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CLUSTAL O(1.2.4) multiple sequence alignment


XM_007904793.1      ------------------------------------------------------------        0
XM_006008085.1      ------------------------------------------------------------        0
XM_024264445.1      AAACAATCTTAGGCGGGACGGCGGCGGTGGGGGTTGAGGGGGCGTGTTCAGATGGACATA       60
XM_022744743.1      ------------------------------------------------------------        0
NM_131056.1         ------------------------------------------------------------        0
XM_027031912.1      ------------------------------------------------------------        0


XM_007904793.1      ---------------GCACCCTGTACTGGT----TTGAAGAAACAT---------CTACC       32
XM_006008085.1      ------------------------------------------------------------        0
XM_024264445.1      TAAAAGAAGGCAAAGCCCTCCACTCTGCCCTACACCCAGCAGCTGCCCCGGTCTTCCTCG      120
XM_022744743.1      TCAACCTGCTCTCAG-CTGCCACTGCTCCTCCTCTTCATCACAGACTCACC---TCCTCC       56
NM_131056.1         -------------------------------------CCATATC-------CACCA       12
XM_027031912.1      ------------------------------------------------------------        0


XM_007904793.1      AGGTAAG--CTTTTTGTCTGCGAAGTGCTGAGATGATGCTCTGGAATCGCTTTGGGTTCG       90
XM_006008085.1      -------------------------------ATGGCCCTCTGGGTTCGAGTCCTCCCTC       28
XM_024264445.1      CCGTACAAGAACCTCCTCTGTTCTCCAGGATGGCAGCGCTGTGGCTCCAGACGTTTTCCT      180
XM_022744743.1      TCCTCCTCCTCCTCCACCAACTCTACAGCATGGCGGCGCTGTGGCTCCAGTCTGTCTCTC      116
NM_131056.1         TTCCTCGCCTCTGCTTCGAGAACAGTGTGACCATGGCAGTGTGGCTTCAGGCTGGTGCTC       72
XM_027031912.1      -----------------------------ATGGCAGCGTGGATCCAGGCTGGTACTC       28
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XM_007904793.1      TGGCTCTGTTGATGGCTCTCTCCGGCCCGAAGCCGTCCGAGACAGTACCAACCCAACGCC      150
XM_006008085.1      TGTTTCTACTGATCGCCCTCTCAGCTCCCAGCACCACGCAAGCTATTGCTAACCAGCATC       88
XM_024264445.1      TGCTGTGTCTGCTCATCGTGTCGT---TTCCAGGCTCCCGAGCCATCCCTCCACAGCACC      237
XM_022744743.1      TGCTGGTCTTACTGATCGTATCGTGGCCGGGCTCCCAGGCCGTCGCCCCCCCGCAGCACC      176
NM_131056.1         TGTTGGTCCTGTTGGTCGTGTCCA---GTGTAAGCACTAACCCAGGCACACCGCAGCACC      129
XM_027031912.1      TTCTGCTCCTGTTGGCTCTGTCCA---CTGCAGGAGCCAACGCTGCCGCTCCCCAACACC       85
                     *         *   *      * **                    *      ** *  *


XM_007904793.1      TGTGCGGCTCTCACCTGGTGGATGCTCTGTACTTTGTGTGCGGAGAAAGGGGCTTCTTCT      210
XM_006008085.1      TATGTGGCTCCCACCTGGTGGAGGCTCTCTACCTGGTCTGTGGGGAAAAGGGCTTCTTCT      148
XM_024264445.1      TGTGTGGCTCTCACCTGGTGGAAGCTCTGTACCTGGTCTGTGGAGACAGAGGCTTCTTCT      297
XM_022744743.1      TTTGCGGCTCGCACCTGGTCGACGCCCTGTACCTGGTCTGTGGGGACAGAGGCTTCTTCT      236
NM_131056.1         TGTGTGGATCTCATCTGGTCGATGCCCTTTATCTGGTCTGTGGCCCAACAGGCTTCTTCT      189
XM_027031912.1      TGTGCGGATCTCACTTGGTCGACGCCCTCTACCTTGTCTGTGGCCCATCAGGCTTCTTTT      145
                     * ** ** ** **   **** ** ** ** **  * ** ** **        ******** *


XM_007904793.1      ACTCACCCAAACAGATAAGGGACGTGGGGCCGCTTTCGGCATTCCGAGACCTAGAGCCCC      270
XM_006008085.1      ACTCACCCCGAGGCAGAAGAGAGATCGAACAGTCACTGATTAA----------------      191
XM_024264445.1      ACAACCCCAAGAGAGACGTGGACCCTCTTGCTGGGTTTCTGTCCCCAAAGATGGGGGGCG      357
XM_022744743.1      ACAACCCCAAGAGAGACGTCGACCCTCTGCTGGGTTTCCTCCCTCCCAAGGCGGGTGGAG      296
NM_131056.1         ACAACCCCAAGAGAGACGTTGAGCCCCTTCTGGGTTTCCTTCCTCCTAAATCTGCCCAGG      249
XM_027031912.1      ACAACCCCAAGAGAGAGGTGGACCCACTGCTGGGTTTCCTTTCCTCCAAGGCGGGTCAGG      205
                    **    ***              **


XM_007904793.1      C------GCTGGATACTGAGATGGAGGACAGGTTTCCCCACCGGCAGCAGTTGGCTGGGA      324
XM_006008085.1      -------GAGCGGCCTGGAGAACGAGGTTGAGGAGCTCCCCTTCCAGCAACAAGGGACCA      244
XM_024264445.1      C------CACAGGTACCGGGAACGAAGTGGCCGAGTTCGCCTTCAAGGACCAGATGGAGA      411
XM_022744743.1      CTGCGGCGGCGGGCGGTGAAAACGAAGTGGCCGAGTTCGCCTTCAAGGACCAGATGGAGA      356
NM_131056.1         A-----------------AACTGAGGTGGCTGACTTTGCATTTAAAGATCATGCCGAGC      291
XM_027031912.1      A-----------------GGGTGAGATGGCCGAGTACCCGTACAGAGAGCACGCGGAGC      247
                                      **                            *


XM_007904793.1      GTAAAATGAAGCGAGGAATCGTCGAGCAATGCTGCCATAACACGTGCTCCCTGGTGAACC      384
XM_006008085.1      TGAAGGAAAAGAGGGGCATAGTAGAACAGTGCTGTCACAACACCTGCTCCCTGTACCAGC      304
XM_024264445.1      TGATGGTTAAGAGAGGTATCGTTGAGCAGTGCTGCCACAAGCCGTGCAACCTCTTTGACT      471
XM_022744743.1      TGATGGTGAAGCGAGGCATCGTGGAGCAGTGCTGCCACAAGCCCTGCAACATCTTCGACC      416
NM_131056.1         TGATAAGGAAGAGAGGCATTGTAGAGCAGTGCTGCCACAAACCCTGCAGCATCTTTGAGC      351
XM_027031912.1      TGATGGTAAAGAGGGGCATCGTGGAACAGTGCTGCCACAAACCCTGCAGCATCTTTGACC      307
                     *      *** * ** ** ** ** ** ***** ** **   * ***   * *      *


XM_007904793.1      TCGAGGGCTACTGTAACTAACAGACATGCCAATCGCTGGCACTGAGCAGCGTTCATTCCC      444
XM_006008085.1      TAGAAAACTACTGCAACTGA----------------------------------------      324
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XM_024264445.1     TGGAGAACTACTGCAACTGAGCAGGAACCGGACTCTGCCAGAACCCAACAAGAACCCAGA      531
XM_022744743.1     TGCAGAACTACTGCAACTGAACGGCTCTCCGCCCGGCTTCCTTCCCCTCCCCCACCCTCG      476
NM_131056.1        TGCAGAACTACTGTAACTGAAGAGATTTGCCCACCGCCAATGCCAGAAACACCTGTTTGC      411
XM_027031912.1     TGCAGAACTACTGCAACTAG----------------------------------------      327
                   *   *   ****** ****


XM_007904793.1     AACAACAAGGCAGTCCCTG------TC--CCTG---------------------------      469
XM_006008085.1     ------------------------------------------------------------      324
XM_024264445.1     GCTGGACCACTGCGTCCAGATA---TT-----------------TAAATAAAGTTTTGT      570
XM_022744743.1     CATCGAAAGAGCGGCAGTGCTGTCCTCTCTCTGAAACCCTGCTGACAAATGAAGTCTTCA      536
NM_131056.1        A-------CACAGGCCTTAATGCTCTCCGTTTGTT--TTTACAGAAAAAATAAAACT---      459
XM_027031912.1     ------------------------------------------------------------      327


XM_007904793.1     -----GGACGATGTTT-TTTTTTTATTAA-----------------------      492
XM_006008085.1     ---------------------------------------------------      324
XM_024264445.1     GAACTGAA-------------------------------------------      578
XM_022744743.1     CAAATGGATGAAATTATTTTTCCTAGAAAATAAAGTTTTGTGAATTGAGAAAA      589
NM_131056.1        -------ATCAAATGA-----------------------------------      468
XM_027031912.1     ---------------------------------------------------      327
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