Fig.1

```
SEQID22     MLLLGAVLLLLALPGHDQETTTQGPGVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDG 60
SEQID23     ------------------------------------------------------------
SEQID24     MLLLGAVLLLLALPGHDQETTTQGPGVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDG 60
SEQID25     MLLLGAVLLLLALPGHDQETTTQGPGVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDG 60

SEQID22     TPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLE 120
SEQID23     ------------------------MPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLE 36
SEQID24     TPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGA------------ 108
SEQID25     TPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLE 120

SEQID22     TYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVSLFKKDK 180
SEQID23     TYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVSLFKKDK 96
SEQID24     ------------------------------------------------------------ 108
SEQID25     TYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLY---------------------- 158

SEQID22     AMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYAD--NDND-STFTGF 237
SEQID23     AMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYAD--NDND-STFTGF 153
SEQID24     ----------------------LLS-PTCPFALPRSSTISKTTMMAP--LVNSTATFLGC 143
SEQID25     ------------------------------------------------------------ 158

SEQID22     LLYHDTN---------- 244
SEQID23     LLYHDTN---------- 160
SEQID24     T----T-LP-TTSQSI- 153
SEQID25     ---------LHRLSSLP 166
```

Fig. 2

```
SEQID28   MLLLQALLFLLILPSHAEDDVTTTEELAPALVPPPKGTCAGWMAGIPGHPGHNGTPGRDG 60
SEQID30   MLLLQALLFLLILPSHAEDDVTTTEELAPALVPPPKGTCAGWMAGIPGHPGH-------- 52
SEQID29   MLLLQALLFLLILPSHAEDDVTTTEELAPALVPPPKGTCAGWMAGIPGHPGHNGTPGRDG 60
SEQID26   MLLLQALLFLLILPSHAEDDVTTTEELAPALVPPPKGTCAGWMAGIPGHPGHNGTPGRDG 60
SEQID27   ------------------------------------------------------------

SEQID28   ---TPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPGTPGRKGEPGEAA-------SL 113
SEQID30   ------------------------------------------------------------ 52
SEQID29   ---TPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPGTPGRKGEPGEAAY-------- 110
SEQID26   RDGTPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPGTPGRKGEPGEAAYMYRSAFSV 120
SEQID27   ----------------------------MTGAEGPRGFPGTPGRKGEPGEAAYVYRSAFSV 33

SEQID28   ------------------------------------------------------------ 109
SEQID30   ------------------------------------------------------------ 52
SEQID29   ------------------------------------------------------------ 110
SEQID26   GLETRVTVPNVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSYHITVYMKDVKVSLFK 180
SEQID27   GLETRVTVPNVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSYHITVYMKDVKVSLFK 93

SEQID28   ------------------------------------------------------------FPMYP 118
SEQID30   ----------------IKIK-------FEGHP-----PG---------------------- 63
SEQID29   ----------------------------------------VYRSAFSVGLETRVTVP 129
SEQID26   KDKAVLFTYDQYQEKNVDQA--------SGSVLLHLEVGDQVWLQ---------------- 217
SEQID27   KDKAVLFTYDQYQEKNVDQA--------SGSVLLHLEVGDQVWLQ---------------- 130

SEQID28   FALLRSSTTNRIIMTAALASSTATFRDSTTSLTTSRCT--- 156
SEQID30   --RLNCAKIWHFLQD------------------------- 76
SEQID29   NVPIRFTKIFYNQQN-HYDGSTGKFYCNIPGLYIYWLSSLP 169
SEQID26   --VYGDGDHNGLYADNVNDSTFTGFLLYHDTN---------- 247
SEQID27   --VYGDGDHNGLYADNVNDSTFTGFLLYHDTN---------- 160
```

Fig. 3

```
SEQID31         MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP---------------- 44
SEQID32         MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP-------------HVV 47

SEQID31         PAKLQPRALAGWLRPEDGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQD 104
SEQID32         PALPLSNQLCDLEQQRHWASVFSQSTKDSGSDLTVSGRTWGLRV---------------- 91

SEQID31         ILWEEAKEAPADK------------ 117
SEQID32         LNRLFPPSSRERSRRSHQPSCSPEL 116
```

Fig. 4

```
SEQID33   MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAYHLAKMGAH 60
SEQID38   ------------------------------MLQGKKVIVTGASKGIGREMAYHLAKMGAH 30
SEQID36   MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAYHLAKMGAH 60
SEQID35   MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAYHLAKMGAH 60
SEQID37   MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAYHLAKMGAH 60
SEQID39   MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAYHLAKMGAH 60
SEQID34   MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAYHLAKMGAH 60

SEQID33   VVVTARSKETLQKVVSHCLELGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLILNH 120
SEQID38   VVVTARSKETLQKVVSHCLELGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLILNH 90
SEQID36   VVVTARSKETLQKVVSHCLELGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLILNH 120
SEQID35   VVVTARSKETLQKVVSHCLELGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLILNH 120
SEQID37   VVVTASS------------------AHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLILNH 102
SEQID39   VVVTARSKETLQKVVSHCLELGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLILNH 120
SEQID34   VVVTASS------------------AHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLILNH 102

SEQID33   ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAALPMLKQSNGSIVVVSSLAGKVAYPMV 180
SEQID38   ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAALPMLKQSNGSIVVVSSLAGKVAYPMV 150
SEQID36   ITNTSLNLFHDDIHHVR------------------PMLKQSNGSIVVVSSLAGKVAYPMV 162
SEQID35   ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAALPMLKQSNGSIVVVSSLAGKVAYPMV 180
SEQID37   ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAALPMLKQSNGSIVVVSSLAGKVAYPMV 162
SEQID39   ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAALPMLKQSNGSIVVVSSLA-------- 172
SEQID34   ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAALPMLKQSNGSMCAL------------ 150

SEQID33   AAYSASKFALDGFFSSIRKEYSVSRVNVSITLCVLGLIDTETAMKAVSGIVHMQAAPKEE 240
SEQID38   AAYSASKFALDGFFSSIRKEYSVSRVNVSITLCVLGLIDTETAMKAVSGIVHMQAAPKEE 210
SEQID36   AAYSASKFALDGFFSSIRKEYSVSRVNVSITLCVLGLIDTETAMKAVSGIVHMQAAPKEE 222
SEQID35   AAYSASKFALDGFFSSIRKEYSVSRVNVSITLCVLGLIDTETAMKAVSGIVHMQAAPKEE 240
SEQID37   AAYSASKFALDGFFSSIRKEYSVSRVNVSITLCVLGLIDTETAMKAVSGIVHMQAAPKEE 222
SEQID39   ------------------------------------------ETAMKAVSGIVHMQAAPKEE 192
SEQID34   ------------------------------------------LLECYHVVHLSSX---- 163

SEQID33   CALEIIKGGALRQEEVYYDSSLWTTLLIRNPCRKILEFLYSTSYNMDRFINK--- 292
SEQID38   CALEIIKGGALRQEEVYYDSSLWTTLLIRNPCRKILEFLYSTSYNMDRFINK--- 262
SEQID36   CALEIIKGGALRQEEVYYDSSLWTTLLIRNPCRKILEFLYSTSYNMDRFINK--- 274
SEQID35   CALEIIKGGALRQEEVYYDSSLWTTLLIRNPCRKILEFLYSTSYNMEGLFCLMFI 295
SEQID37   CALEIIKGGALRQEEVYYDSSLWTTLLIRNPCRKILEFLYSTSYNMDRFINK--- 274
SEQID39   CALEIIKGGALRQEEVYYDSSLWTTLLIRNPCRKILEFLYSTSYNMDRFINK--- 244
SEQID34   ---------------------------------------------------------
```

Fig. 5

```
SEQID40         MAVMKNYLLPILVLFLAYYYYSTNEEFRPEMLQGKKVIVTGASKGIGREMAYHLSKMGAH 60
SEQID41         MAVMKNYLLPILVLFLAY------------------------------------------ 18
SEQID42         MAVMKNYLLPILVLFLAYYYYSTNEEFRPEMLQGKKVIVTGASKGIGREMAYHLSKMGAH 60

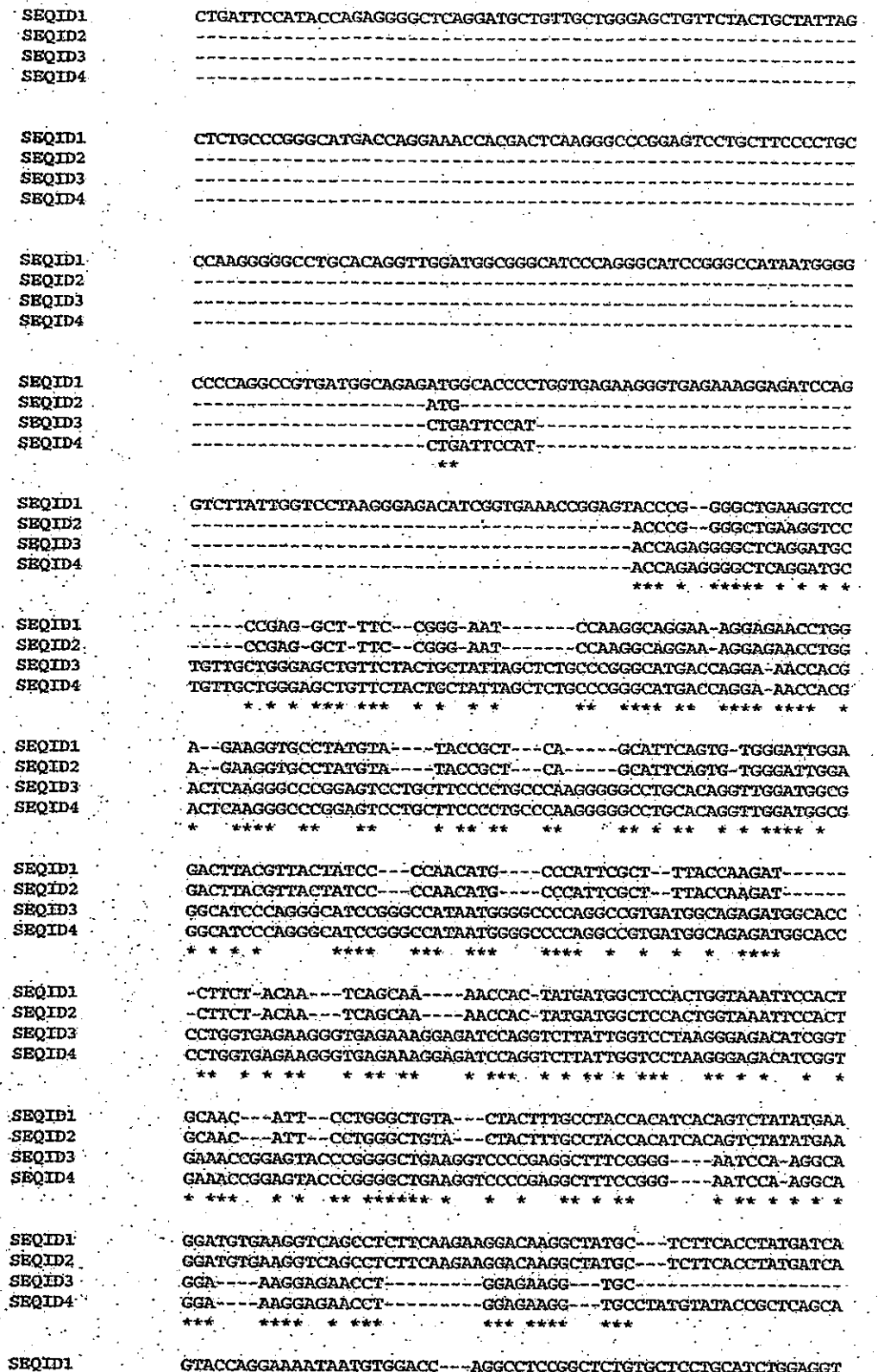
SEQID40         VVLTARSEEGLQKVVSRCLELGAASAHYIAGTMEDMTFAEQFIVKAGKLMGGLDMLILNH 120
SEQID41         YYYSTNEEFRLQKVVSRCLELGAASAHYIAGTMEDMTFAEQFIVKAGKLMGGLDMLILNH 78
SEQID42         VVLTARSEEGLQKVVSRCLELGAASAHYIAGTMEDMTFAEQFIVKAGKLMGGLDMLILNH 120

SEQID40         ITQTSLSLFHDDIHSVRRVMEVNFLSYVVMSTAALPMLKQSNGSIAVISSLAGKMTQPMI 180
SEQID41         ITQTSLSLFHDDIHSVRRVMEVNFLSYVVMSTAALPMLKQSNGSIAVISSLAGKMTQPMI 138
SEQID42         ITQTSLSLFHDDIHSVRRVMEVNFLSYVVMSTAALPMLKQSNGSIAVISSLAGGRTVPQQ 180

SEQID40         APYSASKFALDGFFSTIRTELYITKVNVSITLCVLGLIDTETAMKEISGIINAQASPKEE 240
SEQID41         APYSASKFALDGFFSTIRTELYITKVNVSITLCVLGLIDTETAMKEISGIINAQASPKEE 198
SEQID42         RSRSVTPDSRGP------------------------------------------------ 192

SEQID40         CALEIIKGTALRKSEVYYDKSPLTPILLGNPGRKIMEFFSLRYYNKDMFVSN 292
SEQID41         CALEIIKGTALRKSEVYYDKSPLTPILLGNPGRKIMEFFSLRYYNKDMFVSN 250
SEQID42         ------------------------------------------------------
```

Fig. 6


SEQID1 CTGATTCCATACCAGAGGGGCTCAGGATGCTGTTGCTGGGAGCTGTTCTACTGCTATTAG
SEQID2 ----------
SEQID3 ----------
SEQID4 ----------
SEQID1 CTCTGCCCGGGCATGACCAGGAAACCACGACTCAAGGGCCCGGAGTCCTGCTTCCCCTGC
SEQID2 ----------
SEQID3 ----------
SEQID4 ----------
SEQID1 CCAAGGGGGCCTGCACAGGTTGGATGGCGGGCATCCCAGGGCATCCGGGCCATAATGGGG
SEQID2 ----------
SEQID3 ----------
SEQID4 ----------
SEQID1 CCCCAGGCCGTGATGGCAGAGATGGCACCCCTGGTGAGAAGGGTGAGAAAGGAGATCCAG
SEQID2 ----------ATG----------
SEQID3 ----------CTGATTCCAT----------
SEQID4 ----------CTGATTCCAT----------
** *
SEQID1 GTCTTATTGGTCCTAAGGGAGACATCGGTGAAACCGGAGTACCCG--GGGCTGAAGGTCC
SEQID2 ----------ACCCG--GGGCTGAAGGTCC
SEQID3 ----------ACCAGAGGGGCTCAGGATGC
SEQID4 ----------ACCAGAGGGGCTCAGGATGC
*** * ***** * * * *
SEQID1 -----CCGAG-GCT-TTC--CGGG-AAT-------CCAAGGCAGGAA-AGGAGAACCTGG
SEQID2 -----CCGAG-GCT-TTC--CGGG-AAT-------CCAAGGCAGGAA-AGGAGAACCTGG
SEQID3 TGTTGCTGGGAGCTGTTCTACTGCTATTAGCTCTGCCCGGGCATGACCAGGA-AACCACG
SEQID4 TGTTGCTGGGAGCTGTTCTACTGCTATTAGCTCTGCCCGGGCATGACCAGGA-AACCACG
* * * *** *** * * * * ** **** ** **** **** *
SEQID1 A--GAAGGTGCCTATGTA----TACCGCT---CA-----GCATTCAGTG-TGGGATTGGA
SEQID2 A--GAAGGTGCCTATGTA----TACCGCT---CA-----GCATTCAGTG-TGGGATTGGA
SEQID3 ACTCAAGGGCCCGGAGTCCTGCTTCCCCTGCCCAAGGGGGCCTGCACAGGTTGGATGGCG
SEQID4 ACTCAAGGGCCCGGAGTCCTGCTTCCCCTGCCCAAGGGGGCCTGCACAGGTTGGATGGCG
* **** ** ** * ** ** ** ** * ** * * **** *
SEQID1 GACTTACGTTACTATCC---CCAACATG----CCCATTCGCT--TTACCAAGAT------
SEQID2 GACTTACGTTACTATCC---CCAACATG----CCCATTCGCT--TTACCAAGAT------
SEQID3 GGCATCCCAGGGCATCCGGGCCATAATGGGGCCCCAGGCCGTGATGGCAGAGATGGCACC
SEQID4 GGCATCCCAGGGCATCCGGGCCATAATGGGGCCCCAGGCCGTGATGGCAGAGATGGCACC
* * * * **** *** *** **** * * * * ****
SEQID1 -CTTCT-ACAA---TCAGCAA----AACCAC-TATGATGGCTCCACTGGTAAATTCCACT
SEQID2 -CTTCT-ACAA---TCAGCAA----AACCAC-TATGATGGCTCCACTGGTAAATTCCACT
SEQID3 CCTGGTGAGAAGGGTGAGAAAGGAGATCCAGGTCTTATTGGTCCTAAGGGAGACATCGGT
SEQID4 CCTGGTGAGAAGGGTGAGAAAGGAGATCCAGGTCTTATTGGTCCTAAGGGAGACATCGGT
** * * ** * ** ** * *** * * ** * *** ** * * * * *
SEQID1 GCAAC---ATT--CCTGGGCTGTA---CTACTTTGCCTACCACATCACAGTCTATATGAA
SEQID2 GCAAC---ATT--CCTGGGCTGTA---CTACTTTGCCTACCACATCACAGTCTATATGAA
SEQID3 GAAACCGGAGTACCCGGGGCTGAAGGTCCCCGAGGCTTTCCGGG----AATCCA-AGGCA
SEQID4 GAAACCGGAGTACCCGGGGCTGAAGGTCCCCGAGGCTTTCCGGG----AATCCA-AGGCA
* *** * * ** ****** * * * ** * ** * ** * * * *
SEQID1 GGATGTGAAGGTCAGCCTCTTCAAGAAGGACAAGGCTATGC---TCTTCACCTATGATCA
SEQID2 GGATGTGAAGGTCAGCCTCTTCAAGAAGGACAAGGCTATGC---TCTTCACCTATGATCA
SEQID3 GGA----AAGGAGAACCT----------GGAGAAGG---TGC----------
SEQID4 GGA----AAGGAGAACCT----------GGAGAAGG---TGCCTATGTATACCGCTCAGCA
*** **** * *** *** **** ***
SEQID1 GTACCAGGAAAATAATGTGGACC---AGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGT

```
SEQID2          GTACCAGGAAAATAATGTGGACC---AGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGT
SEQID3          ----------------------------------GTTACTATCC-CCAACATGCCCATTC
SEQID4          TT--CAG---------TGTGGGATTGGAGACTTACGTTACTATCC-CCAACATGCCCATTC
                                                  *   ** * * **  ***    *

SEQID1          GGGCGACCAAG-TCTGGCTCCAGGTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTG
SEQID2          GGGCGACCAAG-TCTGGCTCCAGGTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTG
SEQID3          GCTTTACCAAGATCTT-CTACA-----ATCAGCAAAACCACTATGATGG-CTCCA--CTG
SEQID4          GCTTTACCAAGATCTT-CTACA-----ATCAGCAAAACCACTATGATGG-CTCCA--CTG
                *    ****** ***  ** **     **  * **    *   * .**** *** *  ***

SEQID1          ATAA-TGACAATG----ACTCC--------AC----------------------------
SEQID2          ATAA-TGACAATG----ACTCC--------AC----------------------------
SEQID3          GTAAATTCCACTGCAACATTCCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATA
SEQID4          GTAAATTCCACTGCAACATTCCTGGGCTGTAC----------------------------
                 *** *  ** **     * ***         **

SEQID1          ------------------------------------------------------------
SEQID2          ------------------------------------------------------------
SEQID3          TGAAGGATGTGAAGGTCAGCCTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATC
SEQID4          ------------------------------------------------------------

SEQID1          ------------------------------------------------------------
SEQID2          ------------------------------------------------------------
SEQID3          AGTACCAGGAAAATAATGTGGACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGG
SEQID4          ------------------------------------------------------------

SEQID1          ------------------------------------------------------------
SEQID2          ------------------------------------------------------------
SEQID3          GCGACCAAGTCTGGCTCCAGGTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATA
SEQID4          ------------------------------------------------------------

SEQID1          ----------------CTTCACAGGCTTTCTTCTCTACCATGACACCAACTGATCACCAC
SEQID2          ----------------CTTCACAGGCTTTCTTCTCTACCATGACACCAACTGA--------
SEQID3          ATGACAATGACTCCACCTTCACAGGCTTTCTTCTCTACCATGACACCAACTGA--------
SEQID4          ----------------CTTCACAGGCTTTCTTCTCTACCATGACACCAACTGA--------
                               ************************************

SEQID1          TAACTCAGAGCCTCCTCCAGGCCAAACAGCCCCAAAGTCAATTAAAGGCTTTCAGTACGG
SEQID2          ------------------------------------------------------------
SEQID3          ------------------------------------------------------------
SEQID4          ------------------------------------------------------------

SEQID1          TTAGGAAGTTGATTATTATTTAGTTGGAGGCCTTTAGATATTATTCATTCATTTACTCAT
SEQID2          ------------------------------------------------------------
SEQID3          ------------------------------------------------------------
SEQID4          ------------------------------------------------------------
```

Fig. 7

```
SEQID5          ATGAGACCTGGCCACTTTCTCCTCATTTCTGTCTGTACGATTGTCAGTGGATCTGACGAC  60
SEQID6          ----------------------------------GCTCATTCATCTTTTAATTCA-----  21
SEQID7          ATGAGACCTGGCCACTTTCTCCTCATTTCTGTCTGTACGATTGTCAGTGGATCTGACGAC  60
SEQID8          ------------------------------------------------------------
SEQID9          ------------------------------------------------------------

SEQID5          ACCAAAAGGGCTCAGGATGCTACTGTTGCAAGCTCTCCTGTTCCTCTTAATCCTGCCCAG  120
SEQID6          CCCATAAAGGCTTTGAAAACTAAGGCTGGAGATGAACTTAT-----AGGAGCCTGCCAGG  76
SEQID7          ACCAAAAGGGCTCAGGATGCTACTGTTGCAAGCTCTCCTGTTCCTCTTAATCCTGCCCAG  120
SEQID8          ------------------------------------------------------------
SEQID9          ------------------------------------------------------------

SEQID5          TCATGCCGAAGATGACGTTACTACAACTGAAGAGCTAGCTCCTGCTTTGGTCCCTCCACC  180
SEQID6          CCGTG--GAGAGTGAGGAAGCAGAGATGACGGAGATGATGTCTTTCCTTGTCCTGTGA--  132
SEQID7          TCATGCCGAAGATGACGTTACTACAACTGAAGAGCTAGCTCCTGCTTTGGTCCCTCCACC  180
SEQID8          ------------------------------------------------------------
SEQID9          ------------------------------------------------------------

SEQID5          CAAGGGAACTTGTGCAGGTTGGATGGCAGGCATCCCAGGACATCCTGGCCACAATGGCAC  240
SEQID6          -AATGGATTGTGGGTAGA---GGTTCCGGAGATAATGCCTCTTGCTGGAAACAGT-----  183
SEQID7          CAAGGGAACTTGTGCAGGTTGGATGGCAGGCATCCCAGGACATCCTGGCCACAATGGCAC  240
SEQID8          ------------------------------------------------------------
SEQID9          ------------------------------------------------------------

SEQID5          ACCAGGCCGTGATGGCAGAGATGGCACTCCTGGAGAGAAGGGAGAGAAAGGAGATGCAGG  300
SEQID6          -CTGGGCAGTTCTGTT---CCCGCCATTC----ACAGAATTCTTCTCACTT---TCTAGG  232
SEQID7          ACCAGGCCGTGATGGCAGAGATGGCACTCCTGGAGAGAAGGGAGAGAAAGGAGATGCAGG  300
SEQID8          ------------------------------------------------------------
SEQID9          ------------------------------------------------------------

SEQID5          TCTTCTTGGTCCTAAGGGTGAGACAGGAGATGTTGGAATGACAGGAGCTGAAGGGCCACG  360
SEQID6          TCTTCTTGGTCCTAAGGGTGAGACAGGAGATGTTGGAATGACAGGAGCTGAAGGGCCACG  292
SEQID7          TCTTCTTGGTCCTAAGGGTGAGACAGGAGATGTTGGAATGACAGGAGCTGAAGGGCCACG  360
SEQID8          ------------------------------------------------------------
SEQID9          ------------------------------------------------------------

SEQID5          GGGCTTCCCCGGAACCCCTGGCAGGAAAGGAGAGCCTGGAGAAGCCGCTTATGTGTATCG  420
SEQID6          GGGCTTCCCCGGAACCCCTGGCAGGAAAGGAGAGCCTGGAGAAGCCGCTTATGTGTATCG  352
SEQID7          GGGCTTCCCCGGAACCCCTGGCAGGAAAGGAGAGCCTGGAGAAGCCGC------------  408
SEQID8          ------------------------------------------------------------
SEQID9          ------------------------------------------------------------

SEQID5          CTCAGCGTTCAGTGTGGGGCTGGAGACCCGCGTCACTGTTCCCAATGTACCCATTCGCTT  480
SEQID6          CTCAGCGTTCAGTGTGGGGCTGGAGACCCGCGTCACTGTTCCCAATGTACCCATTCGCTT  412
SEQID7          ----------------------------------GTCACTGTTCCCAATGTACCCATTCGCTT  437
SEQID8          ------------------------------------ATGAGACC--TGGCCACTTTCTCCT  23
SEQID9          ------------------------------------ATGAGACC--TGGCCACTTTCTCCT  23
                                                     **  **  **  * * *** * *

SEQID5          TACTAAGATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTACTG  540
SEQID6          TACTAAGATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTACTG  472
SEQID7          TACTAAGATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTACTG  497
SEQID8          CATTTCTGTCTG-TACGATTGTCAG--TGGATCTGACGACACCAAAAG-GGCTCAGGATG  79
SEQID9          CATTTCTGTCTG-TACGATTGTCAG--TGGATCTGACGACACCAAAAG-GGCTCAGGATG  79
                 * *.   ***  *** *   ***  *   * ***** ** **   *   *    **

SEQID5          CAACATTCCGGGACTCTACTACTTCTCTTACCACATCACGGTGTACATGAAAGATGTGAA  600
SEQID6          CAACATTCCGGGACTCTACTACTTCTCTTACCACATCACGGTGTACATGAAAGATGTGAA  532
SEQID7          CAACATTCCGGGACTCTACTACTTCTCTTACCACATCACGGTGTACATGAAAGATGTGAA  557
SEQID8          CTACTGTTGCAAGCTCTCCTGTTCCTCTTAATCCTGCCCAGT---CATGCCGAAGATGAC  136
SEQID9          CTACTGTTGCAAGCTCTCCTGTTCCTCTTAATCCTGCCCAGT---CATGCCGAAGATGAC  136
```

```
                  * **  *      **** **  * ******   *  * * **   ****    *  ***

SEQID5          GGTGAGCCTCTTCAAGAAGGACAAGGCCGTTCTCTTCACCTACGACCAGTATCAGGAAAA 660
SEQID6          GGTGAGCCTCTTCAAGAAGGACAAGGCCGTTCTCTTCACCTACGACCAGTATCAGGAAAA 592
SEQID7          GGTGAGCCTCTTCAAGAAGGACAAGGCCGTTCTCTTCACCTACGACCAGTATCAGGAAAA 617
SEQID8          GTTACTACAACT---GAAGAGCTAGCTCCTGCTTTGGTCCCTCCACCCA----AGGGAAC 189
SEQID9          GTTACTACAACT---GAAGAGCTAGCTCCTGCTTTGGTCCCTCCACCCA----AGGGAAC 189
                * *    *   *   **** * **  * * ** *   **  * ***      *** **

SEQID5          GAATGTGGACCAGGCCTCTGGCTCTGTGCTCCTCCATCTGGAGGTGGGAGACCAAGTCTG 720
SEQID6          GAATGTGGACCAGGCCTCTGGCTCTGTGCTCCTCCATCTGGAGGTGGGAGACCAAGTCTG 652
SEQID7          GAATGTGGACCAGGCCTCTGGCTCTGTGCTCCTCCATCTGGAGGTGGGAGACCAAGTCTG 677
SEQID8          TTGTGCAGGTTGGATGGCAGGCATCCCAGGACATC--CTGGCCACAATG----GCACACC 243
SEQID9          TTGTGCAGGTTGGATGGCAGGCATCCCAGGACATC--CTGGCCACATAA----AAATATA 243
                   **  *    *    * ***          *  *  ****

SEQID5          GCTCCAGGTGTATGGGGATGGGGACCACAATGGACTCTATGCAGATAACGTCAACGACTC 780
SEQID6          GCTCCAGGTGTATGGGGATGGGGACCACAATGGACTCTATGCAGATAACGTCAACGACTC 712
SEQID7          GCTCCAGGTGTATGGGGATGGGGACCACAATGGACTCTATGCAGATAACGTCAACGACTC 737
SEQID8          AGGCCGTGATGGCAGAGA-TGGCACTCCTGGA----GAGAAGGGAGAGAAAGGA-GATGC 297
SEQID9          ATTC----------GAGG-GGCATCCACCAGG----CCGGCTGAATTGTGCCAA-AATAT 287
                   *          * *  *  *  *                  *       *  *

SEQID5          TACATTTACTGGCTTTCTTCTCTACCATGATACCAACTGACTGCAACTACCCATAGCCCA 840
SEQID6          TACATTTACTGGCTTTCTTCTCTACCATGATACCAACTGACTGCAACTACCCATAGCCCA 772
SEQID7          TACATTTACTGGCTTTCTTCTCTACCATGATACCAACTGACTGCAACTACCCATAGCCCA 797
SEQID8          AGGTCTTCTTGGTCCTAAGGGTGAGACAGGAGATGTTGGAATGACAGGAGCTGAAGGGCC 357
SEQID9          GGCACTTCCTG-----CAAGATAA---------------------------------- 306
                     **  **          *

SEQID5          TACACCAGGAGAATCATGGAACAGTCGACACACTTTCAGCTTAGTTTGAGAGATTGATTT 900
SEQID6          TACACCAGGAGAATCATGGAACAGTCGACACACTTTCAGCTTAGTTTGAGAGATTGATTT 832
SEQID7          TACACCAGGAGAATCATGGAACAGTCGACACACTTTCAGCTTAGTTTGAGAGATTGATTT 857
SEQID8          ACGGGGCTTCCCCGGAACCCCTGGCAGGAAAGGAGAGCCTGGAGAAGCCGCTTATGTGTA 417
SEQID9          ------------------------------------------------------------

SEQID5          TATTGCTTAGTTTGAGAGTCCTGAGTATTATCCACACGTGTACTCACTTGTTCATTAAAC 960
SEQID6          TATTGCTTAGTTTGAGAGTCCTGAGTATTATCCACACGTGTACTCACTTGTTCATTAAAC 892
SEQID7          TATTGCTTAGTTTGAGAGTCCTGAGTATTATCCACACGTGTACTCACTTGTTCATTAAAC 917
SEQID8          TCGCTCAGCGTTCAGTGTGGGGCTGGAGACCCGCGTCACTGTTCCCAATGTACCCATTCG 477
SEQID9          ------------------------------------------------------------

SEQID5          GACTTTATAAAAAATAATTTGTGTTCCTAGTCCAGAAAAAAAGGCACTCCCTGGTCTCCA 1020
SEQID6          GACTTTATAAAAAATAATTTGTGTTCCTAGTCCAGAAAAAAAGGCACTCCCTGGTCTCCA 952
SEQID7          GACTTTATAAAAAATAATTTGTGTTCCTAGTCCAGAAAAAAAGGCACTCCCTGGTCTCCA 977
SEQID8          CTTTACTAAGATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTA 537
SEQID9          ------------------------------------------------------------

SEQID5          CGACTCTTACATGGTAGCAATAACAGAATGAAAATCACATTTGGTATGGGGGCTTCACAA 1080
SEQID6          CGACTCTTACATGGTAGCAATAACAGAATGAAAATCACATTTGGTATGGGGGCTTCACAA 1012
SEQID7          CGACTCTTACATGGTAGCAATAACAGAATGAAAATCACATTTGGTATGGGGGCTTCACAA 1037
SEQID8          CTGCAACATTCCGGGACTCTACATTTACTGGCTTTCTTCTCTACCATGATACCAACTGAC 597
SEQID9          ------------------------------------------------------------

SEQID5          TATTCGCATGACTGTCTGGAAGTAGACCATGCTATTTTTCTGCTCACTGTACACAAATAT 1140
SEQID6          TATTCGCATGACTGTCTGGAAGTAGACCATGCTATTTTTCTGCTCACTGTACACAAATAT 1072
SEQID7          TATTCGCATGACTGTCTGGAAGTAGACCATGCTATTTTTCTGCTCACTGTACACAAATAT 1097
SEQID8          TGCAACTACCCATAGCCCATACACCAGGAGAATCATGGAACAGTCGACACACTTTCAGCT 657
SEQID9          ------------------------------------------------------------

SEQID5          TGTTCACATAAACCCTATAATGTAAATATGAAATACAGTGATTACTCTTCTCACAGGCTG 1200
SEQID6          TGTTCACATAAACCCTATAATGTAAATATGAAATACAGTGATTACTCTTCTCACAGGCTG 1132
SEQID7          TGTTCACATAAACCCTATAATGTAAATATGAAATACAGTGATTACTCTTCTCACAGGCTG 1157
```

```
SEQID8          TAGTTTGAGAGATTGATTTTATTGCTTAGTTTGAGAGTCCTGAGTATTATCCACACGTGT 717
SEQID9          ------------------------------------------------------------

SEQID5          ASTGTATGAATTCTAAAGACCCATAAGTATTAAAGTGGTAGGGATAAATTGGAAAAAAAA 1260
SEQID6          AGTGTATGAATTCTAAAGACCCATAAGTATTAAAGTGGTAGGGATAAATTGG-------- 1184
SEQID7          AGTGTATGAATTCTAAAGACCCATAAGTATTAAAGTGGTAGGGATAAATTGG-------- 1209
SEQID8          ACTCACTTGTTCATTAAACGACTTTATAAAAAATAATTTGTGTTCCTAGTCCAGAAAAAA 777
SEQID9          ------------------------------------------------------------

SEQID5          AAAAAAAAAAAGAAAAACTTTAGAGCACACTGGCGGCCGTTACTAG--------------- 1306
SEQID6          ------------------------------------------------------------
SEQID7          ------------------------------------------------------------
SEQID8          AGGCACTCCCTGGTCTCCACGACTCTTACATGGTAGCAATAACAGAATGAAAATCACATT 837
SEQID9          ------------------------------------------------------------

SEQID5          ------------------------------------------------------------
SEQID6          ------------------------------------------------------------
SEQID7          ------------------------------------------------------------
SEQID8          TGGTATGGGGGCTTCACAATATTCGCATGACTGTCTGGAAGTAGACCATGCTATTTTTCT 897
SEQID9          ------------------------------------------------------------

SEQID5          ------------------------------------------------------------
SEQID6          ------------------------------------------------------------
SEQID7          ------------------------------------------------------------
SEQID8          GCTCACTGTACACAAATATTGTTCACATAAACCCTATAATGTAAATATGAAATACAGTGA 957
SEQID9          ------------------------------------------------------------

SEQID5          ------------------------------------------------------------
SEQID6          ------------------------------------------------------------
SEQID7          ------------------------------------------------------------
SEQID8          TTACTCTTCTCACAGGCTGAGTGTATGAATTCTAAAGACCCATAAGTATTAAAGTGGTAG 1017
SEQID9          ------------------------------------------------------------

SEQID5          ------------
SEQID6          ------------
SEQID7          ------------
SEQID8          GGATAAATTGG 1028
SEQID9          ------------
```

Fig. 8

```
SEQID10         ACTCTGGATGGGTGCTGTTTAGACAAACGCCGTCTCCTATATAAGACCTGACAGCACAGG 60
SEQID11         ACTCTGGATGGGTGCTGTTTAGACAAACGCCGTCTCCTATATAAGACCTGACAGCACAGG 60
                ************************************************************

SEQID10         CACCACTCCGCCAGGACTGCAGGCCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCC 120
SEQID11         CACCACTCCGCCAGGACTGCAGGCCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCC 120
                ************************************************************

SEQID10         CCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCA 180
SEQID11         CCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCA 180
                ************************************************************

SEQID10         GGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAG 240
SEQID11         GGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG--GTGAGACCTCCCCACAAAG 238
                ***************************************  * ** *     * *  ***

SEQID10         CCACCAGCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGT 300
SEQID11         CCCCACATGTTGTTCCAGCCCTGCCACTTAGCAA-CCAGCTCTGT----------GACCT 287
                ** *       * * ****** *     *****  *  **** *          ** *

SEQID10         CAAGCAGAAGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGA 360
SEQID11         GGAGCAGCAGCGCCATCTC-TGGGCTTCA-GTCTTCTCCCAGAGCACAAAGGACTCTGGG 345
                  ***** ** * **     **  **  * ***   * * *   * *   **   ***

SEQID10         ATCAAGCTGTCAGGGGTTCAGTACCAGCAGCACAGCC--AGGCCCTGGGGAAGTTTCTTC 418
SEQID11         TCTGACCT--CACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTC 403
                   * **  **  * *** * *    **     **     * ***    *   *  ***

SEQID10         AGGACATCCTCTGGGAAGAG-GCCAAAGAGGCCCCAGCCGACAAGTGATCGCCCACAAGC 477
SEQID11         CCCCTTCCAGCAGAGAAAGGAGTCGAAGAAGCC--ACCAGCCAAGCTGCAGCCC-CGAGC 460
                      *  * * ***  * * * **** ***  * * * ****     **** * ***

SEQID10         CTTACTCACCTCTCTCTAAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGC 537
SEQID11         TCTAGCAGGCTGGCTCC--GCCCGGAAGA--------TGGA---------GGTCAAGCAGA 502
                  **     **  ***   *    ****        ***          * *   ****

SEQID10         AACTCCCACGACTGTTGTACAAGCTCAGGAGGCGAATAAATGTTCAAACTGTATGCTGAT 597
SEQID11         AGGGGCAGAGGATGAACTGGAAGTCCGGG---TCGGTACCTCTGCAG-TTTTATGCTTCT 558
                *    *   *  **   * *** * **       **  * * **   * ******  *

SEQID10         GTTCCAAATGGGAATTTATTTCAAAGAGGAAAAGTTAATATTTTACTTTAAAAAAATCAA 657
SEQID11         GTGGCAGCGAGGAGGGTGGGG---------------------------------------- 579
                **  **    ***   *

SEQID10         AATAATAC 665
SEQID11         --------
```

Fig. 9

```
SEQID15          ------------------------------------------------------------
SEQID17          GGTGAAAAGGGAAAACCTGCCCAAATCCAGTTTTTGTTTCAGTAACTTCCTTTGAGACAA 60
SEQID16          ------------------------------------------------------------
SEQID12          ------------------------------------------------------------
SEQID14          ------------------------------------------------------------
SEQID18          ------------------------------------------------------------
SEQID13          ------------------------------------------------------------

SEQID15          ------------------------------------------------------------
SEQID17          AGTCAGGAATCTGAGAGTAAGCACCTGCTAAGGGTGGGACAGGGGCTCTGTCTGGTATGC 120
SEQID16          ------------------------------------------------------------
SEQID12          ------------------------------------------------------------
SEQID14          ------------------------------------------------------------
SEQID18          ------------------------------------------------------------
SEQID13          ------------------------------------------------------------

SEQID15          ------------------------------------------------------------
SEQID17          CTCTCCCATGTTAAGAGCTAACAATAGTAATGGATAAGTCTCCAGGGCAACCAGGACCAC 180
SEQID16          ------------------------------------------------------------
SEQID12          ------------------------------------------------------------
SEQID14          ------------------------------------------------------------
SEQID18          ------------------------------------------------------------
SEQID13          ------------------------------------------------------------

SEQID15          ------------------------------------------------------------
SEQID17          TTCCAAGCATTCCTGTCTTGGGCTGCCTCGAGGGCTCCTCTGTCCTTTGGGGAGTACTGA 240
SEQID16          ------------------------------------------------------------
SEQID12          ------------------------------------------------------------
SEQID14          ------------------------------------------------------------
SEQID18          ------------------------------------------------------------
SEQID13          ------------------------------------------------------------

SEQID15          ------------------------------------------------------------
SEQID17          TTGATGCCTGATGCCCAGAACTGGCCCACTCTGGCTTCTCTTTGGAGCTGTCTCTGCAGG 300
SEQID16          ------------------------------------------------------------
SEQID12          ------------------------------------------------------------
SEQID14          ------------------------------------------------------------
SEQID18          ------------------------------------------------------------
SEQID13          ------------------------------------------------------------

SEQID15          ------------------------------------------------------------GCA 3
SEQID17          CGCCTTCTGGCTGCCAGCTCGGTCCTAGCATAAGGGACTTCTTCCTTGGCCTGGGTTTCA 360
SEQID16          ------------------------------------------------------------GCA 3
SEQID12          ------------------------------------------------------------GCA 3
SEQID14          ------------------------------------------------------------GCA 3
SEQID18          ------------------------------------------------------------GCA 3
SEQID13          ------------------------------------------------------------GCA 3
                                                                               **

SEQID15          CTGCCTGAGACTACTC--CAGCCTCCCCCGTCCCTGATGTCACAATTCAGAGGCTGCTGC 61
SEQID17          CCTTCTTGTATCAGGTGGCAGACCAGCTGGTTTCAG----TCCCAAATCAG-GTCTTCTGA 416
SEQID16          CTGCCTGAGACTACTC--CAGCCTCCCCCGTCCCTGATGTCACAATTCAGAGGCTGCTGC 61
SEQID12          CTGCCTGAGACTACTC--CAGCCTCCCCCGTCCCTGATGTCACAATTCAGAGGCTGCTGC 61
SEQID14          CTGCCTGAGACTACTC--CAGCCTCCCCCGTCCCTGATGTCACAATTCAGAGGCTGCTGC 61
SEQID18          CTGCCTGAGACTACTC--CAGCCTCCCCCGTCCCTGATGTCACAATTCAGAGGCTGCTGC 61
SEQID13          CTGCCTGAGACTACTC--CAGCCTCCCCCGTCCCTGATGTCACAATTCAGAGGCTGCTGC 61
                 *   **   *  *     *** *   *  **  * *   ** *** **** * ** ***.

SEQID15          CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTCTGTGTGTCCTACAGGAGTCT 119
SEQID17          CTCCTCCCAGAAACCAACCAACTTCTGAGCAGGAAATC-CTGCCCCTCCCCAAAGAGTGG 475
SEQID16          CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTCTGTGTGTCCTACAGGAGTCT 119
SEQID12          CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTCTGTGTGTCCTACAGGAGTCT 119
```

```
SEQID14         CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTCTGTGTGTCCTACAGGAGTCT 119
SEQID18         CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTCTGTGTGTCCTACAGGAGTCT 119
SEQID13         CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTCTGTGTGTCCTACAGGAGTCT 119
                ** **           *  **  ****   ***  ** ***   ***   * ****

SEQID15         TCAG--GCCAGCTCCCTGTCGGATGGCTTTTATGAAAAAATATCTCCTCCCCATTCTGGG 177
SEQID17         GAAACCGCAAAGGAAGAGAGAGATGAAACAGAAGGAAAGGCAGAGGAGGAGGGAGAGAGA 535
SEQID16         TCAG--GCCAGCTCCCTGTCGGATGGCTTTTATGAAAAAATATCTCCTCCCCATTCTGGG 177
SEQID12         TCAG--GCCAGCTCCCTGTCGGATGGCTTTTATGAAAAAATATCTCCTCCCCATTCTGGG 177
SEQID14         TCAG--GCCAGCTCCCTGTCGGATGGCTTTTATGAAAAAATATCTCCTCCCCATTCTGGG 177
SEQID18         TCAG--GCCAGCTCCCTGTCGGATGGCTTTTATGAAAAAATATCTCCTCCCCATTCTGGG 177
SEQID13         TCAG--GCCAGCTCCCTGTCGGATGGCTTTTATGAAAAAATATCTCCTCCCCATTCTGGG 177
                  *   ** *       *   ****     * * ***   *                *

SEQID15         GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCAGACC---------- 225
SEQID17         GAGAAGAGAAGAAAAAGAAAAAAGAACATCAATAAAAAGAAGTCAGATTTGTTCGAAATC 595
SEQID16         GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCAGACC---------- 225
SEQID12         GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCAGACC---------- 225
SEQID14         GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCAGACC---------- 225
SEQID18         GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCAGACC---------- 225
SEQID13         GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCAGACC---------- 225
                *         *   *  *  *     *  *** *  * *** *****

SEQID15         ---AGAGATGCTCCAAGGAAAGAAAGTGATTGTCACAGGGGCCAGCAAAGGGATCGGAAG 282
SEQID17         TTGAGAGATGCTCCAAGGAAAGAAAGTGATTGTCACAGGGGCCAGCAAAGGGATCGGAAG 655
SEQID16         ---AGAGATGCTCCAAGGAAAGAAAGTGATTGTCACAGGGGCCAGCAAAGGGATCGGAAG 282
SEQID12         ---AGAGATGCTCCAAGGAAAGAAAGTGATTGTCACAGGGGCCAGCAAAGGGATCGGAAG 282
SEQID14         ---AGAGATGCTCCAAGGAAAGAAAGTGATTGTCACAGGGGCCAGCAAAGGGATCGGAAG 282
SEQID18         ---AGAGATGCTCCAAGGAAAGAAAGTGATTGTCACAGGGGCCAGCAAAGGGATCGGAAG 282
SEQID13         ---AGAGATGCTCCAAGGAAAGAAAGTGATTGTCACAGGGGCCAGCAAAGGGATCGGAAG 282
                   ************************************************************

SEQID15         AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAGGTCAAA 342
SEQID17         AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAGGTCAAA 715
SEQID16         AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAG------ 336
SEQID12         AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAGGTCAAA 342
SEQID14         AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAGGTCAAA 342
SEQID18         AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAGGTCAAA 342
SEQID13         AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAG------ 336
                ************************************************

SEQID15         AGAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTTGGAGCAGCCTCAGCACACTA 402
SEQID17         AGAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTTGGAGCAGCCTCAGCACACTA 775
SEQID16         ----------------------------------------------CTCAGCACACTA 348
SEQID12         AGAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTTGGAGCAGCCTCAGCACACTA 402
SEQID14         AGAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTTGGAGCAGCCTCAGCACACTA 402
SEQID18         AGAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTTGGAGCAGCCTCAGCACACTA 402
SEQID13         ----------------------------------------------CTCAGCACACTA 348
                                                             ************

SEQID15         CATTGCTGGCACCATGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA 462
SEQID17         CATTGCTGGCACCATGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA 835
SEQID16         CATTGCTGGCACCATGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA 408
SEQID12         CATTGCTGGCACCATGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA 462
SEQID14         CATTGCTGGCACCATGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA 462
SEQID18         CATTGCTGGCACCATGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA 462
SEQID13         CATTGCTGGCACCATGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA 408
                ************************************************************

SEQID15         GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCT 522
SEQID17         GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCT 895
SEQID16         GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCT 468
SEQID12         GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCT 522
SEQID14         GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCT 522
SEQID18         GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCT 522
SEQID13         GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCT 468
                ************************************************************
```

```
SEQID15         TTTTCATGATGATATTCACCATGTGCGC---------------------------------- 550
SEQID17         TTTTCATGATGATATTCACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT 955
SEQID16         TTTTCATGATGATATTCACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT 528
SEQID12         TTTTCATGATGATATTCACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT 582
SEQID14         TTTTCATGATGATATTCACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT 582
SEQID18         TTTTCATGATGATATTCACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT 582
SEQID13         TTTTCATGATGATATTCACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT 528
                ****************************

SEQID15         ----------------------CCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 588
SEQID17         GGTCCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 1015
SEQID16         GGTCCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 588
SEQID12         GGTCCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 642
SEQID14         GGTCCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 642
SEQID18         GGTCCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 642
SEQID13         GGTCCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCAT-------GT 581
                                  ******************************       **

SEQID15         CTCCTCTCTGGCTGGGAAAGTGGCTTATCCAATGGTTGCTGCC-TATTCTGCAAGCAAGT 647
SEQID17         CTCCTCTCTGGCTGGGAAAGTGGCTTATCCAATGGTTGCTGCC-TATTCTGCAAGCAAGT 1074
SEQID16         CTCCTCTCTGGCTGGGAAAGTGGCTTATCCAATGGTTGCTGCC-TATTCTGCAAGCAAGT 647
SEQID12         CTCCTCTCTGGCTGGGAAAGTGGCTTATCCAATGGTTGCTGCC-TATTCTGCAAGCAAGT 701
SEQID14         CTCCTCTCTGGCTGGGAAAGTGGCTTATCCAATGGTTGCTGCC-TATTCTGCAAGCAAGT 701
SEQID18         CTCCTCTCTGGCTG-------------------------------------------------- 656
SEQID13         GCGCTCTTCTGCTGGAA--------------------TGCTATCATGTTGTGCATCTGAGC 622
                   ****.   ****

SEQID15         TTGCTTTGGATGGGTTCTTCTCCTCCATCAGAAAGGAATATTCAGTGTCCAGGGTCAATG 707
SEQID17         TTGCTTTGGATGGGTTCTTCTCCTCCATCAGAAAGGAATATTCAGTGTCCAGGGTCAATG 1134
SEQID16         TTGCTTTGGATGGGTTCTTCTCCTCCATCAGAAAGGAATATTCAGTGTCCAGGGTCAATG 707
SEQID12         TTGCTTTGGATGGGTTCTTCTCCTCCATCAGAAAGGAATATTCAGTGTCCAGGGTCAATG 761
SEQID14         TTGCTTTGGATGGGTTCTTCTCCTCCATCAGAAAGGAATATTCAGTGTCCAGGGTCAATG 761
SEQID18         -------------------------------------------------------------
SEQID13         A-GTNGTTGATGG-----TCTCTCTCAT----AGAAGATATCAGG----CAGGCATGATA 668

SEQID15         TATCAATCACTCTCTGTGTTCTTGGCCTCATAGACACAGAAACAGCCATG-AAGGCAGTT 766
SEQID17         TATCAATCACTCTCTGTGTTCTTGGCCTCATAGACACAGAAACAGCCATG-AAGGCAGTT 1193
SEQID16         TATCAATCACTCTCTGTGTTCTTGGCCTCATAGACACAGAAACAGCCATG-AAGGCAGTT 766
SEQID12         TATCAATCACTCTCTGTGTTCTTGGCCTCATAGACACAGAAACAGCCATG-AAGGCAGTT 820
SEQID14         TATCAATCACTCTCTGTGTTCTTGGCCTCATAGACACAGAAACAGCCATG-AAGGCAGTT 820
SEQID18         ----------------------------------------AAACAGCCATG-AAGGCAGTT 676
SEQID13         TACT-----------------TTGGTCTGCTATACCAGACGCTAGGCGTCTGATGCA--- 708
                                                        ** * *   * ***

SEQID15         TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 826
SEQID17         TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 1253
SEQID16         TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 826
SEQID12         TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 880
SEQID14         TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 880
SEQID18         TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 736
SEQID13         -------------------------------------------------------------

SEQID15         GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG 886
SEQID17         GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG 1313
SEQID16         GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG 886
SEQID12         GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG 940
SEQID14         GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG 940
SEQID18         GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG 796
SEQID13         -------------------------------------------------------------

SEQID15         ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTCTACTCAACGAGCTATAATATGGAC 946
SEQID17         ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTCTACTCAACGAGCTATAATATGGAC 1373
SEQID16         ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTCTACTCAACGAGCTATAATATGGAC 946
SEQID12         ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTCTACTCAACGAGCTATAATATGGAC 1000
SEQID14         ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTCTACTCAACGAGCTATAATATGGA- 999
```

```
SEQID18         ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTCTACTCAACGAGCTATAATATGGAC 856
SEQID13         ------------------------------------------------------------

SEQID15         AGATTCATAAACAAGTAGGAACTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACTG 1006
SEQID17         AGATTCATAAACAAGTAGGAACTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACTG 1433
SEQID16         AGATTCATAAACAAGTAGGAACTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACTG 1006
SEQID12         AGATTCATAAACAAGTAGGAACTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACTG 1060
SEQID14         ------------------------------------------------------GGGACTG 1006
SEQID18         AGATTCATAAACAAGTAGGAACTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACTG 916
SEQID13         ------------------------------------------------------------

SEQID15         TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCCCAG 1066
SEQID17         TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCCCAG 1493
SEQID16         TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCCCAG 1066
SEQID12         TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCCCAG 1120
SEQID14         TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCCCAG 1066
SEQID18         TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCCCAG 976
SEQID13         ------------------------------------------------------------

SEQID15         AGACATGCAAGTCATGGGTCACACCTGACAAATGGAAGGAGTTCCTCTAACATTTGCAAA 1126
SEQID17         AGACATGCAAGTCATGGGTCACACCTGACAAATGGAAGGAGTTCCTCTAACATTTGCAAA 1553
SEQID16         AGACATGCAAGTCATGGGTCACACCTGACAAATGGAAGGAGTTCCTCTAACATTTGCAAA 1126
SEQID12         AGACATGCAAGTCATGGGTCACACCTGACAAATGGAAGGAGTTCCTCTAACATTTGCAAA 1180
SEQID14         AGACATGCAAGTCATGGGTCACACCTGACAAATGGAAGGAGTTCCTCTAACATTTGCAAA 1126
SEQID18         AGACATGCAAGTCATGGGTCACACCTGACAAATGGAAGGAGTTCCTCTAACATTTGCAAA 1036
SEQID13         ------------------------------------------------------------

SEQID15         ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT 1186
SEQID17         ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT 1613
SEQID16         ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT 1186
SEQID12         ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT 1240
SEQID14         ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT 1186
SEQID18         ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT 1096
SEQID13         ------------------------------------------------------------

SEQID15         AGTAAACATAGGTATAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT 1246
SEQID17         AGTAAACATAGGTATAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT 1673
SEQID16         AGTAAACATAGGTATAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT 1246
SEQID12         AGTAAACATAGGTATAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT 1300
SEQID14         AGTAAACATAGGTATAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT 1246
SEQID18         AGTAAACATAGGTATAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT 1156
SEQID13         ------------------------------------------------------------

SEQID15         ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA 1306
SEQID17         ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA 1733
SEQID16         ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA 1306
SEQID12         ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA 1360
SEQID14         ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA 1306
SEQID18         ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA 1216
SEQID13         ------------------------------------------------------------

SEQID15         ACTGGTAGCTATAACTTGAGCTTATTCAGGATGGTTTCTTTAAAACCATAAACTGTACAA 1366
SEQID17         ACTGGTAGCTATAACTTGAGCTTATTCAGGATGGTTTCTTTAAAACCATAAACTGTACAA 1793
SEQID16         ACTGGTAGCTATAACTTGAGCTTATTCAGGATGGTTTCTTTAAAACCATAAACTGTACAA 1366
SEQID12         ACTGGTAGCTATAACTTGAGCTTATTCAGGATGGTTTCTTTAAAACCATAAACTGTACAA 1420
SEQID14         ACTGGTAGCTATAACTTGAGCTTATTCAGGATGGTTTCTTTAAAACCATAAACTGTACAA 1366
SEQID18         ACTGGTAGCTATAACTTGAGCTTATTCAGGATGGTTTCTTTAAAACCATAAACTGTACAA 1276
SEQID13         ------------------------------------------------------------

SEQID15         ATGAAATTTTTCAATATTTGTTTCTTAT 1394
```

```
SEQID17         ATGAAATTTTTCAATATTTGTTTCTTAT 1821
SEQID16         ATGAAATTTTTCAATATTTGTTTCTTAT 1394
SEQID12         ATGAAATTTTTCAATATTTGTTTCTTAT 1448
SEQID14         ATGAAATTTTTCAATATTTGTTTCTTAT 1394
SEQID18         ATGAAATTTTTCAATATTTGTTTCTTAT 1304
SEQID13         ----------------------------
```

Fig. 10

```
SEQID19         ACTGTTGGCCTCTGGAWTCAGAGGCTGCTGCCTGCCTGGGAGGTTGTAGAAAGCTCTGCA 60
SEQID20         ACTGTTGGCCTCTGGAWTCAGAGGCTGCTGCCTGCCTGGGAGGTTGTAGAAAGCTCTGCA 60
SEQID21         ACTGTTGGCCTCTGGAWTCAGAGGCTGCTGCCTGCCTGGGAGGTTGTAGAAAGCTCTGCA 60
                ************************************************************

SEQID19         GGTTTTCTTCGTGTGTCCTACAGGGCGCCCTGAGCCAGGTCCCTGTTTGATGGCAGTTAT 120
SEQID20         GGTTTTCTTCGTGTGTCCTACAGGGCGCCCTGAGCCAGGTCCCTGTTTGATGGCAGTTAT 120
SEQID21         GGTTTTCTTCGTGTGTCCTACAGGGCGCCCTGAGCCAGGTCCCTGTTTGATGGCAGTTAT 120
                ************************************************************

SEQID19         GAAAAATTACCTCCTCCCGATCCTGGTGCTCTTCCTGGCCTACTACTACTATTCTACAAA 180
SEQID20         GAAAAATTACCTCCTCCCGATCCTGGTGCTCTTCCTGGCCTACTACTACTATTCTACAAA 180
SEQID21         GAAAAATTACCTCCTCCCGATCCTGGTGCTCTTCCTGGCCTACTACTACTATTCTACAAA 180
                ************************************************************

SEQID19         TGAAGAGTTCAGACCAGAAATGCTCCAGGGAAAGAAAGTGATTGTCACTGGGGCCAGCAA 240
SEQID20         TGAAGAGTTCAGAC---------------------------------------------- 194
SEQID21         TGAAGAGTTCAGACCAGAAATGCTCCAGGGAAAGAAAGTGATTGTCACTGGGGCCAGCAA 240
                **************

SEQID19         AGGGATTGGAAGAGAAATGGCATATCATCTGTCAAAAATGGGAGCCCATGTGGTATTGAC 300
SEQID20         ------------------------------------------------------------
SEQID21         AGGGATTGGAAGAGAAATGGCATATCATCTGTCAAAAATGGGAGCCCATGTGGTATTGAC 300

SEQID19         TGCCAGGTCGGAGGAAGGTCTCCAGAAGGTAGTGTCTCGCTGCCTTGAACTCGGAGCAGC 360
SEQID20         --------------------TCCAGAAGGTAGTGTCTCGCTGCCTTGAACTCGGAGCAGC 234
SEQID21         TGCCAGGTCGGAGGAAGGTCTCCAGAAGGTAGTGTCTCGCTGCCTTGAACTCGGAGCAGC 360
                                    ****************************************

SEQID19         CTCTGCTCACTACATTGCTGGCACTATGGAAGACATGACATTTGCGGAGCAATTTATTGT 420
SEQID20         CTCTGCTCACTACATTGCTGGCACTATGGAAGACATGACATTTGCGGAGCAATTTATTGT 294
SEQID21         CTCTGCTCACTACATTGCTGGCACTATGGAAGACATGACATTTGCGGAGCAATTTATTGT 420
                ************************************************************

SEQID19         CAAGGCGGGAAAGCTCATGGGCGGACTGGACATGCTTATTCTAAACCACATCACTCAGAC 480
SEQID20         CAAGGCGGGAAAGCTCATGGGCGGACTGGACATGCTTATTCTAAACCACATCACTCAGAC 354
SEQID21         CAAGGCGGGAAAGCTCATGGGCGGACTGGACATGCTTATTCTAAACCACATCACTCAGAC 480
                ************************************************************

SEQID19         CTCGCTGTCTCTCTTCCATGACGACATCCACTCTGTGCGAAGAGTCATGGAGGTCAACTT 540
SEQID20         CTCGCTGTCTCTCTTCCATGACGACATCCACTCTGTGCGAAGAGTCATGGAGGTCAACTT 414
SEQID21         CTCGCTGTCTCTCTTCCATGACGACATCCACTCTGTGCGAAGAGTCATGGAGGTCAACTT 540
                ************************************************************

SEQID19         CCTCAGCTACGTGGTCATGAGCACAGCCGCCTTGCCCATGCTGAAGCAGAGCAATGGCAG 600
SEQID20         CCTCAGCTACGTGGTCATGAGCACAGCCGCCTTGCCCATGCTGAAGCAGAGCAATGGCAG 474
SEQID21         CCTCAGCTACGTGGTCATGAGCACAGCCGCCTTGCCCATGCTGAAGCAGAGCAATGGCAG 600
                ************************************************************

SEQID19         CATTGCCGTCATCTCCTCCTTGGCTGGGAAAATGACCCAGCCTATGATTGCTCCCTACTC 660
SEQID20         CATTGCCGTCATCTCCTCCTTGGCTGGGAAAATGACCCAGCCTATGATTGCTCCCTACTC 534
SEQID21         CATTGCCGTCATCTCCTCCTTGGCTGGGGGAA-GAACAGTTCCACAACAGAGA---AGTC 656
                ****************************  ** ** *    * *  *  *     * **

SEQID19         TGCAAGCAAGTTTGCTCTGGATGGGTTCTTTTCCACCATTAGAACAGAACTCTACATAAC 720
SEQID20         TGCAAGCAAGTTTGCTCTGGATGGGTTCTTTTCCACCATTAGAACAGAACTCTACATAAC 594
SEQID21         -----GCAGTGTTACTCCTGAC---------TCCCGC-----GGCCCGTGATTAATATCAC 698
                     ***  ** *** **          * ** *    *  * *.  *  * ** **
```

```
SEQID19         CAAGGTCAACGTGTCCATCACTCTCTGTGTCCTTGGCCTCATAGACACAGAAACAGCTAT 780
SEQID20         CAAGGTCAACGTGTCCATCACTCTCTGTGTCCTTGGCCTCATAGACACAGAAACAGCTAT 654
SEQID21         CAGCCACAGAATGGAC-TGGAACCCTGTATC---GATCTGGTGGGATTGGATATAACGAA 754
                **   **   **  * *    * **** **   *  **  * *     ** * * * *

SEQID19         GAAGGAA--ATCTCTGGGATAATTAACGCCCAAGCTTCTCCCAAGGAGGAGTGCGCCCTG 838
SEQID20         GAAGGAA--ATCTCTGGGATAATTAACGCCCAAGCTTCTCCCAAGGAGGAGTGCGCCCTG 712
SEQID21         CATAGAATTACTCCTGAGACTACCAGAACTGAA---TAGTTCAAATCAAATCATGCC--- 808
                 *  ***  *   *** **  *  *   *  **   *    ***     *    ***

SEQID19         GAGATCATCAAAGGCACAGCTCTACGCAAAAGCGAGGTGTACTATGACAAATCGCCTTTG 898
SEQID20         GAGATCATCAAAGGCACAGCTCTACGCAAAAGCGAGGTGTACTATGACAAATCGCCTTTG 772
SEQID21         -AGAATATC--AGACAAATCCAAATGGCAAAAC-AGTTGCA------------------- 845
                 ***  ***  ** ** * *   * *  *** * ** ** *

SEQID19         ACTCCAATCCTGCTTGGGAACCCAGGAAGGAAGATCATGGAATTTTTTTCATTACGATAT 958
SEQID20         ACTCCAATCCTGCTTGGGAACCCAGGAAGGAAGATCATGGAATTTTTTTCATTACGATAT 832
SEQID21         ------------------------------------------------------------

SEQID19         TATAATAAGGACATGTTTGTAAGTAACTAGGAACTCCTGAGCCCTGGTGAGTGGTCTTAG 1018
SEQID20         TATAATAAGGACATGTTTGTAAGTAACTAGGAACTCCTGAGCCCTGGTGAGTGGTCTTAG 892
SEQID21         ------------------------------------------------------------

SEQID19         AACAGTCCTGCCTGATACTTCTGTAAGCCCTACCCACAAAAGTATCTTTCCAGAGATACA 1078
SEQID16         AACAGTCCTGCCTGATACTTCTGTAAGCCCTACCCACAAAAGTATCTTTCCAGAGATACA 952
SEQID21         ------------------------------------------------------------

SEQID19         CAAATTTTGGGGTACACCTCATCATGAGAAATTCTTGCAACACTTGCACAGTGAAAATGT 1138
SEQID20         CAAATTTTGGGGTACACCTCATCATGAGAAATTCTTGCAACACTTGCACAGTGAAAATGT 1012
SEQID21         ------------------------------------------------------------

SEQID19         AATTGTAATAAATGTCACAAACCACTTTGGGGCCTGCAGTTGTGAACTTGATTGTAACTA 1198
SEQID20         AATTGTAATAAATGTCACAAACCACTTTGGGGCCTGCAGTTGTGAACTTGATTGTAACTA 1072
SEQID21         ------------------------------------------------------------

SEQID19         TGGATATAAACACATAGTGGTTGTATCGGCTTTACCTCACACTGAATGAAACAATGATAA 1258
SEQID20         TGGATATAAACACATAGTGGTTGTATCGGCTTTACCTCACACTGAATGAAACAATGATAA 1132
SEQID21         ------------------------------------------------------------

SEQID19         CTAATGTAACATTAAATATAATAAAGGTAATATCAACTTTGTAAATGCA 1307
SEQID20         CTAATGTAACATTAAATATAATAAAGGTAATATCAACTTTGTAAATGCA 1181
SEQID21         --------------------------------------------------
```