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CLUSTAL O(1.2.4) multiple sequence alignment


JQ678788.1                        ------------------------AGTTGTTTAGCTGGAAAAGATGATGGAGCCGGGC
34
NC_003070.9:c26796532-26795052    CGACACACTTCCACATTCATGATTCCACAAATTCTAATGGATTTGAACAAATAT-GGGAC
59
                                           *     **    ****   **  *    *    ** *


JQ678788.1                        CGTTTTTTCTTTGAACCTTCGCCGTCGTCGGCGGTTTGCCAGCAAGGTGGTGGTGGCAAC
94
NC_003070.9:c26796532-26795052    CAATTTTTATTTGTTTCAACTCCTAAATGTGGGACCAATTAACAAGGT--TGATGTATTC
117
                                  *  ***** ****   *  * **    *  * *       * ******  ** **     *


JQ678788.1                        ATGTTGTTCCTCGGCAATCCTGATCACGGTTTTCGAGGG--CAAAGATCGATGATGGGAT
152
NC_003070.9:c26796532-26795052    TTCTTGTTCTTCCTCGTTCATTAATAGTTTGATTGAGCATGCACGCTTCTCTCAACCCAC
177
                                    * ****** **  *  ** * *  *   *  * ***    **     **  * *    *


JQ678788.1                        TGATGGA--TCAGGAGAGCTCACGG------AGGCGACCTTTTTTCAGCTCCTCCTCGTC
204
NC_003070.9:c26796532-26795052    CAGTCCAAGTCAAACCTCCTCAAGCCATCCCCTAATCCTATATATCAGTTTCTTCTCGCA
237
                                      *  *   ***      **** *             *   * * **** * ** ****


JQ678788.1                        GCAGGAC-----------GAACTGTTCGAC---GAGGAATACTACGACGAGCAGCT----
246
NC_003070.9:c26796532-26795052    AACCACCTCACAATCTATCAACAGTTTTAAAAAAAGACATAACTCAACCAATCTCACTTT
297
                                        *            *** ***   *    **  ***   * ** *      *


JQ678788.1                        -----GCCGGAGAAGAAGCGCCGCCTCACTTCTGACCAGGTGCATATGCTGGAGAAGAGC
301
NC_003070.9:c26796532-26795052    GAAAAAGACATGAACAAAACCCGCCTTCGTGCTCTCTC----CCCACCTTCCGGTAACTA
353
                                         *** **  ******   * **  *      *   *    *    * *


JQ678788.1                        TTTGAGACAGAGAACAAGCTGGAGCCGGAGCG-AAAGACGCAGCTGGCCAAGAAGCTAGG
360
NC_003070.9:c26796532-26795052    TTT-TCTCTTTAAACAGTATTAATCATGTGTTTTGCTATTCACATCACCAAATTATTCAT
412
                                  *** *    **** *  * * *        * ** *  ****      *


JQ678788.1                        ACTGCAGCCGAGACAGGTGGCCGTGTGGTTCCAGAACCGCCGCGCTCGGTGGAAGACCAA
420
NC_003070.9:c26796532-26795052    -----AGTTTAAAGAGGTCGATGTAGAATTCAT---------------AGATATACATG
451
                                       **   * * **** * **   ***                *  * **


JQ678788.1                        GCAGCTCGAGCGCGATTACGACCTTCTCAAGTCTTCCTATGACACCCTTTT---------
471
NC_003070.9:c26796532-26795052    TGTACATACGTGACTTTGTGACGATATATCGTTTTAATTTGTTAAATTTTGATCCCTTCT
511
                                      *     * *  **  ***  * *  ** **  * **  *    ***


JQ678788.1                        -GTCTGATTACGACTCCATCCTCAAGGAGAATCAGAAGCTCAAATCCCAGGTGGTTTCCA
530
NC_003070.9:c26796532-26795052    CTTAGGTATGCAACACCGTAAGAGATGTCGAT------------TGAGAGGTCGAAA---
556
                                     *  *  * * ** ** *    * *  **           *    **** *


JQ678788.1                        TAAACGAGAAGCTTGGAGGTAAAGAGCAGGCTAGTAGCACAAAAGCAACAGCATTTGCAG
590
NC_003070.9:c26796532-26795052    -CTACGTAAGGCCAGAAGTTAAACAA-CGCAACTTCTCAAAAGATGAAGACGATCTCATC
614
                                    *** * **  * ** **** *   *      * ** ** * ** * ** *
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JQ678788.1                       CGGA-------TGATCACGATGACGAGAAGCGCGGC---------CCTCTTCTTCCAGCC
634
NC_003070.9:c26796532-26795052   CTCAAGCTTCATGCACTTCTTGGCAATAGGTTCGTATTCATTCTTCTTATTCTTTAATTC
674
                                 *  *      **  *    ** * * *  **          *  * ***** *  *

JQ678788.1                       GGTGATCAGTTGACGGAGGTTGTTCCGATAACTAGTCTCCAGTA---TAGCTGCAG--CG
689
NC_003070.9:c26796532-26795052   AATAGTAATGTGAACG-GTACGTGCTAATAATCATTTTGATGTTATGTTTTTTCAGATGG
733
                                  *  * * ***  * *    ** * ****  * *   **     *   * ***    *

JQ678788.1                       TCA-AGGTG----GA---------GGACCGCCTGAGCTCAGGGAGCGGAGGAAGTGCCGT
735
NC_003070.9:c26796532-26795052   TCATTGATAGCGGGAAGATTGCCAGGACGAACCGACAACGAAGTTAGGATCCATTGGGAA
793
                                 *** * *      **         ****   * **   *   *   ***   * **

JQ678788.1                       GGTGGACGAGGCC-GAAGGCCCTCAGCCTGTGGACAGCAGTGATTCCTATAATTTCCCAA
794
NC_003070.9:c26796532-26795052   ACTTACCTAAAAAGGAAGCTCGTAAAAATGGGAATCG--ACCCAACCAATCATCGTCTCC
851
                                  *   * *    **** * *   ** * *  *       ** ** **    *

JQ678788.1                       ACA------ACATC------------------CACAATTACTACTCTCATGATCATGACA
830
NC_003070.9:c26796532-26795052   ACCATCACACCAACTACATTTCTAGACGTCACCTCCATTCTTCACATAAGGAACATGAAA
911
                                 **       ** *                  * * ***   *    * * ** ***** *

JQ678788.1                       CTCATCATCATCATCATCATCATCAATACACGGCGCCACA--------------------
870
NC_003070.9:c26796532-26795052   CCAAGATTATTAGTGATCAATCTTCTTCGGTATCCGAATCATGTGGTGTAACAATTTTGC
971
                                 *  *   *  *  * ****   *   *      *   *

JQ678788.1                       --TGATCATGTAGAACATCATCGTAGAGGAGTCCACTCAGAAGAAGATGACGGTA-----
923
NC_003070.9:c26796532-26795052   CCATTCCAAGTACCAATTGCTCGGAGGATAGTACTAGTACCGGACGAAGTCATTTGCCTG
1031
                                    ** ***  *  * *** **   *** *    *   ** ** * *  *

JQ678788.1                       -----------GCGATGACGGCCAGTGTTACTTCT--CCGATGTCTTTGCAGCCGCAGCA
970
NC_003070.9:c26796532-26795052   ACCTAAACATTGGTCTCATCCCGGCCGTGACTTCTTTGCCAGCTCTTTGCCTTCAGGACT
1091
                                            *   * *  *   ** ******  * * *******    *     *

JQ678788.1                       GCGGAGCAGCAAGCAG-----------CACAGGAGGAAGG--------------------
999
NC_003070.9:c26796532-26795052   CTAGCGAATCCTCTACCAATGGTTCAACAGGTCAAGAAACGCTTCTTCTATTCCGATGAG
1151
                                   * * * *    *            **   * ***

JQ678788.1                       --------TGTTTCTTT-------------------------------------------
1008
NC_003070.9:c26796532-26795052   AAATGGTGTATTTGTTTGTACACATTTGTTATATTACAAATGCACATATTATAATATTCA
1211
                                         * *** ***

JQ678788.1                       -----------------------------------------GAACTGGTGGGGATGGTCA
1027
NC_003070.9:c26796532-26795052   CTAGAGAGATGGTATAACGATGTTTGAAATATGTTAATCCTGAATTGGACCGGCTGGTCA
1271
                                                                          *** ***   ** ******

JQ678788.1                       TAAATGG-----------------------------------------------------
1034
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NC_003070.9:c26796532-26795052    TTGAACAACTATTCTCTTAAATGTCCGGTTCTGTTTTCAGTGATTAGTATTATAGTAGAT
1331
                                  *   *

JQ678788.1                        ------------------------------------------------------------
1034
NC_003070.9:c26796532-26795052    CGTTAATAACTAACCGACGATAACCGCTGCTTATTTGATCAATCAAGCTGTAAGAAATTA
1391


JQ678788.1                        ----------------------------------------------CTAAATCCCCTAA
1047
NC_003070.9:c26796532-26795052    TAGCTAATACAGCAATGTTAACGGTGCACATTGACGGGAAGTATTAATTAACTCTCTTAA
1451
                                                                           *** ** * ***

JQ678788.1                        ATTG------------------------    1051
NC_003070.9:c26796532-26795052    AATGGACAAGTATGTTCATTTTCCTCCAAA  1481
                                  * **
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