Ciona intestinalis EST Clones: Heart

RIKEN clone ID: CiAD062K07
Vector : pBluescript II SK(−)

5'-EST	KhC10: 531736..532247
3'-EST	KhC10: 531388..532116

●Plasmid DNA purification

Date : 110421 Culture : LB (100 ug/ml Ampicillin) 3 ml →37°C O/N

Date : 110422 Purification : QIAGEN Miniprep kit→dH_2O 100 ul

●Digestion by restriction enzyme / Concentration calibration

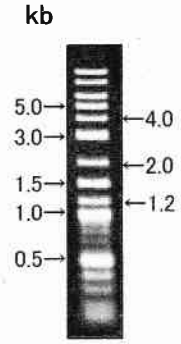
Date : 110422

DNA concentration (O.D.): 196.01 ng/ul

DNA	0.5 ul
Enzyme (Pst I +KpnI)	0.5+0.5 ul
Buffer M	1 ul
dH_2O	7.5 ul
Total	10 ul

Electrophoresis: 1% agarose gel, 1 × TAE Buffer

Marker: 2-Log DNA Ladder (NEB#N3200L)



<Expected digestion pattern >

878, 2905 bp

●Adjust plasmid DNA solution to 25 ng/ul ～preparation for shipping～

Date : 110509 Shipped : 25 ng/ul, 40 ul

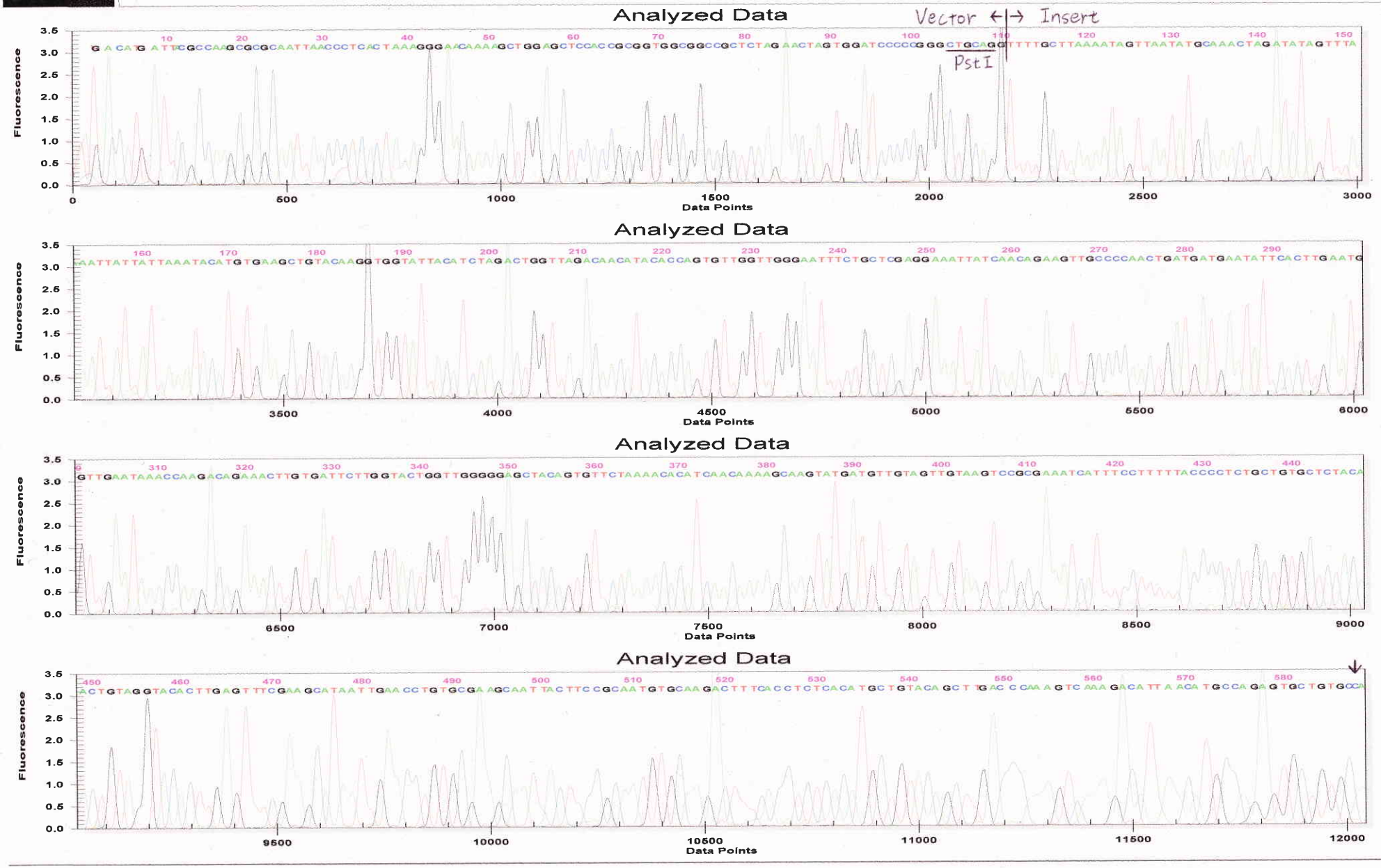
Final concentration: 25 ng/ul

DNA (196.01 ng/ul)	86.0	ul
10 × TE	67.4	ul
dH_2O	520.9	ul
Total	674.3	ul

Project : GNP
Sample : 6730_CiAD062K07_Reverse2.A07_11042810QX
Result : 6730_CiAD062K07_Reverse2.A07_11042810QX

System : System 1

Operator : 1.110428.furu
Instrument : System 1 (Ver. 9.0.25)

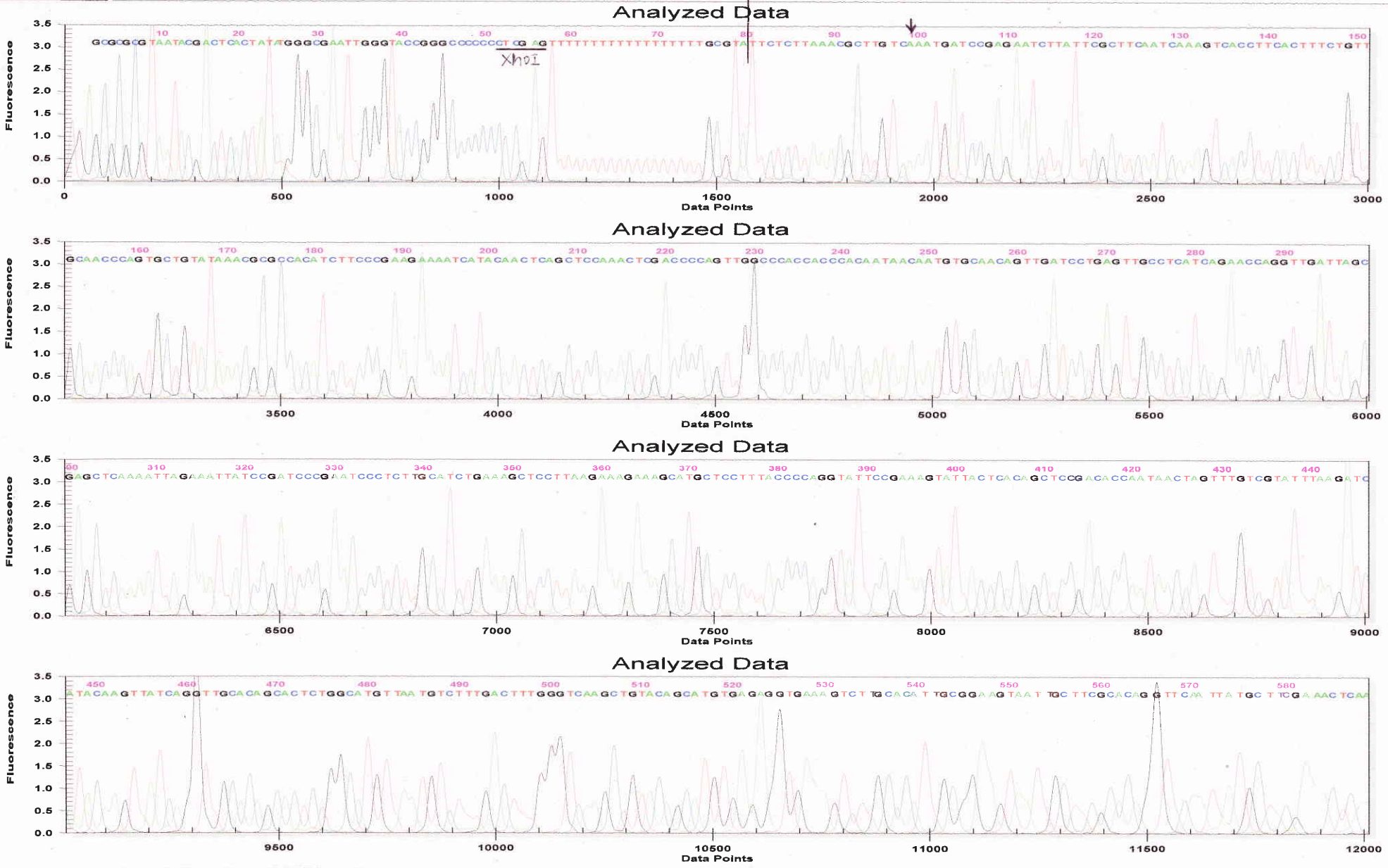


Project : GNP
Sample : 6730_CiAD062K07_M13.B07_11042810QX
Result : 6730_CiAD062K07_M13.B07_11042810QX

System : System 1

Operator : 1.110428.furu
Instrument : System 1 (Ver. 9.0.25)

Vector ← | → Insert



[GENETYX : Homology Data]

Date : 2011.04.28

Query Sequence
  File Name :
  Sequence Name : ciad062k07_5EST
  Sequence Size : 512

Target Sequence
  File Name : 6730_CiAD062K07_Reverse2.A07_11042810QX
  Sequence Name : 6730_CiAD062K07_Reverse2.A07_11042810QX
  Sequence Size : 697

  Unit Size to Compare = 6
  Pick up Location No. = 1

Query Range: 1 - 512
Sbjct Range: 110 - 621
512 bp, INT.Score: 2042, OPT.Score: 2042
Identity: 511 / 512 (99%)
Strand: Plus / Plus

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Query  1    TTTTGCTTAA AATAGTTAAT ATGCAAACTA GATATAGTTT AAAATTATTA TTAAATACAT  60
            |||||||||| |||||||||| |||||||||| |||||||||| |||||||||| ||||||||||
Sbjct  110  TTTTGCTTAA AATAGTTAAT ATGCAAACTA GATATAGTTT AAAATTATTA TTAAATACAT  169

Query  61   GTGAAGCTGT ACAAGGTGGT ATTACATCTA GACTGGTTAG ACAACATACA CCAGTGTTGG  120
            |||||||||| |||||||||| |||||||||| |||||||||| |||||||||| ||||||||||
Sbjct  170  GTGAAGCTGT ACAAGGTGGT ATTACATCTA GACTGGTTAG ACAACATACA CCAGTGTTGG  229

Query  121  TTGGGAATTT CTGCTCGAGG AAATTATCAA CAGAAGTTGC CCCAACTGAT GATGAATATT  180
            |||||||||| |||||||||| |||||||||| |||||||||| |||||||||| ||||||||||
Sbjct  230  TTGGGAATTT CTGCTCGAGG AAATTATCAA CAGAAGTTGC CCCAACTGAT GATGAATATT  289

Query  181  CACTTGAATG GTTGAATAAA CCAAGACAGA AACTTGTGAT TCTTGGTACT GGTTGGGGGA  240
            |||||||||| |||||||||| |||||||||| |||||||||| |||||||||| ||||||||||
Sbjct  290  CACTTGAATG GTTGAATAAA CCAAGACAGA AACTTGTGAT TCTTGGTACT GGTTGGGGGA  349

Query  241  GCTACAGTGT TCTAAAACAC ATCAACAAAA GCAAGTATGA TGTTGTAGTT GTAAGTCCGC  300
            |||||||||| |||||||||| |||||||||| |||||||||| |||||||||| ||||||||||
Sbjct  350  GCTACAGTGT TCTAAAACAC ATCAACAAAA GCAAGTATGA TGTTGTAGTT GTAAGTCCGC  409

Query  301  GAAATCATTT CCTTTTTACC CCTCTGCTGT GCTCTACAAC TGTAGGTACA CTTGAGTTTC  360
            |||||||||| |||||||||| |||||||||| |||||||||| |||||||||| ||||||||||
Sbjct  410  GAAATCATTT CCTTTTTACC CCTCTGCTGT GCTCTACAAC TGTAGGTACA CTTGAGTTTC  469

Query  361  GAAGCATAAT TGAACCTGTG CGAAGCAATT ACTTCCGCAA TGTGCAAGAC TTTCACCTCT  420
            |||||||||| |||||||||| |||||||||| |||||||||| |||||||||| ||||||||||
Sbjct  470  GAAGCATAAT TGAACCTGTG CGAAGCAATT ACTTCCGCAA TGTGCAAGAC TTTCACCTCT  529

Query  421  CACATGCTGT ACAGCTTGAC CCAAAGTCAA AGACATTAAC ATGCCAGAGT GCTGTGCAAC  480
            |||||||||| |||||||||| |||||||||| |||||||||| |||||||||| ||||||| ||
Sbjct  530  CACATGCTGT ACAGCTTGAC CCAAAGTCAA AGACATTAAC ATGCCAGAGT GCTGTGCCAC  589

Query  481  CTGATAACTT GTATGATCTT AAATACGACA AA  512
            |||||||||| |||||||||| |||||||||| ||
Sbjct  590  CTGATAACTT GTATGATCTT AAATACGACA AA  621
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[GENETYX : Homology Data]

Date : 2011.04.28

Query Sequence
  File Name :
  Sequence Name : ciad062k07_3EST
  Sequence Size : 729

Target Sequence
  File Name : 6730_CiAD062K07_M13.B07_11042810QX
  Sequence Name : 6730_CiAD062K07_M13.B07_11042810QX
  Sequence Size : 700

  Unit Size to Compare = 6
  Pick up Location No. = 1

Query Range: 2 - 618
Sbjct Range: 80 - 700
621 bp, INT.Score: 2188, OPT.Score: 2405
Identity: 614 / 621 (98%)
Strand: Plus / Plus

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Query  2    TTCTCTTAAA CGCTTGTC-A ATGATCCGAG AATCTTATTC GCTTCAATCA AAGTCACCTT  60
            |||||||||| |||||||| | |||||||||| |||||||||| |||||||||| ||||||||||
Sbjct  80   TTCTCTTAAA CGCTTGTCAA ATGATCCGAG AATCTTATTC GCTTCAATCA AAGTCACCTT  139

Query  61   CACTTTCTGT TGCAACCCAG TGCTGTATAA ACGCGCCACA TCTTCCCGAA GAAAATCATA  120
            |||||||||| |||||||||| |||||||||| |||||||||| |||||||||| ||||||||||
Sbjct  140  CACTTTCTGT TGCAACCCAG TGCTGTATAA ACGCGCCACA TCTTCCCGAA GAAAATCATA  199

Query  121  CAACTCAGCT CCAAACTCGA CCCCAGTTGG CCCACCACCC ACAATAACAA TGTGCAACAG  180
            |||||||||| |||||||||| |||||||||| |||||||||| |||||||||| ||||||||||
Sbjct  200  CAACTCAGCT CCAAACTCGA CCCCAGTTGG CCCACCACCC ACAATAACAA TGTGCAACAG  259

Query  181  TTGATCCTGA GTTGCCTCAT CAGAACCAGG TTGATTAGCG AGCTCAAAAT TAGAAATTAT  240
            |||||||||| |||||||||| |||||||||| |||||||||| |||||||||| ||||||||||
Sbjct  260  TTGATCCTGA GTTGCCTCAT CAGAACCAGG TTGATTAGCG AGCTCAAAAT TAGAAATTAT  319

Query  241  CCGATCCCGA ATCCCTCTTG CATCTGAAAG CTCCTTAAGA AAGAAAGCAT GCTCCTTTAC  300
            |||||||||| |||||||||| |||||||||| |||||||||| |||||||||| ||||||||||
Sbjct  320  CCGATCCCGA ATCCCTCTTG CATCTGAAAG CTCCTTAAGA AAGAAAGCAT GCTCCTTTAC  379

Query  301  CCCAGGTATT CCGAAAGTAT TACTCACAGC TCCGACACCA ATAACTAGTT TGTCGTATTT  360
            |||||||||| |||||||||| |||||||||| |||||||||| |||||||||| ||||||||||
Sbjct  380  CCCAGGTATT CCGAAAGTAT TACTCACAGC TCCGACACCA ATAACTAGTT TGTCGTATTT  439

Query  361  AAGATCATAC AAGTTATCAG GTTGCACAGC ACTCTGGCAT GTTAATGTCT TTGACTTTGG  420
            |||||||||| |||||||||| |||||||||| |||||||||| |||||||||| ||||||||||
Sbjct  440  AAGATCATAC AAGTTATCAG GTTGCACAGC ACTCTGGCAT GTTAATGTCT TTGACTTTGG  499

Query  421  GTCAAGCTGT ACAGCATGTG AGAGGTGAAA GTCTTGCACA TTGCGGAAGT AATTGCTTCG  480
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Sbjct  500  GTCAAGCTGT ACAGCATGTG AGAGGTGAAA GTCTTGCACA TTGCGGAAGT AATTGCTTCG  559

Query  481  CACAGGTTCA ATTATGCTTC GAAACTCAAG TGTACCTACA GTTGTAGAGC ACAGCAGAGG  540
            |||||||||| |||||||||| |||||||||| |||||||||| |||||||||| ||||||||||
Sbjct  560  CACAGGTTCA ATTATGCTTC GAAACTCAAG TGTACCTACA GTTGTAGAGC ACAGCAGAGG  619

Query  541  GGTAAAAAGG AAATGATTTC GCGGACTTAC -AACTACAAC ATCATA-CTT G-CTTTTGTT  597
            |||||||||| |||||||||| |||||| ||| |||||||||| |||||| || | ||||.|||
Sbjct  620  GGTAAAAAGG AAATGATTTC GCGGACCTAC AAACTACAAC ATCATACCTG GCCTTTNGTT  679

Query  598  GATGTGTTTT AGAACACTGT A  618
            |||||||||| |||||||||| |
Sbjct  680  GATGTGTTTT AGAACACTGT A  700
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