCATTTAACAGTTCA TTTAAA CAGTTCATTA TAACTGTTTAAAAATATATATGCTTATAGT CAAAAGCTGTTGTGGTGTGTGTGTGTA 7463
gi|58331165|ref|NM_008817.2| -GTTTAAAAATATATATGCTTATAGT CAAAAGCTGTTGTGGTGTGTGTGTGTA 6624
gi|73947372|ref|XM_533574.2| 6282
gi|50872144|ref|NM_001002887.1| CCGACCTCACCTGGTA CTCTCGGTTTTGCTTTTTTTTTTGAGGAGGAGAGAGCAACAAATTA CAATATA TTTTGTAA GCATCTTA ---GAGCTTTAGAAAGATCTATTGTGAGCTGTTTGAACCCCTATCAGTATCTTTTTGACTA 8149
.....8260.....8270.....8280.....8290.....8300.....8310.....8320.....8330.....8340.....8350.....8360.....8370.....8380.....8390.....8400



gi|226053125|ref|NM_001146184.1| GCGTTATAGTTAGCATTATTTTCTTAAATTTCTTGAAATGTTCTTTATGGTAGTGTACTAAAAAGTTTATGATCACATTTTCATTTGTGAACATAAATTTGAACTCATTATCACACACTTGGAAAAACAGAAAA GTGGAGGAAAAAAAT 7661
gi|114679299|ref|XM_001141226.1| GCGTTATAGTTAGCATTATTTTCTTAAATTTCTTGAAATGTTCTTTATGGTAGTGTACTAAAAAGTTTATGATCACATTTTCATTTGTGAACATAAATTTGAACTCATTATCACACACTTGGAAAAACAGAAAA GTGGAGGAAAAAAAT 7613
gi|58331165|ref|NM_008817.2| 6624
gi|73947372|ref|XM_533574.2| 6282
gi|50872144|ref|NM_001002887.1| ACGGACTGGTTCTCTACCTTTCTACA TAA CCCCCTCACAGTGTAGGCGTGAAAGGCAGAGCGCTTTGCCCGCTTCCCGGTGTGAAAGGAAAGTCCGTCTGCTCCCTTTCAAGGCGCTCGTCTACA CCGACA CTGTGAAACCTCGTCTG 8299
.....8410.....8420.....8430.....8440.....8450.....8460.....8470.....8480.....8490.....8500.....8510.....8520.....8530.....8540.....8550



gi|226053125|ref|NM_001146184.1| CATATCCCCACCATCCAAAGACATATACCTCCTCTTATCTTGTTCA TTTCTGTTTCTGTGCACAGGTTTATGATTATAACTGTGTCAAAA TGTATATTTCAAAA TAGCTGTTACATTACCCTTTGTGGAATTA TGGTTAAATAC TTTCACT 7811
gi|114679299|ref|XM_001141226.1| CATATCCCCACCATCCAAAGACATATACCTCCTCT-ATCTTGTTCA TTTCTGTTTCTGTGCACAGGTTTATGATTATAACTGTGTCAAAA TGTATATTTCAAAA TAGCTGTTACATTACCCTTTGTGGAATTA TGGTTAAATAC TTTCACT 7762
gi|58331165|ref|NM_008817.2| 6624
gi|73947372|ref|XM_533574.2| 6282
gi|50872144|ref|NM_001002887.1| TGTCA GCTTTCCGTACCGTGAATTGGCC TTTTGTAA CCTCTTTTGGTTGGTTC CCGTTGGTTCCACCCTTTGTAA CCTTGCAGTGGGCTCTA TGC AAAAACA CTA CAAGTTTTTGTTA TTTTATTTT-TTAA CCCCCTTGA TGTCTCT 8448
.....8560.....8570.....8580.....8590.....8600.....8610.....8620.....8630.....8640.....8650.....8660.....8670.....8680.....8690.....8700



gi|226053125|ref|NM_001146184.1| TTAA TTTTTTCAAATGTTCCCTATAATAATGTCCGTATAACAGTGTATTA TGTGTTCTCCA ATTGGTGTGCATAATA CATACCCAGAGGAAAAATTA GAAAAATAAGTAAATTA TTTTAAAAATTA CCTATATT CCAA CACCTAACAA 7961
gi|114679299|ref|XM_001141226.1| TTAA TTTTTTCAAATGTTCCCTATAATAATGTCCGTATAACAGTGTATTA TGTGTTCTCCA ATTGGTGTGCATAATA CATACCCAGAGGAAAAATTA GAAAAATAAGTAAATTA TTTTAAAAATTA CCTATATT CCAA CACCTAACAA 7912
gi|58331165|ref|NM_008817.2| 6624
gi|73947372|ref|XM_533574.2| 6282
gi|50872144|ref|NM_001002887.1| TCGATAGTGAATTTTACAAAAGCCGAAGCTTTTCCCTGTGAGTCTTA CATCTTCCTTTAAAGAGTGGGTTGTA CCA TCACTAGATCACGCGTGCCTAA TGAAAGTTGAGAA CCGCGGGGAGGGGGCTCTCTCTGTTGTAATA CCG 8598
.....8710.....8720.....8730.....8740.....8750.....8760.....8770.....8780.....8790.....8800.....8810.....8820.....8830.....8840.....8850



gi|226053125|ref|NM_001146184.1| CTACTGCTAACATCTTGATCTGTTTCTCTATCTTGTTCAGTGCA CACGCTTGTGATAAACAGTGTAAATATGTTGTCATAAAGTCTTAAATGAAAAGATGTGAAAATAA C TAAAATAGTGTGTGCATTGTGGGAATTTGGTTAAATA 8111
gi|114679299|ref|XM_001141226.1| CTACTGCTAACATCTTGATCTGTTTCTCTATCTTGTTCAGTGCA CACGCTTGTGATAAACAGTGTAAATATGTTGTCATAAAGTCTTAAATGAAAAGATGTGAAAATAA C TAAAATAGTGTGTGCATTGTGGGAATTTGGTTAAATA 8062
gi|58331165|ref|NM_008817.2| 6624
gi|73947372|ref|XM_533574.2| 6282
gi|50872144|ref|NM_001002887.1| TTGAGGGCTTACGACTTCA TTA CTTCCCTTTGCGGCTTCCTGCTTAA GTGACCA GTAGCAACGTGGCCTTGGCCCTCCGTGCC CCGTGCAGAGTCTGCACCCCTGGGTGCCAGGAGCTAGCATCCCTTAGAGCTTTCCAGCTTGA 8747
.....8860.....8870.....8880.....8890.....8900.....8910.....8920.....8930.....8940.....8950.....8960.....8970.....8980.....8990.....9000



gi | 226053125 | ref | NM_001146184.1 | TTTTGTCTCAAATTCCTTAAATAATCTTTGGTGTTTGGTAATAAATTTTATGTA TGTAATTTCCATTACAAATATAATACATACTCATACAAAACTTTGGAAATTCAGTAAAGAAAATTCACACATATCCCAACACCCAAACAATT 8261
gi | 114679299 | ref | XM_001141226.1 | TTTTGTCTCAAATTCCTTAAATAATCTTTGGTGTTTGGTAATAAATTTTATGTA TGTAATTTCCATTACAAATATAATACATACTCATACAAAACTTTGGAAATTCAGTAAAGAAAATTCACACATATCCCAACACCCAAACAATT 8212
gi | 58331165 | ref | NM_008817.2 | ----- 6624
gi | 73947372 | ref | XM_533574.2 | ----- 6282
gi | 50872144 | ref | NM_001002887.1 | GACTTCATCCCTCTCCAACCTGTGACCCCTCAACCAACCCCAATGTCTAACCTTGCAATTTAAAAAATAAGAAAAAGCTTTCTTTACAGCCCACTCGAGCTCGACACGGACTCAGGTTCCCGGCCAGCCTTAATTGTTTGGTTGCC 8897
.....9010.....9020.....9030.....9040.....9050.....9060.....9070.....9080.....9090.....9100.....9110.....9120.....9130.....9140.....9150



gi | 226053125 | ref | NM_001146184.1 | AAAGTAAACATCTTGATCTGTGCACTAGTCTGTGATTATTAGGGTGTAGTGATAAGTATGCATAAATGTCAAAGATGGGAAAGAAAGATGAAAAACAAGAAATAGTGTGTGGTGTGTGGGAATATGGTTATTTTGTTCGGTTCC 8411
gi | 114679299 | ref | XM_001141226.1 | AAAGTAAACATCTTGATCTGTGCACTAGTCTGTGATTATTAGGGTGTAGTGATAAGTATGCATAAATGTCAAAGATGGGAAAGAAAGATGAAAAACAAGAAATAGTGTGTGGTGTGTGGGAATATGGTTATTTTGTTCGGTTCC 8362
gi | 58331165 | ref | NM_008817.2 | ----- 6624
gi | 73947372 | ref | XM_533574.2 | ----- 6282
gi | 50872144 | ref | NM_001002887.1 | ATCTGTCCCCCTCTCAAGGTCGGCCCTTCTGACAAAGCACCCCGCTGCCCTCAGAGCGGCCCTGTCCCGCCCGCCAGTCTCTGTGCTGCGCTCCCAAGCTGACCTCGCCGCTCTGGGGTCTCCTGCGTCTGCTCCCTTTGTGCCCTCCCT 9047
.....9160.....9170.....9180.....9190.....9200.....9210.....9220.....9230.....9240.....9250.....9260.....9270.....9280.....9290.....9300



gi | 226053125 | ref | NM_001146184.1 | TTGAAAGGTCATCATTCTAGTGTTTGGTAGTCCACCCTTACTACATATAATTTCCATTATATGAAATGTGTTCAATATAGAAACTTTGAAAGTTACAGAAATGTAGAAAGAGAACTCACCCATGTTTTCACCATCCAAAGAGTGTGGTT 8561
gi | 114679299 | ref | XM_001141226.1 | TTGAAAGGTCATCATTCTAGTGTTTGGTAGTCCACCCTTACTACATATAATTTCCATTATATGAAATGTGTTCAATATAGAAACTTTGAAAGTTACAGAAATGTAGAAAGAGAACTCACCCATGTTTTCACCATCCAAAGAGTGTGGTT 8512
gi | 58331165 | ref | NM_008817.2 | ----- 6624
gi | 73947372 | ref | XM_533574.2 | ----- 6282
gi | 50872144 | ref | NM_001002887.1 | TTGCTTCCCCGCCCTCTTTCGAATAAATGACTATTATGAAATTTCTTGGCTTTGAGTGGCTGGCAAAAAAATTTAAAAAATTTTTTTAAAACTTAAAAAAGAGGATCTTGTAAGCTGCAAGTGAGCAGAAAGCTAAGAGCAGATTG 9197
.....9310.....9320.....9330.....9340.....9350.....9360.....9370.....9380.....9390.....9400.....9410.....9420.....9430.....9440.....9450



gi | 226053125 | ref | NM_001146184.1 | AACATCTTGAATATTTTTCATCTTGTCTGTGACAGGTTTTGGTTGTTAATATGGTTGTGGTCAATCTATCTGTAATAGTGTCAACAAATAAAAAATAAGTTAAAAATAAATAATTTAAAAA----- 8689
gi | 114679299 | ref | XM_001141226.1 | AACATCTTGAATATTTTTCATCTTGTCTGTGACAGGTTTTGGTTGTTAATATGGTTGTGGTCAATCTATCTGTAATAGTGTCAACAAATAAAAAATAAGTTAAAAATAAATAATTT----- 8634
gi | 58331165 | ref | NM_008817.2 | ----- 6624
gi | 73947372 | ref | XM_533574.2 | ----- 6282
gi | 50872144 | ref | NM_001002887.1 | TTTGGGACAGCAGAGTGCAGATCTGCTCGGGAAGCCCGCTCTGGAAGCCCGCTCTCCTAG-GTCCCTGCCATGAGGGCTGGGAAAAGCTGTCTAGAGCTGGAGGAAAGCCCAAAGTCAAGGAGAGCCAAAGAAAGGGGTCTGACCGCTTACC 9346
.....9460.....9470.....9480.....9490.....9500.....9510.....9520.....9530.....9540.....9550.....9560.....9570.....9580.....9590.....9600



gi | 226053125 | ref | NM_001146184.1 | ----- 8689
gi | 114679299 | ref | XM_001141226.1 | ----- 8634
gi | 58331165 | ref | NM_008817.2 | ----- 6624
gi | 73947372 | ref | XM_533574.2 | ----- 6282
gi | 50872144 | ref | NM_001002887.1 | AGACCTGGGAGGGCAGGGTCTGACAGAGGAAACATCAGAAAGCAGGGAAGTGGAAAGCCCAAGTGGGGAGGGTTGAATGAAATGAGCAGGGTGTCTGGCAGTTAAGAGAAAGGGGCCCTTGGTGGCTGGTGTCCATGAGGGCAGCTGCATC 9496
.....9610.....9620.....9630.....9640.....9650.....9660.....9670.....9680.....9690.....9700.....9710.....9720.....9730.....9740.....9750



gi | 226053125 | ref | NM_001146184.1 | ----- 8689
gi | 114679299 | ref | XM_001141226.1 | ----- 8634
gi | 58331165 | ref | NM_008817.2 | ----- 6624
gi | 73947372 | ref | XM_533574.2 | ----- 6282
gi | 50872144 | ref | NM_001002887.1 | ACAAGACCCAAACATTTGGAGCGGACGCCCGGAGCCCGAGGGGCTGCAAGCTGGGAGCCAGCTGCTGGCGTAAAGGGGTGAACCTGGCTGTTTATCTGCTGCTGGCGGCCAACCTGGTACAGTGTTTTACAGAGAGCCCGCTGCCAGCGCTC 9646
.....9760.....9770.....9780.....9790.....9800.....9810.....9820.....9830.....9840.....9850.....9860.....9870.....9880.....9890.....9900



gi|226053125|ref|NM_001146184.1|----- 8689
gi|114679299|ref|XM_001141226.1|----- 8634
gi|58331165|ref|NM_008817.2|----- 6624
gi|73947372|ref|XM_533574.2|----- 6282
gi|50872144|ref|NM_001002887.1|C GTTCCAACCGTCCCTTTGGTCA GTGAGCGATCAGGAA CAAC TGA CAAATGCCAAAAACAGGAGGAAAGGTGAAAGGGA GTGTGTCCGCGCACTCTGAACGCAGCTGTCTAGAAA GGATAATCATGGAGAGTTACGTAGTGACCTGGAGATA 9796
.....9910.....9920.....9930.....9940.....9950.....9960.....9970.....9980.....9990.....10000.....10010.....10020.....10030.....10040.....10050

gi|226053125|ref|NM_001146184.1|----- 8689
gi|114679299|ref|XM_001141226.1|----- 8634
gi|58331165|ref|NM_008817.2|----- 6624
gi|73947372|ref|XM_533574.2|----- 6282
gi|50872144|ref|NM_001002887.1|ATTTACGGAA TACCAAGTGGAAAAA CCAAGGACACAGAA TTA TTTATAC TACAA TTACAGCTGTTTAAAAATGTA TGC TTA TTAGT CAAAAGCTGTGGTGGTGGTGC TGTGGT AGGCTTA TTAGTTAGCA TTA TTTTCTTAAA TTTCTTTC 9946
.....10060.....10070.....10080.....10090.....10100.....10110.....10120.....10130.....10140.....10150.....10160.....10170.....10180.....10190.....10200

gi|226053125|ref|NM_001146184.1|----- 8689
gi|114679299|ref|XM_001141226.1|----- 8634
gi|58331165|ref|NM_008817.2|----- 6624
gi|73947372|ref|XM_533574.2|----- 6282
gi|50872144|ref|NM_001002887.1|AATGTTTATGGTATGTGTTACTCAAAGCTTA TAA TCA CGTCTCCATTGTGAACATAATTTGAGCTCATTATTCAAGCACTCAGAGAATA CAGAAAAGTGGAGGGAAAAAAATCCATATA CCCACCATCCAAAGATGACAGATA TGC TCT 10096
.....10210.....10220.....10230.....10240.....10250.....10260.....10270.....10280.....10290.....10300.....10310.....10320.....10330.....10340.....10350

gi|226053125|ref|NM_001146184.1|----- 8689
gi|114679299|ref|XM_001141226.1|----- 8634
gi|58331165|ref|NM_008817.2|----- 6624
gi|73947372|ref|XM_533574.2|----- 6282
gi|50872144|ref|NM_001002887.1|CACTACA TTGTTTA TTTCTTTCTGTGCACA GGCCTTA TAACTGTGTCCCAAA CGTGTACTCAGATTAAAGTGTTAGCTTTTGTGGAATTA TGGTTAAACGCCTTTCATCTCTAA TGTTTTCA GATGGCCCTTAAAA TAGTTTCTGTATAACAA 10246
.....10360.....10370.....10380.....10390.....10400.....10410.....10420.....10430.....10440.....10450.....10460.....10470.....10480.....10490.....10500

gi|226053125|ref|NM_001146184.1|----- 8689
gi|114679299|ref|XM_001141226.1|----- 8634
gi|58331165|ref|NM_008817.2|----- 6624
gi|73947372|ref|XM_533574.2|----- 6282
gi|50872144|ref|NM_001002887.1|AGTTGATTCTGCTTCTTCAATTAGCAAGCATAATACACACCCAGAGGAATAA TTGGAAAA TACAAAA TAAATGAGAAAA GAA CAAAAAAGTGC CCAATA TTCCCAACGCCAACGCCTACTGTTAACATCTTGTTCCTCCATCTCGT 10396
.....10510.....10520.....10530.....10540.....10550.....10560.....10570.....10580.....10590.....10600.....10610.....10620.....10630.....10640.....10650

gi|226053125|ref|NM_001146184.1|----- 8689
gi|114679299|ref|XM_001141226.1|----- 8634
gi|58331165|ref|NM_008817.2|----- 6624
gi|73947372|ref|XM_533574.2|----- 6282
gi|50872144|ref|NM_001002887.1|ATCAGTGCACAAGCTTTGTGATTTATGACC GTGGTGAATATGTGTGCATACAGTCTAAAA TAAAAAAT CACA GAAAA TAA TAAAGTAGTGTGTCTATTGTGGCATTATGGTTAACTATCTTGTCTCAAA TTTCTTGAATGATCTTTG 10546
.....10660.....10670.....10680.....10690.....10700.....10710.....10720.....10730.....10740.....10750.....10760.....10770.....10780.....10790.....10800

gi|226053125|ref|NM_001146184.1|----- 8689
gi|114679299|ref|XM_001141226.1|----- 8634
gi|58331165|ref|NM_008817.2|----- 6624
gi|73947372|ref|XM_533574.2|----- 6282
gi|50872144|ref|NM_001002887.1|GTGTTTGGAGTATTAAATCTTATGTTATGTTTTCCATTAAAATTCTTAAATACATACTCATGGCATA CCTGGGGGAGATTAGTAAAGCAAAAGAAATTCA CGCATA TCTGACACCCAAACAATCATTGCTGTTAAACCTTGATCTGTG 10696
.....10810.....10820.....10830.....10840.....10850.....10860.....10870.....10880.....10890.....10900.....10910.....10920.....10930.....10940.....10950

gi|226053125|ref|NM_001146184.1|----- 8689
gi|114679299|ref|XM_001141226.1|----- 8634
gi|58331165|ref|NM_008817.2|----- 6624
gi|73947372|ref|XM_533574.2|----- 6282
gi|50872144|ref|NM_001002887.1|CACAGTCAGGACGGGGGTGTCTGTGGTCA GAAATGCAGAGGGTTGAA GAGGAGAAAGAAAGCA GTCAAGGAACGGT CGTGTGGTCTTTTCCGGCGTTAAGCCTGTGGGGTTCCGTTTCTGGGAAGCCCTGTCTCGTTGTGTCCCGGTCA CCG 10846
.....10960.....10970.....10980.....10990.....11000.....11010.....11020.....11030.....11040.....11050.....11060.....11070.....11080.....11090.....11100

gi|226053125|ref|NM_001146184.1|----- 8689
gi|114679299|ref|XM_001141226.1|----- 8634
gi|58331165|ref|NM_008817.2|----- 6624
gi|73947372|ref|XM_533574.2|----- 6282
gi|50872144|ref|NM_001002887.1|ACCTTTTATGACCGGGTGCCTCCATTGTAACTGCAGTGTCTGCTCACGTGAGAAAACCCGGCACCTTACAGAAAGTGTGGAAGAGAGGCGTGCCCGTGTGCGCCATCACCCAAAGACCAGGTTAACATCTGGACACGTTTTCTTCATCTTGTCT 10996
.....11110.....11120.....11130.....11140.....11150.....11160.....11170.....11180.....11190.....11200.....11210.....11220.....11230.....11240.....11250

gi|226053125|ref|NM_001146184.1|----- 8689
gi|114679299|ref|XM_001141226.1|----- 8634
gi|58331165|ref|NM_008817.2|----- 6624
gi|73947372|ref|XM_533574.2|----- 6282
gi|50872144|ref|NM_001002887.1|CTGTGCACAGGTTTTGGTTTGTGTAAGTA TGGTTGGTGGT CAGTTCTATCTGTAAATCGTGTCA CCAATAAAAAATAA GTTGAA 11076
.....11260.....11270.....11280.....11290.....11300.....11310.....11320.....11330