```
CLUSTAL O(1.2.1) multiple sequence alignment


original        ATGTCCGCAGTAAAAGCAGCCCGCTACGGCAAGGACAATGTCCGCGTCTACAAGGTTCAC      60
optimized       ATGTCTGCCGTCAAAGCTGCCAGATACGGTAAAGACAATGTCAGAGTTTACAAAGTCCAT      60
                ***** ** ** ***** *** * ***** ** ********* * ** ***** ** **

original        AAGGACGAGAAGACCGGTGTCCAGACGGTGTACGAGATGACCGTCTGTGTGCTTCTGGAG      120
optimized       AAGGACGAAAAGACTGGTGTCCAGACCGTTTACGAAATGACTGTCTGCGTCTTGTTGGAG      120
                ******** ***** ********** ** ***** ***** ***** **  *  *****

original        GGTGAGATTGAGACCTCTTACACCAAGGCCGACAACAGCGTCATTGTCGCAACCGACTCC      180
optimized       GGTGAAATCGAAACTTCTTACACAAAGGCCGATAATTCTGTCATCGTTGCCACTGACTCT      180
                ***** ** ** ** ******** ******** **    ***** ** ** ** *****

original        ATTAAGAACACCATTTACATCACCGCCAAGCAGAACCCCGTTACTCCTCCCGAGCTGTTC      240
optimized       ATCAAGAACACCATCTACATCACCGCTAAACAGAACCCAGTTACCCCACCTGAGTTGTTC      240
                ** ********** ********** ** ******** ***** ** ** *** *****

original        GGCTCCATCCTGGGCACACACTTCATTGAGAAGTACAACCACATCCATGCCGCTCACGTC      300
optimized       GGTTCTATCTTGGGTACTCACTTCATTGAGAAATACAACCACATCCATGCCGCCCACGTT      300
                ** ** *** **** ** ************** ******************** *****

original        AACATTGTCTGCCACCGCTGGACCCGGATGGACATTGACGGCAAGCCACACCCTCACTCC      360
optimized       AATATCGTCTGTCACAGATGGACAAGAATGGACATCGACGGAAAGCCTCATCCTCACTCT      360
                ** ** ***** *** * *****  * ******** ***** ***** ** ********

original        TTCATCCGCGACAGCGAGGAGAAGCGGAATGTGCAGGTGGACGTGGTCGAGGGCAAGGGC      420
optimized       TTCATCAGAGACTCTGAGGAGAAAAGAAATGTCCAAGTCGACGTTGTCGAGGGTAAGGGA      420
                ****** * ***   ********  * ***** ** ** ***** ******** *****

original        ATCGATATCAAGTCGTCTCTGTCCGGCCTGACCGTGCTGAAGAGCACCAACTCGCAGTTC      480
optimized       ATTGACATTAAGTCTTCTTTGTCTGGATTGACAGTCTTGAAGTCTACAAATTCTCAGTTT      480
                ** ** ** ***** *** **** **  **** **  *****   ** ** ** *****

original        TGGGGCTTCCTGCGTGACGAGTACACCACACTTAAGGAGACCTGGGACCGTATCCTGAGC      540
optimized       TGGGGTTTCTTGAGAGATGAATACACAACCTTGAAGGAAACCTGGGATAGAATCTTGTCT      540
                ***** *** ** * ** ** ***** **  * ***** ********  * *** **

original        ACCGACGTCGATGCCACTTGGCAGTGGAAGAATTTCAGTGGACTCCAGGAGGTCCGCTCG      600
optimized       ACCGATGTTGACGCCACTTGGCAATGGAAGAACTTTTCTGGTTTGCAGGAGGTCAGATCT      600
                ***** ** ** ********** ******** **   ***  * ********* * **

original        CACGTGCCTAAGTTCGATGCTACCTGGGCCACTGCTCGCGAGGTCACTCTGAAGACTTTT      660
optimized       CACGTTCCTAAGTTCGATGCCACATGGGCAACCGCCAGAGAGGTCACTTTGAAAACTTTC      660
                ***** ************** ** ***** ** **  * ********* **** *****

original        GCTGAAGATAACAGTGCCAGCGTGCAGGCCACTATGTACAAGATGGCAGAGCAAATCCTG      720
optimized       GCCGAAGATAACTCTGCCTCTGTTCAAGCAACCATGTACAAAATGGCCGAGCAGATCTTG      720
                ** *********  ****   ** ** ** ** ******** ***** ***** *** **

original        GCGCGCCAGCAGCTGATCGAGACTGTCGAGTACTCGTTGCCTAACAAGCACTATTTCGAA      780
optimized       GCTAGACAGCAGTTGATTGAAACCGTCGAATACTCTTTGCCAAACAAACACTACTTCGAG      780
                **  * ****** **** ** ** ***** ***** ***** ***** ***** *****

original        ATCGACCTGAGCTGGCACAAGGGCCTCCAAAACACCGGCAAGAACGCCGAGGTCTTCGCT      840
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optimized       ATTGACTTGTCTTGGCACAAGGGTTTGCAGAACACTGGAAAGAATGCAGAGGTTTTCGCT     840
                ** *** **   **********  * ** ***** ** ***** ** ***** ******

original        CCTCAGTCGGACCCCAACGGTCTGATCAAGTGTACCGTCGGCCGGTCCTCTCTGAAGTCT     900
optimized       CCACAGTCTGACCCAAACGGTTTGATTAAGTGCACCGTTGGTAGATCTTCTTTGAAGTCT     900
                ** ***** ***** ****** **** ***** ***** **  * ** *** ********

original        AAATTGT  907
optimized       AAGTTGC  907
                ** ***
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