CLUSTAL 2.1 multiple sequence alignment

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Sulu_1              ------------------------------------------------------------
V1197               ------------------------------------------------------------
CM                  ------------------------------------------------------------
Unigene0038420      TTCAAAACTCTCACCTTTCCTTCTTGTTTTGTTCTTTCTCTTTTTCTCTCACACAAATAC

Sulu_1              --------------ATGGGTTCTTGCAAACCCCAACAAGAACATGTTCATGGACCTATCA
V1197               --------------ATGGGTTCTTGCAAACCCCAACAAGAACATGTTCATGGACCTATCA
CM                  --------------ATGGGTTCTTGCAAACCCCAACAAGAACATGTTCATGGACCTATCA
Unigene0038420      ACCTATCTATCTACATGGGTTCTTGCAAACCCCAACAAGAACATGTTCATGGACCTATCA
                                   ******************************************

Sulu_1              TCATAGGTGCCGGTCCTTCAGGCCTAGCCGTGGCTGCGTGTCTCTCGGAGCACAAAGTCC
V1197               TCATAGGTGCCGGTCCTTCAGGCCTAGCCGTGGCTGCGTGTCTCTCGGAGCACAAAGTCC
CM                  TCATAGGTGCCGGTCCTTCAGGCCTAGCCGTGGCTGCGTGTCTCTCGGAGCACAAAGTCC
Unigene0038420      TCATAGGTGCCGGTCCTTCAGGCCTAGCCGTGGCTGCGTGTCTCTCGGAGCACAAAGTCC
                    ************************************************************

Sulu_1              CTTTCGTGATTCTTGAGAGAAGCAACTGCATAGCCTCTCTTTGGCAACACAAAACCTACG
V1197               CTTTCGTGATTCTTGAGAGAAGCAACTGCATAGCCTCTCTTTGGCAACACAAAACCTACG
CM                  CTTTCGTGATTCTTGAGAGAAGCAACTGCATAGCCTCTCTTTGGCAACACAAAACCTACG
Unigene0038420      CTTTCGTGATTCTTGAGAGAAGCAACTGCATAGCCTCTCTTTGGCAACACAAAACCTACG
                    ************************************************************

Sulu_1              ACCGTCTCAAACTCCACCTCCCAAAGCAGTTCTGCGAGCTTCCCTTGAAAGGTTTTCCCC
V1197               ACCGTCTCAAACTCCACCTCCCAAAGCAGTTCTGCGAGCTTCCCTTGAAAGGTTTTCCCC
CM                  ACCGTCTCAAACTCCACCTCCCAAAGCAGTTCTGCGAGCTTCCCTTGAAAGGTTTTCCCC
Unigene0038420      ACCGTCTCAAACTCCACCTCCCAAAGCAGTTCTGCGAGCTTCCCTTGAAAGGTTTTCCCC
                    ************************************************************

Sulu_1              ACAACTTCCCCAAGTACCCCACAAAGTACCAGTTCATATCCTACATGGAGTCCTACGCCT
V1197               ACAACTTCCCCAAGTACCCCACAAAGTACCAGTTCATATCCTACATGGAGTCCTACGCCT
CM                  ACAACTTCCCCAAGTACCCCACAAAGTACCAGTTCATATCCTACATGGAGTCCTACGCCT
Unigene0038420      ACAACTTCCCCAAGTACCCCACAAAGTACCAGTTCATATCCTACATGGAGTCCTACGCCT
                    ************************************************************

Sulu_1              CACACTTCAACATCCACCCCAGGTTCAACCAAACAGTCGAAACTGCTCACTTTGATAAAG
V1197               CACACTTCAACATCCACCCCAGGTTCAACCAAACAGTCGAAACTGCTCACTTTGATAAAG
CM                  CACACTTCAACATCCACCCCAGGTTCAACCAAACAGTCGAAACTGCTCACTTTGATAAAG
Unigene0038420      CACACTTCAACATCCACCCCAGGTTCAACCAAACAGTCGAAACTGCTCACTTTGATAAAG
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Sulu_1          CCTCTCAGCTTTGGCTCGTTAGGACTCAGCACTGTCAGCTTCTCTCTCCTTGGCTCGTCG
V1197           CCTCTCAGCTTTGGCTCGTTAGGACTCAACACTGTGAGCTTCTCTCTCCTTGGCTCGTGG
CM              CCTCTCAGCTTTGGCTCGTTAGGACTCAACACTGTGAGCTTCTCTCTCCTTGGCTCGTGG
Unigene0038420  CCTCTCAGCTTTGGCTCGTTAGGACTCAACACTGTGAGCTTCTCTCTCCTTGGCTCGTGG
                *************************** ****** ******************** *

Sulu_1          TGGCCACCGGGGAGAATGCTGAGCCTGTGCTTCCTAGAATTCATGGCATGGACCATTTCT
V1197           TGGCCACCGGGGAGAATGCTGAGCCTGTGCTTCCTAGAATTCATGGCATGGACCATTTTT
CM              TGGCCACCGGGGAGAATGCTGAGCCTGTGCTTCCTAGAATTCATGGCATGGACCATTTTT
Unigene0038420  TGGCCACCGGGGAGAATGCTGAGCCTGTGCTTCCTAGAATTCATGGCATGGACCATTTTT
                ******************************************************** *

Sulu_1          CTGGCTCCATTGCTCACACCAGTGTCTACAAGTCTGGCTCTGAGTACACAAACCAGAAGG
V1197           CTGGCTCCATTGCTCACACCAGTGTCTACAAGTCTGGCTCTGAGTACACAAACCAGAAGG
CM              CTGGCTCCATTGCTCACACCAGTGTCTACAAGTCTGGCTCTGAGTACACAAACCAGAAGG
Unigene0038420  CTGGCTCCATTGCTCACACCAGTGTCTACAAGTCTGGCTCTGAGTACACAAACCAGAAGG
                ************************************************************

Sulu_1          TTCTCGTCATTGGCTGTGGCAATTCAGGAATGGAAGTTAGCTTAGACCTTTGCAGACACA
V1197           TTCTCGTCATTGGCTGTGGCAATTCAGGAATGGAAGTTAGCTTAGACCTTTGCAGACACA
CM              TTCTCGTCATTGGCTGTGGCAATTCAGGAATGGAAGTTAGCTTAGACCTTTGCAGACACA
Unigene0038420  TTCTCGTCATTGGCTGTGGCAATTCAGGAATGGAAGTTAGCTTAGACCTTTGCAGACACA
                ************************************************************

Sulu_1          ATGCCTCCCCTTACATGGTTGCAAGGAACACAGTGCATGTCCTTCCTAGGGAGATGTTTG
V1197           ATGCCTCCCCTTACATGGTTGCAAGGAACACAGTGCATGTCCTTCCTAGGGAGATGTTTG
CM              ATGCCTCCCCTTACATGGTTGCAAGGAACACAGTGCATGTCCTTCCTAGGGAGATGTTTG
Unigene0038420  ATGCCTCCCCTTACATGGTTGCAAGGAACACAGTGCATGTCCTTCCTAGGGAGATGTTTG
                ************************************************************

Sulu_1          GCTTCTCAACTTTTGGCATAGCCATGGCTCTTTACAAGTGGTTTCCCATCAAAGTTGTAG
V1197           GCTTCTCAACTTTTGGCATAGCCATGGCTCTTTACAAGTGGTTTCCCATCAAAGTTGTAG
CM              GCTTCTCAACTTTTGGCATAGCCATGGCTCTTTACAAGTGGTTTCCCATCAAAGTTGTAG
Unigene0038420  GCTTCTCAACTTTTGGCATAGCCATGGCTCTTTACAAGTGGTTTCCCATCAAAGTTGTAG
                ************************************************************

Sulu_1          ACAAAATTCTCTTACTTGTGACCAACTTCATGTTGGGAAACACAAATCACTATGGCATCA
V1197           ACAAAATTCTCTTACTTGTGACCAACTTCATGCTGGGAAACACAAATCACTATGGCATCA
CM              ACAAAATTCTCTTACTTGTGACCAACTTCATGCTGGGAAACACAAATCACTATGGCATCA
Unigene0038420  ACAAAATTCTCTTACTTGTGACCAACTTCATGCTGGGAAACACAAATCACTATGGCATCA
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Sulu_1          AAAGGCCTAAAACAGGCCCAATAGAGCTGAAACTAGCCACAGGGAAAACCCCAGTCCTTG
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V1197              AAAGGCCTAAAACAGGTCCAATAGAGCTGAAACTAGCCACAGGGAAAACCCCAGTCCTTG
CM                 AAAGGCCTAAAACAGGTCCAATAGAGCTGAAACTAGCCACAGGGAAAACCCCAGTCCTTG
Unigene0038420     AAAGGCCTAAAACAGGTCCAATAGAGCTGAAACTAGCCACAGGGAAAACCCCAGTCCTTG
                   *************** ****************************************

Sulu_1             ATGTGGGTCAAGTTGCACAGATCAAATGTGGCAACATAAAGGTGATGGAAGGTGTGAAGG
V1197              ATGTGGGTCAAGTTGCACAGATCAAATGTGGCAACATAAAGGTGATGGAAGGTGTGAAGG
CM                 ATGTGGGTCAAGTTGCACAGATCAAATGTGGCAACATAAAGGTGATGGAAGGTGTGAAGG
Unigene0038420     ATGTGGGTCAAGTTGCACAGATCAAATGTGGCAACATAAAGGTGATGGAAGGTGTGAAGG
                   ************************************************************

Sulu_1             AGATAACTAGAAAAGGTGCGAAATTTATGGATGGACAAGAAAAGGAATTTGATGCTATAA
V1197              AGATAACAAGAAAAGGTGCGAAATTTATGGATGGACAAGAAAAGGAATTTGATGCTATAA
CM                 AGATAAC-AGAAAAGGTGCGAAATTTATGGATGGACAAGAAAAGGAATTTGATGCTATAA
Unigene0038420     AGATAAC-AGAAAAGGTGCGAAATTTATGGATGGACAAGAAAAGGAATTTGATGCTATAA
                   ******* ****************************************************

Sulu_1             TATTGGCAACAGGGTACAAGAGCAACGTGCCTGCTTGGCTTAAGGGTTGTGATTTTTTCA
V1197              TATTGGCAACAGGGTACAAGAGCAACGTGCCTGCTTGGCTTAAGGGTTGTGATTTTTTCA
CM                 TATTGGCAACAGGGTACAAGAGCAACGTGCCTGCTTGGCTTAAGGGTTGTGATTTTTTCA
Unigene0038420     TATTGGCAACAGGGTACAAGAGCAACGTGCCTGCTTGGCTTAAGGGTTGTGATTTTT---
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Sulu_1             CTGAGGATGGAATGCCGAAAACACCCTTTCCCCATGGGTGGAAAGGGGAGCAGGGATTGT
V1197              CTGAGGATGGAATGCCGAAAACACCCTTTCCCCATGGGTGGAAAGGGGAGCAGGGATTGT
CM                 CTGAGGATGGAATGCCGAAAACACCCTTTCCCCATGGGTGGAAAGGGGAGCAGGGATTGT
Unigene0038420     ------------------------------------------------------------

Sulu_1             ATACGGTGGGGTTCACCAGAAGAGGCATTCAAGGAACATCTTGTGATGCAATCAAGATCG
V1197              ATACGGTGGGGTTCACCAGAAGAGGCATTCAAGGAACATCTTGTGATGCAATCAAGATCG
CM                 ATACGGTGGGGTTCACCAGAAGAGGCATTCAAGGAACATCTTGTGATGCAATCAAGATCG
Unigene0038420     ------------------------------------------------------------

Sulu_1             CTGAAGACATAGCCTCGCAGTGGAGAACCGTAGAGAACAAGAATCAATGCAATTCACATA
V1197              CTGAAGACATAGCCTCGCAGTGGAGAACCGTAGAGAACAAGAATCAATGCAATTCACATA
CM                 CTGAAGACATAGCCTCGCAGTGGAGAACCGTAGAGAACAAGAATCAATGCAATTCACATA
Unigene0038420     ------------------------------------------------------------

Sulu_1             TCATCCTTCTCACTTCATAA
V1197              TCATCCTTCTCACTTCATAA
CM                 TCATCCTTCTCACTTCATAA
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Unigene0038420 ----------