

Supplementary Information for

**iMiRNA-SSF: Improving the Identification of MicroRNA Precursors by
Combining Negative Sets with Different Distributions**
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Supplementary S1. The benchmark dataset S contains 4666 sequences, which are classified into subset S^+ with 1612 Human pre-microRNAs (positive samples) and subset S^- with 1612 Xue pseudo miRNAs and 1442 Zou pseudo miRNAs (negative samples).

(1). 1612 Human pre-microRNAs

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CUUCUCCGCCUCUCGGCUGCAUCCACAGAGUCUGGCUGGCUCGC
>random_seq_from_cds__NO_65 RANDOM_LENGTH 75 SEQ_LENGTH 58
GC_CONTENT 0.568965517241379 BASEPAIR 21 FREE_ENERGY
-21.60 LEN_BP_RATIO 2.76190476190476
UUGGCGACUUUGUGCUGUACCGUUGAAUAGUAGGCCAGCUUGGUUAACGACCCGCCCUAUGUCGA
UGGCGAAGCG
>random_seq_from_cds__NO_71 RANDOM_LENGTH 89 SEQ_LENGTH 73
GC_CONTENT 0.616438356164384 BASEPAIR 29 FREE_ENERGY
-35.10 LEN_BP_RATIO 2.51724137931034
CACCUUGGUCUGGUGCUGACAUCUCCAGGGUCCAUUGGAGAGAAGGUCCCCGGGGGCAGU
UCUGACACAGGGUGUCCUGACUCU
>random_seq_from_cds__NO_76 RANDOM_LENGTH 78 SEQ_LENGTH 64
GC_CONTENT 0.671875 BASEPAIR 22 FREE_ENERGY -26.30
LEN_BP_RATIO 2.90909090909091
AGGACGGCAGAGCUGGGGCGUAGCAGGGGGCUCCCAGGAAGGUGAGAUACAGCACCCAGCCUCAA
GACGUCGGUUUUG
>random_seq_from_cds__NO_80 RANDOM_LENGTH 70 SEQ_LENGTH 61

GC_CONTENT 0.573770491803279 BASEPAIR 23 FREE_ENERGY
-19.90 LEN_BP_RATIO 2.65217391304348
GCAUAGUUGAUGAAGAAGAGCUGCUCUAGGGUGAGAUAUCCAGGCCGGCAGCUGCUGGUCCUUGCC
ACCCU
>random_seq_from_cds__NO_86 RANDOM_LENGTH 84 SEQ_LENGTH 75
GC_CONTENT 0.546666666666667 BASEPAIR 25 FREE_ENERGY
-23.10 LEN_BP_RATIO 3
GCGCCACCUUGAGGUUCUGCAGACUGUUCUCAAGUACAGGUCCUCUGAGAAGUUCAGCAUUGG
AGUACUCCUCGUCCAGGCG
>random_seq_from_cds__NO_93 RANDOM_LENGTH 77 SEQ_LENGTH 57
GC_CONTENT 0.56140350877193 BASEPAIR 20 FREE_ENERGY
-15.80 LEN_BP_RATIO 2.85
AGAGUCCAGUAAAUCCCCUUCAGGCCAAACUGGCUUUGCAGCUCCUCCAGUCCCAUCCGGUGGU
ACAAGGCGAUGA
>random_seq_from_cds__NO_112 RANDOM_LENGTH 110 SEQ_LENGTH 94
GC_CONTENT 0.542553191489362 BASEPAIR 34 FREE_ENERGY
-32.91 LEN_BP_RATIO 2.76470588235294
UUCAGCAAGGUCAAGGUCCUCCACUGAUCUCUGCCUCCCGGUGGCUGCUGAAGCGCGGAGAGC
UGUUCUAGUGGAAGAAACCGGACUUUUUCGAAAAUUGCCAGCC
>random_seq_from_cds__NO_117 RANDOM_LENGTH 88 SEQ_LENGTH 79
GC_CONTENT 0.683544303797468 BASEPAIR 27 FREE_ENERGY
-27.20 LEN_BP_RATIO 2.92592592592593
GCAGGCGGACGUGGUCCUGGUUCUGCAGCAGGAGGAUUGGGUGGCUCUAUGGCGAGAGGCUCCGG
GACGGAGAGACGGAUGGUUCC
>random_seq_from_cds__NO_129 RANDOM_LENGTH 94 SEQ_LENGTH 61
GC_CONTENT 0.655737704918033 BASEPAIR 22 FREE_ENERGY
-23.60 LEN_BP_RATIO 2.77272727272727
AUGCUCACGUAUUCUUGCAGUCGCGCCGUUCUGCCAGCGCCAUGUAGCGGCCGUCCUGGUGAA
GGUGAUUCCUUGCAGACAAGCUUUCGGG
>random_seq_from_cds__NO_130 RANDOM_LENGTH 85 SEQ_LENGTH 75
GC_CONTENT 0.453333333333333 BASEPAIR 26 FREE_ENERGY
-22.10 LEN_BP_RATIO 2.88461538461538
UAUUUGAUGUAAGACACGGAUUUUGUGCACAAGGACCAGACGGUUAUCCGCAGCAUGGAAUCCG
UGGUGUUGAGAAUGUGGCGC
>random_seq_from_cds__NO_132 RANDOM_LENGTH 110 SEQ_LENGTH 106
GC_CONTENT 0.575471698113208 BASEPAIR 37 FREE_ENERGY
-32.90 LEN_BP_RATIO 2.86486486486486
CCUGCACCAGCCCUCGCUUGUACAUGGCGCACAGGAUGAAGAGCGAGUCUGCCGACCACUCGAUG
UGCUGGAUCUGGUCUAGGCACGUGUACAGCUGAAGGAUCUGAAGG
>random_seq_from_cds__NO_135 RANDOM_LENGTH 72 SEQ_LENGTH 67
GC_CONTENT 0.701492537313433 BASEPAIR 23 FREE_ENERGY
-26.40 LEN_BP_RATIO 2.91304347826087
UUCGGCGUGGCUGGCCGGAGCUGCCAGGAGGUGCUGCGCAAGGGCUGUCUCCGCUCCAGGCUC
CUGAGCG

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>random_seq_from_cds__NO_140  RANDOM_LENGTH 89  SEQ_LENGTH  80
  GC_CONTENT  0.5875 BASEPAIR  29  FREE_ENERGY  -31.00
  LEN_BP_RATIO  2.75862068965517
UGGAGUCCCGAUUUCAGAGCAAGUCUGGCUAUCUGAGAUACAGCUGUGAGAGCCGGAUCCGGAGU
UACCUGAGGGAGGGUGAGCUCCUA
>random_seq_from_cds__NO_149  RANDOM_LENGTH 71  SEQ_LENGTH  49
  GC_CONTENT  0.693877551020408  BASEPAIR  20  FREE_ENERGY
-28.50  LEN_BP_RATIO  2.45
CGGAGAGUGUCCUGGCUCUCUCGCAGGGGCAGGCGGGGUCACAGAGGAUGCUCGAGAGAGAGG
UCGGCU
>random_seq_from_cds__NO_153  RANDOM_LENGTH 70  SEQ_LENGTH  53
  GC_CONTENT  0.566037735849057  BASEPAIR  19  FREE_ENERGY
-17.70  LEN_BP_RATIO  2.78947368421053
UGCAUAUGUCACAGGUCCUUUGUCCACUGCGCUGGAGAAACUAUUUGGAGGACAGGGACUGCAA
AUCUG
>random_seq_from_cds__NO_159  RANDOM_LENGTH 90  SEQ_LENGTH  71
  GC_CONTENT  0.577464788732394  BASEPAIR  24  FREE_ENERGY
-30.30  LEN_BP_RATIO  2.958333333333333
UCACGGCCUUGGCGAUCCUCUUUGGGUUGGUCACUGUGAGAUCAUCCCCACUACCUGGAUCCU
GCACUGGCUGUGAACUUCUGCCAAG
>random_seq_from_cds__NO_187  RANDOM_LENGTH 77  SEQ_LENGTH  58
  GC_CONTENT  0.551724137931034  BASEPAIR  22  FREE_ENERGY
-20.90  LEN_BP_RATIO  2.63636363636364
ACGGCCAUGACACUGUCCUUGUGCUCUCGCAGCACCUCCAUCACUGUGUGGAUGUGAUUCUGUA
GUUGCCAUCCAG
>random_seq_from_cds__NO_196  RANDOM_LENGTH 97  SEQ_LENGTH  76
  GC_CONTENT  0.565789473684211  BASEPAIR  28  FREE_ENERGY
-35.40  LEN_BP_RATIO  2.71428571428571
UGCAAAGACGGUGCUAUGGACUGAAUGCGAAUGAUUGGCUGGUUGGGGUCAUAUGUCCUGGCAC
AGCCAAUUC AAGGUCCCGGCACAUCAGAAGUU
>random_seq_from_cds__NO_197  RANDOM_LENGTH 70  SEQ_LENGTH  56
  GC_CONTENT  0.517857142857143  BASEPAIR  21  FREE_ENERGY
-18.80  LEN_BP_RATIO  2.66666666666667
UUGGGGAAACAUUUGCAGCUCUAAGGAUGUGAGCCUGAGGCAGCUGCUUUGAGAUUCGUCGGAA
CACAU
>random_seq_from_cds__NO_198  RANDOM_LENGTH 84  SEQ_LENGTH  78
  GC_CONTENT  0.487179487179487  BASEPAIR  31  FREE_ENERGY
-28.00  LEN_BP_RATIO  2.51612903225806
GAUAAUAGAGGUCCAGGCUUGGGUGAGGUCCUUGACAUCCUGAUUUAUGUACUCCUGGCAC
CACUCUUGGGCCUCCAUA
>random_seq_from_cds__NO_204  RANDOM_LENGTH 68  SEQ_LENGTH  46
  GC_CONTENT  0.5 BASEPAIR  20  FREE_ENERGY  -20.12  LEN_BP_RATIO
  2.3
UAGCCAGGUAUCAUUCUGGAUGGCUUUCACCCCUCCACUAAGGCCUCAUUGACAUCUGGCCAGU
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GAC

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>random_seq_from_cds__NO_207  RANDOM_LENGTH 80  SEQ_LENGTH 74
  GC_CONTENT 0.716216216216216  BASEPAIR 24  FREE_ENERGY
-31.00 LEN_BP_RATIO 3.083333333333333
CCCUCGGUGCUGGCAGUGGGUGGCAGUGGCGGCCGUGGUGGCGGCAGUGGUGGCGUUGGUGAU
GUUGGCCCCGCUGGC
>random_seq_from_cds__NO_219  RANDOM_LENGTH 82  SEQ_LENGTH 74
  GC_CONTENT 0.581081081081081  BASEPAIR 22  FREE_ENERGY
-26.45 LEN_BP_RATIO 3.363636363636363
UUGGCUUGGGUCUCAUCAUUAACCAGGGUCCACUUUUCACAGCACUGCUGGUGGAGUUGACCCC
AUUCCCCAAGGCCUCG
>random_seq_from_cds__NO_222  RANDOM_LENGTH 78  SEQ_LENGTH 64
  GC_CONTENT 0.578125  BASEPAIR 22  FREE_ENERGY -28.20
  LEN_BP_RATIO 2.90909090909091
CCGGCCGUGCCUCCGGCUGCUGUAGCUUAUUUAUUAUGCCUGAUGAGAGAUUCUAGAAUGGCAG
GGGUGGGGCCUUU
>random_seq_from_cds__NO_239  RANDOM_LENGTH 90  SEQ_LENGTH 72
  GC_CONTENT 0.458333333333333  BASEPAIR 29  FREE_ENERGY
-26.90 LEN_BP_RATIO 2.48275862068966
GGUAGAACUCAUCCAGAGGCAAGUUUCCAUUGUUGACCAGCAUUUCACUAGUGCUAUAGUCAGCA
GGAAUCCUGACUUGACUUGGAUUCU
>random_seq_from_cds__NO_242  RANDOM_LENGTH 87  SEQ_LENGTH 75
  GC_CONTENT 0.586666666666667  BASEPAIR 27  FREE_ENERGY
-29.50 LEN_BP_RATIO 2.77777777777778
AAGUAGGGUACUUCUGUAGGGUCUACUACAUAAGCCAGUGCUGGCCACCAACUGUCCCAGGGUC
CACAGAGCCACCCUGCCUUUUG
>random_seq_from_cds__NO_256  RANDOM_LENGTH 82  SEQ_LENGTH 62
  GC_CONTENT 0.564516129032258  BASEPAIR 23  FREE_ENERGY
-21.14 LEN_BP_RATIO 2.69565217391304
UUGCUCGAGCCAGCAUGCUGAUGCAAGUGAAGACUGUGGCAUCCACCUGCAUUGCCUUCUGCCUC
CUUAUGGGCGAAGUCCU
>random_seq_from_cds__NO_261  RANDOM_LENGTH 84  SEQ_LENGTH 68
  GC_CONTENT 0.617647058823529  BASEPAIR 28  FREE_ENERGY
-36.80 LEN_BP_RATIO 2.42857142857143
CCGGCUCUCCACCAGGGUGGACUAGCUGGACUGGGGGAGGUCCCAAUCCAUAGAGGCCUUGGU
GAGAGCUGUACCCCAGCAG
>random_seq_from_cds__NO_275  RANDOM_LENGTH 110 SEQ_LENGTH 99
  GC_CONTENT 0.686868686868687  BASEPAIR 35  FREE_ENERGY
-45.30 LEN_BP_RATIO 2.82857142857143
GCUCGAAGCGGACGAAGCGGACGCCCGGCCCGUAGUCGGUGAAGGUGUGGGAGAUCUCAUCA
GCCCCCGCCGUCACUGUCUUGGGGCACUGCCACCUGCCCGCUGCU
>random_seq_from_cds__NO_280  RANDOM_LENGTH 73  SEQ_LENGTH 60
  GC_CONTENT 0.6  BASEPAIR 21  FREE_ENERGY -19.10  LEN_BP_RATIO
2.85714285714286
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GCCUCCAAGUCCUCCUCCCCACACGGGUUACGCAGAAGGUUGCGGCGCCGCUUGCUCAGGAAG
UAGAACUG

>random_seq_from_cds__NO_289 RANDOM_LENGTH 97 SEQ_LENGTH 83
GC_CONTENT 0.590361445783133 BASEPAIR 28 FREE_ENERGY
-34.00 LEN_BP_RATIO 2.96428571428571

UUUUGUCACAUCUACGAGAAUGUGCCUCAAGUCCAGCUGGUGGACCUUGUAGCCGAGGGCUAC
UGGGAGGAGCUACUAGACACAUCCGGCCGGA

>random_seq_from_cds__NO_292 RANDOM_LENGTH 78 SEQ_LENGTH 56
GC_CONTENT 0.660714285714286 BASEPAIR 19 FREE_ENERGY
-23.30 LEN_BP_RATIO 2.94736842105263

CCUCUCCAGCAUGGGGGCAGGGACACCCAGUACUGGGCAGGCUGGUAUGGGCCCCGAGUCACCA
ACAGCAGCAUUGU

>random_seq_from_cds__NO_310 RANDOM_LENGTH 89 SEQ_LENGTH 84
GC_CONTENT 0.630952380952381 BASEPAIR 27 FREE_ENERGY
-35.40 LEN_BP_RATIO 3.11111111111111

UCCCAAUGGGCCCCAGCCCCCAGCUGAAGGGAGCACUGGCGACUUCGCUCUCCAGUUGGGACU
GAUUGUGGGUGUGACAGCCUUGG

>random_seq_from_cds__NO_318 RANDOM_LENGTH 77 SEQ_LENGTH 60
GC_CONTENT 0.516666666666667 BASEPAIR 21 FREE_ENERGY
-20.70 LEN_BP_RATIO 2.85714285714286

UGGCCGUGGAAAGUGUCAAAAUUCUCCCAAGAGGGGAUCUGAAGGAGGAGUGGCUGCCUUG
UGGAUUUUGUGG

>random_seq_from_cds__NO_336 RANDOM_LENGTH 97 SEQ_LENGTH 82
GC_CONTENT 0.475609756097561 BASEPAIR 25 FREE_ENERGY
-20.92 LEN_BP_RATIO 3.28

UUUGACCGCUAAAAGGCAUGGCCUGGUUCUCUACAAUGAAAUUGAAUAUGCACAAGCAGCUGU
AAAAGAGACCAAAGGGAGGAAAUCGGUGGGA

>random_seq_from_cds__NO_349 RANDOM_LENGTH 71 SEQ_LENGTH 57
GC_CONTENT 0.491228070175439 BASEPAIR 19 FREE_ENERGY
-16.30 LEN_BP_RATIO 3

CUGCCUGGACCAGAAACUUCAGGUCUCUCAGACGGAGCCUGCAAAAUCUGACUUGUCUAAACUG
GAAUCA

>random_seq_from_cds__NO_351 RANDOM_LENGTH 99 SEQ_LENGTH 78
GC_CONTENT 0.576923076923077 BASEPAIR 28 FREE_ENERGY
-27.70 LEN_BP_RATIO 2.78571428571429

AGGAAGCACCUCAAGCCUGAGCAGCCUGCAGAUGGGGUAAGUGCUGUGGAUCUGGAGAAGCUGGA
AGCCAGGAAAAGGCGCUUUGCAGAUCCAAUUUA

>random_seq_from_cds__NO_398 RANDOM_LENGTH 110 SEQ_LENGTH 79
GC_CONTENT 0.443037974683544 BASEPAIR 26 FREE_ENERGY
-17.40 LEN_BP_RATIO 3.03846153846154

CCAUCCACUCCUCCUCAGUCAUGUACUUCUGACCUAAGCAAGAUUCCCUCCACAGAGAAUUCGU
CCCAAGAAAUCAGUGUUGAGGAAAGGACUCCAACCAAAGCAUCUG

>random_seq_from_cds__NO_410 RANDOM_LENGTH 82 SEQ_LENGTH 71
GC_CONTENT 0.633802816901408 BASEPAIR 28 FREE_ENERGY

-38.70 LEN_BP_RATIO 2.53571428571429
CGGGUGCGGUUACUGCUGCAUCUGGUGGUGUAACGGCCACAACAGGCACGGUGACAAUGGCAGGG
GCAGUGAUUGCGCCGUC
>random_seq_from_cds__NO_424 RANDOM_LENGTH 80 SEQ_LENGTH 66
GC_CONTENT 0.590909090909091 BASEPAIR 23 FREE_ENERGY
-26.90 LEN_BP_RATIO 2.8695652173913
UCGCUCGAGCCACAGCCCCUGUGCAGUCAGAGGUACUAGUCAUGCAGUCUGAGUACCGACUGCAC
CCCUAUACUGUGCCA
>random_seq_from_cds__NO_440 RANDOM_LENGTH 110 SEQ_LENGTH 87
GC_CONTENT 0.586206896551724 BASEPAIR 21 FREE_ENERGY
-17.38 LEN_BP_RATIO 4.14285714285714
CAGAUCUCCCCGCCUGUGAGUUCUCUGAGAGUCACCUGUCCCGCCUGGCCCCUGACCUCCUUGC
CAGCAUCUCCAACAUCUCUCCCCACCUCAUGAUUGUCAUUGCCUC
>random_seq_from_cds__NO_441 RANDOM_LENGTH 87 SEQ_LENGTH 74
GC_CONTENT 0.662162162162162 BASEPAIR 27 FREE_ENERGY
-34.90 LEN_BP_RATIO 2.74074074074074
CGUGUGAGAUGGAGGAGUUUGUGGGGUCGUGAAGGCUCUCAGGGAACCCUGUGACUCUGCAG
GAGCUGUGGGGCCCCUGUCCCC
>random_seq_from_cds__NO_450 RANDOM_LENGTH 119 SEQ_LENGTH 93
GC_CONTENT 0.602150537634409 BASEPAIR 34 FREE_ENERGY
-37.60 LEN_BP_RATIO 2.73529411764706
AGACCAGUUUCCGGGUGGACGUUCCCUUCGACCUGCCUGAGAUCUUCUUUUUUGUGGCGCUGGGG
GGGUCUCUGUGGCAUCCUGGGCAGCGCUUACCUCUUCUGUCAGCGAAUCUUCUU
>random_seq_from_cds__NO_468 RANDOM_LENGTH 110 SEQ_LENGTH 88
GC_CONTENT 0.443181818181818 BASEPAIR 33 FREE_ENERGY
-29.60 LEN_BP_RATIO 2.66666666666667
AGUUUCUCACGCUCUUCUAUGGACUGCAGAUACUGCUGCUUGCCUUCUGAGAUUCAUCCUUCUU
CUUCAAAUAAGGCUCAUUGGAUUUGUACUGUGCAUAGAAGUUGCU
>random_seq_from_cds__NO_481 RANDOM_LENGTH 75 SEQ_LENGTH 62
GC_CONTENT 0.596774193548387 BASEPAIR 21 FREE_ENERGY
-20.50 LEN_BP_RATIO 2.95238095238095
GGUCCCAAGUGGCCUCUCACUACCUGAUGGUCCCCGGUGGAAAGCACAACAUGGACUUCUACGU
GGAGGCCUC
>random_seq_from_cds__NO_487 RANDOM_LENGTH 86 SEQ_LENGTH 58
GC_CONTENT 0.672413793103448 BASEPAIR 21 FREE_ENERGY
-27.10 LEN_BP_RATIO 2.76190476190476
UGGGAACCUUGAAGUGAGCCCCCAGUCACAGUCAGGGGCAAGGAUACCCGUGGGCAGGAUUC
UCUUCGGGGACAGCUGUUAUC
>random_seq_from_cds__NO_489 RANDOM_LENGTH 77 SEQ_LENGTH 54
GC_CONTENT 0.537037037037037 BASEPAIR 19 FREE_ENERGY
-18.90 LEN_BP_RATIO 2.84210526315789
CCCUGUGAAGCUCUAUUCUGACUGGCUGUCCGUGGGCCACGUGGACGAGUUCUGAGCUUUGUGC
CAGCACCCGACA
>random_seq_from_cds__NO_501 RANDOM_LENGTH 81 SEQ_LENGTH 55

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GC_CONTENT    0.672727272727273    BASEPAIR    23    FREE_ENERGY
-33.70    LEN_BP_RATIO    2.39130434782609
UCAGGCAGCUGGGCCUGCCCACCGCCUCAAGAGAGGGUGUGGGUGACUCUGCUGUCUGACUACGA
GGUGUGCAAGGAGGGC
>random_seq_from_cds__NO_502    RANDOM_LENGTH    87    SEQ_LENGTH    71
GC_CONTENT    0.549295774647887    BASEPAIR    22    FREE_ENERGY
-20.22    LEN_BP_RATIO    3.22727272727273
GAUGUGCUGACCCCAGAGCAGGCUCGCGUCCUGGAAGCUUUUUGGGUAUGAGAUGGCUGAAUUCA
AGGUGACCAUCAAUAUCAUGUG
>random_seq_from_cds__NO_509    RANDOM_LENGTH    89    SEQ_LENGTH    76
GC_CONTENT    0.460526315789474    BASEPAIR    27    FREE_ENERGY
-18.20    LEN_BP_RATIO    2.81481481481481
UCCAGCAAAGCCAUGAUCCAGAUCCCAGAGGUAGACAGAUGAGACGCCACCUUCAAUUUACCAGG
UCUCGAUACUGGUCAAAGGCAUUG
>random_seq_from_cds__NO_512    RANDOM_LENGTH    84    SEQ_LENGTH    70
GC_CONTENT    0.514285714285714    BASEPAIR    27    FREE_ENERGY
-23.40    LEN_BP_RATIO    2.59259259259259
CUGGUCAACAGAAGACAGGAGAUCUCACAUAGACUGGGGACCCAGGUCGAUCAGGUCGCUGAGG
UUUUUCUGGAUUUGCUGGG
>random_seq_from_cds__NO_516    RANDOM_LENGTH    75    SEQ_LENGTH    49
GC_CONTENT    0.673469387755102    BASEPAIR    19    FREE_ENERGY
-24.80    LEN_BP_RATIO    2.57894736842105
CCUGGGGAGGAGACCAGGCUGGAGAUGGACAAGUUCUUUUUCUGGGCCUCUCCAAGGACGUACA
ACACCAAUGC
>random_seq_from_cds__NO_521    RANDOM_LENGTH    110    SEQ_LENGTH    80
GC_CONTENT    0.5625    BASEPAIR    24    FREE_ENERGY    -27.80
LEN_BP_RATIO    3.33333333333333
AAGAAUAAAACUGAUGUGGAGUAUGAGAGUGACGAGAAAGCCAGGGGCACGAGGCUGGACGGCCU
GGACCUCGUUGACACCUGGAAGAGCUUCAAACCGAGAUACAAGGC
>random_seq_from_cds__NO_522    RANDOM_LENGTH    110    SEQ_LENGTH    95
GC_CONTENT    0.568421052631579    BASEPAIR    34    FREE_ENERGY
-30.50    LEN_BP_RATIO    2.79411764705882
ACUCCCACUUCUUGGAACCGCACGGAACUCCUGACCCUUGACCCCAAAUGUGGACUACCUA
UUGGGGUCUCUUCGAGCCAGGGACAUGCAGUACGAGCUGAACAG
>random_seq_from_cds__NO_529    RANDOM_LENGTH    84    SEQ_LENGTH    78
GC_CONTENT    0.705128205128205    BASEPAIR    28    FREE_ENERGY
-33.90    LEN_BP_RATIO    2.78571428571429
GGCCCAUGGCGCACCUGCUGCACGGCGUCCACGAGCAGAAUACGUCCCCACGUGAUGGCGUA
UGCAGCCUGCAUCGGGGCC
>random_seq_from_cds__NO_551    RANDOM_LENGTH    86    SEQ_LENGTH    47
GC_CONTENT    0.74468085106383    BASEPAIR    19    FREE_ENERGY
-31.60    LEN_BP_RATIO    2.47368421052632
UGGAGGUGGUGUCUUUUUUUUUGGUGGUGGUGGAGCACCUCGCCUUUUUUUUUCCUCCUCCUC
UUCUUCUUCUACUGCAUAGCCA
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>random_seq_from_cds__NO_553 RANDOM_LENGTH 86 SEQ_LENGTH 59
GC_CONTENT 0.711864406779661 BASEPAIR 21 FREE_ENERGY
-27.30 LEN_BP_RATIO 2.80952380952381
UAUCCACCUCUCCCCCACCACGACCCCGACCUCUAAUUGGAGGUGGCAUGCGAGGAGGAGGGUG
GUAGUAAUAAUCUUCUACCG

>random_seq_from_cds__NO_567 RANDOM_LENGTH 84 SEQ_LENGTH 67
GC_CONTENT 0.477611940298507 BASEPAIR 19 FREE_ENERGY
-17.60 LEN_BP_RATIO 3.52631578947368
GUCUGAAAUAUUUCAAGUCUUCUGCCACCUUCUGUGGGAGGCCUGCCUCUAUCAGUGUCUU
GUAGUGUUCUGUGUGAGUU

>random_seq_from_cds__NO_578 RANDOM_LENGTH 71 SEQ_LENGTH 65
GC_CONTENT 0.523076923076923 BASEPAIR 23 FREE_ENERGY
-18.30 LEN_BP_RATIO 2.82608695652174
CUGGGGUUGGGAAAACAGUAAAUAGCUUGCGAAAACACGAGCAUGUUGGAAGCUUUGCCAGGGAC
CUAGUG

>random_seq_from_cds__NO_595 RANDOM_LENGTH 90 SEQ_LENGTH 63
GC_CONTENT 0.492063492063492 BASEPAIR 22 FREE_ENERGY
-18.10 LEN_BP_RATIO 2.86363636363636
CCCUAAAAUGAUGACCUUGCACCAGCAAUGCAUCCGAGUACUAAAAACAACAUCGAUUGCAAUC
UUUGAAGUGGGAGGAGUCCCAUACU

>random_seq_from_cds__NO_605 RANDOM_LENGTH 88 SEQ_LENGTH 75
GC_CONTENT 0.613333333333333 BASEPAIR 26 FREE_ENERGY
-27.10 LEN_BP_RATIO 2.88461538461538
UCUGUCCCCAUGCGCCUAGGAUCCUGUGACCCUCAACAUGAAGAUGGUGAUGCCCUCCUGGGU
UUGACCUGAUGGGGCUGAGUCCA

>random_seq_from_cds__NO_611 RANDOM_LENGTH 73 SEQ_LENGTH 64
GC_CONTENT 0.578125 BASEPAIR 19 FREE_ENERGY -27.74
LEN_BP_RATIO 3.36842105263158
GCUCCUGUCCUCAGGGAGAUGGCAGCUGUGAAGGAAUUUCUUGAGAAGCUGCUGCCUCCUGUCUA
ACUCAGGC

>random_seq_from_cds__NO_620 RANDOM_LENGTH 78 SEQ_LENGTH 65
GC_CONTENT 0.584615384615385 BASEPAIR 21 FREE_ENERGY
-20.20 LEN_BP_RATIO 3.0952380952381
ACACCAGGUUCUUCACCCCGUGGGCCUUCGAUCCUCCAGAAGCUGGAUGGUCCCGUCAGGUU
AACUCUGUAAUAA

>random_seq_from_cds__NO_626 RANDOM_LENGTH 80 SEQ_LENGTH 68
GC_CONTENT 0.470588235294118 BASEPAIR 23 FREE_ENERGY
-19.20 LEN_BP_RATIO 2.95652173913043
AGGCUCUUCAUUGAUUCUUGGCUCAAGGAGUUGUAUUUAGUGUGACGACUGUUGACCUGAAAAG
GGAAGCCAGCAGACC

>random_seq_from_cds__NO_639 RANDOM_LENGTH 71 SEQ_LENGTH 49
GC_CONTENT 0.63265306122449 BASEPAIR 19 FREE_ENERGY
-20.80 LEN_BP_RATIO 2.57894736842105
AGCGGCACAGAGCAGGAUGACCUCUUCAGCUUCUGACCUACAGGCUGGACAGAUGGUGGGGGGCC

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CCUGGG
>random_seq_from_cds__NO_659  RANDOM_LENGTH 75  SEQ_LENGTH  59
  GC_CONTENT  0.610169491525424  BASEPAIR  19  FREE_ENERGY
  -23.50  LEN_BP_RATIO  3.10526315789474
UCCUGAGGAUCGUGCAGCCACGUGGCUGGGAUCUGCCACAACAUCUGGUCUGCUGCCCAAGGA
GCUGCUGGAA
>random_seq_from_cds__NO_661  RANDOM_LENGTH 87  SEQ_LENGTH  80
  GC_CONTENT  0.625  BASEPAIR  28  FREE_ENERGY  -35.10
  LEN_BP_RATIO  2.85714285714286
ACCCAGGGUCCCCACUGACUCCCGACUGCAGAUCAGCCUGGAGACGAGGUUGUCCAGAUCAACG
AGCAGGUGGUGGGUGGGAUGGC
>random_seq_from_cds__NO_669  RANDOM_LENGTH 70  SEQ_LENGTH  58
  GC_CONTENT  0.517241379310345  BASEPAIR  21  FREE_ENERGY
  -16.60  LEN_BP_RATIO  2.76190476190476
CCAUGAUGUGUACAAACCCUUCAUCUUCGUCUGAUACCCUGACAGAUCUGAGCAUGGUGGGUG
CGUCA
>random_seq_from_cds__NO_673  RANDOM_LENGTH 110 SEQ_LENGTH  99
  GC_CONTENT  0.626262626262626  BASEPAIR  35  FREE_ENERGY
  -45.00  LEN_BP_RATIO  2.82857142857143
CAGUGAAGAGGCACUGGAAGGAAUGGUACGGGGCUGAGGCAGGGUGGCGUGUCCCUAGGCC
AGCCACAGCCCUGACCCAGGAACAGUGGCGGAGCUCUUUCAUGC
>random_seq_from_cds__NO_675  RANDOM_LENGTH 110 SEQ_LENGTH  97
  GC_CONTENT  0.618556701030928  BASEPAIR  32  FREE_ENERGY
  -39.00  LEN_BP_RATIO  3.03125
CUGCAGGUCCUAGAAGAAGUGCUGGGUGACCCUGAGCUGACAGGAGAGAAGUUCGCCAGUGGAA
GGAGCAGAACCGGGAGCUGUACUCAGAGGGCCUGGGGGCCUGGGG
>random_seq_from_cds__NO_682  RANDOM_LENGTH 84  SEQ_LENGTH  72
  GC_CONTENT  0.5694444444444444  BASEPAIR  26  FREE_ENERGY
  -21.71  LEN_BP_RATIO  2.76923076923077
CAUGGAGCCUUGUGGAGGGGUGCUGGCUGGUUCCGGUUUUUAUGGAUGAGAAAUUGGAGAGGUUGA
UUAGGGCUGAGGGGCCAAA
>random_seq_from_cds__NO_698  RANDOM_LENGTH 72  SEQ_LENGTH  64
  GC_CONTENT  0.765625  BASEPAIR  24  FREE_ENERGY  -32.00
  LEN_BP_RATIO  2.666666666666667
CCAGGUCUGUGGGCCGCGUCCGGCAGAGAUGGCCUCUGGACUGGGGGGCGAGGCCAGGGCUGCA
CAGGGCC
>random_seq_from_cds__NO_710  RANDOM_LENGTH 73  SEQ_LENGTH  67
  GC_CONTENT  0.656716417910448  BASEPAIR  20  FREE_ENERGY
  -20.90  LEN_BP_RATIO  3.35
GACCGCUGGUAUGCCAUCUGCCACCCACUAUUGUUAAGAGCACAGCCCGGCGGGCCCGUGGCUC
CAUCCUGG
>random_seq_from_cds__NO_713  RANDOM_LENGTH 80  SEQ_LENGTH  62
  GC_CONTENT  0.645161290322581  BASEPAIR  21  FREE_ENERGY
  -27.10  LEN_BP_RATIO  2.95238095238095
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ACUGGGCCUCAUGGCCAUGGCCUAUUUCCAGAUUAUUCGCAAGCUCUGGGGCCGCCAGGAUCCCC
GGCACCACCUCAGCA

>random_seq_from_cds__NO_714 RANDOM_LENGTH 84 SEQ_LENGTH 75
GC_CONTENT 0.7333333333333333 BASEPAIR 27 FREE_ENERGY
-38.60 LEN_BP_RATIO 2.777777777777778
CUGGUGCGGAACUGGAAGCGCCCCUCAGACCAGCUGGGGGACCUGGAGCAGGGCCUGAGUGGAGA
GCCCCAGCCCCGGGCCCGC

>random_seq_from_cds__NO_716 RANDOM_LENGTH 85 SEQ_LENGTH 78
GC_CONTENT 0.628205128205128 BASEPAIR 25 FREE_ENERGY
-24.92 LEN_BP_RATIO 3.12
UUCGCCUCUGCUACCUGCCCAUCAGCGUCCUCA AUGUCCUUAAGAGGGGUGUUCGGGAUGUUC
GCCAAGCCAGUGACCGCGAA

>random_seq_from_cds__NO_717 RANDOM_LENGTH 110 SEQ_LENGTH 87
GC_CONTENT 0.586206896551724 BASEPAIR 22 FREE_ENERGY
-25.64 LEN_BP_RATIO 3.95454545454545
GCUGUCUACGCCUGCUUACCUUCUCCCACUGGCUGGUGUACGCCAACAGCGCUGCCAACCCCAU
CAUCUACAACUCCUCAGUGGGCAAUUCGGGAGCAGUUUAAGG

>random_seq_from_cds__NO_720 RANDOM_LENGTH 64 SEQ_LENGTH 52
GC_CONTENT 0.596153846153846 BASEPAIR 20 FREE_ENERGY
-19.00 LEN_BP_RATIO 2.6
AUGGGUGGGUACUGCUGCUCCAUCGGCAUGGCCCAAAGCAGUCAGAGGGAUUACAGUGGCCAG

>random_seq_from_cds__NO_723 RANDOM_LENGTH 110 SEQ_LENGTH 89
GC_CONTENT 0.685393258426966 BASEPAIR 30 FREE_ENERGY
-42.70 LEN_BP_RATIO 2.966666666666667
AAGCCUGCCGUCCUUCUCUGCCAAUCUGACCAGGGAGCCCAGGUGACCCUGGAGCACCUGGCCU
GCCCCGAGCACCAUCCUCCUGGAGGCCUGGUCGUCCCGGAGC

>random_seq_from_cds__NO_725 RANDOM_LENGTH 90 SEQ_LENGTH 65
GC_CONTENT 0.723076923076923 BASEPAIR 21 FREE_ENERGY
-28.90 LEN_BP_RATIO 3.0952380952381
GAUUUCAUCAUAUUCACCAUGUCUCCCAUGGAGCCAGGCACACCAGGCAAGCCAGGGCUCCCC
GAAGGCCCGGAGCUCCAGGGUGGC

>random_seq_from_cds__NO_728 RANDOM_LENGTH 84 SEQ_LENGTH 77
GC_CONTENT 0.714285714285714 BASEPAIR 30 FREE_ENERGY
-43.70 LEN_BP_RATIO 2.566666666666667
CCCCUCUUUGCCAGCUGCACCAUCCGUACCAGGUUCGCCUUGGGGGCCAGGGUGUCCAGGGGGG
CCGGGCUGGCCUGGGAGGC

>random_seq_from_cds__NO_739 RANDOM_LENGTH 78 SEQ_LENGTH 63
GC_CONTENT 0.698412698412698 BASEPAIR 23 FREE_ENERGY
-30.80 LEN_BP_RATIO 2.73913043478261
CCCGGAGGACCAGGUAGGCCUGGGCUCCCAACACAGCCAGGAUCUCCUCACUGUUGUCACCCCC
GGGCCUCCUGGC

>random_seq_from_cds__NO_763 RANDOM_LENGTH 68 SEQ_LENGTH 51
GC_CONTENT 0.705882352941177 BASEPAIR 19 FREE_ENERGY
-22.40 LEN_BP_RATIO 2.68421052631579

UGGACCAGGCAGGCCCGCUCACCCUJUUCCCUCCCCUUGGGGCCAGAGGGAGCAAGUGUGACCAUU
GCU

>random_seq_from_cds__NO_766 RANDOM_LENGTH 73 SEQ_LENGTH 59
GC_CONTENT 0.610169491525424 BASEPAIR 23 FREE_ENERGY
-22.70 LEN_BP_RATIO 2.56521739130435

UAGACCUUGCCUUCAGACUGUGGAUUGAUCUCAUUGAGCUCUUGCUCUGGGUGUCCCGGCGGGC
CUUGGAGG

>random_seq_from_cds__NO_790 RANDOM_LENGTH 99 SEQ_LENGTH 81
GC_CONTENT 0.703703703703704 BASEPAIR 26 FREE_ENERGY
-38.00 LEN_BP_RATIO 3.11538461538462

GGACGGCAGACAUCAGGUGAGCGCCAGCAGGGGCAGCACCCACGCAGGAGCUCAGAGUGAGGCC
CAUGGCGUCCUGGCCGAGGCUGAGCUGAGCAGG

>random_seq_from_cds__NO_792 RANDOM_LENGTH 80 SEQ_LENGTH 62
GC_CONTENT 0.451612903225806 BASEPAIR 22 FREE_ENERGY
-19.70 LEN_BP_RATIO 2.81818181818182

CGGCCUCUGCUUCUUGGAUUUGUCGGAGAUGCCAUCACGUGCCAUGAGCUUGUUGAAGACGAUG
AUUCCGAUGAGCAUG

>random_seq_from_cds__NO_821 RANDOM_LENGTH 70 SEQ_LENGTH 59
GC_CONTENT 0.661016949152542 BASEPAIR 22 FREE_ENERGY
-26.20 LEN_BP_RATIO 2.68181818181818

CAGCCCGGGUCGCCCUGUCUGCGCAUGUAUAGCCAGGCUCAUCUGCAGACCUCGGCCACUG
GGUUU

>random_seq_from_cds__NO_830 RANDOM_LENGTH 85 SEQ_LENGTH 60
GC_CONTENT 0.783333333333333 BASEPAIR 21 FREE_ENERGY
-32.80 LEN_BP_RATIO 2.85714285714286

CGAGAAGGCCCGUAGAGCACACCCGAGGCCAGGGCAGAGCAGGCACUGGGGGCGGGGUCGAAGG
CGGUGGCCAGGCGCAGGGAC

>random_seq_from_cds__NO_834 RANDOM_LENGTH 102 SEQ_LENGTH 89
GC_CONTENT 0.471910112359551 BASEPAIR 32 FREE_ENERGY
-26.60 LEN_BP_RATIO 2.78125

UCUUAUGUGAGCUCUACCACUGGGGGAGAGUGUGAUCACAAGAGAGAUGGUGGAGAUGCUCUUUU
CUGAUGAUUCUGACCUGCAGUUAGCAACCACACAGAA

>random_seq_from_cds__NO_848 RANDOM_LENGTH 100 SEQ_LENGTH 87
GC_CONTENT 0.551724137931034 BASEPAIR 26 FREE_ENERGY
-20.60 LEN_BP_RATIO 3.34615384615385

CGAGAACCAGGAGAUUCUACCAGAAGGCCUUCGACCUCAUUGAGCACUACUUUGGUGUAGAAGACG
AUGAUAGCAGCCUGGCUCCCAAGUCGAUGAAACG

>random_seq_from_cds__NO_854 RANDOM_LENGTH 83 SEQ_LENGTH 57
GC_CONTENT 0.596491228070175 BASEPAIR 19 FREE_ENERGY
-20.90 LEN_BP_RATIO 3

GUGAAACUUAUAAGCAGCAGACGGACAUCGUGUGAAUUGGGCUGGGGGCCUGCACCAUGCAAA
GAAGUCCGAGGCAUCUGG

>random_seq_from_cds__NO_855 RANDOM_LENGTH 88 SEQ_LENGTH 62
GC_CONTENT 0.5 BASEPAIR 22 FREE_ENERGY -19.80 LEN_BP_RATIO

2.81818181818182
CUUCUGUUACGUCAAUGAUAUCGUCUUGGCCAUCCUGGAACUGCUAAAGGUAUCACCAGAGGGUG
CUGUACAUGACAUGAUUAUUA
>random_seq_from_cds__NO_870 RANDOM_LENGTH 89 SEQ_LENGTH 81
GC_CONTENT 0.62962962962963 BASEPAIR 29 FREE_ENERGY
-32.50 LEN_BP_RATIO 2.79310344827586
CCAAGGCCUCUUCGUCAGAUGGUUGAGGCCAUCCGCUACUGCCAUGGCUGUGGUGGGCCAC
CGGGACCUCAAAUGUGAGAACGCC
>random_seq_from_cds__NO_872 RANDOM_LENGTH 88 SEQ_LENGTH 72
GC_CONTENT 0.611111111111111 BASEPAIR 25 FREE_ENERGY
-27.86 LEN_BP_RATIO 2.88
GUACAGCCUAUGCUGCCCCGAGGUGCUGCAGGGCAUCCCCACGAUAGCAAAAAAGGUGAUGC
UGGAGCAUGGGUGUGGUCCUGUA
>random_seq_from_cds__NO_881 RANDOM_LENGTH 81 SEQ_LENGTH 70
GC_CONTENT 0.5 BASEPAIR 24 FREE_ENERGY -22.74 LEN_BP_RATIO
2.91666666666667
ACAUCUUCUAAACCAGGAUCCUUCUGGAGAGUGCAACCCAGACUUGCGUCUCCGUGGACAUCAG
AAGGAAGGCUAUGGGC
>random_seq_from_cds__NO_884 RANDOM_LENGTH 69 SEQ_LENGTH 62
GC_CONTENT 0.451612903225806 BASEPAIR 21 FREE_ENERGY
-19.60 LEN_BP_RATIO 2.95238095238095
CUGGCAUCUACUCCAUGAGUCUCUGUUUGGGUCAGUUGCUGAUGAUCAGAAACUUAUGAUGUUGG
GAUA
>random_seq_from_cds__NO_885 RANDOM_LENGTH 119 SEQ_LENGTH 67
GC_CONTENT 0.477611940298507 BASEPAIR 23 FREE_ENERGY
-22.09 LEN_BP_RATIO 2.91304347826087
CUCGUUCAACAUAUACUCCAACCAAGCCACUCAGUUGAUGCUCACACUGCUGAAGUGAACUGC
CUUUCUUAUCCUUAUAGUGAGUUAUUCUUGCCACAGGAUCAGCUGACAAG
>random_seq_from_cds__NO_894 RANDOM_LENGTH 109 SEQ_LENGTH 93
GC_CONTENT 0.602150537634409 BASEPAIR 34 FREE_ENERGY
-34.70 LEN_BP_RATIO 2.73529411764706
UUGACACCAACAGCGAUGGCACCAUAGACUUUCGGGAGUUCAUCAUUGCGCUGAGCGUGACCUCG
CGCGGCCCGCUGGAGCAGAAGCUCUUGUGGGCCUUCAGCAUGUA
>random_seq_from_cds__NO_905 RANDOM_LENGTH 82 SEQ_LENGTH 72
GC_CONTENT 0.430555555555556 BASEPAIR 29 FREE_ENERGY
-21.70 LEN_BP_RATIO 2.48275862068966
UAUCAUCUGUUUUGAGGUGCUUAGGUGAAGGAGAAGUCAUGAAAGAUGGACCCCUUUUCUUUACC
CUGAGACUUAGACGAUU
>random_seq_from_cds__NO_906 RANDOM_LENGTH 72 SEQ_LENGTH 65
GC_CONTENT 0.492307692307692 BASEPAIR 19 FREE_ENERGY
-17.14 LEN_BP_RATIO 3.42105263157895
CCUUUGCCGCCUCAGCCUUGACAGGAGAAAGUGUAUGAAAGACAAAGUUUCUUGAAUUUCGAGGA
GCACUGG
>random_seq_from_cds__NO_907 RANDOM_LENGTH 79 SEQ_LENGTH 65

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GC_CONTENT    0.553846153846154    BASEPAIR    22    FREE_ENERGY
-21.50    LEN_BP_RATIO    2.9545454545454545
GGUUAUGGUCAGAGAGAGCAGCCAGUUUCUGAAGCACAGCUUUGGGCUGGUUUAGCAGUGAGCCU
GUCUUCACCCUGUU
>random_seq_from_cds__NO_939    RANDOM_LENGTH    110    SEQ_LENGTH    94
GC_CONTENT    0.372340425531915    BASEPAIR    30    FREE_ENERGY
-18.50    LEN_BP_RATIO    3.1333333333333333
UUGUCUGCUCAGAACCUUUACUAUGGUGAUCACUGUUCAUUUCAGUAGUAUUUGCAGUGUCUAUG
AUUUCUUUGUGAUGGCUUGACUGAUUUUAGAUGACCUUCAUAG
>random_seq_from_cds__NO_946    RANDOM_LENGTH    85    SEQ_LENGTH    67
GC_CONTENT    0.432835820895522    BASEPAIR    25    FREE_ENERGY
-15.90    LEN_BP_RATIO    2.68
CUUUUAUCAUGUAUGUCUUUUUGGAACUCUUUCUGUCAGUGGUAAGUCUGUAGAGUUUCCAGAC
UGAAGACUCAGCUCUAAGCA
>random_seq_from_cds__NO_953    RANDOM_LENGTH    81    SEQ_LENGTH    63
GC_CONTENT    0.5555555555555556    BASEPAIR    23    FREE_ENERGY
-21.80    LEN_BP_RATIO    2.73913043478261
CUGGCCAAUUACUUUGAGGUGGACAUCCCUAAGAUCGACGUGUACCACUACGAGGUGGACAUCAA
GCCGGAUAAGUGUCCC
>random_seq_from_cds__NO_954    RANDOM_LENGTH    67    SEQ_LENGTH    52
GC_CONTENT    0.5    BASEPAIR    19    FREE_ENERGY    -16.20    LEN_BP_RATIO
2.73684210526316
CGUAGAGUCAACCGGGGAAGUGGUGGAAUACAUGGUCCAGCAUUUCAAGCCUCAGAUUUUGGUG
AU
>random_seq_from_cds__NO_980    RANDOM_LENGTH    110    SEQ_LENGTH    98
GC_CONTENT    0.612244897959184    BASEPAIR    34    FREE_ENERGY
-39.60    LEN_BP_RATIO    2.88235294117647
CACACGCUCUGUCUCUAUCCAGCACCUGCCUACUAUGCCCGCCUGGUGGCUUCCGGGCACGAU
ACCACCGUGGACAAGGAGCAUGACAGGUGGAGAGGGGAGCCAC
>random_seq_from_cds__NO_1004    RANDOM_LENGTH    80    SEQ_LENGTH    70
GC_CONTENT    0.628571428571429    BASEPAIR    27    FREE_ENERGY
-31.40    LEN_BP_RATIO    2.59259259259259
AUGGUGGUGGACUCCAUGAGCAGCGCGUAGUCGGCCGUCAGGGCCUCUGGAUGCCCUCCUCGUU
GUUCUUCACCAGCGC
>random_seq_from_cds__NO_1020    RANDOM_LENGTH    81    SEQ_LENGTH    73
GC_CONTENT    0.534246575342466    BASEPAIR    25    FREE_ENERGY
-19.41    LEN_BP_RATIO    2.92
GUUGUCCACAUUGAGAAUCCGGAAUCCUGUCAGGUUCACGCCUGAGUAGCGGUAGGGCUCCAGGU
CUAAAGCGUAGAGAUC
>random_seq_from_cds__NO_1023    RANDOM_LENGTH    71    SEQ_LENGTH    53
GC_CONTENT    0.566037735849057    BASEPAIR    19    FREE_ENERGY
-17.40    LEN_BP_RATIO    2.78947368421053
GGAGCUGACGGAUCUUCAGGCGGAUGUUGUAUCUUGAUGGGCCAUGAUGAGCUCCUGCAGUCGG
AUGAGC
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>random_seq_from_cds__NO_1025 RANDOM_LENGTH 90 SEQ_LENGTH 64
  GC_CONTENT 0.640625 BASEPAIR 25 FREE_ENERGY -31.90
  LEN_BP_RATIO 2.56
UAGAGGUUCACGUAGAAGGUGUCCUUGUUGUCCAGCGGGUGGUGCUCCAACGCAGCUGGAUGUG
GGGCACCUCCAGGGCAUUGCAGAUG
>random_seq_from_cds__NO_1031 RANDOM_LENGTH 72 SEQ_LENGTH 57
  GC_CONTENT 0.385964912280702 BASEPAIR 21 FREE_ENERGY
  -16.80 LEN_BP_RATIO 2.71428571428571
AAGCUAAAUAUGCAGCAAUUGCUAUCCAAAACCUUGGAUCUUUCAGCAGUGCUUUUAUCAAAGCAG
CUAAACA
>random_seq_from_cds__NO_1057 RANDOM_LENGTH 96 SEQ_LENGTH 89
  GC_CONTENT 0.539325842696629 BASEPAIR 33 FREE_ENERGY
  -42.80 LEN_BP_RATIO 2.6969696969697
CGAGACUUGAAUCUGCCCACAAUACAUUUGCGGUCAUUGAGGAGCAUGCCAUUCAUCUUCUGA
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>random_seq_from_cds__NO_1062 RANDOM_LENGTH 86 SEQ_LENGTH 73
  GC_CONTENT 0.63013698630137 BASEPAIR 24 FREE_ENERGY
  -35.84 LEN_BP_RATIO 3.04166666666667
CAGGUCGCCACGUACAGGGAGGCCAUGGGGUAGCUGCUGGCCGCAGCGUUCAUGAUGGCCACCA
CCAAGCGGUCUUGUACGUGG
>random_seq_from_cds__NO_1064 RANDOM_LENGTH 92 SEQ_LENGTH 69
  GC_CONTENT 0.420289855072464 BASEPAIR 26 FREE_ENERGY
  -24.10 LEN_BP_RATIO 2.65384615384615
CAUCACAGAUAAUUCAGAUUCCUCUGGAUUAUGAAACAGGAAAAGCACCGAGGAUUUGCUUUUGUU
GAAUUUGAGUUGGCAGAGGGGAUGCUGC
>random_seq_from_cds__NO_1106 RANDOM_LENGTH 88 SEQ_LENGTH 63
  GC_CONTENT 0.555555555555556 BASEPAIR 22 FREE_ENERGY
  -19.91 LEN_BP_RATIO 2.86363636363636
GCUUGGUGGAACCGUGGGGACAUAAGAAAGCAUGCCCUUUAUUGAGGCCUUCGUCAGUCCAUAU
UCAAGGUCAAAAGAGAGAACUUU
>random_seq_from_cds__NO_1112 RANDOM_LENGTH 89 SEQ_LENGTH 71
  GC_CONTENT 0.52112676056338 BASEPAIR 19 FREE_ENERGY
  -18.90 LEN_BP_RATIO 3.73684210526316
UGUCAUUAAGGCUCUGGAGCAUUCUGCACUGGCCAUCAACCACAAAUUGGAAAUCAAGGUACAUA
GAUUCUGCGGACUUGGAGCCCAUC
>random_seq_from_cds__NO_1114 RANDOM_LENGTH 78 SEQ_LENGTH 71
  GC_CONTENT 0.52112676056338 BASEPAIR 27 FREE_ENERGY
  -23.10 LEN_BP_RATIO 2.62962962962963
UCCAAGCAAUUGCCUGGGCUCGGAAUCAGAAAAGCCUUUUUUGGGGCGUGUGCUUAGGGAUGCA
GUUGGCAGUGGUU
>random_seq_from_cds__NO_1134 RANDOM_LENGTH 77 SEQ_LENGTH 55
  GC_CONTENT 0.6 BASEPAIR 21 FREE_ENERGY -26.30 LEN_BP_RATIO
  2.61904761904762
ACAGGAGGGGGCACCAGUGAUCGACACAUUCGCAUCUGGAAUGUGUGCUCUGGGGCCUGUCUGAG
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UGCCGUGGAUGC
>random_seq_from_cds__NO_1143 RANDOM_LENGTH 85 SEQ_LENGTH 78
  GC_CONTENT 0.602564102564103 BASEPAIR 27 FREE_ENERGY
  -32.20 LEN_BP_RATIO 2.88888888888889
GUCUGCGUGGGCAUCGUGGGCAGUGGGCUGCCCUGGCCGAUGCUCAGAACCCCAGCCUCUUUGU
AAAGAUUCUCAUCGUGGAGA
>random_seq_from_cds__NO_1172 RANDOM_LENGTH 84 SEQ_LENGTH 75
  GC_CONTENT 0.44 BASEPAIR 24 FREE_ENERGY -19.10
  LEN_BP_RATIO 3.125
GGAUCAUCGAUGUUGUCUACAAUGCAUCUAAUAACGAGCUGGUUCGUACCAAGACCCUGGUGAAG
AAUUGCAUCGUGCUCAUCG
>random_seq_from_cds__NO_1181 RANDOM_LENGTH 92 SEQ_LENGTH 83
  GC_CONTENT 0.686746987951807 BASEPAIR 28 FREE_ENERGY
  -38.90 LEN_BP_RATIO 2.96428571428571
CGGGGGCAAUGUGUGUCUCAAGGGCAUGGGCGGCCCGCAGGUCCGGCUGCCCUGGGUGGUCAGG
AAGCCCAGAGCCACGUGGACUGUGAA
>random_seq_from_cds__NO_1196 RANDOM_LENGTH 94 SEQ_LENGTH 76
  GC_CONTENT 0.644736842105263 BASEPAIR 25 FREE_ENERGY
  -36.90 LEN_BP_RATIO 3.04
UCAGAGCCCAGUGGGUCAGAAGGUGGGGCACCAGGUGGGCUUGGGGAGGCAGGAUGGUGACCAC
AUGCUGGCUGCUGGCUUCACAGUGGGUAA
>random_seq_from_cds__NO_1208 RANDOM_LENGTH 77 SEQ_LENGTH 70
  GC_CONTENT 0.685714285714286 BASEPAIR 23 FREE_ENERGY
  -28.70 LEN_BP_RATIO 3.04347826086957
GGAGCCCUGCCUGCUGUGAUGGUUGGGGGCACUAGGUGGGCAGUGGAGGUCAUCAGGGUGCAGAC
AGGGCCGCCCCA
>random_seq_from_cds__NO_1212 RANDOM_LENGTH 81 SEQ_LENGTH 74
  GC_CONTENT 0.554054054054054 BASEPAIR 31 FREE_ENERGY
  -30.50 LEN_BP_RATIO 2.38709677419355
UCCCAUAGAGUGAUACUUGGACUUUACUGGCAGUGAGGGCUGCCUGGAGGUGGAGGCCAAGUGCU
UCGGGUGUGAGGAUGU
>random_seq_from_cds__NO_1217 RANDOM_LENGTH 85 SEQ_LENGTH 75
  GC_CONTENT 0.56 BASEPAIR 25 FREE_ENERGY -23.80
  LEN_BP_RATIO 3
GCGGCGAUCGAGUCAUCAUGGAAGCGAAUGGGUUGGGGACCUCAGGGUUUUCGGAGCUGAAGAA
UGACACAUUCCUGCGAGCAG
>random_seq_from_cds__NO_1223 RANDOM_LENGTH 84 SEQ_LENGTH 67
  GC_CONTENT 0.597014925373134 BASEPAIR 24 FREE_ENERGY
  -28.60 LEN_BP_RATIO 2.79166666666667
GUUGAGGGUGGUGGCUCAAGCACCAUGGCUCAGGCCAAGCGCUGGCUCUAUCAGAGACCUCAGGC
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>random_seq_from_cds__NO_1243 RANDOM_LENGTH 67 SEQ_LENGTH 57
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  -15.10 LEN_BP_RATIO 2.85
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CCGAUGAAAAAUGCCUUUGAAGUGAAGGUAGCUGAGGCCACUGCUAUGUCAUAGGCCAGUUUUA
CC

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GC_CONTENT 0.577777777777778 BASEPAIR 28 FREE_ENERGY
-32.30 LEN_BP_RATIO 3.21428571428571

UGGAGGAGGAGCUUGGCUCCAGCCAGCUGGCCAAGAGAAAACCUGAAGGCAGGUCCUGUGAUGA
UGAAGACUGGCAACCUGGCCUAGUGGACUCCUAGGAA

>random_seq_from_cds__NO_1251 RANDOM_LENGTH 85 SEQ_LENGTH 62
GC_CONTENT 0.725806451612903 BASEPAIR 19 FREE_ENERGY
-33.00 LEN_BP_RATIO 3.26315789473684

AGGGUCCUCUGGGCUCUCGAGCAUUGGGCCUGAAAAGGGCUGGGGUCCGCCGGGCCCUCCAUGAC
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>random_seq_from_cds__NO_1257 RANDOM_LENGTH 81 SEQ_LENGTH 66
GC_CONTENT 0.515151515151515 BASEPAIR 23 FREE_ENERGY
-20.90 LEN_BP_RATIO 2.8695652173913

GUCUUCUCCCAUCCUCAUCAUUCUUAUGAGACCUUCCGCCUUAUGUUGGAGUCCUCCAGAAAAG
GAAGUGUUGGUCUGGU

>random_seq_from_cds__NO_1265 RANDOM_LENGTH 84 SEQ_LENGTH 70
GC_CONTENT 0.585714285714286 BASEPAIR 26 FREE_ENERGY
-25.30 LEN_BP_RATIO 2.69230769230769

UCUAAGGCCUUGGAGCCCCAGCUGUCAGGGUAAGAUGCUGGUCCUGGAUUUAUUCUGGCGGUGA
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>random_seq_from_cds__NO_1272 RANDOM_LENGTH 72 SEQ_LENGTH 60
GC_CONTENT 0.616666666666667 BASEPAIR 21 FREE_ENERGY
-22.30 LEN_BP_RATIO 2.85714285714286

CCGUCAGAUCCGGCCACCCCUGAUGGUUCUGACUGCACUUCAGACCUGGCAGGGUGGAACCACU
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>random_seq_from_cds__NO_1273 RANDOM_LENGTH 77 SEQ_LENGTH 57
GC_CONTENT 0.666666666666667 BASEPAIR 19 FREE_ENERGY
-26.80 LEN_BP_RATIO 3

UAAGUGGGGGCUCGGGAUGAGGUACUCCAGGCUGCCUGGGAUGCUGCCUCCACUGCCAUCACCU
UCGUCUCCACC

>random_seq_from_cds__NO_1275 RANDOM_LENGTH 98 SEQ_LENGTH 86
GC_CONTENT 0.813953488372093 BASEPAIR 37 FREE_ENERGY
-63.10 LEN_BP_RATIO 2.32432432432432

CCUGGCCUGCUGCUUCGUGGCGGCGGCCUGGCCUUGCGCUGGUCCGGGCGCCGGACGGCGCGGG
GCGCGGUGGUCCGGGCGCGACAGAGGCAGCGAG

>random_seq_from_cds__NO_1276 RANDOM_LENGTH 86 SEQ_LENGTH 62
GC_CONTENT 0.741935483870968 BASEPAIR 25 FREE_ENERGY
-46.00 LEN_BP_RATIO 2.48

CGGGCCUGGAGAACAUGGACAGGGCGGCGCAGCGCUUCCGGCUCCAGGAACCCAGACCUGGACUC
AGAGGCGCUGCUAGCCCUGCC

>random_seq_from_cds__NO_1280 RANDOM_LENGTH 82 SEQ_LENGTH 71
GC_CONTENT 0.704225352112676 BASEPAIR 24 FREE_ENERGY

-30.90 LEN_BP_RATIO 2.9583333333333333
UGAAGGGGUGCCGGCGGAGUGCGACAGCGUAGUGGUGCAUGUGCUGAAGCUGCAGGGUGCCGUGC
CCUUCGUGCACACCAAU
>random_seq_from_cds__NO_1284 RANDOM_LENGTH 71 SEQ_LENGTH 56
GC_CONTENT 0.642857142857143 BASEPAIR 20 FREE_ENERGY
-21.20 LEN_BP_RATIO 2.8
AGAGCCUGGCACUGUGCCUGCGAGCCUGCUGUGUGAGGACAUGUCCGCUUGGACCCACUGUG
CCUCCC
>random_seq_from_cds__NO_1286 RANDOM_LENGTH 87 SEQ_LENGTH 74
GC_CONTENT 0.702702702702703 BASEPAIR 26 FREE_ENERGY
-33.70 LEN_BP_RATIO 2.84615384615385
CUAUACCAUGCCCUCCCCGGCCAUGAGGCGGGCCGUGCUGGAGACCAAACAGAGCCUUGAGGCUG
CGGGGCACACGGCUGGUUCCU
>random_seq_from_cds__NO_1306 RANDOM_LENGTH 86 SEQ_LENGTH 66
GC_CONTENT 0.560606060606061 BASEPAIR 25 FREE_ENERGY
-27.30 LEN_BP_RATIO 2.64
CAGUGGUAUCUCCUGGUUUCUCUACUGCAUGGCCUGUACCCUGAGCACCAGCAUCGUUGUAGAG
AGGAGGUCCGCGAGAUCCUAG
>random_seq_from_cds__NO_1310 RANDOM_LENGTH 83 SEQ_LENGTH 72
GC_CONTENT 0.555555555555556 BASEPAIR 24 FREE_ENERGY
-24.40 LEN_BP_RATIO 3
ACUGAGAAUGCAUCCAAACGCCAUCCCUUUGCCUUUAUGCCCUUCUCUGCUGGGCCAGGGAACU
GCAUUGGGCAGCAGUUUG
>random_seq_from_cds__NO_1319 RANDOM_LENGTH 82 SEQ_LENGTH 49
GC_CONTENT 0.510204081632653 BASEPAIR 19 FREE_ENERGY
-20.90 LEN_BP_RATIO 2.57894736842105
CACCUCAGCACGGAGGUCCUUGUCUGACAAGAUGCUCCCAUCUCCAUCUUUGGCCAAGAGGAGG
AUAUCCAGAAAAUCCAA
>random_seq_from_cds__NO_1322 RANDOM_LENGTH 68 SEQ_LENGTH 59
GC_CONTENT 0.542372881355932 BASEPAIR 19 FREE_ENERGY
-17.20 LEN_BP_RATIO 3.10526315789474
GGUCACUAAUGGCCUGUAUGUAGGACUGAGAAUCCCUGUCCACCUGGAUGCUGCCUGAUGGCU
GAA
>random_seq_from_cds__NO_1324 RANDOM_LENGTH 106 SEQ_LENGTH 94
GC_CONTENT 0.574468085106383 BASEPAIR 32 FREE_ENERGY
-35.60 LEN_BP_RATIO 2.9375
AGGAGCUCUCCCAUUUGUCCCAGCAUCACUCGUACAGAGUCUGCCAUGAGCCCCACAUAGGGCU
UCAGGAUGUCAUAGUGGAAGGCUGGGGUCAGCAUCCGUCGA
>random_seq_from_cds__NO_1335 RANDOM_LENGTH 96 SEQ_LENGTH 69
GC_CONTENT 0.405797101449275 BASEPAIR 27 FREE_ENERGY
-19.40 LEN_BP_RATIO 2.555555555555556
AUUCCAUUUUAACAUCUGAAAGCAUACAUAUGAGGUGAUGGCUCAUUCUGUGAAAUGAUGCUGG
GAUAAGUGGGAGAAGAUUUGCAGCACUCAGG
>random_seq_from_cds__NO_1336 RANDOM_LENGTH 67 SEQ_LENGTH 57

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GC_CONTENT    0.43859649122807 BASEPAIR   21 FREE_ENERGY
-18.20 LEN_BP_RATIO  2.71428571428571
ACACAAGCGUGGAGGUCUAUGAGCACAUCAACUCGAUGUCUCUGGAUUAUAUCAUGAAAUGCUCU
UU
>random_seq_from_cds__NO_1345 RANDOM_LENGTH 83 SEQ_LENGTH    73
GC_CONTENT    0.465753424657534  BASEPAIR   27 FREE_ENERGY
-15.70 LEN_BP_RATIO  2.7037037037037
UUGAGGUUCUCUCAGGAGAAUUCUGAUCAGAGACACCCCUAUGCCUACUUACCAUUCUCAGCUGG
AUCAAGGGAACUGCAUUG
>random_seq_from_cds__NO_1346 RANDOM_LENGTH 82 SEQ_LENGTH    70
GC_CONTENT    0.485714285714286  BASEPAIR   22 FREE_ENERGY
-21.10 LEN_BP_RATIO  3.18181818181818
GGCAGGAGUUUGCCAUGAUUGAGUUAAAGGUAACCAUUGCCUUGAUUCUGCUCCACUUCAGAGUG
ACUCCAGACCCCACCAG
>random_seq_from_cds__NO_1349 RANDOM_LENGTH 110 SEQ_LENGTH    99
GC_CONTENT    0.494949494949495  BASEPAIR   31 FREE_ENERGY
-23.70 LEN_BP_RATIO  3.19354838709677
CCUACCAGAUGUACCUUGGAAGCAGGAGCCAUGACUUUCAGCUACAUAUUGAGCAGGGGGUGU
GUGAUUUGGUUUUAUGUGAAGCUGCCUCCCCUAAGACGUUGGCUU
>random_seq_from_cds__NO_1352 RANDOM_LENGTH 82 SEQ_LENGTH    64
GC_CONTENT    0.46875  BASEPAIR   20 FREE_ENERGY  -15.50
LEN_BP_RATIO  3.2
AGAGGAUCAUGGUGCCAAUAUCGAAGAAGUGUUACAACGAGGAGAAGCACUCUCAGGCAUUGGA
UUCAAAGGCUAACAAUU
>random_seq_from_cds__NO_1354 RANDOM_LENGTH 88 SEQ_LENGTH    66
GC_CONTENT    0.772727272727273  BASEPAIR   24 FREE_ENERGY
-30.10 LEN_BP_RATIO  2.75
UGUUAAUAGUGUAUGUCCGAUUCUGGUGGCUGUGAGAUGGUGCCCCGCCUGCUGCUGCGCGCCUG
GCCCCGGGGCCCCGCGGUUGGUC
>random_seq_from_cds__NO_1372 RANDOM_LENGTH 68 SEQ_LENGTH    49
GC_CONTENT    0.591836734693878  BASEPAIR   19 FREE_ENERGY
-23.40 LEN_BP_RATIO  2.57894736842105
GCCCUC CAGGCACAGUGCUGGUGAGCUUCAGCAGAUGAUGGUUGAGUGCUC CAAGUACCAUGGCC
AGC
>random_seq_from_cds__NO_1373 RANDOM_LENGTH 99 SEQ_LENGTH    72
GC_CONTENT    0.5694444444444444  BASEPAIR   24 FREE_ENERGY
-27.90 LEN_BP_RATIO  3
UGACCAAAGAAGCAGCAAUGGGGCCAGGGCUUUGACCGACACUUGUUUGCUCUGCGGCAUCUGGC
AGCAGCCAAAGGGAUCAUCUUGCCUGAGCUCUAC
>random_seq_from_cds__NO_1378 RANDOM_LENGTH 110 SEQ_LENGTH    96
GC_CONTENT    0.3333333333333333  BASEPAIR   27 FREE_ENERGY
-20.81 LEN_BP_RATIO  3.55555555555556
CUGGACAAGAUAAUAAAUAUCUCGUAAGCCUUCUGGAUCCCUUGGAUUGAUUGACAUCAUAAGG
GAACCAAUUUUUGAUGUUGUAAAAGAAAUGUGUUAUCUCCAAUG
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>random_seq_from_cds__NO_1406 RANDOM_LENGTH 75 SEQ_LENGTH 58
  GC_CONTENT 0.431034482758621 BASEPAIR 20 FREE_ENERGY
  -17.10 LEN_BP_RATIO 2.9
CAAGUUCAUCAUGACUAUGGCACCCAUUACAUCACAUCUGGAUCCAUGGGUGGCAUUUAUGAAU
AUAUCCUGGU

>random_seq_from_cds__NO_1417 RANDOM_LENGTH 75 SEQ_LENGTH 66
  GC_CONTENT 0.560606060606061 BASEPAIR 21 FREE_ENERGY
  -23.40 LEN_BP_RATIO 3.14285714285714
CAAUGGGGGUAUCUCUCCGAUAGGAGACCUCACAGGCUAGGCCUUGGGAUCCAACAGGACAGAU
GCAGUCACAG

>random_seq_from_cds__NO_1420 RANDOM_LENGTH 102 SEQ_LENGTH 88
  GC_CONTENT 0.636363636363636 BASEPAIR 30 FREE_ENERGY
  -35.60 LEN_BP_RATIO 2.93333333333333
GAUGAUGGCUGGGUUGUACUGCACAGCGUCUCCCCACUCCUGCAUCAGGUCCGCCGUCGGCAGCU
CCUGGUAUGCCAGGGUGGUGAUGUGCUCACUUGCCCC

>random_seq_from_cds__NO_1423 RANDOM_LENGTH 81 SEQ_LENGTH 64
  GC_CONTENT 0.484375 BASEPAIR 21 FREE_ENERGY -17.60
  LEN_BP_RATIO 3.04761904761905
CAUGGCCUCUUGUUAUAACGAGGGUGUAUUAUAAAUGCCCCAAGCACAGCCUCUGUGAUGU
AGUGGGUCCCAAAAU

>random_seq_from_cds__NO_1470 RANDOM_LENGTH 110 SEQ_LENGTH 105
  GC_CONTENT 0.419047619047619 BASEPAIR 33 FREE_ENERGY
  -31.40 LEN_BP_RATIO 3.18181818181818
GAGAUGUCAAUGCUGAAUGCAUAUAAACCCAAGGAGCAAGGCUAAAGAGCUACCUCUUCUGCUG
UACGCUUUAUGGAAGAAUUGGGUGAGUGGCCUUGGAAAAAUCU

>random_seq_from_cds__NO_1473 RANDOM_LENGTH 85 SEQ_LENGTH 74
  GC_CONTENT 0.445945945945946 BASEPAIR 26 FREE_ENERGY
  -29.82 LEN_BP_RATIO 2.84615384615385
GUGCAUGCUUUUUGAGUAUAUUAUCAGGGGGAUCUCCAUGAGUCCUCAUCAUGAGAUGCCAC
ACUCUGAUGUUGGCUGCAGC

>random_seq_from_cds__NO_1495 RANDOM_LENGTH 110 SEQ_LENGTH 96
  GC_CONTENT 0.572916666666667 BASEPAIR 28 FREE_ENERGY
  -27.79 LEN_BP_RATIO 3.42857142857143
ACUCUCAGGCUUCAGAGAUUUAACAGCCACCUGCUCUCCUUGUAUUGUCCCUUCGGGGUCAUACC
UGCAGAGCUCAACCUUCCCAAAGUGGCCUCCUCCCAAGUCACGG

>random_seq_from_cds__NO_1507 RANDOM_LENGTH 86 SEQ_LENGTH 71
  GC_CONTENT 0.577464788732394 BASEPAIR 27 FREE_ENERGY
  -25.30 LEN_BP_RATIO 2.62962962962963
GGUUGGAGAUUCCUCGGGGCUUGGGCUGGCAGCAGCGUUUJAGCAUGAAGCUGAUGUUAUCCGU
GCGCAGGAUCUGCUUCUUGAG

>random_seq_from_cds__NO_1522 RANDOM_LENGTH 86 SEQ_LENGTH 66
  GC_CONTENT 0.454545454545455 BASEPAIR 24 FREE_ENERGY
  -18.20 LEN_BP_RATIO 2.75
AUUUUUCUGCUUCUUGGAGAAUGACGCCACACUGACUGCUCAUUGUCGUUGGUCCAUGCCAAU
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UGGUGAAAUAGAACCCUCAUC
>random_seq_from_cds__NO_1530 RANDOM_LENGTH 90 SEQ_LENGTH 73
  GC_CONTENT 0.397260273972603 BASEPAIR 25 FREE_ENERGY
  -15.90 LEN_BP_RATIO 2.92
UUCUGGAACCACAUGCUUCUAUGUACUGCACUGCUGAAUGUCCCAAACAUUUUAAGAGACACUG
AUAUGUGGAAAAGACAUUUCUUCUG
>random_seq_from_cds__NO_1558 RANDOM_LENGTH 89 SEQ_LENGTH 76
  GC_CONTENT 0.368421052631579 BASEPAIR 26 FREE_ENERGY
  -15.70 LEN_BP_RATIO 2.92307692307692
GGCCAAAGGAAGACAUGAUUUGCUGGAUCUGAAACCAUUUACAGAAUAUGAAUUUCAGAUUUCU
CUAAGCUACAUCUUUAUAAGGGAA
>random_seq_from_cds__NO_1563 RANDOM_LENGTH 74 SEQ_LENGTH 56
  GC_CONTENT 0.607142857142857 BASEPAIR 20 FREE_ENERGY
  -25.20 LEN_BP_RATIO 2.8
CGUAUUAACAUAUAUGAACCGUGUGAGGCAGGGUUGCUGGCUCCUCGCCAGGUCUCUGCAAACU
CAGAGGGCA
>random_seq_from_cds__NO_1571 RANDOM_LENGTH 100 SEQ_LENGTH 81
  GC_CONTENT 0.481481481481481 BASEPAIR 26 FREE_ENERGY
  -22.83 LEN_BP_RATIO 3.11538461538462
CAUGGUGGGCAUUUUCUCAACGCAUUACUCCAGCAAAAAGGUGUUUGUUCUCCUAGCAGCCCUC
AGACCUCAGUGGUGUAGCAGAGAAAUCCAGAUC
>random_seq_from_cds__NO_1579 RANDOM_LENGTH 82 SEQ_LENGTH 67
  GC_CONTENT 0.626865671641791 BASEPAIR 23 FREE_ENERGY
  -21.60 LEN_BP_RATIO 2.91304347826087
GAUAAGGUGGGGGAUGCCCUGGAGGAAGUGCUCAGCAAAGCCCUGAGUCAGCGCACGAUCACUGU
CGGGGUGUACGAAGCGG
>random_seq_from_cds__NO_1582 RANDOM_LENGTH 71 SEQ_LENGTH 63
  GC_CONTENT 0.80952380952381 BASEPAIR 23 FREE_ENERGY
  -34.90 LEN_BP_RATIO 2.73913043478261
UGCGCGUCAGCAACCCGGGCCGGCUGGCGGAGCUCCUGCUCUUGGAGACCGACGCUGGCCCCGCG
GCGAGC
>random_seq_from_cds__NO_1585 RANDOM_LENGTH 110 SEQ_LENGTH 100
  GC_CONTENT 0.76 BASEPAIR 37 FREE_ENERGY -57.80
  LEN_BP_RATIO 2.7027027027027
CCUGAACGGUGACAUGAGCAACACUACCGUCGUCCCCAGCACUGCAGGUCCGGGCCCCAGCGGCG
GGCCCCGUGGCGGAGGUGGUGGUGGCGGCGGAGGCGGCGGCACCG
>random_seq_from_cds__NO_1587 RANDOM_LENGTH 73 SEQ_LENGTH 62
  GC_CONTENT 0.516129032258065 BASEPAIR 21 FREE_ENERGY
  -19.60 LEN_BP_RATIO 2.95238095238095
UUCGCCUUUGCCAGUCUCAUCUCGUGUCUGCUUUGUUAAGUCCAUGAUCCAGACUCAGCAGUUG
UGGCACAG
>random_seq_from_cds__NO_1633 RANDOM_LENGTH 81 SEQ_LENGTH 68
  GC_CONTENT 0.426470588235294 BASEPAIR 24 FREE_ENERGY
  -16.90 LEN_BP_RATIO 2.83333333333333
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UUUUCUACUAUAAGUACCAGAGCGAAUGUAUGUCUCCACGGGGUUGACACCACAUGCAUGGACCU
UGAUUAGAACCCUGAU

>random_seq_from_cds__NO_1636 RANDOM_LENGTH 87 SEQ_LENGTH 73
GC_CONTENT 0.506849315068493 BASEPAIR 25 FREE_ENERGY
-18.10 LEN_BP_RATIO 2.92

UGCCCAUAAUCCCAGAAUAAAGCCCCAGGAGGAUGCCAGUCUUUCAGCUUCGGUUUCCUGGUGU
AUUAUCUGAGCUACAGGAAGUU

>random_seq_from_cds__NO_1646 RANDOM_LENGTH 110 SEQ_LENGTH 90
GC_CONTENT 0.433333333333333 BASEPAIR 33 FREE_ENERGY
-26.30 LEN_BP_RATIO 2.72727272727273

AACACUGUAGCUGGUUUGGAUUUCUAGGAUUACAGGCCAUUAUCAUCUGCAAGCAUJAGGACAAU
GUGACCUGUCAGGAAUACCUAGCCUCUUGACACUUCUAUAAACAG

>random_seq_from_cds__NO_1655 RANDOM_LENGTH 87 SEQ_LENGTH 77
GC_CONTENT 0.649350649350649 BASEPAIR 32 FREE_ENERGY
-45.80 LEN_BP_RATIO 2.40625

GAGGCCAGGAGGUCCAUGGGGGCCUGGGACACCAUGGGGCCAUGGGGUACAGGUGGCCCUAAA
GGAUUUACUGGGCCACCAAUC

>random_seq_from_cds__NO_1675 RANDOM_LENGTH 89 SEQ_LENGTH 82
GC_CONTENT 0.609756097560976 BASEPAIR 28 FREE_ENERGY
-25.00 LEN_BP_RATIO 2.92857142857143

CACCAGGCCCGGGUCCAGCAUACCACAAACGCCCCUAAGACAGUCAUCACCGUCUUAUJAGC
UUAUGGGUGUCCUCCGGCGGCUG

>random_seq_from_cds__NO_1680 RANDOM_LENGTH 68 SEQ_LENGTH 53
GC_CONTENT 0.415094339622642 BASEPAIR 19 FREE_ENERGY
-16.70 LEN_BP_RATIO 2.78947368421053

UUUUUGAAACUGGGCCUGUGUUAAACAUCAGGAAUACAUAGGCAAUCCAGCGAAGAAAUCGGCA
GCA

>random_seq_from_cds__NO_1683 RANDOM_LENGTH 109 SEQ_LENGTH 91
GC_CONTENT 0.373626373626374 BASEPAIR 31 FREE_ENERGY
-24.50 LEN_BP_RATIO 2.93548387096774

CAGUGUUGCUCCAUUAUAAAAAAGUCCAUGUGCUUGUCAUAGUGACACUCAUUAUGUCAUUG
UCGUGAAACAGUACGUGAUCUUAAGGGAAGAAACAUCUCACUAG

>random_seq_from_cds__NO_1709 RANDOM_LENGTH 70 SEQ_LENGTH 50
GC_CONTENT 0.44 BASEPAIR 20 FREE_ENERGY -19.00
LEN_BP_RATIO 2.5

CAUCAAUUGAAAAACACAGUGACUGUGGAUAAUACUGUGGGCAACGACACUAUGUUUCUAGUUAC
GUGGC

>random_seq_from_cds__NO_1727 RANDOM_LENGTH 82 SEQ_LENGTH 63
GC_CONTENT 0.492063492063492 BASEPAIR 20 FREE_ENERGY
-17.20 LEN_BP_RATIO 3.15

GAAGACAAAGGCUGACUAUGUGAGACCAAACUUGAGACCUACAAAAAUGGCUGAUGUUCUGGUU
GCUGAGUCUACUCCUCC

>random_seq_from_cds__NO_1738 RANDOM_LENGTH 82 SEQ_LENGTH 62
GC_CONTENT 0.483870967741936 BASEPAIR 22 FREE_ENERGY

-18.31 LEN_BP_RATIO 2.81818181818182
CGGAUGGGGAAGACAACACUAUAAGUGGGUGCUUUAACGAGGUCAAACAAAGUGGUGCCAUCAUC
CACACAGUCGCUUUGG
>random_seq_from_cds__NO_1774 RANDOM_LENGTH 94 SEQ_LENGTH 73
GC_CONTENT 0.465753424657534 BASEPAIR 24 FREE_ENERGY
-20.20 LEN_BP_RATIO 3.04166666666667
GGAAAAUUUCACAGUGGAUGCAACUCCAAAUGGCCUAUCUCAGUAUUCAGGAACUGCAAAGG
GUGGGCACUUGGGCAUACAAUCUUAAGC
>random_seq_from_cds__NO_1787 RANDOM_LENGTH 87 SEQ_LENGTH 57
GC_CONTENT 0.385964912280702 BASEPAIR 20 FREE_ENERGY
-15.50 LEN_BP_RATIO 2.85
AUUGAAAAGCUCACUGGUAACUUUGAAUAACAAUGGAUAUGAUGGCAUUGUCAUUGCAAUUAUC
CCAGUGUACCAGAAGAUGAAAA
>random_seq_from_cds__NO_1833 RANDOM_LENGTH 71 SEQ_LENGTH 62
GC_CONTENT 0.564516129032258 BASEPAIR 23 FREE_ENERGY
-22.40 LEN_BP_RATIO 2.69565217391304
UCCUGGAGGUUUCUGUGGGCAGCUGCACCUUCUGGCCCAUCUGCUGUUCAUAGUGGGCAAUAGC
CUUUUG
>random_seq_from_cds__NO_1844 RANDOM_LENGTH 79 SEQ_LENGTH 68
GC_CONTENT 0.529411764705882 BASEPAIR 25 FREE_ENERGY
-25.20 LEN_BP_RATIO 2.72
UCUGGAUUCGCCAUCAGUCGCCCAUAGUGUUCUCAAUGAGGCACAUUGGGCCUGUCAUGUGGAU
CUCUGAUGCCAUGA
>random_seq_from_cds__NO_1846 RANDOM_LENGTH 102 SEQ_LENGTH 60
GC_CONTENT 0.4 BASEPAIR 25 FREE_ENERGY -15.30 LEN_BP_RATIO
2.4
UGAUACAAGAUAAAAUAAAUACAACACACCCAAAUACAGGAUGAUAGUUCGUGUGACAAACAGA
GAUAUCAUUUGUCAGGAUUGCUUAUGCCCGUAUAGAG
>random_seq_from_cds__NO_1849 RANDOM_LENGTH 62 SEQ_LENGTH 51
GC_CONTENT 0.490196078431373 BASEPAIR 21 FREE_ENERGY
-21.80 LEN_BP_RATIO 2.42857142857143
CAAGUGGAGGUGACUGGUGAUGAAUACA AUGUGGAAAGCAUUGAUGGUCAGCCAGGUGCCUU
>random_seq_from_cds__NO_1855 RANDOM_LENGTH 98 SEQ_LENGTH 76
GC_CONTENT 0.5 BASEPAIR 26 FREE_ENERGY -29.50 LEN_BP_RATIO
2.92307692307692
GAAGAAGGAUCGGGUAGCUCAAAAGAAGGCAAGCUUCCUCAGAGCUCAGGAGCGGGCUGCUGAGA
GCUAAAUCAAAGCUCUGCCUGCUUUACAGGAG
>random_seq_from_cds__NO_1864 RANDOM_LENGTH 68 SEQ_LENGTH 52
GC_CONTENT 0.557692307692308 BASEPAIR 20 FREE_ENERGY
-18.00 LEN_BP_RATIO 2.6
CCACUGCAAUGCCGAUGGCCAUUGUGUUGUGUCCUUUCAAUUAUGUCCAGGCGCAGCUGGUGUCC
GUG
>random_seq_from_cds__NO_1869 RANDOM_LENGTH 81 SEQ_LENGTH 59
GC_CONTENT 0.627118644067797 BASEPAIR 22 FREE_ENERGY

-27.70 LEN_BP_RATIO 2.6818181818181818
GUAGUUGACGCCAGAGUUCGGGGACCUGGCGCCUCAUUCUGCUUGGCUGUGAGCAGUUCUGUGU
GGCUUCCUGGGCACA
>random_seq_from_cds__NO_1877 RANDOM_LENGTH 92 SEQ_LENGTH 75
GC_CONTENT 0.6666666666666667 BASEPAIR 30 FREE_ENERGY
-37.30 LEN_BP_RATIO 2.5
GGUUGCCCACGUAGCAGCGCACCAGGCCGGGAUGGAGUCGAAGCUCUCCAUCUCGAACUGGUAC
UGCACGCGGCUGUAGGCCUCGCUGAGU
>random_seq_from_cds__NO_1887 RANDOM_LENGTH 110 SEQ_LENGTH 97
GC_CONTENT 0.463917525773196 BASEPAIR 33 FREE_ENERGY
-27.00 LEN_BP_RATIO 2.93939393939394
AGUCAAAUCUGGUGGCAUCACACAGCAGGAGGCAAGAUUAACUUGGUUACUAUUUGGUUUUACCC
UGUGCCCACUGAUACAGCUGUCCAACUGUGUUUUGUCUAGAUA
>random_seq_from_cds__NO_1897 RANDOM_LENGTH 89 SEQ_LENGTH 78
GC_CONTENT 0.487179487179487 BASEPAIR 27 FREE_ENERGY
-24.50 LEN_BP_RATIO 2.88888888888889
ACAGGGUUCAGGUCAGGAAGCAGGUCGUCCUUCGGGAUUUGAUCUUCAUUGUGACGAUAUAGCC
AUCUCCAAAUCUUGGACUUGAGAU
>random_seq_from_cds__NO_1911 RANDOM_LENGTH 72 SEQ_LENGTH 52
GC_CONTENT 0.538461538461538 BASEPAIR 19 FREE_ENERGY
-16.40 LEN_BP_RATIO 2.73684210526316
AUCCCAUACAGCAGGAGCAGUGCCACAAGGGCAGGAAGGUUUUCUGGAGAAGUGUAGGCUUUCU
CUGAAAC
>random_seq_from_cds__NO_1914 RANDOM_LENGTH 80 SEQ_LENGTH 57
GC_CONTENT 0.491228070175439 BASEPAIR 20 FREE_ENERGY
-20.30 LEN_BP_RATIO 2.85
GAAGGACAUGGAGAAAUCACGCAGAUGGCAACCACAGCAUCCACUGAAGUGGUCAGCCACUGUA
AUCUCUGAGAGCUGC
>random_seq_from_cds__NO_1930 RANDOM_LENGTH 110 SEQ_LENGTH 101
GC_CONTENT 0.475247524752475 BASEPAIR 29 FREE_ENERGY
-25.17 LEN_BP_RATIO 3.48275862068966
CUUAUUUGGAAGAAGGAAGAUAAAGUUCUUGACCAAUGCACUCCACCAGCUUUGCCUCUGGAACAU
GGUGGAGAACUACAUCAUCAGCUCAUUUACAUCSCCAUCCAGG
>random_seq_from_cds__NO_1940 RANDOM_LENGTH 98 SEQ_LENGTH 83
GC_CONTENT 0.542168674698795 BASEPAIR 24 FREE_ENERGY
-28.90 LEN_BP_RATIO 3.458333333333333
AGUCCGUGUAUUCUUCUGGGUGCUCUGGAUCCUGGUUUCUUGUAGGGGCUCGGUCUUUUC
CAGGGCUCUUUCUUCUGGUUGAACACCCUU
>random_seq_from_cds__NO_1946 RANDOM_LENGTH 92 SEQ_LENGTH 65
GC_CONTENT 0.476923076923077 BASEPAIR 26 FREE_ENERGY
-21.70 LEN_BP_RATIO 2.5
ACAGGAAGAGGAUGAAUGGGUCGCUGUAAUGUAGGAUUCUCCAUGCCAUGAUGAAUAUCGUCAG
GAGGAAGAUGCUCUACGACAUGAUGGA
>random_seq_from_cds__NO_1953 RANDOM_LENGTH 84 SEQ_LENGTH 77

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GC_CONTENT    0.519480519480519    BASEPAIR    28    FREE_ENERGY
-22.40    LEN_BP_RATIO    2.75
CAUGUCAGGGAUACCACUCCGGCCCGAACAUGUUUCCUCCAGUAGAGAGAGGGCACGUUGG
UGAGCUGAGUUUCAUCAU
>random_seq_from_cds__NO_1959    RANDOM_LENGTH    81    SEQ_LENGTH    70
GC_CONTENT    0.4    BASEPAIR    28    FREE_ENERGY    -19.70    LEN_BP_RATIO
2.5
CUGGAUCAUUGCAUUACAAAAGGAUGCUUGUUCUUCUGUCAUAAGAAUAGAUAGGAUCCUCCU
GUGGAGUCAAUCCCCA
>random_seq_from_cds__NO_1970    RANDOM_LENGTH    72    SEQ_LENGTH    49
GC_CONTENT    0.469387755102041    BASEPAIR    20    FREE_ENERGY
-18.90    LEN_BP_RATIO    2.45
UGUUGGGGAAAUGGCCAUUCAUGAUGGCUGUAGAGUGGGUUGGCAUCCUUAACCAGAUCAAGAC
CAGAAAU
>random_seq_from_cds__NO_1998    RANDOM_LENGTH    70    SEQ_LENGTH    58
GC_CONTENT    0.431034482758621    BASEPAIR    20    FREE_ENERGY
-16.60    LEN_BP_RATIO    2.9
UCUUCGGUUAACUGUUCGGGAGGGAAUCACUGCUUGAACACUGAAACAGUAGUUUUCUCCUUUA
UCCAC
>random_seq_from_cds__NO_2005    RANDOM_LENGTH    63    SEQ_LENGTH    54
GC_CONTENT    0.796296296296296    BASEPAIR    19    FREE_ENERGY
-27.10    LEN_BP_RATIO    2.84210526315789
ACCUGGGCGAAGACCCAGCCGAGCAGGAGCGUCCGAGCGACGGCGGUCUCGGGGCGCGGGACC
>random_seq_from_cds__NO_2007    RANDOM_LENGTH    84    SEQ_LENGTH    61
GC_CONTENT    0.459016393442623    BASEPAIR    22    FREE_ENERGY
-17.50    LEN_BP_RATIO    2.77272727272727
CUGACGAACUACUCUCAGGCAGUGUUCUCAGUAGUCCGAACUCUAAUAUGAGCAGCAUGGUAGUU
ACAGGCCAAUGGUAUGAU
>random_seq_from_cds__NO_2020    RANDOM_LENGTH    90    SEQ_LENGTH    69
GC_CONTENT    0.405797101449275    BASEPAIR    24    FREE_ENERGY
-16.50    LEN_BP_RATIO    2.875
AGACAGCGCUCUAAUACAGAUGGCUGAUGGAAACCAAUCACAACUUGGCCAUGAAUCAUCUAAU
GGACAGAAAAUGUAUGGAAAAAUUA
>random_seq_from_cds__NO_2031    RANDOM_LENGTH    75    SEQ_LENGTH    54
GC_CONTENT    0.518518518518518    BASEPAIR    21    FREE_ENERGY
-24.50    LEN_BP_RATIO    2.57142857142857
UCCAUGAGUUCAGCUAUACGUGGAACUGGUUCCCUUUCUGGUGACUCACAGUAGCUGGACUCUG
UCCAUCCAG
>random_seq_from_cds__NO_2038    RANDOM_LENGTH    81    SEQ_LENGTH    75
GC_CONTENT    0.546666666666667    BASEPAIR    27    FREE_ENERGY
-27.30    LEN_BP_RATIO    2.77777777777778
UUGUCCAGGGCAUACAUGGGGCCAGAGGUUGUCCCGGAUGAUUCUGGGGGAAACAUUUGUCA
CAAUGUCCCUUAUCA
>random_seq_from_cds__NO_2053    RANDOM_LENGTH    88    SEQ_LENGTH    77
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GC_CONTENT    0.493506493506494    BASEPAIR    30    FREE_ENERGY
-27.80    LEN_BP_RATIO    2.566666666666667
UGGGGGAGGCAGCGAAGGAUUUCUGAUCUGUGGGGAUACUCAUUGCUUUGAAUACCCUCAGUAGCA
AAUUGCUGCAAUCCACCAAUAU
>random_seq_from_cds__NO_2061    RANDOM_LENGTH    85    SEQ_LENGTH    62
GC_CONTENT    0.483870967741936    BASEPAIR    22    FREE_ENERGY
-15.40    LEN_BP_RATIO    2.81818181818182
AUGAGUCUGUCCAGAGAAUGUGCUGAGUUUCGAUGACCUUACUGCAGACGCUUUAGCUGAACCU
GAAAGUCUCACAAAUCAAAA
>random_seq_from_cds__NO_2065    RANDOM_LENGTH    80    SEQ_LENGTH    71
GC_CONTENT    0.535211267605634    BASEPAIR    23    FREE_ENERGY
-20.90    LEN_BP_RATIO    3.08695652173913
UGGUGUUCUGGAACAGGCUCUCAUCCAGUAUGCCCUUCGCACCUUGGGAAGUCGGGGCUACAUU
CCCAUUUAUACCCCC
>random_seq_from_cds__NO_2071    RANDOM_LENGTH    73    SEQ_LENGTH    57
GC_CONTENT    0.56140350877193    BASEPAIR    23    FREE_ENERGY
-20.00    LEN_BP_RATIO    2.47826086956522
AAUAUUGUCUCAGGGUUCUUUGAAUCAUGCUGCCAGUAAGAAGCUUGACCUGGAGGCCUGGUUUC
CGGGCUCA
>random_seq_from_cds__NO_2072    RANDOM_LENGTH    63    SEQ_LENGTH    54
GC_CONTENT    0.62962962962963    BASEPAIR    22    FREE_ENERGY
-25.10    LEN_BP_RATIO    2.45454545454545
GGAGCCUUCGUGAGUUGGUCUCCUGUUCUAAUUGCACGGAUUACCAGGCUCGCCGGCUUCGA
>random_seq_from_cds__NO_2082    RANDOM_LENGTH    85    SEQ_LENGTH    76
GC_CONTENT    0.684210526315789    BASEPAIR    24    FREE_ENERGY
-28.60    LEN_BP_RATIO    3.166666666666667
CCUGCAAGCUGGCACAGGCCCCCGGGCUCAGGGCAGGGGAAAGGUCACCAGAAGAGUCCUGGGU
GGGCGUCGAAAAGGAAUGU
>random_seq_from_cds__NO_2096    RANDOM_LENGTH    94    SEQ_LENGTH    81
GC_CONTENT    0.592592592592593    BASEPAIR    29    FREE_ENERGY
-29.30    LEN_BP_RATIO    2.79310344827586
CAGGCUGGAUCUCUGUGGCUGCUGAACUGGACCGGGAGGAAGUUGAUUUCUACAGCUUUGGGGUA
GAAGCUCGAGACCAUGGCACUCCAGCACU
>random_seq_from_cds__NO_2098    RANDOM_LENGTH    88    SEQ_LENGTH    80
GC_CONTENT    0.5875    BASEPAIR    27    FREE_ENERGY    -29.10
LEN_BP_RATIO    2.96296296296296
GCGGCUCAAUGAGGAUGCAGCUGUGGGCACCAGCGUGGUGACGGUGUCAGCUGUGGACCGUGAUG
CUCAUAGUGUCAUACCUACCAG
>random_seq_from_cds__NO_2103    RANDOM_LENGTH    110    SEQ_LENGTH    84
GC_CONTENT    0.595238095238095    BASEPAIR    27    FREE_ENERGY
-32.60    LEN_BP_RATIO    3.11111111111111
AUCGAUGCAGACACGGGGCUGUCACCACCCAGGCUGAGCUGGACUAUGAAGACCAAGUGUCUUA
CACCCUGGCCAUUACUGCUCGGGACAAUGGCAUUCCCCAGAAGUC
>random_seq_from_cds__NO_2110    RANDOM_LENGTH    64    SEQ_LENGTH    47
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GC_CONTENT    0.531914893617021    BASEPAIR    19    FREE_ENERGY
-17.30    LEN_BP_RATIO    2.47368421052632
AACAUCCUGAGGUCUUUCAGCUGGACAUCUUCUCCGGGGAGCUGACAGCCCUGGUAGACUUAG
>random_seq_from_cds__NO_2119    RANDOM_LENGTH    86    SEQ_LENGTH    75
GC_CONTENT    0.6666666666666667    BASEPAIR    25    FREE_ENERGY
-24.00    LEN_BP_RATIO    3
CUGCCUGCGGGAGCCCUGCGAGAACUACAUGCUGCGUGUCGGUGCUGCGCUUCGACUCCUCCG
CGCCCUUCAUCGCCUCCUCCU
>random_seq_from_cds__NO_2120    RANDOM_LENGTH    87    SEQ_LENGTH    83
GC_CONTENT    0.734939759036145    BASEPAIR    28    FREE_ENERGY
-33.70    LEN_BP_RATIO    2.96428571428571
CCGUGCUCUUCGGCCCAUCCACCCCGUCGGAGGGCUGCGCUGCCGCUGCCCGCCCGGCUUCACG
GGUGACUACUGCGAGACCGAGG
>random_seq_from_cds__NO_2127    RANDOM_LENGTH    85    SEQ_LENGTH    70
GC_CONTENT    0.642857142857143    BASEPAIR    26    FREE_ENERGY
-31.10    LEN_BP_RATIO    2.69230769230769
ACUGUUGGGUCAGACAGGGCUCCACAGGGCCAUCAGAGCAGAAGGUGGCUGUGGUGACCGUGG
AUGGCUGUGACACAGGAGUG
>random_seq_from_cds__NO_2128    RANDOM_LENGTH    71    SEQ_LENGTH    63
GC_CONTENT    0.650793650793651    BASEPAIR    24    FREE_ENERGY
-32.30    LEN_BP_RATIO    2.625
GCCUUGCGCUUCGGAUCUGUCCUGGGCAACUACUCCUGUGCUGCCCAGGGCACCCAGGGUGGCAG
CAAGAA
>random_seq_from_cds__NO_2160    RANDOM_LENGTH    90    SEQ_LENGTH    61
GC_CONTENT    0.655737704918033    BASEPAIR    20    FREE_ENERGY
-27.00    LEN_BP_RATIO    3.05
UGCCCUGGGCCUGGCUCAGCUGGUCUUCUCCUGGGAAUCAACCAGGCUGACCUCCUGUUUGCC
UGCACAGUCAUUGCCAUCCUGCUGC
>random_seq_from_cds__NO_2166    RANDOM_LENGTH    73    SEQ_LENGTH    51
GC_CONTENT    0.627450980392157    BASEPAIR    19    FREE_ENERGY
-18.90    LEN_BP_RATIO    2.68421052631579
UCCUAUGUGGUGCUUAGCAAGGAGGUCCGAAAGCACUCAAGCUUGCCUGCAGCCGCAAGCCCAG
CCCUGACC
>random_seq_from_cds__NO_2173    RANDOM_LENGTH    73    SEQ_LENGTH    63
GC_CONTENT    0.6666666666666667    BASEPAIR    22    FREE_ENERGY
-26.10    LEN_BP_RATIO    2.86363636363636
CCCCUGAGGAGCGGCUGCGGGAGAAUGGAGAUGCCUGUCUCGAGAGGGGUCCCUAGGCCCCCU
CCAGGCUC
>random_seq_from_cds__NO_2186    RANDOM_LENGTH    68    SEQ_LENGTH    48
GC_CONTENT    0.5208333333333333    BASEPAIR    19    FREE_ENERGY
-24.60    LEN_BP_RATIO    2.52631578947368
GCUAGGCCAGUGAAUAGAUGGGGUCCUGGUGAACGUGUAGGUUUGCCAGCAUUGACCUUCGUC
UGU
>random_seq_from_cds__NO_2198    RANDOM_LENGTH    77    SEQ_LENGTH    62
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GC_CONTENT    0.387096774193548    BASEPAIR    22    FREE_ENERGY
-15.10    LEN_BP_RATIO    2.81818181818182
GAGGGCUAUACAUCAUCUGAGUGAGAGGAUGAAAAGGGAGAUCUGUUUGCACAAAAUUCUUCGCA
AAAUCUGAUGAU
>random_seq_from_cds__NO_2200    RANDOM_LENGTH    102    SEQ_LENGTH    81
GC_CONTENT    0.382716049382716    BASEPAIR    27    FREE_ENERGY
-19.60    LEN_BP_RATIO    3
GCCAAAUUCAGUCCGAAUAAAAGGUGUUUAUGAUGAGAUCUGUAAUAUCCUUAAGUUCUCCCAU
AAUCCUCACCUUCGAUAUAGCUUGGACUGUCCAAAAG
>random_seq_from_cds__NO_2211    RANDOM_LENGTH    79    SEQ_LENGTH    52
GC_CONTENT    0.557692307692308    BASEPAIR    19    FREE_ENERGY
-17.75    LEN_BP_RATIO    2.73684210526316
AAUUAGCCCACUCAUGGCACAACCCUAUGUGAGCAUCAAUUCUCUACAAUUUUCUCAAUGCUGCUG
GGCUCCAUCAGUGG
>random_seq_from_cds__NO_2218    RANDOM_LENGTH    97    SEQ_LENGTH    75
GC_CONTENT    0.52    BASEPAIR    26    FREE_ENERGY    -20.30
LEN_BP_RATIO    2.88461538461538
GACUCAUGCAUACGAUUCACUUCGUAUCUUCACCAGCACCAUAUCAUAGGCACUGAGGGCUG
CACAGAAAUGAUGCAGGUGACUCCUCGAAG
>random_seq_from_cds__NO_2221    RANDOM_LENGTH    102    SEQ_LENGTH    68
GC_CONTENT    0.544117647058823    BASEPAIR    23    FREE_ENERGY
-21.80    LEN_BP_RATIO    2.95652173913043
UAAUUCGUUCUAAUUGGUUCAGGUAGCUAAGAUGCGGAGUCAUUAAGCUGGUAAUUCUGCAGCUCU
CUCGAAGCAGGCUUGCACCCACCAUCCUCCACAAC
>random_seq_from_cds__NO_2234    RANDOM_LENGTH    85    SEQ_LENGTH    74
GC_CONTENT    0.621621621621622    BASEPAIR    26    FREE_ENERGY
-29.30    LEN_BP_RATIO    2.84615384615385
UCACAAAGAUGGCUGUCUGGGGCAACAAGUAGCAUGCCCAUGACUCUGGGGUACUGGGACAUCGG
UGGGGCUGGCCCACGCCAUC
>random_seq_from_cds__NO_2239    RANDOM_LENGTH    68    SEQ_LENGTH    53
GC_CONTENT    0.509433962264151    BASEPAIR    20    FREE_ENERGY
-17.50    LEN_BP_RATIO    2.65
UGGGGAAGCGGCCAUGGUUUGCAGGAGACAAGGAUCACCUUUGUGGAUUUCCUUGCCUAUGAUGU
CCU
>random_seq_from_cds__NO_2247    RANDOM_LENGTH    88    SEQ_LENGTH    75
GC_CONTENT    0.52    BASEPAIR    25    FREE_ENERGY    -20.50
LEN_BP_RATIO    3
UCAUUUGCUGCAGUGUUGUGGUAUAAAUGGCACGAGUGAUUGGACCAGUGGCCACCAGCAUCU
GCCCCUCAGAUCGAAAAGUGGAG
>random_seq_from_cds__NO_2263    RANDOM_LENGTH    110    SEQ_LENGTH    84
GC_CONTENT    0.476190476190476    BASEPAIR    28    FREE_ENERGY
-19.53    LEN_BP_RATIO    3
UGAAGAACGGCCAAGGUUUUGCACUAGUAUAUUCUAUUACAGCUCAGUCCACGUUUAACGACUUA
CAGGACCUGAGGGAACAGAUUUUACGGGUUAAGGACACGGAAGAU
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>random_seq_from_cds__NO_2276 RANDOM_LENGTH 110 SEQ_LENGTH 87
  GC_CONTENT 0.540229885057471 BASEPAIR 28 FREE_ENERGY
-29.80 LEN_BP_RATIO 3.10714285714286
UGGAACGGAACACAUCACUAGAUCUGGGAACUGGAUCAUCAUGUCAUGUUGGGCAGUGGAU
GCGAUUGCAGACGAACCAGGAGGAGUUUGCUCCACUCAUCAGG
>random_seq_from_cds__NO_2277 RANDOM_LENGTH 90 SEQ_LENGTH 76
  GC_CONTENT 0.605263157894737 BASEPAIR 29 FREE_ENERGY
-28.50 LEN_BP_RATIO 2.62068965517241
ACUGCGGCCAUAGAUGGACAGGCGGGGCUCAGCAUGCUGGUACUUGGCCUCCACCAGGUCCGCAC
CUACCUCUUUGAUGAUAGUGGCAA
>random_seq_from_cds__NO_2285 RANDOM_LENGTH 77 SEQ_LENGTH 67
  GC_CONTENT 0.522388059701492 BASEPAIR 25 FREE_ENERGY
-23.50 LEN_BP_RATIO 2.68
AGGAAGGUUGUCUGUUCGGAAGGGGUCCUCUCCUUCUUCACAGGAGGAGUAAAGACCUGGAUAG
AAGCUCUCAUUU
>random_seq_from_cds__NO_2288 RANDOM_LENGTH 85 SEQ_LENGTH 78
  GC_CONTENT 0.371794871794872 BASEPAIR 27 FREE_ENERGY
-17.10 LEN_BP_RATIO 2.88888888888889
UGGAGAUGAGGAAAUGUAUUCAUCAUUGUGGGACAGUUUGGUGGAAGAUGUUUCACUAGUGGAA
UGGACAAAUUAACAGUCUUC
>random_seq_from_cds__NO_2294 RANDOM_LENGTH 95 SEQ_LENGTH 75
  GC_CONTENT 0.466666666666667 BASEPAIR 26 FREE_ENERGY
-18.50 LEN_BP_RATIO 2.88461538461538
UAACUCUUGGCCAGUUCGUGGGCUUGUUUUGUAUCAACUGUCCUUGUUGGCAAUACACUUGUU
UCCACUAGCACCAUAGGUACAUCAUCCGA
>random_seq_from_cds__NO_2334 RANDOM_LENGTH 75 SEQ_LENGTH 58
  GC_CONTENT 0.5 BASEPAIR 19 FREE_ENERGY -15.40 LEN_BP_RATIO
3.05263157894737
UUGCACAUGAUGACAGGUGUGAUGUACCUACAGUUUGUACCCAAGUCUCACCUCUUCUUCACUGC
CGGAAAAGAU
>random_seq_from_cds__NO_2339 RANDOM_LENGTH 85 SEQ_LENGTH 66
  GC_CONTENT 0.5 BASEPAIR 21 FREE_ENERGY -19.77 LEN_BP_RATIO
3.14285714285714
AAAAUGAAGGAACACAAAGCCAUUUGUAAAGCUGCAGGGAAAGAGGGUCCACUUCCAGCAACC
CCAUCCUAAUGGCUUAUGGC
>random_seq_from_cds__NO_2360 RANDOM_LENGTH 87 SEQ_LENGTH 66
  GC_CONTENT 0.621212121212121 BASEPAIR 25 FREE_ENERGY
-31.80 LEN_BP_RATIO 2.64
ACUUGCCCACAGAGGCUGGGAAAGGAUGAUAGGCUGGGAGAAUGGUCUGAGCUACCUGCCCGUCC
UGCUGGGGCAUCAUGGCAGUGG
>random_seq_from_cds__NO_2366 RANDOM_LENGTH 87 SEQ_LENGTH 75
  GC_CONTENT 0.52 BASEPAIR 23 FREE_ENERGY -18.40
  LEN_BP_RATIO 3.26086956521739
ACAUAGGGUUGGGUGAGGCCUGUAAGAUCACAGGGGAUGUAAUCAUUGGAGAGGAUGUGGUGUCG
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GAAACAUACGUGUGAGGAGAUU
>random_seq_from_cds__NO_2385 RANDOM_LENGTH 110 SEQ_LENGTH 90
  GC_CONTENT 0.5111111111111111 BASEPAIR 30 FREE_ENERGY
  -29.12 LEN_BP_RATIO 3
UGUUCUUGUUCACCAGGAAGGGAUCGCGUGUCAUCCUCUGUUUCUUAUAGCAGCUGACUUCUC
ACCAUAAUAGGGGUACACCAUGAGUUCUCCUUGGGAGUCCCGCUU
>random_seq_from_cds__NO_2392 RANDOM_LENGTH 81 SEQ_LENGTH 72
  GC_CONTENT 0.7083333333333333 BASEPAIR 27 FREE_ENERGY
  -30.40 LEN_BP_RATIO 2.666666666666667
CUGGCAGGGGCUACUGGCACAGCCUGACUCGCAGUCCCGGGACUGGGGCAGAAGCAGCGGGGUC
CAGAGGCGGUGGCAC
>random_seq_from_cds__NO_2396 RANDOM_LENGTH 98 SEQ_LENGTH 83
  GC_CONTENT 0.566265060240964 BASEPAIR 29 FREE_ENERGY
  -28.60 LEN_BP_RATIO 2.86206896551724
AGGGGUUGGAGAGGCACUCGUUGAUGUCUCCUCACAACGCUCCCAAGCCAGGCAAGCAG
CGACAACUGUAGCCUCCAAUCCUAUCCAUGCAC
>random_seq_from_cds__NO_2403 RANDOM_LENGTH 84 SEQ_LENGTH 60
  GC_CONTENT 0.6333333333333333 BASEPAIR 21 FREE_ENERGY
  -23.20 LEN_BP_RATIO 2.85714285714286
UUCACCAGGUCCUGACAGUUUUUCCAGUGUAGCCCAGGGGGCAGCUGCAGCGGUAGGUACCCA
GGCCAUAACACACGUUCC
>random_seq_from_cds__NO_2422 RANDOM_LENGTH 94 SEQ_LENGTH 80
  GC_CONTENT 0.5125 BASEPAIR 28 FREE_ENERGY -25.30
  LEN_BP_RATIO 2.85714285714286
AUGCACACCUUUGAAACCCUGGCAUGCACAGACAUGUGAAGCCUCCAAUCUUAUCCAGACAGGUA
GCAUCAUUCUGGCAGGGGUCUGAAUGGCA
>random_seq_from_cds__NO_2423 RANDOM_LENGTH 81 SEQ_LENGTH 61
  GC_CONTENT 0.557377049180328 BASEPAIR 22 FREE_ENERGY
  -15.40 LEN_BP_RATIO 2.77272727272727
CUCAUUGAUGUCCAUCUCACAACGAGGUCCUGCAUAACCCUUCAGACACUCACAGUGGAAGGCGC
CAUCCGUGUUCACACA
>random_seq_from_cds__NO_2424 RANDOM_LENGTH 97 SEQ_LENGTH 74
  GC_CONTENT 0.567567567567568 BASEPAIR 26 FREE_ENERGY
  -34.26 LEN_BP_RATIO 2.84615384615385
UUUUCUGCAUGCUCACAAGGAUUGCUAUUGGCCCAUGGCACAUUCAUCCACAUCUUCUGUGCAG
UCAGCCCCUUGUAGCCUUGUGGGCAGGUGCA
>random_seq_from_cds__NO_2443 RANDOM_LENGTH 101 SEQ_LENGTH 83
  GC_CONTENT 0.55421686746988 BASEPAIR 25 FREE_ENERGY
  -31.64 LEN_BP_RATIO 3.32
AGGCUGCUAUGGAGGGACUCAAUUGGCCAGGAUUUGAUGGGACAGCCAUCAAGCGUUGACUGGUGU
UUUGUUCGGGGUCCACCAAAGGCAAGAGGAGGAGG
>random_seq_from_cds__NO_2453 RANDOM_LENGTH 87 SEQ_LENGTH 64
  GC_CONTENT 0.421875 BASEPAIR 20 FREE_ENERGY -15.09
  LEN_BP_RATIO 3.2
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CCUUCACAUUUCCUUUCACUUUCACCAAGCCAGAAAUGAUACGAUUUGGCAGGUCAUCAUUUAAG
GUUGGAUGCUGACUCAGAGCUC

>random_seq_from_cds__NO_2465 RANDOM_LENGTH 96 SEQ_LENGTH 83
GC_CONTENT 0.662650602409639 BASEPAIR 31 FREE_ENERGY
-38.40 LEN_BP_RATIO 2.67741935483871

CCAGCCAAUCCCAGCCAUCCCCUGUGACUCCAAGAGUGGGGGCCAUACCCCUAAAAGCACUCCCU
GGCCCAGGUGGGAGCAUGGGGCUGAAGAAUG

>random_seq_from_cds__NO_2489 RANDOM_LENGTH 97 SEQ_LENGTH 80
GC_CONTENT 0.6375 BASEPAIR 30 FREE_ENERGY -42.10
LEN_BP_RATIO 2.66666666666667

UACGCCCAGGUGGCUCAGACAUGCUGCCUGCUCAGCAGAAGAUGGUGCCACUGCCAUUUGGUGAG
CACCCCAGCAGGAGUAUGGCAUGGGCCCCAG

>random_seq_from_cds__NO_2493 RANDOM_LENGTH 86 SEQ_LENGTH 55
GC_CONTENT 0.6 BASEPAIR 22 FREE_ENERGY -23.10 LEN_BP_RATIO
2.5

AACCUCAAGUCCCCCAGACUCCAUCGCAGCUGGCAGGCAUGCUGGCGGGCCAGCUGCUGCUGC
UCCAUAAGUCCCCCCCUGU

>random_seq_from_cds__NO_2518 RANDOM_LENGTH 84 SEQ_LENGTH 72
GC_CONTENT 0.638888888888889 BASEPAIR 23 FREE_ENERGY
-32.62 LEN_BP_RATIO 3.1304347826087

GGAGGUGGCACUGGGGGUGGGAAGGAGCCAGGAGGCAUGCCCUGGUGGAGGAAGCCAGACC
CCAAUGAUGAUACCACAGG

>random_seq_from_cds__NO_2547 RANDOM_LENGTH 70 SEQ_LENGTH 64
GC_CONTENT 0.5625 BASEPAIR 24 FREE_ENERGY -26.20
LEN_BP_RATIO 2.66666666666667

GGUCAACACUGGACGUAUGAGGGGCCACAUGGUCAGGACCAUUGGCCAGCCUCUUACCCUGAGU
GUGGA

>random_seq_from_cds__NO_2554 RANDOM_LENGTH 85 SEQ_LENGTH 67
GC_CONTENT 0.462686567164179 BASEPAIR 27 FREE_ENERGY
-24.20 LEN_BP_RATIO 2.48148148148148

AGUGUGCUCUGGACAGUUUUUAUAGAAGGUCCAGAUUUCAAUGGAACAGGCUGGAAAAGCUUC
AGGGGACAUUGUUCUCCACA

>random_seq_from_cds__NO_2556 RANDOM_LENGTH 67 SEQ_LENGTH 61
GC_CONTENT 0.540983606557377 BASEPAIR 20 FREE_ENERGY
-15.60 LEN_BP_RATIO 3.05

GGCAGGAUCCUCGUAUACCACAGGGUGAAAUGCUGAGUCUAGGUGUAGGAAUCUUGGUUGGCUGU
CU

>random_seq_from_cds__NO_2562 RANDOM_LENGTH 71 SEQ_LENGTH 58
GC_CONTENT 0.482758620689655 BASEPAIR 21 FREE_ENERGY
-20.50 LEN_BP_RATIO 2.76190476190476

UCCAUGGCUUUGUAGGGAUAGGAAGCGUCUGAGUCGAUGCCCUUGUUAUCAUGAUGUACUGGA
AAGCCG

>random_seq_from_cds__NO_2592 RANDOM_LENGTH 98 SEQ_LENGTH 78
GC_CONTENT 0.461538461538462 BASEPAIR 26 FREE_ENERGY

-23.50 LEN_BP_RATIO 3
GUGUUGCUUUUUGGGUCUUUAUGCUCCUGGGUAUAAGGAACUUUGAAGCACCAUGCUCCUUUAAGUCU
UUAUUACCCUGUGGGUCAGUGUCUACCUCUCCC
>random_seq_from_cds__NO_2625 RANDOM_LENGTH 106 SEQ_LENGTH 97
GC_CONTENT 0.628865979381443 BASEPAIR 33 FREE_ENERGY
-37.00 LEN_BP_RATIO 2.93939393939394
GGAUGUCCUUGGGUCUCAAUGACCCUUGUGCAGCUUUGGGGCCCGGGCUCAGAGCCCACGUCCAC
CACAUAGAUGCGAGAGGAGAUGAGACUGGGCAGCACCAGCU
>random_seq_from_cds__NO_2629 RANDOM_LENGTH 78 SEQ_LENGTH 68
GC_CONTENT 0.647058823529412 BASEPAIR 24 FREE_ENERGY
-26.40 LEN_BP_RATIO 2.83333333333333
AAGCGUUUUUGGGGUCGCGGUCCGACUUUGGGCGGGGGUCCGGCCCCAGGACAGUUUUACCGC
AUUCCGUCCACUC
>random_seq_from_cds__NO_2630 RANDOM_LENGTH 78 SEQ_LENGTH 74
GC_CONTENT 0.608108108108108 BASEPAIR 27 FREE_ENERGY
-24.40 LEN_BP_RATIO 2.74074074074074
CCGAUCCUUCAUUGGAUCCGGCGUCUGCACUUUACAGAGGUCCAUCACGCGGACCCAGGAACCC
CAUGGUGACCGGG
>random_seq_from_cds__NO_2633 RANDOM_LENGTH 88 SEQ_LENGTH 73
GC_CONTENT 0.493150684931507 BASEPAIR 27 FREE_ENERGY
-29.42 LEN_BP_RATIO 2.7037037037037
UUCUCGGCCAGAUGGUGGAUUGAUGAGGAGCUUCUGGGAGAUGGACACAGCUAUAGUCCUAGAGC
UAUUCAUUCAUUGGCUGACCAGGG
>random_seq_from_cds__NO_2636 RANDOM_LENGTH 97 SEQ_LENGTH 68
GC_CONTENT 0.573529411764706 BASEPAIR 24 FREE_ENERGY
-25.50 LEN_BP_RATIO 2.83333333333333
CAGUGCUAAGCCAGACCGAGGCCCGCGACUUAGUAGAACGUGCAUGCGAGUGCUGUACUACCGA
GAUGCCCGUUCUUACAACCGGGUUUCAAUCG
>random_seq_from_cds__NO_2655 RANDOM_LENGTH 100 SEQ_LENGTH 85
GC_CONTENT 0.517647058823529 BASEPAIR 31 FREE_ENERGY
-27.91 LEN_BP_RATIO 2.74193548387097
UGAGGACACUCGGUCUCUAGCAAUUUCUUCAGGUCAUCCCGUAGACGGCAUGGAAAUCCCCU
UAUCAGGGAGUACUUGUGGUAGACGUCGAUGAUG
>random_seq_from_cds__NO_2674 RANDOM_LENGTH 84 SEQ_LENGTH 78
GC_CONTENT 0.474358974358974 BASEPAIR 25 FREE_ENERGY
-19.29 LEN_BP_RATIO 3.12
AGUUUGAGUAUCGGACAUGUCAUGCUGCCCAAGGACAUAAGCAAGCUGGUCCUAAAACCCAUCU
GAUGUCUGAAUCUGAAUGG
>random_seq_from_cds__NO_2675 RANDOM_LENGTH 95 SEQ_LENGTH 85
GC_CONTENT 0.576470588235294 BASEPAIR 27 FREE_ENERGY
-26.90 LEN_BP_RATIO 3.14814814814815
AGGAAUCUUGGCGUUCAGCAGAGUCAGGGAUGGGUCCAUAUAUGAUGCAUGAACCAGGAACCUC
ACAUCUUGCUGUCCGGCGCCCACUACCCA
>random_seq_from_cds__NO_2676 RANDOM_LENGTH 85 SEQ_LENGTH 69

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GC_CONTENT    0.579710144927536    BASEPAIR    25    FREE_ENERGY
-24.00    LEN_BP_RATIO    2.76
AGAAACCAAAGAAAUGACUUAGCUCUCGGAGGCUACAGCCUCCCCGUCGCGGCUCUCCGUCUCCU
CCGGGAUGUCCUGCAUUCUG
>random_seq_from_cds__NO_2686    RANDOM_LENGTH    86    SEQ_LENGTH    79
GC_CONTENT    0.518987341772152    BASEPAIR    26    FREE_ENERGY
-23.41    LEN_BP_RATIO    3.03846153846154
CCUCCCUUCUUGCGGUGAUCUCAGCUGAUUUCCAUUUCGAUCCCCUCUGGCUAGAGUCUGAGUCAG
CUCUGCAGAGUUCAAUGGAGC
>random_seq_from_cds__NO_2689    RANDOM_LENGTH    68    SEQ_LENGTH    63
GC_CONTENT    0.682539682539683    BASEPAIR    20    FREE_ENERGY
-29.30    LEN_BP_RATIO    3.15
UCCUGCAGCAGCCGUCGCCACGAGGGGACUCAAGGGACUCAGAGCGGAAAAGGCCCCUGGGCAG
GGU
>random_seq_from_cds__NO_2698    RANDOM_LENGTH    82    SEQ_LENGTH    68
GC_CONTENT    0.661764705882353    BASEPAIR    24    FREE_ENERGY
-34.00    LEN_BP_RATIO    2.833333333333333
ACCAGCAGGAUGCACUCCUGUACCCCGUGCCGCUUGAGCACGGCGGGGCGGGUCACUUUCCCGGA
UGAAUUGCUGGAAGCGU
>random_seq_from_cds__NO_2703    RANDOM_LENGTH    87    SEQ_LENGTH    77
GC_CONTENT    0.480519480519481    BASEPAIR    22    FREE_ENERGY
-18.19    LEN_BP_RATIO    3.5
AUCUUCAGUGUCCUCAUUGGUGCAGCUCUGUCUGGAUUAGCUCCAUAGAUGACAUCUUGCUGCU
UCAUCACCUCCUUUUUAUGCUG
>random_seq_from_cds__NO_2706    RANDOM_LENGTH    70    SEQ_LENGTH    54
GC_CONTENT    0.462962962962963    BASEPAIR    19    FREE_ENERGY
-16.60    LEN_BP_RATIO    2.84210526315789
GCGCAGCCCCAGGGGAGACUCAUCAUUGAAAUGUCCAGCAAUGUUGGUGGUAGAAACACUCUUG
GCUAA
>random_seq_from_cds__NO_2721    RANDOM_LENGTH    110    SEQ_LENGTH    79
GC_CONTENT    0.379746835443038    BASEPAIR    25    FREE_ENERGY
-19.60    LEN_BP_RATIO    3.16
UGAUUUUCCAGUUGCCAGAGAAGUUGGGCAUAAUGGUGAAUGAAUACAAGAAAAUUCUUUUGCUG
AAAGGAUUUGAGCUCAUGGAUGAUUAUCAUUUUAUCAUAAUUAAG
>random_seq_from_cds__NO_2726    RANDOM_LENGTH    89    SEQ_LENGTH    75
GC_CONTENT    0.586666666666667    BASEPAIR    24    FREE_ENERGY
-20.10    LEN_BP_RATIO    3.125
CAAAAAGAAUAAGGUGUCCCAAGAGCAGAGUAAGCCCCAGGUCCUCAGGAGCCAGCACAUUCG
CAGCUGUGGAUCAUCCCCACUAC
>random_seq_from_cds__NO_2742    RANDOM_LENGTH    72    SEQ_LENGTH    61
GC_CONTENT    0.508196721311475    BASEPAIR    23    FREE_ENERGY
-21.90    LEN_BP_RATIO    2.65217391304348
UUCUUGGGUCUCAAACGUGAAGGGCUUCUUUGCUUUCAGUACCAUAACUGGCAAACAGCGCUUCU
GAAACCC
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>random_seq_from_cds__NO_2743 RANDOM_LENGTH 89 SEQ_LENGTH 75
  GC_CONTENT 0.5066666666666667 BASEPAIR 25 FREE_ENERGY
-25.10 LEN_BP_RATIO 3
UUCUCUGAUAGAUUCCUGCUGGGCCACCAUCUGUUUCUGUUCAGGCCUUAACAUGAGGAGAGACU
UUUGGUGCAGCACGUUGCUUUGCG
>random_seq_from_cds__NO_2756 RANDOM_LENGTH 90 SEQ_LENGTH 75
  GC_CONTENT 0.64 BASEPAIR 26 FREE_ENERGY -30.50
  LEN_BP_RATIO 2.88461538461538
ACCCUUGGUGUGGGUCUGAAUCAGAGGAUCUGGCGUGGCAUCCCGUAGCCAGUCAUGCCUGCCUG
AGACGCCCCGCGGUUGGUGCCCAUC
>random_seq_from_cds__NO_2757 RANDOM_LENGTH 110 SEQ_LENGTH 87
  GC_CONTENT 0.540229885057471 BASEPAIR 34 FREE_ENERGY
-36.10 LEN_BP_RATIO 2.55882352941176
UGUAACCCGAUCACGUUCUUGCCCUCUUGCAGCUGGUUAUCCGAGAAGUUCGAGGAUUCUCCUU
GGAUUUCCUUAGGGAACCAGUUGGGAUCCCCAGAGAAGAGCCCAU
>random_seq_from_cds__NO_2766 RANDOM_LENGTH 75 SEQ_LENGTH 63
  GC_CONTENT 0.53968253968254 BASEPAIR 24 FREE_ENERGY
-25.90 LEN_BP_RATIO 2.625
AGCUGAUCCUGGAGGUUAGCAGCCCAAGUCCUAGAAGACAAGGGUGUUGGCUUCGGGCUGGUAGA
CUCUGAGAAG
>random_seq_from_cds__NO_2795 RANDOM_LENGTH 109 SEQ_LENGTH 64
  GC_CONTENT 0.46875 BASEPAIR 24 FREE_ENERGY -24.40
  LEN_BP_RATIO 2.666666666666667
CUUCUUCUCCUCUUCUCCUCUUCUCCUCUGAGCGGUCAUGGACUCGAUUUUCAUCAUAAUGGAGUAA
UGACCAGUGUCCUCAUGCUGUCAGAGUCCUUAUCUUCACCUGA
>random_seq_from_cds__NO_2796 RANDOM_LENGTH 86 SEQ_LENGTH 60
  GC_CONTENT 0.6 BASEPAIR 20 FREE_ENERGY -22.90 LEN_BP_RATIO
3
GCUCUCUGUGUCUGUGCCUCGACUUCUGUGCUGGUGCGGUUGGGGCCACCAUCAUCCCAGUCA
AGCUCAAACUCAGGUCUGAGG
>random_seq_from_cds__NO_2801 RANDOM_LENGTH 87 SEQ_LENGTH 74
  GC_CONTENT 0.608108108108108 BASEPAIR 28 FREE_ENERGY
-34.90 LEN_BP_RATIO 2.64285714285714
GAUUUUUCGGGUCCUGUUGGGCCACCUCAGGCUUGGGCCGAGUUCUAGUAGGCGCCGAGCAAAG
GUGGCAGCUGUCUUGAAGUUCU
>random_seq_from_cds__NO_2802 RANDOM_LENGTH 72 SEQ_LENGTH 56
  GC_CONTENT 0.535714285714286 BASEPAIR 21 FREE_ENERGY
-22.00 LEN_BP_RATIO 2.666666666666667
UGAGCUUGAAGAACAGAUUGAGGGCUGUACGCAGCACCAGGAUCAUGUGCACAGGCUGCAGGUUU
GAGUGGG
>random_seq_from_cds__NO_2809 RANDOM_LENGTH 87 SEQ_LENGTH 67
  GC_CONTENT 0.582089552238806 BASEPAIR 26 FREE_ENERGY
-29.00 LEN_BP_RATIO 2.57692307692308
CAGAUCCUGAGUUGGACUUGUUCUCCUUGGUUGGGGGCACAAAGAAACCAUCUUCAGCCCCACCAG
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CUGCCCCAGGGGAUUAUCCCA
>random_seq_from_cds__NO_2813 RANDOM_LENGTH 77 SEQ_LENGTH 70
GC_CONTENT 0.5 BASEPAIR 24 FREE_ENERGY -16.50 LEN_BP_RATIO
2.91666666666667
AGCAGCUUGGCAUUAGGGUCA AUGUCUGGGAUCUGUCUCCUUCUCUGGGUCA AUGUCUCCUUUA
GGCUCUCAGCUU
>random_seq_from_cds__NO_2814 RANDOM_LENGTH 89 SEQ_LENGTH 68
GC_CONTENT 0.529411764705882 BASEPAIR 25 FREE_ENERGY
-19.60 LEN_BP_RATIO 2.72
CUUCAUCUAAGCCAUGGGUAGCAGCUGUGAGAUAGGCCAGGACUCUCUGUCCACAGUUCUUCAG
GAUCCGCACACGCUCUGACACAUC
>random_seq_from_cds__NO_2822 RANDOM_LENGTH 81 SEQ_LENGTH 69
GC_CONTENT 0.463768115942029 BASEPAIR 20 FREE_ENERGY
-15.27 LEN_BP_RATIO 3.45
GACAGCAUUAUUUGAUGUGGUUGCUUGUGGUUAUAGAUAAAUACCCACUCUCAUCCAGGCCCCAC
UCUUGACACGAAUGUU
>random_seq_from_cds__NO_2823 RANDOM_LENGTH 87 SEQ_LENGTH 76
GC_CONTENT 0.447368421052632 BASEPAIR 29 FREE_ENERGY
-24.00 LEN_BP_RATIO 2.62068965517241
CUCAUGAAUGUUACAUAAGCAUCCAGUUUGCGGUACAGAUCAAAUGGCCGUGUUUGGCUAGU
AGUGCUACAUGUGACAUGUCUG
>random_seq_from_cds__NO_2830 RANDOM_LENGTH 86 SEQ_LENGTH 77
GC_CONTENT 0.506493506493506 BASEPAIR 22 FREE_ENERGY
-21.95 LEN_BP_RATIO 3.5
UAGCAUAUUGCCAUGAACAGCAUAGGCUGGCCGUUCCCGUCCAGCUUAAACACAAUCAUACCAC
CAUCAUGGCCUGCUGCAAAG
>random_seq_from_cds__NO_2834 RANDOM_LENGTH 70 SEQ_LENGTH 49
GC_CONTENT 0.591836734693878 BASEPAIR 20 FREE_ENERGY
-24.00 LEN_BP_RATIO 2.45
AGGGGCAUAGUGGGUGGAAGGCAGCCAGUUUACUCCACGAUCGUGACCCCUUAGUACAUGCU
UCACC
>random_seq_from_cds__NO_2842 RANDOM_LENGTH 80 SEQ_LENGTH 72
GC_CONTENT 0.458333333333333 BASEPAIR 23 FREE_ENERGY
-15.50 LEN_BP_RATIO 3.1304347826087
CUUCUGAGUUUCCUUGGCUGCUGGCCUUCUCAUCUUCUCCCAUGAGACGAAUGUUGGCUUUUCC
CGGAAUUCAUUUAGU
>random_seq_from_cds__NO_2845 RANDOM_LENGTH 97 SEQ_LENGTH 86
GC_CONTENT 0.546511627906977 BASEPAIR 33 FREE_ENERGY
-26.00 LEN_BP_RATIO 2.60606060606061
UCCUUCAGUGUAUCGAUCACUAGGCCUGUGCUCAUUAACUCCAUCUCCAACUCAGCUGCUUUGG
AUGCCAGGCCUCGCUGUCCUGCCGAAGGCGG
>random_seq_from_cds__NO_2854 RANDOM_LENGTH 81 SEQ_LENGTH 63
GC_CONTENT 0.603174603174603 BASEPAIR 20 FREE_ENERGY
-19.70 LEN_BP_RATIO 3.15

CAUGGCGGGGUCCCCGGGGGUCACACACAUACAGAUUGUGGUCAUUUUCUGGCAAGAGGUCCACA
UCGUGCAAGAACAGGC

>random_seq_from_cds__NO_2856 RANDOM_LENGTH 110 SEQ_LENGTH 91
GC_CONTENT 0.659340659340659 BASEPAIR 28 FREE_ENERGY
-38.00 LEN_BP_RATIO 3.25

UGUCCAUUUCCAGCCCUGGUGGAUGACAUAAGAUGCCAUAAGCAAGCUGCUGGGCGUGCAAGAAG
GGGUGCAGGUGGUAGAGCAGCAGGCGCAGGUGGUGCUCCGGGCA

>random_seq_from_cds__NO_2862 RANDOM_LENGTH 82 SEQ_LENGTH 59
GC_CONTENT 0.576271186440678 BASEPAIR 20 FREE_ENERGY
-22.01 LEN_BP_RATIO 2.95

UUGGUUGAACAAAGCAGGCGGCCUUGGGAGAGCCUCAGCUCUGCUAUAUCCUGGAUGCCAUCCUGU
UUCUGUAUGGAAUUGUC

>random_seq_from_cds__NO_2864 RANDOM_LENGTH 81 SEQ_LENGTH 60
GC_CONTENT 0.533333333333333 BASEPAIR 22 FREE_ENERGY
-21.20 LEN_BP_RATIO 2.72727272727273

GACUUACGAGACUCUGAAGCAUGAGAAAACCACCACAGUAGUUCACUGGGUGGCAGGCUGUGUUC
AAGUCCACGAAAUAG

>random_seq_from_cds__NO_2873 RANDOM_LENGTH 68 SEQ_LENGTH 63
GC_CONTENT 0.634920634920635 BASEPAIR 24 FREE_ENERGY
-28.50 LEN_BP_RATIO 2.625

GUGUUGUCCUCUAUGGGGUGGCAGCCAUGUGACAUGUUGGAGGCUCGGGCCGAGUGAUGGCU
GCG

>random_seq_from_cds__NO_2887 RANDOM_LENGTH 84 SEQ_LENGTH 62
GC_CONTENT 0.580645161290323 BASEPAIR 20 FREE_ENERGY
-22.24 LEN_BP_RATIO 3.1

CAGCUGCCAAUAUGGAAGGGCUGGACUCAGAAGAAGGGGAUGGAGCCUGGUGCCCUGAGAUUC
AGUGGAACCGAUGACCUG

>random_seq_from_cds__NO_2902 RANDOM_LENGTH 80 SEQ_LENGTH 66
GC_CONTENT 0.575757575757576 BASEPAIR 24 FREE_ENERGY
-22.80 LEN_BP_RATIO 2.75

GCUGACAUAUGAACCUCCAAGGAGUGACAGGAGGCAACACAUACUCAGUGCCUGCCGUCACCAU
GGACCUGCUCUCAGG

>random_seq_from_cds__NO_2903 RANDOM_LENGTH 82 SEQ_LENGTH 51
GC_CONTENT 0.509803921568627 BASEPAIR 19 FREE_ENERGY
-20.80 LEN_BP_RATIO 2.68421052631579

AAAAGAUGUGGCUGUGGAGGAGUCCCCAGGAAACUCCUAACUUUCAAGAGAAGCUGGGAGAAG
GACAGUUUGGGGAGGGU

>random_seq_from_cds__NO_2914 RANDOM_LENGTH 98 SEQ_LENGTH 79
GC_CONTENT 0.468354430379747 BASEPAIR 28 FREE_ENERGY
-29.70 LEN_BP_RATIO 2.82142857142857

AUAUGGUUUUGUGCUUCUAACUGGUGCUGCCAGCUUUAUAUGGUGGCCACCUAGCCAUCAUG
UUCCAAGGCCCGCAAGAAGUACAAAGUGGAGG

>random_seq_from_cds__NO_2921 RANDOM_LENGTH 89 SEQ_LENGTH 66
GC_CONTENT 0.515151515151515 BASEPAIR 24 FREE_ENERGY

-20.10 LEN_BP_RATIO 2.75
CCCGUUGGAUGUCCCCUGGUAAAAGACGCCAGCUGCUAGUCCAAAAGUGGUUAUCAUUGGCUCUUUC
UAGAACCUCAGCUUCAGUGUCAAAA
>random_seq_from_cds__NO_2938 RANDOM_LENGTH 82 SEQ_LENGTH 56
GC_CONTENT 0.607142857142857 BASEPAIR 20 FREE_ENERGY
-18.90 LEN_BP_RATIO 2.8
UACCGUGUCCUUACCUCGGAGCAGAAGGCCAAAGCCCUGAAGGGCCAGUUCAACUUUGACCACCC
GGGAUGCCUUUGACAAU
>random_seq_from_cds__NO_2974 RANDOM_LENGTH 83 SEQ_LENGTH 73
GC_CONTENT 0.493150684931507 BASEPAIR 26 FREE_ENERGY
-22.90 LEN_BP_RATIO 2.80769230769231
ACUGUGAAGUGAUGAUAGGGAAUGAAGUCCCUGCCUCGGCAGUGGUCACAUCUGUGGGCAUCUUUC
UUCUAAAAAGCGGGCACA
>random_seq_from_cds__NO_2975 RANDOM_LENGTH 81 SEQ_LENGTH 54
GC_CONTENT 0.481481481481481 BASEPAIR 20 FREE_ENERGY
-17.60 LEN_BP_RATIO 2.7
UUUCAAGUGCAUGGCUUUUCUCUGGUCCUUGAGCCACAGCUCGUAGGCUGUUUUCUGCAUCAUAG
GGUUACAGAAUCGAAU
>random_seq_from_cds__NO_2980 RANDOM_LENGTH 86 SEQ_LENGTH 69
GC_CONTENT 0.463768115942029 BASEPAIR 26 FREE_ENERGY
-23.30 LEN_BP_RATIO 2.65384615384615
UUUCCUUUUAAUGACGUUGGAGGUGACAGGUUUUUCAGUCUGACACCACUUGUGAGGUGACAGAC
UUCUUCACUUUCCUUAUCACU
>random_seq_from_cds__NO_2981 RANDOM_LENGTH 84 SEQ_LENGTH 64
GC_CONTENT 0.390625 BASEPAIR 24 FREE_ENERGY -17.80
LEN_BP_RATIO 2.66666666666667
AUGGAGAGUAACCAUGUUUAACUUCUCUGUUAGCUUAAUGGAAUACUCUGAACAGGUUAUUCAG
GUCCUAUUUGUCUUUUCU
>random_seq_from_cds__NO_2997 RANDOM_LENGTH 72 SEQ_LENGTH 48
GC_CONTENT 0.5 BASEPAIR 19 FREE_ENERGY -21.50 LEN_BP_RATIO
2.52631578947368
GACAGAAGUGAUGUGCAUAUAGGCAUCCUGGAUGGCUGGGCCUAUCUCUUCUGCUUUGUCUUGGU
CUUCAAA
>random_seq_from_cds__NO_3009 RANDOM_LENGTH 66 SEQ_LENGTH 54
GC_CONTENT 0.555555555555556 BASEPAIR 19 FREE_ENERGY
-19.10 LEN_BP_RATIO 2.84210526315789
AAGGCGACCCUACGGAGAAGCAACUUCAGAUCAUCCUGGAGGAUGCACCUCUCUGGCAGAGAUUC
A
>random_seq_from_cds__NO_3011 RANDOM_LENGTH 71 SEQ_LENGTH 52
GC_CONTENT 0.557692307692308 BASEPAIR 20 FREE_ENERGY
-20.80 LEN_BP_RATIO 2.6
CCCCAAUGCCAUGUACUCCCUCUGCUGGACUUUGUCCCUACGGACAGUCACCGCUGGAAGUACG
UCAACG
>random_seq_from_cds__NO_3017 RANDOM_LENGTH 72 SEQ_LENGTH 62

GC_CONTENT 0.661290322580645 BASEPAIR 20 FREE_ENERGY
-19.00 LEN_BP_RATIO 3.1
UGCCGCUCUCUGCCUCUGCCUGCCCCACACCCACCAUGGCUGUGAGCACUAUUCGGGUCUC
GAGGACA
>random_seq_from_cds__NO_3023 RANDOM_LENGTH 81 SEQ_LENGTH 66
GC_CONTENT 0.696969696969697 BASEPAIR 26 FREE_ENERGY
-29.60 LEN_BP_RATIO 2.53846153846154
CACCUGGACAGCAGUGGCCUCGCAUCCCUUCGCGGGCUGGGGUGGCCAGGAGCGGGUGGGCACC
AUUCUCCUUCUCACU
>random_seq_from_cds__NO_3031 RANDOM_LENGTH 70 SEQ_LENGTH 57
GC_CONTENT 0.421052631578947 BASEPAIR 19 FREE_ENERGY
-16.90 LEN_BP_RATIO 3
AUUCCUUGUGCUGUCCCUUGAAGAUCUGCCAGUUGAUCUGGUUGGAACUGUAAGCUACAUAGA
ACUCU
>random_seq_from_cds__NO_3040 RANDOM_LENGTH 73 SEQ_LENGTH 61
GC_CONTENT 0.491803278688525 BASEPAIR 19 FREE_ENERGY
-20.00 LEN_BP_RATIO 3.21052631578947
CAUAGGCAUGUUGCUGUCCUUAUGUAGUAUUCUUUUUGGCAGAUUAGGAGGGGACCUAUCAAGC
CUGAGUGA
>random_seq_from_cds__NO_3048 RANDOM_LENGTH 102 SEQ_LENGTH 57
GC_CONTENT 0.456140350877193 BASEPAIR 21 FREE_ENERGY
-15.91 LEN_BP_RATIO 2.71428571428571
UAACAUCAGUUUUGUAGGGGUCAUCAUAGGGCACAAUUAUUCAGCAUAGUCAUCUUCACUG
CUCUGGACCUCUCCUUUGGAAUGAUCUCAAUGUAAU
>random_seq_from_cds__NO_3058 RANDOM_LENGTH 81 SEQ_LENGTH 72
GC_CONTENT 0.513888888888889 BASEPAIR 20 FREE_ENERGY
-21.90 LEN_BP_RATIO 3.6
GUCUGGCUGAGGUCUAAAGAAAGGGUUGUAUGGCUGAGGUCUGGAGAAAGGGUUGUAUGGCUGAG
GUCUGGAGAAAUGGGC
>random_seq_from_cds__NO_3059 RANDOM_LENGTH 86 SEQ_LENGTH 67
GC_CONTENT 0.552238805970149 BASEPAIR 25 FREE_ENERGY
-20.90 LEN_BP_RATIO 2.68
AUCUGACCGAGGGCUGGGGAAAGGUUCUCUGAAUGAGUUCUGGAGAGAGAGUCGUGUGGCUGAG
GUCUGGAGAGAGGUUUGUCUG
>random_seq_from_cds__NO_3063 RANDOM_LENGTH 83 SEQ_LENGTH 59
GC_CONTENT 0.525423728813559 BASEPAIR 23 FREE_ENERGY
-26.50 LEN_BP_RATIO 2.56521739130435
UCUGAUAAAGACCUGGAGGACAGCUUGCCUGACCAGUGUCAUUGAGGAAUUCUGAUUAUGGUCA
GGAAGUGAGGCUAUCCAG
>random_seq_from_cds__NO_3077 RANDOM_LENGTH 84 SEQ_LENGTH 49
GC_CONTENT 0.448979591836735 BASEPAIR 20 FREE_ENERGY
-16.50 LEN_BP_RATIO 2.45
CAUAGUCAGCAUCACUCUCUUAUCUUCAGGUUCUAAACGAUCAUGCAUUUCCGUGUAGCCAUG
ACUGUAGAUUCUGGAGGUU

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>random_seq_from_cds__NO_3105 RANDOM_LENGTH 87 SEQ_LENGTH 58
  GC_CONTENT 0.482758620689655 BASEPAIR 24 FREE_ENERGY
  -25.40 LEN_BP_RATIO 2.416666666666667
CCCCAGAGGUUGGAGCAGUUCAUCGCUAUUGGCUUAUUAACAUGUAGUUCUGAGCAUUCACAGC
CUCUGCAUGCUGGAGUUACUGC
>random_seq_from_cds__NO_3107 RANDOM_LENGTH 87 SEQ_LENGTH 79
  GC_CONTENT 0.569620253164557 BASEPAIR 27 FREE_ENERGY
  -27.70 LEN_BP_RATIO 2.92592592592593
GCCUACAGUACAUGGUUCCCUGCCCAGGAGUGGUGAGGGCUGGACAUUGCACCCCUGGAGUAGGA
AGUGAUGCUAUGCCCUUUGCAG
>random_seq_from_cds__NO_3117 RANDOM_LENGTH 95 SEQ_LENGTH 73
  GC_CONTENT 0.616438356164384 BASEPAIR 19 FREE_ENERGY
  -26.25 LEN_BP_RATIO 3.84210526315789
CAGGUUGGCAAGGGUGCAGACCAGUGUCCAGAGUCAAUUGCAGCGGAGCAUGUCCAAGCCCUCAC
UCUGUAGCCGGGCGGCACUCAAAUUUACA
>random_seq_from_cds__NO_3122 RANDOM_LENGTH 66 SEQ_LENGTH 49
  GC_CONTENT 0.591836734693878 BASEPAIR 20 FREE_ENERGY
  -19.60 LEN_BP_RATIO 2.45
CAGAAGCCAAGCAUUCAGCUUGCUGGGCCCAUUUACUUGGUACCCGUCAGUGCAGUGGAAGCUG
C
>random_seq_from_cds__NO_3127 RANDOM_LENGTH 97 SEQ_LENGTH 82
  GC_CONTENT 0.51219512195122 BASEPAIR 25 FREE_ENERGY
  -21.40 LEN_BP_RATIO 3.28
UUGUUGUAGGUUCAUUAUCAGCCAGUUCUCAGCCUCGUUGGUGAGAGCCUUUUUGGUUCCCAC
CCAUGUCCAUGUCUUAUUGUUCUUUCGGAUCC
>random_seq_from_cds__NO_3128 RANDOM_LENGTH 81 SEQ_LENGTH 63
  GC_CONTENT 0.365079365079365 BASEPAIR 24 FREE_ENERGY
  -19.20 LEN_BP_RATIO 2.625
CAAUCCAGUAGUAGGAGCUGUAGUAGGGUAGGACCUUAUUGAGGUAUAUCAAUUUCAUUUUUAUUC
UGGAUGGCCACUAAGU
>random_seq_from_cds__NO_3129 RANDOM_LENGTH 77 SEQ_LENGTH 50
  GC_CONTENT 0.44 BASEPAIR 19 FREE_ENERGY -15.90
  LEN_BP_RATIO 2.63157894736842
CUGUGUAGCGAUUCUGGCAGUAUUUACGGGAAAUAUCCAUGAGUAUGC UUUUGUGCUGUA AUGA
UAAGUCCAUGCU
>random_seq_from_cds__NO_3145 RANDOM_LENGTH 81 SEQ_LENGTH 74
  GC_CONTENT 0.445945945945946 BASEPAIR 23 FREE_ENERGY
  -22.41 LEN_BP_RATIO 3.21739130434783
UUAAAGGAUGUAAGAAGGCUUUUGGUAGCUUCCAUCUGAUUCAAGGCUUUGGCAGCUGCCUGGCA
GGAACAAAUUUCUUUG
>random_seq_from_cds__NO_3147 RANDOM_LENGTH 79 SEQ_LENGTH 61
  GC_CONTENT 0.60655737704918 BASEPAIR 22 FREE_ENERGY
  -27.60 LEN_BP_RATIO 2.77272727272727
CAAGGGAAUGUUGGACUCAGUGGGAGCCUUCACAGGUAGGUAGCAGGCCAGACCAGUGUCCUGUG
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GCUCCACAUGUCCG
>random_seq_from_cds__NO_3153 RANDOM_LENGTH 70 SEQ_LENGTH 51
  GC_CONTENT 0.568627450980392 BASEPAIR 20 FREE_ENERGY
  -18.60 LEN_BP_RATIO 2.55
GGAUUUGCUGUGUCCACUGCCCUUGAGUGGUGCAUUAACCUGGCUGGUCCUGCAACAUGAAG
CCUUC
>random_seq_from_cds__NO_3164 RANDOM_LENGTH 97 SEQ_LENGTH 72
  GC_CONTENT 0.527777777777778 BASEPAIR 22 FREE_ENERGY
  -19.80 LEN_BP_RATIO 3.27272727272727
CAGGUGUGUGUACCUUUGCUGACAAUAAGCACUGGCCUCAUCAUAAGUCAUAGCUUCCGUGGAGG
UGUUGUAAGACCAGGCUCCACUCUCUUUAUG
>random_seq_from_cds__NO_3166 RANDOM_LENGTH 70 SEQ_LENGTH 52
  GC_CONTENT 0.557692307692308 BASEPAIR 19 FREE_ENERGY
  -16.70 LEN_BP_RATIO 2.73684210526316
UGAUUGGAGCUGGGUCAGUGGCCUAAUUUCUCUGAAGUCUGUGUGGAUGAGGGACUUGAGCCC
ACUUG
>random_seq_from_cds__NO_3175 RANDOM_LENGTH 90 SEQ_LENGTH 56
  GC_CONTENT 0.410714285714286 BASEPAIR 21 FREE_ENERGY
  -15.70 LEN_BP_RATIO 2.66666666666667
GAACAACAGAUGAAUCGGUGGUUCAACCAUGAAAUAUGGCCUUGAGCCUCAAAAACAAGAUACA
UUAUGAAGGAACCUGUACUAAAUGA
>random_seq_from_cds__NO_3186 RANDOM_LENGTH 74 SEQ_LENGTH 63
  GC_CONTENT 0.507936507936508 BASEPAIR 24 FREE_ENERGY
  -21.30 LEN_BP_RATIO 2.625
AAAAUGCUCAGAUUCUGCUGUCUCUGGCCAAUGGGAGGUGGUCACUAUGCAUGAAGAGAAGCAAG
AGUCAGCCA
>random_seq_from_cds__NO_3233 RANDOM_LENGTH 97 SEQ_LENGTH 69
  GC_CONTENT 0.739130434782609 BASEPAIR 26 FREE_ENERGY
  -37.57 LEN_BP_RATIO 2.65384615384615
GUUUCAGCUGGUCCCGCUCGCCUCAGGGUGCCAGCUCUCCUCUGCAGCCCCUCCUGGGUCUC
CUGGGGCCUGGCAGCCUGGUCCAAGGUCAAUU
>random_seq_from_cds__NO_3236 RANDOM_LENGTH 80 SEQ_LENGTH 62
  GC_CONTENT 0.693548387096774 BASEPAIR 23 FREE_ENERGY
  -28.62 LEN_BP_RATIO 2.69565217391304
GCCUUCUGAGCUGAGCUGUCCUGGCCCCCAUCCACACCAGGCAGGCCAGAAGCAGCAGCUG
GACAGCUGGCAUCUC
>random_seq_from_cds__NO_3249 RANDOM_LENGTH 86 SEQ_LENGTH 69
  GC_CONTENT 0.565217391304348 BASEPAIR 23 FREE_ENERGY
  -20.80 LEN_BP_RATIO 3
UCUACAUGUGACUUCGAACUUGGCCUGAAGCUGAUGAAGGAACCAUCCUGCUUGAACGUCGCA
GCAGCGAGCCCAGCAUGAAGG
>random_seq_from_cds__NO_3254 RANDOM_LENGTH 87 SEQ_LENGTH 63
  GC_CONTENT 0.587301587301587 BASEPAIR 23 FREE_ENERGY
  -23.71 LEN_BP_RATIO 2.73913043478261
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AGAGACUUCAACAUCCUGGCUUCCCGACUGUGAGGGUUCUUCAAGGCCUUUACCAAGAACGGCU
CGGGAGCAGUAUUUCCAGGUGG

>random_seq_from_cds__NO_3258 RANDOM_LENGTH 81 SEQ_LENGTH 74
GC_CONTENT 0.567567567567568 BASEPAIR 22 FREE_ENERGY
-21.70 LEN_BP_RATIO 3.36363636363636

CCUGCUGUCCGAAUGGCUCUGUCUCCCGAGUCCCGUGGCUCAUGGAAUCCAGGUCCUUCUAU
ACCGCUUACCGCAGA

>random_seq_from_cds__NO_3274 RANDOM_LENGTH 80 SEQ_LENGTH 60
GC_CONTENT 0.583333333333333 BASEPAIR 23 FREE_ENERGY
-33.00 LEN_BP_RATIO 2.60869565217391

GGCUCUAUCCUGUCCUUAUGGGCCUGCUGGCCAUGUACACCUACUCCAGGCCAAGUAAGG
GCCCUGAAGGGCCAU

>random_seq_from_cds__NO_3278 RANDOM_LENGTH 90 SEQ_LENGTH 61
GC_CONTENT 0.688524590163934 BASEPAIR 23 FREE_ENERGY
-28.90 LEN_BP_RATIO 2.65217391304348

GGUCACCAAGUCCUGUCACCGUGCGACGCCGGCAGCCCACCUGCAGCACGGGGCAGCCUCC
UGACCGACUACAACAACCAGGCCGA

>random_seq_from_cds__NO_3302 RANDOM_LENGTH 92 SEQ_LENGTH 81
GC_CONTENT 0.530864197530864 BASEPAIR 29 FREE_ENERGY
-21.50 LEN_BP_RATIO 2.79310344827586

ACUAUGGAGAUUCAACUGCAGGCACCUCCGGAUUGCCAACCCUGUCCGUGUCCUGGAGGUUCA
AGUUGUGCUGUUGUCCCAAGACAAAG

>random_seq_from_cds__NO_3308 RANDOM_LENGTH 70 SEQ_LENGTH 58
GC_CONTENT 0.637931034482759 BASEPAIR 21 FREE_ENERGY
-21.30 LEN_BP_RATIO 2.76190476190476

UCUGCAGAGUGGGCAAGGCUGUGAGAGGGUGUGACUGCCAUGCCUUGGGCUCCACCAAUGGGCAG
UGUGA

>random_seq_from_cds__NO_3312 RANDOM_LENGTH 88 SEQ_LENGTH 71
GC_CONTENT 0.47887323943662 BASEPAIR 22 FREE_ENERGY
-20.30 LEN_BP_RATIO 3.22727272727273

CAGGAAUAGAGAGUCUCAUAGCAAACCUUGGAACUGGGGAUGAGAUGGUGACAGAUAAGCCUU
CGAGGAUAGACUAAAGGAAGCAG

>random_seq_from_cds__NO_3328 RANDOM_LENGTH 110 SEQ_LENGTH 85
GC_CONTENT 0.505882352941176 BASEPAIR 27 FREE_ENERGY
-24.20 LEN_BP_RATIO 3.14814814814815

CAAGAAGCCGAGAUCAAUGCCAGAAAAGCCAAAAACUCUGUJACUAGCCUCCUCAGCAUUAUUA
UGACCUCUUGGAGCAGCUGGGGGCAGCUGGAUACAGUGGACCUGA

>random_seq_from_cds__NO_3331 RANDOM_LENGTH 89 SEQ_LENGTH 78
GC_CONTENT 0.538461538461538 BASEPAIR 24 FREE_ENERGY
-17.50 LEN_BP_RATIO 3.25

CCAUCUGGCUGCUUCAACACCCGUCCAUGAAAAGCCCUAGCCUAGACUUCUCUCCGAGUGCUU
UCCAAAUCUGUAGUUGCGCAGUCU

>random_seq_from_cds__NO_3334 RANDOM_LENGTH 88 SEQ_LENGTH 79
GC_CONTENT 0.455696202531646 BASEPAIR 27 FREE_ENERGY

-18.30 LEN_BP_RATIO 2.92592592592593
UGCCUCCACUUGGCUGCCUUUCUUAAGCUGAGGUUCUGUUGUCUGGUUAAUAGCAUCAGCUUUUU
CACUUCCUUGGGUUAUCUGGA
>random_seq_from_cds__NO_3360 RANDOM_LENGTH 83 SEQ_LENGTH 60
GC_CONTENT 0.5 BASEPAIR 20 FREE_ENERGY -22.50 LEN_BP_RATIO
3
UACUUCUAUGCCUUUGUUGCAUCGGGCUGCAGCUCCUUGCCACUGCAGCUACAACAAUUCUGGCU
GCUAGUCCUUGUAAU
>random_seq_from_cds__NO_3377 RANDOM_LENGTH 78 SEQ_LENGTH 70
GC_CONTENT 0.442857142857143 BASEPAIR 20 FREE_ENERGY
-18.00 LEN_BP_RATIO 3.5
AGGAUUUAUCAAGCUGUGCAGGGAGAUGUGGGGAAGGGUAAUUCUAGAGAUGCCACCUGCAACUGU
GAUUUAACUGUC
>random_seq_from_cds__NO_3417 RANDOM_LENGTH 80 SEQ_LENGTH 57
GC_CONTENT 0.473684210526316 BASEPAIR 22 FREE_ENERGY
-16.63 LEN_BP_RATIO 2.59090909090909
GCAUUCGAGGGUCAUUUUUCUGGAUGCUAAGUCCAUCAGUCCACCAUCUCCAGCUCGCAGAA
UUACUGAAGUUUGG
>random_seq_from_cds__NO_3419 RANDOM_LENGTH 95 SEQ_LENGTH 81
GC_CONTENT 0.469135802469136 BASEPAIR 29 FREE_ENERGY
-18.90 LEN_BP_RATIO 2.79310344827586
CUGGCGUUUUACCAUGAUUAAAAGAUGCAGGGUACCCCAAACCAUUUUCAAAGGAUUUGGAG
GACUAAACUGGACAAUAGUGGCAGCGUUU
>random_seq_from_cds__NO_3436 RANDOM_LENGTH 68 SEQ_LENGTH 49
GC_CONTENT 0.510204081632653 BASEPAIR 19 FREE_ENERGY
-21.30 LEN_BP_RATIO 2.57894736842105
CCGUAGAUGCUCAGGGACUUGAGGAGGGUAGAUCAUCUCUGCCUGAGUAUCUUUGACUGUGGGAG
GAU
>random_seq_from_cds__NO_3441 RANDOM_LENGTH 82 SEQ_LENGTH 62
GC_CONTENT 0.403225806451613 BASEPAIR 27 FREE_ENERGY
-19.10 LEN_BP_RATIO 2.2962962962963
UUUGUAGCCAUGUCAGCAUUGUAAGUUGGUGGACUGUCAAAUCAAUGUGAUCUGGCAUGUCAAC
ACAUAACUCAUAAUUGC
>random_seq_from_cds__NO_3445 RANDOM_LENGTH 84 SEQ_LENGTH 60
GC_CONTENT 0.5 BASEPAIR 24 FREE_ENERGY -20.00 LEN_BP_RATIO
2.5
AGCAGCAGGGCGGGCGAGCAUUCUAUGUUCUUAAGGGUUCUUGAUAAAGACAGAGUGCCUUUGU
CUUGGAAUACAUCUUGGAU
>random_seq_from_cds__NO_3452 RANDOM_LENGTH 90 SEQ_LENGTH 78
GC_CONTENT 0.371794871794872 BASEPAIR 24 FREE_ENERGY
-20.47 LEN_BP_RATIO 3.25
CCCUUCAUAAUUCACUUCUUAUUCUUAUGUAAUUCUGUUCUUGUAAUCCACAUAAACAGUACAUG
GUUCCCAAGCAAACAGGUGGGGAUG
>random_seq_from_cds__NO_3461 RANDOM_LENGTH 97 SEQ_LENGTH 73

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GC_CONTENT    0.479452054794521    BASEPAIR    25    FREE_ENERGY
-19.81    LEN_BP_RATIO    2.92
GCACUUUAAUUCUGGUACAUUUUGGUGUGAGAGACCAUCCGUAUGUGAGACAUUCUACCUCUCU
GUCUUCUUUCCUCCAGCUGUGUAGUAGCCAGU
>random_seq_from_cds__NO_3466    RANDOM_LENGTH    85    SEQ_LENGTH    67
GC_CONTENT    0.328358208955224    BASEPAIR    24    FREE_ENERGY
-15.50    LEN_BP_RATIO    2.791666666666667
UUUUGUCUAUGCUCAUUGGAAAAGUAAAAGCUUUUAAAAGUAUAGUAAUAUUGGGCAAUUCUCCA
UUUUCACAUGAGGAAAACC
>random_seq_from_cds__NO_3468    RANDOM_LENGTH    77    SEQ_LENGTH    69
GC_CONTENT    0.666666666666667    BASEPAIR    27    FREE_ENERGY
-38.20    LEN_BP_RATIO    2.55555555555556
GCCUUGGAGGAAUAAGGGUCUCCUGGGAGCCUGGUGUUGGUCGAGGCUGCCCAGGGAGGACCCG
AGGUUCAGGCAU
>random_seq_from_cds__NO_3489    RANDOM_LENGTH    81    SEQ_LENGTH    67
GC_CONTENT    0.567164179104478    BASEPAIR    23    FREE_ENERGY
-18.40    LEN_BP_RATIO    2.91304347826087
UCCCAAACAUCUGCAUGCCGAUGACAGCGUAGAUGAAGAAGAGCAUGACGAUGAGCAGAGCCAC
GUAGGGUAGGGCCCUG
>random_seq_from_cds__NO_3498    RANDOM_LENGTH    95    SEQ_LENGTH    77
GC_CONTENT    0.584415584415584    BASEPAIR    25    FREE_ENERGY
-29.70    LEN_BP_RATIO    3.08
CAUUGGAGUCUAUGGCCUUGUACAGCAGCCUGAGGCCAUCCCUCGAAGGUGGAGACCGUGAAGAG
GGACAUCAUGGCUGAGAGCACAUUGUCGAA
>random_seq_from_cds__NO_3511    RANDOM_LENGTH    73    SEQ_LENGTH    64
GC_CONTENT    0.609375    BASEPAIR    23    FREE_ENERGY    -26.60
LEN_BP_RATIO    2.78260869565217
GGCAGAAGUCAGGCUCUCCGCCUCGGCCAGGUUGUCCACGGCAAUGGCCAGGAAGACAUUGAGCA
GGAUGUCA
>random_seq_from_cds__NO_3514    RANDOM_LENGTH    84    SEQ_LENGTH    69
GC_CONTENT    0.536231884057971    BASEPAIR    23    FREE_ENERGY
-16.70    LEN_BP_RATIO    3
UGAGGGCUUGGGGAAAGUUGUCAAAAGUUGCUGCGCCGUACUUCUGUGUCUCAAAGUCAUACCUC
CCCCAAAGAGCUGCAUGC
>random_seq_from_cds__NO_3534    RANDOM_LENGTH    88    SEQ_LENGTH    67
GC_CONTENT    0.582089552238806    BASEPAIR    27    FREE_ENERGY
-34.30    LEN_BP_RATIO    2.48148148148148
UCAGGCAGAACAAGGCCCGGGUGGCCUUGGCAGAAUCUCAGGAACUGGCUUCUUGGGCUGUUUC
UUCCUCAGGCCUUCAUCCUGGGG
>random_seq_from_cds__NO_3540    RANDOM_LENGTH    90    SEQ_LENGTH    74
GC_CONTENT    0.567567567567568    BASEPAIR    26    FREE_ENERGY
-23.30    LEN_BP_RATIO    2.84615384615385
GCCAUAGCCUUGGGCCCAUACUUCUUGCCGUAAGCAGGACUUGCAGUAAAUCUCCUCACCAUGCA
CGGCCACAGUGGUACUGUCCAGAUU
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>random_seq_from_cds__NO_3544 RANDOM_LENGTH 69 SEQ_LENGTH 55
GC_CONTENT 0.763636363636364 BASEPAIR 21 FREE_ENERGY
-29.50 LEN_BP_RATIO 2.61904761904762
CCAAGGCGCCCGGCGGGCGGGCGGCAUGGCCAAGGCCAGCGGGCUGAGCUGAAGGUCUUCAAG
UCCG
>random_seq_from_cds__NO_3546 RANDOM_LENGTH 110 SEQ_LENGTH 86
GC_CONTENT 0.604651162790698 BASEPAIR 31 FREE_ENERGY
-40.70 LEN_BP_RATIO 2.7741935483871
AAAAAGCUGCAGCUUUAUGAGCCCGAAUGGAGCGACGAUAUGGCCAAGGCGCCCAAAGGCUUAGG
CAAGGUGGGGUCCAAGGGCCGUGAAGCUCCGUGAUGUCCAAGAC
>random_seq_from_cds__NO_3549 RANDOM_LENGTH 84 SEQ_LENGTH 72
GC_CONTENT 0.666666666666667 BASEPAIR 25 FREE_ENERGY
-31.70 LEN_BP_RATIO 2.88
CUCUCCAGCAAGGCCAAGGGCGAAAAGAGCUCUGGGCCUGUCCCCUCUGCCAAGGGCCAGGAGGA
GCGCGCCUCCUCAAGGUG
>random_seq_from_cds__NO_3551 RANDOM_LENGTH 78 SEQ_LENGTH 65
GC_CONTENT 0.615384615384615 BASEPAIR 23 FREE_ENERGY
-27.10 LEN_BP_RATIO 2.82608695652174
AAAGAGGACAGUGCAGAAUGUCCUGGAUCUCCGGCAGAACCUUGGAAGAGACCAUGUCCAGCCUGC
GAGGGUCCAGGU
>random_seq_from_cds__NO_3552 RANDOM_LENGTH 92 SEQ_LENGTH 71
GC_CONTENT 0.619718309859155 BASEPAIR 23 FREE_ENERGY
-19.20 LEN_BP_RATIO 3.08695652173913
GACUCACAGGCUCCUGGAGAUGACCUGCUACGACAGCGAUGAUGCCAACCCACGCAGCGUGUCC
AGCCUCUCCAACCGCUCGUCCCCUCUG
>random_seq_from_cds__NO_3571 RANDOM_LENGTH 93 SEQ_LENGTH 77
GC_CONTENT 0.584415584415584 BASEPAIR 23 FREE_ENERGY
-20.70 LEN_BP_RATIO 3.34782608695652
CAUCCAGUGAUACCACCAUGCUUCAAGGUCCAGAUUCUGCAUGCUACAAGCUCAGCAUCUGGG
GGCCUCUCCCUCCUGCUUACCCCA
>random_seq_from_cds__NO_3572 RANDOM_LENGTH 89 SEQ_LENGTH 68
GC_CONTENT 0.529411764705882 BASEPAIR 20 FREE_ENERGY
-20.20 LEN_BP_RATIO 3.4
GUCCGGCACCCAUCCUCAAUAUUAACUCAGCCAGCUUCUCCAGGGCCUGGAGCUAAUGAGUGGU
UUCAGUGUGCCAAAAGAGACCCGC
>random_seq_from_cds__NO_3574 RANDOM_LENGTH 86 SEQ_LENGTH 64
GC_CONTENT 0.640625 BASEPAIR 19 FREE_ENERGY -19.20
LEN_BP_RATIO 3.36842105263158
AGCAGUACUCCCGUCCCCACCCACCCUGCUCCCCUGCUGCUCCACAGAAGAAGAGACGGAAGA
GCUGACUUGGAGUGGAAGCCC
>random_seq_from_cds__NO_3575 RANDOM_LENGTH 82 SEQ_LENGTH 69
GC_CONTENT 0.579710144927536 BASEPAIR 19 FREE_ENERGY
-21.70 LEN_BP_RATIO 3.63157894736842
CAGAGCUGGGCAACUGGACAGGUAAUCAGCGGAUCGGAACACUCUCCCAAGAAAGGGCUCAGG
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GUACCAGCUUCAGUCCC
>random_seq_from_cds__NO_3584 RANDOM_LENGTH 78 SEQ_LENGTH 63
  GC_CONTENT 0.507936507936508 BASEPAIR 21 FREE_ENERGY
  -16.50 LEN_BP_RATIO 3
AUCUCAAGCCUCAACAGCAUCACUAGCCAUUCCAGCAUCGGCAGCAGCAAGGAUGCUGAUGCAGAA
AAAGAAGAAAAAA
>random_seq_from_cds__NO_3594 RANDOM_LENGTH 83 SEQ_LENGTH 68
  GC_CONTENT 0.470588235294118 BASEPAIR 20 FREE_ENERGY
  -16.80 LEN_BP_RATIO 3.4
UUCCAAGUGUUCAAGGGACUAUAUUUCUAAAAUGGACCCAGCCUCUACCCUGGGACUAAGCACUG
AGUCCAUCAUGGCUACA
>random_seq_from_cds__NO_3614 RANDOM_LENGTH 82 SEQ_LENGTH 77
  GC_CONTENT 0.597402597402597 BASEPAIR 26 FREE_ENERGY
  -27.30 LEN_BP_RATIO 2.96153846153846
CAGCAGCUUGGCGAUCUCCAUCUCCGUCUUGCCUCCACAGAUGUGUCGCGUGGUUGUGGAAGCGGA
GCUCGGUCAGCGUGUUG
>random_seq_from_cds__NO_3617 RANDOM_LENGTH 110 SEQ_LENGTH 99
  GC_CONTENT 0.505050505050505 BASEPAIR 33 FREE_ENERGY
  -24.10 LEN_BP_RATIO 3
AACUCCAGAGCCUCAGUAAACCGGACCAAGAUCUCAUUUGUGAUGCAGUCUGAGUUGUUGACGUU
CACCUCAGUCAUCUCGGGGUCAUUGUUCUUCACUCUCUCCAGAGG
>random_seq_from_cds__NO_3618 RANDOM_LENGTH 87 SEQ_LENGTH 59
  GC_CONTENT 0.677966101694915 BASEPAIR 22 FREE_ENERGY
  -26.90 LEN_BP_RATIO 2.68181818181818
CUCAUCAAAUAUGCUGGGAGCUGCCUCCUCCUCCACCUUGGCCGGUCCUUCAGAGGGCUUGGUGG
GGCCACUGGGCGUCUGUUUCUC
>random_seq_from_cds__NO_3627 RANDOM_LENGTH 75 SEQ_LENGTH 52
  GC_CONTENT 0.596153846153846 BASEPAIR 20 FREE_ENERGY
  -15.80 LEN_BP_RATIO 2.6
CACAGAAGUUGAGCAUGGCCUCCCGGUUGUACACACCCGUGGACUGUUUCUCCGUCUGGUUUCUC
UGCCGCAGCC
>random_seq_from_cds__NO_3638 RANDOM_LENGTH 68 SEQ_LENGTH 58
  GC_CONTENT 0.655172413793103 BASEPAIR 24 FREE_ENERGY
  -26.90 LEN_BP_RATIO 2.41666666666667
CGGGAUGCCACCUUCUGCUUCAUCGUGUCGUGGCGGUGGCUGAUGUGGCCGUGGGUGCCCUGGU
CAU
>random_seq_from_cds__NO_3641 RANDOM_LENGTH 77 SEQ_LENGTH 52
  GC_CONTENT 0.769230769230769 BASEPAIR 20 FREE_ENERGY
  -31.40 LEN_BP_RATIO 2.6
GUGACCCCGGAGGGCGGCGGUGGCAUAGCCGGCUGCUGGAUCCUCUCCUUCGUGGUGGGACU
GACCCUAUGUU
>random_seq_from_cds__NO_3649 RANDOM_LENGTH 68 SEQ_LENGTH 56
  GC_CONTENT 0.607142857142857 BASEPAIR 20 FREE_ENERGY
  -24.61 LEN_BP_RATIO 2.8
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GUCGGGCAGCUUUGCUGGAACAGCCGCCCGCUGCACAGCUGUAGAAGCUGGACCGUUCCCGAGG
AUU

>random_seq_from_cds__NO_3652 RANDOM_LENGTH 97 SEQ_LENGTH 81
GC_CONTENT 0.654320987654321 BASEPAIR 26 FREE_ENERGY
-30.60 LEN_BP_RATIO 3.11538461538462

UGGAUGAGGGGGUAUCGGCCUGGUUGCAGGAGAAGCCGGCAAAGUCAUCUAAGUCCAGUGCCCA
GACCAUGGCCCGCCAGUCCCUUCUGCUUCA

>random_seq_from_cds__NO_3654 RANDOM_LENGTH 72 SEQ_LENGTH 57
GC_CONTENT 0.56140350877193 BASEPAIR 20 FREE_ENERGY
-17.90 LEN_BP_RATIO 2.85

UGAUCCUGGAUUCUCUGUUUGGUGGCCCCCUUCCAGGAGCAGACCUUCAUAGUAGGCCAGCAUCC
CUCCUUC

>random_seq_from_cds__NO_3658 RANDOM_LENGTH 71 SEQ_LENGTH 43
GC_CONTENT 0.558139534883721 BASEPAIR 19 FREE_ENERGY
-20.15 LEN_BP_RATIO 2.26315789473684

AAUCCAGGUUCCUGGGCGAUUUUGUCCACCUCGUAUCCAGCAUCCACAUAGGUCUGCCAGCUGG
AACCGC

>random_seq_from_cds__NO_3661 RANDOM_LENGTH 82 SEQ_LENGTH 75
GC_CONTENT 0.5333333333333333 BASEPAIR 26 FREE_ENERGY
-20.00 LEN_BP_RATIO 2.88461538461538

GGCCGAGUUGACAAAGGUCUGACGGUUGUUGGCCGUGGCUACCAUAUCUGUGAACCUUCUGAGUG
CCGAAAUUCCAGCCUCC

>random_seq_from_cds__NO_3670 RANDOM_LENGTH 68 SEQ_LENGTH 54
GC_CONTENT 0.5555555555555556 BASEPAIR 21 FREE_ENERGY
-23.10 LEN_BP_RATIO 2.57142857142857

UCAGGUCCAGCAAGAUCAGUGACCGGAGGCCCUCAUGGAACUGCCCACUUCUGGAUCUCAUUG
UGU

>random_seq_from_cds__NO_3687 RANDOM_LENGTH 85 SEQ_LENGTH 77
GC_CONTENT 0.532467532467532 BASEPAIR 27 FREE_ENERGY
-24.50 LEN_BP_RATIO 2.85185185185185

UGUCCUGGCUGAGAAAGCCACUGACUGUCCUGUUGAAUAGCGGAGGGUGAGUUCUGUUCUUAUG
UGCUGUAGCUGGAGGAAUC

>random_seq_from_cds__NO_3699 RANDOM_LENGTH 110 SEQ_LENGTH 99
GC_CONTENT 0.484848484848485 BASEPAIR 36 FREE_ENERGY
-25.00 LEN_BP_RATIO 2.75

CCAACCAUCUCAUUGUAGGUAGGAUUGCAGGUUUUCCGGGCCACUUUGGUUUUCCUCUJAGUGGU
UUUCUGAGGGUCAGGAAGGAGGUAAAUUUUCACAUAGGGGUCAGG

>random_seq_from_cds__NO_3704 RANDOM_LENGTH 89 SEQ_LENGTH 76
GC_CONTENT 0.513157894736842 BASEPAIR 26 FREE_ENERGY
-26.30 LEN_BP_RATIO 2.92307692307692

UGGAACUCCUCAAGGUCCGUGGAUGUAGGUGGCCUCGUGAGUGUUCUCUCGCAUCACCUUUAC
CACAUUAUCAUAGCCUUUGUUGG

>random_seq_from_cds__NO_3708 RANDOM_LENGTH 100 SEQ_LENGTH 88
GC_CONTENT 0.556818181818182 BASEPAIR 30 FREE_ENERGY

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-29.80 LEN_BP_RATIO 2.9333333333333333
GGCAUCGUACACAUACUUGAGGUCCUCCAGGUCUGAGAGUUCAGGGAUCCCACAGGACAACAUC
AGGCCAGAAGGUUGAGGAAGAGGUGGGUGUGCUU
>random_seq_from_cds__NO_3720 RANDOM_LENGTH 71 SEQ_LENGTH 62
GC_CONTENT 0.596774193548387 BASEPAIR 22 FREE_ENERGY
-24.61 LEN_BP_RATIO 2.81818181818182
GCCACAGCAGCACAGUAAGGCUGCCAGCAGAUACUGGUAGCGGAUGCUGAACUGAGAGUCCUUGA
GGCCGU
>random_seq_from_cds__NO_3726 RANDOM_LENGTH 90 SEQ_LENGTH 80
GC_CONTENT 0.5875 BASEPAIR 27 FREE_ENERGY -29.30
LEN_BP_RATIO 2.96296296296296
UGUCUUUAAGCUUGCGCUGGUCUUCUCCCGGAGGCUGCCAAACUCAUAGCGGGGCUGAACUUG
UCUCCAGGGGGCUGGUGAACUUGA
>random_seq_from_cds__NO_3736 RANDOM_LENGTH 69 SEQ_LENGTH 57
GC_CONTENT 0.684210526315789 BASEPAIR 20 FREE_ENERGY
-20.30 LEN_BP_RATIO 2.85
CACGGCGCCAGGGCGUUGCAGAUGGCCUUGACGGACUGGACCACCCUGUCAGCCUUCAGUGGGA
AGUC
>random_seq_from_cds__NO_3739 RANDOM_LENGTH 81 SEQ_LENGTH 66
GC_CONTENT 0.515151515151515 BASEPAIR 24 FREE_ENERGY
-22.00 LEN_BP_RATIO 2.75
GUAGCCGAAUGUCA AUGUCAAAACUUGCGGCAGUAUUGGAUGUACUCAUGACUGCCCAAGGCAUGC
UUGCUCUGCAGGAAC
>random_seq_from_cds__NO_3745 RANDOM_LENGTH 70 SEQ_LENGTH 58
GC_CONTENT 0.655172413793103 BASEPAIR 20 FREE_ENERGY
-22.00 LEN_BP_RATIO 2.9
CUCCUGGCCACGGGUUUUCCAGAGGUGUCUUUGCUGAAGUCCAGCGGCCUCGGCCCUCCUCCA
GCCCC
>random_seq_from_cds__NO_3763 RANDOM_LENGTH 78 SEQ_LENGTH 61
GC_CONTENT 0.39344262295082 BASEPAIR 24 FREE_ENERGY
-18.90 LEN_BP_RATIO 2.54166666666667
UUUGAAUGAGUCAGUAUCAGAGCAGUUAGGUGUUGGAAUAAAAGUUGAAGCUGCUGAUACUGAAC
AAACAAGUGAAGA
>random_seq_from_cds__NO_3771 RANDOM_LENGTH 80 SEQ_LENGTH 69
GC_CONTENT 0.565217391304348 BASEPAIR 21 FREE_ENERGY
-23.74 LEN_BP_RATIO 3.28571428571429
GCCCUUGUCUCCUCUUCAGGCUUGGAGUUCAGCCCUGGGAUCCCAAACCACCUUCGGGCCUGUCU
UGAAGACCAGCCCC
>random_seq_from_cds__NO_3774 RANDOM_LENGTH 81 SEQ_LENGTH 67
GC_CONTENT 0.641791044776119 BASEPAIR 24 FREE_ENERGY
-28.80 LEN_BP_RATIO 2.79166666666667
UGGGGGGCAACCUGGUCAUCAUGAACCCACCAAGGCACAGGAUGCCGGGGUCUACCAGUGCCUG
GCCUCAACCCAGUGG
>random_seq_from_cds__NO_3791 RANDOM_LENGTH 110 SEQ_LENGTH 95
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GC_CONTENT    0.621052631578947    BASEPAIR    34    FREE_ENERGY
-42.70    LEN_BP_RATIO    2.79411764705882
CAGGUCCCCAGGAGGUGUGGUGGUGAGGGACAUUGGCGACACCACCAUCCAGCUCAGCUGGAGC
CGUGGCUUCGACAACCACAGCCCCAUCGCUAAGUACACCCUGCAA
>random_seq_from_cds__NO_3800    RANDOM_LENGTH    84    SEQ_LENGTH    77
GC_CONTENT    0.701298701298701    BASEPAIR    24    FREE_ENERGY
-32.76    LEN_BP_RATIO    3.208333333333333
GUGACCGUGAGGGCCUACAACCGGGCUGGCACUGGGCCUGCCAGCCCUUCUGCCAACGCCACGAC
CAUGAAGCCCCGCUCCGCG
>random_seq_from_cds__NO_3804    RANDOM_LENGTH    72    SEQ_LENGTH    62
GC_CONTENT    0.629032258064516    BASEPAIR    20    FREE_ENERGY
-18.00    LEN_BP_RATIO    3.1
AUCGUGAGGAAUGGAGGGCACAAGCAUGAUGGUGGAGAAACAUGGCAGUCCGCCAGCACACCACCC
CUGGCAC
>random_seq_from_cds__NO_3810    RANDOM_LENGTH    82    SEQ_LENGTH    76
GC_CONTENT    0.565789473684211    BASEPAIR    24    FREE_ENERGY
-26.50    LEN_BP_RATIO    3.166666666666667
UCAUCCAUCAAGGAGGUUUGGACUGCAUCCGGUGGGGGCCGUAAGGAUUUUUCUUCUGGGUCUUC
UACCUCAGGGGCAAUGG
>random_seq_from_cds__NO_3821    RANDOM_LENGTH    84    SEQ_LENGTH    70
GC_CONTENT    0.471428571428571    BASEPAIR    24    FREE_ENERGY
-18.40    LEN_BP_RATIO    2.916666666666667
AUCUCGUGGAUGAUUUGGACUUUUAAGAUGGGUGAAGGGAAUCGAAACCUCUGGUCACAGUCGC
CUGAAAGAACAUCCACUG
>random_seq_from_cds__NO_3831    RANDOM_LENGTH    100    SEQ_LENGTH    84
GC_CONTENT    0.511904761904762    BASEPAIR    25    FREE_ENERGY
-27.10    LEN_BP_RATIO    3.36
CUAUAUUAUGUACCUCGAGACCAUCUAGCUUAUCGAUAUGAGGUGCUGAAAAUUAUUGGCAAGG
GGAGUUUUGGGCAGGUGGCCAGGGUCUAUGAUCAC
>random_seq_from_cds__NO_3837    RANDOM_LENGTH    84    SEQ_LENGTH    66
GC_CONTENT    0.454545454545455    BASEPAIR    19    FREE_ENERGY
-17.70    LEN_BP_RATIO    3.47368421052632
CCAGUCUCGGUUCUACAGAGCUCAGAAUUAUCUUAGGAAGCCGCUACAGCACACCAAUUGACA
UAUGGAGUUUUGGCUGCAU
>random_seq_from_cds__NO_3865    RANDOM_LENGTH    81    SEQ_LENGTH    75
GC_CONTENT    0.586666666666667    BASEPAIR    22    FREE_ENERGY
-26.70    LEN_BP_RATIO    3.40909090909091
GGGGUGCAAGCCAUCUGCCUGGAGUUGCCACAGAGCCUUGUUGAAGGUGGGUGUCAGGUCAGGCA
ACGAAGACAUCUCCAG
>random_seq_from_cds__NO_3870    RANDOM_LENGTH    86    SEQ_LENGTH    70
GC_CONTENT    0.671428571428571    BASEPAIR    26    FREE_ENERGY
-30.40    LEN_BP_RATIO    2.69230769230769
CCCUGGAGAGUUCGCCUGAGGGAGAGGAUGGCACUGGCCACCUGAGCCACCUCUGCUCUGUGA
CUGCGGGCUGCUGAGAACUG
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>random_seq_from_cds__NO_3880 RANDOM_LENGTH 68 SEQ_LENGTH 55
  GC_CONTENT 0.581818181818182 BASEPAIR 20 FREE_ENERGY
  -21.10 LEN_BP_RATIO 2.75
CAGAUGCAGGUCUCCUGAAUGGAAGCUCCCGGGCGCCGGUCCGGAAAUAGUGCAGCUGACACCG
CUC
>random_seq_from_cds__NO_3888 RANDOM_LENGTH 70 SEQ_LENGTH 65
  GC_CONTENT 0.661538461538462 BASEPAIR 24 FREE_ENERGY
  -27.30 LEN_BP_RATIO 2.708333333333333
ACUGGCACCGAACAUCCUGCCAGCUCUGAGGCCGACCCUGGCGGACCCGAGGGAAGGUGGAGGUG
CAGUC
>random_seq_from_cds__NO_3890 RANDOM_LENGTH 85 SEQ_LENGTH 69
  GC_CONTENT 0.623188405797101 BASEPAIR 25 FREE_ENERGY
  -25.30 LEN_BP_RATIO 2.76
UGGAAUCUCCUGUCCAGGUCCAGCUGCAGAGAGACAGGGUUCACAUCCAUCUUGUGACUGCCACC
AGCGCAUGGGGCCGAGGAU
>random_seq_from_cds__NO_3903 RANDOM_LENGTH 110 SEQ_LENGTH 94
  GC_CONTENT 0.595744680851064 BASEPAIR 31 FREE_ENERGY
  -41.20 LEN_BP_RATIO 3.03225806451613
ACUCCAUCUCCAGGGUUCAGUUUUGGGCCACACUGCCUCCGGGUGCAGUUGCCCACACUGCA
AUUGCCCACACUGGCUGGCGCCAUGGGAGAACCCAUGAUGUUCA
>random_seq_from_cds__NO_3904 RANDOM_LENGTH 84 SEQ_LENGTH 70
  GC_CONTENT 0.542857142857143 BASEPAIR 28 FREE_ENERGY
  -29.60 LEN_BP_RATIO 2.5
GGAAGGGGAAGGUGUCCUGGAUGGGAACAUGGUGCUGCGACUGAUCCAGCUCAUCUCCUCAUCU
UCUUCAUCCACAUAUUAU
>random_seq_from_cds__NO_3908 RANDOM_LENGTH 72 SEQ_LENGTH 55
  GC_CONTENT 0.581818181818182 BASEPAIR 22 FREE_ENERGY
  -30.00 LEN_BP_RATIO 2.5
GUUGAGGGCUAUGCCGGGUGGCAUGUUUCCAGGGAAUCUGGAAGCGUUUAGAGUCCUGUGUAGC
CAGAUGA
>random_seq_from_cds__NO_3918 RANDOM_LENGTH 99 SEQ_LENGTH 84
  GC_CONTENT 0.416666666666667 BASEPAIR 26 FREE_ENERGY
  -20.42 LEN_BP_RATIO 3.23076923076923
GACUCCAAGUCGAUCAACUUUGCAAUAGGGAAAAGAGAUGCUAUAGCAGUUUCUUUGACAAU
CUAGCAGUCCUCAUCUUUUGGAUCAAUUAAAAGC
>random_seq_from_cds__NO_3933 RANDOM_LENGTH 82 SEQ_LENGTH 58
  GC_CONTENT 0.396551724137931 BASEPAIR 23 FREE_ENERGY
  -19.87 LEN_BP_RATIO 2.52173913043478
ACAGCAGAAAGCUGAGUUCUCAGAUCAGAAACAUCAGAAGGAAAUAGAAAUAUGUGUUUGAAGA
CUUCUCAGCUUACUGGG
>random_seq_from_cds__NO_3939 RANDOM_LENGTH 81 SEQ_LENGTH 70
  GC_CONTENT 0.428571428571429 BASEPAIR 28 FREE_ENERGY
  -17.60 LEN_BP_RATIO 2.5
AAGUCAGCGCAUUAAGUUAACAGGAAGACACUUCUGCUCACCAGAAUGUUGUUGCUGAAACCU
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UAAGUGCCCUUGAGAA

>random_seq_from_cds__NO_3956 RANDOM_LENGTH 62 SEQ_LENGTH 54
GC_CONTENT 0.4444444444444444 BASEPAIR 20 FREE_ENERGY
-21.90 LEN_BP_RATIO 2.7

GAAGACAUACCAGGAGGUGAAUUUGGUGAACAACCAAUGAACAGCACCCUGUGUCUUUGGC

>random_seq_from_cds__NO_3959 RANDOM_LENGTH 67 SEQ_LENGTH 55
GC_CONTENT 0.4545454545454545 BASEPAIR 21 FREE_ENERGY
-18.00 LEN_BP_RATIO 2.61904761904762

CUGCAGACCUAUGUUGACUCAUUAAGGCCGAAAAUUUGGUCUUGUCAACGAAUCUGAGAAACUU
UC

>random_seq_from_cds__NO_3978 RANDOM_LENGTH 85 SEQ_LENGTH 60
GC_CONTENT 0.5166666666666667 BASEPAIR 20 FREE_ENERGY
-16.40 LEN_BP_RATIO 3

GGAGAAAACACAAGAGCUUGAGUCUCAUCAAAGUGAGUGUCUCCAUGCAUUCAGGUGGCAGAGG
CAGAGGUGAAGGAAAAGACG

>random_seq_from_cds__NO_3979 RANDOM_LENGTH 94 SEQ_LENGTH 88
GC_CONTENT 0.4545454545454545 BASEPAIR 32 FREE_ENERGY
-25.71 LEN_BP_RATIO 2.75

GAACUCCUUCAGACUUUGUCCUCUGAUGUGAGUGAGCUGUJAAAAGACAAAACUCAUCUCCAGGA
AAAGCUGCAGAGUUUGGAAAAGGACUCAC

>random_seq_from_cds__NO_3996 RANDOM_LENGTH 78 SEQ_LENGTH 69
GC_CONTENT 0.420289855072464 BASEPAIR 24 FREE_ENERGY
-18.70 LEN_BP_RATIO 2.875

UAUUGUUUUGCAAUCUUCAGUGAAUGGCCUCAUUAAGAAGUAGAAGAUGGCAAGCAGAAACUGG
AGAAGAAGGAUGA

>random_seq_from_cds__NO_4018 RANDOM_LENGTH 84 SEQ_LENGTH 55
GC_CONTENT 0.5454545454545454 BASEPAIR 19 FREE_ENERGY
-18.91 LEN_BP_RATIO 2.89473684210526

CCCACAGUGCUUGCUUCCCGGGUGGAGAGUGACACGACCAUJAAUGUUAUGAAAUGGAAGACGGU
CUCCACGAUUAUCCUGGUG

>random_seq_from_cds__NO_4032 RANDOM_LENGTH 83 SEQ_LENGTH 70
GC_CONTENT 0.457142857142857 BASEPAIR 24 FREE_ENERGY
-23.50 LEN_BP_RATIO 2.916666666666667

AAUAAUCAAUUGCCUUGGUCGCUAUUAUUGGUAUUCUCUGGGGUAGUCAUCCUGGUACUCGCAUGA
UACUCAUCAGGGUAUUCU

>random_seq_from_cds__NO_4035 RANDOM_LENGTH 110 SEQ_LENGTH 82
GC_CONTENT 0.524390243902439 BASEPAIR 30 FREE_ENERGY
-27.80 LEN_BP_RATIO 2.733333333333333

AAAUUGUCGAGUUGUCCACCGGUCUGUAAUGUUAGCUUCUGAUCAUAGAUGUCUCUUCUGGUACCU
GGUGCUAACAUCCUGCCUGGCGUGGCUCCUUUAUUAGUGCCCAU

>random_seq_from_cds__NO_4058 RANDOM_LENGTH 82 SEQ_LENGTH 73
GC_CONTENT 0.438356164383562 BASEPAIR 26 FREE_ENERGY
-22.30 LEN_BP_RATIO 2.80769230769231

AUAUGCAGGAUACAUAUACCUGUUUCACUAGUAGGACGAAUGGCAAUUGGUUCUGCCAGCUCGGUU

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UUGCCAGAUCUUGUAAC
>random_seq_from_cds__NO_4059 RANDOM_LENGTH 82 SEQ_LENGTH 67
  GC_CONTENT 0.492537313432836 BASEPAIR 21 FREE_ENERGY
  -16.50 LEN_BP_RATIO 3.19047619047619
CCAAGCAACCCUCUGGGGCAAAGUCAGCAACAUGAGUCUUCUCUUUCUCUAAUGCACUUUGAGAC
ACAAACAUGGGGAAGUA
>random_seq_from_cds__NO_4071 RANDOM_LENGTH 90 SEQ_LENGTH 82
  GC_CONTENT 0.402439024390244 BASEPAIR 26 FREE_ENERGY
  -19.96 LEN_BP_RATIO 3.15384615384615
AGCCACUCUAUUGUAAAGGACCAAGGAAUCCUCAGAUGUAGUACAAUUAUUUAUUCAGAGAAGGUG
UUGGUCUUUCCUAAAAGGAGCAGA
>random_seq_from_cds__NO_4084 RANDOM_LENGTH 84 SEQ_LENGTH 71
  GC_CONTENT 0.464788732394366 BASEPAIR 22 FREE_ENERGY
  -17.23 LEN_BP_RATIO 3.22727272727273
AAACUGCUCAUUCUCUGUCAUGGUAUUCUGUUGUUCUCAGGGCAUGUGUAACACCUUCGAUGCUGU
CAACUAUGGGGCAGGCAAA
>random_seq_from_cds__NO_4085 RANDOM_LENGTH 95 SEQ_LENGTH 76
  GC_CONTENT 0.407894736842105 BASEPAIR 24 FREE_ENERGY
  -19.60 LEN_BP_RATIO 3.16666666666667
AUCAUAUGUUGGAUAAACACUUGUAUUUUAUUUCCAGUUCUUGGAUGUGGUUGAAUUUUGCAGCGA
UAAAGGGUUGGAUCUCUCAUGCAUCCAUG
>random_seq_from_cds__NO_4102 RANDOM_LENGTH 89 SEQ_LENGTH 75
  GC_CONTENT 0.56 BASEPAIR 29 FREE_ENERGY -28.80
  LEN_BP_RATIO 2.58620689655172
CUGAUAGCCGACUGGCCGGUGGUGGUCUUGGGCAUGUGCACCAUGUUCAUCGUAGUCUGUGCCUU
GGUUGGAGUAUUAGUGCCAGAGCU
>random_seq_from_cds__NO_4111 RANDOM_LENGTH 81 SEQ_LENGTH 68
  GC_CONTENT 0.455882352941176 BASEPAIR 21 FREE_ENERGY
  -22.51 LEN_BP_RATIO 3.23809523809524
CACGCCAGCUUAAAUAACAGCAUGCUCUUCUCUCCCACAGAGAAAGGGGAGAGCAUGAUGAACA
UUUACUUGGACAACUU
>random_seq_from_cds__NO_4140 RANDOM_LENGTH 94 SEQ_LENGTH 85
  GC_CONTENT 0.541176470588235 BASEPAIR 27 FREE_ENERGY
  -18.30 LEN_BP_RATIO 3.14814814814815
CUUGAACUAUGGCCACACUCUUGCCAGCAGAUGGGGGACUGCUUGUGCCACCAGUGCUCUCCUA
CCACUAGCAGCUUUGUCCAGAUCAAAAC
>random_seq_from_cds__NO_4142 RANDOM_LENGTH 72 SEQ_LENGTH 66
  GC_CONTENT 0.5303030303030303 BASEPAIR 21 FREE_ENERGY
  -20.10 LEN_BP_RATIO 3.14285714285714
UGCAGGGCAGAGUAAAGCCAGCCGGAUUGCAGAAUUCUCUGCCUAGGAAUUUUUCCUCCACCCA
GUGCAGC
>random_seq_from_cds__NO_4155 RANDOM_LENGTH 77 SEQ_LENGTH 58
  GC_CONTENT 0.603448275862069 BASEPAIR 22 FREE_ENERGY
  -24.40 LEN_BP_RATIO 2.63636363636364
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UAUGAAGCGCUAUCAGGGGUGCCACCACUGAGGGCUUCGAAGACUUCACCGGAGGCAUUGCUGA
GUGGUAUGAGUU

>random_seq_from_cds__NO_4167 RANDOM_LENGTH 67 SEQ_LENGTH 58
GC_CONTENT 0.517241379310345 BASEPAIR 22 FREE_ENERGY
-16.60 LEN_BP_RATIO 2.63636363636364

AGAUCUCUGCCUUUGAGCUGCAGACCAUCCUGAGAAGGGUUCUAGCAAAGCGGCCAAGAUUAUCAA
GU

>random_seq_from_cds__NO_4168 RANDOM_LENGTH 86 SEQ_LENGTH 79
GC_CONTENT 0.506329113924051 BASEPAIR 30 FREE_ENERGY
-25.80 LEN_BP_RATIO 2.633333333333333

CAGAUGGCUUCAGCAUCGAGACAUGCAAAAUUAUGGUUGACAUGCUAGAUGUCGGACGGGAGUGG
CAAGCUGGGGCGUAAGGAGUU

>random_seq_from_cds__NO_4172 RANDOM_LENGTH 110 SEQ_LENGTH 93
GC_CONTENT 0.56989247311828 BASEPAIR 33 FREE_ENERGY
-40.50 LEN_BP_RATIO 2.81818181818182

AUCCUCCUCACUUCAGUGCUGGGCUUUGCCAUCUACUGGUUCAUCUCCCGGGACAAAGAGGAAAC
UUUGCCACUUGAAGAUGGGUGGGGGCCAGGCACGAGGUCCGC

>random_seq_from_cds__NO_4187 RANDOM_LENGTH 84 SEQ_LENGTH 71
GC_CONTENT 0.633802816901408 BASEPAIR 27 FREE_ENERGY
-31.80 LEN_BP_RATIO 2.62962962962963

UGUCGGUGCUGGAGCGGCAAUGACCUAUGGCUGGAGCCUCCUUGGCACGAGCGCACCAUCCGAGG
CACAGCUGCACUUCUGCAC

>random_seq_from_cds__NO_4191 RANDOM_LENGTH 80 SEQ_LENGTH 68
GC_CONTENT 0.647058823529412 BASEPAIR 21 FREE_ENERGY
-27.70 LEN_BP_RATIO 3.23809523809524

GCAGCGGGUGCCCUCGGUCAUUGGUGCUUCAGGGUCACAGUCGCCUGAGCUCCAUAGUCCCCA
AGGUCCAGGGUGUGC

>random_seq_from_cds__NO_4207 RANDOM_LENGTH 94 SEQ_LENGTH 87
GC_CONTENT 0.793103448275862 BASEPAIR 33 FREE_ENERGY
-47.00 LEN_BP_RATIO 2.63636363636364

GGGAGGUGCUGGUUGGAGCCGUCGUCGCGGACGCGCAGCCACUCGACGGUCACCCGGGCCUGGGCG
CUGCGCGGGGACAGCCGCCCGUGCCUGUG

>random_seq_from_cds__NO_4209 RANDOM_LENGTH 84 SEQ_LENGTH 70
GC_CONTENT 0.671428571428571 BASEPAIR 26 FREE_ENERGY
-26.50 LEN_BP_RATIO 2.69230769230769

CAUGCCGAACACCAGCAGGUGUGUGCUGGCCUCCGACGCCAGGAACCUGCCGGCCACCUCCUGG
AAGCUCUGGCUGAACCUCU

>random_seq_from_cds__NO_4216 RANDOM_LENGTH 86 SEQ_LENGTH 76
GC_CONTENT 0.513157894736842 BASEPAIR 28 FREE_ENERGY
-24.60 LEN_BP_RATIO 2.71428571428571

UUUGCAGGGAGGCAAGUGAGGCCUAUCUGGUUGCCUUUUUGAAGACACCAACCUGUGUCUAUC
CAUGCCAAACGUGUAACAAU

>random_seq_from_cds__NO_4233 RANDOM_LENGTH 89 SEQ_LENGTH 74
GC_CONTENT 0.851351351351351 BASEPAIR 28 FREE_ENERGY

-49.00 LEN_BP_RATIO 2.64285714285714
CUCCGCCGCGCCCCAGCCGCCGCCUCCCCGGGCUCGGGCUCUCCCCUGAGGCGCCCGGGCCGC
GACCGGAUCCAGGUGGCGAGGGCG
>random_seq_from_cds__NO_4243 RANDOM_LENGTH 82 SEQ_LENGTH 68
GC_CONTENT 0.544117647058823 BASEPAIR 25 FREE_ENERGY
-25.90 LEN_BP_RATIO 2.72
CUCAUAGUUGACAUCGAUGGGAUCCUUGCUGCUAUCAUCAUCAGACCCUCCCCUGAGCAGACUGUAGG
CCACCUCGAUGUCCAGC
>random_seq_from_cds__NO_4251 RANDOM_LENGTH 110 SEQ_LENGTH 90
GC_CONTENT 0.555555555555556 BASEPAIR 32 FREE_ENERGY
-32.70 LEN_BP_RATIO 2.8125
UUGUAGUAGGAGUUGGUUCCUUAACGAUGUCCACCAGGCCAAGGGUGGCACUGAAGACCUUCCC
ACCUUUCUCCAGGACAUGCGCAGAGUGUCCAGUCCCAGAAUCAG
>random_seq_from_cds__NO_4267 RANDOM_LENGTH 110 SEQ_LENGTH 75
GC_CONTENT 0.586666666666667 BASEPAIR 20 FREE_ENERGY
-18.24 LEN_BP_RATIO 3.75
GCCUUGCACCAUCCAUCCUGGCCUUUGCCCUGUCACUCCUCCAGCUUCCGCUGUCUUCUUGA
CUUUCUGCUGGUCAUCCACCGAAGCUCAGAGAACCCAUCCACCU
>random_seq_from_cds__NO_4274 RANDOM_LENGTH 82 SEQ_LENGTH 66
GC_CONTENT 0.545454545454545 BASEPAIR 22 FREE_ENERGY
-20.00 LEN_BP_RATIO 3
CUUCAUUGGUGGUGCUGCCCACCUUGAGUGCCGUCUCAUACUUGUGCUUCAGAUGCUUGCCCACC
UCAUGGAAAGGCGCCAA
>random_seq_from_cds__NO_4275 RANDOM_LENGTH 73 SEQ_LENGTH 52
GC_CONTENT 0.692307692307692 BASEPAIR 22 FREE_ENERGY
-29.70 LEN_BP_RATIO 2.36363636363636
CUGCCGCCAGCAGGUCCGCACCCUGCAUGAGCCUGACACGCCGUGGCACUUGCAGGUGGUCUCCA
CCCCAGCC
>random_seq_from_cds__NO_4284 RANDOM_LENGTH 88 SEQ_LENGTH 73
GC_CONTENT 0.698630136986301 BASEPAIR 28 FREE_ENERGY
-34.60 LEN_BP_RATIO 2.60714285714286
ACCCGAUCUGGUGGGUCGUGGCUGUUGGGCCACAGUAUCCUCCCUGGGCUCGCAGCCCAUCCU
GUGUGCCAGCAUCCCGGGCCUGG
>random_seq_from_cds__NO_4287 RANDOM_LENGTH 85 SEQ_LENGTH 68
GC_CONTENT 0.676470588235294 BASEPAIR 25 FREE_ENERGY
-35.00 LEN_BP_RATIO 2.72
UUGCCUCAGCCGGUGUGGCCUUUGCAGUGACACGCUCAUGUGCAGAAGGCACGGCCGCAUCUGU
GGCUGCAGCAGCCGCCACCA
>random_seq_from_cds__NO_4297 RANDOM_LENGTH 75 SEQ_LENGTH 48
GC_CONTENT 0.625 BASEPAIR 20 FREE_ENERGY -29.05
LEN_BP_RATIO 2.4
GCCAGGACAAGAUCCGGCCCCUGUGGCGCCACUACUCCAGAACACACAAGGGCCUGAUCUUCGU
GGUGGACAGC
>random_seq_from_cds__NO_4304 RANDOM_LENGTH 72 SEQ_LENGTH 58

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>random_seq_from_cds__NO_4359 RANDOM_LENGTH 87 SEQ_LENGTH 76
  GC_CONTENT 0.5 BASEPAIR 24 FREE_ENERGY -18.40 LEN_BP_RATIO
  3.166666666666667
GAUGAGACAUGGAUUGUCUGCUGAGUGCCAUGCUGCUGCCAAAAUCACCAGCCCAUCACCAGUUU
UGCUCUUAAGUCCAAUAUCGAA
>random_seq_from_cds__NO_4367 RANDOM_LENGTH 97 SEQ_LENGTH 85
  GC_CONTENT 0.482352941176471 BASEPAIR 26 FREE_ENERGY
  -16.40 LEN_BP_RATIO 3.26923076923077
CCAAAUAUUGAGCUUCUCUUUGCACACCAGACAAGCCCAUCCACCUUCAUCUAUGUUAUUGGUCA
GCUGGUCAUCGACCUUCAGCCAAUGUUAGGGC
>random_seq_from_cds__NO_4391 RANDOM_LENGTH 90 SEQ_LENGTH 83
  GC_CONTENT 0.843373493975904 BASEPAIR 29 FREE_ENERGY
  -45.20 LEN_BP_RATIO 2.86206896551724
CAGCCCCAGGAGCUUCCGGGCCUCCGGGAGUCCGGCCGUGCGGGGCGCAGCCGCCCUUGUCCC
CGGGAGGCGCCGCCGGCCCGCGCCG
>random_seq_from_cds__NO_4400 RANDOM_LENGTH 90 SEQ_LENGTH 84
  GC_CONTENT 0.666666666666667 BASEPAIR 28 FREE_ENERGY
  -32.90 LEN_BP_RATIO 3
CCGUUGGGAGAAAAGGCGAGAGAAAGCACGGGGCCACGGUGGCCUGUGAAAAGCCUCACCGAGUU
CCCCUGCUGAGCGCUCCACAGCCGG
>random_seq_from_cds__NO_4402 RANDOM_LENGTH 75 SEQ_LENGTH 70
  GC_CONTENT 0.6 BASEPAIR 27 FREE_ENERGY -29.00 LEN_BP_RATIO
  2.59259259259259
UAUAUCCUCAGCGGGUACGUCCGAUCAAUGACCACAGCCUGGCGGUGCGGUCGUGGGACCCGCU
GGCGAAGUAC
>random_seq_from_cds__NO_4410 RANDOM_LENGTH 86 SEQ_LENGTH 76
  GC_CONTENT 0.473684210526316 BASEPAIR 25 FREE_ENERGY
  -23.50 LEN_BP_RATIO 3.04
CACAGGGCAGUAUUGUUGUCACUUUGGAGGUAGCGGAUAAGGUAGUUGUAGCUGUCUUCUUGGAG
ACGGACCACGUACUUGUUAUC
>random_seq_from_cds__NO_4411 RANDOM_LENGTH 69 SEQ_LENGTH 59
  GC_CONTENT 0.491525423728814 BASEPAIR 20 FREE_ENERGY
  -15.10 LEN_BP_RATIO 2.95
UAGGAAUGCUCGAAGCUUGAAGUUAGAUAGGAUGUCCUGGAUGGUUUGAGUGGUCUGUAGCUGCU
CAAU
>random_seq_from_cds__NO_4412 RANDOM_LENGTH 110 SEQ_LENGTH 87
  GC_CONTENT 0.494252873563218 BASEPAIR 33 FREE_ENERGY
  -25.30 LEN_BP_RATIO 2.63636363636364
GACAUCCUUCUGGCUAGCAUUCUGCAGAAACAUUCCAUGGAAGCGGCUGUAAAAACUUCCACUG
UGCUCUUCGGACUGUUUUGGACCAGGUUGAGAUGGAGGUAGACAA
>random_seq_from_cds__NO_4414 RANDOM_LENGTH 81 SEQ_LENGTH 66
  GC_CONTENT 0.53030303030303 BASEPAIR 22 FREE_ENERGY
  -20.90 LEN_BP_RATIO 3
CAGUCGUCCAAACUGUACUUCAUAUUGCUGGGGUUCUGCCUGGCAAGGGGCGUCAGACACUAUGU
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UGGCACAACCAGAUUC
>random_seq_from_cds__NO_4416 RANDOM_LENGTH 87 SEQ_LENGTH 63
  GC_CONTENT 0.587301587301587 BASEPAIR 25 FREE_ENERGY
  -26.60 LEN_BP_RATIO 2.52
CCAUCUGAGUCCACGUACUGCCGCGUUUGAGGUAGCAGGACACUGCCAUCUGAAUCUGCUCGGU
ACGCACUCGUUUCAUAAUGCGG
>random_seq_from_cds__NO_4423 RANDOM_LENGTH 94 SEQ_LENGTH 79
  GC_CONTENT 0.531645569620253 BASEPAIR 29 FREE_ENERGY
  -28.20 LEN_BP_RATIO 2.72413793103448
UGAUCGCUGAGGACGGGCUCUCUUGGGGAAAAUUGAGAAAUGCGAGUUCUUAGAAAUGAUCGA
CGAGAAGGGCCUCAUGCGCUCACGGGUUC
>random_seq_from_cds__NO_4432 RANDOM_LENGTH 95 SEQ_LENGTH 81
  GC_CONTENT 0.518518518518518 BASEPAIR 21 FREE_ENERGY
  -19.54 LEN_BP_RATIO 3.85714285714286
UUGCUGAUGGUGUGGUUGGAGUUUAUGAAUGUCACAAUGCUGGGGAAACCAGGGAAUGGGCCUU
GACGAAGGAGAAGUCGGUGAAGCACAUGGA
>random_seq_from_cds__NO_4434 RANDOM_LENGTH 89 SEQ_LENGTH 78
  GC_CONTENT 0.666666666666667 BASEPAIR 22 FREE_ENERGY
  -26.94 LEN_BP_RATIO 3.54545454545455
AAAUGGGAACAGAUCGAGGGCAACUCCAAGCUGAGGCACGUGGGCAGCAACCUGUGCCUGGACAG
UCGCACGGCCAAGAGCGGGGGCCU
>random_seq_from_cds__NO_4457 RANDOM_LENGTH 97 SEQ_LENGTH 84
  GC_CONTENT 0.607142857142857 BASEPAIR 28 FREE_ENERGY
  -36.40 LEN_BP_RATIO 3
GCUGAUUGUGCUCAGGUAUGCGGAUGAGGAGCUCCAGCUGGACUUCGAUGACUUCUCAACUGCC
UGGUCCGGCUGGAGAAUGCGAGCCGGGGUGUU
>random_seq_from_cds__NO_4462 RANDOM_LENGTH 87 SEQ_LENGTH 76
  GC_CONTENT 0.421052631578947 BASEPAIR 26 FREE_ENERGY
  -18.80 LEN_BP_RATIO 2.92307692307692
AGGUGCUCUGAUAUGGAAGAUUAUUGACUGAAUCAGAAAUAAAUUGGAUGGUGUCAGACAAA
AGAUAUUCCAGGUAGCCCAAGA
>random_seq_from_cds__NO_4470 RANDOM_LENGTH 84 SEQ_LENGTH 78
  GC_CONTENT 0.615384615384615 BASEPAIR 26 FREE_ENERGY
  -31.50 LEN_BP_RATIO 3
GCUUCCUGGUGCUGGGCUACUUGCUCUACCUGGUCUUCGGCGCAGUGGUCUUCUCCUCGGUGGAG
CUGCCCUAUGAGGACCUGC
>random_seq_from_cds__NO_4472 RANDOM_LENGTH 72 SEQ_LENGTH 55
  GC_CONTENT 0.672727272727273 BASEPAIR 19 FREE_ENERGY
  -21.80 LEN_BP_RATIO 2.89473684210526
GGCGUGUCGGUGCUCAGCAACGCCUCGGGCAACUGGAACUGGGACUUCACCUCCGCGCUCUUCUU
CGCCAGC
>random_seq_from_cds__NO_4474 RANDOM_LENGTH 81 SEQ_LENGTH 55
  GC_CONTENT 0.654545454545455 BASEPAIR 20 FREE_ENERGY
  -22.00 LEN_BP_RATIO 2.75
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>random_seq_from_cds__NO_4503 RANDOM_LENGTH 81 SEQ_LENGTH 55
GC_CONTENT 0.454545454545455 BASEPAIR 20 FREE_ENERGY
-18.10 LEN_BP_RATIO 2.75

UGAUCAGAAGAAAGAACUGUGAGGGCUUCUAGUGCAGACUGCAAAGUCCUUAUUGGCAUCUGAAC
GGCAGGUAGAAACGGU

>random_seq_from_cds__NO_4504 RANDOM_LENGTH 88 SEQ_LENGTH 57
GC_CONTENT 0.421052631578947 BASEPAIR 21 FREE_ENERGY
-23.40 LEN_BP_RATIO 2.71428571428571

UCCAGAAUUUCACUCCUGUGGUUGUAUAAGGGUGUGAUAUUUUUCAACAGGAAAGAGAGGCA
CACCCAUUGAUGAUGAAUAUAU

>random_seq_from_cds__NO_4527 RANDOM_LENGTH 71 SEQ_LENGTH 63
GC_CONTENT 0.73015873015873 BASEPAIR 21 FREE_ENERGY
-24.79 LEN_BP_RATIO 3

CCGCCGACACCUCCACCGCCUCUGCAGCAGGUAGCGCGCUCGCUUGCGCGUCAGGGCGUCCGCC
UGGCC

>random_seq_from_cds__NO_4532 RANDOM_LENGTH 89 SEQ_LENGTH 70
GC_CONTENT 0.8 BASEPAIR 29 FREE_ENERGY -44.90 LEN_BP_RATIO
2.41379310344828

GCCCGUCCUCGCGGGGCCGAAACAUGGCCCGACGGCUGCUAGCACUCCACGGCAGCCUCGGCG
CCAGGCGCGGCCACCCGGCGAGC

>random_seq_from_cds__NO_4537 RANDOM_LENGTH 81 SEQ_LENGTH 58
GC_CONTENT 0.448275862068966 BASEPAIR 21 FREE_ENERGY
-20.40 LEN_BP_RATIO 2.76190476190476

ACCCACUCCAUAUGAGUGACACUUGACAGCGGAUGUCAUUGGUCGAAGAGUUGAAGUUAUGG
AGAACAUGCAACAGUA

>random_seq_from_cds__NO_4553 RANDOM_LENGTH 110 SEQ_LENGTH 104
GC_CONTENT 0.509615384615385 BASEPAIR 33 FREE_ENERGY
-29.00 LEN_BP_RATIO 3.15151515151515

UGCCGGGGCUCCAUGACAAUUCAAAAGGUGAAGGGAUUGCUGUCACGUCUUCUCAAAGUUCUGU
GUCAGACCUUCUGUUGUCCUAUGAAAGUCCCAAAGAAGCCGGGCA

>random_seq_from_cds__NO_4557 RANDOM_LENGTH 86 SEQ_LENGTH 79
GC_CONTENT 0.518987341772152 BASEPAIR 27 FREE_ENERGY
-17.90 LEN_BP_RATIO 2.92592592592593

CUCCCACCUAAGGAAAGCCGGCACCCAGAUUGAGAACAUCGAGGAAGACUUCAGGAAUGGCCUUA
AGCUCAUGCUGCUUUUGGAAG

>random_seq_from_cds__NO_4563 RANDOM_LENGTH 78 SEQ_LENGTH 72
GC_CONTENT 0.555555555555556 BASEPAIR 24 FREE_ENERGY
-17.00 LEN_BP_RATIO 3

UCGUGAACACCCUAAAACCCGAUGAAAGAGCCAUCAUGACGUACGUCUCUUGCUUCUACCACGCU
UUUGCGGGCGCGG

>random_seq_from_cds__NO_4567 RANDOM_LENGTH 72 SEQ_LENGTH 61
GC_CONTENT 0.60655737704918 BASEPAIR 25 FREE_ENERGY

-32.90 LEN_BP_RATIO 2.44
CUGCGGAUCAGCAACCGUCCUGCCUUAUGCCCUCGAGGGCAAGAUGGUGUCGGGAUUAUUGCUG
GUGCCUG
>random_seq_from_cds__NO_4581 RANDOM_LENGTH 75 SEQ_LENGTH 55
GC_CONTENT 0.490909090909091 BASEPAIR 19 FREE_ENERGY
-19.50 LEN_BP_RATIO 2.89473684210526
GAUGAAUGAGUUCAGAGCCUCCUUAACCACUUUGACAGGGAGGAAGAAUGGCCUGAUGGAUCAU
GAGGAUUUCA
>random_seq_from_cds__NO_4582 RANDOM_LENGTH 87 SEQ_LENGTH 79
GC_CONTENT 0.556962025316456 BASEPAIR 32 FREE_ENERGY
-38.70 LEN_BP_RATIO 2.46875
GAGCCUGCCUGAUUUCCAUGGGUUAUGACCUGGGGUGAAGCCGAAUUUGCCC GAUUAUGACCCU
GGUAGAUCCCAACGGGCAAGGC
>random_seq_from_cds__NO_4588 RANDOM_LENGTH 98 SEQ_LENGTH 74
GC_CONTENT 0.418918918918919 BASEPAIR 26 FREE_ENERGY
-18.90 LEN_BP_RATIO 2.84615384615385
CUGAAAGGCAACAAUGACAUUUAAGUAUAACUCAGCCUGAUGUCAUUUACCAAUCCAUAAGGG
AAUACUUGCUGGCUGGGGCAGAUUAUCAUGAAA
>random_seq_from_cds__NO_4593 RANDOM_LENGTH 73 SEQ_LENGTH 55
GC_CONTENT 0.527272727272727 BASEPAIR 21 FREE_ENERGY
-17.60 LEN_BP_RATIO 2.61904761904762
UGCCAAUGCCAAGGGCAGCCUUGUUUGCACUCCAAAUCUUUUUGAGGAGAAAUAUGCUCCCCGG
CCUAUCUU
>random_seq_from_cds__NO_4594 RANDOM_LENGTH 84 SEQ_LENGTH 64
GC_CONTENT 0.53125 BASEPAIR 27 FREE_ENERGY -28.91
LEN_BP_RATIO 2.37037037037037
UGAUUUCAGGGACGAUCGUUGAUAAAAGUGGGCGGACUCUUUCCGGACAGACAGGAGAGGGAUUU
GUCAUCAGCGUGUCUCAUG
>random_seq_from_cds__NO_4597 RANDOM_LENGTH 78 SEQ_LENGTH 71
GC_CONTENT 0.464788732394366 BASEPAIR 22 FREE_ENERGY
-21.29 LEN_BP_RATIO 3.22727272727273
UGAUGGCCAAGCACCUAAAGGGAUUUUGCUAUGGAUGGCUUGGUCAAUAUAGUUGGAGGAUGCUG
UGGGUCAACACCA
>random_seq_from_cds__NO_4602 RANDOM_LENGTH 86 SEQ_LENGTH 81
GC_CONTENT 0.45679012345679 BASEPAIR 26 FREE_ENERGY
-19.40 LEN_BP_RATIO 3.11538461538462
CCAAUUUUGCUGUGAUUGAAGCUGGGUUAAGUGCUGCCAAGGGAAGUGCAUUGUCAAUAGCAUU
AGUCUGAAGGAAGGAGAGGAC
>random_seq_from_cds__NO_4607 RANDOM_LENGTH 89 SEQ_LENGTH 78
GC_CONTENT 0.461538461538462 BASEPAIR 28 FREE_ENERGY
-26.60 LEN_BP_RATIO 2.78571428571429
AGAAGCAAUGCAUGGGGUUUUCCUUUACCAUGCAAUCAAGGUCUGGCAUGGACAUGGGGAUAGUG
AAUGCUGGAAACCUCCUGUGUAU
>random_seq_from_cds__NO_4612 RANDOM_LENGTH 70 SEQ_LENGTH 54

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GC_CONTENT    0.5 BASEPAIR    20 FREE_ENERGY   -15.20 LEN_BP_RATIO
2.7
GCUGUUGGCCACCUUAUCCCUUUC AUGGAAAAAGAAAGAGAAGAAACCAGAGUGCUUAACGGCAC
AGUAG
>random_seq_from_cds__NO_4633 RANDOM_LENGTH 87 SEQ_LENGTH    79
GC_CONTENT    0.594936708860759 BASEPAIR    29 FREE_ENERGY
-32.10 LEN_BP_RATIO 2.72413793103448
CUGGCAGACUGACACGCUGCAGUGCAGAUGCACCCGGUCCCCUGAGGGCCUGUUUCUCCACUGUA
GGGUUCACAAAGCUGAAGGUGA
>random_seq_from_cds__NO_4634 RANDOM_LENGTH 69 SEQ_LENGTH    56
GC_CONTENT    0.589285714285714 BASEPAIR    19 FREE_ENERGY
-21.30 LEN_BP_RATIO 2.94736842105263
AGAUGCUGAAGCGCUGGUGGUGAGAGGGAAAUGGAAGAUCCAAGGCUUUCUGGACAGGGAUCAGC
UGGG
>random_seq_from_cds__NO_4637 RANDOM_LENGTH 109 SEQ_LENGTH    100
GC_CONTENT    0.52 BASEPAIR    36 FREE_ENERGY   -32.80
LEN_BP_RATIO 2.77777777777778
GGUAGUCACCAACACCGUAGUAAGAGCCAUAGUUUUUAUCCUUUGGCAAUCUGAAGUCCAGAGU
GAGGGGUCCAGGCUGGGUCUCAGGAAAGGGUGGUGGGAGAGUGA
>random_seq_from_cds__NO_4664 RANDOM_LENGTH 68 SEQ_LENGTH    48
GC_CONTENT    0.416666666666667 BASEPAIR    19 FREE_ENERGY
-16.00 LEN_BP_RATIO 2.52631578947368
AGCUUUAUAACUGGGGUCUGGCAUGCGUUCUGUCACACCUCCAAUCUUAAGUUCAUCGUAGAU
CUC
>random_seq_from_cds__NO_4672 RANDOM_LENGTH 110 SEQ_LENGTH    96
GC_CONTENT    0.625 BASEPAIR    32 FREE_ENERGY   -43.20
LEN_BP_RATIO 3
AGCCCCGGGGCAAAGAGCCUGAUGAGACUGUGCACAGUUUUGCCCAGCGCCGUUGGACCUGAG
GGUGGCGUCUCUAGCCAUGGACAGUCUCUGCCGUGGAGUGUUUGC
>random_seq_from_cds__NO_4678 RANDOM_LENGTH 78 SEQ_LENGTH    66
GC_CONTENT    0.515151515151515 BASEPAIR    24 FREE_ENERGY
-21.80 LEN_BP_RATIO 2.75
CCAUCUGCCUGUCCAGGGGAUUUGGACAUUUGGUGCCAUCUUCAGAAGAUAUCCAGGAGUCCUGGGA
AUCGUGUAUGACU
>random_seq_from_cds__NO_4694 RANDOM_LENGTH 75 SEQ_LENGTH    70
GC_CONTENT    0.471428571428571 BASEPAIR    25 FREE_ENERGY
-17.60 LEN_BP_RATIO 2.8
CAAGCCAGACAGGAGCUUGGAUCUAGGAGGCAGUAUGGUAAUAAAUUUGUGGAUGCGCUUCAGG
AGCGUGGUUU
>random_seq_from_cds__NO_4699 RANDOM_LENGTH 84 SEQ_LENGTH    66
GC_CONTENT    0.515151515151515 BASEPAIR    21 FREE_ENERGY
-16.60 LEN_BP_RATIO 3.14285714285714
UGGGUGGCGUUGGUAGGAUGGAUCAGAAUAUUGCCAAGUACAAGGUGAAGAUAUCCGAGGCAUGAAG
UGGUACUCAAGCUUUAUUG
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>random_seq_from_cds__NO_4707 RANDOM_LENGTH 84 SEQ_LENGTH 66
  GC_CONTENT 0.575757575757576 BASEPAIR 19 FREE_ENERGY
  -19.63 LEN_BP_RATIO 3.47368421052632
CUUUCUCCUGCGUGUCCCUGCUUCUCCUCGCCGGUCUCCUCCGCAGGGUUCUCUUCUUCUUGUUU
CUGGGACAUGUUAGCCGUC
>random_seq_from_cds__NO_4708 RANDOM_LENGTH 102 SEQ_LENGTH 78
  GC_CONTENT 0.474358974358974 BASEPAIR 24 FREE_ENERGY
  -19.30 LEN_BP_RATIO 3.25
UUCUUUUGGGGGUGUGUACCAGCCCGUUUUUUUCGUGGAUCUGCACCAAGGACUUGUAGGACUGC
UGUGCUCUUGUCAGACUGUAUUGAGACUUUGUUGGCU
>random_seq_from_cds__NO_4717 RANDOM_LENGTH 84 SEQ_LENGTH 74
  GC_CONTENT 0.608108108108108 BASEPAIR 26 FREE_ENERGY
  -26.10 LEN_BP_RATIO 2.84615384615385
GGGUCAUCAGACUCCACCGACCAGAUGGGGGGCACAGCAGGGUAUGACUCCCGUGAUGUUGCAGU
GGAUGCGGACAGGAUCCCC
>random_seq_from_cds__NO_4719 RANDOM_LENGTH 81 SEQ_LENGTH 61
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  -28.10 LEN_BP_RATIO 3.05
GAACUCGCAGCUCAGCUCGUCCAGGCAGGCGCUGGCAAUGCGGAAGCGCUCGUGGCCGCGGUGGA
AGAUGGACUCGAGCAG
>random_seq_from_cds__NO_4728 RANDOM_LENGTH 89 SEQ_LENGTH 77
  GC_CONTENT 0.519480519480519 BASEPAIR 22 FREE_ENERGY
  -24.43 LEN_BP_RATIO 3.5
CAAGCCAGGGUCACUGUUCAUGGUCUGAACGAUUUCAUGCCCCUGGUUGAGCACAACCCAGUUU
GGGUCAAUCUGAGCAUCACCCUCA
>random_seq_from_cds__NO_4757 RANDOM_LENGTH 86 SEQ_LENGTH 72
  GC_CONTENT 0.458333333333333 BASEPAIR 25 FREE_ENERGY
  -15.60 LEN_BP_RATIO 2.88
GAUGAAAUUUUAAACUUAGACACUCAGCUCAGGCCUGCUUCCAUGGGCGAACAGUGGUCCAA
GUACAAAUGGCUGUCAGUUCU
>random_seq_from_cds__NO_4763 RANDOM_LENGTH 87 SEQ_LENGTH 75
  GC_CONTENT 0.466666666666667 BASEPAIR 26 FREE_ENERGY
  -19.11 LEN_BP_RATIO 2.88461538461538
GUGCUGGUGCCUGCUGCUAAAGUUUGUCCUGCUCCCGAAGCACUGGUCACACAACCAACUGAAU
GCAGAGAGUAAUAGUAAACUCA
>random_seq_from_cds__NO_4768 RANDOM_LENGTH 78 SEQ_LENGTH 69
  GC_CONTENT 0.420289855072464 BASEPAIR 28 FREE_ENERGY
  -18.30 LEN_BP_RATIO 2.46428571428571
AGUGAUGGUUGUCAUUGUUUGAGGAGGUUUUAAUGCAUUUCAUUGGCCGAUUCUACAAAUGAAU
GAGGACUGAGCCA
>random_seq_from_cds__NO_4770 RANDOM_LENGTH 89 SEQ_LENGTH 53
  GC_CONTENT 0.471698113207547 BASEPAIR 19 FREE_ENERGY
  -15.50 LEN_BP_RATIO 2.78947368421053
UUCAUAUCUUAAUAAUUAUCCCAUUUAGUCCCGUGGUGGAGACCAUUCUACAUGAAGUUCUGUA
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GAACUGAUUUUCUGCAUCUUAGGU

>random_seq_from_cds__NO_4772 RANDOM_LENGTH 75 SEQ_LENGTH 58
GC_CONTENT 0.482758620689655 BASEPAIR 19 FREE_ENERGY
-17.80 LEN_BP_RATIO 3.05263157894737

CAGAAAAAUCGUACUUGGCAAUGGAACCAGAUUCCAGAUGGUAGCUGAGGUUUC AUGACCUUCG
UAGGAAACAC

>random_seq_from_cds__NO_4779 RANDOM_LENGTH 94 SEQ_LENGTH 84
GC_CONTENT 0.464285714285714 BASEPAIR 26 FREE_ENERGY
-21.97 LEN_BP_RATIO 3.23076923076923

UUACAAGGCUGACAUCUCCAGUCUGAGGAUCAAAUCCAAAGUAAUGGUCUUUGCAUUGGUCAC
AACGUUGCCCAGCAAUGGAAGCAUCUUGG

>random_seq_from_cds__NO_4780 RANDOM_LENGTH 78 SEQ_LENGTH 55
GC_CONTENT 0.509090909090909 BASEPAIR 21 FREE_ENERGY
-19.50 LEN_BP_RATIO 2.61904761904762

CAAACACACUGACCAGUCAGGCUAUUACAGAUGUGAUUAACUGCACCAGUUGUAUGGCAUGAGCA
UGGCAGGCAGCCA

>random_seq_from_cds__NO_4787 RANDOM_LENGTH 88 SEQ_LENGTH 67
GC_CONTENT 0.432835820895522 BASEPAIR 23 FREE_ENERGY
-22.72 LEN_BP_RATIO 2.91304347826087

AAGUCCUUUGGCUUCUUUUUUGCACUCACACUGCCCAGAGUGAGGAUUGCAGAAUUGUUCACUG
AGCCAUGGAGGUACACUGGCAG

>random_seq_from_cds__NO_4794 RANDOM_LENGTH 81 SEQ_LENGTH 64
GC_CONTENT 0.453125 BASEPAIR 22 FREE_ENERGY -17.70
LEN_BP_RATIO 2.90909090909091

UGGAAUGGCUGUUGCAUUGACAAGGUUUACA AUUGAAAGCGUAAACUUGAUCACCUUGGCGGAAA
GGCUUGUCAUUUAAAA

>random_seq_from_cds__NO_4803 RANDOM_LENGTH 90 SEQ_LENGTH 78
GC_CONTENT 0.564102564102564 BASEPAIR 27 FREE_ENERGY
-28.70 LEN_BP_RATIO 2.88888888888889

UUCAACCGUGACACUCUAUUAUCAGCUGUGUCUCCUGCAUCAUUAGGAAUGCAGUACCGCUGUGC
CAAAGGGUGGACCCGCGGGUGGCUG

>random_seq_from_cds__NO_4838 RANDOM_LENGTH 84 SEQ_LENGTH 72
GC_CONTENT 0.597222222222222 BASEPAIR 25 FREE_ENERGY
-26.80 LEN_BP_RATIO 2.88

ACUAAAAGGCCUGUGAGGCUGGAAGAGUGACACGCUAUGGGAUUGCAGGUCCUUGGUCACUACCUC
CGGCGGCAGCGAGAUCCEA

>random_seq_from_cds__NO_4841 RANDOM_LENGTH 97 SEQ_LENGTH 80
GC_CONTENT 0.6 BASEPAIR 26 FREE_ENERGY -33.00 LEN_BP_RATIO
3.07692307692308

GAUGGGAUUCUUUUUGGGAUGGUGGGGGCCUAUGACUGGGGAGGCUCUGUGCUAUGGCUUGAAGG
AGGCCACCGCCUUUUUCCCCCACGAAUGGCAC

>random_seq_from_cds__NO_4849 RANDOM_LENGTH 72 SEQ_LENGTH 48
GC_CONTENT 0.5625 BASEPAIR 19 FREE_ENERGY -23.00
LEN_BP_RATIO 2.52631578947368

UCCAUCUGACCCCAUCACUGGAGGUGACCCACAGGCCAUCAGUGUGGUUCAGAGGGACUGUAGG
CGGCGAG

>random_seq_from_cds__NO_4852 RANDOM_LENGTH 86 SEQ_LENGTH 62
GC_CONTENT 0.548387096774194 BASEPAIR 22 FREE_ENERGY
-18.80 LEN_BP_RATIO 2.81818181818182

CUACACUCCAUGUGCUGGGAUACAUCAGAUUACCUCGGCCAGUGGCCUUGACUGUGACCUUUG
CCUUGGACAAUACUACAAAGC

>random_seq_from_cds__NO_4853 RANDOM_LENGTH 88 SEQ_LENGTH 67
GC_CONTENT 0.611940298507463 BASEPAIR 23 FREE_ENERGY
-31.00 LEN_BP_RATIO 2.91304347826087

CAGGGCCUGUGCUGAAUGAGGGCUCACCCACCUCUAUACAAAAGCUGGGUCCCUUCUCAAAGGA
UUGUGGCCUGACAAUGAAUGUG

>random_seq_from_cds__NO_4855 RANDOM_LENGTH 110 SEQ_LENGTH 99
GC_CONTENT 0.484848484848485 BASEPAIR 28 FREE_ENERGY
-26.70 LEN_BP_RATIO 3.53571428571429

CGGAAAGUGCUGGUAUCUACAACUCUGGAGAACAGAAAGGAAAAUGCUUACAAUACGAGCCUGAG
UCUCAUCUUCUCUAGAAACCUCACCUGGCCAGUCUCACUCCUCA

>random_seq_from_cds__NO_4864 RANDOM_LENGTH 98 SEQ_LENGTH 80
GC_CONTENT 0.5875 BASEPAIR 25 FREE_ENERGY -29.70
LEN_BP_RATIO 3.2

CCGAAGAGGGCAGUGUCCUACAGCUGACUGAAGCCUCCCGUUGGAGUGAGGAGCCUCUUGGAGGU
GGUUCAGACCCGGCCUAUCCUCAUCUCCUGUG

>random_seq_from_cds__NO_4865 RANDOM_LENGTH 68 SEQ_LENGTH 61
GC_CONTENT 0.59016393442623 BASEPAIR 22 FREE_ENERGY
-31.50 LEN_BP_RATIO 2.77272727272727

GAUCCUCAUAGGCAGUGUCCUGGGAGGGUUGCUCCUGCUUGCUCUCCUUGUCUUCUGCCUGUGGA
AGG

>random_seq_from_cds__NO_4881 RANDOM_LENGTH 85 SEQ_LENGTH 60
GC_CONTENT 0.65 BASEPAIR 22 FREE_ENERGY -30.60
LEN_BP_RATIO 2.72727272727273

UCAGCACCCUGGCUCUGGCCAUGGCGGGAGGAAGGCUGGCCUUGGUCCUGCCUCAGAGCCCAUUG
CUCACACUCUCCUUGGACC

>random_seq_from_cds__NO_4885 RANDOM_LENGTH 70 SEQ_LENGTH 58
GC_CONTENT 0.689655172413793 BASEPAIR 22 FREE_ENERGY
-27.80 LEN_BP_RATIO 2.63636363636364

GGAGCGUGUUGCGGCGAGCCAUGGGGAGGUGGAGCGACUUGAGCGUCAUGGCCUCCAUGCCCCGC
ACCAU

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GC_CONTENT 0.636363636363636 BASEPAIR 21 FREE_ENERGY
-25.90 LEN_BP_RATIO 2.61904761904762

GCUGUUCAUACCUCAGGCUGUGGCGCUUGUUCACAGUGCCGUGGUGCUUGGUGGCCGUGAGGG

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GC_CONTENT 0.73134328358209 BASEPAIR 26 FREE_ENERGY
-38.90 LEN_BP_RATIO 2.57692307692308

GGGUCACCAGGUCCGGGUCGUCGCCGUCGACGUACUUGGGCGGUGGCUGGCCAGGUCUGGGGUG
CUGGUGGCAGGUCGUG

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GC_CONTENT 0.523076923076923 BASEPAIR 21 FREE_ENERGY
-21.60 LEN_BP_RATIO 3.0952380952381

AUUAUUCUUUGGGUUCUCUGGUCAGAUGGACUGACAAGUUUGUUGCUGUAGACCCCUUGGGCC
CAUAAGGGACAGUGUAGG

>random_seq_from_cds__NO_4892 RANDOM_LENGTH 81 SEQ_LENGTH 74
GC_CONTENT 0.554054054054054 BASEPAIR 25 FREE_ENERGY
-20.52 LEN_BP_RATIO 2.96

GGUGCCUCUCCCGCAUCUCCGGUUGGCUGUACACCAGAUCUCCUGGCUGGUUGUAGGCAUGGGUG
UUGAUAAUGUUGAGGU

>random_seq_from_cds__NO_4906 RANDOM_LENGTH 70 SEQ_LENGTH 59
GC_CONTENT 0.593220338983051 BASEPAIR 22 FREE_ENERGY
-17.70 LEN_BP_RATIO 2.68181818181818

GGCAUUCUUGCCUGUGCUUCCACCGACAGCGUGCACUCGAUAACAUGCUGUCCAGCAGGCGA
AUCCG

>random_seq_from_cds__NO_4911 RANDOM_LENGTH 80 SEQ_LENGTH 69
GC_CONTENT 0.478260869565217 BASEPAIR 26 FREE_ENERGY
-22.70 LEN_BP_RATIO 2.65384615384615

CAUCAUCAUCAUCGGUGUGGGUUGUCUCUUAUGAGUUAGUUGCUGUCAUUCUUGAUGACGACCU
CUAAUCCGUGGUGCC

>random_seq_from_cds__NO_4928 RANDOM_LENGTH 80 SEQ_LENGTH 66
GC_CONTENT 0.666666666666667 BASEPAIR 22 FREE_ENERGY
-24.80 LEN_BP_RATIO 3

AACCCAUCGGACUCCCAUCUCGAUCCAGGCUGCAGGAUCCAGUAGCAGCUGGGGCACCUGGCC
CAGAGGUUCUGCCAC

>random_seq_from_cds__NO_4931 RANDOM_LENGTH 87 SEQ_LENGTH 75
GC_CONTENT 0.693333333333333 BASEPAIR 28 FREE_ENERGY
-38.00 LEN_BP_RATIO 2.67857142857143

CAGCAGGAUCCAGCCUCCUUCAGUCUCCCUUGAGGGGGUGGCCUCUGCUCUCCAGUGGGG
UCCCACCUGGGGGAGGUGGGGG

>random_seq_from_cds__NO_4932 RANDOM_LENGTH 81 SEQ_LENGTH 72
GC_CONTENT 0.597222222222222 BASEPAIR 28 FREE_ENERGY
-28.90 LEN_BP_RATIO 2.57142857142857

ACCUGAGGUAGAAGCCCAGGGGAGUGGAGUCUGGAAGGGUCUCCCCGAGCUCAUCCUCCUCGCUC
UCUUCUCUGCUCUCCU

>random_seq_from_cds__NO_4939 RANDOM_LENGTH 95 SEQ_LENGTH 86
GC_CONTENT 0.686046511627907 BASEPAIR 29 FREE_ENERGY
-29.30 LEN_BP_RATIO 2.96551724137931

GGCCUGGCUCAGUCCCGCAGCAGACUCACCCAUGGCAGGCUCUGACCCCAACAUGACCUCUGGG
GAGGCUUGGUCACCCCUUGGGGCCACAUCA

>random_seq_from_cds__NO_4950 RANDOM_LENGTH 71 SEQ_LENGTH 53
GC_CONTENT 0.490566037735849 BASEPAIR 19 FREE_ENERGY

-18.60 LEN_BP_RATIO 2.78947368421053
CCCUAGAGACCUCCGUCGCUGUUGAGUCUCUUUUUCAAGAGUUCUCA AUGUCUCUUGGUCCUGU
CUUCUA
>random_seq_from_cds__NO_4957 RANDOM_LENGTH 82 SEQ_LENGTH 72
GC_CONTENT 0.513888888888889 BASEPAIR 23 FREE_ENERGY
-27.80 LEN_BP_RATIO 3.1304347826087
UCUCCCUUUCUAGUGUCUCAUGGCUCUGGUUUUCCAGAGUCUUCAGUGACUCUUGAAUCUCCUCU
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>random_seq_from_cds__NO_4961 RANDOM_LENGTH 83 SEQ_LENGTH 77
GC_CONTENT 0.701298701298701 BASEPAIR 26 FREE_ENERGY
-36.60 LEN_BP_RATIO 2.96153846153846
GGGACUGGCCUGUACUGGCCUCUUGCCGCUGGCCCCAGGCUCUCUGGUCCAGGCAGGACGCUG
GCAGGAAUGGCCACCCUG
>random_seq_from_cds__NO_4963 RANDOM_LENGTH 71 SEQ_LENGTH 53
GC_CONTENT 0.622641509433962 BASEPAIR 19 FREE_ENERGY
-17.20 LEN_BP_RATIO 2.78947368421053
CUGAGGUGUGGGGGGAUGGGGGUGCUGGCCAAGGUAGGGGUACGGGCCUGGAGGAAUUCUUGGU
UCUUA
>random_seq_from_cds__NO_4970 RANDOM_LENGTH 89 SEQ_LENGTH 80
GC_CONTENT 0.725 BASEPAIR 24 FREE_ENERGY -32.69
LEN_BP_RATIO 3.33333333333333
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CCUCGCCAGUCGCCUUGCCAGCU
>random_seq_from_cds__NO_4974 RANDOM_LENGTH 75 SEQ_LENGTH 64
GC_CONTENT 0.78125 BASEPAIR 23 FREE_ENERGY -27.00
LEN_BP_RATIO 2.78260869565217
CCAGGUUGUCGCGGCCACCUCGGCCGCGUGCUUCUCCCGCCAGCGUUGGUCAACGAGGGCCCGC
AGGGCCGCCA
>random_seq_from_cds__NO_4997 RANDOM_LENGTH 81 SEQ_LENGTH 69
GC_CONTENT 0.492753623188406 BASEPAIR 23 FREE_ENERGY
-18.20 LEN_BP_RATIO 3
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GAUGGAGCUCACAGGU
>random_seq_from_cds__NO_4999 RANDOM_LENGTH 82 SEQ_LENGTH 65
GC_CONTENT 0.523076923076923 BASEPAIR 24 FREE_ENERGY
-24.10 LEN_BP_RATIO 2.70833333333333
GUGUAACUGGACAGCUUUGCAGAGGUCUUUGUGGAUAUCUGGGCUCUGUAAGAGCCUGUGUCUUC
CAUCUUCAGGUUGCUGA
>random_seq_from_cds__NO_5002 RANDOM_LENGTH 86 SEQ_LENGTH 74
GC_CONTENT 0.5 BASEPAIR 27 FREE_ENERGY -26.40 LEN_BP_RATIO
2.74074074074074
AACUCCAGGGGAAGAGUUACUGACUCCCCAGAAUCCCGUUCACCAUCA AUGGGGUUAAGCUGCU
UUGUGAAACUACAUCCUCCUG
>random_seq_from_cds__NO_5019 RANDOM_LENGTH 89 SEQ_LENGTH 76

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GC_CONTENT    0.473684210526316    BASEPAIR    26    FREE_ENERGY
-23.90    LEN_BP_RATIO    2.92307692307692
UCAUUGGGAGAAGCUGUCUUUGCUCGGUGCUUAUCAUCUCUGAAGGAUGAGAGAAUUCAAGCUAG
CAAAAAGCUGAAGGGUCCCCAGAA
>random_seq_from_cds__NO_5031    RANDOM_LENGTH    110    SEQ_LENGTH    103
GC_CONTENT    0.621359223300971    BASEPAIR    36    FREE_ENERGY
-41.20    LEN_BP_RATIO    2.8611111111111111
CCCUUCAUCUCAGGGUCCAGAGGUGACUGGUGUGGAUCCUGCUCGCUGUGCCAAGAUGGCCCUCC
AGAUGCGGCAUACCAUCCCUCCCCUGAUGCGGGUGUAGAUGAGG
>random_seq_from_cds__NO_5034    RANDOM_LENGTH    69    SEQ_LENGTH    52
GC_CONTENT    0.615384615384615    BASEPAIR    19    FREE_ENERGY
-15.50    LEN_BP_RATIO    2.73684210526316
GCACCAGGGCCUGGUACUCCCGUCCUCCCCGCCAGGAUUUCGCGCAGCCCGAUCAGUCUCUGC
CCUC
>random_seq_from_cds__NO_5039    RANDOM_LENGTH    69    SEQ_LENGTH    58
GC_CONTENT    0.706896551724138    BASEPAIR    21    FREE_ENERGY
-28.90    LEN_BP_RATIO    2.76190476190476
CUGGGCGAGCUGCCGGCGGUUGGGAGUGUGGAUGUGUGCCCCGAGGCAGCGCAGCAGCUCUCCA
CAUG
>random_seq_from_cds__NO_5046    RANDOM_LENGTH    110    SEQ_LENGTH    100
GC_CONTENT    0.53    BASEPAIR    32    FREE_ENERGY    -30.50
LEN_BP_RATIO    3.125
CCAUCUCA AUGACAGUGCAGCCCAGUGACCAGAUGUCAGCUGCUUCCCAUACCCGCGUGGGCCC
UGGUCAAUGAUUUCUGGGCCAUUAUCUGCAGAGUCCCCUGUGAA
>random_seq_from_cds__NO_5078    RANDOM_LENGTH    72    SEQ_LENGTH    66
GC_CONTENT    0.636363636363636    BASEPAIR    21    FREE_ENERGY
-27.59    LEN_BP_RATIO    3.14285714285714
ACUUCUCCGGCGGUGGUGUCUGUGGAUGGGCGGCCCGUGAGACUCCAACUCUGUGACACUGCCGG
ACAGGGA
>random_seq_from_cds__NO_5101    RANDOM_LENGTH    71    SEQ_LENGTH    63
GC_CONTENT    0.571428571428571    BASEPAIR    21    FREE_ENERGY
-18.30    LEN_BP_RATIO    3
CCCUUCCUCGUCGUGGUACCCAACCUGUGGGUUCUCUAGAACUAAAGUCUGCCUGCCAGGUGACU
GCUGGA
>random_seq_from_cds__NO_5103    RANDOM_LENGTH    92    SEQ_LENGTH    78
GC_CONTENT    0.551282051282051    BASEPAIR    28    FREE_ENERGY
-30.20    LEN_BP_RATIO    2.78571428571429
CUUGAGUCAUGUCCUGGUGAGACGGUUGUGGCAGAAGAUCCCGCCGGGCUGAAGGGUCCCUUGC
UACUACACCAGAAGCAGGCAUUGGCUU
>random_seq_from_cds__NO_5111    RANDOM_LENGTH    95    SEQ_LENGTH    91
GC_CONTENT    0.450549450549451    BASEPAIR    27    FREE_ENERGY
-21.73    LEN_BP_RATIO    3.37037037037037
AGUCAGGUUGACAAUGGCUCAAAAGAAAGGAGGAGAACGGUUAAGUAUUUUAAACCAAGAGCCUUU
GCUGAGGAGAACAAAAGACCAGCUGGACUC
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>random_seq_from_cds__NO_5117 RANDOM_LENGTH 87 SEQ_LENGTH 79
GC_CONTENT 0.468354430379747 BASEPAIR 27 FREE_ENERGY
-17.90 LEN_BP_RATIO 2.92592592592593
UUUCCCUUAACGGCACCUUCUUCUUAAGAUGGAGCUUUUUGAAGGCAUGCGAGAGAGCACCAAGGAU
UUCAUCUCUGUUGGCAGAAUUG
>random_seq_from_cds__NO_5128 RANDOM_LENGTH 75 SEQ_LENGTH 52
GC_CONTENT 0.480769230769231 BASEPAIR 19 FREE_ENERGY
-18.80 LEN_BP_RATIO 2.73684210526316
GAUGAAAUGAGGCACAAGCUGGCUGGAUUGAGGGGGCAGCCAUCUUUCUCAGUGAUCAUCGU
GGUGUUAGUG
>random_seq_from_cds__NO_5129 RANDOM_LENGTH 67 SEQ_LENGTH 58
GC_CONTENT 0.517241379310345 BASEPAIR 21 FREE_ENERGY
-15.80 LEN_BP_RATIO 2.76190476190476
ACUGCCUUUAUGAUUGGAGCAAAGAGAAGCAAUUCGGGGCUGCAGUGCCGAUUGAACAGGA
GC
>random_seq_from_cds__NO_5137 RANDOM_LENGTH 75 SEQ_LENGTH 57
GC_CONTENT 0.526315789473684 BASEPAIR 20 FREE_ENERGY
-22.76 LEN_BP_RATIO 2.85
GUACUCCCAUCUACAUCAGUACUUGUCAAGUUCUUCAUCAUCGGCAUCACUGUACUGGUGGUG
GCUGUGCCAG
>random_seq_from_cds__NO_5149 RANDOM_LENGTH 110 SEQ_LENGTH 85
GC_CONTENT 0.576470588235294 BASEPAIR 26 FREE_ENERGY
-30.30 LEN_BP_RATIO 3.26923076923077
AACGAGAAAGGCGAGGGUAGAGCAAGAAAAGCUGGACAAGAUCUGGCCUAAGCUUCGGGUCCUGG
CGCGAUCUUCUCCCACUGACAAGCACACCCUGGUGAAAAGGGCAUA
>random_seq_from_cds__NO_5151 RANDOM_LENGTH 82 SEQ_LENGTH 57
GC_CONTENT 0.508771929824561 BASEPAIR 19 FREE_ENERGY
-18.30 LEN_BP_RATIO 3
GGAUGUUGGUUUUGCCAUGGGGCAUCGCAGGCACAGAUGUAGCAAAGGAGGCUUCAGACAUCAUC
CUAACAGAUGACAACUU
>random_seq_from_cds__NO_5152 RANDOM_LENGTH 73 SEQ_LENGTH 60
GC_CONTENT 0.516666666666667 BASEPAIR 22 FREE_ENERGY
-22.10 LEN_BP_RATIO 2.72727272727273
CACCAGCAUUGUGAAGGCAGUGAUGUGGGGACGAAAUGUCUAUGACAGCAUCUCCAAGUCCUGC
AGUCCAG
>random_seq_from_cds__NO_5156 RANDOM_LENGTH 82 SEQ_LENGTH 71
GC_CONTENT 0.422535211267606 BASEPAIR 24 FREE_ENERGY
-20.41 LEN_BP_RATIO 2.95833333333333
CAUUCUAUCAGCUCAUUGUCAUCUUUAUCCUUGUCUUUGCGGGGUGAGAAUUCUUUGAUUAUGA
UAGUGGGAGGAAGGCAC
>random_seq_from_cds__NO_5164 RANDOM_LENGTH 89 SEQ_LENGTH 77
GC_CONTENT 0.506493506493506 BASEPAIR 23 FREE_ENERGY
-17.59 LEN_BP_RATIO 3.34782608695652
UAAGUUUGGACUAGGGUGCUCCUGUUGGAUGGUGAGGUCACUCCAUAUGCCAAUACAAACAACA
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AUGCGGUGGAUUGCAACCAAGUGC
>random_seq_from_cds__NO_5182 RANDOM_LENGTH 82 SEQ_LENGTH 71
  GC_CONTENT 0.71830985915493 BASEPAIR 23 FREE_ENERGY
  -32.10 LEN_BP_RATIO 3.08695652173913
GGGACGGAGCGGGAGGCCGAGGCUGGGGGCAGGUCCCCGGCGCACGCCCAUAAGCAGAAUCCCCAG
GGCCAGACUGACUCCCA
>random_seq_from_cds__NO_5209 RANDOM_LENGTH 110 SEQ_LENGTH 89
  GC_CONTENT 0.426966292134831 BASEPAIR 30 FREE_ENERGY
  -28.30 LEN_BP_RATIO 2.966666666666667
AACAUUGAUGAUUCUGGGCUAGAGCUUGAUAAUAACAAUGCAGCAAUGGCAAUUGAUCCAGUAA
UGGAUGGUGCUAGUGAAAUUGAAUUGAUUAGUAUUCAGGCCUCAUCCCA
>random_seq_from_cds__NO_5210 RANDOM_LENGTH 89 SEQ_LENGTH 70
  GC_CONTENT 0.428571428571429 BASEPAIR 23 FREE_ENERGY
  -17.60 LEN_BP_RATIO 3.04347826086957
CACUUAUGGAAAAAGAUGACAGUGCACAGACGAGGAUACAUAAGACUUCUGGUAACGCCACUGU
UGAUCACUUAUCCAAGUAUCUGGC
>random_seq_from_cds__NO_5225 RANDOM_LENGTH 78 SEQ_LENGTH 65
  GC_CONTENT 0.430769230769231 BASEPAIR 23 FREE_ENERGY
  -19.80 LEN_BP_RATIO 2.82608695652174
AAAGAGUCUUGACAUUGGAAUGGCUGAGGAUGUAGGAACAAAUUCUGCAACUUGUUCUAUGAAA
UCAGGGUUCAGCU
>random_seq_from_cds__NO_5232 RANDOM_LENGTH 71 SEQ_LENGTH 49
  GC_CONTENT 0.551020408163265 BASEPAIR 20 FREE_ENERGY
  -20.24 LEN_BP_RATIO 2.45
GUGUUCUGGCUUCUUGGGAUGAGGCACACACCACAUCCAGAUUCCCUUGGUGUGAGACUUCACUG
UGGAGC
>random_seq_from_cds__NO_5244 RANDOM_LENGTH 65 SEQ_LENGTH 51
  GC_CONTENT 0.529411764705882 BASEPAIR 19 FREE_ENERGY
  -16.80 LEN_BP_RATIO 2.68421052631579
UCUGAAUCUCGUUACCUCCCAGCAGACCAGGAGUAUACUGUUGGCUGUAGGAAUAUGUUGGGC
>random_seq_from_cds__NO_5252 RANDOM_LENGTH 89 SEQ_LENGTH 66
  GC_CONTENT 0.454545454545455 BASEPAIR 21 FREE_ENERGY
  -17.40 LEN_BP_RATIO 3.14285714285714
AACAAACCUACAGAAUAUCAUCUAUAACCCGGGUAUACCCGUUUGUUGGCACCAUUCUGAUCAGC
UGGAUCCUGGAACUUUGAUUGUGA
>random_seq_from_cds__NO_5270 RANDOM_LENGTH 99 SEQ_LENGTH 89
  GC_CONTENT 0.50561797752809 BASEPAIR 26 FREE_ENERGY
  -27.03 LEN_BP_RATIO 3.42307692307692
CCGCAUGCCCUAUAUCUCAGACAAGCACCCUCGACAAACCUUGGAAGUGAUUAACCUUCUGAGAA
AGCACCGGGAGCUAUGUGAUGUGGUGCUAGUUGU
>random_seq_from_cds__NO_5276 RANDOM_LENGTH 80 SEQ_LENGTH 73
  GC_CONTENT 0.493150684931507 BASEPAIR 24 FREE_ENERGY
  -22.70 LEN_BP_RATIO 3.041666666666667
GUGUUCAAUGCAGUGAUGGCCUGGGUCAAAUACAGUAUUCAGGAAAGACGUCCUCAAUACCCCA
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GGGUGCUGCAGCAUG
>random_seq_from_cds__NO_5280 RANDOM_LENGTH 82 SEQ_LENGTH 70
  GC_CONTENT 0.485714285714286 BASEPAIR 27 FREE_ENERGY
  -25.80 LEN_BP_RATIO 2.59259259259259
CAGACCAAUGAAUGGAGAAUGGUGGCUUCAUGAGCAAAGGAGAUGCGGAGUUGGGUCAGUGU
UCUUGAUGAUCUGUUAU
>random_seq_from_cds__NO_5281 RANDOM_LENGTH 110 SEQ_LENGTH 94
  GC_CONTENT 0.5 BASEPAIR 30 FREE_ENERGY -31.10 LEN_BP_RATIO
  3.13333333333333
AUGCAGUAGGAGGCCAUGAUGGAUCCUCUUAUCUCAAUAGUGUUGAAAGGGUAUGACCCCAAAC
AAACCAGUGGAGCAGUGAUGUGGCCCUACAAGCACCUGCAGGAC
>random_seq_from_cds__NO_5294 RANDOM_LENGTH 80 SEQ_LENGTH 65
  GC_CONTENT 0.538461538461538 BASEPAIR 24 FREE_ENERGY
  -24.80 LEN_BP_RATIO 2.70833333333333
GAUGGCCAUGGCAGUCAGUGGCAGCAGAAAGAGGCAGCAGAAGGUGAAGAGGUUAUAGGUGGUCU
CUUGCCAUGAGCCU
>random_seq_from_cds__NO_5296 RANDOM_LENGTH 72 SEQ_LENGTH 60
  GC_CONTENT 0.6 BASEPAIR 20 FREE_ENERGY -20.40 LEN_BP_RATIO
  3
UGCCCCAGAAGUUCCUACACCUGAACGGGAUCCAAGCGGGUUGAGUACUGCUGCCUGGCGGU
CCAAUCC
>random_seq_from_cds__NO_5301 RANDOM_LENGTH 84 SEQ_LENGTH 65
  GC_CONTENT 0.523076923076923 BASEPAIR 25 FREE_ENERGY
  -27.50 LEN_BP_RATIO 2.6
UGCAGCUGUUCUACUUCCUUUUCUCUUGGAGCCCUGGCCGAUCGGGCAUUGAUGAGAACAAGGG
CUGUGUAGAGGGCAAUCUC
>random_seq_from_cds__NO_5307 RANDOM_LENGTH 64 SEQ_LENGTH 58
  GC_CONTENT 0.689655172413793 BASEPAIR 23 FREE_ENERGY
  -27.60 LEN_BP_RATIO 2.52173913043478
GGUGUGCUGCGGAAACUGGGGCGCCGUGAGCUGUCUGGGCCUGUCCAGUUCCTCAAGCCAG
>random_seq_from_cds__NO_5309 RANDOM_LENGTH 85 SEQ_LENGTH 66
  GC_CONTENT 0.636363636363636 BASEPAIR 26 FREE_ENERGY
  -26.60 LEN_BP_RATIO 2.53846153846154
CUCUCUCUGCCCUCAGCCUUGCCCCGCUCAGGGCUGUAUUAAGGUGGCAUGAGGCCCAUUGAG
CCCUGCCUUGGCCAAGUUGU
>random_seq_from_cds__NO_5311 RANDOM_LENGTH 82 SEQ_LENGTH 74
  GC_CONTENT 0.662162162162162 BASEPAIR 28 FREE_ENERGY
  -40.20 LEN_BP_RATIO 2.64285714285714
GGCAGCUGCCCGUCUGGGAGCCCAAGGUGUAGGUGAGGGUAUCUGCUCCUUGGGCCCGUCUGG
AGGGGUCUUGACCACUG
>random_seq_from_cds__NO_5316 RANDOM_LENGTH 90 SEQ_LENGTH 81
  GC_CONTENT 0.62962962962963 BASEPAIR 25 FREE_ENERGY
  -30.42 LEN_BP_RATIO 3.24
UGCAGGUGUGGGUCUUCUUUGCAGCCAGCAGCUCCCCCGUGAGGCUCGGUGCUGUCUCUGUGGGC
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CCUGUCCAUUCUAUUUCCAGCGCCC
>random_seq_from_cds__NO_5322 RANDOM_LENGTH 94 SEQ_LENGTH 77
  GC_CONTENT 0.519480519480519 BASEPAIR 25 FREE_ENERGY
  -16.31 LEN_BP_RATIO 3.08
CUCUGCCCAGCGUCUCUCCGAUCCUGUCUUUGAGAGAAACGAGCUCCUCCUCCUCUUUCUCCUG
UUCUCAAGGUGAGCCUCGAUCAGCGCCUG
>random_seq_from_cds__NO_5332 RANDOM_LENGTH 80 SEQ_LENGTH 65
  GC_CONTENT 0.615384615384615 BASEPAIR 21 FREE_ENERGY
  -23.90 LEN_BP_RATIO 3.0952380952381
ACCUCGAUCAUCUUCUGGUACAUGUCCUCCGCAGGCUGGGCUUCUCCGGGCCUUCGUGAGCUC
CUCUCCAGGUAGGU
>random_seq_from_cds__NO_5334 RANDOM_LENGTH 71 SEQ_LENGTH 58
  GC_CONTENT 0.603448275862069 BASEPAIR 24 FREE_ENERGY
  -21.20 LEN_BP_RATIO 2.41666666666667
UCUGGUUGUAGCGCUCCCCGUCCUACACAUCCCAUGGUAGGCAGGUACGAAGGGCCUCAGC
ACAUCC
>random_seq_from_cds__NO_5335 RANDOM_LENGTH 64 SEQ_LENGTH 53
  GC_CONTENT 0.622641509433962 BASEPAIR 20 FREE_ENERGY
  -20.80 LEN_BP_RATIO 2.65
ACCAUCAGCCGGUCCAGGCAGCGCUGCUCUGACUCACAGUGCUUCUUCAGGAUCCUGCCAUUGG
>random_seq_from_cds__NO_5339 RANDOM_LENGTH 81 SEQ_LENGTH 73
  GC_CONTENT 0.684931506849315 BASEPAIR 29 FREE_ENERGY
  -45.20 LEN_BP_RATIO 2.51724137931034
CCCUGGAGGAGGCCGAGGAAGAGGACAGUUUCCUCAGGGGCAGGUUGCCCCGAGGGCUUCCUG
CGUCUCCUCCAAGGCC
>random_seq_from_cds__NO_5346 RANDOM_LENGTH 71 SEQ_LENGTH 60
  GC_CONTENT 0.633333333333333 BASEPAIR 20 FREE_ENERGY
  -23.20 LEN_BP_RATIO 3
CACAGUCGUCUCCUCUGGCCUUUGCCCACUUCAGGCUCCCAGAGCCCGGAUGCCACAGGGCA
GAUAUC
>random_seq_from_cds__NO_5348 RANDOM_LENGTH 86 SEQ_LENGTH 65
  GC_CONTENT 0.707692307692308 BASEPAIR 27 FREE_ENERGY
  -36.80 LEN_BP_RATIO 2.40740740740741
CUGCCUCUCCACCAGGGCCUCUGGGGGCUGCAGGUCCUCAAGCUCACGGGCUCUCCAGACGGCU
CAGUGAGGGCAAGAUCCUGUG
>random_seq_from_cds__NO_5360 RANDOM_LENGTH 82 SEQ_LENGTH 64
  GC_CONTENT 0.734375 BASEPAIR 25 FREE_ENERGY -31.40
  LEN_BP_RATIO 2.56
GCAGUACACAGCCAUCAUGCAGCGCGCUGGCUCAGCGGUGGCCGCGGGGAAUGUGACAUCAGCG
GCGCCGGGCGCUUGGGG
>random_seq_from_cds__NO_5361 RANDOM_LENGTH 110 SEQ_LENGTH 78
  GC_CONTENT 0.756410256410256 BASEPAIR 31 FREE_ENERGY
  -48.10 LEN_BP_RATIO 2.51612903225806
CUGGAGGAGGCAGCUCGCCUCAGCUGCGCUGUGCACACCUCGCCCGGGGGAGGACGCAGACCCGG
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GCAGGCGGCAGGGAUGUCGGCGAAGGAGAGGCCAAAGGGCAAAGU
>random_seq_from_cds__NO_5381 RANDOM_LENGTH 84 SEQ_LENGTH 65
  GC_CONTENT 0.538461538461538 BASEPAIR 20 FREE_ENERGY
  -19.40 LEN_BP_RATIO 3.25
CUCCUGCACUGGCUCCAUCCGCUAUA AAAACCUUGACAGACCAUGAGCCCAGUGGGAUAGUGAGGG
UUGAGGCUCACCCAGAGAA
>random_seq_from_cds__NO_5390 RANDOM_LENGTH 92 SEQ_LENGTH 83
  GC_CONTENT 0.481927710843373 BASEPAIR 27 FREE_ENERGY
  -18.20 LEN_BP_RATIO 3.07407407407407
CUGUGUCCACAGCGUUCAAGGCAAACAGUGAGUUUUUCCAGAUUCUCAGUCAGAAUGGAGCACCU
CAGGCAGAUGUGAGCAUGUACAGUCUU
>random_seq_from_cds__NO_5402 RANDOM_LENGTH 110 SEQ_LENGTH 97
  GC_CONTENT 0.65979381443299 BASEPAIR 33 FREE_ENERGY
  -42.10 LEN_BP_RATIO 2.93939393939394
UGGGGAGCAGCGGGUCG CAGGAGCAGCUUGUCAGCAUCGCCUCCUCCAGUGAGGCCAGUGGGCAC
CGUGUGGAGGAGACGAAGGCGGAGCAGGAUGACCUUGCAGCAGGU
>random_seq_from_cds__NO_5409 RANDOM_LENGTH 73 SEQ_LENGTH 61
  GC_CONTENT 0.639344262295082 BASEPAIR 19 FREE_ENERGY
  -17.94 LEN_BP_RATIO 3.21052631578947
CCAUGUCCACCC CAGAGACAGGCCAGGGAUGCUACCCUCUUCUGUGAGCCUGGACCCUGAAC
AUGCAGCC
>random_seq_from_cds__NO_5415 RANDOM_LENGTH 81 SEQ_LENGTH 63
  GC_CONTENT 0.634920634920635 BASEPAIR 23 FREE_ENERGY
  -29.20 LEN_BP_RATIO 2.73913043478261
CAGCCCCCGGAACUGCACCGGAAGGCCUGCAUGGGCUGCCCUUGUCCGAGGGCUUGCAGCCUAC
CCAGCUUUCUUUUUC
>random_seq_from_cds__NO_5430 RANDOM_LENGTH 71 SEQ_LENGTH 63
  GC_CONTENT 0.714285714285714 BASEPAIR 21 FREE_ENERGY
  -32.80 LEN_BP_RATIO 3
CACCCAGUGAGCCUCCUGCUGCAGGUGCCCAAUGUGGGAGGCGGCUUGGAGGCCUGGCACAUCCG
GGGUUG
>random_seq_from_cds__NO_5437 RANDOM_LENGTH 79 SEQ_LENGTH 69
  GC_CONTENT 0.579710144927536 BASEPAIR 23 FREE_ENERGY
  -19.12 LEN_BP_RATIO 3
GCCCAGAACUUUGGUCUCCAGCAUCUCUCCAGCGGCCACUUCUUGCGGGAGAACAUCAAGGCCAG
CACCGGAAGUUGGU
>random_seq_from_cds__NO_5467 RANDOM_LENGTH 82 SEQ_LENGTH 53
  GC_CONTENT 0.547169811320755 BASEPAIR 19 FREE_ENERGY
  -16.30 LEN_BP_RATIO 2.78947368421053
CCGUCGCUAUAUCCG CAGACUCCGGGCUAUCCGGGAGCUCAAUAGGAACUGUAGAAGAUUUGAAA
AAUAAUGAAAGCCAAUG
>random_seq_from_cds__NO_5469 RANDOM_LENGTH 102 SEQ_LENGTH 82
  GC_CONTENT 0.573170731707317 BASEPAIR 27 FREE_ENERGY
  -24.20 LEN_BP_RATIO 3.03703703703704
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CUGUGCUGAUGCUGGCCUACUUGACGAGAGCUUCCUGAGAAGAUGUCUGAAUUUUUAUGGCCUUC
UCAUUCAGCUGCUGCUCCGCAUCCUGGACCCCGCAUA

>random_seq_from_cds__NO_5479 RANDOM_LENGTH 90 SEQ_LENGTH 71
GC_CONTENT 0.492957746478873 BASEPAIR 24 FREE_ENERGY
-17.60 LEN_BP_RATIO 2.95833333333333

AGCAACUUUGUGGCCCAAGUGCCGUGACCUGAAAGUUGAAAACCCUGAGAAUACGGCUUUGAA
CCAAAGAAGCUGUUGGACCAACUGA

>random_seq_from_cds__NO_5480 RANDOM_LENGTH 83 SEQ_LENGTH 77
GC_CONTENT 0.480519480519481 BASEPAIR 24 FREE_ENERGY
-20.10 LEN_BP_RATIO 3.20833333333333

CGGAUUAUUACUUACAGCUGGACUGUGCUCGGUUCGCGAAAGCCAUUGCUGACGACCAGGAGAU
CUACAGUAAGGAAUUGUU

>random_seq_from_cds__NO_5488 RANDOM_LENGTH 72 SEQ_LENGTH 65
GC_CONTENT 0.676923076923077 BASEPAIR 27 FREE_ENERGY
-36.00 LEN_BP_RATIO 2.40740740740741

AGGCCUGGGGAUGGCCGAGGGAAUGGGCAGUUGACUGGAAGAUUUAGCAGCUGCUCCUGCGGCC
GGGGCAG

>random_seq_from_cds__NO_5491 RANDOM_LENGTH 110 SEQ_LENGTH 81
GC_CONTENT 0.666666666666667 BASEPAIR 31 FREE_ENERGY
-43.27 LEN_BP_RATIO 2.61290322580645

GAGGGCCUCUUCCAGAUGUAGCCCGGAGAGCCUGACUGACCCCUCCUAUCAUUACUCCGGAG
UCGAGGCGUCAGGCUGCUUGGGGAGGGGUGCUCGCGUCAAGA

>random_seq_from_cds__NO_5498 RANDOM_LENGTH 84 SEQ_LENGTH 73
GC_CONTENT 0.438356164383562 BASEPAIR 23 FREE_ENERGY
-16.30 LEN_BP_RATIO 3.17391304347826

GUGCAUUUGCCCAGUAUAACAUGGAUCAGUUCACGCCUGUGAAGAUAGAAGGAUAUGAAGAU
GGUCUUAUUACAGAGCAC

>random_seq_from_cds__NO_5518 RANDOM_LENGTH 69 SEQ_LENGTH 61
GC_CONTENT 0.557377049180328 BASEPAIR 20 FREE_ENERGY
-18.51 LEN_BP_RATIO 3.05

GCUGAGCAUUUCCUGGGACCAGGAGACAGAGAUGUGCCUAUUCUGCAUUGUCUCCAACCCUG
UCAG

>random_seq_from_cds__NO_5519 RANDOM_LENGTH 83 SEQ_LENGTH 62
GC_CONTENT 0.645161290322581 BASEPAIR 20 FREE_ENERGY
-26.40 LEN_BP_RATIO 3.1

CUGGGACUUGGCCACAGUCACGCCUGGGAUAGCUGUCAUCAUGAGGCAGGCACCAGGGAAGGCC
UCCUACAAAGAUGUGCUG

>random_seq_from_cds__NO_5530 RANDOM_LENGTH 110 SEQ_LENGTH 79
GC_CONTENT 0.417721518987342 BASEPAIR 26 FREE_ENERGY
-19.00 LEN_BP_RATIO 3.03846153846154

UAUAUUCUUUAAGAACCAAUUCCAGUCUAAGUCUGGAAUGGUCAAGUUUGCAAGAGUCCCAA
CAUUCAAUCACAAACUCCUCUUCUUCAUCAUUAAGAGAUCUGGGCU

>random_seq_from_cds__NO_5535 RANDOM_LENGTH 85 SEQ_LENGTH 63
GC_CONTENT 0.444444444444444 BASEPAIR 22 FREE_ENERGY

-17.40 LEN_BP_RATIO 2.86363636363636

GAAGCAGUCCAACUUGUACCAUCUUAUUCUCAGUCCUGUGUCAAGGAUAGGUUUAGUAAAAGU
CGGAGGGUGAUUUCAGCAG

>random_seq_from_cds__NO_5549 RANDOM_LENGTH 87 SEQ_LENGTH 60
GC_CONTENT 0.65 BASEPAIR 23 FREE_ENERGY -28.00
LEN_BP_RATIO 2.60869565217391

UUGCAUCUCAUGCUGUGCUCAGCGGUUGGCCACGCGGCCAGGAAGUGCAGGGCAGUGGCGCUU
UGAUCAUACACAGCAAACAGGA

>random_seq_from_cds__NO_5553 RANDOM_LENGTH 109 SEQ_LENGTH 96
GC_CONTENT 0.59375 BASEPAIR 32 FREE_ENERGY -32.70
LEN_BP_RATIO 3

AGGUCAGAGGCAUAGUGAGGCUGGAUCAGCAGCAGGCAGGCGCUCUCAGUGAAGGGCACUUGAGU
CACCGAGAAGUUGUCCUGGAUGUCACUCCAGUGCUGGAAGGUGC

>random_seq_from_cds__NO_5556 RANDOM_LENGTH 93 SEQ_LENGTH 78
GC_CONTENT 0.551282051282051 BASEPAIR 28 FREE_ENERGY
-26.80 LEN_BP_RATIO 2.78571428571429

CCAGUCUCCAUCUGUCACAGCCUGCAUGAACCUGUCAAUUCUCAGCAGCAACAUCAGUUC
UGUGAAGUCCAGAGAGCGUGGGAGGACC

>random_seq_from_cds__NO_5557 RANDOM_LENGTH 71 SEQ_LENGTH 65
GC_CONTENT 0.646153846153846 BASEPAIR 22 FREE_ENERGY
-27.10 LEN_BP_RATIO 2.95454545454545

ACAGGGGUAUAGAGAGCCAGGCCUGCACAAACGGCUGCUUCAGGUGCAGGCCUGGGGUCUGUGAA
CACGCC

>random_seq_from_cds__NO_5560 RANDOM_LENGTH 78 SEQ_LENGTH 66
GC_CONTENT 0.651515151515151 BASEPAIR 21 FREE_ENERGY
-24.10 LEN_BP_RATIO 3.14285714285714

GCCUGUCAGCUGUGUGGUCCAAGGCUCCAGAUAGAGAGAGGCCAGGGUGCCAAAGACAGCCGUU
GGGGAGAGGACGG

>random_seq_from_cds__NO_5578 RANDOM_LENGTH 89 SEQ_LENGTH 79
GC_CONTENT 0.594936708860759 BASEPAIR 27 FREE_ENERGY
-26.20 LEN_BP_RATIO 2.92592592592593

GCUCCAGCUUCUGGUCAUGAUUCACCAGCUGUCCACCCUGCGGGACCAGCUCCUGACAGCCCACU
CGGAGCAGAAGAACAUGGCUGCCA

>random_seq_from_cds__NO_5588 RANDOM_LENGTH 77 SEQ_LENGTH 63
GC_CONTENT 0.619047619047619 BASEPAIR 22 FREE_ENERGY
-25.60 LEN_BP_RATIO 2.86363636363636

UUCCCCGAGUCCCGAAACAGCAGCCACAUCAAGAGGCCCAUGAACGCCUUCAUGGUGGGCCAA
GGAUGAGCGGAG

>random_seq_from_cds__NO_5603 RANDOM_LENGTH 68 SEQ_LENGTH 58
GC_CONTENT 0.620689655172414 BASEPAIR 19 FREE_ENERGY
-19.60 LEN_BP_RATIO 3.05263157894737

CACUGGCCACCUUCAGAAAUAUGUCCCGUGGUUCCCCGGGGCCCCACAUCUGGGUCUCACAGAU
GAC

>random_seq_from_cds__NO_5607 RANDOM_LENGTH 87 SEQ_LENGTH 78

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GC_CONTENT    0.641025641025641    BASEPAIR    29    FREE_ENERGY
-29.31    LEN_BP_RATIO    2.68965517241379
CACUGCGCUGGACUCCAAGGUGACACGGCGUCCAUGCCUUCUCGUUGCUC AACCCAGGAGAGG
CCCUGCACCAUGGCCAGCUGCC
>random_seq_from_cds__NO_5612    RANDOM_LENGTH    99    SEQ_LENGTH    79
GC_CONTENT    0.721518987341772    BASEPAIR    32    FREE_ENERGY
-36.40    LEN_BP_RATIO    2.46875
CCUUCGUGCGUUCGCCGUAGGCGGCGAUGACCUGUAGGUCCCGCAAGUGCUGUGUGCGGACGCUC
UGCUGCGCCCAACACGCUCGUCCCGCGCCGGCCC
>random_seq_from_cds__NO_5624    RANDOM_LENGTH    68    SEQ_LENGTH    56
GC_CONTENT    0.535714285714286    BASEPAIR    21    FREE_ENERGY
-22.90    LEN_BP_RATIO    2.666666666666667
CGUCACAGGUUCUGUAGCGCUGACAGCCUCGGCUGGUCGUUUUAUUGGCAUCCAGAAUCUCGGGAA
AGC
>random_seq_from_cds__NO_5625    RANDOM_LENGTH    87    SEQ_LENGTH    65
GC_CONTENT    0.676923076923077    BASEPAIR    27    FREE_ENERGY
-37.00    LEN_BP_RATIO    2.40740740740741
CGGAGGACUGCAGGAGCACCAUGGAGGCUCUCGAGGGCUGCCCUGCAGAGCCUCCUGGUCUGGGU
UCCCACAACAUAUAGGGGCAUGC
>random_seq_from_cds__NO_5627    RANDOM_LENGTH    82    SEQ_LENGTH    76
GC_CONTENT    0.684210526315789    BASEPAIR    28    FREE_ENERGY
-31.40    LEN_BP_RATIO    2.71428571428571
CUCCUGCUGGCCUGGGCCGGGGAGGCCUGAGAGCCAUGGGGUAGCUGUGAAGUAGGCCUGGCCAAG
CAGUGCUGAGUCGGGGA
>random_seq_from_cds__NO_5629    RANDOM_LENGTH    80    SEQ_LENGTH    69
GC_CONTENT    0.710144927536232    BASEPAIR    28    FREE_ENERGY
-39.10    LEN_BP_RATIO    2.46428571428571
GCGCUGGCGGGCCUCGAAGGGGACGUGGGUGGUUCCUGGAAGGCCCGCCGCUCCACUUUGGGGCC
ACUGACAGGCUCCGU
>random_seq_from_cds__NO_5634    RANDOM_LENGTH    90    SEQ_LENGTH    76
GC_CONTENT    0.605263157894737    BASEPAIR    26    FREE_ENERGY
-28.50    LEN_BP_RATIO    2.92307692307692
CGGAGCCUGGUCUUGGAAGAGGAGACCACUUCCUGCUGAAGCUAGCUGAGCGCGUCAAGGCCAC
AUCCAUCUCAGGCACCAGUACAACG
>random_seq_from_cds__NO_5641    RANDOM_LENGTH    85    SEQ_LENGTH    78
GC_CONTENT    0.551282051282051    BASEPAIR    24    FREE_ENERGY
-21.50    LEN_BP_RATIO    3.25
CCUGGGAAGCAGAGAUAGGAGAGUCCGGCUGGUUGCUGAAGAUCGAAGAAUCCAAAACCCACAG
GACAAUGUCUGGAGGCUCCC
>random_seq_from_cds__NO_5648    RANDOM_LENGTH    64    SEQ_LENGTH    51
GC_CONTENT    0.6666666666666667    BASEPAIR    20    FREE_ENERGY
-20.70    LEN_BP_RATIO    2.55
UCCACGGGGACUGGGGCUGGCUCACGUAUCCGGCUC AUGGGGUGGGACUCCAUCAACGAGGUGG
>random_seq_from_cds__NO_5652    RANDOM_LENGTH    84    SEQ_LENGTH    77
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GC_CONTENT    0.649350649350649    BASEPAIR    27    FREE_ENERGY
-35.00    LEN_BP_RATIO    2.85185185185185
CACCAUUGCGGCCGACGAGAGCUUCACAGGUGCCGACCUUGGUGUGCGGCGUCUCAAGCUCAACA
CGGAGGUGCGCAGUGUGGG
>random_seq_from_cds__NO_5655    RANDOM_LENGTH    87    SEQ_LENGTH    79
GC_CONTENT    0.708860759493671    BASEPAIR    27    FREE_ENERGY
-27.90    LEN_BP_RATIO    2.92592592592593
GGAGGUGAGGGGCCAGUGCGUGCGGCACUCAGAGGAGCGGGACACACCCAAGAUGUACUGCAGCG
CGGAGGGCGAGUGGCUCGUGCC
>random_seq_from_cds__NO_5681    RANDOM_LENGTH    97    SEQ_LENGTH    64
GC_CONTENT    0.546875    BASEPAIR    22    FREE_ENERGY    -18.90
LEN_BP_RATIO    2.90909090909091
CCCGCCGGCACCUCUGAUCUACUUCUGCAUGUCACACUGCAGCAGCAACACAAUGGAUGGGUCAC
UCUUGGCUGCCUCCUUGAACUCCUCCAAUGUA
>random_seq_from_cds__NO_5688    RANDOM_LENGTH    94    SEQ_LENGTH    76
GC_CONTENT    0.565789473684211    BASEPAIR    23    FREE_ENERGY
-26.10    LEN_BP_RATIO    3.30434782608696
ACCGUGGGUAUGCAGACAGUCCUUCAAAAGGCAGGAGCAGCUCCAUAUGUGCAGGCAUUUGACUC
GCUGCUUGCUGGUCCUGUGGCAGAGUACU
>random_seq_from_cds__NO_5694    RANDOM_LENGTH    110    SEQ_LENGTH    100
GC_CONTENT    0.65    BASEPAIR    30    FREE_ENERGY    -36.40
LEN_BP_RATIO    3.33333333333333
CCUGGAGCAAACGGGGGCCUGUGGCAAAGAACUGAGCGGACUGCCAUCUGGACCCUCUGCCGG
AUCAUGUCCUCCUCCCCUCCACCAUGCCCCCUCCUCCCCCAGU
>random_seq_from_cds__NO_5700    RANDOM_LENGTH    75    SEQ_LENGTH    68
GC_CONTENT    0.470588235294118    BASEPAIR    23    FREE_ENERGY
-16.00    LEN_BP_RATIO    2.95652173913043
UUGGCCUGGUAUUCGAUGACGUGGUGGGCAUUGUGGAGAUAAUCAACAGUAAGGAUGUCAAGUU
CAGGGUAAUG
>random_seq_from_cds__NO_5727    RANDOM_LENGTH    97    SEQ_LENGTH    75
GC_CONTENT    0.56    BASEPAIR    29    FREE_ENERGY    -28.20
LEN_BP_RATIO    2.58620689655172
UCUGCCCCUGCCAAAACAGACUGUGUGCAUCUCCUUUCAGAAGUUAACGGUAUCCCCGGCCUGG
AGCUGUAAAGGGGUCCUUAUGCAGAGCUGG
>random_seq_from_cds__NO_5744    RANDOM_LENGTH    100    SEQ_LENGTH    91
GC_CONTENT    0.450549450549451    BASEPAIR    34    FREE_ENERGY
-26.20    LEN_BP_RATIO    2.67647058823529
UUCCACAAGGGUUUCACUCUAUUAAAUCAGGAAGGCCUUUGUAGAUGUCUUAUCAUUAUUGCUU
UCUUCUGUUGGAAGGGCCCUGAUUCCUGUGGCCA
>random_seq_from_cds__NO_5746    RANDOM_LENGTH    97    SEQ_LENGTH    53
GC_CONTENT    0.509433962264151    BASEPAIR    21    FREE_ENERGY
-26.50    LEN_BP_RATIO    2.52380952380952
AGUUCACUUUUCUCAUUCCAAACGUCUCACAACAGGCCGUGAGAAAUGUCCUUAUGUUCUUCAA
ACAGAGAAACCUGGGACAUCUGCGGCCUCAGG
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>random_seq_from_cds__NO_5778 RANDOM_LENGTH 71 SEQ_LENGTH 60
  GC_CONTENT 0.65 BASEPAIR 22 FREE_ENERGY -26.50
  LEN_BP_RATIO 2.72727272727273
UGGUCGGGGUUCAGAUAGAUUCGACCCCGCAUGGCCAGCUCUAUCAGGAUGCCCCUCGCAGG
CCUGAU
>random_seq_from_cds__NO_5780 RANDOM_LENGTH 84 SEQ_LENGTH 63
  GC_CONTENT 0.46031746031746 BASEPAIR 20 FREE_ENERGY
  -20.29 LEN_BP_RATIO 3.15
CCAUAAGAGUAAGGCGGAUAUCCUJAGAGUCUCCAGAAUCUUAUUGUCUGGACUUUCUCCCAA
UUACUGUCUUCUCACUUU
>random_seq_from_cds__NO_5793 RANDOM_LENGTH 79 SEQ_LENGTH 69
  GC_CONTENT 0.550724637681159 BASEPAIR 23 FREE_ENERGY
  -29.70 LEN_BP_RATIO 3
AAUUGGGAGCCAGGUCCUGAUUCCUCUUCAGCAAGGCCUCACUGAAGGAAGUUUCAUCAGGUGCU
GGCUUGACCCGGGG
>random_seq_from_cds__NO_5795 RANDOM_LENGTH 109 SEQ_LENGTH 93
  GC_CONTENT 0.548387096774194 BASEPAIR 32 FREE_ENERGY
  -36.30 LEN_BP_RATIO 2.90625
UCUGUCACCCCUCAUAAUGAGCCUCUUUGAUCUCUCCGGGGCUUUUUCGGCUUUCUGGACCU
CGGAGGCCACAGAGAUCUUUUUUGGAGGGAUGACUCGAGAUG
>random_seq_from_cds__NO_5817 RANDOM_LENGTH 95 SEQ_LENGTH 74
  GC_CONTENT 0.540540540540541 BASEPAIR 26 FREE_ENERGY
  -31.40 LEN_BP_RATIO 2.84615384615385
AUUAUGAAACUGUCCUGUCCUGGGAAUUCUCCAUUCCUAAGCCAGACAUGAUCACCCGUUUGGA
AGGGGAGGAGGAGUCUCAGAAUUCUGACGA
>random_seq_from_cds__NO_5824 RANDOM_LENGTH 81 SEQ_LENGTH 61
  GC_CONTENT 0.540983606557377 BASEPAIR 21 FREE_ENERGY
  -19.30 LEN_BP_RATIO 2.9047619047619
AAGGGUUCAAGGCAAGCUUGGGUUGGUGUCGAAGAAUGAUGAGAAGGUAUGACCUGUCUCUGAGG
CAUAAAGUGCCCGUGC
>random_seq_from_cds__NO_5826 RANDOM_LENGTH 63 SEQ_LENGTH 55
  GC_CONTENT 0.490909090909091 BASEPAIR 19 FREE_ENERGY
  -15.40 LEN_BP_RATIO 2.89473684210526
CGCAUGACUAUGAGGUAGCUCAGAUUGGGGAAUGCAGAUGAGACGCCCAUUUGUUUAGAGGUGC
>random_seq_from_cds__NO_5830 RANDOM_LENGTH 77 SEQ_LENGTH 61
  GC_CONTENT 0.60655737704918 BASEPAIR 20 FREE_ENERGY
  -17.60 LEN_BP_RATIO 3.05
GACUGAAGACUUGAUGCAGGACUGGUUGGAAGUGGUGUGGAGACGGAGGACAGGAGCAGUGCCCA
AGCAGCGAGGGA
>random_seq_from_cds__NO_5847 RANDOM_LENGTH 71 SEQ_LENGTH 59
  GC_CONTENT 0.694915254237288 BASEPAIR 19 FREE_ENERGY
  -22.80 LEN_BP_RATIO 3.10526315789474
CCGGAGGUCUGCUUCUCGGGGACGUGGCUCCCAACUUUGAGGCCAAUACCACCGUCGGCCGCAUC
CGUUUC
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>random_seq_from_cds__NO_5848 RANDOM_LENGTH 67 SEQ_LENGTH 50
GC_CONTENT 0.6 BASEPAIR 19 FREE_ENERGY -18.29 LEN_BP_RATIO
2.63157894736842
CACGACUUUCUGGGAGACUCGAUGGGGCAUUCUCUUCUCCACCCUCGGGACUUUACCCAGUGU
GC

>random_seq_from_cds__NO_5851 RANDOM_LENGTH 72 SEQ_LENGTH 49
GC_CONTENT 0.489795918367347 BASEPAIR 19 FREE_ENERGY
-17.40 LEN_BP_RATIO 2.57894736842105
AGCAGAGAAGGAUGAAAAGGGCAUGCCUGUGACAGCUCGUGUGGGUGUUUGUUUUUGGUCCUGAU
AAGAAGC

>random_seq_from_cds__NO_5865 RANDOM_LENGTH 88 SEQ_LENGTH 67
GC_CONTENT 0.597014925373134 BASEPAIR 22 FREE_ENERGY
-24.60 LEN_BP_RATIO 3.04545454545455
GACAGUUA AUGAAUGGGAGCUUCUCCAUGGACGGGACAGGACAAUCCUAUCAGGACUUGAGGGAU
GGGAGCCCCUAUGGAAUCCCCCA

>random_seq_from_cds__NO_5866 RANDOM_LENGTH 87 SEQ_LENGTH 65
GC_CONTENT 0.553846153846154 BASEPAIR 23 FREE_ENERGY
-19.90 LEN_BP_RATIO 2.82608695652174
GUCUCCAUCCUCCAUAUCGUCCUGCCAUCCACGCUCUUUGCUCAAUGGGCUGGAUJACACGG
UGGACAGUAAUUUGGGCAUCAU

>random_seq_from_cds__NO_5871 RANDOM_LENGTH 87 SEQ_LENGTH 79
GC_CONTENT 0.455696202531646 BASEPAIR 22 FREE_ENERGY
-17.04 LEN_BP_RATIO 3.59090909090909
UAUAUCAUUAGCUUUAAAAGAGAUGAGCACCUUCAAGACAAUGCUGCCUGCCCGGUCCUUCACU
GCCUGACUCUUGGUGUUGAUAG

>random_seq_from_cds__NO_5873 RANDOM_LENGTH 88 SEQ_LENGTH 69
GC_CONTENT 0.550724637681159 BASEPAIR 21 FREE_ENERGY
-17.20 LEN_BP_RATIO 3.28571428571429
AUCUUCUUCGUCCACGAACUUGUUCUGUCAUAUUCAUCCACGUCCACCUUCCGGAAGCGGGCCG
ACGACACUGUGUUCUUCGACAU

>random_seq_from_cds__NO_5874 RANDOM_LENGTH 75 SEQ_LENGTH 66
GC_CONTENT 0.636363636363636 BASEPAIR 23 FREE_ENERGY
-21.70 LEN_BP_RATIO 2.8695652173913
UCAGUGGGUCGGAGAGGCAUCCUCCAAGCCCAGCAGCUCUCUGACGAGUCUCUCUCCAAACUGCG
CCCGGCUGUA

>random_seq_from_cds__NO_5879 RANDOM_LENGTH 81 SEQ_LENGTH 67
GC_CONTENT 0.626865671641791 BASEPAIR 23 FREE_ENERGY
-22.60 LEN_BP_RATIO 2.91304347826087
CAUGGACAGUGGGAGGCCGGUGCAGUCACUCUCCGCGCGGAGCAAGCCGCAGCAGUAAAUCC
CCUUGCUUCUCAAACU

>random_seq_from_cds__NO_5889 RANDOM_LENGTH 68 SEQ_LENGTH 51
GC_CONTENT 0.745098039215686 BASEPAIR 19 FREE_ENERGY
-25.20 LEN_BP_RATIO 2.68421052631579
AUGGAUUAUAGGGCGGCCGAGGCGUCGACUCCAUCCACAGCUGUCGCGUGCCUCUGGCCCAAGGAG

CUC

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>random_seq_from_cds__NO_5926 RANDOM_LENGTH 82 SEQ_LENGTH 68
  GC_CONTENT 0.441176470588235 BASEPAIR 23 FREE_ENERGY
-15.30 LEN_BP_RATIO 2.95652173913043
AGAUUAUCACAGAAACCACUGGUAGAGAGAACACUAUAUGAAGCCUCCUCUGAAGGGAACUCUUCUG
AUGAUUCUGAAGAUGAG
>random_seq_from_cds__NO_5940 RANDOM_LENGTH 77 SEQ_LENGTH 60
  GC_CONTENT 0.433333333333333 BASEPAIR 20 FREE_ENERGY
-15.60 LEN_BP_RATIO 3
CUGUGAUGCAUCCAUCUGGUGAUAGUGACACAACGAUGUUAGAAUCUGAAUGUCAAGCUCCUGUA
CAGAAGGGUAU
>random_seq_from_cds__NO_5948 RANDOM_LENGTH 67 SEQ_LENGTH 57
  GC_CONTENT 0.87719298245614 BASEPAIR 25 FREE_ENERGY
-42.00 LEN_BP_RATIO 2.28
GCCGCGCCGCCGCCGUCGCGCCGCCACGCCGAGGCCAGGCGGCCGCGCGGCAGGG
AA
>random_seq_from_cds__NO_5949 RANDOM_LENGTH 100 SEQ_LENGTH 91
  GC_CONTENT 0.538461538461538 BASEPAIR 26 FREE_ENERGY
-26.60 LEN_BP_RATIO 3.5
CUGGCGCUGAAGACCCUGGGGACAGAUGGCCUUUUUCUCUUUCCUCCUUGGACACUGACGGGGA
UAUGUACAUCAGCCUGAGGAGUCAAACCCAUG
>random_seq_from_cds__NO_5950 RANDOM_LENGTH 84 SEQ_LENGTH 71
  GC_CONTENT 0.549295774647887 BASEPAIR 27 FREE_ENERGY
-25.20 LEN_BP_RATIO 2.62962962962963
CUGAGAAGCUAACAGGGGUCUUGUUCUGUCACCCAGACUGGAGUGCAGUGGUGCAGUCACAGCUC
ACUGCAGCCUCAACUCCCC
>random_seq_from_cds__NO_5978 RANDOM_LENGTH 84 SEQ_LENGTH 62
  GC_CONTENT 0.451612903225806 BASEPAIR 21 FREE_ENERGY
-16.30 LEN_BP_RATIO 2.95238095238095
CACUCUUUGUAACUUGGAAACUCAGGAGCCUUUGGAAAGUACUGCUGCAGUUUGCUCCAAGCCUC
UUUAGAAACAAGCCUUCUU
>random_seq_from_cds__NO_5992 RANDOM_LENGTH 73 SEQ_LENGTH 68
  GC_CONTENT 0.441176470588235 BASEPAIR 26 FREE_ENERGY
-24.60 LEN_BP_RATIO 2.61538461538462
AGCUGCAAGUUCAGAGUGCAAGGAAGGCUAAGAAGUCGAAUCUUUCUUGUUGCAUUCUGUUUGCU
UUGACAGU
>random_seq_from_cds__NO_6016 RANDOM_LENGTH 106 SEQ_LENGTH 70
  GC_CONTENT 0.557142857142857 BASEPAIR 22 FREE_ENERGY
-26.14 LEN_BP_RATIO 3.18181818181818
AUUUUGUAUUUUUCAUCAAUAAAAGAACUUGAGUUUGCCAAUCAUAGGGCGGUAUAUUCUGUGGAG
AUCCUUCAGGGCUGCCCCCAGUGUGAGCUCUGAGGCUUCC
>random_seq_from_cds__NO_6028 RANDOM_LENGTH 81 SEQ_LENGTH 50
  GC_CONTENT 0.62 BASEPAIR 19 FREE_ENERGY -21.40
  LEN_BP_RATIO 2.63157894736842
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UCCACUGCAGCCCUUCUACCGCUGGAGGACGUGGGUCCCUCCUGGGGGUUGUUAUGAUCCCUGCU
CUCCAUGAUGUCGUCG

>random_seq_from_cds__NO_6031 RANDOM_LENGTH 93 SEQ_LENGTH 86
GC_CONTENT 0.383720930232558 BASEPAIR 33 FREE_ENERGY
-23.70 LEN_BP_RATIO 2.60606060606061

CUUCAAAUGAACAACAAGAGCUUUUCUGUCAGAAGUUGCAGCAGUGUUGUAUACUGUUUGAUUUC
AUGGACUCUGUUUCAGACUUGAAGAGCA

>random_seq_from_cds__NO_6042 RANDOM_LENGTH 96 SEQ_LENGTH 78
GC_CONTENT 0.320512820512821 BASEPAIR 25 FREE_ENERGY
-18.36 LEN_BP_RATIO 3.12

UUGUACUUCUGGAAUAACGAAUAUAUUCUAGUUUGAUUGAGGAGAACAUAUGAUAAAAUUCUGCC
AAUUAUGUUUGCCAGUUUGUACAAAAUUUCC

>random_seq_from_cds__NO_6050 RANDOM_LENGTH 110 SEQ_LENGTH 92
GC_CONTENT 0.717391304347826 BASEPAIR 33 FREE_ENERGY
-51.90 LEN_BP_RATIO 2.78787878787879

UGCCCAUGGGGGCCCUUGCCUGGGUACCCAGGGGGCCAGGAGGUCCUGGAGGACCCAUCAU
GCCACCGCACCCAGGGCUUCCCGCUUGGCACUCACGGCGACCUC

>random_seq_from_cds__NO_6059 RANDOM_LENGTH 79 SEQ_LENGTH 54
GC_CONTENT 0.722222222222222 BASEPAIR 19 FREE_ENERGY
-25.60 LEN_BP_RATIO 2.84210526315789

UCCCAUCCUUGCCGUUGAUGCCUGGGGGGCCCGUUGCUCUUUCGGGCCUGUGAUCCCUUGGGG
UCCACGAAUACCG

>random_seq_from_cds__NO_6062 RANDOM_LENGTH 70 SEQ_LENGTH 51
GC_CONTENT 0.686274509803922 BASEPAIR 20 FREE_ENERGY
-29.90 LEN_BP_RATIO 2.55

CCCCGGUGGUCCAGGAUGCCUUGCUCUCCAGAGGCACCCACAUCUCCCUUGGGACCCCGGCUUC
CCUG

>random_seq_from_cds__NO_6065 RANDOM_LENGTH 78 SEQ_LENGTH 72
GC_CONTENT 0.666666666666667 BASEPAIR 24 FREE_ENERGY
-36.90 LEN_BP_RATIO 3

UGGGGGCCCCGAUGGUCCAUCUGGUCCAGGGUCCCCCUUGGGGCCUCGGAUCCAAUCUCACCA
GGGAGGCCAACAG

>random_seq_from_cds__NO_6070 RANDOM_LENGTH 82 SEQ_LENGTH 63
GC_CONTENT 0.666666666666667 BASEPAIR 21 FREE_ENERGY
-28.50 LEN_BP_RATIO 3

UCCCGGUGGACCUCUCAAUCUGCGCCAGAGCGAGCACUACCACCUGGAGGAGAACAAGGAGGCUG
CGGGGGGAGGCCGUAGC

>random_seq_from_cds__NO_6076 RANDOM_LENGTH 84 SEQ_LENGTH 64
GC_CONTENT 0.4375 BASEPAIR 20 FREE_ENERGY -18.40
LEN_BP_RATIO 3.2

AGAUGUGAAACCUGGCUUCAACAUCAGCAUUCUGAAAAUAUUAUCACCAUGAUGUCUGAGAGU
GUUCGGAUGAUGCUGGAAC

>random_seq_from_cds__NO_6078 RANDOM_LENGTH 88 SEQ_LENGTH 58
GC_CONTENT 0.586206896551724 BASEPAIR 19 FREE_ENERGY

-20.60 LEN_BP_RATIO 3.05263157894737
AAGUGUGCCUUCAGCCACCAGGGCAGCAUCCAGUUGGACAGGUACCCUGGACUCAUACCUGAAAAG
CAGUGUUCAACCUUAGCAAAAUC
>random_seq_from_cds__NO_6099 RANDOM_LENGTH 75 SEQ_LENGTH 59
GC_CONTENT 0.559322033898305 BASEPAIR 23 FREE_ENERGY
-32.10 LEN_BP_RATIO 2.56521739130435
GCCAGAGGCUGGAAUGUGGACAGUGAAGGACCUCAAGCAGUGGAAGGCACUCUGUUCGCAUUACU
GGCCUCAGUA
>random_seq_from_cds__NO_6108 RANDOM_LENGTH 70 SEQ_LENGTH 61
GC_CONTENT 0.475409836065574 BASEPAIR 22 FREE_ENERGY
-15.10 LEN_BP_RATIO 2.77272727272727
AAUGUUACAGUCACUCCUGGAGAGAGAGCAGUUUUAACAUGUCUCAUCAUCAGUGCGGUGGAUUA
CAAUC
>random_seq_from_cds__NO_6149 RANDOM_LENGTH 84 SEQ_LENGTH 67
GC_CONTENT 0.432835820895522 BASEPAIR 22 FREE_ENERGY
-16.90 LEN_BP_RATIO 3.04545454545455
GAGAAAAGGAAAUCAAUAUGAAGUUGAUGUCUUGGGUGCCACCAGCUAUAAGAAGGAGGAGAUGA
AACAUUCUACUUCUUGUG
>random_seq_from_cds__NO_6155 RANDOM_LENGTH 86 SEQ_LENGTH 62
GC_CONTENT 0.516129032258065 BASEPAIR 22 FREE_ENERGY
-18.00 LEN_BP_RATIO 2.81818181818182
AUGGAACCACCUAGUCUGGAAGAUGCUGGAAAAAUGCUGAAUGAGACUGUGUUGGUGAGCAACCC
UGUACAGCUGGAGUGUAAGGC
>random_seq_from_cds__NO_6170 RANDOM_LENGTH 87 SEQ_LENGTH 78
GC_CONTENT 0.423076923076923 BASEPAIR 26 FREE_ENERGY
-18.40 LEN_BP_RATIO 3
UCAUGUAUCUGACACAGGCCGUUAUGUGUGUGUUGCUGUGAAUGUAGCAGGAAUGACUGACAAAA
AAUAUGACUUAAGUGUCCAUGG
>random_seq_from_cds__NO_6173 RANDOM_LENGTH 84 SEQ_LENGTH 56
GC_CONTENT 0.482142857142857 BASEPAIR 22 FREE_ENERGY
-18.90 LEN_BP_RATIO 2.54545454545455
CUACGGCUGAUGCAGACCACAAUGGAAGAUGCUGGCCAAUAUACUUGCGUUGUAAGGAAUGCAGC
UGGUGAAGAAAGAAAAAUC
>random_seq_from_cds__NO_6177 RANDOM_LENGTH 96 SEQ_LENGTH 77
GC_CONTENT 0.532467532467532 BASEPAIR 27 FREE_ENERGY
-22.40 LEN_BP_RATIO 2.85185185185185
UGGCUUCCAGUCCAGCUGGCCACAAGAGCAGGAGCUUCAGUCUUAUGUAUUUGGUAUCUCCUAC
AAUUGCUGGUGUAGGUAGUGAUGGCAACCCU
>random_seq_from_cds__NO_6192 RANDOM_LENGTH 110 SEQ_LENGTH 82
GC_CONTENT 0.48780487804878 BASEPAIR 29 FREE_ENERGY
-26.20 LEN_BP_RATIO 2.82758620689655
UGGUGAACAAUUUCAUCUCUUGACCUGUGAGGUCUCUGGUUUUCCACCUCUGACCUCAGCUGG
CUCAAGAAUGAACAGCCCAUCAAAACUGAACACAAAUAUCUCAUU
>random_seq_from_cds__NO_6209 RANDOM_LENGTH 80 SEQ_LENGTH 60

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GC_CONTENT    0.65    BASEPAIR    22    FREE_ENERGY    -32.00
LEN_BP_RATIO  2.72727272727273
UACUGAUGGAACCCAGCUCCAGUAUGGCCUGGCUUAGAGAUGGCCAGCCUCUGGGGCUUGAUG
CCCAUCUGACAGUCA
>random_seq_from_cds__NO_6215    RANDOM_LENGTH 66    SEQ_LENGTH    55
GC_CONTENT    0.490909090909091    BASEPAIR    20    FREE_ENERGY
-17.60    LEN_BP_RATIO  2.75
AACUGAUGAGCCCCGGGAUAUCACUGUGUUACGGAACAGACAAGUGACAUUGGAAUGCAAGUCAG
A
>random_seq_from_cds__NO_6218    RANDOM_LENGTH 82    SEQ_LENGTH    64
GC_CONTENT    0.453125    BASEPAIR    19    FREE_ENERGY    -17.99
LEN_BP_RATIO  3.36842105263158
CUACAAGAGAAUUUAUUCUCACUGUAAAUGGUUCCUCCAAACAUAAGGGGGGCCCCCAGAGCCU
UGUAAUUCUUUAAAUA
>random_seq_from_cds__NO_6230    RANDOM_LENGTH 67    SEQ_LENGTH    48
GC_CONTENT    0.583333333333333    BASEPAIR    19    FREE_ENERGY
-21.80    LEN_BP_RATIO  2.52631578947368
CAUGCAGUUCUCCUAGUGGGCGGCUUACAGAUCUCCAGAGCUGUCCGAGAGGAUGCUGGCACUUA
CA
>random_seq_from_cds__NO_6231    RANDOM_LENGTH 90    SEQ_LENGTH    70
GC_CONTENT    0.585714285714286    BASEPAIR    24    FREE_ENERGY
-28.44    LEN_BP_RATIO  2.91666666666667
UGUGUGUGGCCAGAACCCGGCUGGUACAGCCUUGGGCAAAAUCAAGUAAAUGUCCAAGGUUCC
UCCAGUCAUUAGCCCUCAUCUAAAG
>random_seq_from_cds__NO_6232    RANDOM_LENGTH 84    SEQ_LENGTH    75
GC_CONTENT    0.493333333333333    BASEPAIR    28    FREE_ENERGY
-18.10    LEN_BP_RATIO  2.67857142857143
GAAUAUGUUUAUUGCUGUGGACAAGCCCAUCACGUUAUCCUGUGAAGCAGAUGGCCUCCCUCCGCC
UGACAUAUACAUGGCAUAAA
>random_seq_from_cds__NO_6237    RANDOM_LENGTH 87    SEQ_LENGTH    74
GC_CONTENT    0.527027027027027    BASEPAIR    25    FREE_ENERGY
-26.30    LEN_BP_RATIO  2.96
AUGUUGUGGGCUGGAGGAUUCUGGCUUCUAUACCUGUGUUGCUAACAAUGCUGCAGGUGAAGAUAC
ACACACUGUCAGCCUGACUGUG
>random_seq_from_cds__NO_6249    RANDOM_LENGTH 85    SEQ_LENGTH    62
GC_CONTENT    0.580645161290323    BASEPAIR    24    FREE_ENERGY
-25.10    LEN_BP_RATIO  2.58333333333333
AGCCUUGUCCAGGUGGAUGGUAGCUGGUCGGAAUGGAGUCUUUGGGAAGAAUGCACAAGGAGCUG
UGGACGCGGCAACCAAACCA
>random_seq_from_cds__NO_6262    RANDOM_LENGTH 90    SEQ_LENGTH    85
GC_CONTENT    0.376470588235294    BASEPAIR    28    FREE_ENERGY
-16.42    LEN_BP_RATIO  3.03571428571429
GGUUCAGCAAUGAGAAAGAUAGUUUCUAUUCUAAAUCCCAUUUAUUGGACAACAGCAAAGGAAAU
AGGAGAAGCAGUCAUUGGCUUACC
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>random_seq_from_cds__NO_6277 RANDOM_LENGTH 84 SEQ_LENGTH 65
  GC_CONTENT 0.507692307692308 BASEPAIR 24 FREE_ENERGY
  -20.40 LEN_BP_RATIO 2.708333333333333
CUUCAAGUGUAUCUGUCCACCAGGACAACAUUUUUAUAGGGGACGGGAAAUCUUGCGCUGGAUUGG
AGAGGCUGCCAAAUUAUGG
>random_seq_from_cds__NO_6283 RANDOM_LENGTH 67 SEQ_LENGTH 53
  GC_CONTENT 0.528301886792453 BASEPAIR 19 FREE_ENERGY
  -15.30 LEN_BP_RATIO 2.78947368421053
GGGUUCUGCCUCAAGAACUGUCCACCCAAUGAUUUGGAAUGUGCCUUGAGCCCAUAUGCCUUGG
AA
>random_seq_from_cds__NO_6284 RANDOM_LENGTH 84 SEQ_LENGTH 72
  GC_CONTENT 0.5 BASEPAIR 22 FREE_ENERGY -17.80 LEN_BP_RATIO
  3.27272727272727
UACAAACUCGUCUCCCUCCCAUUGGAAUAGCCACCAAUCAAGAUUUAAUCCGGCUGGUUGCAUA
CACACAGGAUGGAGUGAUG
>random_seq_from_cds__NO_6285 RANDOM_LENGTH 88 SEQ_LENGTH 76
  GC_CONTENT 0.473684210526316 BASEPAIR 28 FREE_ENERGY
  -31.60 LEN_BP_RATIO 2.71428571428571
CAUCCAGGACAACUUUCCUCAUGGUAGAUGAGGAACAGACUGUCCUUUUGCCUUGAGGGAUGA
AAACCUGAAAGGAGUGGUGUAUA
>random_seq_from_cds__NO_6295 RANDOM_LENGTH 79 SEQ_LENGTH 67
  GC_CONTENT 0.626865671641791 BASEPAIR 24 FREE_ENERGY
  -28.70 LEN_BP_RATIO 2.791666666666667
CUGUGGGCUGCUCCAGGUCUGAGGUCUCAGGGGCUGGGCUCUUGGCUUCAUCCUUGGGACACACA
AGGGACUCCAGCAG
>random_seq_from_cds__NO_6301 RANDOM_LENGTH 74 SEQ_LENGTH 66
  GC_CONTENT 0.621212121212121 BASEPAIR 22 FREE_ENERGY
  -28.20 LEN_BP_RATIO 3
CCCAUAGGAGGGAGGCCAGCUGUCCGGAGUGGCUUGAGGGGCAUAGGAGGAAGGCUGGACCUUA
GAGAUGGCC
>random_seq_from_cds__NO_6311 RANDOM_LENGTH 87 SEQ_LENGTH 75
  GC_CONTENT 0.64 BASEPAIR 28 FREE_ENERGY -37.40
  LEN_BP_RATIO 2.67857142857143
GGGUAGCUGUGCUGCAGAGAGCUGAACCUGUCAGUCAUCUUGGUGGCUGACCGGCCUCCGCACU
GACAGCGGUGACCCUGGCAUAG
>random_seq_from_cds__NO_6315 RANDOM_LENGTH 67 SEQ_LENGTH 59
  GC_CONTENT 0.711864406779661 BASEPAIR 22 FREE_ENERGY
  -25.90 LEN_BP_RATIO 2.68181818181818
CCGUCAGCUCCAGGCGGUCCUGGUGGCCGUCGCCACUCGUCGUCGUCGUCGUCGUCGUCUCCUGGGU
CC
>random_seq_from_cds__NO_6320 RANDOM_LENGTH 86 SEQ_LENGTH 81
  GC_CONTENT 0.679012345679012 BASEPAIR 27 FREE_ENERGY
  -32.42 LEN_BP_RATIO 3
CUGUCUUUGCCCAGAGCAUCCCGUGGAACCUGGAGCGGAUUAACCCUCCACGGUACCGGGCGGAU
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GAAUACCAGCCCCCGGACGG
>random_seq_from_cds__NO_6322 RANDOM_LENGTH 83 SEQ_LENGTH 78
  GC_CONTENT 0.602564102564103 BASEPAIR 28 FREE_ENERGY
  -26.50 LEN_BP_RATIO 2.78571428571429
CAUGGUCACCGACUUCGAGAAUGUGCCCGAGGAGGACGGGACCCGCUUCCACAGACAGGGCCAGC
AAGUGUGACAGUCAUGGC
>random_seq_from_cds__NO_6356 RANDOM_LENGTH 84 SEQ_LENGTH 66
  GC_CONTENT 0.651515151515151 BASEPAIR 22 FREE_ENERGY
  -24.20 LEN_BP_RATIO 3
GCCCAUGCUGACAGCCUCACCCAGGAUGCUGCUCCUUCUUCUCCUCGAAGCCUCCAGGCCUGG
GCACAGAGACACCGCUGUC
>random_seq_from_cds__NO_6372 RANDOM_LENGTH 70 SEQ_LENGTH 62
  GC_CONTENT 0.645161290322581 BASEPAIR 21 FREE_ENERGY
  -25.50 LEN_BP_RATIO 2.95238095238095
AAGCCCUAGGAGGGGAAGGCUGGGAGAAGCUAUCAUUGGUGCCCUCCUCUGCCC GCCUGCAUUAU
GGCAC
>random_seq_from_cds__NO_6394 RANDOM_LENGTH 86 SEQ_LENGTH 67
  GC_CONTENT 0.388059701492537 BASEPAIR 26 FREE_ENERGY
  -16.90 LEN_BP_RATIO 2.57692307692308
UUCCCGGUUGAUCGUGGAUUAUUUGAGGGAUAAAGUAGCCAAUUAUUUGGUGCAGCUCAAUGUCU
UUCUGAAGAUUAAGGAUUAUU
>random_seq_from_cds__NO_6405 RANDOM_LENGTH 73 SEQ_LENGTH 60
  GC_CONTENT 0.616666666666667 BASEPAIR 19 FREE_ENERGY
  -24.20 LEN_BP_RATIO 3.15789473684211
GUGGGAAGGAGCACUCCCCUCACAGUAAUAGGCCGAGUAGCCUUGGGGAGCGAUGACCCAGUCC
CAGCCAGC
>random_seq_from_cds__NO_6410 RANDOM_LENGTH 110 SEQ_LENGTH 92
  GC_CONTENT 0.608695652173913 BASEPAIR 27 FREE_ENERGY
  -30.34 LEN_BP_RATIO 3.40740740740741
GUGACAUC CAGCACCAGCCAGCCUCGUCUCCAGCUCGGAGCGUCUGAAGAUC CAAAAAGAACAA
GUCAGACUCCCCUGUUGGACUGCUCCUGGACCACCU GGAACAUGC
>random_seq_from_cds__NO_6415 RANDOM_LENGTH 84 SEQ_LENGTH 76
  GC_CONTENT 0.789473684210526 BASEPAIR 27 FREE_ENERGY
  -40.70 LEN_BP_RATIO 2.81481481481481
CGAGCACCGCCAGGAUCUCGCGCUGCAGUCCCGGCGCUCGCGCGCGCCAGACGUCGUGGGGA
CAGCCGGGCGGGGUCGCA
>random_seq_from_cds__NO_6437 RANDOM_LENGTH 97 SEQ_LENGTH 76
  GC_CONTENT 0.565789473684211 BASEPAIR 28 FREE_ENERGY
  -29.00 LEN_BP_RATIO 2.71428571428571
AUGUUGACUAUAUAUCCUGUUGAAACGUGGCUUCCUCCAGUCCUGAUCGACGGAACUCUGCGAGG
AUGGCUCUCAGGAAGCUCUGUCCAGAACAGA
>random_seq_from_cds__NO_6444 RANDOM_LENGTH 77 SEQ_LENGTH 60
  GC_CONTENT 0.533333333333333 BASEPAIR 21 FREE_ENERGY
  -16.41 LEN_BP_RATIO 2.85714285714286
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UUUGGCCUGUUAGCUUCCUGCAAGAUUUGCACAUAGACUUGGUGGGGCUCGUCAGCUUCAUGCC
AUUGACCUCAAU

>random_seq_from_cds__NO_6451 RANDOM_LENGTH 110 SEQ_LENGTH 91
GC_CONTENT 0.516483516483517 BASEPAIR 29 FREE_ENERGY
-29.60 LEN_BP_RATIO 3.13793103448276

CUUUUACUAUUACCUAGAAACCCGAAGCUGCUGCCUAAUCCGAUUCAUAGUCAAGACAGAACUCU
UUCUGCGGAUACGAUGGGGAGUAGAGGUCGCUUCAUUCUGGGCUU

>random_seq_from_cds__NO_6454 RANDOM_LENGTH 72 SEQ_LENGTH 62
GC_CONTENT 0.483870967741936 BASEPAIR 23 FREE_ENERGY
-20.00 LEN_BP_RATIO 2.69565217391304

UGAAGCCUUCUUGUCAUCCUCAGUAUAAGAGAGUCCAGUCUCUCUGGUUUUCUCUGGGGCUUUA
GAGCUGG

>random_seq_from_cds__NO_6457 RANDOM_LENGTH 81 SEQ_LENGTH 70
GC_CONTENT 0.571428571428571 BASEPAIR 24 FREE_ENERGY
-28.90 LEN_BP_RATIO 2.91666666666667

GGAGGCGGAGUGCCUUGAUUCAAUCCUUUUGGCCACAUGUUCUGCUGGGGUCCAAGAAGGGCUCU
CUGCACUCUUACUCUU

>random_seq_from_cds__NO_6458 RANDOM_LENGTH 87 SEQ_LENGTH 63
GC_CONTENT 0.555555555555556 BASEPAIR 20 FREE_ENERGY
-20.00 LEN_BP_RATIO 3.15

GGCUCUCACGGGUUUCUGGCACUUGGCUGCACUCUCUUGUGGUUUUAUUAACUCCGCAAUAGUU
CUGAGGAAAGUGGCCUGAAUUU

>random_seq_from_cds__NO_6468 RANDOM_LENGTH 85 SEQ_LENGTH 71
GC_CONTENT 0.647887323943662 BASEPAIR 23 FREE_ENERGY
-18.90 LEN_BP_RATIO 3.08695652173913

GGCCCGUUCGAGGAAUUGUAAUAGCUCCCCAGGAAGACCAGGAUCCAGAAGCCGUUGCCCGCGG
ACAGCUCGCCCUUCUCCUUC

>random_seq_from_cds__NO_6469 RANDOM_LENGTH 85 SEQ_LENGTH 53
GC_CONTENT 0.716981132075472 BASEPAIR 21 FREE_ENERGY
-26.70 LEN_BP_RATIO 2.52380952380952

CUGUUCACGUUCUCCUGCACACCCCCAGGGCCAGCUGGUGCGGUCCCCAACCUCCACCUCCCA
GUAGUGGCGGCCUGAGGUGA

>random_seq_from_cds__NO_6477 RANDOM_LENGTH 77 SEQ_LENGTH 72
GC_CONTENT 0.75 BASEPAIR 23 FREE_ENERGY -32.40
LEN_BP_RATIO 3.1304347826087

GCUCCCAGAGCGCUCGCAGGCCGCACACAGGAGGCGCAGCUCGUCGCCACAGAAGGCGGCCAGU
GGCUCGCGGUGC

>random_seq_from_cds__NO_6495 RANDOM_LENGTH 83 SEQ_LENGTH 72
GC_CONTENT 0.625 BASEPAIR 22 FREE_ENERGY -25.90
LEN_BP_RATIO 3.27272727272727

CUGAGGAGCUCAUCUACCCAGACCGCAGGCUGGAGACCAAGUAUCCGGUGUGUCCGAUGGCAAG
AGGUUCCUGGGCUCUGGA

>random_seq_from_cds__NO_6500 RANDOM_LENGTH 86 SEQ_LENGTH 78
GC_CONTENT 0.615384615384615 BASEPAIR 28 FREE_ENERGY

-24.70 LEN_BP_RATIO 2.78571428571429
GGCAUUGGGGAUGAAGCUCUGCCCACGGUCCUGGUCGGCGUGUUAUCGAACAGCCCACGCCGU
UUGUGUCCUGUUCUCCAGC
>random_seq_from_cds__NO_6507 RANDOM_LENGTH 72 SEQ_LENGTH 58
GC_CONTENT 0.655172413793103 BASEPAIR 20 FREE_ENERGY
-20.40 LEN_BP_RATIO 2.9
CCCUGCGGGGUGAGCUGCAGUCCUCAGAUCUCUCCACCACAGCAAGCUGGACCCCGACAUGGCC
UUCUGUG
>random_seq_from_cds__NO_6518 RANDOM_LENGTH 83 SEQ_LENGTH 59
GC_CONTENT 0.457627118644068 BASEPAIR 21 FREE_ENERGY
-23.12 LEN_BP_RATIO 2.80952380952381
AGUGACCUGGAUUAUUCUGUUGUAGCCCAGCAGGAAUAUGGGCACCUCUUGCUGUAGCGACAACA
GUAAAACUGCCACUCCCG
>random_seq_from_cds__NO_6519 RANDOM_LENGTH 110 SEQ_LENGTH 81
GC_CONTENT 0.592592592592593 BASEPAIR 27 FREE_ENERGY
-25.10 LEN_BP_RATIO 3
AUCCAGCACUGACUCGAAGUAGCGGCUCUGGAAUCCUGCCACCAGCCCAUUGUUGGAGCACGUCU
GGUACCCAUUCCAUGCCAGCCCUGUUGAUCUCCUCCACCAGCAC
>random_seq_from_cds__NO_6520 RANDOM_LENGTH 81 SEQ_LENGTH 75
GC_CONTENT 0.573333333333333 BASEPAIR 24 FREE_ENERGY
-22.80 LEN_BP_RATIO 3.125
UCCGUGGGUUCCCCAGGCUCUGUGGCGUGGGCAUGCAGGCGUAGUCCAUUGUCUGUCAGAACC
UCCUUCUUGCUGAAG
>random_seq_from_cds__NO_6531 RANDOM_LENGTH 68 SEQ_LENGTH 48
GC_CONTENT 0.458333333333333 BASEPAIR 19 FREE_ENERGY
-17.40 LEN_BP_RATIO 2.52631578947368
UUUUAAUUGGUGACGGAGCUGGUUCAAAGUUGCAAUGGGAGCUUUUGAUAAAACCAGACCUGUA
GGU
>random_seq_from_cds__NO_6540 RANDOM_LENGTH 81 SEQ_LENGTH 63
GC_CONTENT 0.666666666666667 BASEPAIR 24 FREE_ENERGY
-28.80 LEN_BP_RATIO 2.625
CUGCUGCACACGGAUGGUCCUUGGCCAGCUCCUGGCCACUACAUUGCCAUCAUGGGCUGCCG
CCCGCCAUCAGUGUUC
>random_seq_from_cds__NO_6541 RANDOM_LENGTH 87 SEQ_LENGTH 77
GC_CONTENT 0.688311688311688 BASEPAIR 20 FREE_ENERGY
-31.70 LEN_BP_RATIO 3.85
UUACCUGGUAGGCUCCACAUGGCCGAGUUUCUGCAGACUGGUGGUGACCCUGAGUGGCUGCUGG
GCCUCCACCGGGCCCCCGAGAA
>random_seq_from_cds__NO_6543 RANDOM_LENGTH 75 SEQ_LENGTH 62
GC_CONTENT 0.661290322580645 BASEPAIR 24 FREE_ENERGY
-26.90 LEN_BP_RATIO 2.583333333333333
CAGGGCCUUGCUGAAGACCGGCGAGCACACUUGGUCCUGGCCGAGCUCAUUCAGGCUCUGGUCC
UGCUCACCCA
>random_seq_from_cds__NO_6548 RANDOM_LENGTH 67 SEQ_LENGTH 53

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GC_CONTENT    0.584905660377358    BASEPAIR    20    FREE_ENERGY
-17.80    LEN_BP_RATIO    2.65
UCGGAUAUGAGGACUUCACUCGGAGAGGGGCUCAGGCACCCCUACCUUCCGGGCCAGGGAUUA
UA
>random_seq_from_cds__NO_6549    RANDOM_LENGTH    89    SEQ_LENGTH    80
GC_CONTENT    0.6    BASEPAIR    32    FREE_ENERGY    -39.30    LEN_BP_RATIO
2.5
CCUGGGAAGACCAUGGCUACUCGCUGAUCCAGCGGCUUUACCCUGAGGGUGGGCAGCUGCUGGAU
GAGAAGUUCAGGCAGCCUAUAGC
>random_seq_from_cds__NO_6557    RANDOM_LENGTH    87    SEQ_LENGTH    51
GC_CONTENT    0.529411764705882    BASEPAIR    19    FREE_ENERGY
-17.20    LEN_BP_RATIO    2.68421052631579
CUUGACAGAUUCUGAUCUCCCGUAUGGCCGUGUGGUAUCUCUCCAGCUUCUCUCCCAACUUCACU
GUGUUGUCUGGGAGCUUCAUGC
>random_seq_from_cds__NO_6558    RANDOM_LENGTH    110    SEQ_LENGTH    103
GC_CONTENT    0.553398058252427    BASEPAIR    38    FREE_ENERGY
-40.80    LEN_BP_RATIO    2.71052631578947
UGGCACCUGCGAGUUAGGGUUGUUUCCGAGUUUUCUUUCUUGGGUUUCAUCCCGAAAGGAGAUGG
UCCUGGGGCGUGGAGCGUUUGAGGGAGCUGCUGUAGGUUCGCUGUG
>random_seq_from_cds__NO_6559    RANDOM_LENGTH    109    SEQ_LENGTH    92
GC_CONTENT    0.66304347826087    BASEPAIR    28    FREE_ENERGY
-39.65    LEN_BP_RATIO    3.28571428571429
UGGGUGAGGACAUUUCUGCCUCUCCUCCUUGCUGGGGAUUUCACCCUGGAGUGUGACGGGUGG
GAGGCGGGAGGCCACAGUCGGAGGGUCUGAAGCCCCCUGCUUUG
>random_seq_from_cds__NO_6568    RANDOM_LENGTH    90    SEQ_LENGTH    78
GC_CONTENT    0.628205128205128    BASEPAIR    28    FREE_ENERGY
-38.10    LEN_BP_RATIO    2.78571428571429
CUGCCUCCGCUCUGCCGUGUUCUGAGGAUGCUCUGGAUGUCCUCGUCCUCAUCUUUGGAGGCUG
GGGCAGUGGCUUGGGCACCUCUGC
>random_seq_from_cds__NO_6569    RANDOM_LENGTH    90    SEQ_LENGTH    85
GC_CONTENT    0.611764705882353    BASEPAIR    31    FREE_ENERGY
-35.10    LEN_BP_RATIO    2.74193548387097
UUUUUCCACGCUCGGUAGUCCUCUCAGAAGCAGAGGCCUGCCGGUCUCCAUCUGGCUGAGCCUG
GGAGCCUCAUCGUCCGUGGUGGAGC
>random_seq_from_cds__NO_6571    RANDOM_LENGTH    88    SEQ_LENGTH    75
GC_CONTENT    0.6133333333333333    BASEPAIR    28    FREE_ENERGY
-33.00    LEN_BP_RATIO    2.67857142857143
CCUGCUGACAGCCAUAUGGCGGCGGAUUUGAAGCCUCGGGAGCCUAGCAGCAGUGGCGACUG
CUAUGCCGGCUGAGCAUGUGGCC
>random_seq_from_cds__NO_6576    RANDOM_LENGTH    86    SEQ_LENGTH    74
GC_CONTENT    0.378378378378378    BASEPAIR    22    FREE_ENERGY
-18.55    LEN_BP_RATIO    3.36363636363636
GAUCUUGGCUCUACAAGAGAAAUUGCUGUACAGAUACAUCUGUUAUUACAGCCAUUGGAAUAA
AAAUGGAAGGCUUAGAGUGUC
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>random_seq_from_cds__NO_6595 RANDOM_LENGTH 81 SEQ_LENGTH 70
  GC_CONTENT 0.428571428571429 BASEPAIR 25 FREE_ENERGY
-18.80 LEN_BP_RATIO 2.8
UGGAUGAUCGUAUUUCUUUGGAACAACCACCAAUGGAAGUGACACCCCAAUCCAGAGAAUAU
CAAGAAUCACCUGGAA
>random_seq_from_cds__NO_6614 RANDOM_LENGTH 67 SEQ_LENGTH 58
  GC_CONTENT 0.620689655172414 BASEPAIR 20 FREE_ENERGY
-24.60 LEN_BP_RATIO 2.9
GCCAGAGCUGCGCGGUGAGGAAGACCAUCUCAGAUGGGGAUCCCCACAGUGUUCACCUGGUCCUU
GA
>random_seq_from_cds__NO_6615 RANDOM_LENGTH 90 SEQ_LENGTH 70
  GC_CONTENT 0.628571428571429 BASEPAIR 25 FREE_ENERGY
-26.00 LEN_BP_RATIO 2.8
GUCCCAGCAGGCUGUAGGCGAUGCGCUUCUGGUGGCCGGCAGCCGCACCCCAAUCCUCUUGAUG
UCGCUCGUUGGUCAUCUGCACCACC
>random_seq_from_cds__NO_6619 RANDOM_LENGTH 72 SEQ_LENGTH 52
  GC_CONTENT 0.711538461538462 BASEPAIR 21 FREE_ENERGY
-28.70 LEN_BP_RATIO 2.47619047619048
GGCGGCACGCUCCUGCUGCCAGCACUGCAUCAUGAGCUGGUAGAUGGCGGAGGGGCAGUCCAUG
GGUGUGG
>random_seq_from_cds__NO_6629 RANDOM_LENGTH 66 SEQ_LENGTH 58
  GC_CONTENT 0.672413793103448 BASEPAIR 21 FREE_ENERGY
-16.60 LEN_BP_RATIO 2.76190476190476
AAUACCCGCAAGUUGCCAGAUCUCCUCCGGGGCACAGCGUCUGGAAUUCGUGCACCUCUGCUGCCG
G
>random_seq_from_cds__NO_6632 RANDOM_LENGTH 67 SEQ_LENGTH 50
  GC_CONTENT 0.64 BASEPAIR 19 FREE_ENERGY -23.10
  LEN_BP_RATIO 2.63157894736842
GAGACGCUAAGCGAGGUGGUGCUGCGGCCUCCAGCCUCACCUUGGGGGCUCUCCUGUCUGGUUGA
UG
>random_seq_from_cds__NO_6642 RANDOM_LENGTH 84 SEQ_LENGTH 73
  GC_CONTENT 0.671232876712329 BASEPAIR 26 FREE_ENERGY
-35.40 LEN_BP_RATIO 2.80769230769231
CCUGGAAGGCCAGGUAGAAGCCUUUGCGGGUGAGCGGCCCCACGGAGCGCUCCUCCACGUUCAGC
UUCACGUGGCGUGCCUCGA
>random_seq_from_cds__NO_6657 RANDOM_LENGTH 75 SEQ_LENGTH 60
  GC_CONTENT 0.566666666666667 BASEPAIR 20 FREE_ENERGY
-23.90 LEN_BP_RATIO 3
AACUCCACGUUUUCUGCUACCUUGGAACCGAGGAGUCUCUUCUCCUUCUUCUUCUUCUUCUUCUUC
GAGCCCGACU
>random_seq_from_cds__NO_6663 RANDOM_LENGTH 86 SEQ_LENGTH 56
  GC_CONTENT 0.5 BASEPAIR 23 FREE_ENERGY -20.50 LEN_BP_RATIO
2.43478260869565
UGUCAAGAAUUUGGCCUGGGUGGACUCAGACCAGCUCUCCUCUAUCAGCAUUUUUGGUGUCUCCAG
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UGAUCAAAAAGAGAGUGGUUG
>random_seq_from_cds__NO_6666 RANDOM_LENGTH 72 SEQ_LENGTH 64
  GC_CONTENT 0.703125 BASEPAIR 20 FREE_ENERGY -20.70
  LEN_BP_RATIO 3.2
UGCAGCGUUCAGCCAGCUCCACCGUGCGCCGUGUGGAAGCCGCGGCCACAGCACAGCAGCUCACAG
CCGUCGA
>random_seq_from_cds__NO_6667 RANDOM_LENGTH 82 SEQ_LENGTH 78
  GC_CONTENT 0.6666666666666667 BASEPAIR 29 FREE_ENERGY
-36.20 LEN_BP_RATIO 2.68965517241379
UGGCCUUGGACGUCUUGUUGCAUGUGCGGCCCCUCGUGCCCAGCACGCCGUGCGCAUGUCCUGC
UCACAGAAGUCGGGGCU
>random_seq_from_cds__NO_6683 RANDOM_LENGTH 86 SEQ_LENGTH 67
  GC_CONTENT 0.552238805970149 BASEPAIR 24 FREE_ENERGY
-25.00 LEN_BP_RATIO 2.791666666666667
CUUUACCUGGUGACUGUUCUCCUUGGUCACUCGACGGGAAUCCUCCAGCUGAGUGAUGAUGGUC
UGCACACGGUCAUUCGCCGCC
>random_seq_from_cds__NO_6687 RANDOM_LENGTH 86 SEQ_LENGTH 80
  GC_CONTENT 0.6625 BASEPAIR 30 FREE_ENERGY -40.90
  LEN_BP_RATIO 2.666666666666667
AUGAUCACCUCGUGGCGGCAGGUGGGGCAGCGGAAACGGCCUCCAGACAUGGACACUGAGCUGCC
CCGGCUGGUCCAGUAGGGAUU
>random_seq_from_cds__NO_6721 RANDOM_LENGTH 110 SEQ_LENGTH 75
  GC_CONTENT 0.5466666666666667 BASEPAIR 29 FREE_ENERGY
-33.30 LEN_BP_RATIO 2.58620689655172
AGCACACGAUGUAUUUUGCCUGAUUUAGAUCUGGGGGCUGGUGGGGGCCAUAGCCUUGGCAGCUU
GCUGGGCUAACCAGUACUUAUAUCUUUUGGUCUUGGGCUUCUCAA
>random_seq_from_cds__NO_6731 RANDOM_LENGTH 72 SEQ_LENGTH 54
  GC_CONTENT 0.703703703703704 BASEPAIR 21 FREE_ENERGY
-34.01 LEN_BP_RATIO 2.57142857142857
CCUCUCCAGCCUCCUGAGGACCCGGGGCUGCGUGAGCGAGCAGAGGCUUAAGGUCUUCAGCGGGG
CGCUCCA
>random_seq_from_cds__NO_6734 RANDOM_LENGTH 78 SEQ_LENGTH 61
  GC_CONTENT 0.688524590163934 BASEPAIR 21 FREE_ENERGY
-30.10 LEN_BP_RATIO 2.9047619047619
UCCUACCGCAUUGGGGAGGACGGCUCCAUCUGCGUCUUGUACGAGGAGGCCCCACUGGCCGCCUC
CUGUGGGCUCCUC
>random_seq_from_cds__NO_6751 RANDOM_LENGTH 68 SEQ_LENGTH 53
  GC_CONTENT 0.452830188679245 BASEPAIR 19 FREE_ENERGY
-15.50 LEN_BP_RATIO 2.78947368421053
AAGAAGUUCAGCACAAGACUUGAGAAAACUCUGUGAGAGACUCAGGGGUAUGGAUUCUAGCACU
CCC
>random_seq_from_cds__NO_6754 RANDOM_LENGTH 83 SEQ_LENGTH 71
  GC_CONTENT 0.366197183098592 BASEPAIR 24 FREE_ENERGY
-16.30 LEN_BP_RATIO 2.958333333333333
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UGAUGAAGCUUAUGACCUGCUUGAUAAACUUCUAGAUCUAAAUCCAGCUUCAAGAAUAACAGCAG
AAGAAGCUUUGUUGCAUC

>random_seq_from_cds__NO_6758 RANDOM_LENGTH 87 SEQ_LENGTH 80
GC_CONTENT 0.5375 BASEPAIR 26 FREE_ENERGY -20.62
LEN_BP_RATIO 3.07692307692308

AUUUGGAUGGAGAGCUCUGUCUAGGGGCUGGGGUUGGAGCGUGAGUUGGUCGAUGGUGUGGUAGA
AGUCACAGGGGUCAAUUC AAC

>random_seq_from_cds__NO_6763 RANDOM_LENGTH 72 SEQ_LENGTH 54
GC_CONTENT 0.7222222222222222 BASEPAIR 19 FREE_ENERGY
-23.70 LEN_BP_RATIO 2.84210526315789

UGCUGAGUGGCAGGAAAGAGACCCGGCUGGCCCAUGCGAUGGGCUGAGCCCCGGCAUCACCUG
AGCGACU

>random_seq_from_cds__NO_6768 RANDOM_LENGTH 110 SEQ_LENGTH 86
GC_CONTENT 0.476744186046512 BASEPAIR 31 FREE_ENERGY
-26.60 LEN_BP_RATIO 2.7741935483871

UCACGGAUUGGCUCGUGUCCAGCCUCAAACACAAUGUACCUGGUACACAGGAUCUUCAACAUCU
CUUCCAAUAUUGUCCUGGUACACAGCUUGUUCACACUGCUUAUCC

>random_seq_from_cds__NO_6770 RANDOM_LENGTH 87 SEQ_LENGTH 78
GC_CONTENT 0.538461538461538 BASEPAIR 20 FREE_ENERGY
-19.55 LEN_BP_RATIO 3.9

CAGCCCGCUGGGCUGUUUUUAUGGCCACAAUCUGUGAUUCCCUUCCUCCACAAACAUAUCC
AAAGGCCCGGUGAUCUGUAAUG

>random_seq_from_cds__NO_6774 RANDOM_LENGTH 72 SEQ_LENGTH 61
GC_CONTENT 0.524590163934426 BASEPAIR 20 FREE_ENERGY
-17.21 LEN_BP_RATIO 3.05

AAAGUGGCUUCACUGCGAUCCUGACCCUUCUUCUUGGAGUCUUCUUGGCGCUGGUUUUCACAG
CUACUUG

>random_seq_from_cds__NO_6789 RANDOM_LENGTH 72 SEQ_LENGTH 59
GC_CONTENT 0.576271186440678 BASEPAIR 20 FREE_ENERGY
-20.34 LEN_BP_RATIO 2.95

UACCGGGUGGACCAUUACUUAGGCAAGCAGGGCUGUGGCGAGAUCUGCCUUUCCGAGACCAGA
ACCGCAA

>random_seq_from_cds__NO_6790 RANDOM_LENGTH 68 SEQ_LENGTH 60
GC_CONTENT 0.6166666666666667 BASEPAIR 20 FREE_ENERGY
-20.80 LEN_BP_RATIO 3

GGCUUUGGACGGCCUCUGGAACCGGCACCAUGUGGAGCGGGUGGAGAUCAUCAUGAAAGAGACCG
UGG

>random_seq_from_cds__NO_6793 RANDOM_LENGTH 85 SEQ_LENGTH 77
GC_CONTENT 0.61038961038961 BASEPAIR 29 FREE_ENERGY
-28.00 LEN_BP_RATIO 2.6551724137931

AGUCUACAGUGAGCAGGUGCGCAGAGAGCUGCAGAAGCCAGACAGCUUCCACAGCCUGACGCCG
ACCUUCGCAGGUGGUCCUAG

>random_seq_from_cds__NO_6806 RANDOM_LENGTH 87 SEQ_LENGTH 62
GC_CONTENT 0.725806451612903 BASEPAIR 19 FREE_ENERGY

-23.81 LEN_BP_RATIO 3.26315789473684
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CACACCGCCGCAUGAGCCUUAG
>random_seq_from_cds__NO_6819 RANDOM_LENGTH 62 SEQ_LENGTH 55
GC_CONTENT 0.654545454545455 BASEPAIR 19 FREE_ENERGY
-17.80 LEN_BP_RATIO 2.89473684210526
ACGGGGAUGACAUGCCAAGCUCGGAGCUCCUACCUGGUAGACGAGGUGCUGUGGGGCCACC
>random_seq_from_cds__NO_6822 RANDOM_LENGTH 92 SEQ_LENGTH 55
GC_CONTENT 0.763636363636364 BASEPAIR 20 FREE_ENERGY
-30.40 LEN_BP_RATIO 2.75
GGUGGAGGAGGAGGGGGCGGGGGAGGGGGCGGGUGGGGAAGCUGGGGCUGACAAGGAGCAGAAUG
GCUGCCUGCCACCCCAGAGAGUGAGU
>random_seq_from_cds__NO_6825 RANDOM_LENGTH 88 SEQ_LENGTH 56
GC_CONTENT 0.517857142857143 BASEPAIR 21 FREE_ENERGY
-19.10 LEN_BP_RATIO 2.66666666666667
CCACCACUGCCUCCACUACCGCUGCCACCCUGAAGAAGAGAGGGAACCACAGCACAGGCCUGUG
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>random_seq_from_cds__NO_6830 RANDOM_LENGTH 81 SEQ_LENGTH 67
GC_CONTENT 0.567164179104478 BASEPAIR 23 FREE_ENERGY
-21.00 LEN_BP_RATIO 2.91304347826087
AACAAACUGCCCCUGAGCCACAAGGUCUACAUGAGGAACUCUAAGUAUCCCCAGGAUCUGGUGAU
GAUGGAGGGGAAGAUG
>random_seq_from_cds__NO_6831 RANDOM_LENGTH 65 SEQ_LENGTH 56
GC_CONTENT 0.589285714285714 BASEPAIR 21 FREE_ENERGY
-25.60 LEN_BP_RATIO 2.66666666666667
AUGAGCUACUGCACUACUGGGCAGAUGUGGGCCCGCAGCAGCUACCUGGGGCAGUGUCAAUCU
>random_seq_from_cds__NO_6832 RANDOM_LENGTH 98 SEQ_LENGTH 77
GC_CONTENT 0.402597402597403 BASEPAIR 26 FREE_ENERGY
-19.60 LEN_BP_RATIO 2.96153846153846
UACCAGUGCUGAUCAUUUAUAUGUCAACGUAUCUGAGCUCUCUGGUCAAUUUUGAGGAAUCUC
AGACGUUUUUCGGCUUAUAUAAGCUCUAACUA
>random_seq_from_cds__NO_6835 RANDOM_LENGTH 79 SEQ_LENGTH 60
GC_CONTENT 0.55 BASEPAIR 19 FREE_ENERGY -24.90
LEN_BP_RATIO 3.15789473684211
AAGAGGGGCUCCUCAUCCUUCUGGUAAGAAGGCUAAUGUUGACUUCUGGGAGAAGUAGCCCUU
CAGGGAGAUGAGAU
>random_seq_from_cds__NO_6861 RANDOM_LENGTH 79 SEQ_LENGTH 54
GC_CONTENT 0.481481481481481 BASEPAIR 20 FREE_ENERGY
-16.90 LEN_BP_RATIO 2.7
UAGAUGAGGAGGAAGGAUGGGUGGGGAUUUGAAUCUUCCUCAGAUCGAAACGCAUACAUUUCU
GACCAUAAGGCCCU
>random_seq_from_cds__NO_6874 RANDOM_LENGTH 82 SEQ_LENGTH 73
GC_CONTENT 0.657534246575342 BASEPAIR 25 FREE_ENERGY
-28.40 LEN_BP_RATIO 2.92

CAGGCUGCAGCUGGACAGAGUGGCAGAGGCGGCUGAGGCUUGGGCAGCCAGGUCCCGUAAGCAG
GCGACUUCAGGAAGCGU

>random_seq_from_cds__NO_6880 RANDOM_LENGTH 84 SEQ_LENGTH 54
GC_CONTENT 0.62962962962963 BASEPAIR 19 FREE_ENERGY
-22.70 LEN_BP_RATIO 2.84210526315789

AUUUGUGAAGAAAGAUCCCCAGACGUGUCUUGAACUCUUUGGCUCCUCUCCAGGCAGGUGGUGGG
GAAGGCGGCCAGGGUGCGG

>random_seq_from_cds__NO_6884 RANDOM_LENGTH 84 SEQ_LENGTH 65
GC_CONTENT 0.661538461538462 BASEPAIR 23 FREE_ENERGY
-27.30 LEN_BP_RATIO 2.82608695652174

AGGAUGCUGUGGGCUCCAUGAUGCAGGGUCGGUGCUGCUGCUGGGCUGGGCAGAGUCAGGGCUG
GGCAGAGGGUGGAGGUAG

>random_seq_from_cds__NO_6886 RANDOM_LENGTH 62 SEQ_LENGTH 50
GC_CONTENT 0.66 BASEPAIR 19 FREE_ENERGY -19.60
LEN_BP_RATIO 2.63157894736842

GUUGUCCUCAGUCCUGUCGGGCACUCCAGUCUCGUCUGCGGAGGGGCCUUGACGGCAAUC

>random_seq_from_cds__NO_6887 RANDOM_LENGTH 110 SEQ_LENGTH 98
GC_CONTENT 0.530612244897959 BASEPAIR 35 FREE_ENERGY
-35.40 LEN_BP_RATIO 2.8

ACUGUCUGCUCCUAAAGUUGCCAACAGCACGGAUAUCCUGGUAAGUCACAUAGGCCAGCUCUCU
UGUUGGCCUUGUCCUCAGUCAGGUGCUUGAAGCUCAGAGAGCAGC

>random_seq_from_cds__NO_6893 RANDOM_LENGTH 81 SEQ_LENGTH 72
GC_CONTENT 0.6944444444444444 BASEPAIR 25 FREE_ENERGY
-35.80 LEN_BP_RATIO 2.88

AUCCAGCUCCUUUUGGCCCGGCAGCCGGCCUGCCGGCAGGCAUCGCACAACUUGGCCUCGGGU
CCGUGGGGAGUGGCGU

>random_seq_from_cds__NO_6894 RANDOM_LENGTH 81 SEQ_LENGTH 64
GC_CONTENT 0.6875 BASEPAIR 23 FREE_ENERGY -34.70
LEN_BP_RATIO 2.78260869565217

CGAGGCAGGUGCCUGGCGCCGUCGCGGGAGGCGCCGUCUGCGGGUACAGCGGUGUGUAGUAGGUA
GCAGUAGCUGGGCAGA

>random_seq_from_cds__NO_6898 RANDOM_LENGTH 110 SEQ_LENGTH 83
GC_CONTENT 0.373493975903614 BASEPAIR 30 FREE_ENERGY
-23.20 LEN_BP_RATIO 2.76666666666667

CCUUGCAUUUGAUAUGUCUGUGUCCAUCUGGGAGAGUCUUAUAUUGAACUUAACUUAUUUA
AGACUUCUUGGUUGCCUGGGGAUAUGAGGUAUGAUUUCACCAUCU

>random_seq_from_cds__NO_6919 RANDOM_LENGTH 63 SEQ_LENGTH 50
GC_CONTENT 0.62 BASEPAIR 19 FREE_ENERGY -18.50
LEN_BP_RATIO 2.63157894736842

GCAUGACCAUCGCUGCCUACCAGACCCUGUACGAGAGCAGCGUGGCGUUUGGCAUGAGGAAGG

>random_seq_from_cds__NO_6922 RANDOM_LENGTH 73 SEQ_LENGTH 55
GC_CONTENT 0.5454545454545454 BASEPAIR 19 FREE_ENERGY
-16.90 LEN_BP_RATIO 2.89473684210526

GAAGCACAAUGAGGAGAUUCAGUCCUGAAGCGAACAAAUCAGCAGCUGAAGGGCCCAACUGGAA

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GGCAUUAU
>random_seq_from_cds__NO_6923 RANDOM_LENGTH 99 SEQ_LENGTH 81
  GC_CONTENT 0.4444444444444444 BASEPAIR 26 FREE_ENERGY
  -18.00 LEN_BP_RATIO 3.11538461538462
UGCACCAAAGAAGUGAAAUGUCCUGCUCUUCUCUCGAUGCAACUCUAUCGUCACAGUCAAGAAA
AAUAAGAGACACAUGGCUGAGGUGAAUGCAUCCC
>random_seq_from_cds__NO_6932 RANDOM_LENGTH 97 SEQ_LENGTH 85
  GC_CONTENT 0.647058823529412 BASEPAIR 32 FREE_ENERGY
  -38.30 LEN_BP_RATIO 2.65625
UGCAUCUGCCUCAGAGCCCGAGUACAUGGAGGAGGGUGCGGCGGCAGCACAUUGGAGCGUUGUACC
AGCUUCCUGGUGGAUGAGCUGGGCGUGGUGGA
>random_seq_from_cds__NO_6937 RANDOM_LENGTH 72 SEQ_LENGTH 59
  GC_CONTENT 0.542372881355932 BASEPAIR 20 FREE_ENERGY
  -18.30 LEN_BP_RATIO 2.95
CUGGAGCUCUUGGCUCAAGACUAUAAGCUGCGAAUUAAGCAGAUUACGGAGGAAGUGGAGAGGCA
GGGUGUC
>random_seq_from_cds__NO_6940 RANDOM_LENGTH 68 SEQ_LENGTH 51
  GC_CONTENT 0.568627450980392 BASEPAIR 19 FREE_ENERGY
  -19.90 LEN_BP_RATIO 2.68421052631579
UCCACGGCCAUCACCAACUCCCUGCAGACCAUGCAGCAGGACAUGAUAGGAUGGCUUGAAACCCC
UCC
>random_seq_from_cds__NO_6955 RANDOM_LENGTH 78 SEQ_LENGTH 60
  GC_CONTENT 0.4666666666666667 BASEPAIR 24 FREE_ENERGY
  -20.30 LEN_BP_RATIO 2.5
GUGAAAAUGAUGUUAAGUGGUGUGGCUUGUUUGCUGUUUUCAUAGCUUUGCUGCCCAUCCUUGG
ACAUCGAGACUAU
>random_seq_from_cds__NO_6958 RANDOM_LENGTH 110 SEQ_LENGTH 81
  GC_CONTENT 0.481481481481481 BASEPAIR 29 FREE_ENERGY
  -23.60 LEN_BP_RATIO 2.79310344827586
AAGAGUUAAAUUAAAAGUCAGCAGCACAGACAAGGCAGAUCAUCAUUUGGAAAUGGUAUCC
AGCUCCUGGCGAUAAUGUGUGUCUCCUGUAUUUGUUGGAGCCCAU
>random_seq_from_cds__NO_6969 RANDOM_LENGTH 78 SEQ_LENGTH 55
  GC_CONTENT 0.618181818181818 BASEPAIR 21 FREE_ENERGY
  -26.40 LEN_BP_RATIO 2.61904761904762
CCCGCACGUGUACCGUUUCUCCUCAUAAGAGGUAUCCGUGAACUCCAGGAGCAGGCGGAUGGCGU
GCGCCAGCCCCAC
>random_seq_from_cds__NO_6979 RANDOM_LENGTH 110 SEQ_LENGTH 72
  GC_CONTENT 0.3472222222222222 BASEPAIR 24 FREE_ENERGY
  -16.50 LEN_BP_RATIO 3
AAAUUAUGACAUUUUCAAAAAUCUACAUAUUUGAUCAGUCUUUUUAUGAUCUAUCGUGCAA
ACCAGUGAAAUCAAGAAGAAGAAAAGGAACUGAGAAGAACUACA
>random_seq_from_cds__NO_6985 RANDOM_LENGTH 89 SEQ_LENGTH 58
  GC_CONTENT 0.46551724137931 BASEPAIR 22 FREE_ENERGY
  -19.30 LEN_BP_RATIO 2.63636363636364
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GGCAUUCUGCUGAAUGUACCACCAUUUAUAACAGAGGUGAACAUACAAGUGGCAUGUAUGCCAU
CAGACCCAGCAACUCUCAAGUUUU

>random_seq_from_cds__NO_6989 RANDOM_LENGTH 86 SEQ_LENGTH 60
GC_CONTENT 0.4333333333333333 BASEPAIR 21 FREE_ENERGY
-18.40 LEN_BP_RATIO 2.85714285714286

UACUGGCAAUGUCCCCAAUGCAAUCCCGGAAAACAAAGAUUUGGUGUUUUCUACUUGGGAUCACA
AAGCAAAAGGACACUUCAACU

>random_seq_from_cds__NO_7016 RANDOM_LENGTH 62 SEQ_LENGTH 57
GC_CONTENT 0.614035087719298 BASEPAIR 22 FREE_ENERGY
-26.10 LEN_BP_RATIO 2.59090909090909

CAGCAGAGUUAGGGUGCCUCCUCCAGGGGUGGAGGUGGAGUUCAGCCCCCGAUUAUUGU

>random_seq_from_cds__NO_7025 RANDOM_LENGTH 73 SEQ_LENGTH 60
GC_CONTENT 0.6166666666666667 BASEPAIR 21 FREE_ENERGY
-22.70 LEN_BP_RATIO 2.85714285714286

CACCACCCACUACUACCGUGUCAUGCAGCUGUGUUUCUGGUGGGAGCUCUUUGACCGGAUCCUG
GAGCGGGG

>random_seq_from_cds__NO_7026 RANDOM_LENGTH 94 SEQ_LENGTH 86
GC_CONTENT 0.5 BASEPAIR 27 FREE_ENERGY -23.90 LEN_BP_RATIO
3.18518518518519

UGUCUACACAGAGAAGGAUGCCAGUCUGGUGAUCCAGCAGGUCUUGUCGGCAGUGAAAUACCUAC
AUGAGAAUGGCAUCGUCCACAGAGACUUA

>random_seq_from_cds__NO_7035 RANDOM_LENGTH 110 SEQ_LENGTH 80
GC_CONTENT 0.7 BASEPAIR 25 FREE_ENERGY -31.60 LEN_BP_RATIO
3.2

CUGACCCAAUUAACCGGCCAGCAUGGCCGCGGCCACUCGCCCCUGGUGGCAGGUCCCUCAACUG
CCUGGUCAAUGGCUCCUCCACAUCAGCAGCAGCCUGGUGCCCAU

>random_seq_from_cds__NO_7039 RANDOM_LENGTH 79 SEQ_LENGTH 67
GC_CONTENT 0.597014925373134 BASEPAIR 25 FREE_ENERGY
-27.70 LEN_BP_RATIO 2.68

GAUCCUGUCUGGCUCGCUUAGGAUUCUGCAGGUCACCAGGUGGUGAGGCCUUGCUUGCUGAGAUG
CUCCGGAGAGAAUG

>random_seq_from_cds__NO_7049 RANDOM_LENGTH 102 SEQ_LENGTH 96
GC_CONTENT 0.6354166666666667 BASEPAIR 35 FREE_ENERGY
-37.20 LEN_BP_RATIO 2.74285714285714

GUCAGGGACUUAUCAUUGGCCAGAAUGUCACAGGCCCUUGCUCCUCAGGUCUUCGAGGCAGGAGG
CGGCCACGCCUGCUGUUCGCGGCUGUAGUUGCGGCG

>random_seq_from_cds__NO_7051 RANDOM_LENGTH 96 SEQ_LENGTH 91
GC_CONTENT 0.538461538461538 BASEPAIR 31 FREE_ENERGY
-26.60 LEN_BP_RATIO 2.93548387096774

GCUGUGGCUGAAGAGGCUCUGGGUGCUCUUGGAGGUGGCUGUGCAUGUGGUCGUGGGUAAAGUGC
UUCUGAUUAUUGUUCCAGACAGAGUCAAGCG

>random_seq_from_cds__NO_7053 RANDOM_LENGTH 79 SEQ_LENGTH 65
GC_CONTENT 0.553846153846154 BASEPAIR 23 FREE_ENERGY
-26.90 LEN_BP_RATIO 2.82608695652174

CCCAGUAUUUCUGGUUCGUCUUGAAGGUCCGUUGGCAGCGACUAGAGGACACGACUGAGCUAGGG
GGUCUGGCCCCAAA

>random_seq_from_cds__NO_7066 RANDOM_LENGTH 72 SEQ_LENGTH 61
GC_CONTENT 0.639344262295082 BASEPAIR 19 FREE_ENERGY
-21.70 LEN_BP_RATIO 3.21052631578947

UCCCGCUGCUCCUCAACCCUGCGCAGCUGAAAACCCUUGACGGAUGGCUGAAAGCAGGUCGCUAC
GGGCAUC

>random_seq_from_cds__NO_7072 RANDOM_LENGTH 73 SEQ_LENGTH 56
GC_CONTENT 0.517857142857143 BASEPAIR 19 FREE_ENERGY
-19.60 LEN_BP_RATIO 2.94736842105263

AUCUUUUGGGUCCAGCCAAACCAGAUCCUCUUUGGUUGUCCACUGGGUAACCUGAAUUCUGCUGG
UGGAGGAG

>random_seq_from_cds__NO_7076 RANDOM_LENGTH 110 SEQ_LENGTH 68
GC_CONTENT 0.397058823529412 BASEPAIR 24 FREE_ENERGY
-19.95 LEN_BP_RATIO 2.83333333333333

CUAUGCUUUCUCUUCUCUUUCAUGAUAUCCUUGGUGUCCUGCAGCAUCUUCUCCUCCAAAGAUC
AAAGAAGUAUGAAGGGUCUGUGUAGAAUUUGAGUGCCUCUUUCC

>random_seq_from_cds__NO_7079 RANDOM_LENGTH 87 SEQ_LENGTH 76
GC_CONTENT 0.552631578947368 BASEPAIR 25 FREE_ENERGY
-24.90 LEN_BP_RATIO 3.04

CCUUCUUCUCCUUGGGAUCCAGCUGAGUGACUUUAACCGUAGUCGGUCGACCCUCUCAGCAAG
GGAGCUUACCCGAGAGGCAAAG

>random_seq_from_cds__NO_7092 RANDOM_LENGTH 90 SEQ_LENGTH 72
GC_CONTENT 0.680555555555556 BASEPAIR 27 FREE_ENERGY
-33.20 LEN_BP_RATIO 2.66666666666667

GUGGAAGGUAGUGACCAGCACAGCCAGCGCCUGCUCCAGAGAACUGCACAUCAUGCGGCUGGCGC
UGCUCUGGGCCCUGGGCUCUCCUGG

>random_seq_from_cds__NO_7093 RANDOM_LENGTH 73 SEQ_LENGTH 57
GC_CONTENT 0.701754385964912 BASEPAIR 21 FREE_ENERGY
-28.70 LEN_BP_RATIO 2.71428571428571

CGCGGGCAGCCUCUGCCUCCUGGCCGCUCCCAAUAUAGGGUGGCACUGAGGAGCAGCAGGCA
GAGUCAGA

>random_seq_from_cds__NO_7098 RANDOM_LENGTH 100 SEQ_LENGTH 91
GC_CONTENT 0.571428571428571 BASEPAIR 24 FREE_ENERGY
-26.75 LEN_BP_RATIO 3.79166666666667

GGUCCUCCAUUAUUUCGCGAAUCCAAGAUCUCCACCUGCCAGGCCACACCUGUGCCUGAGCUG
GCGGGAAUCUGUACACACUCAGAAGCCACCAGAGC

>random_seq_from_cds__NO_7101 RANDOM_LENGTH 94 SEQ_LENGTH 74
GC_CONTENT 0.662162162162162 BASEPAIR 26 FREE_ENERGY
-26.20 LEN_BP_RATIO 2.84615384615385

AAUGUACGAGUGGCACUAGUGGGCCUGGAGGCCUGGACCCAGCGUGACCUGGUGGAGAUCAAGCCC
AAACCAGCUGUCACCCUCGAAAACUCC

>random_seq_from_cds__NO_7114 RANDOM_LENGTH 84 SEQ_LENGTH 73
GC_CONTENT 0.534246575342466 BASEPAIR 28 FREE_ENERGY

-29.30 LEN_BP_RATIO 2.60714285714286
AUAGACCAUCGAUGCCAGCGUGUGGAUCUCCUGGGGCACAGGAAUGUCGAAGCAAUGCCAUGG
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>random_seq_from_cds__NO_7120 RANDOM_LENGTH 98 SEQ_LENGTH 78
GC_CONTENT 0.641025641025641 BASEPAIR 27 FREE_ENERGY
-35.80 LEN_BP_RATIO 2.88888888888889
AGUGUCCUCGCUCUACCUCUGAGAUGGCGGACGGGGAGCUGAACGUGGACAGCCUCAUCACCCGG
CUGCUGGAGGGUACGAGGAUGUCGUCCAGGAAA
>random_seq_from_cds__NO_7150 RANDOM_LENGTH 89 SEQ_LENGTH 75
GC_CONTENT 0.466666666666667 BASEPAIR 19 FREE_ENERGY
-18.30 LEN_BP_RATIO 3.94736842105263
GCAGUCUCUUGGUACUUUUGAUGCACAGCGUUUAUGGCAGUUGAAUUUGCAAUCCUUUACACUGC
AUUCCUUGGCGAAAGAGGCCUUUC
>random_seq_from_cds__NO_7153 RANDOM_LENGTH 79 SEQ_LENGTH 65
GC_CONTENT 0.492307692307692 BASEPAIR 19 FREE_ENERGY
-16.40 LEN_BP_RATIO 3.42105263157895
GUCUUGAACUGAGAGGCCGGGUCCUGGUAAGAUACA AUUUGACAGACGUCUCUUUCUACUCCA
CUACAGUUUUUGG
>random_seq_from_cds__NO_7179 RANDOM_LENGTH 68 SEQ_LENGTH 61
GC_CONTENT 0.540983606557377 BASEPAIR 19 FREE_ENERGY
-16.10 LEN_BP_RATIO 3.21052631578947
GUGGAGAAGUGGGAGCACGCAGUCAUGGUAACAGGAGAAACGUGGACUUCAGGAACUCUUUGU
CUC
>random_seq_from_cds__NO_7203 RANDOM_LENGTH 73 SEQ_LENGTH 62
GC_CONTENT 0.483870967741936 BASEPAIR 23 FREE_ENERGY
-20.00 LEN_BP_RATIO 2.69565217391304
AGCAUGUUAGCCUAGGUUUUGUUUGGGCAAGCUGUCGACUUGGCCGUCUAAUAGACUGUUUUUGC
UGUAUCUU
>random_seq_from_cds__NO_7254 RANDOM_LENGTH 82 SEQ_LENGTH 71
GC_CONTENT 0.591549295774648 BASEPAIR 25 FREE_ENERGY
-23.80 LEN_BP_RATIO 2.84
GAACCGCCGUUCUUCUGACACUGGCUCCAAGGCACCCCCACCUUCAAGGGUCUCACUUAUGGAC
CAGUCAGUAAGAGAAGG
>random_seq_from_cds__NO_7256 RANDOM_LENGTH 71 SEQ_LENGTH 64
GC_CONTENT 0.75 BASEPAIR 26 FREE_ENERGY -39.40
LEN_BP_RATIO 2.46153846153846
CCAGCGGCGCUUUGCGGAGGAGCUGAGGGUGGGCUGUGCCGCGCUGCGGAUCCUGGCUGCAGAGC
GUGGCG
>random_seq_from_cds__NO_7257 RANDOM_LENGTH 64 SEQ_LENGTH 50
GC_CONTENT 0.64 BASEPAIR 19 FREE_ENERGY -19.30
LEN_BP_RATIO 2.63157894736842
AUGCUGGUUUCUACACUUGCAAAGCGGUCAAUGAGUAUGGUGCUCGGCAGUGCGAGGCCCGCUU
>random_seq_from_cds__NO_7270 RANDOM_LENGTH 69 SEQ_LENGTH 63
GC_CONTENT 0.476190476190476 BASEPAIR 24 FREE_ENERGY

-18.60 LEN_BP_RATIO 2.625
CAGCUCaucugcagucacAUUUAGUGAAGAAACUAUAUGGUCUAUACUGCUGGCUCAUCAGGUGA
CUGG
>random_seq_from_cds__NO_7280 RANDOM_LENGTH 89 SEQ_LENGTH 76
GC_CONTENT 0.421052631578947 BASEPAIR 21 FREE_ENERGY
-17.50 LEN_BP_RATIO 3.61904761904762
UCGUUCUUGGUUACCAUGUAUAUUUUUGCUGGAGGCAUAACAUGGGAAACAUUGGUCGACAAC
UGGCAAUGGUACGAAUGUAAAAGUU
>random_seq_from_cds__NO_7292 RANDOM_LENGTH 89 SEQ_LENGTH 80
GC_CONTENT 0.4875 BASEPAIR 29 FREE_ENERGY -19.20
LEN_BP_RATIO 2.75862068965517
CAUGGGCAGCUAUCGAUGUACCUGCAAAAUAGGAUUUGGCCGGAUCCUACCUUUUCAAGUUGUG
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>random_seq_from_cds__NO_7293 RANDOM_LENGTH 78 SEQ_LENGTH 57
GC_CONTENT 0.526315789473684 BASEPAIR 20 FREE_ENERGY
-16.00 LEN_BP_RATIO 2.85
GAAGAGAAAGGGCCUGUUACCGACUUGUCAGUUCUGGAAGACAGUGUAUGCACCCUCUGUCUGU
UCACCUCACCAAG
>random_seq_from_cds__NO_7295 RANDOM_LENGTH 79 SEQ_LENGTH 70
GC_CONTENT 0.485714285714286 BASEPAIR 23 FREE_ENERGY
-22.20 LEN_BP_RATIO 3.04347826086957
CGGUUCUGGCGUUCAUAGACGCAGGCCAAUCCAUCACCAUGUAGGUAAAGGACCUGUAUUUGUC
AAGCCAAAGAACAC
>random_seq_from_cds__NO_7301 RANDOM_LENGTH 82 SEQ_LENGTH 72
GC_CONTENT 0.541666666666667 BASEPAIR 23 FREE_ENERGY
-24.00 LEN_BP_RATIO 3.1304347826087
GUUCAGUGAACAACAGAGGAAAUGUGUGGGAUUAUGAUGAGUGUACUCAGGUCCAACACCUCUGC
UCCCAGGGCCGUGUGA
>random_seq_from_cds__NO_7309 RANDOM_LENGTH 70 SEQ_LENGTH 61
GC_CONTENT 0.524590163934426 BASEPAIR 22 FREE_ENERGY
-17.90 LEN_BP_RATIO 2.77272727272727
AUCUCUGUGCUCAUGGGCAGUGCAGGAACACUGAGGGCUCUUUCAUGUGUGUGUGACCAGGGU
UACAG
>random_seq_from_cds__NO_7314 RANDOM_LENGTH 88 SEQ_LENGTH 64
GC_CONTENT 0.59375 BASEPAIR 25 FREE_ENERGY -24.90
LEN_BP_RATIO 2.56
GCUGGCUCUUCCGUGCCUCUGUUAUCAGGGCUUUAAGCCCCACAGGAUGGGCAAGGGUGUGU
GGGAUGUGAAUGAAUGUGAACUG
>random_seq_from_cds__NO_7321 RANDOM_LENGTH 87 SEQ_LENGTH 74
GC_CONTENT 0.459459459459459 BASEPAIR 27 FREE_ENERGY
-20.40 LEN_BP_RATIO 2.74074074074074
GAUGAAUGUCAAGACCCCAGUAGUUGUAUUGAUGGCCAGUGUGUAAUACAGAGGGCUCUUACAA
CUGCUUCUGUACUCACCCAUG
>random_seq_from_cds__NO_7326 RANDOM_LENGTH 74 SEQ_LENGTH 61

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GC_CONTENT    0.409836065573771    BASEPAIR    20    FREE_ENERGY
-18.40    LEN_BP_RATIO    3.05
GGUUUUCUAAAUAGCUUUGAGGAGUUACAGGCUGAGGAAUGCGGCAUCCUCA AUGGAUGUGAAAA
UGGUCG CUG
>random_seq_from_cds__NO_7336    RANDOM_LENGTH    73    SEQ_LENGTH    65
GC_CONTENT    0.492307692307692    BASEPAIR    24    FREE_ENERGY
-20.20    LEN_BP_RATIO    2.708333333333333
UUGGUAACCACUUC CUGCCAUCA AAGCUAGCUACUAUAAAUGUUUUCUGUGCUUGCAAGGUAAG
UGGCC CAG
>random_seq_from_cds__NO_7354    RANDOM_LENGTH    109    SEQ_LENGTH    82
GC_CONTENT    0.304878048780488    BASEPAIR    33    FREE_ENERGY
-16.26    LEN_BP_RATIO    2.484848484848484
UUUUUUUCUUGUUUGUAGAGAUUUC AUGAUCCUGAAAUC CAUCUUAAGGAGUAUAACUUCAGUC
UAUAAGUAUUUUUAAGUAAUCAGUUAGAGUGUAAGUUUUGCGA
>random_seq_from_cds__NO_7364    RANDOM_LENGTH    85    SEQ_LENGTH    76
GC_CONTENT    0.552631578947368    BASEPAIR    23    FREE_ENERGY
-21.96    LEN_BP_RATIO    3.30434782608696
GGACCUGUAGUAGCGAUGCAGCACCAGGAUGAAGUCAGUGAUGGUCAGCAUCCCCACAAAGCUC
UGCUCUUGCUGUCCCAUAG
>random_seq_from_cds__NO_7382    RANDOM_LENGTH    90    SEQ_LENGTH    73
GC_CONTENT    0.493150684931507    BASEPAIR    24    FREE_ENERGY
-21.04    LEN_BP_RATIO    3.041666666666667
UGAUCCAAAAGAAGAUCAAAUACAGUGCAAGUAGCAUGGCAGCACAGCGUUGUGCAUCCAGGU
CUAGCGUGUCUCCUGUCUUCUGU
>random_seq_from_cds__NO_7407    RANDOM_LENGTH    85    SEQ_LENGTH    65
GC_CONTENT    0.553846153846154    BASEPAIR    24    FREE_ENERGY
-24.00    LEN_BP_RATIO    2.708333333333333
GGCAUCUGUUUCUGCAGUUUGAGGUGUUAAGGCACGUGCCCUGGAACUCCAGCCCGUAGAUCACU
GGUGCAUCGUCCUCAUGAU
>random_seq_from_cds__NO_7412    RANDOM_LENGTH    72    SEQ_LENGTH    64
GC_CONTENT    0.40625    BASEPAIR    23    FREE_ENERGY    -16.30
LEN_BP_RATIO    2.78260869565217
GACAGCACUUUCAAACCUGGAUUCAGAAUAUGAACAAUAUAUCUCCUCCCUUGGACAGU
UUGCUGA
>random_seq_from_cds__NO_7439    RANDOM_LENGTH    72    SEQ_LENGTH    64
GC_CONTENT    0.609375    BASEPAIR    22    FREE_ENERGY    -21.30
LEN_BP_RATIO    2.90909090909091
GAAGCUCUGGGUCCUCUGUCCAAUGCUAUGGUCCUGCAGCCCCUGCACCCAUGCCUAGGAAGUC
GCAGGCA
>random_seq_from_cds__NO_7442    RANDOM_LENGTH    96    SEQ_LENGTH    88
GC_CONTENT    0.545454545454545    BASEPAIR    30    FREE_ENERGY
-31.80    LEN_BP_RATIO    2.933333333333333
GCUGACUGAGAUGGACCUCGAGGAGGCGGGAAGAGUUAAAAGAACGCUGUACUCAGUGUGCUGCU
GUCUCAUGGGGUCUACUGAUGAAGGCAAU
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>random_seq_from_cds__NO_7453 RANDOM_LENGTH 82 SEQ_LENGTH 67
  GC_CONTENT 0.402985074626866 BASEPAIR 22 FREE_ENERGY
-17.30 LEN_BP_RATIO 3.04545454545455
UAGCUUAACUUGCCACGUGGUAAAAAUGACUGGAAUGGGAGAAGUGGAUUUUCUGACAUUUGAUC
CUAUAGCUAAAAUGGCA
>random_seq_from_cds__NO_7461 RANDOM_LENGTH 71 SEQ_LENGTH 61
  GC_CONTENT 0.426229508196721 BASEPAIR 19 FREE_ENERGY
-17.30 LEN_BP_RATIO 3.21052631578947
UCUCUUCUCCUCCUGCUCAGAAUAAAGACUCCCCUUCUCCAUGAAGAAGUGAGCUUAGUUGAGA
AGAAAC
>random_seq_from_cds__NO_7465 RANDOM_LENGTH 87 SEQ_LENGTH 79
  GC_CONTENT 0.493670886075949 BASEPAIR 29 FREE_ENERGY
-20.10 LEN_BP_RATIO 2.72413793103448
GAGAGAAAACCCCGCCGCUUUGUCAUCUCCCCAUCGAGUACCAUGAUAUCUGGCAGAUGUAUA
AGAAGGCAGAGGCUUCCUUUUG
>random_seq_from_cds__NO_7476 RANDOM_LENGTH 72 SEQ_LENGTH 62
  GC_CONTENT 0.451612903225806 BASEPAIR 21 FREE_ENERGY
-16.40 LEN_BP_RATIO 2.95238095238095
AGAGGAUGGGAGUGAUGUCAAGUCCAACAGAGAAUUCUUUJACCUUGGAUGCUGACUUCUAAUCU
ACACAUU
>random_seq_from_cds__NO_7490 RANDOM_LENGTH 79 SEQ_LENGTH 62
  GC_CONTENT 0.5 BASEPAIR 22 FREE_ENERGY -19.00 LEN_BP_RATIO
2.81818181818182
AAUCCUGUCCCGGUAGCAGCAAGGGUCUUCACGAUGGCUUUGCUAUCAUUACAUUUGACUGCAUA
AAAGGGGGUGACAC
>random_seq_from_cds__NO_7503 RANDOM_LENGTH 85 SEQ_LENGTH 79
  GC_CONTENT 0.759493670886076 BASEPAIR 29 FREE_ENERGY
-38.40 LEN_BP_RATIO 2.72413793103448
AGGCUGCGGGCAGCAGGGGCGUGGCACACGGCUAGGCAGCGCUCGGCGCUCAGGCCUGCCACGCU
CAGCACCGUGGCGUAGGCGC
>random_seq_from_cds__NO_7511 RANDOM_LENGTH 77 SEQ_LENGTH 72
  GC_CONTENT 0.638888888888889 BASEPAIR 22 FREE_ENERGY
-21.20 LEN_BP_RATIO 3.27272727272727
UGCCAGCUGAAAAGGGGCUUGUGGACAGGAUGAGAGGCCUGGACCCCAGCACGCCAGCCCAAGU
GAUCGCUCCCAG
>random_seq_from_cds__NO_7520 RANDOM_LENGTH 73 SEQ_LENGTH 55
  GC_CONTENT 0.490909090909091 BASEPAIR 21 FREE_ENERGY
-18.40 LEN_BP_RATIO 2.61904761904762
CAGCAAACAAGACGGAUUCUCCUCCAGGAAAAGAGGAUAAACGAAGCCGACAUCUUGGUGCUGA
CGGCGUCU
>random_seq_from_cds__NO_7534 RANDOM_LENGTH 99 SEQ_LENGTH 86
  GC_CONTENT 0.383720930232558 BASEPAIR 29 FREE_ENERGY
-15.10 LEN_BP_RATIO 2.96551724137931
UUGAAAAGAAGCCAGAAAAGUUUAAAGUCCAGUGUUUGACAGACAUCAAAACCUGUUUUUCCCC
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AACACAGAACCCUUUUUAUGCUGCUUUUGGAAACC
>random_seq_from_cds__NO_7547 RANDOM_LENGTH 81 SEQ_LENGTH 72
  GC_CONTENT 0.5972222222222222 BASEPAIR 25 FREE_ENERGY
  -21.20 LEN_BP_RATIO 2.88
GGCCAUCAUCUUGAGGGACGCCAUGUCUGCCCGGUCCACGCCACAGCAUAGAGCUCAAUACCAG
AUGCUUGGGCCCGAGC
>random_seq_from_cds__NO_7548 RANDOM_LENGTH 81 SEQ_LENGTH 66
  GC_CONTENT 0.6060606060606060 BASEPAIR 22 FREE_ENERGY
  -24.80 LEN_BP_RATIO 3
CGCCACCUCAUUCACCUGGUCCUGGGGCCUCCCAUCUGUAACAAUGAUGGCCACCUUAGGGAUGU
UAGAAGAGGGCUCUCG
>random_seq_from_cds__NO_7549 RANDOM_LENGTH 82 SEQ_LENGTH 70
  GC_CONTENT 0.6 BASEPAIR 27 FREE_ENERGY -28.10 LEN_BP_RATIO
  2.59259259259259
AGCCCCUGCCUCCACUGUGAAGGCUUCGUCCAUUGCUGUCUGGAUGGCUAGGCCUGACAUGGUGC
CUGUUGACAAGGGUGUG
>random_seq_from_cds__NO_7553 RANDOM_LENGTH 99 SEQ_LENGTH 87
  GC_CONTENT 0.839080459770115 BASEPAIR 35 FREE_ENERGY
  -57.30 LEN_BP_RATIO 2.48571428571429
GGCGGCGUCCAGGGCUGCCCCGGGACCUCGGGUCUCCAGCCUCCGGAAGCCCGGGCGGGCCACG
GGGUCGGGGCGGCGGAGGGCAGCAGCAGCAGCG
>random_seq_from_cds__NO_7554 RANDOM_LENGTH 89 SEQ_LENGTH 77
  GC_CONTENT 0.662337662337662 BASEPAIR 24 FREE_ENERGY
  -34.70 LEN_BP_RATIO 3.208333333333333
GCCAGAGCAGCAGGAGGAGUCCCGGGAGGCGGCGCGGGGGCCGGGCGCGGCAUUAUAGAGGAU
GAUAGUAAGUUCUCCUGGAGCAAG
>random_seq_from_cds__NO_7560 RANDOM_LENGTH 110 SEQ_LENGTH 96
  GC_CONTENT 0.3854166666666667 BASEPAIR 29 FREE_ENERGY
  -19.43 LEN_BP_RATIO 3.31034482758621
GGCACUGACAAUAUAUUCAGAAUGGAAGUCCUUAAGAGCAACUAACAGGUUCUUGAUCAGACUGA
CUAUCUUUUCUUAAGUUAUAUAUUCACUGUCCAGCCAACUA
>random_seq_from_cds__NO_7568 RANDOM_LENGTH 89 SEQ_LENGTH 75
  GC_CONTENT 0.4533333333333333 BASEPAIR 23 FREE_ENERGY
  -17.39 LEN_BP_RATIO 3.26086956521739
AAUUCUUGAGUAAUCUGUACCAAGCCAUAACACGUUAUCCUUGAGUCCUGGAAACUGGCUUG
GCCUCCUGAGUCAACAGUCCUG
>random_seq_from_cds__NO_7570 RANDOM_LENGTH 78 SEQ_LENGTH 60
  GC_CONTENT 0.5 BASEPAIR 20 FREE_ENERGY -18.50 LEN_BP_RATIO
  3
AAACCCACUCAGCAUUGUUCUGCAGAUUUCUUCUCAGCUUUGAAGACACUUCUCUCAGGGUGAGC
CCUGUGUGUCC
>random_seq_from_cds__NO_7571 RANDOM_LENGTH 79 SEQ_LENGTH 71
  GC_CONTENT 0.47887323943662 BASEPAIR 25 FREE_ENERGY
  -24.30 LEN_BP_RATIO 2.84
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AGUGGUACUUGUUGACAUAUAUCAUAAGGACCCUGUGGCCUUGGGCACGUUGUCUUUCAGAGAG
GUUAGCAAGCCAGA

>random_seq_from_cds__NO_7574 RANDOM_LENGTH 80 SEQ_LENGTH 63
GC_CONTENT 0.619047619047619 BASEPAIR 25 FREE_ENERGY
-23.90 LEN_BP_RATIO 2.52

CGUCAUCUUCAUCAUAUCAUGCCCACGGUGCCUACGGCUGGGGAGGCUGCUGAGGUGGAGAUG
CCUUUCUUGUCUUUC

>random_seq_from_cds__NO_7576 RANDOM_LENGTH 92 SEQ_LENGTH 65
GC_CONTENT 0.430769230769231 BASEPAIR 26 FREE_ENERGY
-15.60 LEN_BP_RATIO 2.5

UUGCCAUCUUCUUCAUAUUCUGCACUGAAGUCACGGUGUGCAAUGUCCUUUAGUCUJAGAGGC
UAACGUACCAUCUUCGAUUUUGUGUGU

>random_seq_from_cds__NO_7586 RANDOM_LENGTH 102 SEQ_LENGTH 91
GC_CONTENT 0.428571428571429 BASEPAIR 33 FREE_ENERGY
-28.00 LEN_BP_RATIO 2.75757575757576

AAGCUCUUGUCAUAGACUGGUAGGAUGAUUUUUUGAGGAACCUUAGGUGUCCUUCUAAGGAUCC
UGCAAUGUCAAGGUGUGCCUUUUCUUGGUCAUUGGAA

>random_seq_from_cds__NO_7592 RANDOM_LENGTH 94 SEQ_LENGTH 66
GC_CONTENT 0.454545454545455 BASEPAIR 23 FREE_ENERGY
-18.40 LEN_BP_RATIO 2.8695652173913

CUGAAUAUUCGGAGAAAGAACCGAACCCUUGACAUCUCCUUUGGUAGAUGACUCAAUGGAAAAG
UAAGAGGUGAGGCCUUUCCAAGCUAAGCUU

>random_seq_from_cds__NO_7595 RANDOM_LENGTH 110 SEQ_LENGTH 62
GC_CONTENT 0.467741935483871 BASEPAIR 25 FREE_ENERGY
-21.72 LEN_BP_RATIO 2.48

UUUUUCGUGGUUAAGCUCACAGUACUGUUAUGACUACCCUCCACAAUUUGUUGCUCAGAGACAG
AGCUGUGGCUAACUUCAAUCCCCUUUUUCUUGUCAAUUCUUGUGGU

>random_seq_from_cds__NO_7612 RANDOM_LENGTH 87 SEQ_LENGTH 76
GC_CONTENT 0.5 BASEPAIR 28 FREE_ENERGY -23.00 LEN_BP_RATIO
2.71428571428571

CUGAGAAUCUGGGGAGGCCCAUJUCAUGACCCUUUCCAGAAGAAGUCCAUGCUAUGUGGCCA
GCUUUCAACAGUGUCUUGAUCU

>random_seq_from_cds__NO_7613 RANDOM_LENGTH 84 SEQ_LENGTH 78
GC_CONTENT 0.448717948717949 BASEPAIR 25 FREE_ENERGY
-19.50 LEN_BP_RATIO 3.12

CGUUGCGCAGGUCAGCCUGACUAGAGAAGUCCAGUUUGGGGAUGUCAAUUUGUGGAAGUAUUUA
GUGUUGCUAUCCAGGGUAA

>random_seq_from_cds__NO_7627 RANDOM_LENGTH 84 SEQ_LENGTH 63
GC_CONTENT 0.412698412698413 BASEPAIR 22 FREE_ENERGY
-16.40 LEN_BP_RATIO 2.86363636363636

GCCAAAGAUGCUGAACUUAAGCCUCCUGUAACCAAUUGAUGAUUAAGGUUAUUUUGGUGUCCUG
UAGGCUUCCAGAUACACU

>random_seq_from_cds__NO_7638 RANDOM_LENGTH 92 SEQ_LENGTH 80
GC_CONTENT 0.3 BASEPAIR 25 FREE_ENERGY -15.40 LEN_BP_RATIO

3.2

CAUUAAGUUGAUUUUGGCAUCAUCUAAUGCAAUUUGUAUAUCAUUUUCUGUAAUUCUAUACUUU
UUUGUGAGAGCAGUCAGUUUCUCCUUG

>random_seq_from_cds__NO_7641 RANDOM_LENGTH 100 SEQ_LENGTH 67
GC_CONTENT 0.373134328358209 BASEPAIR 23 FREE_ENERGY
-19.30 LEN_BP_RATIO 2.91304347826087

UUGCAAGGUCUCAAAAAAUGGGAGGUUAAUGGAGUGAACAUUCUUGGUUUUUUAUCAUACUUUACAA
AAGCAACAAUUGUAAAUCUUGGGGCUUCUCAACG

>random_seq_from_cds__NO_7644 RANDOM_LENGTH 75 SEQ_LENGTH 59
GC_CONTENT 0.542372881355932 BASEPAIR 20 FREE_ENERGY
-21.20 LEN_BP_RATIO 2.95

GUUGUAAAUUGGGUCUUGAGUUUCCAGGUGCCUGUCUGCUCAGCUGGAGUAAGCAGGGCACUGA
CUUUGUGUUC

>random_seq_from_cds__NO_7673 RANDOM_LENGTH 82 SEQ_LENGTH 77
GC_CONTENT 0.558441558441558 BASEPAIR 29 FREE_ENERGY
-24.10 LEN_BP_RATIO 2.6551724137931

UCCAUUUGGAGAAGCAGUUUGGCAGGCGACCAGUGGGCGAGGAUCUCACUUCUGGCUUCUGCUUG
CAAACGGGGUAUGGAAA

>random_seq_from_cds__NO_7677 RANDOM_LENGTH 90 SEQ_LENGTH 78
GC_CONTENT 0.525641025641026 BASEPAIR 22 FREE_ENERGY
-22.87 LEN_BP_RATIO 3.54545454545455

UGCUCGCACCCUUCUGCUUGAGUUACAAACUUCAGGGUAUCCACCAAGGCUCUGUCCUCUCUCU
GGAGCUCAUAGGUUGCGCUGACAGA

>random_seq_from_cds__NO_7683 RANDOM_LENGTH 75 SEQ_LENGTH 63
GC_CONTENT 0.53968253968254 BASEPAIR 20 FREE_ENERGY
-17.30 LEN_BP_RATIO 3.15

CUUGGCUCCGGGAGCAAUGACUCCAGAUGAAGAUUUUGCAACUGUAAUCCAGCUCAGUGGGGA
GUUCAAGGC

>random_seq_from_cds__NO_7690 RANDOM_LENGTH 83 SEQ_LENGTH 68
GC_CONTENT 0.352941176470588 BASEPAIR 27 FREE_ENERGY
-16.70 LEN_BP_RATIO 2.51851851851852

UAUUUGGAUCAAAUUAUAAGAUUCCUUCUAUUUUGGCUGAGGCUGGGUCAAGUGAUGGAAGAGAA
ACAGAUUUGUAGAGUUGA

>random_seq_from_cds__NO_7694 RANDOM_LENGTH 81 SEQ_LENGTH 68
GC_CONTENT 0.529411764705882 BASEPAIR 25 FREE_ENERGY
-22.10 LEN_BP_RATIO 2.72

UCUGAAGAAGAACCUCUGGUCCUUGUCUUUAGGCUCCAUUUCCGCAGAGCCUGGAUGGCAGC
UUUCUGGAUCAUCAGU

>random_seq_from_cds__NO_7695 RANDOM_LENGTH 85 SEQ_LENGTH 66
GC_CONTENT 0.454545454545455 BASEPAIR 25 FREE_ENERGY
-21.70 LEN_BP_RATIO 2.64

GAUGGCUUUGUACUUUGGACACAUUUCAGGAUUGAAGACUUGAGUUCUGGAGUUAACUGCUCCAU
GGUUUGGCCCAUAAUUUCCAA

>random_seq_from_cds__NO_7709 RANDOM_LENGTH 70 SEQ_LENGTH 55

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GC_CONTENT    0.581818181818182    BASEPAIR    23    FREE_ENERGY
-31.70    LEN_BP_RATIO    2.39130434782609
CUGGCUGGUCUUCAGGAUGAAGCUGCAGAGCUGGGGAACCUCCAGCUCAACCCUUGCAGUUGAUC
CUGGU
>random_seq_from_cds__NO_7711    RANDOM_LENGTH    80    SEQ_LENGTH    61
GC_CONTENT    0.655737704918033    BASEPAIR    19    FREE_ENERGY
-21.80    LEN_BP_RATIO    3.21052631578947
GUGCUUGAAUCGGGUCGCAUCUUCUUGGACAGACCAGGCUGACAUUUUCCAGCAUUUCCUCUUC
GGCCUGGCGCCCGC
>random_seq_from_cds__NO_7713    RANDOM_LENGTH    67    SEQ_LENGTH    55
GC_CONTENT    0.563636363636364    BASEPAIR    19    FREE_ENERGY
-21.70    LEN_BP_RATIO    2.89473684210526
UGACAGAGGGGCCAUUGGGGAAGGUGGCUAGCUUAUCCCCGCCCCUUCAGAAGAAGGUCAGCAGC
UC
>random_seq_from_cds__NO_7719    RANDOM_LENGTH    67    SEQ_LENGTH    60
GC_CONTENT    0.416666666666667    BASEPAIR    22    FREE_ENERGY
-17.00    LEN_BP_RATIO    2.72727272727273
GAUUUCAUUGAGGAAACGCAGACACUCAAUACCACCAUUGUUGAUGCUCUCCUCUGUGUAGAAGU
CA
>random_seq_from_cds__NO_7730    RANDOM_LENGTH    70    SEQ_LENGTH    58
GC_CONTENT    0.637931034482759    BASEPAIR    22    FREE_ENERGY
-21.60    LEN_BP_RATIO    2.63636363636364
CCAGGGCCGUGCAGAGCAGGACGACGCAGGAGCAGCUGAAGGCAGCCCCACUCUGCUUCUCCUUC
UCCAC
>random_seq_from_cds__NO_7733    RANDOM_LENGTH    82    SEQ_LENGTH    68
GC_CONTENT    0.676470588235294    BASEPAIR    24    FREE_ENERGY
-33.10    LEN_BP_RATIO    2.83333333333333
GCGCAGCCUCCGCGUGGGUUGGGGAUGAGGGUUGUCGGCCUGGGCAUCCUGCUCUCCUGGGC
UUCUCCGACGUGGACCC
>random_seq_from_cds__NO_7734    RANDOM_LENGTH    71    SEQ_LENGTH    55
GC_CONTENT    0.636363636363636    BASEPAIR    20    FREE_ENERGY
-26.90    LEN_BP_RATIO    2.75
ACUGCUGUGGGCACUCCCGUUGGGCUCCUUGGUCUCAAUUGAGGGCAGGGGAGCUGGACUUUGAGG
AAGCUG
>random_seq_from_cds__NO_7742    RANDOM_LENGTH    78    SEQ_LENGTH    66
GC_CONTENT    0.575757575757576    BASEPAIR    19    FREE_ENERGY
-16.20    LEN_BP_RATIO    3.47368421052632
GAACUGCUGCUGGUCCUUCUGGCUCUCGUCUUUCUUAUGUCUUUCAGCAUCUCGUCAGCCACGU
GCUUGGGCAGGAU
>random_seq_from_cds__NO_7744    RANDOM_LENGTH    89    SEQ_LENGTH    71
GC_CONTENT    0.619718309859155    BASEPAIR    21    FREE_ENERGY
-18.90    LEN_BP_RATIO    3.38095238095238
GUAGUAGGACAUGAUGCCCACAGCGAUGGCGCACAGGUAGAGGAAGACGUUGGCCAGGAUCCUCC
CGCAGCAGCUGCAUCCCUUGAGC
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>random_seq_from_cds__NO_7750 RANDOM_LENGTH 72 SEQ_LENGTH 57
  GC_CONTENT 0.614035087719298 BASEPAIR 20 FREE_ENERGY
  -20.80 LEN_BP_RATIO 2.85
CAGCACCAGCAGGGUCUCGUGGCGCUGCCUUUUGAAGUAGGUCUGGUAGAGGUUCUCCAAGGACU
CCGGCAC
>random_seq_from_cds__NO_7764 RANDOM_LENGTH 71 SEQ_LENGTH 52
  GC_CONTENT 0.596153846153846 BASEPAIR 20 FREE_ENERGY
  -17.80 LEN_BP_RATIO 2.6
UGCACUCCAGUCCAUGUGCUCGUGCCUGUGGUACAAGAGCCGCGAGAAGCUGCAGUACUCCAUC
CCCAUG
>random_seq_from_cds__NO_7767 RANDOM_LENGTH 75 SEQ_LENGTH 58
  GC_CONTENT 0.827586206896552 BASEPAIR 21 FREE_ENERGY
  -30.60 LEN_BP_RATIO 2.76190476190476
CGUGUGACAUGGGCCCGCGCCGCGGAGCCGAAAGCCCGAGGCCCGGAGGAGGCGCAGCCCGAGC
CCGACCCCGA
>random_seq_from_cds__NO_7839 RANDOM_LENGTH 84 SEQ_LENGTH 72
  GC_CONTENT 0.666666666666667 BASEPAIR 25 FREE_ENERGY
  -27.70 LEN_BP_RATIO 2.88
UCGGAGGAAGGACUUGAGGUCUCCCCCGCAUGAGCUCCAGCAGGAUGAACCGGGGCAGGGAUU
GCAGGCUCACCCCAUGCA
>random_seq_from_cds__NO_7843 RANDOM_LENGTH 72 SEQ_LENGTH 56
  GC_CONTENT 0.607142857142857 BASEPAIR 22 FREE_ENERGY
  -23.60 LEN_BP_RATIO 2.54545454545455
CAGCUUGUACUCAGGGCUCUGCAGCUCCAUCUGCAUGGCUUGCAGCUCCUGGUGCUUCCGGCGGU
ACACCAA
>random_seq_from_cds__NO_7845 RANDOM_LENGTH 84 SEQ_LENGTH 60
  GC_CONTENT 0.666666666666667 BASEPAIR 19 FREE_ENERGY
  -28.30 LEN_BP_RATIO 3.15789473684211
GUGGCUCGCGGGUGGGUGACACCAAUGCAGGAGACGCCAUCCUCAGCCAGCACCGUCCGUGGUC
ACAGAAGCAGAUGACCUUG
>random_seq_from_cds__NO_7864 RANDOM_LENGTH 72 SEQ_LENGTH 56
  GC_CONTENT 0.571428571428571 BASEPAIR 19 FREE_ENERGY
  -18.40 LEN_BP_RATIO 2.94736842105263
AGUCCUGGUGGAAGUCACAGGCCUGCCCAAGCUGGAGGACUGUCCCAUCCAACAAGUGAAGGAG
CUCUGCA
>random_seq_from_cds__NO_7866 RANDOM_LENGTH 85 SEQ_LENGTH 66
  GC_CONTENT 0.545454545454545 BASEPAIR 25 FREE_ENERGY
  -27.70 LEN_BP_RATIO 2.64
UCCACUGGAGAUGUAUCCAGGGCCACUCGAAAUGGGUUGUCUGGACGCCCGAUUCUCCUGGA
GCACUGUCCAACCCAUGCUU
>random_seq_from_cds__NO_7869 RANDOM_LENGTH 81 SEQ_LENGTH 72
  GC_CONTENT 0.597222222222222 BASEPAIR 27 FREE_ENERGY
  -31.00 LEN_BP_RATIO 2.66666666666667
UGCUUGGAGUCAGCUGAGGUGUUGAGAAGGAGAAAGGAGCCUCUGGGCAUCUCCUAGAACGCU
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CUGCCCCAGGCCCAUC
>random_seq_from_cds__NO_7873 RANDOM_LENGTH 86 SEQ_LENGTH 76
  GC_CONTENT 0.671052631578947 BASEPAIR 27 FREE_ENERGY
  -36.00 LEN_BP_RATIO 2.81481481481481
CCCGAAGAUCUGGAAGAGAAGGCGGGGCGUGGGAGGCGCGAAUUGCCGCGGACAGCCUCCUCUC
UGCCCACUCCGACGCCUUCU
>random_seq_from_cds__NO_7881 RANDOM_LENGTH 84 SEQ_LENGTH 70
  GC_CONTENT 0.528571428571429 BASEPAIR 29 FREE_ENERGY
  -26.20 LEN_BP_RATIO 2.41379310344828
AGGGUUUGCAGUUUUCUGGGACACCAGUGACACACCAGGGUGGUGAACUUGUCCACGCAGGCAUU
GCGGAUCUUCUCCGGGGUG
>random_seq_from_cds__NO_7890 RANDOM_LENGTH 78 SEQ_LENGTH 69
  GC_CONTENT 0.623188405797101 BASEPAIR 23 FREE_ENERGY
  -23.10 LEN_BP_RATIO 3
GAGCUCUACUGGCCACCCUGGACCAUUUUGGUAUGAAGGCCUUGGCCCAUCUCAGUCCCCCGUG
GGUCAGCAGCACA
>random_seq_from_cds__NO_7893 RANDOM_LENGTH 71 SEQ_LENGTH 60
  GC_CONTENT 0.533333333333333 BASEPAIR 24 FREE_ENERGY
  -21.60 LEN_BP_RATIO 2.5
GAUACUGAGAGCUUGCUAGGCAUUCUCCAGCAUCUGGGCAAGGUGAAACCCUCAAGCUUCUGG
UUGAAG
>random_seq_from_cds__NO_7901 RANDOM_LENGTH 96 SEQ_LENGTH 89
  GC_CONTENT 0.49438202247191 BASEPAIR 32 FREE_ENERGY
  -21.80 LEN_BP_RATIO 2.78125
UUGGAACAGCAAUGGUGCAGUGAGUCUCCAGGUAGAAGUGCUCUUGGCCACCGAUGUAUAUCUCC
CCCUGACACAACAUUAUCUGCUUCGGAAAAC
>random_seq_from_cds__NO_7929 RANDOM_LENGTH 66 SEQ_LENGTH 49
  GC_CONTENT 0.387755102040816 BASEPAIR 19 FREE_ENERGY
  -15.50 LEN_BP_RATIO 2.57894736842105
UUUUUUUCUAUAAGGAAUGACUGUAGUCAAAUACUGUGCCGGGCAUAUGACUUCUCUCAUUCU
C
>random_seq_from_cds__NO_7932 RANDOM_LENGTH 89 SEQ_LENGTH 59
  GC_CONTENT 0.457627118644068 BASEPAIR 20 FREE_ENERGY
  -15.66 LEN_BP_RATIO 2.95
GCACCAGCUCCUCAGAGUACUCCUUAUGGCAGUCUCAAUUUCUCCAGGAUUUCAUUUAACUCA
GACACUGAGAGCCUUUUCACUCCU
>random_seq_from_cds__NO_7933 RANDOM_LENGTH 87 SEQ_LENGTH 74
  GC_CONTENT 0.445945945945946 BASEPAIR 25 FREE_ENERGY
  -15.10 LEN_BP_RATIO 2.96
CUCUUCAUAACUGCCGGUACUAGACCUCUUGAGAGUUUGAAUUUCCUGGGAAAGCAUUGAAAGCC
GAUCUGACUGUGUAGGGGUUC
>random_seq_from_cds__NO_7934 RANDOM_LENGTH 109 SEQ_LENGTH 93
  GC_CONTENT 0.451612903225806 BASEPAIR 29 FREE_ENERGY
  -24.42 LEN_BP_RATIO 3.20689655172414
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AUCAUCUUCUGGGUCCGGUGAUUCCUGCAUCAUUUCUUCAAUUCUUCAAUAACCCUGGUCUGCC
GUGAAGAGGGGUUCAUCAUUAACACAGGAGACGAUGAUUGAGUG

>random_seq_from_cds__NO_7948 RANDOM_LENGTH 94 SEQ_LENGTH 85
GC_CONTENT 0.588235294117647 BASEPAIR 32 FREE_ENERGY
-27.60 LEN_BP_RATIO 2.65625

GGGGGGCGGCCCGGGCCGAAGGCUUUCGCAGUGCCUCAAGAACUUGUCCAGGAUGAAGUUGCUG
AAGUUGCGGUUGAGCUGCUCGAAUUCGCG

>random_seq_from_cds__NO_7951 RANDOM_LENGTH 95 SEQ_LENGTH 89
GC_CONTENT 0.786516853932584 BASEPAIR 34 FREE_ENERGY
-47.50 LEN_BP_RATIO 2.61764705882353

GGGCCGUCGCGCUGCCGCGCACCAGCAGCGCCACCAGCUCGCGCGCCUCGCUCAGCACGUGGC
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>random_seq_from_cds__NO_7955 RANDOM_LENGTH 80 SEQ_LENGTH 65
GC_CONTENT 0.815384615384615 BASEPAIR 22 FREE_ENERGY
-36.50 LEN_BP_RATIO 2.95454545454545

CCGCCUGGCCACCGCCGCGCGUUCGCAUCAGUGGCCACGCAAACGGGCCCGGGGGCGCGGAC
CGGAGCUGCCGCCUC

>random_seq_from_cds__NO_7958 RANDOM_LENGTH 88 SEQ_LENGTH 79
GC_CONTENT 0.721518987341772 BASEPAIR 28 FREE_ENERGY
-37.60 LEN_BP_RATIO 2.82142857142857

GCAGGCGGCGCCAGGGUCGAGGCUGGGAGACUCAGAGCCGCUGAGGCUGCCGAGCUCAGGGAG
CCGCUUAGGUAGCUGUCGCGGUC

>random_seq_from_cds__NO_7963 RANDOM_LENGTH 80 SEQ_LENGTH 68
GC_CONTENT 0.838235294117647 BASEPAIR 24 FREE_ENERGY
-47.60 LEN_BP_RATIO 2.83333333333333

GUCCUCGGCGCCCCCGGUGCCGUACAGCAGAGCGGCCGAGCCGCGGCCGCGCGGAGGCGCAGC
AUGUCGGGGCGCCCCG

>random_seq_from_cds__NO_7969 RANDOM_LENGTH 71 SEQ_LENGTH 57
GC_CONTENT 0.684210526315789 BASEPAIR 19 FREE_ENERGY
-23.30 LEN_BP_RATIO 3

GAAGGGCCGGCACAGCUCGGUCUUGUAGCGGUGGAGUUGAUCUGGGAGCCGCCGCCCCCUUCU
GCUGCU

>random_seq_from_cds__NO_7976 RANDOM_LENGTH 85 SEQ_LENGTH 79
GC_CONTENT 0.417721518987342 BASEPAIR 26 FREE_ENERGY
-22.40 LEN_BP_RATIO 3.03846153846154

UGGGCAGGUUUUCUCAAUGAAUUGAAUCCUUGAGUGAAGGCACACAUUGGAUUAGUUGUCACAG
AAACAUUUGAGCUGCCACA

>random_seq_from_cds__NO_7986 RANDOM_LENGTH 98 SEQ_LENGTH 89
GC_CONTENT 0.393258426966292 BASEPAIR 31 FREE_ENERGY
-17.80 LEN_BP_RATIO 2.87096774193548

UUCAAAGUUUUAUGACAAAUUGCUGAUUUUCUUGUAGGCAGAUUCUAUCAUCUGGACUCUCUUGA
GGUUUCUAUUUCCCGUUCUUGCUUUGGGUAUC

>random_seq_from_cds__NO_7997 RANDOM_LENGTH 89 SEQ_LENGTH 76
GC_CONTENT 0.605263157894737 BASEPAIR 26 FREE_ENERGY

-31.20 LEN_BP_RATIO 2.92307692307692
GGAGCUCUGGGAGCCUCUGUUUACUUGGAGACCCAUGGACCCUCCGGGGGUCAAAGAUGAGAGGU
CACCCAUCAUGGCGCCCCCGCAGG
>random_seq_from_cds__NO_7998 RANDOM_LENGTH 78 SEQ_LENGTH 70
GC_CONTENT 0.614285714285714 BASEPAIR 25 FREE_ENERGY
-27.10 LEN_BP_RATIO 2.8
UCCUCGCGUUCGGGCUUCUGCUUGCCGCGGCGACGGCGACUUUUGCCGCGAGCUCAGGAAGGAAUG
UGUCUGUGAAAAC
>random_seq_from_cds__NO_8009 RANDOM_LENGTH 71 SEQ_LENGTH 52
GC_CONTENT 0.673076923076923 BASEPAIR 21 FREE_ENERGY
-24.60 LEN_BP_RATIO 2.47619047619048
AGGAGACGCGCAGUUGGAGAGCGCGGCCGAGGUCGGCUUCGUGCGCUUCUUUCAGGGCAUGCCG
GAGAAG
>random_seq_from_cds__NO_8034 RANDOM_LENGTH 81 SEQ_LENGTH 66
GC_CONTENT 0.5303030303030303 BASEPAIR 21 FREE_ENERGY
-23.04 LEN_BP_RATIO 3.14285714285714
GUCAGCAGAAGUGUCCAUGUGGACUGCAUCUUAGCCCGAGUAGGGGCUUGGUGACAGUCAAUUGA
AAGGAGUCUCCACGUU
>random_seq_from_cds__NO_8038 RANDOM_LENGTH 110 SEQ_LENGTH 92
GC_CONTENT 0.402173913043478 BASEPAIR 30 FREE_ENERGY
-24.42 LEN_BP_RATIO 3.06666666666667
UAACUAUGCUUUUAUCAGGUGAAGAAAGGGUGUCUGUGAUCAAAGUUUUGGGAUUCAUGUUGCAGA
GCUUGCUAAUUUCCUAAGCAUGUAAUAGAGUGUCUAAAACAGAA
>random_seq_from_cds__NO_8049 RANDOM_LENGTH 94 SEQ_LENGTH 81
GC_CONTENT 0.802469135802469 BASEPAIR 32 FREE_ENERGY
-48.10 LEN_BP_RATIO 2.53125
GGUACACCGAGGGCUUCCAGCCCGCCAGGCUGUCGGCCUCCGAGAGCGCGGAGCCGCGGCGGAAG
GUGGCGGGCAGCAGGCCGUGCGGCGCAG
>random_seq_from_cds__NO_8051 RANDOM_LENGTH 69 SEQ_LENGTH 57
GC_CONTENT 0.666666666666667 BASEPAIR 22 FREE_ENERGY
-29.50 LEN_BP_RATIO 2.59090909090909
AGCCCGUAGGCGAUGAGGAAGCCUUCGCCACCGUCGCGGGGUGGUCAUGCCGAAACCCUA
UGGU
>random_seq_from_cds__NO_8076 RANDOM_LENGTH 86 SEQ_LENGTH 77
GC_CONTENT 0.467532467532468 BASEPAIR 24 FREE_ENERGY
-20.50 LEN_BP_RATIO 3.20833333333333
UGCCGGUUUGAGCUGAUGCGUUUCAAGACUUUGUAUAAUGGGGAUAAUCUUCUUUCCUUGAA
GUCUGUAGUGGUUGUCCAGGG
>random_seq_from_cds__NO_8079 RANDOM_LENGTH 63 SEQ_LENGTH 46
GC_CONTENT 0.434782608695652 BASEPAIR 19 FREE_ENERGY
-19.20 LEN_BP_RATIO 2.42105263157895
UGUCUGGGGAGUUUACAGGAACUUGAAUCUGAACCCUGUCAUUAAGUCACUGUGGGGUCAGCA
>random_seq_from_cds__NO_8096 RANDOM_LENGTH 110 SEQ_LENGTH 98
GC_CONTENT 0.418367346938776 BASEPAIR 31 FREE_ENERGY

-21.50 LEN_BP_RATIO 3.16129032258065
GAAGGUACCUGAAGAAGAAGCUGACAGUAUUUCAAAUGAGGAUUCAGCCACAAACAGUAGUGAUA
AUGAAGACCCUCAAGUAAACAUUGUAGAAGAGGGACCCUUUAAA
>random_seq_from_cds__NO_8115 RANDOM_LENGTH 110 SEQ_LENGTH 84
GC_CONTENT 0.357142857142857 BASEPAIR 27 FREE_ENERGY
-19.02 LEN_BP_RATIO 3.11111111111111
AAAUUGUGGACAACUUUUGGGGUAAGUCACAAAAGAAGGAAAUUUGUUGAAAGUGCUGUGAUA
ACUCAAAUUUAUUGCCUCUGCUUUGUGAAUGGGAACCCUGGAAUGC
>random_seq_from_cds__NO_8134 RANDOM_LENGTH 82 SEQ_LENGTH 68
GC_CONTENT 0.426470588235294 BASEPAIR 24 FREE_ENERGY
-19.00 LEN_BP_RATIO 2.83333333333333
GCAUAAUCAGAAUGGCAUGUCUAAUCGCAGCUUUGGUCCAGGUGAAUAGCAUAGGUGAUGGUG
UGCCAUCUUUCUAGAGU
>random_seq_from_cds__NO_8143 RANDOM_LENGTH 70 SEQ_LENGTH 54
GC_CONTENT 0.592592592592593 BASEPAIR 19 FREE_ENERGY
-23.70 LEN_BP_RATIO 2.84210526315789
CCAUAGCUCGGCAGGGCCUGCAAUUUGGUGGAAGAAAUAUCCCAAGGUUUUCGGCCUGUGGCC
CACGG
>random_seq_from_cds__NO_8150 RANDOM_LENGTH 67 SEQ_LENGTH 51
GC_CONTENT 0.823529411764706 BASEPAIR 19 FREE_ENERGY
-29.40 LEN_BP_RATIO 2.68421052631579
CAGCGCAGGGCGCCGUCGGGCACGCAGUUGCAGGGCUCAGGGCAGAGCGCCUCGCGCAGCGCUCG
UG
>random_seq_from_cds__NO_8151 RANDOM_LENGTH 70 SEQ_LENGTH 55
GC_CONTENT 0.727272727272727 BASEPAIR 22 FREE_ENERGY
-33.20 LEN_BP_RATIO 2.5
GCAGCGGCGGCGUCGAGCAGCAGCAGCAGCUUCAGCAGCUGCAGCGCCGAGAACCGCUGCUUCAUC
AUGUC
>random_seq_from_cds__NO_8197 RANDOM_LENGTH 86 SEQ_LENGTH 50
GC_CONTENT 0.56 BASEPAIR 19 FREE_ENERGY -18.38
LEN_BP_RATIO 2.63157894736842
GAGAACUGCAUCCAACAGAGGGGAACAAAUUUCAGCGACCCAUCUGUGGAUCAUUGGAUCGG
CUCACCCAACCAGAUUAUAAC
>random_seq_from_cds__NO_8201 RANDOM_LENGTH 77 SEQ_LENGTH 52
GC_CONTENT 0.346153846153846 BASEPAIR 19 FREE_ENERGY
-16.50 LEN_BP_RATIO 2.73684210526316
AUUAUACUAUCCACACUUGAUUAGGGAGUAACAUGUACUUUUCUAUCAAGUGUUCUUGUACUGU
UUGAUCUGUUUG
>random_seq_from_cds__NO_8237 RANDOM_LENGTH 87 SEQ_LENGTH 70
GC_CONTENT 0.485714285714286 BASEPAIR 22 FREE_ENERGY
-17.50 LEN_BP_RATIO 3.18181818181818
UUCCCCUCCUGAAAGGAUGUCAUCGCAACAGAUAAAGAAGACGUUGCCUCAAAGACCUGGAUGU
GGCCAUCUUGUGGGCUCCAUG
>random_seq_from_cds__NO_8247 RANDOM_LENGTH 82 SEQ_LENGTH 64

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GC_CONTENT    0.515625  BASEPAIR   23  FREE_ENERGY   -22.40
LEN_BP_RATIO  2.78260869565217
AGCCAGCAACUGUAAAGGGAUCACGCUGAGAAUGCCCUGCAAGCAGUCCACUGAGUGGGGCACCU
UGAUCGUUCUUUUUGUG
>random_seq_from_cds__NO_8258  RANDOM_LENGTH 97  SEQ_LENGTH    78
GC_CONTENT    0.512820512820513  BASEPAIR   28  FREE_ENERGY
-26.61  LEN_BP_RATIO  2.78571428571429
GCCCCUUAUGAUCUGCUGGAGUCCAUCUGGAGUUUUGCACAGCUCGUCGGGGUGAUCUCCU
GCAGUUCGUUUAAUUCGAUGGAUAGAAAGACG
>random_seq_from_cds__NO_8264  RANDOM_LENGTH 90  SEQ_LENGTH    74
GC_CONTENT    0.364864864864865  BASEPAIR   26  FREE_ENERGY
-15.60  LEN_BP_RATIO  2.84615384615385
GUUUCAGAUUCGAAGUCAUAGCCUUUGCUUUCCAAAAACUUUUUCAAGUCUUUGUAGUUGGUGA
UGAUUCCAUGUGAAUAACGAUAAA
>random_seq_from_cds__NO_8265  RANDOM_LENGTH 78  SEQ_LENGTH    60
GC_CONTENT    0.566666666666667  BASEPAIR   20  FREE_ENERGY
-18.60  LEN_BP_RATIO  3
UUCCAUAUUUUUAUCAGAGCGCUGGGGGUGGCUAUUGACAGGACUGGGUUCUCCAUGUGUUGCC
CAACGGGUAUGAG
>random_seq_from_cds__NO_8293  RANDOM_LENGTH 83  SEQ_LENGTH    72
GC_CONTENT    0.652777777777778  BASEPAIR   23  FREE_ENERGY
-29.60  LEN_BP_RATIO  3.1304347826087
CUCCGAGGCCUUUGCCACCUCCAACAUCUGCGGCUGCUGGAGCAGGGCCGGCUGCUCUCUGUGC
CCAGGGCCCUAGCCUCC
>random_seq_from_cds__NO_8298  RANDOM_LENGTH 85  SEQ_LENGTH    71
GC_CONTENT    0.577464788732394  BASEPAIR   22  FREE_ENERGY
-21.96  LEN_BP_RATIO  3.22727272727273
CCGAGAACAUCAGCAGGCGGUCACCCGAAACUACAUCACCCACCCCGUGUCAGCCUACAGGACU
GUGUGCAGCGUGAACGGGCC
>random_seq_from_cds__NO_8300  RANDOM_LENGTH 87  SEQ_LENGTH    74
GC_CONTENT    0.554054054054054  BASEPAIR   29  FREE_ENERGY
-26.10  LEN_BP_RATIO  2.55172413793103
UGCUUGAGGUGGCUGGCACCAAGGCGAUUGUUCAGGGUGUUUGAAGGGACAUCAGGGAUUCGAUGC
CAGGAAGACCACUUGCGAAUUU
>random_seq_from_cds__NO_8375  RANDOM_LENGTH 89  SEQ_LENGTH    68
GC_CONTENT    0.338235294117647  BASEPAIR   26  FREE_ENERGY
-16.60  LEN_BP_RATIO  2.61538461538462
GCCCGAAGACCCUUCUACUUAGUUACUGUAGAUGAAAUACAAGAUGACAGCAGUGAUUUGCAUU
UAGUGACUUUGGAUGAAGUAACUG
>random_seq_from_cds__NO_8376  RANDOM_LENGTH 110  SEQ_LENGTH    59
GC_CONTENT    0.355932203389831  BASEPAIR   20  FREE_ENERGY
-16.80  LEN_BP_RATIO  2.95
AAGAGGAUGAAGACUCUCUGGCGGAUUUUACAACCUAAAAGAAGAGCUAAUUUUUGUACUGUU
GAUGAAGUUGGAGAGGAGGAAGAUGGAGAUAAUGAUUUAAAAGUU
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>random_seq_from_cds__NO_8403 RANDOM_LENGTH 99 SEQ_LENGTH 81
  GC_CONTENT 0.604938271604938 BASEPAIR 26 FREE_ENERGY
-28.00 LEN_BP_RATIO 3.11538461538462
AGUCCAGAGAGUUCACAGGCUUCCAGACCCCUACACAGAGCUCAACACAGGCAAGGGGGGAAG
GUGUGGCUUAUCGUGGCCGGCUUCUGCUCUCCCU
>random_seq_from_cds__NO_8409 RANDOM_LENGTH 73 SEQ_LENGTH 66
  GC_CONTENT 0.636363636363636 BASEPAIR 23 FREE_ENERGY
-15.40 LEN_BP_RATIO 2.8695652173913
ACCAGUACCUGUACCAGCUGCGCACCCAUCACCUGAGCCAAAUCACUGAGGCUGCCCUGGCCUG
AAGCUCGG
>random_seq_from_cds__NO_8414 RANDOM_LENGTH 85 SEQ_LENGTH 69
  GC_CONTENT 0.492753623188406 BASEPAIR 26 FREE_ENERGY
-21.50 LEN_BP_RATIO 2.65384615384615
AGUUUGCUGAGGGGAAGCUGUCUGUCUUUGCUGAAACCGUAUGAGAACGAGACUAAGUUGGCCCU
UGUUGGGAACUGGGGCACAA
>random_seq_from_cds__NO_8425 RANDOM_LENGTH 78 SEQ_LENGTH 58
  GC_CONTENT 0.603448275862069 BASEPAIR 19 FREE_ENERGY
-16.30 LEN_BP_RATIO 3.05263157894737
GAACACCCUUAACCCCACCGGGACCAGACGCUCAUCUUCUACGAGAUCGAGAUCUUUGGCGAGC
CGGCCACAGUUGC
>random_seq_from_cds__NO_8435 RANDOM_LENGTH 88 SEQ_LENGTH 69
  GC_CONTENT 0.565217391304348 BASEPAIR 25 FREE_ENERGY
-32.60 LEN_BP_RATIO 2.76
AGCCCCUCAUCCCAUCCAGGGAGGAAGAGUUAUCGAUUGGUGGAGCAAUUCUUUGCCUCCAU
AGGGGAGAGGGAAAAGUGCGGCU
>random_seq_from_cds__NO_8436 RANDOM_LENGTH 97 SEQ_LENGTH 81
  GC_CONTENT 0.493827160493827 BASEPAIR 28 FREE_ENERGY
-28.90 LEN_BP_RATIO 2.89285714285714
CCUACCUGGAGAAGGAUUUUGACACCCUGAAGGGUCUAUGACACACAGCUGGAGAAUGUGGAGGC
CUUUGAGGGCCUGUCUGACUUUUGUAACACCU
>random_seq_from_cds__NO_8438 RANDOM_LENGTH 85 SEQ_LENGTH 67
  GC_CONTENT 0.671641791044776 BASEPAIR 19 FREE_ENERGY
-21.20 LEN_BP_RATIO 3.52631578947368
UCCCGAAGACCCAGCCAUCCCAUGCCCCAAGACAGUUCACCAGCUGGCCGCCAGGGACCC
CAGGAGUGCUUGGUCCGUAU
>random_seq_from_cds__NO_8445 RANDOM_LENGTH 110 SEQ_LENGTH 94
  GC_CONTENT 0.680851063829787 BASEPAIR 35 FREE_ENERGY
-51.32 LEN_BP_RATIO 2.68571428571429
CUGGUCCCGGAGCACGUGGAGUCACGGCCCCUCUACAGCCCCUGCAGCCAGACAUCGAGCAGGG
GGAAGCUGCAGAUGUGGGUCGACCUAUUUCCGAAGGCCCUUGGGGC
>random_seq_from_cds__NO_8473 RANDOM_LENGTH 86 SEQ_LENGTH 72
  GC_CONTENT 0.472222222222222 BASEPAIR 22 FREE_ENERGY
-20.40 LEN_BP_RATIO 3.27272727272727
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  -20.60 LEN_BP_RATIO 2.958333333333333
ACCUGAAGAGGCACAGAAAGUUUCACCUUUCUUGGACCAGCUGACCAGAAGACUGGGACACCAA
CUCCAACCUCUGCUUCUACUCA
>random_seq_from_cds__NO_8509 RANDOM_LENGTH 73 SEQ_LENGTH 48
  GC_CONTENT 0.5 BASEPAIR 20 FREE_ENERGY -19.30 LEN_BP_RATIO
  2.4
CUGUAACCUCCCCUCCAGCUCAUUUGGAGAGAAGCCCAUUGUUAUCUACAAACAGGCCUUUCCA
GAGGGUCA
>random_seq_from_cds__NO_8565 RANDOM_LENGTH 110 SEQ_LENGTH 89
  GC_CONTENT 0.438202247191011 BASEPAIR 28 FREE_ENERGY
  -19.40 LEN_BP_RATIO 3.17857142857143
AAAUACAAGUGAACAUUUCAGAUUUCGAAGGACAUUCCAAUCCAGAGGGGACCCAGUAUUUGCA
GAUCGGAUUACCAGAGAAGAUGAAGACCCACUUUCUGCUUUCUC
>random_seq_from_cds__NO_8582 RANDOM_LENGTH 110 SEQ_LENGTH 75
  GC_CONTENT 0.466666666666667 BASEPAIR 27 FREE_ENERGY
  -23.20 LEN_BP_RATIO 2.777777777777778
UUUCUCAGAAUCCAAUCACACAUCUCUCCAGGUCUCAGAAAGUACACAUGAUGAUAGCAGAGGG
GAACGAAGUGUGAAGGAAUGGAGUGGUAGACAACAGCAGAGAAAU
>random_seq_from_cds__NO_8593 RANDOM_LENGTH 80 SEQ_LENGTH 57
  GC_CONTENT 0.385964912280702 BASEPAIR 19 FREE_ENERGY
  -16.10 LEN_BP_RATIO 3
UGAGGACAGAAAGUUAAAAAAGAACAAGAAGAAUCCCAUGAAGGGAGUUUCCUGGUUUGUCCU
GUGGAAAAUGUGGAG
>random_seq_from_cds__NO_8597 RANDOM_LENGTH 110 SEQ_LENGTH 86
  GC_CONTENT 0.558139534883721 BASEPAIR 27 FREE_ENERGY
  -22.20 LEN_BP_RATIO 3.18518518518519
GAUAAAAGCGCCUGAAGUAAUAGUCCAGGAGAGGAAGCUGCAGAGCAUGUUACAGACCGAGCGGG
AUGCACUAUUCAACAUUGACAGGGAACGGCAGGGCCACCAGAAUC
>random_seq_from_cds__NO_8609 RANDOM_LENGTH 67 SEQ_LENGTH 54
  GC_CONTENT 0.574074074074074 BASEPAIR 21 FREE_ENERGY
  -24.80 LEN_BP_RATIO 2.57142857142857
AAUGAGAUGGCCACAGCAGCUUCCUCUCCUCCUGGAGAAGAGCUAUGAGCUGCCAGAUGGGCA
GG
>random_seq_from_cds__NO_8651 RANDOM_LENGTH 72 SEQ_LENGTH 62
  GC_CONTENT 0.887096774193548 BASEPAIR 21 FREE_ENERGY
  -34.90 LEN_BP_RATIO 2.95238095238095
UCCAGCCGUGCUACGCGGCCCGCCGCCCGGCCGUCUCCGUCGCCCGGGCCUCCCCGAGCCGCC
UCUCGGC
>random_seq_from_cds__NO_8653 RANDOM_LENGTH 87 SEQ_LENGTH 79
  GC_CONTENT 0.683544303797468 BASEPAIR 27 FREE_ENERGY
  -33.20 LEN_BP_RATIO 2.92592592592593
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UGCAGAGUCAGCGCUUUGGGACCAAGGAGGUGGAGGAAGACCUGGGCCGUGCUCUACCCGGCCAG
UCCCCACGGCGUAGCGCGGCUC

>random_seq_from_cds__NO_8663 RANDOM_LENGTH 81 SEQ_LENGTH 69
GC_CONTENT 0.579710144927536 BASEPAIR 23 FREE_ENERGY
-26.60 LEN_BP_RATIO 3

CAUGCCCUUCCCAGGACUCCCUAUACUCAGACCCCUUGGACAGCACGUCUGCUCAGGCAGGAGAG
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>random_seq_from_cds__NO_8666 RANDOM_LENGTH 99 SEQ_LENGTH 79
GC_CONTENT 0.645569620253165 BASEPAIR 20 FREE_ENERGY
-22.02 LEN_BP_RATIO 3.95

CAACCCUGCCACUGAUGACUACGCUGUGCCACCCCCUCGGAGCACAAAGCCCCUCCUUGCUCCCA
AGCCCCAGGGCCCAGCCUUCCCUGAACCUGGUAC

>random_seq_from_cds__NO_8668 RANDOM_LENGTH 69 SEQ_LENGTH 59
GC_CONTENT 0.491525423728814 BASEPAIR 21 FREE_ENERGY
-18.50 LEN_BP_RATIO 2.80952380952381

GUAGGGACUGACAAGACUGGGGUCAAGUCAGAGGGCUCUACCUGAUCUAGUUUUUGAACUUGCAA
ACAA

>random_seq_from_cds__NO_8674 RANDOM_LENGTH 81 SEQ_LENGTH 54
GC_CONTENT 0.518518518518518 BASEPAIR 24 FREE_ENERGY
-43.20 LEN_BP_RATIO 2.25

CAGGAACAUCAGGGAGGAGAUCAUGAAGAACGAGUUGGUCUGAGCCAUCAUGGCUCAGACCA
GCUCAUACUUCAUGCU

>random_seq_from_cds__NO_8679 RANDOM_LENGTH 73 SEQ_LENGTH 65
GC_CONTENT 0.6 BASEPAIR 21 FREE_ENERGY -25.80 LEN_BP_RATIO
3.0952380952381

AGCAGUGGGUCCUGGUCUCCUACAAGUCCUGGGGCAUUGGAGCCCCAAGCAGUGUAAUCCUGG
CUACUGUG

>random_seq_from_cds__NO_8702 RANDOM_LENGTH 110 SEQ_LENGTH 93
GC_CONTENT 0.666666666666667 BASEPAIR 34 FREE_ENERGY
-39.20 LEN_BP_RATIO 2.73529411764706

AGGCGUCGGACGGCAGCCUCCUGGGGGACCUCGGGCACACACCACUUAGCAAGAAGGAGGUUAUC
AAGUGGCAGAGGCCGAGGCUCAGCCGCCAGGCUUUGAUGAGAUGC

>random_seq_from_cds__NO_8706 RANDOM_LENGTH 97 SEQ_LENGTH 73
GC_CONTENT 0.63013698630137 BASEPAIR 28 FREE_ENERGY
-37.60 LEN_BP_RATIO 2.60714285714286

AACGCCUUGAUGCGGACGGGAACGGGGCAUCCACUUUGAGGGACUUUGUGGUUGGCCUCUCCA
UCCUGCUGCGGGGCACAGUCCACGAGAAGCUC

>random_seq_from_cds__NO_8718 RANDOM_LENGTH 81 SEQ_LENGTH 74
GC_CONTENT 0.756756756756757 BASEPAIR 27 FREE_ENERGY
-34.00 LEN_BP_RATIO 2.74074074074074

AGCACAUGAGCCGGCUGUCGGGCCGGAGCUCCGCCACCGAGGCACUGCCUCGUCCAGCACCCAC
GGCCCCGCGCCAGCUCC

>random_seq_from_cds__NO_8741 RANDOM_LENGTH 87 SEQ_LENGTH 67
GC_CONTENT 0.597014925373134 BASEPAIR 22 FREE_ENERGY

-25.50 LEN_BP_RATIO 3.04545454545455
CUCUGGUCCAGCUUCACCUCAAACCAGGCACCAGGGUUACUUAAGAUGGCCCCAGGGCCAUAAGGGU
AGAGACUGAGCAUUAUGAAGAA

>random_seq_from_cds__NO_8743 RANDOM_LENGTH 81 SEQ_LENGTH 73
GC_CONTENT 0.465753424657534 BASEPAIR 24 FREE_ENERGY
-16.00 LEN_BP_RATIO 3.04166666666667
GUGAUGAUGAAGAUUUGGAUGACUUAUUUGUGGGACCUGUUGGGAACUCUGACCUCACCUUAU
CCUUGCCAUCCACCUA

>random_seq_from_cds__NO_8746 RANDOM_LENGTH 82 SEQ_LENGTH 69
GC_CONTENT 0.608695652173913 BASEPAIR 24 FREE_ENERGY
-27.70 LEN_BP_RATIO 2.875
UGAAGCAGAGCAUGUGGAGUCUGCUGACAGCGCUCUCCGGAAAGGAGGCAGAUGCAGAGGGCAAA
CCACAGGGAAGCUGGAA

>random_seq_from_cds__NO_8750 RANDOM_LENGTH 95 SEQ_LENGTH 84
GC_CONTENT 0.75 BASEPAIR 33 FREE_ENERGY -49.40
LEN_BP_RATIO 2.54545454545455
ACUUCGCGGAGCUGGAACGCUGGCCGCGCAGGCCUUGAGGGCUCGCGGCCCCAGUGGCGCGGCCG
CGAUGCGCUCCAUGGCAUCUGGAGGGUGGU

>random_seq_from_cds__NO_8764 RANDOM_LENGTH 82 SEQ_LENGTH 65
GC_CONTENT 0.584615384615385 BASEPAIR 25 FREE_ENERGY
-23.70 LEN_BP_RATIO 2.6
AGGAGCACAGGAUGCCUCCUCCGAGAAGGUCUGCAGCUGAUCCUUGGAGUAGACGUACUGCCAGA
UGCGUCCAUGUCGUUC

>random_seq_from_cds__NO_8767 RANDOM_LENGTH 96 SEQ_LENGTH 78
GC_CONTENT 0.525641025641026 BASEPAIR 23 FREE_ENERGY
-25.33 LEN_BP_RATIO 3.39130434782609
UCUCCUGCAAAGCCAGCUUUAUACCCCCGAACCCGUUGUCGAUGACCACAGGCUGGUUGGCCGA
UGAUGUCGUAGGACUCCAUAUCAGUUGGUGG

>random_seq_from_cds__NO_8770 RANDOM_LENGTH 99 SEQ_LENGTH 75
GC_CONTENT 0.386666666666667 BASEPAIR 26 FREE_ENERGY
-19.42 LEN_BP_RATIO 2.88461538461538
CUUCACUCCUAAAAGGCAAAACUCCACAGUUGUGUUUAGCAGAAUAUCUCCAGGAUGUUCUUG
GUUGCCGCUAUGGAACAAAUAACCUUUCUACAUU

>random_seq_from_cds__NO_8775 RANDOM_LENGTH 72 SEQ_LENGTH 57
GC_CONTENT 0.456140350877193 BASEPAIR 21 FREE_ENERGY
-15.30 LEN_BP_RATIO 2.71428571428571
UCAGAGUAAGAUCGGCGCUUGAAACAUUUUACCCAAUGAAGCCAGCUGGGAAAACUCUAGAAU
CAUCCA

>random_seq_from_cds__NO_8788 RANDOM_LENGTH 84 SEQ_LENGTH 73
GC_CONTENT 0.452054794520548 BASEPAIR 23 FREE_ENERGY
-17.70 LEN_BP_RATIO 3.17391304347826
AGAAUUGUCUUUGGAAGCUCAAGGCAUCAAGCUGACAGAGAAACUGUUGCAGUGAAGGCCAACA
GAAAACAAUGAAGAGGAAU

>random_seq_from_cds__NO_8816 RANDOM_LENGTH 81 SEQ_LENGTH 67

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GC_CONTENT    0.447761194029851    BASEPAIR    25    FREE_ENERGY
-22.00    LEN_BP_RATIO    2.68
GAUGUCAUCUUGAUCAAUGGGCGUUUGAAGGAAGGAGAUACAAUCAUUGUUCUGGAGUAGAAGG
GCCCAUUGUAACUCAG
>random_seq_from_cds__NO_8818    RANDOM_LENGTH    110    SEQ_LENGTH    86
GC_CONTENT    0.441860465116279    BASEPAIR    26    FREE_ENERGY
-22.30    LEN_BP_RATIO    3.30769230769231
GCUCAGGGGGUAAAGAUUCUUGGAAAAGACCUGGAGAAAACAUUGGCUGGUUUACCCCUCCUUGU
GGCUUAUAAAGAAGAUGAAAUCCUGUUCUUAAGGAUGAAUUGA
>random_seq_from_cds__NO_8828    RANDOM_LENGTH    70    SEQ_LENGTH    56
GC_CONTENT    0.678571428571429    BASEPAIR    19    FREE_ENERGY
-27.12    LEN_BP_RATIO    2.94736842105263
GGUGGGCGCUGUUCGCGAGCCAGUGCAGGCCUGUUGGGAGUACUGGACCAGGUGCUGCAUGCUG
CUGUG
>random_seq_from_cds__NO_8830    RANDOM_LENGTH    90    SEQ_LENGTH    78
GC_CONTENT    0.58974358974359    BASEPAIR    26    FREE_ENERGY
-27.00    LEN_BP_RATIO    3
GUAGUCGUAGCUGUGCAGGAUGCUGUUGGUGAUGCUGACGUGGUUGGCCGCAUCUGGUGGAUGC
GCUGUGGGAUGCUGACGAUGGUCGA
>random_seq_from_cds__NO_8833    RANDOM_LENGTH    119    SEQ_LENGTH    107
GC_CONTENT    0.476635514018692    BASEPAIR    36    FREE_ENERGY
-26.30    LEN_BP_RATIO    2.97222222222222
AAUAGUCGAUUGAGUCUUUUGAAUACUUUACAGCGUGGUCCUUUUGAGUCGAAACAUCGCCAG
UACAGGAGGGCCAGGCAUCGGUAACCAUAAUGCAGCCAGUUGUUUGUCUUCUGG
>random_seq_from_cds__NO_8837    RANDOM_LENGTH    86    SEQ_LENGTH    74
GC_CONTENT    0.662162162162162    BASEPAIR    29    FREE_ENERGY
-35.50    LEN_BP_RATIO    2.55172413793103
UCUGCCUCUUGCAGUCCCUGUGGCCGUUGGAGCCUGGAGACCACGGCUUCGUCUGCGGCCGUGAC
UUGUGGAGGGGAAUGUUUUA
>random_seq_from_cds__NO_8840    RANDOM_LENGTH    90    SEQ_LENGTH    72
GC_CONTENT    0.458333333333333    BASEPAIR    25    FREE_ENERGY
-23.00    LEN_BP_RATIO    2.88
UUUAUUGGUAUUGCCACACCGUUGAUGUUAUGUUGCAGUGGUUUGCAGACAAAGUAUUCUGG
UGGAGGUGGCCAGUCUUGAAGAGCU
>random_seq_from_cds__NO_8842    RANDOM_LENGTH    75    SEQ_LENGTH    62
GC_CONTENT    0.612903225806452    BASEPAIR    20    FREE_ENERGY
-22.70    LEN_BP_RATIO    3.1
UUGGAUUUUGGCAAAGCCUUUCUGCAGGUGUGUCCGAGGUGUGGCUGGGCGGUGCGCUCUCAGA
GUCCUUGGUG
>random_seq_from_cds__NO_8844    RANDOM_LENGTH    78    SEQ_LENGTH    58
GC_CONTENT    0.551724137931034    BASEPAIR    23    FREE_ENERGY
-19.20    LEN_BP_RATIO    2.52173913043478
CCUGAUCUCAUCUGUCCUUUAGAGGGGAGAGAAGUUCGUUCCGGCCAAAGGGGACCAGUGUGU
AGAACUGCUCCUC
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>random_seq_from_cds__NO_8848 RANDOM_LENGTH 71 SEQ_LENGTH 58
  GC_CONTENT 0.689655172413793 BASEPAIR 19 FREE_ENERGY
  -28.20 LEN_BP_RATIO 3.05263157894737
ACGGAGGAGCGCAGCUCCUUGCGGUGGCUCGCUCUGUUGUUGCCACAGGGCCUGGUUUUGGUGGG
CUCCGG
>random_seq_from_cds__NO_8850 RANDOM_LENGTH 87 SEQ_LENGTH 75
  GC_CONTENT 0.76 BASEPAIR 30 FREE_ENERGY -46.00
  LEN_BP_RATIO 2.5
GUCCUCUCGGUGCGCCUGGUGGGCUUCUUGCCC GCGGACCUCCGGGCAGGCGCGGGCGGUUCUC
CGCGGGCGCACAGGGCACUGCG
>random_seq_from_cds__NO_8872 RANDOM_LENGTH 110 SEQ_LENGTH 99
  GC_CONTENT 0.464646464646465 BASEPAIR 33 FREE_ENERGY
  -22.90 LEN_BP_RATIO 3
UGGACAAAACCACCGUGUUGGAAAAGGUCAUCGGAUUUUUGCAGAAACACAAUGGAAGUCUCAGC
GCAAACGGAAUCUGUGACAUCAGCAAGACUGGAAGCCUUCAUU
>random_seq_from_cds__NO_8874 RANDOM_LENGTH 75 SEQ_LENGTH 55
  GC_CONTENT 0.490909090909091 BASEPAIR 21 FREE_ENERGY
  -21.80 LEN_BP_RATIO 2.61904761904762
UCAUCUAUGUCUCUGACAGUAUCACGCCUCUCCUUGGGCAUUUACCGGUCGGAUGUCAUGGAUCA
GAAUUUGUUA
>random_seq_from_cds__NO_8883 RANDOM_LENGTH 72 SEQ_LENGTH 60
  GC_CONTENT 0.633333333333333 BASEPAIR 21 FREE_ENERGY
  -27.20 LEN_BP_RATIO 2.85714285714286
UCCGGGUGGAAAGGAGGCAGGAGCUGGCUCUGGAAGACCCGCCAUCCGAGGCCUCCACUCCUCA
GCACUAA
>random_seq_from_cds__NO_8901 RANDOM_LENGTH 88 SEQ_LENGTH 63
  GC_CONTENT 0.46031746031746 BASEPAIR 23 FREE_ENERGY
  -16.90 LEN_BP_RATIO 2.73913043478261
CUACAGAACAAGCCUCCAGGAUUCAUCAACACAAAGAGAAACUUUGGUUUUGUCCUGCUAAGGUG
GAGGAUUCAGGACAUUACUAUUG
>random_seq_from_cds__NO_8929 RANDOM_LENGTH 92 SEQ_LENGTH 67
  GC_CONTENT 0.537313432835821 BASEPAIR 25 FREE_ENERGY
  -23.90 LEN_BP_RATIO 2.68
GCCUUCUUUCAUGUGCCACGCUGGAGUGCCACAGCAUACAUUAUUAUACAGCUCCAGGCUCC
GGAUUUUCGAGCUUACUUGAUAGGAGG
>random_seq_from_cds__NO_8934 RANDOM_LENGTH 87 SEQ_LENGTH 77
  GC_CONTENT 0.584415584415584 BASEPAIR 24 FREE_ENERGY
  -26.10 LEN_BP_RATIO 3.20833333333333
UCCCCGAAUCGCUGGGCUUUGGCCUGUUGAAGAACCUGUCAGAAGAACAAAUCGCGGUCUACAGU
GCCCUUGAUCCAGGACGGGAUGA
>random_seq_from_cds__NO_8946 RANDOM_LENGTH 70 SEQ_LENGTH 51
  GC_CONTENT 0.470588235294118 BASEPAIR 20 FREE_ENERGY
  -15.80 LEN_BP_RATIO 2.55
AAUAGUGGAAGGAUCGCAGUAAUAUAGUUCGGUUCUUCUUGGACCAAAGCUUAACCAUGUUGCA
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GUGGA

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>random_seq_from_cds__NO_8951 RANDOM_LENGTH 83 SEQ_LENGTH 56
  GC_CONTENT 0.410714285714286 BASEPAIR 23 FREE_ENERGY
  -15.20 LEN_BP_RATIO 2.43478260869565
UGGUGGCAGUAGUGUGCCUAGUGACUGUGUGUGUCAUUUAUAGAGUUGACUUGGUUCUAUUUUUAU
AGACAUUUAACGAGAAGA
>random_seq_from_cds__NO_8972 RANDOM_LENGTH 84 SEQ_LENGTH 76
  GC_CONTENT 0.407894736842105 BASEPAIR 24 FREE_ENERGY
  -17.40 LEN_BP_RATIO 3.16666666666667
CUUUGUAAAAAUGAUGUUACUGAUGGAAGAGCAAAUACUGGCUUGAAAGAGCAGCCAAACUUUU
CCCAGGAAGUCCUGCAAUU
>random_seq_from_cds__NO_8976 RANDOM_LENGTH 95 SEQ_LENGTH 69
  GC_CONTENT 0.449275362318841 BASEPAIR 24 FREE_ENERGY
  -22.89 LEN_BP_RATIO 2.875
UUUACAGUGUUUGGAGUCUGAUAAAAGUGACUGGCGAGCAACCAUACAGACUUACUGCUGGCCU
AUGCUGAAUCUUAUGCUUCUUACGCUUUCCA
>random_seq_from_cds__NO_8982 RANDOM_LENGTH 86 SEQ_LENGTH 78
  GC_CONTENT 0.41025641025641 BASEPAIR 26 FREE_ENERGY
  -16.57 LEN_BP_RATIO 3
CUUGGUAGCGAUGAUUAUUGGAAACAUUGAUGUACGAGAACCAGAGCUUGAAGAUUUGACUAGUAU
CGAUGUUGGGUGCUAUUCGAG
>random_seq_from_cds__NO_8997 RANDOM_LENGTH 89 SEQ_LENGTH 74
  GC_CONTENT 0.527027027027027 BASEPAIR 25 FREE_ENERGY
  -23.90 LEN_BP_RATIO 2.96
CCUCAUCGUUGGCCACAGAGAAUUAUGGACCAGACUCAGUGCCUGAUGGAUAUCAGGGGUCACA
GACAUUUC AUGGGGCUCCACUAAC
>random_seq_from_cds__NO_9026 RANDOM_LENGTH 89 SEQ_LENGTH 70
  GC_CONTENT 0.457142857142857 BASEPAIR 23 FREE_ENERGY
  -23.60 LEN_BP_RATIO 3.04347826086957
AAGGAAGGACAGUGGGAUUGCAGUGUGUCUUAUGUAAGAAAUGAAGCCAGUGCUACCAAUGUAU
UGCUUGUCAGUGUCCAAGUAAAACA
>random_seq_from_cds__NO_9046 RANDOM_LENGTH 88 SEQ_LENGTH 70
  GC_CONTENT 0.371428571428571 BASEPAIR 25 FREE_ENERGY
  -17.00 LEN_BP_RATIO 2.8
AGAUGGACAGUACUUUGAACCUUGUUGUCCUUUACCUGAUCUAGUUGAAGUAUCCAGUGGUGAGG
AAAAUGAACAAAGUUGUUUUUAGU
>random_seq_from_cds__NO_9063 RANDOM_LENGTH 110 SEQ_LENGTH 81
  GC_CONTENT 0.37037037037037 BASEPAIR 30 FREE_ENERGY
  -19.90 LEN_BP_RATIO 2.7
UAAAUCUGAAGAACCUGAUUCUAUUACCAAUCCAUUAGUUCACCAUCUGUUUCCUCUGAAACUA
UGGACAAACCUGUAGAUUUGUCAACUAGAAAGGAAUUGAUACAG
>random_seq_from_cds__NO_9090 RANDOM_LENGTH 110 SEQ_LENGTH 90
  GC_CONTENT 0.455555555555556 BASEPAIR 30 FREE_ENERGY
  -22.40 LEN_BP_RATIO 3
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CUUUUCCAUCUUCUUCUUGGGUAAUUUUUGGGAUCUACACUCCUCCAGCUGUAGAGUGGGCUUA
UCAUCUUUCAACACGCAGGACAGGUACAGAUUCUUUCCUUGAGG

>random_seq_from_cds__NO_9111 RANDOM_LENGTH 96 SEQ_LENGTH 84
GC_CONTENT 0.726190476190476 BASEPAIR 29 FREE_ENERGY
-36.80 LEN_BP_RATIO 2.89655172413793
GCGCCCGGUGCCCAACGGGUGGACAGGGUCUCUACCUGCGGCAGUCUGGCCUCUGUCACGCUCG
ACCCGGCCUCCUCCUCCUGCGCCUCCUCUGG

>random_seq_from_cds__NO_9113 RANDOM_LENGTH 75 SEQ_LENGTH 58
GC_CONTENT 0.724137931034483 BASEPAIR 21 FREE_ENERGY
-32.30 LEN_BP_RATIO 2.76190476190476
UGAAAAAGUUGGUGGUGCGGUGCAGCUGGGCCGUGGCUGCGGCUGGUGAGCAGGCGCCGCGAGA
UGCUGAGGCG

>random_seq_from_cds__NO_9115 RANDOM_LENGTH 85 SEQ_LENGTH 76
GC_CONTENT 0.776315789473684 BASEPAIR 25 FREE_ENERGY
-31.20 LEN_BP_RATIO 3.04
GACACCGGCACGCUGUCUCCAUCGCUGCCGCUGCCGCUGCGCCGUGGCGCCCGGACUGAGGCU
CAGGCUGAGGCCGCCCGGAG

>random_seq_from_cds__NO_9117 RANDOM_LENGTH 110 SEQ_LENGTH 99
GC_CONTENT 0.666666666666667 BASEPAIR 35 FREE_ENERGY
-45.70 LEN_BP_RATIO 2.82857142857143
GAUGAUGCUGGUCCUGCAGGUGCCUGGCUCUGCUCCAAGUGGCUGGCCUUGGUGCUGUUGCUGA
AGGAGGCCACGGGGUGCAGUGGGAACUCACGGAGGUGCCAUUGCU

>random_seq_from_cds__NO_9124 RANDOM_LENGTH 67 SEQ_LENGTH 49
GC_CONTENT 0.571428571428571 BASEPAIR 19 FREE_ENERGY
-18.70 LEN_BP_RATIO 2.57894736842105
CCAGCAGCCAGGAGUAGUUGGCCAUGAUGCAGUACUGGAACAGCACCAUGACCAGCUUGCAGCCC
GC

>random_seq_from_cds__NO_9126 RANDOM_LENGTH 92 SEQ_LENGTH 74
GC_CONTENT 0.621621621621622 BASEPAIR 24 FREE_ENERGY
-22.60 LEN_BP_RATIO 3.08333333333333
GGACACGAACAGGUGCAUGUGGAUGUAGUUGCGAGUGCAGUGGAGCCUCCCGAAAGCACAGAGG
AUGCCAAGGGCGACCAGGAGCAUGACC

>random_seq_from_cds__NO_9160 RANDOM_LENGTH 89 SEQ_LENGTH 66
GC_CONTENT 0.46969696969697 BASEPAIR 25 FREE_ENERGY
-21.00 LEN_BP_RATIO 2.64
GUACGAAACAAGAGGGCUGGCAAGGAAGAACCCGUUGUUGUCCAUGCAGGUGCUGGAAUCGGAA
GAACUGGGGUUCUUAUUACUAUGG

>random_seq_from_cds__NO_9161 RANDOM_LENGTH 77 SEQ_LENGTH 64
GC_CONTENT 0.40625 BASEPAIR 22 FREE_ENERGY -17.10
LEN_BP_RATIO 2.90909090909091
AAACAGCCAUGUGUCUCAUUGAAUGCAAUCAGCCAGUUUAUCCACUAGAUUUGUAAGAACAUG
AGAGAUCAGCGA

>random_seq_from_cds__NO_9170 RANDOM_LENGTH 77 SEQ_LENGTH 60
GC_CONTENT 0.85 BASEPAIR 23 FREE_ENERGY -41.70

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LEN_BP_RATIO 2.60869565217391
AUGGACGGGCGUGCCCGGUCGGGCGUGGGGGCCGCCUGCCUUCUGCUGCUGGCGGCCGGCUGGCU
GGGGCCUGAGGC
>random_seq_from_cds__NO_9200 RANDOM_LENGTH 86 SEQ_LENGTH 62
GC_CONTENT 0.419354838709677 BASEPAIR 21 FREE_ENERGY
-15.02 LEN_BP_RATIO 2.95238095238095
UGUCAUCCUCCUUUCAUGAAACUUGAUCAGAAACUGGCAAGCUCUAAAUUUGUUGGGGUUCAUG
GUGUACAGCAAGAUUCGUUUC
>random_seq_from_cds__NO_9211 RANDOM_LENGTH 78 SEQ_LENGTH 66
GC_CONTENT 0.5 BASEPAIR 25 FREE_ENERGY -26.70 LEN_BP_RATIO
2.64
CAUUUGCUCAUAGAAGUCAAAACAGGUCCAUGGGGAUGUCAGAUUUACCCUGUGGAUCUGUCACUC
GGGAAGUGGAGGG
>random_seq_from_cds__NO_9212 RANDOM_LENGTH 81 SEQ_LENGTH 62
GC_CONTENT 0.5 BASEPAIR 21 FREE_ENERGY -19.20 LEN_BP_RATIO
2.95238095238095
CCCACCACUGCUUUCAGCAGUCUUGAAAUUCGGCAGAUUUGCUUGUGAAAGUCUCUGUGAUGAGC
UCAGUGGCCUCCCUU
>random_seq_from_cds__NO_9215 RANDOM_LENGTH 81 SEQ_LENGTH 72
GC_CONTENT 0.5277777777777778 BASEPAIR 24 FREE_ENERGY
-24.30 LEN_BP_RATIO 3
CUGAGCUUCCUGAGGUACUCGGUGAUGUCACUGGUUUGCAGCCCAACGCUGACAGCUGCAUACAA
GGAGUAGGCAGUUAGU
>random_seq_from_cds__NO_9234 RANDOM_LENGTH 85 SEQ_LENGTH 75
GC_CONTENT 0.6133333333333333 BASEPAIR 28 FREE_ENERGY
-26.60 LEN_BP_RATIO 2.67857142857143
CCCCUCUGCACAUGCCGCCACUCGCUCAGGUAGCGGGACACGGGGUCUCGUAGCAGGGUGAUGUA
GUAGAACUUCCUGGGCGUG
>random_seq_from_cds__NO_9235 RANDOM_LENGTH 99 SEQ_LENGTH 92
GC_CONTENT 0.760869565217391 BASEPAIR 35 FREE_ENERGY
-46.70 LEN_BP_RATIO 2.62857142857143
CGCAGCGCGGCGGAGUCGCGGCGGUCCAGCACGCCGGCACGCAGUUGGUGAGCUCGGUCCAGUC
GGCGUGCAGCCCGCAGCUCCAGCCGGUGGAGAAG
>random_seq_from_cds__NO_9237 RANDOM_LENGTH 86 SEQ_LENGTH 76
GC_CONTENT 0.644736842105263 BASEPAIR 31 FREE_ENERGY
-35.20 LEN_BP_RATIO 2.45161290322581
GCCGAAGGUGGUGCCGCCGUCUUCUGGAUGUGCAGGAAGACGAUCACGUCGUCGCCCUUCAUGU
CGAAGCGCAGCGAGCGCUCCA
>random_seq_from_cds__NO_9248 RANDOM_LENGTH 87 SEQ_LENGTH 56
GC_CONTENT 0.607142857142857 BASEPAIR 20 FREE_ENERGY
-23.80 LEN_BP_RATIO 2.8
GAAGAAUCCGGUGGAUGAGACUACGGAUCCGGCGAAUGGCUGACGCAUGGAUCCAAGCAAUCAA
GUCCUUGGCAGAAAAGCAGAAC
>random_seq_from_cds__NO_9263 RANDOM_LENGTH 78 SEQ_LENGTH 53
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GC_CONTENT    0.60377358490566 BASEPAIR   21 FREE_ENERGY
-21.40 LEN_BP_RATIO  2.52380952380952
AACAAAGGACAAGGACAUGCUGAAGGUACAAGGUGACCUGCCAAAGCUCAGAGCUGGCCAAGGACA
UCCUGGUGCCUC
>random_seq_from_cds__NO_9270 RANDOM_LENGTH 80 SEQ_LENGTH    65
GC_CONTENT    0.415384615384615 BASEPAIR   23 FREE_ENERGY
-19.00 LEN_BP_RATIO  2.82608695652174
UUACAACAUCCUGCUCUAUUCUUGGUGCCACUUAUGUUAUUGCGGGGAUUGUCAUUUGUGCAU
UUUGGGUGUACAGGC
>random_seq_from_cds__NO_9272 RANDOM_LENGTH 86 SEQ_LENGTH    66
GC_CONTENT    0.439393939393939 BASEPAIR   19 FREE_ENERGY
-17.30 LEN_BP_RATIO  3.47368421052632
GUUAUUGAAGUGAAAGCAAGGGGAAGAUUUGGUUGUGUCUGGAAAGCCCAGUUGCUAACGAAU
AUGUGGCUGUCAAAAUAUUUC
>random_seq_from_cds__NO_9285 RANDOM_LENGTH 88 SEQ_LENGTH    73
GC_CONTENT    0.383561643835616 BASEPAIR   21 FREE_ENERGY
-15.33 LEN_BP_RATIO  3.47619047619048
CAUCCAUUUGAAGCCUCCAUCUCCUGUCAGAAGCACUGUCCUCUAGAUGUCCUGAAAAUAUC
CUGAUACUUUUUCAAGUGUAUUU
>random_seq_from_cds__NO_9291 RANDOM_LENGTH 77 SEQ_LENGTH    55
GC_CONTENT    0.381818181818182 BASEPAIR   20 FREE_ENERGY
-19.00 LEN_BP_RATIO  2.75
CGAGCUCACUUGAAACGAACAGGAGAUUUUGACAACUGGCUGUCAUUCUCAGGAGUUUCAACUG
AUAAGAAUUUCA
>random_seq_from_cds__NO_9296 RANDOM_LENGTH 110 SEQ_LENGTH   96
GC_CONTENT    0.510416666666667 BASEPAIR   32 FREE_ENERGY
-30.60 LEN_BP_RATIO  3
CGCAGAAGCUAAGGCGGUGUGUGAAUUUGAAGGCGGCCAUCUCGCAACUUACAAGCAGCUAGAGG
CAGCCAGAAAAUUGGGAUUUC AUGUCUGUCUGCUGGAUGGAUG
>random_seq_from_cds__NO_9311 RANDOM_LENGTH 82 SEQ_LENGTH    72
GC_CONTENT    0.458333333333333 BASEPAIR   23 FREE_ENERGY
-18.10 LEN_BP_RATIO  3.1304347826087
AUACCUCGGUAGUUAUUGUCACUGAAGUCCUGCAUGUUCUUCUUACUCGUUCAGUGAUAGGAUC
UGUCACCACUGGUGUGA
>random_seq_from_cds__NO_9316 RANDOM_LENGTH 86 SEQ_LENGTH    58
GC_CONTENT    0.53448275862069 BASEPAIR   24 FREE_ENERGY
-21.90 LEN_BP_RATIO  2.41666666666667
UGUAUAACACCCGAGCUAAUGUUUUCUUGAUUGCGUUUGACUCUCUGCAUCUCAGGAGUGACAGG
GGUUGCGGUGGCUUCCCCAC
>random_seq_from_cds__NO_9323 RANDOM_LENGTH 72 SEQ_LENGTH    48
GC_CONTENT    0.416666666666667 BASEPAIR   19 FREE_ENERGY
-15.70 LEN_BP_RATIO  2.52631578947368
ACACGCAGUAUUUCUGGCGUGUCUUGAACAACUGUAAUUUUUCCUUUACUGUUUUUAAGGUCACA
CUGGUAU
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>random_seq_from_cds__NO_9332 RANDOM_LENGTH 89 SEQ_LENGTH 73
GC_CONTENT 0.438356164383562 BASEPAIR 30 FREE_ENERGY
-27.30 LEN_BP_RATIO 2.433333333333333
UCUUUGUAUUUCACCUAUACUCUGUAAUUCUGUGGCCUCUUUUAGGUGAAGCUGCUCCAGAUUUAU
CGGGUAUGGUGUGGUAGUGGCCUU
>random_seq_from_cds__NO_9333 RANDOM_LENGTH 81 SEQ_LENGTH 73
GC_CONTENT 0.397260273972603 BASEPAIR 26 FREE_ENERGY
-17.90 LEN_BP_RATIO 2.80769230769231
UACUCUUCUCAUACUUCUUCUUGUACUGGUACAGAACUGGCAAGUUGGCUUGUAUUCAGGACAUG
AUUCAUGAUCAGAGAC
>random_seq_from_cds__NO_9337 RANDOM_LENGTH 83 SEQ_LENGTH 64
GC_CONTENT 0.546875 BASEPAIR 22 FREE_ENERGY -25.10
LEN_BP_RATIO 2.90909090909091
GGCCUGUUUGGUGGCCUGUGUGGCCUUCUUGAUGUCUGGUCGAUCAGCCACUGUGGUGUAAUGCA
GGUUCUCUUUGGCAUCUU
>random_seq_from_cds__NO_9341 RANDOM_LENGTH 82 SEQ_LENGTH 67
GC_CONTENT 0.477611940298507 BASEPAIR 22 FREE_ENERGY
-17.50 LEN_BP_RATIO 3.04545454545455
CAGGAUCUGAGGCGUGUCAGGUACGGCAUGGCAGGUUCCUCUUUCCUUGACAUGUUUCUCUUUGU
AUUUCAGCAUCACUUUC
>random_seq_from_cds__NO_9342 RANDOM_LENGTH 97 SEQ_LENGTH 58
GC_CONTENT 0.5 BASEPAIR 24 FREE_ENERGY -23.90 LEN_BP_RATIO
2.416666666666667
UAUUAAAGUAUUCUGAGGGCGAGCACCGUGUUUUUGUCAUCAGUGACAGAAAGCUUGCAACCCU
UGAGGAACUCCCGGUCCAGCUUAUAUCAAAC
>random_seq_from_cds__NO_9343 RANDOM_LENGTH 80 SEQ_LENGTH 64
GC_CONTENT 0.625 BASEPAIR 24 FREE_ENERGY -27.30
LEN_BP_RATIO 2.666666666666667
AUCGCUUUGCUGCAGGGAUGACUUGGCAGCCUGGAGGAAGUCCGGUCGGUCAGGAGUCCACUUC
AGUGGGCUUUGUUGG
>random_seq_from_cds__NO_9356 RANDOM_LENGTH 79 SEQ_LENGTH 71
GC_CONTENT 0.52112676056338 BASEPAIR 21 FREE_ENERGY
-15.60 LEN_BP_RATIO 3.38095238095238
CCAUGUCCUUCACGUCUUUAGCAUGCUUCAAGGCUGUGGUCUGGUUCCAGCGUGAUGAUGGGGU
CUCUCUUUGGUGGC
>random_seq_from_cds__NO_9357 RANDOM_LENGTH 84 SEQ_LENGTH 72
GC_CONTENT 0.430555555555556 BASEPAIR 23 FREE_ENERGY
-18.90 LEN_BP_RATIO 3.1304347826087
AAGUUCAACAUACAGAUACCUGACUCUGAAGCUUCUGCCCUCGCUUGGCUCUAAAAGAUCAGGA
GUAUCAGGAACUGAAGUAA
>random_seq_from_cds__NO_9361 RANDOM_LENGTH 84 SEQ_LENGTH 67
GC_CONTENT 0.477611940298507 BASEPAIR 24 FREE_ENERGY
-18.20 LEN_BP_RATIO 2.791666666666667
ACAUAGCGGCAAUGGAUCACUUGGGGUGUGUAUGGCAGAGAGAUCAUGUGGCCUUGCAUCUUGAA
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GAAGUCUGAUUUGUAGAUC
>random_seq_from_cds__NO_9362 RANDOM_LENGTH 69 SEQ_LENGTH 50
  GC_CONTENT 0.58 BASEPAIR 20 FREE_ENERGY -17.60
  LEN_BP_RATIO 2.5
AACCCACUGACAGCCUCUUGUGUCUUCUUGACUUGGCGGAUCUCAGGGGUAUCGGGAGUUGUAU
GGAU
>random_seq_from_cds__NO_9368 RANDOM_LENGTH 110 SEQ_LENGTH 99
  GC_CONTENT 0.4040404040404040 BASEPAIR 34 FREE_ENERGY
  -29.99 LEN_BP_RATIO 2.91176470588235
GACAAGCUUGUAGUCAUCCUUGUUUCAACAUGUGAGCUUUUAUACUUGAUCAUCAUCACGUAGA
UCAUAAGCAUGCUUGGCAUGGAGGAUUUCAGGAGUGUCCAGACG
>random_seq_from_cds__NO_9370 RANDOM_LENGTH 81 SEQ_LENGTH 64
  GC_CONTENT 0.53125 BASEPAIR 24 FREE_ENERGY -19.90
  LEN_BP_RATIO 2.666666666666667
UUCCUGACGUGAUCAUUGACUUGCAAGUCGGGGUGGCAAAUCCAUCGUGGAGGCGCAGGCGGUA
AUCAAUCUCACUGACU
>random_seq_from_cds__NO_9374 RANDOM_LENGTH 87 SEQ_LENGTH 62
  GC_CONTENT 0.548387096774194 BASEPAIR 23 FREE_ENERGY
  -22.50 LEN_BP_RATIO 2.69565217391304
GACAAGGUGCUGGAAGGCAGGAUGUAGCUGGUGGCUUUCACUCUAUCCAGGCCUCCUUGUACAG
GUUCACUGCUGUAAAGAUUCUU
>random_seq_from_cds__NO_9378 RANDOM_LENGTH 110 SEQ_LENGTH 79
  GC_CONTENT 0.531645569620253 BASEPAIR 27 FREE_ENERGY
  -23.80 LEN_BP_RATIO 2.92592592592593
AGGUCAUCUUUAUACACAUAUCAUCACUCAAGAUCUCCUGGGCGUUUCGGACGCGUAUAACAUUGG
GUUCUCCAGAAGAGACGUCCACUGGUGGAAUAGUGUCGAUACU
>random_seq_from_cds__NO_9386 RANDOM_LENGTH 81 SEQ_LENGTH 74
  GC_CONTENT 0.540540540540541 BASEPAIR 22 FREE_ENERGY
  -19.93 LEN_BP_RATIO 3.36363636363636
AGUGGGAUCCAGCCAAUGCCUCGGAGCCACUCCAGGUCAGCUCUGUAGACAUUCAUCACUCUGUA
GGUCAUAGGCCUUUCU
>random_seq_from_cds__NO_9390 RANDOM_LENGTH 72 SEQ_LENGTH 57
  GC_CONTENT 0.473684210526316 BASEPAIR 21 FREE_ENERGY
  -15.80 LEN_BP_RATIO 2.71428571428571
UCAGCUUUGUAUUUCAGCCUCACUCUGAACGUCAUUGCAGUGAUGGGCAUGAACAAAUGGCACAG
CAUCUGG
>random_seq_from_cds__NO_9392 RANDOM_LENGTH 93 SEQ_LENGTH 74
  GC_CONTENT 0.5 BASEPAIR 27 FREE_ENERGY -21.50 LEN_BP_RATIO
  2.74074074074074
UGUGCAGCAGGGGGUUUCUGUGAGGGUGUACUUUGAUUUGGUGGCAUUCAGUCUUUCCGGUAU
UUAUCAUCAUCGAGGAUCUCGCCACUU
>random_seq_from_cds__NO_9395 RANDOM_LENGTH 85 SEQ_LENGTH 66
  GC_CONTENT 0.590909090909091 BASEPAIR 25 FREE_ENERGY
  -27.40 LEN_BP_RATIO 2.64
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AACAUUCAUCGCUCUGCAGUUCGUAGGCCUUCUUGGCCUGAAUCACAUCGUUCUGGUCGGGCAUG
CAGGUCCACUGGUGCAGGUA

>random_seq_from_cds__NO_9410 RANDOM_LENGTH 82 SEQ_LENGTH 73
GC_CONTENT 0.520547945205479 BASEPAIR 24 FREE_ENERGY
-26.10 LEN_BP_RATIO 3.04166666666667

UGAAUUUGAGCUGGUCUGCAGGCUGGCGAUACUUCUGUCACUCAGGAUUUCUCCAGCUCUCUUC
ACUUUCUGACCUCUAC

>random_seq_from_cds__NO_9420 RANDOM_LENGTH 85 SEQ_LENGTH 69
GC_CONTENT 0.478260869565217 BASEPAIR 28 FREE_ENERGY
-25.10 LEN_BP_RATIO 2.46428571428571

GUCUGACUUUAACAAAUCGUCACUCUGGAGGUCAUAGGCCUUUCGUGCAUGAAUGAUGUCAUUC
UGGUCGGGCAGGCAGAUCCA

>random_seq_from_cds__NO_9422 RANDOM_LENGTH 101 SEQ_LENGTH 61
GC_CONTENT 0.508196721311475 BASEPAIR 22 FREE_ENERGY
-20.20 LEN_BP_RATIO 2.77272727272727

UGUACCUUGUCUUGUAUUUCUAAAAUCUUUCUUGUACUCACGGUCACUCUGCACUUUGGCAAUG
UGGAGGGACCACAUUAUCUUGGGGUCAUCGUGUACU

>random_seq_from_cds__NO_9442 RANDOM_LENGTH 78 SEQ_LENGTH 46
GC_CONTENT 0.478260869565217 BASEPAIR 19 FREE_ENERGY
-21.60 LEN_BP_RATIO 2.42105263157895

AAAAUCUGGGUGGCUCGUUUUUUCUCAUCCUCGAGAGAACCACUAGUCAUCCAGCCAAUGCC
UUUUAGCCACUGA

>random_seq_from_cds__NO_9448 RANDOM_LENGTH 86 SEQ_LENGTH 64
GC_CONTENT 0.453125 BASEPAIR 24 FREE_ENERGY -15.40
LEN_BP_RATIO 2.66666666666667

GCUUUAGCCAGAACAAUGUCAGGUGUAUCAGGCAUGAUGUGGAUCUGAGUCUUGUCUUUGUCCCA
AGCUUCUCUAUAAAGUCUCAU

>random_seq_from_cds__NO_9454 RANDOM_LENGTH 89 SEQ_LENGTH 75
GC_CONTENT 0.413333333333333 BASEPAIR 22 FREE_ENERGY
-17.40 LEN_BP_RATIO 3.40909090909091

CUUGUAUUCUCUUUCACUCUGCAUUUGGCUACAUUCAUGGACAACACAAGUUUUGGGUCAUCUU
GCAGACUCCGGAUCCAACAUGGU

>random_seq_from_cds__NO_9457 RANDOM_LENGTH 86 SEQ_LENGTH 79
GC_CONTENT 0.354430379746835 BASEPAIR 28 FREE_ENERGY
-15.90 LEN_BP_RATIO 2.82142857142857

AAAUAUCUGGUGUAUCAGGCAUCACAUGAAUCUUGGUCUUAUCUUUAUUCCAAUCAUUGGUGUAU
AAAUGCCUUGUUAUGGUAUG

>random_seq_from_cds__NO_9460 RANDOM_LENGTH 73 SEQ_LENGTH 63
GC_CONTENT 0.444444444444444 BASEPAIR 23 FREE_ENERGY
-18.70 LEN_BP_RATIO 2.73913043478261

UGGUCAGCUCAAUGUUCUUGCAUCUGGAAGGAGGAUGUACUUGUGAAUCAGGUGCUUGUAGUUA
GUGUUGGU

>random_seq_from_cds__NO_9465 RANDOM_LENGTH 82 SEQ_LENGTH 62
GC_CONTENT 0.483870967741936 BASEPAIR 22 FREE_ENERGY

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-17.10 LEN_BP_RATIO 2.81818181818182
AAUCUGGGGGAUAUCAGGCAUGAUGUGGACUUUGUUUUGUCAGCCUCCCAUGCUUGUUUGUAGA
GAUGCUUCGUUCAUAAU
>random_seq_from_cds__NO_9470 RANDOM_LENGTH 68 SEQ_LENGTH 59
GC_CONTENT 0.559322033898305 BASEPAIR 23 FREE_ENERGY
-25.30 LEN_BP_RATIO 2.56521739130435
GUCCACCGGGGUGUGGAAGGAGGUCUUGGAUUUCUCAUAUCCCUUCUUGUAUUCGGUCUGACU
GCA
>random_seq_from_cds__NO_9475 RANDOM_LENGTH 81 SEQ_LENGTH 70
GC_CONTENT 0.485714285714286 BASEPAIR 24 FREE_ENERGY
-17.40 LEN_BP_RATIO 2.91666666666667
CAGUUUGUUACUCUUGUUAAGUGCCUGUCCAUGUGUCAUGGCGUAAGUGAACUUCAGCUUCU
CGGGGUGCUGGCGAUA
>random_seq_from_cds__NO_9486 RANDOM_LENGTH 87 SEQ_LENGTH 68
GC_CONTENT 0.397058823529412 BASEPAIR 26 FREE_ENERGY
-16.60 LEN_BP_RATIO 2.61538461538462
ACUCGUCUUUAUACACAUUCAUCACUCUGAAUUUGAUUGACAUUCCUCGUAUGCUCAGACUCAU
GGCGUCAGGUAGGUAUGUGUAA
>random_seq_from_cds__NO_9487 RANDOM_LENGTH 81 SEQ_LENGTH 67
GC_CONTENT 0.477611940298507 BASEPAIR 22 FREE_ENERGY
-18.30 LEN_BP_RATIO 3.04545454545455
UGAUGCAAUGGCUGUUUGUAGUUGACAUUGGUAGCGACAUCUGGGCCAUCUUUGCAGCUGUGAU
GCUAACCAUGUCCCCA
>random_seq_from_cds__NO_9490 RANDOM_LENGTH 78 SEQ_LENGTH 66
GC_CONTENT 0.5 BASEPAIR 23 FREE_ENERGY -24.70 LEN_BP_RATIO
2.8695652173913
AUGUUUCUCGAUGCCUUGGCUGCAGUGAUGGGAAUAGCAUCGCCAGCACAUUGUUGCCCUUGGC
UAUUAAGUCAUAC
>random_seq_from_cds__NO_9500 RANDOM_LENGTH 100 SEQ_LENGTH 77
GC_CONTENT 0.506493506493506 BASEPAIR 25 FREE_ENERGY
-25.20 LEN_BP_RATIO 3.08
GAUGAACUGGGGCAGGUCUGGUGGCAGGUUGUAUUUGUGAAUAAUUCCUCUCCUUUGGCUUUGU
AAGCGAUCAUACUCCUCUGGGCCUGGUUAAUUU
>random_seq_from_cds__NO_9503 RANDOM_LENGTH 89 SEQ_LENGTH 64
GC_CONTENT 0.5625 BASEPAIR 23 FREE_ENERGY -22.40
LEN_BP_RATIO 2.78260869565217
UUUGUAUUCAACCAUCGCUCUGCAGCGCAUAUGCCUUCUUGGCAAGGUCCACAUUGAUGCUAUCA
GGGGGUAGCUGUAACUGUGUAAG
>random_seq_from_cds__NO_9519 RANDOM_LENGTH 84 SEQ_LENGTH 57
GC_CONTENT 0.473684210526316 BASEPAIR 21 FREE_ENERGY
-17.20 LEN_BP_RATIO 2.71428571428571
ACUUGGGCUUGUAGCAGAACAGGAGAGUCUGUAACUUGGGUGAAUUUUGUCUUAUCUGGAUGGAC
UUUGUAGGUGUGCGUCUUU
>random_seq_from_cds__NO_9521 RANDOM_LENGTH 99 SEQ_LENGTH 76
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GC_CONTENT    0.434210526315789    BASEPAIR    29    FREE_ENERGY
-23.40    LEN_BP_RATIO    2.62068965517241
GUAUUCUGCUUUGUAGUUUUUCAUCACUGUUUUGAGCUGUGACUUUCAUGCAGUGUGAAUGGUAU
GGAUCCUCGAAGCUGCCUACAUAUAAUGUCCCAAAA
>random_seq_from_cds__NO_9523    RANDOM_LENGTH    95    SEQ_LENGTH    76
GC_CONTENT    0.460526315789474    BASEPAIR    28    FREE_ENERGY
-19.80    LEN_BP_RATIO    2.71428571428571
CUUUGCUUUUGUCUUUUCAUAGUUUUCCUUGUAUAGUUUCGUCACUUAGGGCAUCUCCUGCUGCC
UUCAGCUGCCUAAGCUGUGGGUUCUCUGAA
>random_seq_from_cds__NO_9526    RANDOM_LENGTH    88    SEQ_LENGTH    78
GC_CONTENT    0.371794871794872    BASEPAIR    24    FREE_ENERGY
-15.67    LEN_BP_RATIO    3.25
UGUGCUAAUGUUAUCAGCAUUCAUUCUGGCAUUUGCAACUUCAAAGCAAGGUGUCACUCCAUII
UGCCUUUGAUUUUAUUUUCAUAG
>random_seq_from_cds__NO_9528    RANDOM_LENGTH    102    SEQ_LENGTH    97
GC_CONTENT    0.556701030927835    BASEPAIR    32    FREE_ENERGY
-29.90    LEN_BP_RATIO    3.03125
AGCCAGAGGCGUGAAUUGAGCUUGCUGUUCAGCGAGACCUUUUUUUGUAGGCAACCAUCACUGAGA
GCUUUCUGGGCCUGGGCAACUCUCCUCAGUUCGGGC
>random_seq_from_cds__NO_9530    RANDOM_LENGTH    85    SEQ_LENGTH    73
GC_CONTENT    0.506849315068493    BASEPAIR    24    FREE_ENERGY
-21.10    LEN_BP_RATIO    3.04166666666667
CGGCCUGGACAAGUUCAGGGGCAUCAGGAGGAAGCAGGUACUUAUCCUUGGUGUCUCCCAGUUC
UGCUUGUAUAAAACCCUAC
>random_seq_from_cds__NO_9552    RANDOM_LENGTH    81    SEQ_LENGTH    64
GC_CONTENT    0.625    BASEPAIR    23    FREE_ENERGY    -31.30
LEN_BP_RATIO    2.78260869565217
UGUUCUGUUAACACCAGUCCCCUUGGCAGCACUCCACGGCUUGGCCAGGGGACGGCGGGGUCUUA
CAGGUCAUCUUUCCU
>random_seq_from_cds__NO_9559    RANDOM_LENGTH    110    SEQ_LENGTH    72
GC_CONTENT    0.513888888888889    BASEPAIR    24    FREE_ENERGY
-23.80    LEN_BP_RATIO    3
ACUGGUGUAAGCAAACCUAGAGUUUCUGACGCUGUCCAGCCCAACAACUAUCUCAUCAGGACAGA
GCCAGAACAAGGAACCCUCUAUUCACCAGAACAGACAUCUCUCA
>random_seq_from_cds__NO_9583    RANDOM_LENGTH    90    SEQ_LENGTH    64
GC_CONTENT    0.578125    BASEPAIR    22    FREE_ENERGY    -23.13
LEN_BP_RATIO    2.90909090909091
UAAAACCAUAUCUGACUCUUCUAGCAGAAAGUCCAACCCAGCCACCUUGGAAGGCUCUGCAGGG
UCUCUCCAGAACCUCUCUGCUGGCA
>random_seq_from_cds__NO_9585    RANDOM_LENGTH    68    SEQ_LENGTH    59
GC_CONTENT    0.474576271186441    BASEPAIR    20    FREE_ENERGY
-16.80    LEN_BP_RATIO    2.95
GAUAACGAUAGAGUUGUUUCUCCGUGGCAACAGCCUUGAGGAAUAUGGCACUAGAUGUUCGCAA
CAA
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>random_seq_from_cds__NO_9589 RANDOM_LENGTH 99 SEQ_LENGTH 84
  GC_CONTENT 0.464285714285714 BASEPAIR 27 FREE_ENERGY
  -19.77 LEN_BP_RATIO 3.11111111111111
GCAAUUAUCGGGACCUCCGGAGCAUUUAUAAAAAGGGAUGGGUGGAAUCAGAACCAUUUUAUUACA
CCUGUGUCGACAUUGGAGCGAGACCGAUUCAAAU
>random_seq_from_cds__NO_9606 RANDOM_LENGTH 87 SEQ_LENGTH 63
  GC_CONTENT 0.46031746031746 BASEPAIR 22 FREE_ENERGY
  -16.55 LEN_BP_RATIO 2.86363636363636
CACUGGAUGCGCCAAGAAAUCUCUUUUGGAAAAUUAAAACUJACGAACAACAAAGGAGCUUCAA
UAACAAUGGCAGGAUGGUGGU
>random_seq_from_cds__NO_9644 RANDOM_LENGTH 88 SEQ_LENGTH 71
  GC_CONTENT 0.549295774647887 BASEPAIR 25 FREE_ENERGY
  -21.90 LEN_BP_RATIO 2.84
CUUUGGCUUGCUUCGUGGCCCUCCAACACCAGGUGAAGCUGUUAGUCCCAGUAUCUGAGGAAG
GGAUCACUGGUUUUUUUUUUUUU
>random_seq_from_cds__NO_9647 RANDOM_LENGTH 94 SEQ_LENGTH 68
  GC_CONTENT 0.338235294117647 BASEPAIR 23 FREE_ENERGY
  -16.30 LEN_BP_RATIO 2.95652173913043
CAGGACUUGACAACUUCUGGAAAUGAUUUUUUCAGUUGGGUAUCACCACUUAUCCAAUAACACG
AUACCAUUUCUUCAAAAAUGGUUGGAACU
>random_seq_from_cds__NO_9658 RANDOM_LENGTH 65 SEQ_LENGTH 54
  GC_CONTENT 0.62962962962963 BASEPAIR 20 FREE_ENERGY
  -22.00 LEN_BP_RATIO 2.7
CAGACUCCCUUCUCCAAGGUGCUCAGCAGCAGUUAACUGCCUGCAUGUCCCCGGAGGUGGCGAC
>random_seq_from_cds__NO_9664 RANDOM_LENGTH 110 SEQ_LENGTH 90
  GC_CONTENT 0.4 BASEPAIR 29 FREE_ENERGY -18.00 LEN_BP_RATIO
  3.10344827586207
AUGGAACUUACUCUCGCCUUCAGUUUGGAAACCUGCAGAAUUAUGAUUGCCAUGUUGGAUGAGAG
AUCACACAGGAAAAAUGGGAUUUAAUGCAUUCAAAGAGCUAUGGG
>random_seq_from_cds__NO_9673 RANDOM_LENGTH 81 SEQ_LENGTH 55
  GC_CONTENT 0.345454545454545 BASEPAIR 20 FREE_ENERGY
  -16.60 LEN_BP_RATIO 2.75
ACACUGAAGGCGGUGUUUUUUUCAAUUCUUUUUGAAAGAUCACCAAUUGCUUUCUUGUUUAACA
AUUUUUGCUGCAUCUG
>random_seq_from_cds__NO_9709 RANDOM_LENGTH 85 SEQ_LENGTH 66
  GC_CONTENT 0.454545454545455 BASEPAIR 22 FREE_ENERGY
  -18.66 LEN_BP_RATIO 3
AUAUUGGCUUUCUGAAUGGCUGUCUUGAAGGGCUUCUCCAGCUCAGUCUCAAGUGCUUCAUGAA
CCGCCUCUCCUUUCCAAUUC
>random_seq_from_cds__NO_9721 RANDOM_LENGTH 84 SEQ_LENGTH 66
  GC_CONTENT 0.484848484848485 BASEPAIR 20 FREE_ENERGY
  -19.26 LEN_BP_RATIO 3.3
GAUGAGCAACUGAAAUGAUUGUGUGCCCAUGCUGAAUCCUJACUCAGCACUUCUUGCACCAUGGC
UUCACUCUCAUUGUCCAGA
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>random_seq_from_cds__NO_9723 RANDOM_LENGTH 69 SEQ_LENGTH 53
  GC_CONTENT 0.584905660377358 BASEPAIR 19 FREE_ENERGY
-16.50 LEN_BP_RATIO 2.78947368421053
UUCUGGCCACCACUCAUCUGGCCUCCUCCUUCUCCAACAAGGGUGUCAAAUUGCCUGUGGCAGGU
CCAU
>random_seq_from_cds__NO_9727 RANDOM_LENGTH 84 SEQ_LENGTH 63
  GC_CONTENT 0.4444444444444444 BASEPAIR 23 FREE_ENERGY
-21.70 LEN_BP_RATIO 2.73913043478261
UUUAAUGACCAUGUUGAGGUCAUUUAGAAUCCUUCACCUCUGGUCUGGAAGGAUAAUGGAAGGUC
ACAUUAUGGAAUUCAAUUU
>random_seq_from_cds__NO_9744 RANDOM_LENGTH 110 SEQ_LENGTH 74
  GC_CONTENT 0.662162162162162 BASEPAIR 28 FREE_ENERGY
-31.20 LEN_BP_RATIO 2.64285714285714
AGAUCCCGGGCGGGGGCACCGAGGGCUACCACGUUCUGCGGGGUACAAGAAAAUCCCCAGGACA
CAGAGCUGGUUUGGAGCCUUUCUUUGAUUUUUAUUGUUUCUAUUAA
>random_seq_from_cds__NO_9758 RANDOM_LENGTH 82 SEQ_LENGTH 70
  GC_CONTENT 0.642857142857143 BASEPAIR 25 FREE_ENERGY
-20.30 LEN_BP_RATIO 2.8
ACUCACUGUGGAUGUGACGCCCCCACUGCCAAGGCCCCACCACCGUUGAGGACAGAGUCGGCG
ACUCCACCCCAGUCAGC
>random_seq_from_cds__NO_9761 RANDOM_LENGTH 85 SEQ_LENGTH 71
  GC_CONTENT 0.408450704225352 BASEPAIR 25 FREE_ENERGY
-17.90 LEN_BP_RATIO 2.84
UGACAUAAGAACUUUCUUCCUGAGUAUACCCAUCAACUCUUUGGGGAUGAGUGAAACUGCUUUU
GGUUACAAGGGUCUAAAGAU
>random_seq_from_cds__NO_9774 RANDOM_LENGTH 81 SEQ_LENGTH 72
  GC_CONTENT 0.7361111111111111 BASEPAIR 26 FREE_ENERGY
-30.60 LEN_BP_RATIO 2.76923076923077
CCGCCGUGAUGGUGGUGGUGGUGAUGCGGCUGCGGGGUCUGAGUGGGGUGCAGCAGCGGCCCGU
GGCCUGCAGGUGUGAG
>random_seq_from_cds__NO_9779 RANDOM_LENGTH 82 SEQ_LENGTH 73
  GC_CONTENT 0.520547945205479 BASEPAIR 28 FREE_ENERGY
-27.70 LEN_BP_RATIO 2.60714285714286
CUGGAAACUGGAGUAGAUGGUGCGGGUUUCCGGACUUUCUUUGGCUUCCGUUCACUAUCCGAA
UUUCAGGCUCAAGGUCC
>random_seq_from_cds__NO_9780 RANDOM_LENGTH 68 SEQ_LENGTH 57
  GC_CONTENT 0.596491228070175 BASEPAIR 21 FREE_ENERGY
-22.20 LEN_BP_RATIO 2.71428571428571
UCCUUCUCCAGGCUCGUUGUUGGUCUGGGGACGAACUGGUUCCAUAGGGAGCGUAGGAGGUGUAGG
CGG
>random_seq_from_cds__NO_9781 RANDOM_LENGTH 81 SEQ_LENGTH 65
  GC_CONTENT 0.6 BASEPAIR 25 FREE_ENERGY -26.20 LEN_BP_RATIO
2.6
CGGUGUAGCCCAGGUCAUAGCUGCUCUUGGCGGAGUAAGGGACGUUGUUGAGGCCCGCUGGCUUGG
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UACUGGUAGGAACCCA
>random_seq_from_cds__NO_9783 RANDOM_LENGTH 68 SEQ_LENGTH 59
  GC_CONTENT 0.711864406779661 BASEPAIR 19 FREE_ENERGY
  -27.10 LEN_BP_RATIO 3.10526315789474
ACCGGAAGGGUGGGCGACUCCUGGGGCUUGUGGAGGCUGCUGCUGCUGCUGUUGCCACCCGG
GCC
>random_seq_from_cds__NO_9793 RANDOM_LENGTH 97 SEQ_LENGTH 86
  GC_CONTENT 0.441860465116279 BASEPAIR 31 FREE_ENERGY
  -29.80 LEN_BP_RATIO 2.7741935483871
GAAGAUGGGCCUUAUGAAGUUGGUGGAGAGACUGAGCAUGAUGAAAGUCUCGUUCCUGUUCUGC
UAACAGUUACUUAGGGUUUUUCUUUGGACUCA
>random_seq_from_cds__NO_9811 RANDOM_LENGTH 84 SEQ_LENGTH 75
  GC_CONTENT 0.386666666666667 BASEPAIR 29 FREE_ENERGY
  -19.10 LEN_BP_RATIO 2.58620689655172
UUGCUGAAACCUUCCAGGUGUAUUUUGGAGGUACAGUUGUUGCGAGCAAGCUAUGAAAUCUGAA
GAUGAAGUGGGAAGUUUAA
>random_seq_from_cds__NO_9812 RANDOM_LENGTH 85 SEQ_LENGTH 65
  GC_CONTENT 0.461538461538462 BASEPAIR 20 FREE_ENERGY
  -15.01 LEN_BP_RATIO 3.25
UAGAGUAUGAAUUCAGGGGUAUAUAACUUAGGUAAACCUCUACAAACCUCGGCACAGCAACCU
GAACAUCAGUGGCCAAAAG
>random_seq_from_cds__NO_9817 RANDOM_LENGTH 89 SEQ_LENGTH 81
  GC_CONTENT 0.506172839506173 BASEPAIR 29 FREE_ENERGY
  -28.12 LEN_BP_RATIO 2.79310344827586
CUGCCGAAAUAUCAGGCUGCCAAUUGCAGGCACUCAGGGUUCGAGUGACUGUGUUUCCCUCAA
GACUGUAGCUCAGUAUUCGGGAGU
>random_seq_from_cds__NO_9824 RANDOM_LENGTH 84 SEQ_LENGTH 72
  GC_CONTENT 0.555555555555556 BASEPAIR 26 FREE_ENERGY
  -28.10 LEN_BP_RATIO 2.76923076923077
UGGGAUAGUGUCGAUAAAAACCCUUCGCACCCAGUUGGGCAUGACAUGGGUGCUGGGUGAGCGG
UGGUGUGUGUUGAUGACGA
>random_seq_from_cds__NO_9825 RANDOM_LENGTH 84 SEQ_LENGTH 70
  GC_CONTENT 0.471428571428571 BASEPAIR 22 FREE_ENERGY
  -18.00 LEN_BP_RATIO 3.18181818181818
UGACAGUGAUGAUGAUGGAGGCAAUGACGAACACCAUGGUGAACAGCAUGUAUUUCCAAUCAAG
GGCACAGCACUGGACGUGG
>random_seq_from_cds__NO_9831 RANDOM_LENGTH 68 SEQ_LENGTH 57
  GC_CONTENT 0.508771929824561 BASEPAIR 19 FREE_ENERGY
  -17.70 LEN_BP_RATIO 3
CUCACAGUAGCUUUUAAAGAUGGCUGGAGGUGUCCACGUGAUGUGGCCAGUGUACUGCAGGAGCA
CUU
>random_seq_from_cds__NO_9838 RANDOM_LENGTH 85 SEQ_LENGTH 68
  GC_CONTENT 0.867647058823529 BASEPAIR 26 FREE_ENERGY
  -47.00 LEN_BP_RATIO 2.61538461538462
```

CGGGGCGGGCGGGCGGGCGGGCAGCGGGCGGCUGCGGGCGGGCGGGCGGGCAGCCUCCGGCUUUGCG
UACCCCGGGACCUCUGAGCG

>random_seq_from_cds__NO_9841 RANDOM_LENGTH 69 SEQ_LENGTH 58
GC_CONTENT 0.672413793103448 BASEPAIR 20 FREE_ENERGY
-20.50 LEN_BP_RATIO 2.9

CCGUAUGUCGCACGGCGUGGGCUUACAGCAGAAUGCGCUCAAGUCAUCGCCGCACGCCUCGCUGG
GAGG

>random_seq_from_cds__NO_9853 RANDOM_LENGTH 81 SEQ_LENGTH 66
GC_CONTENT 0.757575757575758 BASEPAIR 23 FREE_ENERGY
-32.50 LEN_BP_RATIO 2.8695652173913

ACGCCGGGCUCCACGACCCUGCUCCAGGGGGCUCCUGCGCCCCUGGCUUCAAGGACGACACCAA
GGGCCCGCUCAACUUG

>random_seq_from_cds__NO_9858 RANDOM_LENGTH 84 SEQ_LENGTH 74
GC_CONTENT 0.662162162162162 BASEPAIR 25 FREE_ENERGY
-32.60 LEN_BP_RATIO 2.96

AACGACUUUGACGAGUGCGGCCAGAGCGCAGCCAGCAUGUACCUGCCGGGCGUGCGCCUACUAUGU
GGCCCCGUCUGACUUCGCU

>random_seq_from_cds__NO_9860 RANDOM_LENGTH 87 SEQ_LENGTH 79
GC_CONTENT 0.873417721518987 BASEPAIR 28 FREE_ENERGY
-48.70 LEN_BP_RATIO 2.82142857142857

CGGCCUGGAGCGCGCAAGUGGCCGUACCGCGGGCGGGCGGGCGGGCGGGCAGCGCGGGGGGGCGGCA
GCAGCGGGGGCGGGCCCCGGCGG

>random_seq_from_cds__NO_9885 RANDOM_LENGTH 81 SEQ_LENGTH 76
GC_CONTENT 0.815789473684211 BASEPAIR 28 FREE_ENERGY
-45.00 LEN_BP_RATIO 2.71428571428571

GCCUCUGCCUCCGAGCCCGGCCGCUACGUGCGCUCCUGGAUGGAGCCGCGUGCCCCGGCUUCCCGGG
CGGUGCGGGCGGUGGC

>random_seq_from_cds__NO_9903 RANDOM_LENGTH 84 SEQ_LENGTH 73
GC_CONTENT 0.520547945205479 BASEPAIR 21 FREE_ENERGY
-19.80 LEN_BP_RATIO 3.47619047619048

CCAAGAGCUGGAGGAAGACAGAGCCGAAGGCCUGACAAAUAUAAAUGGUCAUGAGUUCGUAUAUG
GUGAACUCCAAGUAUGUGG

>random_seq_from_cds__NO_9908 RANDOM_LENGTH 75 SEQ_LENGTH 69
GC_CONTENT 0.666666666666667 BASEPAIR 21 FREE_ENERGY
-21.40 LEN_BP_RATIO 3.28571428571429

GCCUCCGGGACGGCACUCAAGCAGCCGGCCGUGGUCUACCCUGGAUGAAGAAGGUGCACGUGA
AUUCGGGUGA

>random_seq_from_cds__NO_9910 RANDOM_LENGTH 86 SEQ_LENGTH 54
GC_CONTENT 0.611111111111111 BASEPAIR 20 FREE_ENERGY
-21.90 LEN_BP_RATIO 2.7

AAAAAGAAUUUCAUUUUUAACAGGUAUCUGACAAGGGCGCCGUCGGAUUGAAAUCGCUCACACCCUG
UGUCUGUCGGAGCGCCAGAUC

>random_seq_from_cds__NO_9931 RANDOM_LENGTH 68 SEQ_LENGTH 64
GC_CONTENT 0.75 BASEPAIR 25 FREE_ENERGY -33.50

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LEN_BP_RATIO 2.56
GGGCCUACGAACCGUGCCGCACCUGCCGCGGCAGCUGGGGGCGCGGACUACGGCUUCCUGGGG
UCC
>random_seq_from_cds__NO_9947 RANDOM_LENGTH 89 SEQ_LENGTH 77
GC_CONTENT 0.363636363636364 BASEPAIR 26 FREE_ENERGY
-16.50 LEN_BP_RATIO 2.96153846153846
UGUAGUUAAGAUUGUGAAUCUAGCUUGCAAUAUAUUCUUUGUAUCAUACCAAUUGGUGGGAGGA
ACAAGUGUUUCAUAUGGCCUGAUG
>random_seq_from_cds__NO_9973 RANDOM_LENGTH 75 SEQ_LENGTH 63
GC_CONTENT 0.507936507936508 BASEPAIR 22 FREE_ENERGY
-20.70 LEN_BP_RATIO 2.86363636363636
AAGGCUUGGAUCGUACUUUGGAGCUUCUGUCUGUGCUGUGGACCUCAAUGCAGAUGGCUUCUCAG
AUCUGCUCGU
>random_seq_from_cds__NO_9980 RANDOM_LENGTH 110 SEQ_LENGTH 91
GC_CONTENT 0.395604395604396 BASEPAIR 32 FREE_ENERGY
-19.20 LEN_BP_RATIO 2.84375
GUUGAAAAUGGAUGGCCUUCUGUGUGCAUAGAUCUAACACUUUGUUUCUCAUAUAAGGGCAAGGA
AGUCCAGGUUACAUAUGGUUUUGUUUAUAACAUGAGUUUGGAUG
>random_seq_from_cds__NO_9992 RANDOM_LENGTH 88 SEQ_LENGTH 59
GC_CONTENT 0.372881355932203 BASEPAIR 20 FREE_ENERGY
-17.40 LEN_BP_RATIO 2.95
UUUUAGCCCCAAACUGAUAAGCUGUUCAACAUUUUGGAUGUCCAGGACUACUACUGGAGAAUGC
CACUUUGAAAAUUAUCAAAAGAGU
>random_seq_from_cds__NO_10003 RANDOM_LENGTH 89 SEQ_LENGTH 68
GC_CONTENT 0.617647058823529 BASEPAIR 23 FREE_ENERGY
-37.80 LEN_BP_RATIO 2.95652173913043
CCCUCUGGUAUUCUGGGAGAAAUGGUGACCCUGGUAUUCAGGACAACCAGGGUCCCCUGGUU
CUCCUGGCCCCCCUGGAAUCUGUG
>random_seq_from_cds__NO_10004 RANDOM_LENGTH 94 SEQ_LENGTH 80
GC_CONTENT 0.5375 BASEPAIR 29 FREE_ENERGY -26.00
LEN_BP_RATIO 2.75862068965517
AAUCAUGCCCUACUGGUCCUCAGGAACUAUUCUCCCCAGUAUGAUUCAUAUGAUGUCAAGUCUGG
AGUAGCAGUAGGAGGACUCGCAGGCUAUC
>random_seq_from_cds__NO_10019 RANDOM_LENGTH 110 SEQ_LENGTH
104 GC_CONTENT 0.625 BASEPAIR 36 FREE_ENERGY -41.90
LEN_BP_RATIO 2.88888888888889
CCAUCUGGUCCCCGAGGUCAGCCUGGUGUCAUGGGCUUCCCCGGUCCUAAAGGAAAUGAUGGGUG
CUCCUGGUAAGAAUGGAGAACGAGGUGGCCUGGAGGACCUGGCC
>random_seq_from_cds__NO_10029 RANDOM_LENGTH 80 SEQ_LENGTH 70
GC_CONTENT 0.657142857142857 BASEPAIR 25 FREE_ENERGY
-30.60 LEN_BP_RATIO 2.8
UCCUGGUGCUCGUGGUCUUCUGGUCCUCCUGGUAGUAAUGGGUAACCCAGGACCCCCAGGUCC
CAGCGGUUCUCCAGG
>random_seq_from_cds__NO_10038 RANDOM_LENGTH 70 SEQ_LENGTH 56
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GC_CONTENT 0.607142857142857 BASEPAIR 20 FREE_ENERGY
-26.60 LEN_BP_RATIO 2.8
GGCCCCAGAGGGACCUGUUGGACCCAGUGGACCUCUGGCAAAGAUGGAACCAGUGGACAUCAG
GUCCC
>random_seq_from_cds__NO_10055 RANDOM_LENGTH 81 SEQ_LENGTH 66
GC_CONTENT 0.409090909090909 BASEPAIR 21 FREE_ENERGY
-16.90 LEN_BP_RATIO 3.14285714285714
UUUACGUGGUACACUGGAUGGGUUUGCUGAAAUACAUGUUUCUCCUGUUUCAUGUUGCAGUAAA
CUUUGAUUGCAUCUUC
>random_seq_from_cds__NO_10059 RANDOM_LENGTH 85 SEQ_LENGTH 65
GC_CONTENT 0.753846153846154 BASEPAIR 23 FREE_ENERGY
-38.30 LEN_BP_RATIO 2.82608695652174
UGGCCAGGGGGACCCGGAGGGCCAGGUGGGCCAGGCUCACCAGGAGGGCCCCUCAGGUCCUGCUU
CUCCUACACUGCCUCGUACA
>random_seq_from_cds__NO_10060 RANDOM_LENGTH 81 SEQ_LENGTH 68
GC_CONTENT 0.647058823529412 BASEPAIR 25 FREE_ENERGY
-37.22 LEN_BP_RATIO 2.72
CCUGGAGGUCCA AUUGGCCCAAGUGGCCAGGGUUUCUUCUUUACCUGAAGGACCAACUGGGCC
UGGAGGACCCUCUUGG
>random_seq_from_cds__NO_10063 RANDOM_LENGTH 71 SEQ_LENGTH 57
GC_CONTENT 0.649122807017544 BASEPAIR 21 FREE_ENERGY
-27.71 LEN_BP_RATIO 2.71428571428571
GAACCCCGGAUCUCCUCUUUGUCCUGCAUCUCCUGGAGCACCCACAGGGCCAGGAGUCCAGGGG
CACCCU
>random_seq_from_cds__NO_10065 RANDOM_LENGTH 84 SEQ_LENGTH 66
GC_CONTENT 0.606060606060606 BASEPAIR 24 FREE_ENERGY
-33.80 LEN_BP_RATIO 2.75
GUUCCCCUACAGGACCAUUGGAGCCUGGGGGCCCCACAGGUCCAGGUGGACCUUUAUCUCCUGUU
GCACCAGUUGGUCCUACUU
>random_seq_from_cds__NO_10066 RANDOM_LENGTH 99 SEQ_LENGTH 77
GC_CONTENT 0.649350649350649 BASEPAIR 26 FREE_ENERGY
-34.23 LEN_BP_RATIO 2.96153846153846
UUCCUGGUGUUCGGCGUGGGCCUGGUAGGCCGGGCAUGCCUCUCUCCACGUUGCCCAGGCAU
GCCAACAAUUCUCCUCUGCCCGGUCGUCCAGCU
>random_seq_from_cds__NO_10073 RANDOM_LENGTH 81 SEQ_LENGTH 63
GC_CONTENT 0.603174603174603 BASEPAIR 21 FREE_ENERGY
-21.60 LEN_BP_RATIO 3
UUUUCUCCAGUAGGACCUGCCGGACCUGGAGGGCCCAAAGGACCUGGAAGACCCUCUUGCACCAU
CAUUCCAGCUGUGCC
>random_seq_from_cds__NO_10085 RANDOM_LENGTH 79 SEQ_LENGTH 69
GC_CONTENT 0.666666666666667 BASEPAIR 25 FREE_ENERGY
-32.30 LEN_BP_RATIO 2.76
ACCCUGAGGUCCUGGAGAUCCAGGAGGCCUGCUGAGCCAGGAGGACCAGAGGUACCUGGAGAGC
CCCGUUGGGCCUUU

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>random_seq_from_cds__NO_10133    RANDOM_LENGTH 95  SEQ_LENGTH    78
  GC_CONTENT    0.41025641025641 BASEPAIR    28  FREE_ENERGY
  -17.20 LEN_BP_RATIO  2.78571428571429
GGGUUUGCUUGGUGUACCAGAUGAGUAUGAGGAUAUUUUUGUAAAAUACAAAUUCACACUCUCC
AGAGCAGUAAUUGGCCUUUAUCUUUUAGG
>random_seq_from_cds__NO_10137    RANDOM_LENGTH 86  SEQ_LENGTH    72
  GC_CONTENT    0.4583333333333333  BASEPAIR    24  FREE_ENERGY
  -18.90 LEN_BP_RATIO  3
GGAUUCAGGUUGUUUGAGCCAAUJUUGCAACACUGUCUUCACAUCAUCAAUGCUCUGCCAAAUACCAG
UGCCUGGGUUCAUGUCAAGUU
>random_seq_from_cds__NO_10140    RANDOM_LENGTH 95  SEQ_LENGTH    57
  GC_CONTENT    0.43859649122807 BASEPAIR    21  FREE_ENERGY
  -16.80 LEN_BP_RATIO  2.71428571428571
UCCAUCCACUUGCAUUAGAAAAUCAGCACUCUGUAGGCAUGGUAUUGAUUGUUUCCGUUGUAGCG
UGAUAAUCGUCAUCUUCCAAAGAGCCAUCG
>random_seq_from_cds__NO_10144    RANDOM_LENGTH 80  SEQ_LENGTH    54
  GC_CONTENT    0.6666666666666667  BASEPAIR    19  FREE_ENERGY
  -21.90 LEN_BP_RATIO  2.84210526315789
GUCAGAUAUCCUCCGGGAGCUGCUCUGUGUCUCUGAGAAGGCUGCUAACAUUGCCCGGGCGUGCA
GACAGCAGGAAGCCC
>random_seq_from_cds__NO_10164    RANDOM_LENGTH 93  SEQ_LENGTH    65
  GC_CONTENT    0.430769230769231  BASEPAIR    21  FREE_ENERGY
  -20.33 LEN_BP_RATIO  3.0952380952381
UUCAGAAUGGUCCACCCAGGUGAAAGUUUUAUCCUCCGAGAUGGCUUUCACUGAAUCUUAUAAAA
AGGUGCCAGGCAUUUUUAUCCUUUAGCAA
>random_seq_from_cds__NO_10182    RANDOM_LENGTH 87  SEQ_LENGTH    68
  GC_CONTENT    0.382352941176471  BASEPAIR    19  FREE_ENERGY
  -15.57 LEN_BP_RATIO  3.57894736842105
GAGUAGGUUUUUCUCUUUGGAAACACGACCUAACUGUUCAUCCAGUUGUAUUAACAAGUUUUGAA
GAAGAAUCGUUGCCAUGGUUUC
>random_seq_from_cds__NO_10201    RANDOM_LENGTH 102 SEQ_LENGTH    89
  GC_CONTENT    0.550561797752809  BASEPAIR    31  FREE_ENERGY
  -35.40 LEN_BP_RATIO  2.87096774193548
UGGAGGCGUUGGUCCAGCCACCAUCUGUGCCAAGAAUCCUGCCAGAAACUCAUUGGAAGGGCAC
UGGAACGAACAGAUGCUGGAUAUAGCCUGCAGGCUUA
>random_seq_from_cds__NO_10202    RANDOM_LENGTH 80  SEQ_LENGTH    66
  GC_CONTENT    0.5303030303030303 BASEPAIR    27  FREE_ENERGY
  -28.00 LEN_BP_RATIO  2.44444444444444
UUCUGAAUGAAGUCUCCUUUUGGGCUCGCGCCAGGUGGGAAAGUGGAGUUCAAGAGGACUCUC
AUCAUCAGCUUCCUC
>random_seq_from_cds__NO_10214    RANDOM_LENGTH 102 SEQ_LENGTH    79
  GC_CONTENT    0.518987341772152  BASEPAIR    27  FREE_ENERGY
  -22.70 LEN_BP_RATIO  2.92592592592593
AGGCUGGAUUCAUGAACGAUGGCAGAAUCUUGGCCUGGACAUGGAGCAUUACAGCAAUGCAGGC
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GCCUCCUUGGAUGAAUCAUUAUUCGGUGAUAGAAAUG
>random_seq_from_cds__NO_10223 RANDOM_LENGTH 110 SEQ_LENGTH
 103 GC_CONTENT 0.475728155339806 BASEPAIR 34 FREE_ENERGY
 -33.30 LEN_BP_RATIO 3.02941176470588
UUCAGCUGUUGGAUACUUCAGGAGGUUAUGAGUCAGACAUGAACUGGGAGAAAGGCGAAGGCCAG
CCCUUCGAAUACUUUGUUUAUGGAGCUGCCUGUUCGAGGUUGAA
>random_seq_from_cds__NO_10243 RANDOM_LENGTH 80 SEQ_LENGTH 67
 GC_CONTENT 0.492537313432836 BASEPAIR 24 FREE_ENERGY
 -23.00 LEN_BP_RATIO 2.79166666666667
UCAUCUCGGCGGGUGACAUUUCACUAUAAGAGAAGCAGUCUGAGUUACUUUGGAGGUGUCUGUUC
UCGCACAAGAGGAGU
>random_seq_from_cds__NO_10251 RANDOM_LENGTH 110 SEQ_LENGTH 94
 GC_CONTENT 0.48936170212766 BASEPAIR 35 FREE_ENERGY
 -24.40 LEN_BP_RATIO 2.68571428571429
AACUGCGGGAAGGAUGGAGACCGGUGGAUUCAGUGCAGCAAACAGUGAUGUGUUCUGUGGAUUCU
UACUCUGUACCAAUUCUACUCGAGCUCCACGUAUUGGUCAACUUC
>random_seq_from_cds__NO_10254 RANDOM_LENGTH 84 SEQ_LENGTH 77
 GC_CONTENT 0.571428571428571 BASEPAIR 23 FREE_ENERGY
 -22.26 LEN_BP_RATIO 3.34782608695652
GGCCAUGGGGGUGUGUAGUAAUGAAGCCACUGCAUUUGUGAUUUCACCUGGGCAGGGACAGAUU
GCAGUAUCCGGGAUCCAGU
>random_seq_from_cds__NO_10266 RANDOM_LENGTH 97 SEQ_LENGTH 81
 GC_CONTENT 0.62962962962963 BASEPAIR 30 FREE_ENERGY
 -35.20 LEN_BP_RATIO 2.7
ACUGUCUUGGGGAUGAGACAACAGGAGCGGAUGGAGUCGCUGAGGCCCAUCCAUUGCUGGUAGU
CGGGGUACUCCCCUCGCCGAGCAAGUAUUGU
>random_seq_from_cds__NO_10270 RANDOM_LENGTH 64 SEQ_LENGTH 52
 GC_CONTENT 0.596153846153846 BASEPAIR 21 FREE_ENERGY
 -21.20 LEN_BP_RATIO 2.47619047619048
GGAUCCAGCUGCCCUCAGCACAUUGAGGGAGUGAAUUUCAGUGAGGUGGAAGCGGUCCUGAAC
>random_seq_from_cds__NO_10296 RANDOM_LENGTH 64 SEQ_LENGTH 57
 GC_CONTENT 0.491228070175439 BASEPAIR 22 FREE_ENERGY
 -21.70 LEN_BP_RATIO 2.59090909090909
CCAUCAGCAAACCUUACAGGCCCUAUACAGGUACUUCAUGUCCUGUGAGGUUGUAGAGUGU
>random_seq_from_cds__NO_10311 RANDOM_LENGTH 99 SEQ_LENGTH 84
 GC_CONTENT 0.5 BASEPAIR 31 FREE_ENERGY -33.40 LEN_BP_RATIO
 2.70967741935484
GAAGGUUCCCCACAAUAGAAGUAGCAUCCAUAACAGCUUUGGCAACCAGCUGUUCUCUGUUG
AGCCUGCUUCUGCGUGGACCUUCAGGAAUUUCAU
>random_seq_from_cds__NO_10317 RANDOM_LENGTH 78 SEQ_LENGTH 61
 GC_CONTENT 0.524590163934426 BASEPAIR 24 FREE_ENERGY
 -20.20 LEN_BP_RATIO 2.54166666666667
UCUUGGCUGCAUCGUGAAGUGGUGAGUCAUUUGAUACCCGGUGGUGUUCACCAAUGCCUUAUGC
UGGAGCAAUAUU

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>random_seq_from_cds__NO_10334    RANDOM_LENGTH 85  SEQ_LENGTH    60
  GC_CONTENT    0.6666666666666667  BASEPAIR    24  FREE_ENERGY
  -36.70  LEN_BP_RATIO    2.5
GAUCCUCGGCUGCCGGUUCUCGGCUGCCGAUUAUCCGGCAUCAUGGUGCGGUCGGGGAAUAAGG
GCAGCUGUUGUGCUGUGUAU
>random_seq_from_cds__NO_10342    RANDOM_LENGTH 96  SEQ_LENGTH    72
  GC_CONTENT    0.5  BASEPAIR    24  FREE_ENERGY    -20.60  LEN_BP_RATIO
  3
GCAUUCCAUUCACUGGCCUGCCGACUGACCAUUGGCUCCAAUUUGUCUAUAAGGAUUGCAGCCU
AUAAAUCGGAUUCUACAGGAGAGAGUUAAAA
>random_seq_from_cds__NO_10385    RANDOM_LENGTH 88  SEQ_LENGTH    81
  GC_CONTENT    0.604938271604938  BASEPAIR    27  FREE_ENERGY
  -32.10  LEN_BP_RATIO    3
CGGCUGACCUGGUGGUGUUUGCUGAGCUGUUUGGAACCCAGGGGUGCUGAUCCAGGCUGAGGA
CCGCGUGCACCGCAUUGGACAGA
>random_seq_from_cds__NO_10391    RANDOM_LENGTH 70  SEQ_LENGTH    53
  GC_CONTENT    0.641509433962264  BASEPAIR    19  FREE_ENERGY
  -18.70  LEN_BP_RATIO    2.78947368421053
GUAACAUGGGCCAAACGUACCAAGAAAGUCGGGAUCGUCGGUAAAUACGGGACCCGCUAUGGGGC
CUCCC
>random_seq_from_cds__NO_10393    RANDOM_LENGTH 84  SEQ_LENGTH    59
  GC_CONTENT    0.627118644067797  BASEPAIR    23  FREE_ENERGY
  -25.00  LEN_BP_RATIO    2.56521739130435
GAAGAGACGAGCUGUGGGGAUCUGGCACUGUGGUUCCUGCAUGAAGACAGUGGCUGGCGUGCCU
GGACGUACAAGUACCACUU
>random_seq_from_cds__NO_10400    RANDOM_LENGTH 70  SEQ_LENGTH    58
  GC_CONTENT    0.620689655172414  BASEPAIR    21  FREE_ENERGY
  -27.70  LEN_BP_RATIO    2.76190476190476
GGCAGGGCCAAUGGGAUGAUGGAGUGCUGGUAGACCAGGGCAGACAGCGAUCCCGAAGUUUGGCU
CAUUG
>random_seq_from_cds__NO_10402    RANDOM_LENGTH 87  SEQ_LENGTH    69
  GC_CONTENT    0.565217391304348  BASEPAIR    24  FREE_ENERGY
  -24.50  LEN_BP_RATIO    2.875
CCUUUUUUUAUUCUGCUGCAUGAUGGUUGGAGGUGGCGAAGACACCUUCAUGGCCAGCCCGUACG
CGCCUCGGAAGGAGUGACUGUC
>random_seq_from_cds__NO_10406    RANDOM_LENGTH 110  SEQ_LENGTH
  101  GC_CONTENT    0.673267326732673  BASEPAIR    36  FREE_ENERGY
  -48.00  LEN_BP_RATIO    2.80555555555556
GUCUCCACUGACAUCUUCGCUUCUCUGGCAAGGCUGGUGUUGGGCUCCUUGCCGGAAGGCUG
CGGAGUCUGGUGACGGGGAGGUGGCAGGGCUGCUCAGGCCAGGGU
>random_seq_from_cds__NO_10409    RANDOM_LENGTH 89  SEQ_LENGTH    79
  GC_CONTENT    0.658227848101266  BASEPAIR    31  FREE_ENERGY
  -37.90  LEN_BP_RATIO    2.54838709677419
CCCAGGCUGGGGCUUCCAGGGCUGGCUAUUGCAUUGCUAUGAAGACCGGAGGCCAGGUUGCCUUG
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GUGAGCCCCAGGGUGCCGGCCCCAG

>random_seq_from_cds__NO_10422 RANDOM_LENGTH 71 SEQ_LENGTH 63
GC_CONTENT 0.587301587301587 BASEPAIR 26 FREE_ENERGY
-30.90 LEN_BP_RATIO 2.42307692307692

CUGGACAGGGGAGCGAACCCCAGGGCUACGAGGGGAUGUGGCUUCUGGAGACUGGUUCUCAUACU
GUCCAU

>random_seq_from_cds__NO_10424 RANDOM_LENGTH 92 SEQ_LENGTH 85
GC_CONTENT 0.588235294117647 BASEPAIR 28 FREE_ENERGY
-30.90 LEN_BP_RATIO 3.03571428571429

CUGCUACCCUGUGGGCCACCAGCCCUUCAAAUUCAAUGGCUCCUCCUCUGGAGUCCGGGAGGGG
UCUGAAGUCGCUUCCUUUGGUGAGAGC

>random_seq_from_cds__NO_10429 RANDOM_LENGTH 110 SEQ_LENGTH 98
GC_CONTENT 0.612244897959184 BASEPAIR 32 FREE_ENERGY
-35.10 LEN_BP_RATIO 3.0625

UGUGUAGUGGGGCAGCAGCGGAGGCUGGCUCAGGUCCAGCAUCAGCAUAUUGAGUGUUUCGAUG
GACUGUCAAUCUCUGCUGGGAGGCUGCUCGCGGGAACUCAGGG

>random_seq_from_cds__NO_10430 RANDOM_LENGTH 71 SEQ_LENGTH 61
GC_CONTENT 0.59016393442623 BASEPAIR 21 FREE_ENERGY
-24.30 LEN_BP_RATIO 2.9047619047619

AGACUGGGGAUGGGGUCUCUGCCAAUGGCUGAGGGCUGGGCCUGCUGGCUACAAGACUCUCCAA
GUGGGC

>random_seq_from_cds__NO_10433 RANDOM_LENGTH 72 SEQ_LENGTH 63
GC_CONTENT 0.6666666666666667 BASEPAIR 23 FREE_ENERGY
-34.50 LEN_BP_RATIO 2.73913043478261

GGAGGUGGUCACUGGCUGUGGCCAGGCUGGGUGGGCCCCUCCUCUGGUAGCCAGCUAAACCCU
CCUGUGC

>random_seq_from_cds__NO_10435 RANDOM_LENGTH 67 SEQ_LENGTH 54
GC_CONTENT 0.6666666666666667 BASEPAIR 20 FREE_ENERGY
-23.20 LEN_BP_RATIO 2.7

ACUUGUCCAGACCGUUGGUCAGUGGGGACAGGGCCUCUGGGUAGCCCCCUCACUGGUGUUGGUG
AC

>random_seq_from_cds__NO_10442 RANDOM_LENGTH 71 SEQ_LENGTH 66
GC_CONTENT 0.6515151515151515 BASEPAIR 23 FREE_ENERGY
-21.60 LEN_BP_RATIO 2.8695652173913

CCUCCCUCCAUGCCGUCAUCUCGAUGCCCACUGAAGUUGUCGUAGGAGUCCAGCGGAUGAGGGG
GUCGGA

>random_seq_from_cds__NO_10446 RANDOM_LENGTH 72 SEQ_LENGTH 55
GC_CONTENT 0.5818181818181818 BASEPAIR 20 FREE_ENERGY
-22.80 LEN_BP_RATIO 2.75

CAAGAGCAGUCCUGGCUCGAUGGUGAUGCAGACGCUAGUCUGGCUGUCUCCUGGGAUGUUGCUAG
AUGCCAG

>random_seq_from_cds__NO_10452 RANDOM_LENGTH 87 SEQ_LENGTH 62
GC_CONTENT 0.548387096774194 BASEPAIR 21 FREE_ENERGY
-20.30 LEN_BP_RATIO 2.95238095238095

GCCAAAUCCAGUACCCUUGGCAUGGAGCUUCGUGAUGUCAGGUCUCCGCUCAGAGAGGUUGAAC
AGCCAGGUAGUUGCCUCAUGU

>random_seq_from_cds__NO_10465 RANDOM_LENGTH 71 SEQ_LENGTH 58
GC_CONTENT 0.551724137931034 BASEPAIR 19 FREE_ENERGY
-17.71 LEN_BP_RATIO 3.05263157894737

CAGACCUCUCCUUAGUGUCCACCUGCCACACUUUCAAGAGGCCACUCAUGUCCCCUGUGGCCAC
UAGAGU

>random_seq_from_cds__NO_10469 RANDOM_LENGTH 102 SEQ_LENGTH 67
GC_CONTENT 0.611940298507463 BASEPAIR 21 FREE_ENERGY
-21.46 LEN_BP_RATIO 3.19047619047619

CGUUGCCUCUUCUCCUCUUCUCCUCAAGUCCACAUCUCCAUCCUGGGCCAGGUCAUCC
UGGGUCCGGCGGACCGGGAUCAAGUUCUACCACCUCG

>random_seq_from_cds__NO_10484 RANDOM_LENGTH 87 SEQ_LENGTH 68
GC_CONTENT 0.602941176470588 BASEPAIR 23 FREE_ENERGY
-25.60 LEN_BP_RATIO 2.95652173913043

AAAACCCACACUGUGGGCUCGUGGGCCAAAGUGGAACAGGUGAAGUUCGAUGCCACAUCCAUGC
AUGUCAAGCCUCAGGUGGCUGC

>random_seq_from_cds__NO_10499 RANDOM_LENGTH 99 SEQ_LENGTH 62
GC_CONTENT 0.532258064516129 BASEPAIR 20 FREE_ENERGY
-19.36 LEN_BP_RATIO 3.1

CCUGUCCAUUGAAGAUUUCACUCAGGCCUUUGGGAUGACUCCAGCUGCCUUCUCUGCUCUGCCUC
GAUGGAAGCAACAAAACCUCAAGAAAGAAAAAGG

>random_seq_from_cds__NO_10500 RANDOM_LENGTH 90 SEQ_LENGTH 71
GC_CONTENT 0.802816901408451 BASEPAIR 28 FREE_ENERGY
-47.40 LEN_BP_RATIO 2.53571428571429

ACUAUUUUGACAUGGCUGCGCUGGGCUGCGCGAGGCUGAGGUGGGCGCUGCGAGGGGCCGGCCGU
GGCCUCUGCCCCACGGGGCCAGAG

>random_seq_from_cds__NO_10506 RANDOM_LENGTH 70 SEQ_LENGTH 59
GC_CONTENT 0.559322033898305 BASEPAIR 22 FREE_ENERGY
-16.60 LEN_BP_RATIO 2.68181818181818

GGUGAUUGAUGACUUUAUGACUCGACUGGACCAGCUGCGGGCAGAGAGUGCUUCGGGAACCAGG
UGUCG

>random_seq_from_cds__NO_10509 RANDOM_LENGTH 84 SEQ_LENGTH 57
GC_CONTENT 0.526315789473684 BASEPAIR 22 FREE_ENERGY
-25.00 LEN_BP_RATIO 2.59090909090909

CCCGUGCUGCCUUUCUGGAAGCGAUACCUGGAUGGUUGGAAUGCCAUCUUUCCUUUGGGGAAGA
AGCUGAUUGAUGAGAAGCU

>random_seq_from_cds__NO_10526 RANDOM_LENGTH 82 SEQ_LENGTH 76
GC_CONTENT 0.684210526315789 BASEPAIR 25 FREE_ENERGY
-28.30 LEN_BP_RATIO 3.04

UGCGGAGCCACACGCGCACCGAGUGCAAUGCCACGGCUGUCGGGAUCAUGCGCGCUGCGCACC
UGCUGGCAGAAGCUGCC

>random_seq_from_cds__NO_10529 RANDOM_LENGTH 97 SEQ_LENGTH 84
GC_CONTENT 0.773809523809524 BASEPAIR 31 FREE_ENERGY

-45.80 LEN_BP_RATIO 2.70967741935484
ACGCGCGGUCGCGCCUGCAAUAGCAGCGCCCCGGACCUCAGCGGCUGCGACCUCUGUGCUGCGG
CCGCGGGCACCGCCAGGAGAGCGUGCAGCUCG
>random_seq_from_cds__NO_10543 RANDOM_LENGTH 84 SEQ_LENGTH 78
GC_CONTENT 0.705128205128205 BASEPAIR 27 FREE_ENERGY
-39.40 LEN_BP_RATIO 2.88888888888889
GGCAGCAUGUGCUGCGGCCGCGCCACAACAUCUGCGCCAGACGCGCAGCGAGCGCUGCCACUG
CCGCUUCCACUGGUGCUGU
>random_seq_from_cds__NO_10545 RANDOM_LENGTH 90 SEQ_LENGTH 62
GC_CONTENT 0.580645161290323 BASEPAIR 21 FREE_ENERGY
-23.51 LEN_BP_RATIO 2.95238095238095
CAGAGGUUUCUCCUGUCCCUGCUGCAGCUGCCACAUGUCAGCAUACACCCCACCUCGGGACAAC
AGAGCCUCGUGUCCGUCUCCCUCUCC
>random_seq_from_cds__NO_10550 RANDOM_LENGTH 73 SEQ_LENGTH 65
GC_CONTENT 0.523076923076923 BASEPAIR 19 FREE_ENERGY
-21.14 LEN_BP_RATIO 3.42105263157895
UCAUCCAGCUGUGACACGGCCGUAACGGAUUAUUGUCGGCGAUGGUGUCAUUAAGAGGACAGU
GUCUUGG
>random_seq_from_cds__NO_10553 RANDOM_LENGTH 110 SEQ_LENGTH 92
GC_CONTENT 0.630434782608696 BASEPAIR 31 FREE_ENERGY
-35.92 LEN_BP_RATIO 2.96774193548387
AAGACACGUCCUGCAGAGUCUCCCGCCCAUCGGCAUAGCUGAAGUGCACGUUCUCAAACUCAAU
ACGGCCCUUCUGAAAGCGAAGGGGCCUCGCUCCAGGAAGGUCCUU
>random_seq_from_cds__NO_10554 RANDOM_LENGTH 85 SEQ_LENGTH 76
GC_CONTENT 0.460526315789474 BASEPAIR 25 FREE_ENERGY
-17.00 LEN_BP_RATIO 3.04
CACCUUCUGUCUCCUCUUUCAGCAAGUCAACAUGUUCUCAUGUCAUGAAGUUGGUCUGGAUC
AUCCUGUAGUAGGUGCCAA
>random_seq_from_cds__NO_10580 RANDOM_LENGTH 85 SEQ_LENGTH 72
GC_CONTENT 0.6805555555555556 BASEPAIR 29 FREE_ENERGY
-35.40 LEN_BP_RATIO 2.48275862068966
UGACGAUGACGGUGCAGCCGUCUCCACACCAUCCUGCCAGAAGUCUGCGAUGGUAUGGGACAG
CGGGCCUGCGUGGCUAUGU
>random_seq_from_cds__NO_10585 RANDOM_LENGTH 110 SEQ_LENGTH
100 GC_CONTENT 0.61 BASEPAIR 36 FREE_ENERGY -37.90
LEN_BP_RATIO 2.77777777777778
GGACACACUGCUCACCCGUGAAGGCUCCGGUGGACCCUCUGCCCGGUUGAACAAGGACUUCGUGG
CCAUGUGCUGGCGGCACAGGUCCCUGGUACUCAAGGUAGUGUCA
>random_seq_from_cds__NO_10590 RANDOM_LENGTH 95 SEQ_LENGTH 84
GC_CONTENT 0.630952380952381 BASEPAIR 28 FREE_ENERGY
-33.70 LEN_BP_RATIO 3
CUCCAGCAGCUUCACUCCUGCAGCCAGGCUCAGGGCCUUCUGAUCAGUGACGAUGUAGCCAUAU
UCCUCUGCUGGCGGGCUGAGGGCUGU
>random_seq_from_cds__NO_10594 RANDOM_LENGTH 78 SEQ_LENGTH 71

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GC_CONTENT    0.647887323943662    BASEPAIR    26    FREE_ENERGY
-30.20    LEN_BP_RATIO    2.73076923076923
CAACCCUCCCCGGAUUUCUCCUGCACCCUUGGGCAGUAGCUGCAGCAGGGUCAGGAGUGUGGA
GAGCUGCUCAGGG
>random_seq_from_cds__NO_10599    RANDOM_LENGTH    82    SEQ_LENGTH    62
GC_CONTENT    0.693548387096774    BASEPAIR    21    FREE_ENERGY
-31.90    LEN_BP_RATIO    2.95238095238095
GGCAGGGGCUUCAGCCUUGGGCAGGGGGCCGACACUGACCAUCCUGGGGAGCCUCUGAGACCC
UGGAGCCAUCACGGGAG
>random_seq_from_cds__NO_10602    RANDOM_LENGTH    78    SEQ_LENGTH    69
GC_CONTENT    0.681159420289855    BASEPAIR    25    FREE_ENERGY
-26.90    LEN_BP_RATIO    2.76
GGGCAGCAGGGGCGGAGCCAGUGGGGAUGUCCUGUAAAAGCAGCUCUCCAGCAGGACCAGGUCUC
UUGGGUGCCAAGC
>random_seq_from_cds__NO_10621    RANDOM_LENGTH    81    SEQ_LENGTH    59
GC_CONTENT    0.440677966101695    BASEPAIR    20    FREE_ENERGY
-17.10    LEN_BP_RATIO    2.95
CAAAAAGCUAUGAUGGUGGAGGAGUUCUGGUCAUGAAGUACCUUGCUCUCGGGCUAAUAUCCA
UUUCUCAGUCUCCUUG
>random_seq_from_cds__NO_10633    RANDOM_LENGTH    95    SEQ_LENGTH    80
GC_CONTENT    0.55    BASEPAIR    27    FREE_ENERGY    -32.20
LEN_BP_RATIO    2.96296296296296
GGACAUCCGGGCUCAGUAUGAGACCAUCGCGGCUAAGAACAUUUCUGAAGCUGAGGAGUGGUACA
AGUCGAAGGGUGUCAGACCUGACCCAGGCA
>random_seq_from_cds__NO_10644    RANDOM_LENGTH    81    SEQ_LENGTH    72
GC_CONTENT    0.680555555555556    BASEPAIR    27    FREE_ENERGY
-32.90    LEN_BP_RATIO    2.66666666666667
CAAUAGCUCUGAGCCCCUGCUAGGCCUGCUGGCACUGUCACCGGGAGGACCCGUGGCUGUGCCCA
UGUCUUUGGGCCAUGC
>random_seq_from_cds__NO_10664    RANDOM_LENGTH    86    SEQ_LENGTH    65
GC_CONTENT    0.692307692307692    BASEPAIR    22    FREE_ENERGY
-31.10    LEN_BP_RATIO    2.95454545454545
ACAGCGGCUGACAUAAGGGGCGGAUCGCCUCUUCAGAGAGUGGCAUCAUGGGGAGGGGCGCAGCGC
UGGCCAGCCAGUAGGAUCUGU
>random_seq_from_cds__NO_10677    RANDOM_LENGTH    73    SEQ_LENGTH    68
GC_CONTENT    0.632352941176471    BASEPAIR    21    FREE_ENERGY
-26.64    LEN_BP_RATIO    3.23809523809524
GCCAGGUGAUCCGGAGGGACCCUUUUUAUCCCGGAGGACCUGGUAUCCUGGAUCCCCUGGAGG
CCUCUUGG
>random_seq_from_cds__NO_10683    RANDOM_LENGTH    98    SEQ_LENGTH    86
GC_CONTENT    0.523255813953488    BASEPAIR    24    FREE_ENERGY
-30.42    LEN_BP_RATIO    3.58333333333333
CUUGCAUCCCGGAGUUCUUUAUCACCCUCUUUCUCUGGGAAUCCAUCAUCUCCAGGAGGUCC
AGGUUCCCCAGGUGUUCUUUUUGUGAAAUGAU
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>random_seq_from_cds__NO_10686    RANDOM_LENGTH 84 SEQ_LENGTH    74
  GC_CONTENT    0.662162162162162  BASEPAIR    27 FREE_ENERGY
  -40.10 LEN_BP_RATIO  2.74074074074074
ACCAGGCAGCCCCCGGGGUCCCCUUGGACCUGGAGGACCAGGUAGCCCAUCAUCUCCAAAGGGA
CCUGGGAUUCUGGGAGGC
>random_seq_from_cds__NO_10715    RANDOM_LENGTH 110 SEQ_LENGTH    89
  GC_CONTENT    0.651685393258427  BASEPAIR    31 FREE_ENERGY
  -49.50 LEN_BP_RATIO  2.87096774193548
UGAAAGCCCAAUGGGUCCUGGGGCUCCCAGGGGUCCAAUUGGACCCUGUGGCCUGGUGGUCCUG
GUGGACCCCGAGACCCCUUUUCAGGAACACAGUGGCAAACAGAG
>random_seq_from_cds__NO_10728    RANDOM_LENGTH 74 SEQ_LENGTH    57
  GC_CONTENT    0.526315789473684  BASEPAIR    19 FREE_ENERGY
  -17.60 LEN_BP_RATIO  3
CCCCUAUUGCUUCUGUGCCUGGAUCCACUAAUACGGGUACUGUCCGGGAUCAGAGAAAGACAGG
UGACUCGAU
>random_seq_from_cds__NO_10734    RANDOM_LENGTH 86 SEQ_LENGTH    65
  GC_CONTENT    0.415384615384615  BASEPAIR    23 FREE_ENERGY
  -16.70 LEN_BP_RATIO  2.82608695652174
AUCAGGAAGGUGGAGGUCUCUAUGCACUAGGUCUUAUUCAUGCCAAUCAUGGUGGUGAUUAAU
GACUAUCUGCUUAAUCAGCUU
>random_seq_from_cds__NO_10756    RANDOM_LENGTH 110 SEQ_LENGTH    69
  GC_CONTENT    0.550724637681159  BASEPAIR    20 FREE_ENERGY
  -18.30 LEN_BP_RATIO  3.45
UUAUUUCCAUCAAUUUCACCGUCUCCAUGGCCUCCUUUGGCAUCCUCCUCACUGUUGAAGUCUA
CAAACCAAACCCCUUUGGAGGACCCAGUUUCCCGUCAGUAACU
>random_seq_from_cds__NO_10773    RANDOM_LENGTH 84 SEQ_LENGTH    67
  GC_CONTENT    0.567164179104478  BASEPAIR    21 FREE_ENERGY
  -24.30 LEN_BP_RATIO  3.19047619047619
UGUGGCUCCCUUCUUGCCAGGUGUGGUAACUGCUUUGGCUGGUGUAACUGUCUUCUUGGCAGGUG
UUGCUGCUGCCUUUUUGCC
>random_seq_from_cds__NO_10778    RANDOM_LENGTH 84 SEQ_LENGTH    75
  GC_CONTENT    0.666666666666667  BASEPAIR    25 FREE_ENERGY
  -33.30 LEN_BP_RATIO  3
AUCCCAGGUUGAGGAGGAGAACCCGACUUCUGGAACCGCGAGGCAGCCGAGGCCUGGGUGCCG
CCAAGAAGCUGCAGCCUGC
>random_seq_from_cds__NO_10788    RANDOM_LENGTH 86 SEQ_LENGTH    73
  GC_CONTENT    0.575342465753425  BASEPAIR    28 FREE_ENERGY
  -29.50 LEN_BP_RATIO  2.60714285714286
UGGAGGGGUGGUCGCAUCGACCAUGGUCAUCAUGAAAGCAGGGCUUACCGGGCACUGACUGAGAC
GAUCAUGUUCGACGACGCCAU
>random_seq_from_cds__NO_10794    RANDOM_LENGTH 72 SEQ_LENGTH    57
  GC_CONTENT    0.719298245614035  BASEPAIR    21 FREE_ENERGY
  -28.00 LEN_BP_RATIO  2.71428571428571
GCGUUGCUUCCUCUGCUGGCCGGACCCUGCUGCUGCUGGAGACGGCCACUGCUCCUGACAUGC
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AGGGGCC

>random_seq_from_cds__NO_10823 RANDOM_LENGTH 82 SEQ_LENGTH 73
GC_CONTENT 0.657534246575342 BASEPAIR 24 FREE_ENERGY
-31.92 LEN_BP_RATIO 3.04166666666667

CCCUGAUGGAGAUGACAGAGGCUGCCUGCGCCUGCUGAGCAGGAACCCCGCGGCUUCUACCUC
UUUGUGGAGGGGCGGCC

>random_seq_from_cds__NO_10825 RANDOM_LENGTH 86 SEQ_LENGTH 68
GC_CONTENT 0.602941176470588 BASEPAIR 23 FREE_ENERGY
-25.71 LEN_BP_RATIO 2.95652173913043

CCAGCUCACCAGCGAGGAGACACGCUGACCCUCGUCACCGCUGACCACUCCCAUGUCUUCUCCU
UUGGUGGCUACACCUUGCGAG

>random_seq_from_cds__NO_10833 RANDOM_LENGTH 77 SEQ_LENGTH 72
GC_CONTENT 0.6527777777777778 BASEPAIR 26 FREE_ENERGY
-36.90 LEN_BP_RATIO 2.76923076923077

UGUGUGUACUUGAGCCGGGAAGUGGGUGCUCUGGGCCGUGCUCCCGCACCCACUUCUGAUAGGC
CGUGGUAGGCCA

>random_seq_from_cds__NO_10835 RANDOM_LENGTH 90 SEQ_LENGTH 72
GC_CONTENT 0.5972222222222222 BASEPAIR 27 FREE_ENERGY
-27.80 LEN_BP_RATIO 2.66666666666667

GAAGUUGUCAUAGAGACGGACGAUGCACUCAGCCUUUCGCAGGAAGCGGCUGUAGGAGGCCUCCG
UCCACCAGUGCAGCAGGUUCCUGA

>random_seq_from_cds__NO_10842 RANDOM_LENGTH 106 SEQ_LENGTH 79
GC_CONTENT 0.708860759493671 BASEPAIR 29 FREE_ENERGY
-44.30 LEN_BP_RATIO 2.72413793103448

AGAGGGCGCCAAGCGCCAUGCCAAAGUGGCGAUUGGCCUGGCCCAAGCAGACCCGGGCCAGCUCC
UGUGGCUUGUCGCUGCCCUCCAUCUCCUGUGCCAGCUCGUG

>random_seq_from_cds__NO_10844 RANDOM_LENGTH 89 SEQ_LENGTH 79
GC_CONTENT 0.582278481012658 BASEPAIR 25 FREE_ENERGY
-21.00 LEN_BP_RATIO 3.16

AUGUAGUCUGUCGCCAGCAGCACCACCUCUCCUCUGAGAAGUCCUCCUGGAAGAUCUGGUC
UAGCAGCCACUCCACCGCAACGU

>random_seq_from_cds__NO_10863 RANDOM_LENGTH 85 SEQ_LENGTH 77
GC_CONTENT 0.584415584415584 BASEPAIR 26 FREE_ENERGY
-29.20 LEN_BP_RATIO 2.96153846153846

AGGAGAACCGCACCUACCCCGUGGAGUGGAUCAUCAUUGAUCCUGAAGGCUUCACAGGAGAACGG
GGAGUGGGAGAUAGUCCACC

>random_seq_from_cds__NO_10866 RANDOM_LENGTH 71 SEQ_LENGTH 58
GC_CONTENT 0.586206896551724 BASEPAIR 20 FREE_ENERGY
-23.10 LEN_BP_RATIO 2.9

AGGUGGUGAGAAGACAUCAGUGGCCAUCUCGGUGCUCCUGGCUCAGUCUGUCUCCUGCUGCUCA
UCUCCA

>random_seq_from_cds__NO_10869 RANDOM_LENGTH 81 SEQ_LENGTH 69
GC_CONTENT 0.710144927536232 BASEPAIR 24 FREE_ENERGY
-30.50 LEN_BP_RATIO 2.875

CUGCCGGAGCUCCUGCACAUGUCCCGCCCAGCAGAGGAUGGACCCAGCCCUGGGGCCCUUGGUGCG
GAGGAGCAGCUCCUG

>random_seq_from_cds__NO_10888 RANDOM_LENGTH 77 SEQ_LENGTH 49
GC_CONTENT 0.673469387755102 BASEPAIR 19 FREE_ENERGY
-24.60 LEN_BP_RATIO 2.57894736842105

CUGAAGCAAGCCUCCAGCUGAGUACCUGCCUCAGUGACAUGGCAGCCAGCGGGAAGACCAGCA
AGUCCGAACCGA

>random_seq_from_cds__NO_10891 RANDOM_LENGTH 79 SEQ_LENGTH 69
GC_CONTENT 0.594202898550725 BASEPAIR 19 FREE_ENERGY
-17.14 LEN_BP_RATIO 3.63157894736842

UCACUCUGACCUGCGCCUCCGCUAUGGCCAAGAGGACAUGACGUGAUCGGCUUGACCUUCCGC
AGGGACCUGUACUU

>random_seq_from_cds__NO_10898 RANDOM_LENGTH 94 SEQ_LENGTH 69
GC_CONTENT 0.434782608695652 BASEPAIR 24 FREE_ENERGY
-17.00 LEN_BP_RATIO 2.875

UAACACAGAGAAGACCGUGAAGAAGAUUAAAGCAUUCGGUGGAACAGGUGGCCAAUGUGGUUCUC
UACUCGAGUGAUUAAUACGUCAAGCCCGU

>random_seq_from_cds__NO_10899 RANDOM_LENGTH 86 SEQ_LENGTH 71
GC_CONTENT 0.577464788732394 BASEPAIR 23 FREE_ENERGY
-23.04 LEN_BP_RATIO 3.08695652173913

GGCUAUGGAGGAAGCGCAGAGAAAAGUGCCACCAAACAGCACUUUGACCAAGACGCUGACGCUG
CUGCCCUUGCUGGCCUAACAAU

>random_seq_from_cds__NO_10904 RANDOM_LENGTH 70 SEQ_LENGTH 62
GC_CONTENT 0.741935483870968 BASEPAIR 24 FREE_ENERGY
-31.40 LEN_BP_RATIO 2.58333333333333

GACGUUGAUGAGUGACAUGGCCCGGGCCCUGUGCCGCCUCCCGCGGCGCGGCCUCUGGCUGCUCC
UGGGC

>random_seq_from_cds__NO_10906 RANDOM_LENGTH 82 SEQ_LENGTH 78
GC_CONTENT 0.641025641025641 BASEPAIR 27 FREE_ENERGY
-30.90 LEN_BP_RATIO 2.88888888888889

CAGUUCAGGUAGACAUGGAGGCCGUCGGGAGACGCUGUGGUGUGACUGGGGCAGGACCAUCAG
GGAGCUACAGGGAGCUG

>random_seq_from_cds__NO_10907 RANDOM_LENGTH 68 SEQ_LENGTH 61
GC_CONTENT 0.639344262295082 BASEPAIR 21 FREE_ENERGY
-26.80 LEN_BP_RATIO 2.9047619047619

GCCGACUGCACCUGGCACAUGGCGGAGAAGCUGGGCUGCUUCUGGCCCAAUGCAGAGGUGGACAG
GUU

>random_seq_from_cds__NO_10910 RANDOM_LENGTH 94 SEQ_LENGTH 81
GC_CONTENT 0.679012345679012 BASEPAIR 24 FREE_ENERGY
-35.20 LEN_BP_RATIO 3.375

GCACUGAGGGCAUUGUGUAGCAUGGCGGAGGGCGGCAGCCCAGACGGGCGGGCAGGGCCGGGCUC
CGCAGGGUCGUAAUCUGAAGGAGUGGCUG

>random_seq_from_cds__NO_10924 RANDOM_LENGTH 78 SEQ_LENGTH 66
GC_CONTENT 0.46969696969697 BASEPAIR 23 FREE_ENERGY

-21.30 LEN_BP_RATIO 2.8695652173913
AUCUCCAUGACUUUCUCCAUGGAACGGACAGCGUUUGCAUUGGGUCUUUGCUGUAAAACCUUUUC
UGGGAGAGGAUCA

>random_seq_from_cds__NO_10928 RANDOM_LENGTH 77 SEQ_LENGTH 65
GC_CONTENT 0.723076923076923 BASEPAIR 22 FREE_ENERGY
-30.80 LEN_BP_RATIO 2.95454545454545

GGGGGGUCCAGGCCCGCGGUGAAAGCCAUGUUGACGUUGAAACCCACGCCGGGCCCUUGGCCA
CCCUCAUCAGGA

>random_seq_from_cds__NO_10934 RANDOM_LENGTH 68 SEQ_LENGTH 55
GC_CONTENT 0.636363636363636 BASEPAIR 21 FREE_ENERGY
-23.00 LEN_BP_RATIO 2.61904761904762

CGGUUGAGGGGUUCGUGCCAUAACAGGAGGGUGUGGGCUUCCGAGUGCACCGUCUGUAGCUCCUC
CAG

>random_seq_from_cds__NO_10945 RANDOM_LENGTH 69 SEQ_LENGTH 51
GC_CONTENT 0.666666666666667 BASEPAIR 19 FREE_ENERGY
-19.90 LEN_BP_RATIO 2.68421052631579

GUGCUUGUGCCGGCGGCUGCUCCAGUAAGACCAUGUGCUGCAGAAGAGGGCUGUGCGCUGCCCCU
CCGU

>random_seq_from_cds__NO_10953 RANDOM_LENGTH 71 SEQ_LENGTH 58
GC_CONTENT 0.586206896551724 BASEPAIR 22 FREE_ENERGY
-25.50 LEN_BP_RATIO 2.63636363636364

CAGUAGCGAGGGUCGUGGAAAUGCAGUGGUUCAGAUUCCGGUGGGCCAGCGCCUUCUUUUUAUU
GAGGAC

>random_seq_from_cds__NO_10976 RANDOM_LENGTH 72 SEQ_LENGTH 51
GC_CONTENT 0.705882352941177 BASEPAIR 20 FREE_ENERGY
-29.20 LEN_BP_RATIO 2.55

ACGGGAUGGCCAGAGGCCGGGUACCUCCCCGAGGUCAUGGGUGACGGCCUGGCCAACCAAGAUCAA
CAACCCC

>random_seq_from_cds__NO_10982 RANDOM_LENGTH 88 SEQ_LENGTH 76
GC_CONTENT 0.671052631578947 BASEPAIR 28 FREE_ENERGY
-39.40 LEN_BP_RATIO 2.71428571428571

UCCUGCUGGGGCCUGGUCCUCCAACCUGCCUCCUCGCAUCAUGGCAGCCGGGGGGCUGCAGAUG
AUCGGGUCCAUGAGCAAGGAUUAU

>random_seq_from_cds__NO_10984 RANDOM_LENGTH 92 SEQ_LENGTH 82
GC_CONTENT 0.670731707317073 BASEPAIR 30 FREE_ENERGY
-34.50 LEN_BP_RATIO 2.73333333333333

CCUGGAGGCCGCCUGGUCAAUGUGCUGGAGCCUGGGACUCCUCCUGGUUGGGGCCAAUGGCA
UUUGGGGGCAGCGAGCCGUGGACAUCG

>random_seq_from_cds__NO_10986 RANDOM_LENGTH 75 SEQ_LENGTH 58
GC_CONTENT 0.672413793103448 BASEPAIR 22 FREE_ENERGY
-24.40 LEN_BP_RATIO 2.63636363636364

CCUGGCCAGCACAAGCCAGUGCUGUCGUUUCUUAACCCACGGGGAGUCGUCCACCGGCGUGCUGC
AGCCCCUUGA

>random_seq_from_cds__NO_10987 RANDOM_LENGTH 88 SEQ_LENGTH 67

GC_CONTENT 0.686567164179104 BASEPAIR 23 FREE_ENERGY
-34.60 LEN_BP_RATIO 2.91304347826087
UGGCUUCGGGGAACUCUGCCACAGGGUACAAGUGCCUGCUCUCCUGGUGGAUUCGGUGGCAUCCCUG
GGCGGGACCCCUUUACAUGGA
>random_seq_from_cds__NO_10991 RANDOM_LENGTH 89 SEQ_LENGTH 75
GC_CONTENT 0.746666666666667 BASEPAIR 31 FREE_ENERGY
-37.70 LEN_BP_RATIO 2.41935483870968
GCACCGCGAGGCCGCGCGUAUCUGCAUGGGCGCCUGCAGGCACUGGGGUGCAGCUCUUCGUGA
AGGACCCGGGCGCUCCGGCUUCCC
>random_seq_from_cds__NO_10999 RANDOM_LENGTH 68 SEQ_LENGTH 59
GC_CONTENT 0.745762711864407 BASEPAIR 22 FREE_ENERGY
-34.80 LEN_BP_RATIO 2.68181818181818
UGGGCCACACGCCUGAGGCCGUGCAGAUCCGCGGAAGGAACGCCGCGCGCCUCUGCUGUGUG
GCC
>random_seq_from_cds__NO_11000 RANDOM_LENGTH 84 SEQ_LENGTH 74
GC_CONTENT 0.756756756756757 BASEPAIR 29 FREE_ENERGY
-39.80 LEN_BP_RATIO 2.55172413793103
AGCCGUGACGCCGCCUCUCUGGGGCGAGCGCCCGGGACCUCACCGAGGAGGCCAUCGGUGGUGC
CGUGCAGGGACUGGGCCAC
>random_seq_from_cds__NO_11006 RANDOM_LENGTH 84 SEQ_LENGTH 60
GC_CONTENT 0.7 BASEPAIR 23 FREE_ENERGY -30.60 LEN_BP_RATIO
2.60869565217391
GUCCACGAACCCAGAGGAGGCUGCUGUAGACCCCGUGGAGGCCAGGUGCCUGGUGGGCCCUU
CAGCCGUCUGCAGCCUCGG
>random_seq_from_cds__NO_11009 RANDOM_LENGTH 80 SEQ_LENGTH 74
GC_CONTENT 0.72972972972973 BASEPAIR 28 FREE_ENERGY
-33.10 LEN_BP_RATIO 2.64285714285714
UGGACCCGCGCAGCUGGACAGAGCCUGGGUGAUCUACGAGGGCCCCAGCGGCUACUCCGACCUG
GCGUCCAUCGGGCCG
>random_seq_from_cds__NO_11010 RANDOM_LENGTH 71 SEQ_LENGTH 60
GC_CONTENT 0.633333333333333 BASEPAIR 22 FREE_ENERGY
-30.50 LEN_BP_RATIO 2.72727272727273
GCUCCUGAGGGGGCCUGGUUUUGCCUGCCUGUACGAGAGCGGGGCCAGGACCUCCUAUGAUGA
GAUUUC
>random_seq_from_cds__NO_11019 RANDOM_LENGTH 82 SEQ_LENGTH 71
GC_CONTENT 0.535211267605634 BASEPAIR 23 FREE_ENERGY
-21.54 LEN_BP_RATIO 3.08695652173913
UCUCAGACAUGGUGGUCCUCGAUCAACCAAGACUCAUUACUGAGGACAAGGAAGGGGGCCUUU
CACUGUGACUCUGUUUC
>random_seq_from_cds__NO_11030 RANDOM_LENGTH 87 SEQ_LENGTH 64
GC_CONTENT 0.5 BASEPAIR 22 FREE_ENERGY -17.20 LEN_BP_RATIO
2.90909090909091
UGUUUGUAGGAGCCACUGAUUCAGCCGUGCCAUGUGCAAUGAUGUUGGAACUUGCUCGUGCCUUA
GACAAGAAACUCCUUUCCUUA

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>random_seq_from_cds__NO_11045    RANDOM_LENGTH 75  SEQ_LENGTH    60
  GC_CONTENT    0.45  BASEPAIR    22  FREE_ENERGY    -23.40
  LEN_BP_RATIO  2.72727272727273
GGGAUUUUUGCUGGAUACAGAAAAUUUCCCUUGGCAGUAUUCUGUCAGGGAGUUUGUGUCUGGAA
UAGCAACAGG
>random_seq_from_cds__NO_11059    RANDOM_LENGTH 110 SEQ_LENGTH
106 GC_CONTENT    0.367924528301887  BASEPAIR    32  FREE_ENERGY
-23.90 LEN_BP_RATIO  3.3125
ACUUUAUCCAACAGCUCGAUUGCCAAAGACCGUGUCAAAUGUUGUGUUACAAAAGGAUGCCUGUA
AUAUUUUUUCAGCAGUAGGUCUUUUUUUCGGAUUUUUGGUAAGUG
>random_seq_from_cds__NO_11065    RANDOM_LENGTH 80  SEQ_LENGTH    73
  GC_CONTENT    0.465753424657534  BASEPAIR    24  FREE_ENERGY
-15.40 LEN_BP_RATIO  3.04166666666667
GCAAUUUGCAGUUCUGACAGAGGUCCAGUUACCGUGAUAAAUAUCCUGUAAAGAACCACCUCCAC
AAAACUCCAUGCAAA
>random_seq_from_cds__NO_11068    RANDOM_LENGTH 86  SEQ_LENGTH    68
  GC_CONTENT    0.588235294117647  BASEPAIR    24  FREE_ENERGY
-25.90 LEN_BP_RATIO  2.83333333333333
CCGAUGCGCUGAAUCAGCUCGAAGUCCUCCUGCGGGUUCGGCGGGACAAAUCGAAGCCGGGGUU
CAUCUCAUUUGUUUUUGGGCU
>random_seq_from_cds__NO_11071    RANDOM_LENGTH 92  SEQ_LENGTH    82
  GC_CONTENT    0.51219512195122  BASEPAIR    27  FREE_ENERGY
-23.10 LEN_BP_RATIO  3.03703703703704
GAAUCGGAGGUCAGUUUAGUUGGUGUGGCAAUAUGAUAGGUGGUGCUUCUGUGGAAACCACAGG
CUUUAAUCCCCUGCGGGCUAUAGGCCU
>random_seq_from_cds__NO_11074    RANDOM_LENGTH 90  SEQ_LENGTH    68
  GC_CONTENT    0.720588235294118  BASEPAIR    22  FREE_ENERGY
-26.50 LEN_BP_RATIO  3.09090909090909
ACCAGGAGGCUGUCAUCAGGGGCCAGGCUCAGGCGCCGUCCCCCAUUGUCACCACCGAGGAGCC
CUCCCAGCUGCCACAGCCACACGUC
>random_seq_from_cds__NO_11087    RANDOM_LENGTH 87  SEQ_LENGTH    81
  GC_CONTENT    0.567901234567901  BASEPAIR    24  FREE_ENERGY
-27.15 LEN_BP_RATIO  3.375
ACAUCUUGGGCACCACAUCUCCACGGUACAGCAGGCAGCAGGCCAUGUACUUGCCGUGCCGGGG
AUCACACUUUACCAUCUGGUUG
>random_seq_from_cds__NO_11089    RANDOM_LENGTH 77  SEQ_LENGTH    66
  GC_CONTENT    0.606060606060606  BASEPAIR    25  FREE_ENERGY
-22.00 LEN_BP_RATIO  2.64
UGACUGGUGCAUAGGUGGCCAGGGGAAGUGGAUGCGAGGGUAGGGCACCAGGUUGGUCUGGAAC
UCUGUCAGGUCC
>random_seq_from_cds__NO_11102    RANDOM_LENGTH 82  SEQ_LENGTH    64
  GC_CONTENT    0.46875  BASEPAIR    20  FREE_ENERGY    -16.00
  LEN_BP_RATIO  3.2
GAAAUUUCUGAACGAAUUGUACAGUGGCCUGCAAUAGACGUACAAACCUCUGUUGGACAAAGCUG
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GUUUGGGAUCCAUAACU

>random_seq_from_cds__NO_11108 RANDOM_LENGTH 87 SEQ_LENGTH 57
GC_CONTENT 0.56140350877193 BASEPAIR 20 FREE_ENERGY
-20.40 LEN_BP_RATIO 2.85

CUACAACAGUUUUUAAGGAGAUACUGCUUGGCUGUACUGCGGCAACUCCACCUAGUAAGGACCCA
AGACAGCAAAGUACUCCCCAGG

>random_seq_from_cds__NO_11116 RANDOM_LENGTH 72 SEQ_LENGTH 59
GC_CONTENT 0.542372881355932 BASEPAIR 19 FREE_ENERGY
-22.10 LEN_BP_RATIO 3.10526315789474

AUCGUGGCACAGUUGCCUAAAUGCCGAGAGUGUCGCUUGGACAGUCUCCGCAAGGAUAAGGAGCA
ACAGAAG

>random_seq_from_cds__NO_11121 RANDOM_LENGTH 85 SEQ_LENGTH 78
GC_CONTENT 0.525641025641026 BASEPAIR 24 FREE_ENERGY
-17.86 LEN_BP_RATIO 3.25

ACUGGGUGUGUCCUCGGUGUGGGUUUGGAGUAUGUGUGGACUGCUACCGGAUGAAGAGAAAGAAU
UGCCAACAGGGGUGCUGCUU

>random_seq_from_cds__NO_11125 RANDOM_LENGTH 84 SEQ_LENGTH 58
GC_CONTENT 0.620689655172414 BASEPAIR 22 FREE_ENERGY
-28.40 LEN_BP_RATIO 2.63636363636364

GAAAAACCGACUCUUGGUGCAGUGCUCAGCAGAAUCCUCAGUGUUGGAGCCAGCAGCUGUGGG
UGGGGAAGCAGCCUCCAAG

>random_seq_from_cds__NO_11140 RANDOM_LENGTH 77 SEQ_LENGTH 56
GC_CONTENT 0.428571428571429 BASEPAIR 22 FREE_ENERGY
-18.60 LEN_BP_RATIO 2.54545454545455

UCAUUUAGAAAACGUCUUCAUCAAGAGUAUGGAGUUCAAGGCUGGGCUAUUGUACAGUUUCUUGG
GGAUGUGGUGUU

>random_seq_from_cds__NO_11146 RANDOM_LENGTH 84 SEQ_LENGTH 67
GC_CONTENT 0.462686567164179 BASEPAIR 22 FREE_ENERGY
-22.00 LEN_BP_RATIO 3.04545454545455

AAAAGGGGCCUUCUGUGGAUUGGGGAAAAAUCCAGAGACCCCUGAAGAUUCGGAUUCAACCCUA
UGAAAAGAUAAAGGCCAGG

>random_seq_from_cds__NO_11190 RANDOM_LENGTH 84 SEQ_LENGTH 70
GC_CONTENT 0.528571428571429 BASEPAIR 25 FREE_ENERGY
-18.90 LEN_BP_RATIO 2.8

CCUGCUGCUGUAAUUGUGGAGAAGCCACUGAGUGUACCACCAGCCCAAGGACUUUCCAUUCAGU
GAUUGGCGCAAGAAGUUGA

>random_seq_from_cds__NO_11205 RANDOM_LENGTH 81 SEQ_LENGTH 56
GC_CONTENT 0.410714285714286 BASEPAIR 21 FREE_ENERGY
-18.32 LEN_BP_RATIO 2.66666666666667

UUUCAGCCUCACUUGAUCAAUGUUGAAGGAGUUGGUGUUGCUGAAUUGCUUUUUAACACAAUUCA
GGCAGCUGACAUUGAU

>random_seq_from_cds__NO_11208 RANDOM_LENGTH 87 SEQ_LENGTH 70
GC_CONTENT 0.485714285714286 BASEPAIR 26 FREE_ENERGY
-19.70 LEN_BP_RATIO 2.69230769230769

GGUAUUCUGGGUGGUGCAGUUCUAGCGGAUAUCAUGAAAGACAAAGACAACUUUUGGAUGACCC
GACAAGAGUACCAAGAAAAGGG

>random_seq_from_cds__NO_11209 RANDOM_LENGTH 73 SEQ_LENGTH 64
GC_CONTENT 0.46875 BASEPAIR 21 FREE_ENERGY -18.40
LEN_BP_RATIO 3.04761904761905

UGUCCGUGUGCUAGAGAAACUUGGUGUGACUGUUCGAUAAGAUGAAGUUCACAGAUUGUCUUUGC
UGGACUUC

>random_seq_from_cds__NO_11217 RANDOM_LENGTH 88 SEQ_LENGTH 76
GC_CONTENT 0.592105263157895 BASEPAIR 26 FREE_ENERGY
-34.10 LEN_BP_RATIO 2.92307692307692

UCCUGGGCUGCCCGACUGGCAUUGGGCUUCACAUUCCAAGAAUACCUCCUGUGUGAAUAGUCCUC
UCCAGGGGGACCAGGAGGAGGGA

>random_seq_from_cds__NO_11226 RANDOM_LENGTH 84 SEQ_LENGTH 65
GC_CONTENT 0.6 BASEPAIR 20 FREE_ENERGY -20.74 LEN_BP_RATIO
3.25

AAACGAGUCCCAGGCAUCCGCUGUCCAACUGGGAGAUAGUCUUUCCACCCUUUCGGGGAUGUGGU
UUCCGCCCUUCUUCUUGGC

>random_seq_from_cds__NO_11258 RANDOM_LENGTH 84 SEQ_LENGTH 62
GC_CONTENT 0.516129032258065 BASEPAIR 21 FREE_ENERGY
-17.20 LEN_BP_RATIO 2.95238095238095

GUUAUAGAAGGUGAUGGUGUCUCUGCUCUAAUAAGGCCUGGUGCGUGAACUGCUUUGCCUGUU
CUACCUUGCAACACUAAAUU

>random_seq_from_cds__NO_11261 RANDOM_LENGTH 84 SEQ_LENGTH 67
GC_CONTENT 0.477611940298507 BASEPAIR 23 FREE_ENERGY
-18.90 LEN_BP_RATIO 2.91304347826087

UCAGUUUGGCCUCUACAAAAUCCGUUUGAGGAAAUCUCGAGUAUAGUCUGAGACAUGAGGUGGC
AGCUUUGGGUUUGUUGGCU

>random_seq_from_cds__NO_11291 RANDOM_LENGTH 88 SEQ_LENGTH 78
GC_CONTENT 0.512820512820513 BASEPAIR 28 FREE_ENERGY
-23.70 LEN_BP_RATIO 2.78571428571429

AUUCGCACUGAGUUUGACCAGGAGAUUGACAUGGGCUCACUGAACCCGGGAAAGCAACUGGUUUG
AGAAGAUGAUCAGUGGGAUGUAC

>random_seq_from_cds__NO_11294 RANDOM_LENGTH 80 SEQ_LENGTH 72
GC_CONTENT 0.7083333333333333 BASEPAIR 24 FREE_ENERGY
-26.60 LEN_BP_RATIO 3

GGAGGACUGCGUGGCCACUCACCGGAUCUGCCAGAUCGUGUCCACACGCUCGCCAGCCUGUGCG
CAGCCACCCUGGCCG

>random_seq_from_cds__NO_11299 RANDOM_LENGTH 82 SEQ_LENGTH 69
GC_CONTENT 0.652173913043478 BASEPAIR 20 FREE_ENERGY
-19.80 LEN_BP_RATIO 3.45

CAAGGAGACUCAUGCCAGUGCCCCGUCAAGAUGCUGCCACCUACGUGUGUCUACCCCGGACG
GCACAGGAGAAAGGGGA

>random_seq_from_cds__NO_11312 RANDOM_LENGTH 84 SEQ_LENGTH 61
GC_CONTENT 0.540983606557377 BASEPAIR 23 FREE_ENERGY

-21.20 LEN_BP_RATIO 2.65217391304348
CAGCUUUGCCAAAGUCAUGCAUGAGACAGUGAAGGACCUGGCUCCGAAAUGUGAUGUGUCUUUCC
UGCAGUCAGAGGAUGGCAG
>random_seq_from_cds__NO_11314 RANDOM_LENGTH 68 SEQ_LENGTH 60
GC_CONTENT 0.766666666666667 BASEPAIR 23 FREE_ENERGY
-33.60 LEN_BP_RATIO 2.60869565217391
AGCGGCUGGAAGCGCGGGGCGGCCGGGAGGGGCGAGUCCUCGCCGGCGAGUUCAGCGGACAUCCA
GGC
>random_seq_from_cds__NO_11318 RANDOM_LENGTH 87 SEQ_LENGTH 58
GC_CONTENT 0.603448275862069 BASEPAIR 22 FREE_ENERGY
-32.70 LEN_BP_RATIO 2.63636363636364
UGGGCGGAAAAGGUGUGAGCGGUACUGGGCCCAGGAGCAGGAGCCACUGCAGACUGGGCUUUUC
UGCAUCACUCUGGAUAAAGGAG
>random_seq_from_cds__NO_11322 RANDOM_LENGTH 79 SEQ_LENGTH 74
GC_CONTENT 0.567567567567568 BASEPAIR 25 FREE_ENERGY
-25.60 LEN_BP_RATIO 2.96
GGCAGCUGCUCUGACCCAGGAUGAUCCCACCUGACUUCAGUCUCUUUGAUGUGGUCCUUAAGAU
GAGGAAGCAGCGGC
>random_seq_from_cds__NO_11342 RANDOM_LENGTH 93 SEQ_LENGTH 68
GC_CONTENT 0.426470588235294 BASEPAIR 27 FREE_ENERGY
-19.10 LEN_BP_RATIO 2.51851851851852
UCAAAUCCUCCAUUUUGUUGGUCUGUUCUUGCAUGCUAGUUUAGAGGAUCUUUAAGCAAGCGA
CAAUGAAGGCAUUGCGGAAAAAAUCUGU
>random_seq_from_cds__NO_11354 RANDOM_LENGTH 81 SEQ_LENGTH 65
GC_CONTENT 0.461538461538462 BASEPAIR 20 FREE_ENERGY
-17.10 LEN_BP_RATIO 3.25
CUUUGGAGUCUGGUUUUGAAUCUGUUGGAUCUAUACUCUGAAGUACCUGCAGGGCUCUAUCCAUC
UUAUCCCUCAUCUAUA
>random_seq_from_cds__NO_11384 RANDOM_LENGTH 83 SEQ_LENGTH 61
GC_CONTENT 0.409836065573771 BASEPAIR 21 FREE_ENERGY
-17.30 LEN_BP_RATIO 2.9047619047619
AACUGCAUUUGUUAUAGCUGCUAUUAUAAAAGUGAGGAGGCCAAACGCCAACAAUUGGGAUAG
AGAAAAGAAGCUGUUCUUC
>random_seq_from_cds__NO_11387 RANDOM_LENGTH 84 SEQ_LENGTH 71
GC_CONTENT 0.507042253521127 BASEPAIR 28 FREE_ENERGY
-24.10 LEN_BP_RATIO 2.53571428571429
ACGUGGCUAGAAACUUGGCUGUGGAGCAGUUAACACUGAGUGAAGAAUCCCAGUGCCCCAGCU
GUGUUACAGCAGACUUUCU
>random_seq_from_cds__NO_11394 RANDOM_LENGTH 80 SEQ_LENGTH 65
GC_CONTENT 0.738461538461539 BASEPAIR 22 FREE_ENERGY
-26.50 LEN_BP_RATIO 2.95454545454545
GUCCGGCCUUUAGAGCGCUCCCAGCGAACACAGUCCCAGUCCUGCGGGGUGGGGGCCCCUGCCA
GCUGCCAGGCCCUU
>random_seq_from_cds__NO_11396 RANDOM_LENGTH 80 SEQ_LENGTH 72

GC_CONTENT 0.666666666666667 BASEPAIR 27 FREE_ENERGY
-36.60 LEN_BP_RATIO 2.666666666666667
UGGCAGUUCUGGGUGUCACGGGUACUUUAGGGGCGUGGCACUCCCCUCCUUUGGGUGCCUCC
GUUCGGGCUGUCGCC
>random_seq_from_cds__NO_11397 RANDOM_LENGTH 84 SEQ_LENGTH 75
GC_CONTENT 0.573333333333333 BASEPAIR 28 FREE_ENERGY
-33.00 LEN_BP_RATIO 2.67857142857143
AGGGACCUCGACUGGGCUUGGGGGAUCUAGCAUAGCUUUCUGGGUUUCGCCCAACCUUUGCUGA
UUUGACCUGGUCCCUGGAA
>random_seq_from_cds__NO_11407 RANDOM_LENGTH 100 SEQ_LENGTH 83
GC_CONTENT 0.55421686746988 BASEPAIR 28 FREE_ENERGY
-28.10 LEN_BP_RATIO 2.96428571428571
CAUGGGGAUACCUCUGCUGGGACCUGAAGCACCAGAGUGAAGCAGACAUACUGUGAAUCCUGGUC
CUCUGCAGUGGCAGGAUGCAAAGUGAUGUAGAUCU
>random_seq_from_cds__NO_11421 RANDOM_LENGTH 89 SEQ_LENGTH 75
GC_CONTENT 0.466666666666667 BASEPAIR 27 FREE_ENERGY
-22.80 LEN_BP_RATIO 2.77777777777778
GAUUUUCUGUAGCUGCCACUGACAUAUAUGGAGAUGAGUUAUGCAGAUGUGUUUAUUGGAGCACC
UCUCUUCAUGGAUCGUGGCUCUGA
>random_seq_from_cds__NO_11441 RANDOM_LENGTH 82 SEQ_LENGTH 71
GC_CONTENT 0.492957746478873 BASEPAIR 22 FREE_ENERGY
-20.12 LEN_BP_RATIO 3.22727272727273
UUGGGGUUGUGGAGUUGCUCAGUGCUUGAAGAUUGUCUGCCAAGUUGGGAGAUUAGACAGAGGAA
AGAGUGCAAUCUUGUAC
>random_seq_from_cds__NO_11449 RANDOM_LENGTH 89 SEQ_LENGTH 81
GC_CONTENT 0.604938271604938 BASEPAIR 28 FREE_ENERGY
-35.20 LEN_BP_RATIO 2.89285714285714
CUGAAGGGAGCCAGAUGGGGGGCGUGGUUGUGCUGAGUGGAGGGGGCACCUCUGGCCGGAUGGCAU
UCCUCAUGUCGGGUGUCCUUAAU
>random_seq_from_cds__NO_11450 RANDOM_LENGTH 85 SEQ_LENGTH 60
GC_CONTENT 0.55 BASEPAIR 22 FREE_ENERGY -22.60
LEN_BP_RATIO 2.72727272727273
CAGCUGAUGAAAGGUCUGGGACAGAAACCUCUUACACCUACCUCAUUGCAGGUGGUGACAGGGU
CUGUGGUGGCCUCUAGGGAG
>random_seq_from_cds__NO_11464 RANDOM_LENGTH 69 SEQ_LENGTH 60
GC_CONTENT 0.6 BASEPAIR 21 FREE_ENERGY -18.50 LEN_BP_RATIO
2.85714285714286
GGACAGUCCAAGGCUCGAUGCAUCGAGAGCCUCCUCCGAGCGAUCCACUUUCCCCAGCCACUGUC
AGAU
>random_seq_from_cds__NO_11481 RANDOM_LENGTH 81 SEQ_LENGTH 65
GC_CONTENT 0.492307692307692 BASEPAIR 21 FREE_ENERGY
-19.13 LEN_BP_RATIO 3.0952380952381
AAGAAACUCAUCCUUAUGCUCUGGAGCAGUGUGUAAAGUCGACACCGUCUUGCUCUGAGAAAA
CAUCACCAAAGAGGGA

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>random_seq_from_cds__NO_11515    RANDOM_LENGTH 78 SEQ_LENGTH    55
  GC_CONTENT    0.418181818181818  BASEPAIR    20 FREE_ENERGY
  -16.50 LEN_BP_RATIO    2.75
UGUUUUCCUUCUAUGAAAGGUCGCUAGAGAAGUCCGACUCUUCUAUCUUUGAUGGAGUCGUAACAAG
AAUCACAAACCCG
>random_seq_from_cds__NO_11537    RANDOM_LENGTH 89 SEQ_LENGTH    69
  GC_CONTENT    0.3333333333333333  BASEPAIR    27 FREE_ENERGY
  -19.80 LEN_BP_RATIO    2.55555555555556
UUUUUUUGAUCCAGUUGAAAGUGAUGAAGACAUAAACAAAUGUUCAUGAUGAUGAGCUGGAUUCAA
ACAAAGAAGAUGAUGAAAUUGCUG
>random_seq_from_cds__NO_11546    RANDOM_LENGTH 68 SEQ_LENGTH    59
  GC_CONTENT    0.525423728813559  BASEPAIR    22 FREE_ENERGY
  -15.40 LEN_BP_RATIO    2.68181818181818
AAAGUUGUGUCAAAUCUGCCAGCCAUAAACCAUGGAGGAAGUAGCCCCAGUGAGUGUUAGUGAUGC
AGC
>random_seq_from_cds__NO_11560    RANDOM_LENGTH 88 SEQ_LENGTH    67
  GC_CONTENT    0.567164179104478  BASEPAIR    22 FREE_ENERGY
  -23.36 LEN_BP_RATIO    3.04545454545455
AACAUGCCCCACAAGUUCGGUAUCCACAACUACAAGGUCCCUACCUUCUGCGAUCACUGUGGGUC
CCUGCUCUGGGGACUCUUGCGGC
>random_seq_from_cds__NO_11565    RANDOM_LENGTH 110 SEQ_LENGTH
  104 GC_CONTENT    0.490384615384615  BASEPAIR    35 FREE_ENERGY
  -33.80 LEN_BP_RATIO    2.97142857142857
UGGGCCUGGAUGAGUUCAACUUCUAUCAAGGUGUUGGGCAAAGGCAGCUUUGGCAAGGGUCAUGUU
GGCAGAACUCAAGGGCAAAGAUGAAGUAUAUGCUGUGAAGGUCUU
>random_seq_from_cds__NO_11577    RANDOM_LENGTH 97 SEQ_LENGTH    81
  GC_CONTENT    0.481481481481481  BASEPAIR    28 FREE_ENERGY
  -25.80 LEN_BP_RATIO    2.89285714285714
CGAUGAAGGCCAGGGAUAAAUUUCAAGAGUUGCUUUCGGACACUCCCUUUCUGCUCUUCGGGG
CAGGGUCCCAAACAUGCUUGAUAGUUGCCCU
>random_seq_from_cds__NO_11585    RANDOM_LENGTH 110 SEQ_LENGTH    91
  GC_CONTENT    0.54945054945055  BASEPAIR    29 FREE_ENERGY
  -36.82 LEN_BP_RATIO    3.13793103448276
GCUUGCAGGCCAGCACAGUGAGCUGGGCUGUCCUCCUGUAUUUUGCAUAUCAAGUGAACAUUUC
CGAGGAGCAGGCAUUCUGAUUCUGGGGCCUGUAAGACCUGAAUUU
>random_seq_from_cds__NO_11595    RANDOM_LENGTH 78 SEQ_LENGTH    69
  GC_CONTENT    0.521739130434783  BASEPAIR    27 FREE_ENERGY
  -19.80 LEN_BP_RATIO    2.55555555555556
UCUUCAUGGUCAUGAUGUCCCCAUAGCAGCCGUGGUACAGGCGUGGAUGUAGGUGAGGCUUCAU
GAGUGACUGAAGG
>random_seq_from_cds__NO_11607    RANDOM_LENGTH 90 SEQ_LENGTH    47
  GC_CONTENT    0.595744680851064  BASEPAIR    20 FREE_ENERGY
  -27.50 LEN_BP_RATIO    2.35
UCCCUAUGAUCCAACACCAUAUUGAAGCCUGUGCCCAGGGUCCUGGAAUGCAGGAGAUUCUGCU
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CAUUGGCUUCUACCAACCUGAUGAG
>random_seq_from_cds__NO_11610    RANDOM_LENGTH 88  SEQ_LENGTH    80
  GC_CONTENT    0.575  BASEPAIR    23  FREE_ENERGY    -22.90
  LEN_BP_RATIO  3.47826086956522
UGCUCCGACUCCCCUUGAGUGCUAUGUUGGAAGCCCACCGACGCCAGCGUCACCCUUCUUACU
CCUUGGCACUACGGGCUAACAGG
>random_seq_from_cds__NO_11613    RANDOM_LENGTH 72  SEQ_LENGTH    61
  GC_CONTENT    0.655737704918033  BASEPAIR    19  FREE_ENERGY
-22.10  LEN_BP_RATIO  3.21052631578947
AAUCAGCAGGAUGGGCAAUUGGGAGGACUCACCAGGCUUGUGGCCAGGGGCAGGUACCAUCCGCC
UAGAGCA
>random_seq_from_cds__NO_11616    RANDOM_LENGTH 79  SEQ_LENGTH    71
  GC_CONTENT    0.676056338028169  BASEPAIR    26  FREE_ENERGY
-31.30  LEN_BP_RATIO  2.73076923076923
UCCGAGGGGAUUGUGUACAUCCACCCGACCGCCAAGGUGGCCCCUCGGCUGUGGCUGGGCCCCA
ACGUCUCCAUCGGG
>random_seq_from_cds__NO_11637    RANDOM_LENGTH 110 SEQ_LENGTH    91
  GC_CONTENT    0.373626373626374  BASEPAIR    34  FREE_ENERGY
-27.00  LEN_BP_RATIO  2.67647058823529
ACAUACGCAGGGUAAGUGGUAUCGAUAAUAAUAUCCGAACAACGGGAUUCUUAGCUCCAGCCCU
UUGGGUAUGGAAUUAUUUAUUGUUCUAGGAUUAUUGUUAUCGCAU
>random_seq_from_cds__NO_11639    RANDOM_LENGTH 94  SEQ_LENGTH    74
  GC_CONTENT    0.310810810810811  BASEPAIR    26  FREE_ENERGY
-16.00  LEN_BP_RATIO  2.84615384615385
UUCAUAAAACCCAGUCUGGGAUUCCAUAUAAUAUUUUUAUUUCUCUCCAUAUAAAUGUUAUUUGAA
AAGGUGGAUCUCCUGGUCUUUGUUUCAA
>random_seq_from_cds__NO_11642    RANDOM_LENGTH 95  SEQ_LENGTH    83
  GC_CONTENT    0.349397590361446  BASEPAIR    28  FREE_ENERGY
-17.90  LEN_BP_RATIO  2.96428571428571
CUAGAUUAACAAUUGCCGAUCAGGUGAUAAAGCCGUAUUUGAAGCAUUCACACUUUCCAUGGU
UCUAUUAUCUAAAUGGUAUAUGAUUGUCC
>random_seq_from_cds__NO_11648    RANDOM_LENGTH 82  SEQ_LENGTH    71
  GC_CONTENT    0.47887323943662  BASEPAIR    22  FREE_ENERGY
-17.60  LEN_BP_RATIO  3.22727272727273
GACGAGGAAUGCCUCCCGACACUGCUGGUA AAAAUUCUUGAAAAGAAAGGCCCAAUGUAAGAAGGG
UUAUCCUGGUUGUCCAG
>random_seq_from_cds__NO_11659    RANDOM_LENGTH 81  SEQ_LENGTH    60
  GC_CONTENT    0.4  BASEPAIR    21  FREE_ENERGY    -16.00  LEN_BP_RATIO
2.85714285714286
UUUUUAUCUCUUUUAUUCUCUUAAGAAGGUGUUUCUUUGCCAACAGGAGCUGAAACUACUCUAUUC
UGAGCUUGAAUCUUUU
>random_seq_from_cds__NO_11667    RANDOM_LENGTH 84  SEQ_LENGTH    63
  GC_CONTENT    0.5555555555555556  BASEPAIR    23  FREE_ENERGY
-26.81  LEN_BP_RATIO  2.73913043478261
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GGUUUACUCAUGAUGGCGGCCUUCUCCGGAGAUGGGUGUAAUGCCUGAGAUUGCACAAGCUGUGG
AAGAGAUGGAUUGGCUGCC

>random_seq_from_cds__NO_11679 RANDOM_LENGTH 88 SEQ_LENGTH 62
GC_CONTENT 0.483870967741936 BASEPAIR 22 FREE_ENERGY
-18.70 LEN_BP_RATIO 2.81818181818182

UAAGAAAUACAUGAUAAUCCUAAAUAAGGGGAGCUUCUGAUAAUUGGAGGUGUUGCAGCCCCG
GAUCAGCUCUCUGUUUUGGAAAA

>random_seq_from_cds__NO_11681 RANDOM_LENGTH 84 SEQ_LENGTH 57
GC_CONTENT 0.403508771929825 BASEPAIR 20 FREE_ENERGY
-17.20 LEN_BP_RATIO 2.85

AUCUCAAGUUAGAUUCCUGGUCCUGGAUGAAGCUGGAUGGGCUUCUUUCUCAAGGUUAUUCUGAU
UUUAUAAAUAGGAUGCACA

>random_seq_from_cds__NO_11697 RANDOM_LENGTH 110 SEQ_LENGTH 96
GC_CONTENT 0.604166666666667 BASEPAIR 33 FREE_ENERGY
-40.50 LEN_BP_RATIO 2.90909090909091

CAAGCGUGAGGCCUGUAGCGGGGUCAGGGAAGCCAUUGCAUCGGACCACAGAGGCGUAGAACUU
CGCUGAUGC UUUGGGAUCCUUGGCAGAGAAGGGUCACUGUAGUU

>random_seq_from_cds__NO_11702 RANDOM_LENGTH 99 SEQ_LENGTH 79
GC_CONTENT 0.481012658227848 BASEPAIR 29 FREE_ENERGY
-27.00 LEN_BP_RATIO 2.72413793103448

AUAGUUGAGGUUGUAGGCGAGGACAGUGGUGUAGUGAUUGAACCCAAAAAAGUCAUAGGUGCCGU
UGAUCCUCCUCUUCUCACUCUCUGUAAAUUCUGG

>random_seq_from_cds__NO_11713 RANDOM_LENGTH 90 SEQ_LENGTH 75
GC_CONTENT 0.573333333333333 BASEPAIR 23 FREE_ENERGY
-24.57 LEN_BP_RATIO 3.26086956521739

UCAGGAAACCGUCCGUACAGAAACUCAUCCUCCUGGCCAGUGGCAUGCCGUUGUUGGUAUGAC
CUCUGUGUAGUACCUGGCGGAGGCU

>random_seq_from_cds__NO_11716 RANDOM_LENGTH 88 SEQ_LENGTH 66
GC_CONTENT 0.46969696969697 BASEPAIR 21 FREE_ENERGY
-23.30 LEN_BP_RATIO 3.14285714285714

GGUUUUGUGGUAAAUAUCCUAUCAGUAUCCUCCGUGUUCGGAUUGGUCAGCCCCACUCCGUUUU
CGGUGAUGUAAAUGGGGAUGUCA

>random_seq_from_cds__NO_11721 RANDOM_LENGTH 84 SEQ_LENGTH 71
GC_CONTENT 0.619718309859155 BASEPAIR 26 FREE_ENERGY
-29.00 LEN_BP_RATIO 2.73076923076923

CAUUCGGUCAGCGGCUUCCACAUCUCUGGGGACCCUGGUGACUUGGGCUCUGCCCAGUGUGUAC
UGAGGCUCAGCGAGAUGAC

>random_seq_from_cds__NO_11731 RANDOM_LENGTH 80 SEQ_LENGTH 60
GC_CONTENT 0.5 BASEPAIR 22 FREE_ENERGY -20.10 LEN_BP_RATIO
2.72727272727273

AAAGUGAAGGCUCUGACUUUGGAGGGGAGUUUACUGUAUJAGGUGGUAGCAGUCUUUUUGCCCC
CUUGGUGAGGAAACC

>random_seq_from_cds__NO_11732 RANDOM_LENGTH 78 SEQ_LENGTH 58
GC_CONTENT 0.448275862068966 BASEPAIR 22 FREE_ENERGY

-17.50 LEN_BP_RATIO 2.63636363636364
GUUCUUUUCUAUGAUGCUAGUGAAAAAGUAGGCAGAUUCCUGGGAGUCCUUGACUUGCUGCUGU
CGCUGAAGUUGAC

>random_seq_from_cds__NO_11742 RANDOM_LENGTH 71 SEQ_LENGTH 63
GC_CONTENT 0.650793650793651 BASEPAIR 22 FREE_ENERGY
-25.80 LEN_BP_RATIO 2.86363636363636

GGACCAAGUGAGCCACCCUAAAAGAGGCCACUCCUGGGUCAGAGAUGCCGGGAGGGUGCUGGCC
GGUGCC

>random_seq_from_cds__NO_11744 RANDOM_LENGTH 74 SEQ_LENGTH 56
GC_CONTENT 0.642857142857143 BASEPAIR 20 FREE_ENERGY
-24.50 LEN_BP_RATIO 2.8

CGCUCUCAUUCUGCCAUCCACCAUGAUCCUGCAGGGCCUGAGGCAGGUCCAGUGGAACAGCGUG
GCCAUGGGC

>random_seq_from_cds__NO_11757 RANDOM_LENGTH 97 SEQ_LENGTH 84
GC_CONTENT 0.571428571428571 BASEPAIR 34 FREE_ENERGY
-29.10 LEN_BP_RATIO 2.47058823529412

UGGUGCAGGAUGACCAUGGGCUGAAGCCGUGCAGUCUUGAGGGCCUUGAGGAGUCGCCGGUAGCA
CUGCACUGUUUUCUGUCUGGAUUCUGGGUGC

>random_seq_from_cds__NO_11758 RANDOM_LENGTH 89 SEQ_LENGTH 81
GC_CONTENT 0.555555555555556 BASEPAIR 27 FREE_ENERGY
-31.90 LEN_BP_RATIO 3

UUCCUGCUGGGAGGAGCUGUGCCCAUGACAGAAUACCUUAUAAUGGGUGAUCUGACUGGCAUGG
AGACUGCUGAAGUAUUCUGGCAGG

>random_seq_from_cds__NO_11767 RANDOM_LENGTH 71 SEQ_LENGTH 54
GC_CONTENT 0.351851851851852 BASEPAIR 21 FREE_ENERGY
-16.90 LEN_BP_RATIO 2.57142857142857

UGUUGUAGUCUGCAUUUUGGAUGCAUACUUAUUUGUUGGCUUACAAAAAGGAAGUAUUAUCC
AGUGUG

>random_seq_from_cds__NO_11773 RANDOM_LENGTH 92 SEQ_LENGTH 80
GC_CONTENT 0.625 BASEPAIR 27 FREE_ENERGY -37.00
LEN_BP_RATIO 2.96296296296296

GCGGGAACAGGGGUCUCUGCUGGGGAAGCUGGUCCAGAAUGGAACAGAACCUUCAUCCUGCCAU
UCUUGGACCCCAUGCCCGCCCCUGG

>random_seq_from_cds__NO_11774 RANDOM_LENGTH 85 SEQ_LENGTH 68
GC_CONTENT 0.588235294117647 BASEPAIR 27 FREE_ENERGY
-33.70 LEN_BP_RATIO 2.51851851851852

UACCAGAGGUCUCCAUAAGGACUCCACGGGUUAUUAACAGGGGUGCCCCUCGGAUCCUUGC
UUUGGACUGUGGCCUCAAGU

>random_seq_from_cds__NO_11775 RANDOM_LENGTH 82 SEQ_LENGTH 67
GC_CONTENT 0.626865671641791 BASEPAIR 22 FREE_ENERGY
-24.90 LEN_BP_RATIO 3.04545454545455

AUAAUCAGAUCCGAUGCCUCUGCCAGCGUGGGGUGAGGUCACUGUGGUACCCUGGGACCAUGCA
CUAGACAGCCAAGGAGU

>random_seq_from_cds__NO_11783 RANDOM_LENGTH 71 SEQ_LENGTH 60

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GC_CONTENT    0.5833333333333333    BASEPAIR    19    FREE_ENERGY
-19.80    LEN_BP_RATIO    3.15789473684211
AGACGUUGCUGAUAACCCCAAUAUUGCCACAGUGCAGACCUCAGGGGCGUGCCGACAAGGUC
UAUUUU
>random_seq_from_cds__NO_11796    RANDOM_LENGTH    87    SEQ_LENGTH    76
GC_CONTENT    0.578947368421053    BASEPAIR    24    FREE_ENERGY
-17.00    LEN_BP_RATIO    3.166666666666667
UGGACCGCCUGUAUGAGCUCACACGCAUCGACCGCUGGUUCCUGCACCGAAUGAAGCGUAUCAUC
GCACAUGCCCAGCUGCUAGAAC
>random_seq_from_cds__NO_11806    RANDOM_LENGTH    84    SEQ_LENGTH    68
GC_CONTENT    0.632352941176471    BASEPAIR    21    FREE_ENERGY
-27.12    LEN_BP_RATIO    3.23809523809524
CCCUCCUAUGUGCUGAGCGGUGCUGCUAUGAAUGUGGCCUACACGGAUGGAGACCUGGAGCGCUU
CCUGAGCAGCGCAGCAGCC
>random_seq_from_cds__NO_11811    RANDOM_LENGTH    85    SEQ_LENGTH    68
GC_CONTENT    0.573529411764706    BASEPAIR    28    FREE_ENERGY
-28.70    LEN_BP_RATIO    2.42857142857143
GGGUGUGGACCUAGUAGCCUUGGCCACGCGGGUCAUCAUGGGGGAAGAAGUGGAACCUUGGGGGC
UAAUGACUGGUUCUGGAGUC
>random_seq_from_cds__NO_11813    RANDOM_LENGTH    81    SEQ_LENGTH    62
GC_CONTENT    0.564516129032258    BASEPAIR    24    FREE_ENERGY
-29.60    LEN_BP_RATIO    2.5833333333333333
GAGGUGGCCGGCUUUGGGGAGAGCCGCUGUGAGGCAUACCCUAAGGCCAUGCUAAGCACUGGCCU
UAAGAUCSCCAAGAAG
>random_seq_from_cds__NO_11820    RANDOM_LENGTH    90    SEQ_LENGTH    70
GC_CONTENT    0.7    BASEPAIR    25    FREE_ENERGY    -30.82    LEN_BP_RATIO
2.8
GCCUCUGGCGGGGUAUCACCAUGGUGUGGCAUGCCUAAUACCCGGCCCCCAUCAUUGACGC
CCCUGCUCUGGCCUGGCCAGAAAG
>random_seq_from_cds__NO_11829    RANDOM_LENGTH    72    SEQ_LENGTH    64
GC_CONTENT    0.609375    BASEPAIR    21    FREE_ENERGY    -22.70
LEN_BP_RATIO    3.04761904761905
CCUAUGUGGAGGGUGGAUCUGGAGCAUGAGUGGACAAUCCAGCCACAUGCCCUUCUCCAAGGC
CCACUGG
>random_seq_from_cds__NO_11834    RANDOM_LENGTH    84    SEQ_LENGTH    74
GC_CONTENT    0.621621621621622    BASEPAIR    21    FREE_ENERGY
-21.33    LEN_BP_RATIO    3.52380952380952
AGGUAGCCGAGCCAGGAGCUGAUGGGAACCCUGAUGGCACCCUGCUACCCUCCACCACAGUACC
GAGACAGGCAUCUCCCCAG
>random_seq_from_cds__NO_11835    RANDOM_LENGTH    84    SEQ_LENGTH    69
GC_CONTENT    0.623188405797101    BASEPAIR    19    FREE_ENERGY
-19.22    LEN_BP_RATIO    3.63157894736842
AACCUGGGGACCCUGGCUUGCUGCACCCCCAGACCUCACCCUGCUGCACUCAUUAUGGGGCA
ACAUAUCCUGUCCGUCCAG
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>random_seq_from_cds__NO_11838 RANDOM_LENGTH 72 SEQ_LENGTH 63
GC_CONTENT 0.619047619047619 BASEPAIR 22 FREE_ENERGY
-23.30 LEN_BP_RATIO 2.86363636363636
UGUGCUCAGCUUCUCGGAAGCCACAUCGUCCGUCCAGAAGGGCGAAUCCCUGGCUGACUCCGUGC
AGACCAU

>random_seq_from_cds__NO_11839 RANDOM_LENGTH 74 SEQ_LENGTH 60
GC_CONTENT 0.7166666666666667 BASEPAIR 21 FREE_ENERGY
-28.60 LEN_BP_RATIO 2.85714285714286
GAGCUGCUAUGCCGACGUCGUCGUCGUCCGGCACCCCCAGCCUGGAGCAGUGGAGGCUGGCCGCC
AAGCACUGC

>random_seq_from_cds__NO_11847 RANDOM_LENGTH 84 SEQ_LENGTH 70
GC_CONTENT 0.6 BASEPAIR 22 FREE_ENERGY -31.84 LEN_BP_RATIO
3.18181818181818
GGAAGCAGGAGGAGAAGCACCUGAAGAUGCUGCGGGACAUGACCGGCCUCCCGCACAAACCGAAAG
UGCUCGACUGCGACCAGC

>random_seq_from_cds__NO_11889 RANDOM_LENGTH 78 SEQ_LENGTH 65
GC_CONTENT 0.538461538461538 BASEPAIR 23 FREE_ENERGY
-20.40 LEN_BP_RATIO 2.82608695652174
GUCACCGAGGACGAGGUCGAGUGGAUGAGACAAGGCUGGACUACUUACUACUGAUCCACGUGUGA
GGGAACGGAAGAA

>random_seq_from_cds__NO_11890 RANDOM_LENGTH 83 SEQ_LENGTH 66
GC_CONTENT 0.575757575757576 BASEPAIR 24 FREE_ENERGY
-29.70 LEN_BP_RATIO 2.75
GCCAGGCCAAGAGGGAGCCCGCAGAAAGUUUACGUGGAAGAAACGCUAAGUUAGACUGUGGCCGU
CAGCAUGGCCUCCGUCUC

>random_seq_from_cds__NO_11897 RANDOM_LENGTH 86 SEQ_LENGTH 77
GC_CONTENT 0.662337662337662 BASEPAIR 29 FREE_ENERGY
-33.90 LEN_BP_RATIO 2.6551724137931
GCAGCUUCUCCAGCACAGUGGGUGCUUCAGCAGCUGCAUGAUGAGUGAGGUGCUGGCCUGGCC
GUGGUGGCAUAGGCCGCAAAG

>random_seq_from_cds__NO_11902 RANDOM_LENGTH 71 SEQ_LENGTH 55
GC_CONTENT 0.690909090909091 BASEPAIR 23 FREE_ENERGY
-28.90 LEN_BP_RATIO 2.39130434782609
GGCCUCGGGUGGCUGCUCCAGGCGCGCAGUGUGUCCUGGAUCACCAGCUGGAUCUUGGGCAGGU
AACUCU

>random_seq_from_cds__NO_11906 RANDOM_LENGTH 89 SEQ_LENGTH 76
GC_CONTENT 0.684210526315789 BASEPAIR 28 FREE_ENERGY
-38.60 LEN_BP_RATIO 2.71428571428571
UGGCCGUCUCUCCGAUGAGCGGGAAGCCCAUGGAUCCCUUGGGGAUGGGCAGCUUGCAGCUCUU
GUCGCGAGUGGCGGCCAGCGCAG

>random_seq_from_cds__NO_11911 RANDOM_LENGTH 85 SEQ_LENGTH 66
GC_CONTENT 0.454545454545455 BASEPAIR 23 FREE_ENERGY
-20.10 LEN_BP_RATIO 2.8695652173913
AUGAUAGCCAGAUUUUCUUCUGCAUGGCGGUUACAGGGCAAUCUUUAUGAGCCAGAAGAAGCUGUU


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UCAGCUGUGCCACUUCAUUU
>random_seq_from_cds__NO_11914    RANDOM_LENGTH 72 SEQ_LENGTH    50
  GC_CONTENT    0.58    BASEPAIR    19 FREE_ENERGY    -19.40
  LEN_BP_RATIO  2.63157894736842
GUUAGCUGCUCUUCUCCGACGACCACUUGUACUUUGGGUCUGUGGAGUUGUGUGAGCUGGAGAAG
CCCGGAG
>random_seq_from_cds__NO_11915    RANDOM_LENGTH 97 SEQ_LENGTH    86
  GC_CONTENT    0.523255813953488    BASEPAIR    31 FREE_ENERGY
  -30.00 LEN_BP_RATIO  2.7741935483871
UUUCUGUAGUGGAUGUGGCUGGCUGUUGUAAUGACUGCGGUCGAGAUUCCUCUGACUGAGUCCUA
ACCAAUCCGCUACCAUGACCUUUGACAGUAUC
>random_seq_from_cds__NO_11916    RANDOM_LENGTH 71 SEQ_LENGTH    54
  GC_CONTENT    0.407407407407407    BASEPAIR    19 FREE_ENERGY
  -17.60 LEN_BP_RATIO  2.84210526315789
ACCAUUGGUAACUGGAGGAUGUUGCUGGGUCAAGCAGCUUUUAAUCUCCAUUUUUGCUUCUGAC
UGUACU
>random_seq_from_cds__NO_11917    RANDOM_LENGTH 68 SEQ_LENGTH    63
  GC_CONTENT    0.603174603174603    BASEPAIR    20 FREE_ENERGY
  -18.20 LEN_BP_RATIO  3.15
GGUUGGGGAGAGGAAGGACCUGGGAUUCCUGGAACACUAGGCACCAUGGUGACUGGUCGAACGAG
CUG
>random_seq_from_cds__NO_11924    RANDOM_LENGTH 82 SEQ_LENGTH    71
  GC_CONTENT    0.47887323943662 BASEPAIR    26 FREE_ENERGY
  -26.50 LEN_BP_RATIO  2.73076923076923
AAUCUUGUUGGUUGGGUCUGAUCCAGCCACAAUGACACUGUCAUUACGUGCUGGACCAAUU
UCAGUGUCAUCUCAUGU
>random_seq_from_cds__NO_11937    RANDOM_LENGTH 69 SEQ_LENGTH    52
  GC_CONTENT    0.538461538461538    BASEPAIR    19 FREE_ENERGY
  -16.00 LEN_BP_RATIO  2.73684210526316
AAGCACAGAAACUUGGUAUUGGGAUCAACAUAUUGUGGCCACACCAGGCCGUCUGCUGGACCAU
AUGC
>random_seq_from_cds__NO_11940    RANDOM_LENGTH 110 SEQ_LENGTH    87
  GC_CONTENT    0.448275862068966    BASEPAIR    31 FREE_ENERGY
  -28.30 LEN_BP_RATIO  2.80645161290323
UUGAAGACCUGGCAAGGAUUUCUCUGAAAAAGGAGCCAUUGUAUGUUGGCGUUGAUGAUGAUA
GCGAAUGCAACAGUGGAUGGUCUUGAACAGGGGAUAUGUUGUUUG
>random_seq_from_cds__NO_11950    RANDOM_LENGTH 90 SEQ_LENGTH    75
  GC_CONTENT    0.48    BASEPAIR    27 FREE_ENERGY    -27.50
  LEN_BP_RATIO  2.77777777777778
AUCAUUCAGGCCUGAAGUGAGGGAGCCUUUAUAUUGCCACAGUGUUCAUUGUUCAGCAUUGU
UGGGCUCACCUGGAAUCCAGAACCC
>random_seq_from_cds__NO_11956    RANDOM_LENGTH 99 SEQ_LENGTH    69
  GC_CONTENT    0.536231884057971    BASEPAIR    23 FREE_ENERGY
  -22.10 LEN_BP_RATIO  3
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CCCAACUUCUUGUUAAGAUCUGGAUCUGUGCGUUGGCCUUCUCCACACUGGUUUUUAACUUCAGG
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>random_seq_from_cds__NO_11964 RANDOM_LENGTH 87 SEQ_LENGTH 54
GC_CONTENT 0.407407407407407 BASEPAIR 20 FREE_ENERGY
-16.70 LEN_BP_RATIO 2.7
GAAAAGCUAUCCUCACAUCAUUCAGGACAAAUGUACCCUUCACUUUUUGACCCCAGGGGUGAAUA
AUUCUGGGUCAUAUAUUUGUAG
>random_seq_from_cds__NO_11983 RANDOM_LENGTH 89 SEQ_LENGTH 80
GC_CONTENT 0.5625 BASEPAIR 25 FREE_ENERGY -15.90
LEN_BP_RATIO 3.2
CGGACCUCUUCACCACGCUGGUGGACCUCAAGUGGCGCUGGAACCUCUUCAUCUUCUUCUUCACC
UACACCGUGGCCUGGCUUUUAUG
>random_seq_from_cds__NO_11997 RANDOM_LENGTH 89 SEQ_LENGTH 74
GC_CONTENT 0.513513513513513 BASEPAIR 25 FREE_ENERGY
-23.90 LEN_BP_RATIO 2.96
CCACCAAGAUGUUAUCUGAUCCCAUGAGCCAGUCUGUGGCUGAUUUGCCACCAAAGCUUCAAAG
AUGGCUGGAGGAGCAGCUAGGAUG
>random_seq_from_cds__NO_12001 RANDOM_LENGTH 101 SEQ_LENGTH 82
GC_CONTENT 0.463414634146341 BASEPAIR 25 FREE_ENERGY
-23.44 LEN_BP_RATIO 3.28
GUUACAAGCUCGCUCUUCUUAUUGCUGACUCGUCCUCUCCUUCUCCACCUUUCUGAGGUGA
AGCACAAUAAGGUUAGAGAUUCGGCAGUACUCAGAG
>random_seq_from_cds__NO_12009 RANDOM_LENGTH 95 SEQ_LENGTH 80
GC_CONTENT 0.4 BASEPAIR 29 FREE_ENERGY -21.40 LEN_BP_RATIO
2.75862068965517
UCGGGACAUGAUGGGAGCUGACAAAUUUUAUUCUGUUUCAUGAUUUUGAUCUGUCAUAGUGUC
CACUGAUUGGGUUUGCUGCUGCCAAAUGG
>random_seq_from_cds__NO_12018 RANDOM_LENGTH 88 SEQ_LENGTH 70
GC_CONTENT 0.528571428571429 BASEPAIR 21 FREE_ENERGY
-22.15 LEN_BP_RATIO 3.3333333333333333
UCGAAUGCCUUCUGUCUCAUAUCCAUCAACACCACUGACACGGGAAUUAGUUUCUGCACGUGCUC
CCUGGUGUGCUAAGCUUGGAGAC
>random_seq_from_cds__NO_12027 RANDOM_LENGTH 95 SEQ_LENGTH 76
GC_CONTENT 0.763157894736842 BASEPAIR 29 FREE_ENERGY
-40.00 LEN_BP_RATIO 2.62068965517241
UUCUGGCACUUCUCGGCCACCUCGUCGCGGACCUCAGGUGCUGGCUGCCGGCGCCCGGCUCCGC
UGCCGCCGCGAGGUCCAUUUCAGCAUAUGG
>random_seq_from_cds__NO_12047 RANDOM_LENGTH 84 SEQ_LENGTH 55
GC_CONTENT 0.509090909090909 BASEPAIR 19 FREE_ENERGY
-19.80 LEN_BP_RATIO 2.89473684210526
UAUCAUUCCAACAUCAUGGACUGGUCCUGCAGAUACAUAUCCUCCUGGUCACAAUAGG
ACAGUCCAUGGGUGAUUU
>random_seq_from_cds__NO_12061 RANDOM_LENGTH 84 SEQ_LENGTH 79
GC_CONTENT 0.556962025316456 BASEPAIR 27 FREE_ENERGY

-26.20 LEN_BP_RATIO 2.92592592592593
GGUGGCGAGGGGCUUCCCAUCUCCUGUGGUACUGUCUGGAUAAUGAAUCCCCGCUUCAGGAAAGU
GCUUGAAGCCCUAGUUUCU
>random_seq_from_cds__NO_12073 RANDOM_LENGTH 70 SEQ_LENGTH 61
GC_CONTENT 0.672131147540984 BASEPAIR 22 FREE_ENERGY
-25.60 LEN_BP_RATIO 2.77272727272727
ACGUGGCGCGUCAGCUGCACAUCCUGCAGUCUGAGCCUGUGGUGACCGAUGCGUUCUGGCC
GUGGC
>random_seq_from_cds__NO_12075 RANDOM_LENGTH 85 SEQ_LENGTH 73
GC_CONTENT 0.712328767123288 BASEPAIR 28 FREE_ENERGY
-36.60 LEN_BP_RATIO 2.60714285714286
CAGGCCAGCCUGCCAUGGUCCACGCCUCGUGGACUGCCUGGGGAGUUCGUGCGCAAGACCCU
GGCAACCUGGCUGCGGAGAC
>random_seq_from_cds__NO_12096 RANDOM_LENGTH 87 SEQ_LENGTH 71
GC_CONTENT 0.647887323943662 BASEPAIR 25 FREE_ENERGY
-32.60 LEN_BP_RATIO 2.84
CUUCCUGCUGGUGUGGCUGGUGUCUUCUGUUGCAGGAUUAUGGCCUGGCCGCCGCGGCCUCG
UCCCCACCUUCCACAUGGCCUC
>random_seq_from_cds__NO_12112 RANDOM_LENGTH 84 SEQ_LENGTH 67
GC_CONTENT 0.462686567164179 BASEPAIR 26 FREE_ENERGY
-22.90 LEN_BP_RATIO 2.57692307692308
ACGUCCUCUCUACAAGGAAUAUUGUCCUCUCUGGAGGUUCAACCAUGUUCAGGGACUUUGGACGU
CGCUUGCAAAGAGAUUUGA
>random_seq_from_cds__NO_12137 RANDOM_LENGTH 92 SEQ_LENGTH 80
GC_CONTENT 0.35 BASEPAIR 29 FREE_ENERGY -19.00
LEN_BP_RATIO 2.75862068965517
CUUAGUGCAGAGAAGAAAGCUGGGGCGUGGUCAAGGUUUGCAAUAGGUUAUUAUUUUAACCAUA
CUGAUCACUUUAUCCAUCUUCUUU
>random_seq_from_cds__NO_12146 RANDOM_LENGTH 92 SEQ_LENGTH 88
GC_CONTENT 0.840909090909091 BASEPAIR 35 FREE_ENERGY
-52.90 LEN_BP_RATIO 2.51428571428571
CGGAGCCGCCUUGGCCGGCCCGGGCCGGGCGUGCGCGCCGCCGCUUCAGCCGCAGCUUCAGCU
CGGACUCGGGCUCCAGCCCGGCGUCCG
>random_seq_from_cds__NO_12181 RANDOM_LENGTH 81 SEQ_LENGTH 74
GC_CONTENT 0.486486486486487 BASEPAIR 30 FREE_ENERGY
-26.80 LEN_BP_RATIO 2.46666666666667
CUGCUUCCACUCAUCCUUCACAUGGAGAGUCUUGGAAGCCAUUUCUAAUAGAUGUUGAUGGUG
GAGGUGGGGAGGUGC
>random_seq_from_cds__NO_12184 RANDOM_LENGTH 82 SEQ_LENGTH 74
GC_CONTENT 0.648648648648649 BASEPAIR 22 FREE_ENERGY
-23.70 LEN_BP_RATIO 3.36363636363636
CGGGGAGGAAGAGACCUGAACGUCCUGGCGAAGGUAACGGGGCGUGGACGAACUGAGGGACA
GAUCCGCGUGGGAGU
>random_seq_from_cds__NO_12186 RANDOM_LENGTH 81 SEQ_LENGTH 67

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GC_CONTENT    0.641791044776119    BASEPAIR    23    FREE_ENERGY
-31.70    LEN_BP_RATIO    2.91304347826087
GGAAGGCACUGGAGGCUUGUUGUUCUGAGGAGGAGGAGGGGGAACCGCUUCCCUGUGGAUGGAGG
GCCUGUUGCCCACUGG
>random_seq_from_cds__NO_12189    RANDOM_LENGTH    110    SEQ_LENGTH
102    GC_CONTENT    0.607843137254902    BASEPAIR    36    FREE_ENERGY
-42.40    LEN_BP_RATIO    2.833333333333333
GGCUGCCUGGGGCCUCCGGGCACUGGUGGGGACCCCCGGUUGUGCGGACUUGAUUGAAUGGGUCU
UGGAGUACUAGGUACUGGAGGAGGAAUGCUAUCAGGCUUUGAGCC
>random_seq_from_cds__NO_12191    RANDOM_LENGTH    110    SEQ_LENGTH
103    GC_CONTENT    0.58252427184466    BASEPAIR    35    FREE_ENERGY
-38.80    LEN_BP_RATIO    2.94285714285714
CCUGGGCCACUUGGGGGUGAAAAGGGUUCGCGAUGUGGAUCUCCUCCCGGUGGCAACAAUGG
UGGUCGGCUUCCUCCAGAAUCCAUAUCCUGUUGGCCGUGGAUC
>random_seq_from_cds__NO_12196    RANDOM_LENGTH    87    SEQ_LENGTH    79
GC_CONTENT    0.683544303797468    BASEPAIR    29    FREE_ENERGY
-39.30    LEN_BP_RATIO    2.72413793103448
GCUGGGGGCGUCGCUCCACGUCUGGGGUUGGCUAAUGCUCGGCAGCUGCCUCCUGGCCAGAGCCC
AGGCUGGAUUCUGAUGGCACCA
>random_seq_from_cds__NO_12200    RANDOM_LENGTH    95    SEQ_LENGTH    83
GC_CONTENT    0.433734939759036    BASEPAIR    27    FREE_ENERGY
-18.50    LEN_BP_RATIO    3.07407407407407
ACAUGGGCCAAUUAUUCAGACUGCCUUCGCUUUCUGCAGCCAGAUUAUCAGCAUAGGAAAGGCAAG
AAUUCUUUGAACGCCUCUAUGUAAUGUAUA
>random_seq_from_cds__NO_12204    RANDOM_LENGTH    110    SEQ_LENGTH
103    GC_CONTENT    0.378640776699029    BASEPAIR    28    FREE_ENERGY
-19.51    LEN_BP_RATIO    3.67857142857143
GUUGUGAUGUUUAUUUACUUCUGGCUACAAUUAUUAUUGGAUCCUGGUGGAAGGUCUCUACCU
GCAUAAUCUCAUCUUUGUGGCUUUCUUUUCGGACACCAAUACCU
>random_seq_from_cds__NO_12208    RANDOM_LENGTH    73    SEQ_LENGTH    66
GC_CONTENT    0.575757575757576    BASEPAIR    23    FREE_ENERGY
-24.90    LEN_BP_RATIO    2.8695652173913
GUCCUGGUCCUAGUCUUUGGAGUGCAUUAUCAUCGUGUUCGUAUGCCUGCCUCACUCCUUCACUGG
GCUCGGGU
>random_seq_from_cds__NO_12227    RANDOM_LENGTH    68    SEQ_LENGTH    54
GC_CONTENT    0.592592592592593    BASEPAIR    20    FREE_ENERGY
-19.50    LEN_BP_RATIO    2.7
CAUGGUGGCCCGUGUCUCUGUGUCAUGGGAGUGCAGCAAGGAGGCACUCAAGCGCCAUUAUCA
GCU
>random_seq_from_cds__NO_12234    RANDOM_LENGTH    70    SEQ_LENGTH    63
GC_CONTENT    0.650793650793651    BASEPAIR    20    FREE_ENERGY
-28.60    LEN_BP_RATIO    3.15
CGCUGGGGCUCUUGUCUGUCUCUGUUGCCCAGGGGAAGGGAGCUUCUUGGAGUCGGCCUC
UGGCA
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>random_seq_from_cds__NO_12244 RANDOM_LENGTH 82 SEQ_LENGTH 62
GC_CONTENT 0.516129032258065 BASEPAIR 23 FREE_ENERGY
-26.30 LEN_BP_RATIO 2.69565217391304
UCGAUAUAAGCGGAGAGUGUCAUGUAGAUUUUCUCUCGUAUAAGGGGUGACCCGGUUCAGCAGGAG
AGAGUUGUGCAUGGAGC

>random_seq_from_cds__NO_12265 RANDOM_LENGTH 99 SEQ_LENGTH 88
GC_CONTENT 0.659090909090909 BASEPAIR 31 FREE_ENERGY
-39.40 LEN_BP_RATIO 2.83870967741936
CCUCCAGCUUGCUCUCAUAGUCCCAGCCGCGUCGUCUCCAGCAGGUAGGUGGCCUCCUCCCGCUC
GCGGCGGUACUGGUCCUCCAGUUCUGGAGCCCU

>random_seq_from_cds__NO_12297 RANDOM_LENGTH 71 SEQ_LENGTH 58
GC_CONTENT 0.637931034482759 BASEPAIR 21 FREE_ENERGY
-16.90 LEN_BP_RATIO 2.76190476190476
GUCCCACGCCUGCGGCACAUCAUCACUGUUGAUGGAAAGCCACCGACCUGGUCCGAGUUCCCCAA
GGGCAU

>random_seq_from_cds__NO_12344 RANDOM_LENGTH 78 SEQ_LENGTH 73
GC_CONTENT 0.465753424657534 BASEPAIR 22 FREE_ENERGY
-15.70 LEN_BP_RATIO 3.31818181818182
GAGGUCUJAGAGUAAAUGGUUAUUCUCUUUUAUGGUCAUCAGGCUCACUCUCAGGGUCAUCUUCG
CUCUCUCUCUUA

>random_seq_from_cds__NO_12347 RANDOM_LENGTH 82 SEQ_LENGTH 66
GC_CONTENT 0.439393939393939 BASEPAIR 25 FREE_ENERGY
-22.90 LEN_BP_RATIO 2.64
AAACCCUGAUCAUCCUUAUCUUCUGAGGAGUGAUGUAUUUAUCCUCUUAUCUGUGGACACAUC
AAGGGUUCUGGAUCCU

>random_seq_from_cds__NO_12348 RANDOM_LENGTH 98 SEQ_LENGTH 86
GC_CONTENT 0.802325581395349 BASEPAIR 30 FREE_ENERGY
-46.60 LEN_BP_RATIO 2.86666666666667
GAGCCUUCGUCCGCGCGGGGAGCCGCUUUGGUGGCACGCCGGGAGCUCGCCCAGACCCGGCCCCG
GCCACGAGGGCCCCGAACCCGGUGGGGCAGUCC

>random_seq_from_cds__NO_12351 RANDOM_LENGTH 77 SEQ_LENGTH 64
GC_CONTENT 0.609375 BASEPAIR 21 FREE_ENERGY -25.80
LEN_BP_RATIO 3.04761904761905
CAAAGGGUACGACGAUCUACCCCAUACGGGGGCAUGGAUGGAGUAGGCAUCCCUCCACGAUGU
AUGGGGACCCGC

>random_seq_from_cds__NO_12367 RANDOM_LENGTH 83 SEQ_LENGTH 49
GC_CONTENT 0.612244897959184 BASEPAIR 19 FREE_ENERGY
-23.09 LEN_BP_RATIO 2.57894736842105
UAAUGGCCUGGAGCCAAUCGCCACUGAUACCACAGCAGAGAAUUCAGGGGAGCUUGGAUCCAAC
AAGGCAGUGUUAGGUCCU

>random_seq_from_cds__NO_12376 RANDOM_LENGTH 110 SEQ_LENGTH 58
GC_CONTENT 0.5 BASEPAIR 19 FREE_ENERGY -21.47 LEN_BP_RATIO
3.05263157894737
CUCUCUCUUGCCAGGCACUUUGAGACGCCACUGCAUACCUCACCAAUUCACCCAACUCCUAUA

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ACUUUUUCAAUCUUA AUGCAGGAUGCGUCAUUUUCUUUGGCAAAC
>random_seq_from_cds__NO_12392    RANDOM_LENGTH 110 SEQ_LENGTH
    101 GC_CONTENT    0.495049504950495    BASEPAIR    34 FREE_ENERGY
    -24.60 LEN_BP_RATIO    2.97058823529412
GUAAAACCCCUUUUUGCUUAAUGGCCCUACAUCCCGGAUCUCGGUGUUCAGCUUCAUGAUUCUGU
CACCAAUGUCCACUUGGGUGAAGCUCUCAUCAGCAGCAAUGGUGU
>random_seq_from_cds__NO_12410    RANDOM_LENGTH 102 SEQ_LENGTH    91
    GC_CONTENT    0.428571428571429    BASEPAIR    30 FREE_ENERGY
    -26.16 LEN_BP_RATIO    3.033333333333333
UACUUCUCCAGCUUUCUCCCAUCUCUGAGUGAUGAGGAAUCACUUCUUCUUGGAAAAACUCCUU
ACACUUUUCGGAAAAUGUCAUGCUCUGGAGAAAAGA
>random_seq_from_cds__NO_12426    RANDOM_LENGTH 84 SEQ_LENGTH    62
    GC_CONTENT    0.532258064516129    BASEPAIR    22 FREE_ENERGY
    -22.70 LEN_BP_RATIO    2.81818181818182
CAAGAUCUCAAUA CAAGGCCGAGUCUGUGGAAUGUAUCAGGGUAUAAUUUCGUGGGUUUCGCU
GGUUACAGGCUAUGAUUU
>random_seq_from_cds__NO_12433    RANDOM_LENGTH 82 SEQ_LENGTH    55
    GC_CONTENT    0.545454545454545    BASEPAIR    20 FREE_ENERGY
    -15.50 LEN_BP_RATIO    2.75
CUCUGAUGAGGAAGAGA UCCAGCAUGUGGUAGAGGUGAUUCAA AAUCCACGGCCAAAGUCAUCG
UGGUUUUCUCCAGUGGC
>random_seq_from_cds__NO_12439    RANDOM_LENGTH 97 SEQ_LENGTH    76
    GC_CONTENT    0.565789473684211    BASEPAIR    22 FREE_ENERGY
    -16.32 LEN_BP_RATIO    3.45454545454545
ACUUAGCAGUCUACUCCA UUGCCCACGCCUUGCAAGAUUAUAUACCUGCUUACCUGGGAGAGGG
CUCUUCACCAAUGGCUCCUGUGCAGACA UCAA
>random_seq_from_cds__NO_12470    RANDOM_LENGTH 73 SEQ_LENGTH    66
    GC_CONTENT    0.545454545454545    BASEPAIR    21 FREE_ENERGY
    -22.90 LEN_BP_RATIO    3.14285714285714
GGGGAGUGGGAGCUCUUGGGCAUCAACAAGGCCACCCCAAAGAUGUCCAUGGGCAACAACCUAUA
UGACCAGA
>random_seq_from_cds__NO_12473    RANDOM_LENGTH 90 SEQ_LENGTH    70
    GC_CONTENT    0.585714285714286    BASEPAIR    23 FREE_ENERGY
    -20.50 LEN_BP_RATIO    3.04347826086957
CUUCCUGCUCAUGAUGAAUGACUUGCUCCUGCCAGUGGCACCCCCUCAUCAGGUGUCUACUUC
GCCUGUGCCUGUCCUGAUGGUGG
>random_seq_from_cds__NO_12478    RANDOM_LENGTH 85 SEQ_LENGTH    72
    GC_CONTENT    0.486111111111111    BASEPAIR    24 FREE_ENERGY
    -24.50 LEN_BP_RATIO    3
UCCUCUGGAACACCUAGAAUGGCUUCUGUUUGGCAGAGAUUGGGUUUUUAUGCCUCUCUUCUGAA
AAGACAGCUAAAUGGUGGGC
>random_seq_from_cds__NO_12482    RANDOM_LENGTH 85 SEQ_LENGTH    73
    GC_CONTENT    0.534246575342466    BASEPAIR    27 FREE_ENERGY
    -27.70 LEN_BP_RATIO    2.7037037037037
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AUCCUUCUGGUAAGCUGCACAUGGGCCAUGUGCGUGUCUACACCAUCAGCGACACCAUAGCACGG
UCCAGAAGAUGAGAGGGAU

>random_seq_from_cds__NO_12486 RANDOM_LENGTH 90 SEQ_LENGTH 82
GC_CONTENT 0.548780487804878 BASEPAIR 25 FREE_ENERGY
-26.16 LEN_BP_RATIO 3.28

ACUGGGACCCAGUGGAUCAAACAGUGCUUGCCAAUGAGCAGGUGGAUGAACAUGGCUGUUAUGG
CGUUCUGGAGCAAAGGUGGAACAGA

>random_seq_from_cds__NO_12494 RANDOM_LENGTH 73 SEQ_LENGTH 66
GC_CONTENT 0.606060606060606 BASEPAIR 23 FREE_ENERGY
-18.20 LEN_BP_RATIO 2.8695652173913

CACACCAAUCCCCAUUGUCCACUGCCCAGUCUGUGGCCCCACACCUGUGCCCCUGGAGGACUUGC
CUGUGACC

>random_seq_from_cds__NO_12559 RANDOM_LENGTH 84 SEQ_LENGTH 73
GC_CONTENT 0.479452054794521 BASEPAIR 25 FREE_ENERGY
-16.70 LEN_BP_RATIO 2.92

GGGAUGUCCGUCCAUUGAUACAAACCAAAGAUGGAGAAAAUACGCUACAGUGGUUGGGUACAGU
GCUUUCUUAUUGCGAGU

>random_seq_from_cds__NO_12562 RANDOM_LENGTH 110 SEQ_LENGTH 92
GC_CONTENT 0.402173913043478 BASEPAIR 25 FREE_ENERGY
-16.75 LEN_BP_RATIO 3.68

AUAGGAAAAACUGCAGUCACAGCCAAUUGGAUUAUAGAAGAUAGCUACAAAACUUAAGUUAUCUC
CUAAGAAUCCUCGUAUCCCCAAUUGCAUAUGCUUGAAUUAUUAU

>random_seq_from_cds__NO_12567 RANDOM_LENGTH 88 SEQ_LENGTH 81
GC_CONTENT 0.45679012345679 BASEPAIR 27 FREE_ENERGY
-29.33 LEN_BP_RATIO 3

AACAAAGAAGAGCCUGGAAGGUGGGAGGAACUGACCAGAGUCCAAGGAAAGAAAACCACAGUUAU
CUUACCUUUGGCUCCAUUUGUGA

>random_seq_from_cds__NO_12585 RANDOM_LENGTH 82 SEQ_LENGTH 64
GC_CONTENT 0.5 BASEPAIR 20 FREE_ENERGY -20.20 LEN_BP_RATIO
3.2

UAUUGGUGCCUACGUGGAUCUAAGGAGAAGGGAUCUGUUGAAAGCAAUGGAAGUUCUACAGCAA
CUUUUCCCCUUCGGGCA

>random_seq_from_cds__NO_12591 RANDOM_LENGTH 90 SEQ_LENGTH 68
GC_CONTENT 0.485294117647059 BASEPAIR 24 FREE_ENERGY
-27.30 LEN_BP_RATIO 2.83333333333333

AGAAGGUCAAGGUGUGGUGCUUCUCUGUGGCCACCGCCACAUUUUGGAGGAUUUAUCUUAUGCA
UGGACCUUCAUGAUAACCCCUUAU

>random_seq_from_cds__NO_12611 RANDOM_LENGTH 85 SEQ_LENGTH 75
GC_CONTENT 0.48 BASEPAIR 24 FREE_ENERGY -17.30
LEN_BP_RATIO 3.125

UGAACUCGUCAUUAACGUGGGAGGUCAAUCCAGAAGAACUGCAGAAUGGGGAGGGAUUUGGAUUA
AUCAUCAUGUCCGGCCAGU

>random_seq_from_cds__NO_12619 RANDOM_LENGTH 82 SEQ_LENGTH 63
GC_CONTENT 0.428571428571429 BASEPAIR 22 FREE_ENERGY

-20.20 LEN_BP_RATIO 2.86363636363636

CAUCAGCUGAGCUUCUGGUUCCAUAUUGAAGAAGACUACUAAUUGAAAUAAGAACAGUCAGUGAU
GGUGGAGAUGGAAGCAG

>random_seq_from_cds__NO_12620 RANDOM_LENGTH 81 SEQ_LENGTH 74
GC_CONTENT 0.378378378378378 BASEPAIR 26 FREE_ENERGY
-17.70 LEN_BP_RATIO 2.84615384615385

CAGUGAGAAAUAAGGAUUCAAAAAUGUCAAGGUUUGAGUUCAGAGGAAUUCAAUUCUAGAA
CCUAGCACCCAUUUUC

>random_seq_from_cds__NO_12627 RANDOM_LENGTH 86 SEQ_LENGTH 79
GC_CONTENT 0.518987341772152 BASEPAIR 26 FREE_ENERGY
-19.70 LEN_BP_RATIO 3.03846153846154

CUCGCGCUGCCGUGGACUUUUGGAGAAUGAGUUGAAACUGAUGGAAGAAUUGUCAAGCAAUAUA
AGAGCGAGGCCUCGGCGUGG

>random_seq_from_cds__NO_12630 RANDOM_LENGTH 90 SEQ_LENGTH 78
GC_CONTENT 0.615384615384615 BASEPAIR 25 FREE_ENERGY
-29.60 LEN_BP_RATIO 3.12

CCCACCUUCUUGUGUGUGCCAAGUGCUCGAGCCGUGGUGACCUCAUCUACUUCUGGAAGGA
UGGUGCACCCUGGUGCGGCCCAU

>random_seq_from_cds__NO_12649 RANDOM_LENGTH 88 SEQ_LENGTH 74
GC_CONTENT 0.513513513513513 BASEPAIR 26 FREE_ENERGY
-28.90 LEN_BP_RATIO 2.84615384615385

CUGAUGGCUCCCAGUACUAUGUUCUGCUCAUCAUCACUGAUGGGGUCAUCUCUGACAUGACGCAG
ACCAAGGAGGCCAUCGUCAGCGG

>random_seq_from_cds__NO_12650 RANDOM_LENGTH 86 SEQ_LENGTH 76
GC_CONTENT 0.486842105263158 BASEPAIR 26 FREE_ENERGY
-23.30 LEN_BP_RATIO 2.92307692307692

CCUCCUCAUUGCCCAUGUCUAUCAUAUCGUCGGUGUAGGACCAGCCAUGUUUGAGGGCAAUGGA
AGAGUUGGACGGUGAUGAUGU

>random_seq_from_cds__NO_12665 RANDOM_LENGTH 88 SEQ_LENGTH 75
GC_CONTENT 0.653333333333333 BASEPAIR 25 FREE_ENERGY
-30.10 LEN_BP_RATIO 3

CCGUUGCCUGCAGUCACCCUCUCGUGCUGUGGAUUGGCCUGUGCCCCAACAAAGGGCGGUGCCU
UCAAGCAGACAGAUGACGGGCGC

>random_seq_from_cds__NO_12671 RANDOM_LENGTH 73 SEQ_LENGTH 60
GC_CONTENT 0.666666666666667 BASEPAIR 20 FREE_ENERGY
-22.60 LEN_BP_RATIO 3

GAUCCUGGCAGAGAAGCGGGCAGCAGCACCUGUGGUGUCAGUGCCCUGCAUCCCACCACACAGGG
CUUAGUAA

>random_seq_from_cds__NO_12678 RANDOM_LENGTH 82 SEQ_LENGTH 67
GC_CONTENT 0.701492537313433 BASEPAIR 26 FREE_ENERGY
-31.70 LEN_BP_RATIO 2.57692307692308

ACACCAUCUUCUACCGGGCAGCAGUGCGGCUUCGUGAGCAGGGUGGUGCUGUGCUCCGCCAGGCC
CGGCGCCAGGCAGAAAA

>random_seq_from_cds__NO_12696 RANDOM_LENGTH 110 SEQ_LENGTH

104 GC_CONTENT 0.644230769230769 BASEPAIR 37 FREE_ENERGY
-41.60 LEN_BP_RATIO 2.81081081081081
GGGCUCUCGAGCACCAGCAAGGUGCAAGGCGAGCAGAGCAGUGAGACCAGCGAUAGUGAUUGA
GAUGGACUGCCACUCUCCGCCCUACCUGAGUGCCGUGCGGGCCA
>random_seq_from_cds__NO_12699 RANDOM_LENGTH 88 SEQ_LENGTH 62
GC_CONTENT 0.419354838709677 BASEPAIR 24 FREE_ENERGY
-20.60 LEN_BP_RATIO 2.58333333333333
UGUGAAACAGGGCUGAUGAGAUCGAGAAGAUUUUGUGCCACAAGUUCAUGCGCUUCAUGAUGAUG
CGAGCAGAGAACUUCUUUAUCCU
>random_seq_from_cds__NO_12714 RANDOM_LENGTH 87 SEQ_LENGTH 73
GC_CONTENT 0.534246575342466 BASEPAIR 20 FREE_ENERGY
-18.12 LEN_BP_RATIO 3.65
AGUACCGCAUGGUCUGGAGAUAUCCACAGCAACGUCAGAGGCUCUAAUGUCUUGCUGGACCA
AAAUCUCACCCCAAACUUGCU
>random_seq_from_cds__NO_12731 RANDOM_LENGTH 89 SEQ_LENGTH 70
GC_CONTENT 0.557142857142857 BASEPAIR 22 FREE_ENERGY
-24.50 LEN_BP_RATIO 3.18181818181818
AGCUGGAACAUCUGAAACUUGGUCUCCUGGACAUGCAGGUGUUUGUAGAGGCUGCUGCCCUCGCA
CCACUGGGUCACAAUUGCCAGGU
>random_seq_from_cds__NO_12737 RANDOM_LENGTH 88 SEQ_LENGTH 72
GC_CONTENT 0.513888888888889 BASEPAIR 28 FREE_ENERGY
-30.80 LEN_BP_RATIO 2.57142857142857
UGUGACUUCGAAUUGCAUCCCUCAAUCAUCCUGCUGUCCACAGGCAGGGUGGUGCUGACCAUGUG
GACAUUAGGUGUGGAUGUCGACC
>random_seq_from_cds__NO_12747 RANDOM_LENGTH 110 SEQ_LENGTH
101 GC_CONTENT 0.544554455445545 BASEPAIR 29 FREE_ENERGY
-31.77 LEN_BP_RATIO 3.48275862068966
CCUGUAUGUGCUCCAUCUACUCAUUUUCUACUGCGCAGCCUGGCAUUGGGGUUGGUGACUCU
GAUGGCCAGUUGGGCAGCUCUUCCACGAUGGCUUUGCGGUUCU
>random_seq_from_cds__NO_12755 RANDOM_LENGTH 88 SEQ_LENGTH 74
GC_CONTENT 0.648648648648649 BASEPAIR 28 FREE_ENERGY
-30.00 LEN_BP_RATIO 2.64285714285714
AGAUCAGCUGCCAGUUCAUGCUGUGCCCGAGCUGCCGCCAACUGCAUCGAGGCUGUAGUGGUG
GCUGACAGCUGCCCACAGUGCGG
>random_seq_from_cds__NO_12762 RANDOM_LENGTH 90 SEQ_LENGTH 86
GC_CONTENT 0.651162790697674 BASEPAIR 29 FREE_ENERGY
-45.40 LEN_BP_RATIO 2.96551724137931
CUGGAUGGGCUGCCCACUACAGCCCAGCCUGGACCCAGUCUCCUAUCCAGGAGGAGGGCAG
AAGCUGGGGCAAGGGCAGAAGCUGG
>random_seq_from_cds__NO_12764 RANDOM_LENGTH 84 SEQ_LENGTH 65
GC_CONTENT 0.692307692307692 BASEPAIR 20 FREE_ENERGY
-29.00 LEN_BP_RATIO 3.25
UGGGCAAGGCUGCUCUCGUCCAACUCAGGCCGUGCCUGGCUCUCCAGGGACCCAGUCAAGCCC
AGCCCCACAACAUCUGU

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>random_seq_from_cds__NO_12772    RANDOM_LENGTH 78 SEQ_LENGTH    66
  GC_CONTENT    0.6969696969697    BASEPAIR    24 FREE_ENERGY
  -35.30 LEN_BP_RATIO    2.75
CACCACGGAGAGUUUCAGAGGCAGAGAUGGCGGGCCGAGAGGCCUGUCACUGGGCACAGAGGC
CGAGCUGCCGAAC
>random_seq_from_cds__NO_12781    RANDOM_LENGTH 84 SEQ_LENGTH    72
  GC_CONTENT    0.625    BASEPAIR    25 FREE_ENERGY    -23.80
  LEN_BP_RATIO    2.88
AACCCGCUGAUCUGCGCGCGCGGCUACCACGCCAGCGAUGAUGGGACCAAGUGUGUGGGACGUGA
AUGAGUGUGAGACAGGUGU
>random_seq_from_cds__NO_12783    RANDOM_LENGTH 98 SEQ_LENGTH    79
  GC_CONTENT    0.658227848101266    BASEPAIR    27 FREE_ENERGY
  -36.50 LEN_BP_RATIO    2.92592592592593
UUUGGCCGGGGCUGCAUCGGACGUGAAUGAGUGCUGGGCCUCGCCAGGCCGCCUGUGCCAGCACA
CGUGUGAGAACACACUCGGCUCCUACCGCUGUU
>random_seq_from_cds__NO_12796    RANDOM_LENGTH 84 SEQ_LENGTH    71
  GC_CONTENT    0.450704225352113    BASEPAIR    25 FREE_ENERGY
  -16.80 LEN_BP_RATIO    2.84
ACCUUGACAUCUAUGAACAGCAAGUGAUGACUGCAGCCAAAAGGGAUGUACAGAUUAUAGUGUU
UCCAGAAGAUGGCAUUCAU
>random_seq_from_cds__NO_12817    RANDOM_LENGTH 80 SEQ_LENGTH    59
  GC_CONTENT    0.423728813559322    BASEPAIR    25 FREE_ENERGY
  -19.30 LEN_BP_RATIO    2.36
GAUGACCUGAACUGGUGAAUUUGGGUAAGUAGGAUAUGCCUGAACAUACUGAGUUUAUGGAUUC
AUCGUGGUUGUGGGC
>random_seq_from_cds__NO_12824    RANDOM_LENGTH 64 SEQ_LENGTH    59
  GC_CONTENT    0.576271186440678    BASEPAIR    19 FREE_ENERGY
  -21.11 LEN_BP_RATIO    3.10526315789474
CUUGCCAAUGCCCAGGUGGCUAAGGGUUUCCCAUAGUCUACUGUCCGAUGGCUUCUGCGAGC
>random_seq_from_cds__NO_12825    RANDOM_LENGTH 85 SEQ_LENGTH    69
  GC_CONTENT    0.449275362318841    BASEPAIR    22 FREE_ENERGY
  -18.30 LEN_BP_RATIO    3.13636363636364
UUGCUGGAUUUGCCCGAACUGAAGUCAUGCAGAAGAGUUUGUAGCUGCAAGUUCUUAUUUGGGGUU
GAAACCAAUGAGCAACUGAU
>random_seq_from_cds__NO_12837    RANDOM_LENGTH 82 SEQ_LENGTH    65
  GC_CONTENT    0.492307692307692    BASEPAIR    24 FREE_ENERGY
  -17.40 LEN_BP_RATIO    2.70833333333333
GGGAAGACAACAGCCUUCUGAAGUGGGAAGUUGGGUUGGCUUCAUGAGUUGGAAAGAGACUGGA
AUCUCCAUAUAUGGCA
>random_seq_from_cds__NO_12838    RANDOM_LENGTH 81 SEQ_LENGTH    61
  GC_CONTENT    0.639344262295082    BASEPAIR    22 FREE_ENERGY
  -21.56 LEN_BP_RATIO    2.77272727272727
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AGCCUCACCAGCGUGG
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CUGCCGGAAAACUUC
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  GC_CONTENT    0.553191489361702  BASEPAIR    19 FREE_ENERGY
  -16.62 LEN_BP_RATIO    2.47368421052632
AUGAAUCACCUUUCGUUGGGCACAAACAGGAACGGUAUAUGACUGCUGCUGCUCCUAUGCAAGGGA
CCUACAUCCUCAGUA
>random_seq_from_cds__NO_12972    RANDOM_LENGTH 85 SEQ_LENGTH    56
  GC_CONTENT    0.5 BASEPAIR    22 FREE_ENERGY    -23.40 LEN_BP_RATIO
  2.54545454545455
CACUUUUUUAUCUUCAGACAAAACCAAUUCAGAGCCUGAGUUUGGCCUCUGGCUCUGGCUGUGA
GGUUUGUUCGUCUUCAGCAG
>random_seq_from_cds__NO_12977    RANDOM_LENGTH 89 SEQ_LENGTH    78
  GC_CONTENT    0.58974358974359 BASEPAIR    28 FREE_ENERGY
  -33.90 LEN_BP_RATIO    2.78571428571429
UGAUUGUGACAACACCGGGGGCCCCACACUGAGGUGUCUCUGGCUACAGGGAGACGCAGAAUUG
GGUGUCCAUGUGGGAGCAAAGUG
>random_seq_from_cds__NO_12980    RANDOM_LENGTH 88 SEQ_LENGTH    77
  GC_CONTENT    0.571428571428571  BASEPAIR    26 FREE_ENERGY
  -27.10 LEN_BP_RATIO    2.96153846153846
AGAGUACACCACCAGCAUGUGGGGAGCUUCAUCGCUCAGGGACACUAUGGCUCCAGAUAAAGACA
GGACUCCUCGAGGCUUCUGGUGU
>random_seq_from_cds__NO_13004    RANDOM_LENGTH 110 SEQ_LENGTH    93
  GC_CONTENT    0.505376344086022  BASEPAIR    30 FREE_ENERGY
  -24.93 LEN_BP_RATIO    3.1
GGAGCAAGUUACUCAGAUGGAAAACUGAAAGCCCCUCCUAAACCAUGUGCUGGCAAUCAAGGGAC
CCAGAUACACGGGUGGAGGACCUUUUUUACAACAUAAGCCACGAGGA
>random_seq_from_cds__NO_13013    RANDOM_LENGTH 82 SEQ_LENGTH    73
  GC_CONTENT    0.547945205479452  BASEPAIR    29 FREE_ENERGY
  -25.30 LEN_BP_RATIO    2.51724137931034
CCCUGUCCAGUCAGCCCCAGGCCAUUGUCACAGAGGAUAAGACAGAUUUUCUAGUGGCAGGGCU
AGGCAGCAAGAUGAGGA
>random_seq_from_cds__NO_13014    RANDOM_LENGTH 80 SEQ_LENGTH    65
  GC_CONTENT    0.569230769230769  BASEPAIR    21 FREE_ENERGY
  -23.32 LEN_BP_RATIO    3.0952380952381
GAUGCUUGAACUCCAGCCCCUGCUGAAGUGGCUGCCAAAAAUCAGAGCUUGGAGGGGGAUACAA
CAAAGGGGACUUCAG
>random_seq_from_cds__NO_13019    RANDOM_LENGTH 84 SEQ_LENGTH    75
  GC_CONTENT    0.6 BASEPAIR    26 FREE_ENERGY    -27.10 LEN_BP_RATIO
  2.88461538461538
CGGGAGCCAGCACCGCUCUUUGACCUUGCCAUGCUUGCCUAGAUAGUCCAGAGAGUGGCUGGAC
AGAGGAAGAUGGUCCAAA
>random_seq_from_cds__NO_13020    RANDOM_LENGTH 84 SEQ_LENGTH    55
  GC_CONTENT    0.363636363636364  BASEPAIR    20 FREE_ENERGY
  -16.20 LEN_BP_RATIO    2.75
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GAAGGACUUGCUGAAUACAUUGUUGAGUUUCUGAAGAAGAAGGCUGAGAUGCUUGCAGACUAUUU
CUCUUUGGAAAUUGAUGAG

>random_seq_from_cds__NO_13022 RANDOM_LENGTH 82 SEQ_LENGTH 62
GC_CONTENT 0.451612903225806 BASEPAIR 21 FREE_ENERGY
-16.80 LEN_BP_RATIO 2.95238095238095

UCAUUCUUCGACUAGCCACUGAGGGUGAAUUGGGACGAAGAAAAGGAAUGUUUUGAAAGCCUCAG
UAAAGAAUGCGCUAUGU

>random_seq_from_cds__NO_13032 RANDOM_LENGTH 88 SEQ_LENGTH 59
GC_CONTENT 0.576271186440678 BASEPAIR 20 FREE_ENERGY
-22.10 LEN_BP_RATIO 2.95

CGGCGGGAGGGGAUAAAUCGAUUCAUGUAAAGCUGGACGUGGGCAAGCUGCACACCCAGCCUAAG
UUAGCGGCCAGCUCAGGAUGGU

>random_seq_from_cds__NO_13038 RANDOM_LENGTH 97 SEQ_LENGTH 91
GC_CONTENT 0.582417582417582 BASEPAIR 26 FREE_ENERGY
-35.90 LEN_BP_RATIO 3.5

UGCCAGCCCGUGCCUCAUCCCUCAACUCCAGUGACAUCUUCUUGCUGGUCACAGCCAGCGUCUGC
UACCUCUGGUUUGGGAAGGGCUGUAAUGGUG

>random_seq_from_cds__NO_13040 RANDOM_LENGTH 70 SEQ_LENGTH 59
GC_CONTENT 0.728813559322034 BASEPAIR 21 FREE_ENERGY
-29.30 LEN_BP_RATIO 2.80952380952381

UUCUGGGAGGCCUGGGAGGCCGGGCCCCCUACCCAGCAACAAGAGGGCUGCCUGAGGAGGUCC
CCAGC

>random_seq_from_cds__NO_13045 RANDOM_LENGTH 87 SEQ_LENGTH 71
GC_CONTENT 0.690140845070423 BASEPAIR 24 FREE_ENERGY
-37.30 LEN_BP_RATIO 2.95833333333333

GCGGCUAUCCAGAUGGCCGGGCAAUGGCAGGGCAGGUGCCGUGGCCUGCAGGCCCUCAAGGGCU
CCCAGGACAGCUCAGAGAAUGA

>random_seq_from_cds__NO_13052 RANDOM_LENGTH 92 SEQ_LENGTH 84
GC_CONTENT 0.535714285714286 BASEPAIR 30 FREE_ENERGY
-24.10 LEN_BP_RATIO 2.8

CAGCCUGGCUUGCAAAGGCCUCAUUGAUCUCGAAGAUGUCCACGUCACUCACUGUCAGCCCCUG
CUUUUUGCAAAGCUACUGGGAUGGCAU

>random_seq_from_cds__NO_13072 RANDOM_LENGTH 110 SEQ_LENGTH 84
GC_CONTENT 0.380952380952381 BASEPAIR 29 FREE_ENERGY
-20.90 LEN_BP_RATIO 2.89655172413793

CUCCUUAUCAUAAAUAUCCACCAAUGAAGGGUUUUAUGCUGACACUGCAGAACGAUCCUCCUUC
UUUGGAAACUGGUGUUAAGAUAAAAGAAUGCUGAAAAAAUAUGG

>random_seq_from_cds__NO_13085 RANDOM_LENGTH 63 SEQ_LENGTH 52
GC_CONTENT 0.634615384615385 BASEPAIR 20 FREE_ENERGY
-16.60 LEN_BP_RATIO 2.6

CUGAACAGCUGGUACUGAGCGUGCCCCUGGACACUGCAGGUCACCCAGAGCCCUGCCUCAUGU

>random_seq_from_cds__NO_13087 RANDOM_LENGTH 84 SEQ_LENGTH 65
GC_CONTENT 0.538461538461538 BASEPAIR 21 FREE_ENERGY
-17.90 LEN_BP_RATIO 3.0952380952381

UAUCCUGAGAACAGGCUCCCAUCCUGAAGAAUGAGGUUCAACCUGGUUUUGUGAUCGGAAGCACC
UGAAGGACACCACACAGUC

>random_seq_from_cds__NO_13098 RANDOM_LENGTH 82 SEQ_LENGTH 70
GC_CONTENT 0.585714285714286 BASEPAIR 24 FREE_ENERGY
-25.82 LEN_BP_RATIO 2.916666666666667

UGCCCUGGUGGUCACCAUGCUGGCUGUGGGGAAGAUGGCCACAGCUGCUGCCUUACCAUC
UCCUAUGUGUACUCUGC

>random_seq_from_cds__NO_13112 RANDOM_LENGTH 85 SEQ_LENGTH 71
GC_CONTENT 0.591549295774648 BASEPAIR 24 FREE_ENERGY
-20.86 LEN_BP_RATIO 2.958333333333333

UAUCCUGGGACACUGCUUUUUCGCUGUUGGGCCGUGUUGCUGACAGGGAUCGCCUACAGUCUUC
CCCACUGGCAGCUGCUGUUU

>random_seq_from_cds__NO_13115 RANDOM_LENGTH 75 SEQ_LENGTH 58
GC_CONTENT 0.53448275862069 BASEPAIR 20 FREE_ENERGY
-19.00 LEN_BP_RATIO 2.9

UGCCCAGAAAGAAGGUGACUCGGGCCUCUGUCCUGGACUUCUGUAAGAAUAGGCAGCUCUGCAAG
GUGACCUUGG

>random_seq_from_cds__NO_13125 RANDOM_LENGTH 90 SEQ_LENGTH 70
GC_CONTENT 0.5 BASEPAIR 26 FREE_ENERGY -28.20 LEN_BP_RATIO
2.69230769230769

UGCACAAGGAUGGGCUGACGGUCACUUCUCCAGUACUAAUGUGGGUCCAGGGCACUGGAUAUCAU
CUUGGAGAAGAUGAAGGCUUCGGGC

>random_seq_from_cds__NO_13129 RANDOM_LENGTH 85 SEQ_LENGTH 59
GC_CONTENT 0.525423728813559 BASEPAIR 24 FREE_ENERGY
-17.90 LEN_BP_RATIO 2.458333333333333

AAAUUGCAAAAUUUACCAGCAGAACCCCGAGGCCUACUCACAUACGGAGGAGAAUUUCUUUGGU
CAGUAGCUUUGCUGCUUCCC

>random_seq_from_cds__NO_13131 RANDOM_LENGTH 78 SEQ_LENGTH 58
GC_CONTENT 0.586206896551724 BASEPAIR 21 FREE_ENERGY
-21.11 LEN_BP_RATIO 2.76190476190476

CUGGUCCAGGCUUGCCUUGGUGCCUGUGCACCUCAUUUAGAGGAGAAGCUUAGCCCACCAGUAC
CAUCAUGCUCAGU

>random_seq_from_cds__NO_13133 RANDOM_LENGTH 88 SEQ_LENGTH 78
GC_CONTENT 0.615384615384615 BASEPAIR 26 FREE_ENERGY
-29.60 LEN_BP_RATIO 3

CUGGCAGGCAUGAGACUGGAGGAAGGUGACAUUGCGGGUCAGCCUGGGCACCAGUGACACCCUGU
UUCUCUGGCUCCAAGAGCCCAUG

>random_seq_from_cds__NO_13134 RANDOM_LENGTH 82 SEQ_LENGTH 71
GC_CONTENT 0.549295774647887 BASEPAIR 19 FREE_ENERGY
-22.14 LEN_BP_RATIO 3.73684210526316

CCUGCCCUGGAAGGCCACAUCUUCUGCAACCCGGUUGACUCCAGCACUACAUGGCACUCCUGUG
GCUUUAAAAAUGGCUCC

>random_seq_from_cds__NO_13142 RANDOM_LENGTH 84 SEQ_LENGTH 60
GC_CONTENT 0.766666666666667 BASEPAIR 24 FREE_ENERGY

-32.30 LEN_BP_RATIO 2.5
GAAUCUUGUCUCAGACCCGGGGCCUCCGGAGUGACAUGACGGCGCCCUGGGUGGCCUCGCCCC
CCUCUGGGGAUCGCUGUGC
>random_seq_from_cds__NO_13149 RANDOM_LENGTH 84 SEQ_LENGTH 67
GC_CONTENT 0.686567164179104 BASEPAIR 23 FREE_ENERGY
-33.10 LEN_BP_RATIO 2.91304347826087
GGUGGGCCUGAAGCCACUGCAGCUGCUGGAGAUCAAGGCUCGGGGCGCUUUGGCUGUGUCUGGA
AGGCCAGCUCAUGAAUGA
>random_seq_from_cds__NO_13160 RANDOM_LENGTH 90 SEQ_LENGTH 71
GC_CONTENT 0.549295774647887 BASEPAIR 24 FREE_ENERGY
-27.70 LEN_BP_RATIO 2.958333333333333
CAUCUAAGUUAUUCUGUGGUAGAGAUCUGGGCCUGGCUGUCCAGCCCCUCAGCCUCCGUCCCAGU
AUCUAGGCCCCUCUGUGCUUGCUGGU
>random_seq_from_cds__NO_13173 RANDOM_LENGTH 81 SEQ_LENGTH 71
GC_CONTENT 0.535211267605634 BASEPAIR 23 FREE_ENERGY
-18.20 LEN_BP_RATIO 3.08695652173913
UUCUCCACAUUGGCUUUCAGUAGUGCCUUCAGGGUGUCAUUCUCCUUGUUCAGCCUCGAGUGCC
CAAUGGUGAUGAUGAA
>random_seq_from_cds__NO_13175 RANDOM_LENGTH 77 SEQ_LENGTH 58
GC_CONTENT 0.637931034482759 BASEPAIR 20 FREE_ENERGY
-24.10 LEN_BP_RATIO 2.9
GGCUGCUCAGCGCUGACGCCAGGCCAUCUCACACCGGCACAGGCUCCAUAUAGAGAUGCUGGGA
CAGUGUCCUCAA
>random_seq_from_cds__NO_13181 RANDOM_LENGTH 87 SEQ_LENGTH 52
GC_CONTENT 0.557692307692308 BASEPAIR 19 FREE_ENERGY
-20.90 LEN_BP_RATIO 2.73684210526316
CACCAGGGUCACUAGUACCAAGAUGUCAGCUGGAUGGAAGCAGCUGAGGUUGUCCAGGUUCCCC
ACGCUCCCUUCCUCCUCUUCU
>random_seq_from_cds__NO_13194 RANDOM_LENGTH 87 SEQ_LENGTH 73
GC_CONTENT 0.657534246575342 BASEPAIR 28 FREE_ENERGY
-33.20 LEN_BP_RATIO 2.60714285714286
GACAGGGCGGGUGAAACUUCUGGGGCCGAGAAGUCACGGUCAGGCAGGGGCAUCUGAUCCCAGG
GGCCUUCUCCUCUGAGUCCCA
>random_seq_from_cds__NO_13206 RANDOM_LENGTH 90 SEQ_LENGTH 82
GC_CONTENT 0.536585365853659 BASEPAIR 24 FREE_ENERGY
-30.20 LEN_BP_RATIO 3.416666666666667
CACGGAAGACUGGUCUGCAGCUCACUGCUCAGGCCACUGAAUGGGUAGGAGCAACCACUGACU
GGUCUUAAGAUGUUCACUGUGCUGA
>random_seq_from_cds__NO_13209 RANDOM_LENGTH 82 SEQ_LENGTH 71
GC_CONTENT 0.464788732394366 BASEPAIR 22 FREE_ENERGY
-20.70 LEN_BP_RATIO 3.22727272727273
UGGUUAUUGUCUGGAUGCCGGGUCUUCAAGAACCACAGUCUACGUGUAUCAAUGGCCAGCAGAAA
AAGAGAAUAAUACCGGA
>random_seq_from_cds__NO_13214 RANDOM_LENGTH 71 SEQ_LENGTH 61

GC_CONTENT 0.639344262295082 BASEPAIR 20 FREE_ENERGY
-30.80 LEN_BP_RATIO 3.05
UCCUGGAGGAAGAACCUGUGGCACAUGUGGGUGCACCCGCAUGGAGUGGAAACCACGGGUGCCCU
GGACUU

>random_seq_from_cds__NO_13220 RANDOM_LENGTH 92 SEQ_LENGTH 78
GC_CONTENT 0.448717948717949 BASEPAIR 25 FREE_ENERGY
-19.00 LEN_BP_RATIO 3.12
CAAAGAUUAAAGGGCCAUUUGUGGGCUUUUGCAGGAUUCUACUACACAGCCAGUGCUUUAUAUCU
UUCAGGUAGCUUUUCCUGGACACCUU

>random_seq_from_cds__NO_13237 RANDOM_LENGTH 85 SEQ_LENGTH 81
GC_CONTENT 0.827160493827161 BASEPAIR 32 FREE_ENERGY
-48.10 LEN_BP_RATIO 2.53125
CCGCCCGCUGGCUAUGCGUGCUGGCAGGCGCCUCGCCUGGGCCCUUGGGCCGGCGGGGCGGCCA
GGCGGCCAGGCUGCAGGAGG

>random_seq_from_cds__NO_13244 RANDOM_LENGTH 89 SEQ_LENGTH 69
GC_CONTENT 0.608695652173913 BASEPAIR 25 FREE_ENERGY
-25.26 LEN_BP_RATIO 2.76
AGUGCUCCGAGGGCUCGGGUGGGCUGUAAGGCAGCCAUGGUCUUUUCCAAUAUUGUGUCAUGGC
UAACUUCUUCUGGCUGCUGGUGGA

>random_seq_from_cds__NO_13245 RANDOM_LENGTH 86 SEQ_LENGTH 72
GC_CONTENT 0.597222222222222 BASEPAIR 27 FREE_ENERGY
-26.80 LEN_BP_RATIO 2.66666666666667
GGGCCUCUACCUGUACACCCUGCUUGCCGUCUCCUUCUUCUCUGAGCGGAAGUACUUCUGGGGGU
ACAUAUCAUCGGCUGGGGGG

>random_seq_from_cds__NO_13258 RANDOM_LENGTH 94 SEQ_LENGTH 68
GC_CONTENT 0.573529411764706 BASEPAIR 21 FREE_ENERGY
-17.10 LEN_BP_RATIO 3.23809523809524
AUUUGCCCGCAUCCUCCUACUGACCUAGUGGCAUUAACCUCCAGGAUCCUCAGCAUGGAUUCUC
CUGCCCCUGAAGCUUCUGCCCUUCCAG

>random_seq_from_cds__NO_13260 RANDOM_LENGTH 81 SEQ_LENGTH 61
GC_CONTENT 0.557377049180328 BASEPAIR 21 FREE_ENERGY
-25.40 LEN_BP_RATIO 2.9047619047619
GGAGGUGUCAGUAUGCUUCACUUCAGAGGAAUGGGCAUGUCUGGGCCCAAUCCAGAGGGCCUUGU
ACUGGGAUGUGAUGCU

>random_seq_from_cds__NO_13261 RANDOM_LENGTH 86 SEQ_LENGTH 79
GC_CONTENT 0.468354430379747 BASEPAIR 28 FREE_ENERGY
-35.00 LEN_BP_RATIO 2.82142857142857
GGAGAAUUAUGGAAUUGUGACCUCCUAGGAAUGGGAGACCAUGACCGAGAAUGAGGAGGUGACA
UCAAGCCAAGUAGUUCUCAA

>random_seq_from_cds__NO_13286 RANDOM_LENGTH 86 SEQ_LENGTH 57
GC_CONTENT 0.298245614035088 BASEPAIR 23 FREE_ENERGY
-15.80 LEN_BP_RATIO 2.47826086956522
AACCCUAUGGGUGUAAUGAUUGUAGUAAAGUUUUUAGGCAAAGAAAAACCUUACUGUACAUCAG
AAAAUCCACACAGAUGAAAAA

>random_seq_from_cds__NO_13294 RANDOM_LENGTH 110 SEQ_LENGTH 95
GC_CONTENT 0.663157894736842 BASEPAIR 37 FREE_ENERGY
-48.00 LEN_BP_RATIO 2.56756756756757
ACCUCUUAAGGGCGCUCAGGCUCAGGGGAGGUGCGGGAGCUGGAGCUGCCUUGGGGGCUGCCUU
GGCAUCAUCCUUCUUGGGCUCUGGCUUUUUGGGGGCCAUGCUAAG

>random_seq_from_cds__NO_13298 RANDOM_LENGTH 72 SEQ_LENGTH 67
GC_CONTENT 0.626865671641791 BASEPAIR 23 FREE_ENERGY
-22.20 LEN_BP_RATIO 2.91304347826087
UGGUAUCUGACCCUGGCUGGGGUGGAUGAGGUGGUGGCAUCUGGUGGUGCAUCAGAGGGUAGGGA
GGGGGCU

>random_seq_from_cds__NO_13315 RANDOM_LENGTH 81 SEQ_LENGTH 59
GC_CONTENT 0.440677966101695 BASEPAIR 22 FREE_ENERGY
-16.50 LEN_BP_RATIO 2.68181818181818
AUACUCUUGGGGUUUAGACGAUACGUGUCAUAUAAAAUUUCGAUAUGCCAAGUAUCAUUUCU
GGAGUCUUGGAUUUGU

>random_seq_from_cds__NO_13339 RANDOM_LENGTH 72 SEQ_LENGTH 64
GC_CONTENT 0.6875 BASEPAIR 19 FREE_ENERGY -24.25
LEN_BP_RATIO 3.36842105263158
CAGGGACCCAGGAGCCCCACCACUCUCUCUCCGGGGGACCUCGCUCACCCCUUCUGGCCUG
AAGUCCU

>random_seq_from_cds__NO_13345 RANDOM_LENGTH 84 SEQ_LENGTH 77
GC_CONTENT 0.662337662337662 BASEPAIR 24 FREE_ENERGY
-36.52 LEN_BP_RATIO 3.20833333333333
UCGGAUACCAGGCACUCCAUCUUCUGGGGAUCCCCGGGUCACCAGGGAUCCUGCUGCACCA
GGUUGACCCUGGGGUCCC

>random_seq_from_cds__NO_13349 RANDOM_LENGTH 70 SEQ_LENGTH 57
GC_CONTENT 0.824561403508772 BASEPAIR 22 FREE_ENERGY
-39.00 LEN_BP_RATIO 2.59090909090909
CGCUCUCCCCUGCUGCCAGGGGGCCCCGUGAGUCCUCGGGGUCCUCCUGGCCGGGGCGGCCAU
CUUCA

>random_seq_from_cds__NO_13360 RANDOM_LENGTH 90 SEQ_LENGTH 80
GC_CONTENT 0.7125 BASEPAIR 29 FREE_ENERGY -43.30
LEN_BP_RATIO 2.75862068965517
AGACCCCGGGCACCAGGUGGUCCAGGGUCUCCAUGACCACCCACUGGGCCAGGGGGCCUCUU
GGACCCUGCAGACCCCGGCUUCCCU

>random_seq_from_cds__NO_13373 RANDOM_LENGTH 75 SEQ_LENGTH 68
GC_CONTENT 0.705882352941177 BASEPAIR 23 FREE_ENERGY
-32.01 LEN_BP_RATIO 2.95652173913043
GGUUUGCCAUCUCCUGCCUGGCUUCCCCGGUAAUCCAGGGGGACCAGAGGGGCCAGGGAGGCCCU
GUUCUCCACG

>random_seq_from_cds__NO_13375 RANDOM_LENGTH 75 SEQ_LENGTH 61
GC_CONTENT 0.704918032786885 BASEPAIR 20 FREE_ENERGY
-31.00 LEN_BP_RATIO 3.05
CAGUCCGCUCCGGCCAUCCAGCCCAGGGGGACCCCGGUCACCCCUUUUCUCCUGCUGGGCCUCGG

ACACCUGGGU

>random_seq_from_cds__NO_13384 RANDOM_LENGTH 68 SEQ_LENGTH 48
GC_CONTENT 0.75 BASEPAIR 19 FREE_ENERGY -27.13
LEN_BP_RATIO 2.52631578947368

UGGGCCUGGGGUCCACGUUCGCCCCUUCUCUCCAGCCUCACCCAGGGGCCUGGAAAGCCCCGG
UCA

>random_seq_from_cds__NO_13386 RANDOM_LENGTH 73 SEQ_LENGTH 61
GC_CONTENT 0.704918032786885 BASEPAIR 23 FREE_ENERGY
-29.20 LEN_BP_RATIO 2.65217391304348

CCUUUUUCUCCUUUCUUUCCAGGGGGCCAACGGGGCCUUGGGGUCCAGGGCUUCCGGGAAGAC
CCCCGCAG

>random_seq_from_cds__NO_13392 RANDOM_LENGTH 84 SEQ_LENGTH 75
GC_CONTENT 0.6933333333333333 BASEPAIR 25 FREE_ENERGY
-30.20 LEN_BP_RATIO 3

CCGGGAGGCCAGGGUCGCCAGGAGGCCAACUUGUCCUCUCAGGCCCAUCUCUCCAGGUUCCCC
CUUCUGGCCCCUUGGACA

>random_seq_from_cds__NO_13393 RANDOM_LENGTH 78 SEQ_LENGTH 66
GC_CONTENT 0.6666666666666667 BASEPAIR 26 FREE_ENERGY
-35.60 LEN_BP_RATIO 2.53846153846154

AUACACUGGGCAGGGCUCUGGCCGGGGCCUGAGUAGUGAAGGAUGCCUGACACAGGGCUGUGGCC
AGACCACUGACUG

>random_seq_from_cds__NO_13415 RANDOM_LENGTH 71 SEQ_LENGTH 57
GC_CONTENT 0.701754385964912 BASEPAIR 22 FREE_ENERGY
-27.70 LEN_BP_RATIO 2.59090909090909

GAGUUUCCGGCUCGCCCGGCGGACAGUGAGGACACUGGCACUGCCCUCACGGGGACCCACUCGAGC
AGACAC

>random_seq_from_cds__NO_13417 RANDOM_LENGTH 77 SEQ_LENGTH 68
GC_CONTENT 0.705882352941177 BASEPAIR 26 FREE_ENERGY
-31.00 LEN_BP_RATIO 2.61538461538462

AGGGUCCGCUCAACCCCCUGGGUGCUGCGCACAAUGAUGCGGUACUGGGUGGCACCAGGGACUG
GGCUCCAGGACA

>random_seq_from_cds__NO_13428 RANDOM_LENGTH 85 SEQ_LENGTH 72
GC_CONTENT 0.6527777777777778 BASEPAIR 21 FREE_ENERGY
-28.47 LEN_BP_RATIO 3.42857142857143

GCUUGGCUCAGACAGCACCAGGUCUCGUGGAGCAGAGGUCGAGUCAUCCGCGAGGUCGGGUCACA
GGCACGCCACCAGCAGUCGU

>random_seq_from_cds__NO_13433 RANDOM_LENGTH 84 SEQ_LENGTH 54
GC_CONTENT 0.6111111111111111 BASEPAIR 19 FREE_ENERGY
-22.40 LEN_BP_RATIO 2.84210526315789

AUCACAUCACCCCAGAGCCAAGUGCAUCCAGGCCGAACUCUGUCCCGUGGGUCAUCGCGUACU
GCACUGUGGCAAAGCGCAC

>random_seq_from_cds__NO_13439 RANDOM_LENGTH 68 SEQ_LENGTH 56
GC_CONTENT 0.678571428571429 BASEPAIR 19 FREE_ENERGY
-25.50 LEN_BP_RATIO 2.94736842105263

ACUGUUCUGUGGAGGGGCCAUGGCUGGGGCCACUGACCGAGUCCUCCCUAGCUCUGAGCAGCUGC
GGG

>random_seq_from_cds__NO_13455 RANDOM_LENGTH 73 SEQ_LENGTH 65
GC_CONTENT 0.676923076923077 BASEPAIR 23 FREE_ENERGY
-24.50 LEN_BP_RATIO 2.82608695652174

GAGAGCCGUGUUGUAGGCCCCAGGUCCCCAGGCCAGGUGCUGGCCUUGCCUCCUCAGGCGCU
GCCUCCU

>random_seq_from_cds__NO_13474 RANDOM_LENGTH 84 SEQ_LENGTH 61
GC_CONTENT 0.672131147540984 BASEPAIR 22 FREE_ENERGY
-29.60 LEN_BP_RATIO 2.77272727272727

GAUCCUCAUUGAAGUGGGCAUCCUGUGUGGCUGUCAGCCCAGGCCUGCUGAUGGCUCUCGAA
GGCCAGCAGGUGGGCCAGC

>random_seq_from_cds__NO_13477 RANDOM_LENGTH 95 SEQ_LENGTH 90
GC_CONTENT 0.666666666666667 BASEPAIR 25 FREE_ENERGY
-31.10 LEN_BP_RATIO 3.6

CCAGCCAACCCUGGGCCUCAUCACACAGCCGCACAGCAGCACCCCAGGGCCCCCGGGGACAGGG
CACUGUGGCCAGGACGCCAAACUUUGUCUG

>random_seq_from_cds__NO_13479 RANDOM_LENGTH 75 SEQ_LENGTH 67
GC_CONTENT 0.701492537313433 BASEPAIR 23 FREE_ENERGY
-29.50 LEN_BP_RATIO 2.91304347826087

CCUCUGCGAAGGGACUGUCACAGCUGUUGCAGUGGCGGCCAAGGGCUCUGGGCGACAGGGGCAC
UGCCCGCUGU

>random_seq_from_cds__NO_13500 RANDOM_LENGTH 99 SEQ_LENGTH 88
GC_CONTENT 0.75 BASEPAIR 33 FREE_ENERGY -39.70
LEN_BP_RATIO 2.666666666666667

CGAAAGCCGCCGUUGGGCGCGUCGGUGCAGGUGCCCCCGUUGCGGCAGACGCCCGGCACGCAGCG
GCCGGCCUCGGUGUCCAGCUCGCAGUCCUCUCCC

>random_seq_from_cds__NO_13505 RANDOM_LENGTH 94 SEQ_LENGTH 84
GC_CONTENT 0.678571428571429 BASEPAIR 30 FREE_ENERGY
-28.70 LEN_BP_RATIO 2.8

CCCUGCAGCGCCCGCCCGGCCACGUGGAGCUAGCGCCGAGAAACUCACAUUGAGCACGGUGC
CCCCUACGUCUGUGUCGUUCUGGAUGUUG

>random_seq_from_cds__NO_13508 RANDOM_LENGTH 68 SEQ_LENGTH 51
GC_CONTENT 0.666666666666667 BASEPAIR 22 FREE_ENERGY
-28.50 LEN_BP_RATIO 2.31818181818182

UGCGCCGUCACGCUGUGCAGGCCAUCCUGUGACAGUCACCAACAUGGAGGCCACCAGUGGGCGGU
UAU

>random_seq_from_cds__NO_13513 RANDOM_LENGTH 109 SEQ_LENGTH 78
GC_CONTENT 0.538461538461538 BASEPAIR 24 FREE_ENERGY
-29.35 LEN_BP_RATIO 3.25

GUUCCCUCCACGAUCUGGUACAUAUAUGGGCAUUGGGCCUUCGUCAGGGUCCACUGCAGUGA
UCUGGGCCACCACUGAGCCCACAAUGCUAUUCUCUUUCACCCGC

>random_seq_from_cds__NO_13523 RANDOM_LENGTH 72 SEQ_LENGTH 56
GC_CONTENT 0.589285714285714 BASEPAIR 20 FREE_ENERGY

-23.70 LEN_BP_RATIO 2.8
CCCCCUGGGUGCUGAUGGCCAAAGCGAUUCCGGGUGUUGCCGCCUGUGAUCUGGUAGCUGAUGGC
ACUGUUG
>random_seq_from_cds__NO_13533 RANDOM_LENGTH 72 SEQ_LENGTH 54
GC_CONTENT 0.759259259259259 BASEPAIR 20 FREE_ENERGY
-28.00 LEN_BP_RATIO 2.7
CGCACAGUGGCCGAGCGCGGCCCGGGUUCUGGCCUGGUCGUGGCUUCCACCACCAGCUCAUA
GCUUUC
>random_seq_from_cds__NO_13540 RANDOM_LENGTH 78 SEQ_LENGTH 62
GC_CONTENT 0.596774193548387 BASEPAIR 24 FREE_ENERGY
-29.20 LEN_BP_RATIO 2.58333333333333
CAACCACGCGUAGCACCGCGGUGCCUGCUGCCUCAUUCUCCGGCACCCAGCGUCUGGUAGUUGUAC
UGCGGAAACUGCG
>random_seq_from_cds__NO_13545 RANDOM_LENGTH 86 SEQ_LENGTH 70
GC_CONTENT 0.714285714285714 BASEPAIR 25 FREE_ENERGY
-37.90 LEN_BP_RATIO 2.8
GCGGUGCCCACUCUUUUGCGGGAGCCUGUCCAGCGUUCGCGUGGGAGGACACCGGCUUGGGACC
GUGGUGCCGAAUCAAAAAGUC
>random_seq_from_cds__NO_13550 RANDOM_LENGTH 70 SEQ_LENGTH 58
GC_CONTENT 0.672413793103448 BASEPAIR 21 FREE_ENERGY
-21.00 LEN_BP_RATIO 2.76190476190476
CAAAGAGCUAAGGCUCGCCACCGAU AUGCGCCUUGGCCCCGUAGUGGCAGCUAAGCCUGGGUC
CCAGC
>random_seq_from_cds__NO_13551 RANDOM_LENGTH 84 SEQ_LENGTH 74
GC_CONTENT 0.675675675675676 BASEPAIR 25 FREE_ENERGY
-32.10 LEN_BP_RATIO 2.96
CCUGGUGCCCACCGCCCCCAGCUCCUCCUGGCUGAGGGGAACAAAGAGAGGAGAAGGAGCAGG
AGUAUGGGGGUCGACCGUC
>random_seq_from_cds__NO_13567 RANDOM_LENGTH 75 SEQ_LENGTH 69
GC_CONTENT 0.652173913043478 BASEPAIR 23 FREE_ENERGY
-25.40 LEN_BP_RATIO 3
GGCAUCGGGCCUGGCGGGGUAGUAGCUUGCCUAGAGAUCUCAGCCGCACCCUCUGGCAAGGCCA
UCUUUGUCA
>random_seq_from_cds__NO_13574 RANDOM_LENGTH 71 SEQ_LENGTH 54
GC_CONTENT 0.62962962962963 BASEPAIR 23 FREE_ENERGY
-27.30 LEN_BP_RATIO 2.34782608695652
UGGGGAUGUCAUGCUGUACAGGGCUCUGGGUGGCUGCACCCGCCACACGUGAUUCUCCGGGAGG
GUCUGC
>random_seq_from_cds__NO_13577 RANDOM_LENGTH 71 SEQ_LENGTH 50
GC_CONTENT 0.6 BASEPAIR 20 FREE_ENERGY -27.90 LEN_BP_RATIO
2.5
CACAGGCUCAGCCCACGCACUCACAGCUGUUUGUAACCAUAUCUCCUCGGUACGUGCUGUGGCUG
UGUGGG
>random_seq_from_cds__NO_13583 RANDOM_LENGTH 110 SEQ_LENGTH 87

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GC_CONTENT    0.620689655172414    BASEPAIR    29    FREE_ENERGY
-33.00    LEN_BP_RATIO    3
CAGCCUGGCUUUCUGGGAUUCACCAUGCUAGACCAUGACUCCACUGUCCUGGAGCCUCCAG
UGGAUCCUGGGCUUCCCUACCGGGCUUGGCACCCCCUCCUGACU
>random_seq_from_cds__NO_13589    RANDOM_LENGTH    72    SEQ_LENGTH    50
GC_CONTENT    0.6    BASEPAIR    21    FREE_ENERGY    -24.10    LEN_BP_RATIO
2.38095238095238
CCUGUGAGCCCUGAGUUUGGCCACCGUUGUGCCCUUGGGGUCAGGGGCUUGAGGUUACAACUG
GUAUGAC
>random_seq_from_cds__NO_13597    RANDOM_LENGTH    83    SEQ_LENGTH    64
GC_CONTENT    0.5625    BASEPAIR    24    FREE_ENERGY    -23.70
LEN_BP_RATIO    2.666666666666667
AGCAGGAAAGUUGGUGAUGAUGACCCGUGAGUACUCCAGCACAGCCAUGGCUCGUGGGGCGUGUGU
CAUUCAGCACAUACGCA
>random_seq_from_cds__NO_13608    RANDOM_LENGTH    69    SEQ_LENGTH    62
GC_CONTENT    0.516129032258065    BASEPAIR    22    FREE_ENERGY
-23.50    LEN_BP_RATIO    2.81818181818182
AGGUGCGCUUUAGUAGAUUCAUGGUGUGUGAGUGACCACAUAGCCUGGGGUCUUGUAGUUCUC
ACCC
>random_seq_from_cds__NO_13614    RANDOM_LENGTH    98    SEQ_LENGTH    86
GC_CONTENT    0.593023255813954    BASEPAIR    32    FREE_ENERGY
-33.40    LEN_BP_RATIO    2.6875
GCCGCUUAGCUGGGGUCAGUGUGGAUCUUCUACUGGCUAUGUAGCUUACAAGGAAGGAGAGAC
GCCGGUAUCCUGAGUCGGGAGGCCAAGCCAU
>random_seq_from_cds__NO_13616    RANDOM_LENGTH    80    SEQ_LENGTH    73
GC_CONTENT    0.657534246575342    BASEPAIR    27    FREE_ENERGY
-34.00    LEN_BP_RATIO    2.7037037037037
GCUGCGCGCUCAGAGCCGAGUUCUUGAGCGUCUCGCGGGCCUUCUGCUCGCUCAGGCCGAGGCUA
GUGAAGAGCGACAGG
>random_seq_from_cds__NO_13620    RANDOM_LENGTH    71    SEQ_LENGTH    59
GC_CONTENT    0.661016949152542    BASEPAIR    19    FREE_ENERGY
-21.72    LEN_BP_RATIO    3.10526315789474
CUGGGCACGACCCUGGGCACUGCCUGCCGUUUCUUCUGCUGUAGAGGCUGCCAGACUAUUUCCUG
CCCGUU
>random_seq_from_cds__NO_13622    RANDOM_LENGTH    85    SEQ_LENGTH    71
GC_CONTENT    0.661971830985916    BASEPAIR    28    FREE_ENERGY
-34.50    LEN_BP_RATIO    2.53571428571429
GUACCCUGGUACAGGGUCUGCUCUGUGUCCCGUGUGUCAGCCACUGCCCCCGGAUGGCACCCUG
GGCAAUACCCUGUGCCCGCU
>random_seq_from_cds__NO_13627    RANDOM_LENGTH    82    SEQ_LENGTH    62
GC_CONTENT    0.67741935483871    BASEPAIR    20    FREE_ENERGY
-22.00    LEN_BP_RATIO    3.1
GCUGCCUGGGCCCGCUGCUGUGCCUCGCUUGCCUGCCGACGAGUCUCAGCCACUCUGCUGAGGAU
GCUACCACCUUCUGCCA
```

>random_seq_from_cds__NO_13629 RANDOM_LENGTH 95 SEQ_LENGTH 88
GC_CONTENT 0.636363636363636 BASEPAIR 27 FREE_ENERGY
-27.91 LEN_BP_RATIO 3.25925925925926
UCUCGACAGCCGGCACCCCCACAAGGGCUUGUAGCACAGGGUGCAUCCCCUGGUGCCCCACACAC
CCAGCUCAUUUUAUGUCUGUCAGGCUCAGGG

>random_seq_from_cds__NO_13634 RANDOM_LENGTH 110 SEQ_LENGTH
103 GC_CONTENT 0.650485436893204 BASEPAIR 35 FREE_ENERGY
-53.83 LEN_BP_RATIO 2.94285714285714
UGCUCAGUGGCCUCCCCAAUUUCACGCCCGCAGCUCUCCUCUGUGGCCUCCACAAGCUGUGCAGUGG
AGGCGGUCUGAGGUGUUGCGGGCACCUACGAUGCCCUGCACAAUGC

>random_seq_from_cds__NO_13640 RANDOM_LENGTH 75 SEQ_LENGTH 67
GC_CONTENT 0.656716417910448 BASEPAIR 23 FREE_ENERGY
-29.20 LEN_BP_RATIO 2.91304347826087
GCCACUGGUGAGGUUCCAGAAGUUGGGGCACAGCGGUCACAGCUAGGGCCCUGGACAUUGGGGA
GGCAUGGGCA

>random_seq_from_cds__NO_13642 RANDOM_LENGTH 88 SEQ_LENGTH 77
GC_CONTENT 0.649350649350649 BASEPAIR 26 FREE_ENERGY
-36.20 LEN_BP_RATIO 2.96153846153846
UCGGGCAGCCUGCCCAUGGAAGCCAGGCUUGCAGUGGGCACAGUGUGGACCCUCUGUGUGGUGUA
AACAGCGCAGGCAUUGCCCCGUG

>random_seq_from_cds__NO_13649 RANDOM_LENGTH 110 SEQ_LENGTH 97
GC_CONTENT 0.639175257731959 BASEPAIR 33 FREE_ENERGY
-38.61 LEN_BP_RATIO 2.93939393939394
CACUGGCAGGCCUUGACAGCCUGUGGGGCCAAAGCCAUAUAGCCAGGGGCACAGAGGUCACAGC
GGCGCCCAACCACUCCAGGCUUGCACAGGCACUGACCACCAUGAG

>random_seq_from_cds__NO_13655 RANDOM_LENGTH 84 SEQ_LENGTH 64
GC_CONTENT 0.609375 BASEPAIR 21 FREE_ENERGY -23.70
LEN_BP_RATIO 3.04761904761905
UCAGUCCAACUCUGCCCAUUGCUCAGGGACCCUGGGGCUCUAAGCGCAGCAGCAGGUCAUAGUC
CAUAGCCUUCGGCACAGAG

>random_seq_from_cds__NO_13656 RANDOM_LENGTH 67 SEQ_LENGTH 60
GC_CONTENT 0.616666666666667 BASEPAIR 21 FREE_ENERGY
-18.10 LEN_BP_RATIO 2.85714285714286
GCCACCAGGAACUCCAGGGUCUGACCUUCCUGUAGCCGCACGAAGCCUGAGCCAGUCCAGGAUGG
AG

>random_seq_from_cds__NO_13667 RANDOM_LENGTH 80 SEQ_LENGTH 67
GC_CONTENT 0.686567164179104 BASEPAIR 25 FREE_ENERGY
-37.70 LEN_BP_RATIO 2.68
GAUGCAAGCUCGGUGCACCCAUGCCCUCAGCAUGGGCUGGUGCCCCUGGGGCGGGUGCACACUCU
GAGGCGUGUCCGUAG

>random_seq_from_cds__NO_13670 RANDOM_LENGTH 84 SEQ_LENGTH 69
GC_CONTENT 0.594202898550725 BASEPAIR 25 FREE_ENERGY
-25.40 LEN_BP_RATIO 2.76
GAGCUGUAGGGGUCUGGGAUAGGGAUGGCAGGGUCCAGCACACGAUAGAUGACCCUCGCCUUCAG

UGGAUGGCUCAAUCUCUGA

>random_seq_from_cds__NO_13674 RANDOM_LENGTH 75 SEQ_LENGTH 68
GC_CONTENT 0.588235294117647 BASEPAIR 26 FREE_ENERGY
-22.00 LEN_BP_RATIO 2.61538461538462
CCAUUCUCUGACUGCCACCAGGCUGCCCGCCGUGUGGUGCAAAGCUGGUGACUACAUUCUGGAU
GCGAUGGCGUG

>random_seq_from_cds__NO_13682 RANDOM_LENGTH 75 SEQ_LENGTH 60
GC_CONTENT 0.6666666666666667 BASEPAIR 23 FREE_ENERGY
-28.90 LEN_BP_RATIO 2.60869565217391
CAGCGGCAGGGAAGGAGGCUUUGCCAUCUUGGCUGCACUGGGACUCACAGAGCCACACCCUGGAG
GGCCUCCCC

>random_seq_from_cds__NO_13687 RANDOM_LENGTH 110 SEQ_LENGTH 87
GC_CONTENT 0.597701149425287 BASEPAIR 31 FREE_ENERGY
-32.70 LEN_BP_RATIO 2.80645161290323
GGAAAUGCAAAAAGGUGGUGGAGAAUGGGGCCCUUCUCUCCUGGAAGCUGGGCUGCUCCUGAA
CCAGAACAGUGUGCCUGACAUUCAUGGUGUAGAGGCCCCUGCCAG

>random_seq_from_cds__NO_13688 RANDOM_LENGTH 70 SEQ_LENGTH 63
GC_CONTENT 0.619047619047619 BASEPAIR 20 FREE_ENERGY
-23.80 LEN_BP_RATIO 3.15
GGAGGGCGCAAUGUCUGCUCAGCUUGGCUACCCUGUGGGUUGGCACAUCGCCAAUAAGAAGC
CCCCU

>random_seq_from_cds__NO_13692 RANDOM_LENGTH 89 SEQ_LENGTH 63
GC_CONTENT 0.587301587301587 BASEPAIR 20 FREE_ENERGY
-23.10 LEN_BP_RATIO 3.15
GAAGCUGGCACCACAGUUCUGGCCAGAUUCGCCAACGAUGACCAUUCUGGCUAUGUGGAGCC
UACUGCAGUUGCUACCCUCCAC

>random_seq_from_cds__NO_13695 RANDOM_LENGTH 88 SEQ_LENGTH 70
GC_CONTENT 0.614285714285714 BASEPAIR 23 FREE_ENERGY
-21.74 LEN_BP_RATIO 3.04347826086957
AUCACCAGAUUGGAAACUGCCUCACCGCCUACUCGUUAUUCGCACCACCACCAGUGGAGUGCCCCG
UGGCGGAGAACCCAACCAGCGCC

>random_seq_from_cds__NO_13700 RANDOM_LENGTH 85 SEQ_LENGTH 72
GC_CONTENT 0.5833333333333333 BASEPAIR 24 FREE_ENERGY
-25.80 LEN_BP_RATIO 3
CUGGCCUUCGCCUUUGGAGACCGAAACUGUAGCACCAUCACCCUGCAGAAUAUCACCCGGGGCUC
CAUCGUGGUGGAAUGGACCA

>random_seq_from_cds__NO_13702 RANDOM_LENGTH 86 SEQ_LENGTH 76
GC_CONTENT 0.618421052631579 BASEPAIR 25 FREE_ENERGY
-27.40 LEN_BP_RATIO 3.04
UCGGCCUGCCUUCUCCAACGCCCUAGAGCCUGACUUUAAGGCCACAAGCAUCACUGUGACGGGCU
CUGGCAGUUGUCGGCACCUAC

>random_seq_from_cds__NO_13703 RANDOM_LENGTH 72 SEQ_LENGTH 58
GC_CONTENT 0.672413793103448 BASEPAIR 20 FREE_ENERGY
-27.22 LEN_BP_RATIO 2.9

AGUUUAUCCCUGUGGUACCACCCAGGAGAGUGCCCUCAGAGGCGCCGCCACAGAAGUGCCUGAC
AGGGACC

>random_seq_from_cds__NO_13704 RANDOM_LENGTH 81 SEQ_LENGTH 67
GC_CONTENT 0.582089552238806 BASEPAIR 27 FREE_ENERGY
-28.70 LEN_BP_RATIO 2.48148148148148

CUGAGAAGAGCAGUGAGGAUGAUGUCUACCUGCACACAGUCAUUCGGCCGUGGUGGUCGCAGCC
AUCCUGCUCAUUGCUG

>random_seq_from_cds__NO_13706 RANDOM_LENGTH 110 SEQ_LENGTH 88
GC_CONTENT 0.636363636363636 BASEPAIR 24 FREE_ENERGY
-24.13 LEN_BP_RATIO 3.66666666666667

AUCUUUGCAGACGAACUGGACGACUCCAAGCCCCACCCUCCUCCAGCAUGCCACUCAUUCUGCA
GGAGGAGAAGGCUCCCCUACCCCUCCUGAGUACCCCAACCAGAG

>random_seq_from_cds__NO_13715 RANDOM_LENGTH 89 SEQ_LENGTH 74
GC_CONTENT 0.567567567567568 BASEPAIR 24 FREE_ENERGY
-23.00 LEN_BP_RATIO 3.08333333333333

ACACACUUGUUGUAUGUGGCAGAGAAGAAGCGCCCCAAGGCCGAGUCCUUCUUUCAGACCAAAGC
CUUGGACGUCAGUGCCAGCGAUGA

>random_seq_from_cds__NO_13722 RANDOM_LENGTH 82 SEQ_LENGTH 68
GC_CONTENT 0.544117647058823 BASEPAIR 25 FREE_ENERGY
-25.00 LEN_BP_RATIO 2.72

GAGAACUUCUCUGGGAUCUACUGCAGCCUUCUGCCUUUGGGAUGCUGGUCAGCUGACAGCCAGAG
AGUGGUCUUUGACUCGG

>random_seq_from_cds__NO_13726 RANDOM_LENGTH 85 SEQ_LENGTH 57
GC_CONTENT 0.56140350877193 BASEPAIR 19 FREE_ENERGY
-18.60 LEN_BP_RATIO 3

ACAGCCACCCCAGAGCAAGAGAAUGUGCAGUAUGGCUGGCCUUGACUUUGAAGCAAUCCUGCUG
CAGCCUGGCAGCCCUCCAGA

>random_seq_from_cds__NO_13730 RANDOM_LENGTH 78 SEQ_LENGTH 64
GC_CONTENT 0.5625 BASEPAIR 24 FREE_ENERGY -29.40
LEN_BP_RATIO 2.66666666666667

CAUGUGGCCUUUAUGGGUGGUUCCUUGGUGGCUUCAUUUCCUGCCACUUGAUUGGUCAGUACCC
AGAGACCUACAGG

>random_seq_from_cds__NO_13734 RANDOM_LENGTH 84 SEQ_LENGTH 62
GC_CONTENT 0.548387096774194 BASEPAIR 21 FREE_ENERGY
-22.40 LEN_BP_RATIO 2.95238095238095

AGACCCGAAUGUGCCUGUUCGGGCUCCUGCUCUAUCCAAAAGCACCCACGCAUUAUCAGAGGU
GGAGUGGAGUCAGACAGC

>random_seq_from_cds__NO_13747 RANDOM_LENGTH 68 SEQ_LENGTH 51
GC_CONTENT 0.588235294117647 BASEPAIR 20 FREE_ENERGY
-21.90 LEN_BP_RATIO 2.55

CCACGGUUGGCUAUGAUGCCAGAGCAUUGAGUGGCAGGUGCACACCAAAGCGGGCCUCACAGUG
UGC

>random_seq_from_cds__NO_13750 RANDOM_LENGTH 81 SEQ_LENGTH 61
GC_CONTENT 0.59016393442623 BASEPAIR 22 FREE_ENERGY

-16.70 LEN_BP_RATIO 2.77272727272727

GGUGAUCCAGCUUCACGAUGCCCCUGAGGAAUCAGAUUCUUAUGCACUCGCCUCAGCUUGGCCCCG
CUUCUGCCCCGUUCUUG

>random_seq_from_cds__NO_13754 RANDOM_LENGTH 99 SEQ_LENGTH 70
GC_CONTENT 0.8 BASEPAIR 20 FREE_ENERGY -23.30 LEN_BP_RATIO
3.5

CGGCCGGGACUUGGAGGCGGUGCGGCGGGGUGCGGUUCAGUCGGUCGGCGGCGGCAGCGGA
GGAGGAGGAGGAGGAGGAGGAGGAGGAGGAUGAG

>random_seq_from_cds__NO_13760 RANDOM_LENGTH 99 SEQ_LENGTH 87
GC_CONTENT 0.459770114942529 BASEPAIR 25 FREE_ENERGY
-20.74 LEN_BP_RATIO 3.48

AGAGCUGAAGAAGAUUCUGGAUGACUGGGGGGAGACAUGCAAAGGCUGUGCAGAAAAGUCUGACU
ACAUCCGGAAGAUAAAUGAACUGAUGCCUAAAUA

>random_seq_from_cds__NO_13771 RANDOM_LENGTH 94 SEQ_LENGTH 67
GC_CONTENT 0.671641791044776 BASEPAIR 27 FREE_ENERGY
-36.40 LEN_BP_RATIO 2.48148148148148

GGGGGCCUUGGAGAGUGUGGUGGCAGGCAGUGAGGGGGCUGCUGAGGGUGCUAUCACCAUCGAGC
UGGCCUCCUACCCCAUCAGUGACUUUGCC

>random_seq_from_cds__NO_13775 RANDOM_LENGTH 89 SEQ_LENGTH 82
GC_CONTENT 0.597560975609756 BASEPAIR 25 FREE_ENERGY
-22.50 LEN_BP_RATIO 3.28

AUGCGGCCAGUUAACGGGCGCCGCCUCUACAAGGACUUUGUGCUCACGUCUAGUUUGAUGGCC
CCUUUCGCCAGCUGACACCCACA

>random_seq_from_cds__NO_13776 RANDOM_LENGTH 81 SEQ_LENGTH 66
GC_CONTENT 0.545454545454545 BASEPAIR 24 FREE_ENERGY
-27.50 LEN_BP_RATIO 2.75

AUGAGGUCCGCUUUGACCGCUUUGGUGAUGGUUAUUGGCCGCUACAACAUCUUCACCUAUCUGCGU
GCAGGCAGUGGGCGCU

>random_seq_from_cds__NO_13784 RANDOM_LENGTH 80 SEQ_LENGTH 73
GC_CONTENT 0.63013698630137 BASEPAIR 24 FREE_ENERGY
-28.40 LEN_BP_RATIO 3.04166666666667

CGGCCACGCUUCAUCAGUCCUGCCUCACAGGUGGCCAUCUGCCUGGCACUUAUCUCGGGCCAGCU
GCUCAUCGUGGUCGC

>random_seq_from_cds__NO_13793 RANDOM_LENGTH 99 SEQ_LENGTH 88
GC_CONTENT 0.568181818181818 BASEPAIR 31 FREE_ENERGY
-34.60 LEN_BP_RATIO 2.83870967741936

GCCUGGGCUGUCAGAAAGUAGAGGGUGGCACCUGGCUAUGUGGUGACCGUGUUGACCUGGCCAGG
CACCAACCCUACACUCUCCUCCAUCUUGCUCUAAAC

>random_seq_from_cds__NO_13796 RANDOM_LENGTH 68 SEQ_LENGTH 57
GC_CONTENT 0.56140350877193 BASEPAIR 20 FREE_ENERGY
-23.40 LEN_BP_RATIO 2.85

CCAGAACCAUCCACAUGACCUUUGGCCUGGAUGAGGAGGUUGGGGGUCACCAAGGCAUGGAGCU
GUU

>random_seq_from_cds__NO_13798 RANDOM_LENGTH 81 SEQ_LENGTH 64

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GC_CONTENT    0.6875 BASEPAIR   24 FREE_ENERGY   -27.20
LEN_BP_RATIO  2.666666666666667
CUGUCUUUUUAUGAGUGAGCGGAGUCCCUGGUGGGUGCGGGUUACCAGCACUGGGAGGCCAGGCCA
UGCCUCACGCUUCAUG
>random_seq_from_cds__NO_13801    RANDOM_LENGTH 86 SEQ_LENGTH    77
GC_CONTENT    0.584415584415584    BASEPAIR   26 FREE_ENERGY
-34.00 LEN_BP_RATIO  2.96153846153846
CAGCUUUGACUUCUGUGGCACCGGAUGUGGACUUCAAGGGCUUUUGAGGAGCAGCUGCAGAGC
UGGUGCCAGGCAGCUGGCGAG
>random_seq_from_cds__NO_13804    RANDOM_LENGTH 71 SEQ_LENGTH    47
GC_CONTENT    0.617021276595745    BASEPAIR   20 FREE_ENERGY
-18.80 LEN_BP_RATIO  2.35
CUCACCCAUGAACCGCACACCCUGUGCUGCUGCAGACCACGAUGAACGGCUGCAUGAGGCUGUGU
UCCUCC
>random_seq_from_cds__NO_13807    RANDOM_LENGTH 87 SEQ_LENGTH    69
GC_CONTENT    0.652173913043478    BASEPAIR   24 FREE_ENERGY
-30.40 LEN_BP_RATIO  2.875
UUUGGCCGGCACAGCCUGAGCCCCUUGGCAAUACGGGCACGAGCACGCUUCCCAAGCUUGGGGUG
GGCAAUGUAGGCAAGUCGAUCG
>random_seq_from_cds__NO_13811    RANDOM_LENGTH 81 SEQ_LENGTH    71
GC_CONTENT    0.647887323943662    BASEPAIR   22 FREE_ENERGY
-27.30 LEN_BP_RATIO  3.22727272727273
AGAAGUUCCGGUUUAUGAAGUGGUGGUUUGUCCCUGGUCAGGGCCAUGCCCAGCUGGGCCCAGAAG
CUGCGCUGACCACUGG
>random_seq_from_cds__NO_13814    RANDOM_LENGTH 67 SEQ_LENGTH    53
GC_CONTENT    0.69811320754717 BASEPAIR   19 FREE_ENERGY
-22.70 LEN_BP_RATIO  2.78947368421053
CACUGACCCGGUCCGUGUGGGCCAGCACAAACAGCGUCUUGCGGCUGCCAUGACCCGAGGCCAC
AG
>random_seq_from_cds__NO_13819    RANDOM_LENGTH 72 SEQ_LENGTH    63
GC_CONTENT    0.666666666666667    BASEPAIR   24 FREE_ENERGY
-24.80 LEN_BP_RATIO  2.625
GGUCCUGUGCAAAGAUGCUGAGGCCUGGAGCUGGCCCGGACUGCCACACUUCACCCGGCUGGGC
AGACCGG
>random_seq_from_cds__NO_13835    RANDOM_LENGTH 84 SEQ_LENGTH    72
GC_CONTENT    0.486111111111111    BASEPAIR   21 FREE_ENERGY
-19.30 LEN_BP_RATIO  3.42857142857143
AUUGAAGGACAGGUUAAGCUUGCGCAGCUGUGUUAGGCCCUUGGAAGGCCUUGGUUUUAGUGAUGC
AUUUGUAGAGGAAGUUCUC
>random_seq_from_cds__NO_13837    RANDOM_LENGTH 78 SEQ_LENGTH    63
GC_CONTENT    0.634920634920635    BASEPAIR   21 FREE_ENERGY
-19.00 LEN_BP_RATIO  3
CGGCUCAGGUGGCUGAAGGUAUCGGGAUGUAGCUGGGGGAAGUGACGAGGGCACUCCAUGCAGGG
GUUGGGAGCGUGG
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>random_seq_from_cds__NO_13840    RANDOM_LENGTH 62 SEQ_LENGTH    56
  GC_CONTENT    0.714285714285714    BASEPAIR    21 FREE_ENERGY
  -27.50 LEN_BP_RATIO    2.666666666666667
GAGGUUGCCCAGGCCAAGGAGGGCACCCGGGGCCACCUCAGUGCCUGCCUGCAGGGGUUCU
>random_seq_from_cds__NO_13842    RANDOM_LENGTH 71 SEQ_LENGTH    58
  GC_CONTENT    0.517241379310345    BASEPAIR    21 FREE_ENERGY
  -20.20 LEN_BP_RATIO    2.76190476190476
AUGGCUGAGGGACAGGGGAUAUGAGGGAUUUGGGCAGCGCAGGCACAGUCAUGAUGUUGUUGUAGC
UCAGGU
>random_seq_from_cds__NO_13844    RANDOM_LENGTH 74 SEQ_LENGTH    66
  GC_CONTENT    0.575757575757576    BASEPAIR    23 FREE_ENERGY
  -21.60 LEN_BP_RATIO    2.8695652173913
GGGCAGUUCCACUUGAGGUUGAGAUGCCGCAGGCUGGGCAGGUGGGCAAAGUCAGAAUCAUGGAG
GUGGUGGAU
>random_seq_from_cds__NO_13862    RANDOM_LENGTH 88 SEQ_LENGTH    82
  GC_CONTENT    0.634146341463415    BASEPAIR    29 FREE_ENERGY
  -33.90 LEN_BP_RATIO    2.82758620689655
CCUGUGUGGUUGCCCUCAGAGGCUGCAGGGGCCUGUUUGCUUCCAGCACCAGCGGGGACUUGUU
GCUGGCUGACUUGGACUCCUCAG
>random_seq_from_cds__NO_13865    RANDOM_LENGTH 86 SEQ_LENGTH    68
  GC_CONTENT    0.676470588235294    BASEPAIR    22 FREE_ENERGY
  -27.86 LEN_BP_RATIO    3.09090909090909
GCGAGGCCGAUACGCUCAUGAUGACCCGCCGGGCCUUGUCUGUCCACUCCUCGUCCUCCCCCA
GGGCCCAUGGUCAAUGGGGU
>random_seq_from_cds__NO_13892    RANDOM_LENGTH 97 SEQ_LENGTH    72
  GC_CONTENT    0.388888888888889    BASEPAIR    25 FREE_ENERGY
  -23.00 LEN_BP_RATIO    2.88
AGGUGUAUUUGAAGAAGAUGCCACAGCUAUUUCCAACUAUAUGAACCAGUUGUAUCAAGCUAUGC
AUCGGAUUUAUGAUGCACAGGAAUGAAUUAAG
>random_seq_from_cds__NO_13894    RANDOM_LENGTH 99 SEQ_LENGTH    76
  GC_CONTENT    0.407894736842105    BASEPAIR    22 FREE_ENERGY
  -17.54 LEN_BP_RATIO    3.45454545454545
CUACAUUGCAACAGUUUUCAAAAGUUUAUGAUGAGGCCUUAGCUCUUGUCAUGCAGUGCUUUAAC
UCAACUUGCUGAUGCCAUGAUGUCCCCAUUACC
>random_seq_from_cds__NO_13901    RANDOM_LENGTH 84 SEQ_LENGTH    70
  GC_CONTENT    0.528571428571429    BASEPAIR    25 FREE_ENERGY
  -18.61 LEN_BP_RATIO    2.8
AGUAAAACAGGCUUGGUGUCAUCUACCUGGGACAGACAGUUUUACUUCACGCAGGGUGGAAUUU
AAUGAGUCAGGCCCGUGGG
>random_seq_from_cds__NO_13902    RANDOM_LENGTH 68 SEQ_LENGTH    57
  GC_CONTENT    0.543859649122807    BASEPAIR    21 FREE_ENERGY
  -19.50 LEN_BP_RATIO    2.71428571428571
GAUGUAGCAGGAGGCCUGGCCAUGGACAUAGACAACUGUUCAGUGAUGGCUGUGGACUGUGAAGA
CAG
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>random_seq_from_cds__NO_13912    RANDOM_LENGTH 110 SEQ_LENGTH    97
  GC_CONTENT    0.391752577319588    BASEPAIR    35 FREE_ENERGY
  -25.10 LEN_BP_RATIO    2.77142857142857
GGGAGAAGUGAAAGUAAUCUGUCAUCAGUCUGCUAUUAUUAUUGAGUCAAAACAAUGAGGGGGAAAA
GGAUAUGUGAUUCUGUUGGACUGGCAAACAGAUAGCUUUGCAUG
>random_seq_from_cds__NO_13918    RANDOM_LENGTH 110 SEQ_LENGTH    98
  GC_CONTENT    0.418367346938776    BASEPAIR    31 FREE_ENERGY
  -20.90 LEN_BP_RATIO    3.16129032258065
UUUAGGCGGCACAAAUGUUUUAGGGAGCGAGGGUUUGCUUAAGAUAAAAUGUAUUUCUGACCAGA
UCCCCUGUUUUUGGAGCACAGCUUUCAACUUUGAACAGAUCCGAA
>random_seq_from_cds__NO_13928    RANDOM_LENGTH 119 SEQ_LENGTH
  106 GC_CONTENT    0.433962264150943    BASEPAIR    30 FREE_ENERGY
  -25.73 LEN_BP_RATIO    3.53333333333333
GGCAAUCCUGUUUGUUUGCAAAAAGUAGCAGCACUGCAUCUCUCAAUUAUCUACCAGAAGCCA
UUUUCUGCAGCUCAUCUGCUACUCCUGAAUUCUUUCACGAUCGUUGCUAUCUA
>random_seq_from_cds__NO_13934    RANDOM_LENGTH 84 SEQ_LENGTH    70
  GC_CONTENT    0.628571428571429    BASEPAIR    23 FREE_ENERGY
  -26.70 LEN_BP_RATIO    3.04347826086957
UACAGGAUGGCAUCCUCCCCGGAUCAGGCGGAGCAGGUCCAGGUAGGCUGUUCUUGCCAUGUCC
ACUUGGGCACCAGACAGGA
>random_seq_from_cds__NO_13937    RANDOM_LENGTH 90 SEQ_LENGTH    83
  GC_CONTENT    0.602409638554217    BASEPAIR    27 FREE_ENERGY
  -33.80 LEN_BP_RATIO    3.07407407407407
UAGCAGUGCACCCUAGCAGCCUGGAGGUGUAUGACAGUGGUCUGGUUCCAAGCCUCGUGCUGGU
CAGCUCCGGAUUGCGUCAGGGUCUG
>random_seq_from_cds__NO_13943    RANDOM_LENGTH 71 SEQ_LENGTH    58
  GC_CONTENT    0.5 BASEPAIR    20 FREE_ENERGY    -19.60 LEN_BP_RATIO
  2.9
GAAGUCUUGGUUCAGAAUGGCAGUGUAGGAGUGCUGGAAGAACUCCAAGAGGCUGACUGCCAGGA
AAUGGA
>random_seq_from_cds__NO_13957    RANDOM_LENGTH 64 SEQ_LENGTH    57
  GC_CONTENT    0.596491228070175    BASEPAIR    20 FREE_ENERGY
  -18.10 LEN_BP_RATIO    2.85
CCAGGUAUCCCCAAUGACACUCGGUGCACUGGGCUGCCCAUCAUGCGGAGGUUACUGGAACCG
>random_seq_from_cds__NO_13967    RANDOM_LENGTH 86 SEQ_LENGTH    55
  GC_CONTENT    0.527272727272727    BASEPAIR    23 FREE_ENERGY
  -20.60 LEN_BP_RATIO    2.39130434782609
CUUACCAUCAGGCUUGAGGCUUUUUUAUCCAUCUUCACCACGGAGCAGCAAGACCAUGUCAAGUC
GGUGGAGUAUCUGAGAAAUA
>random_seq_from_cds__NO_13975    RANDOM_LENGTH 89 SEQ_LENGTH    79
  GC_CONTENT    0.746835443037975    BASEPAIR    28 FREE_ENERGY
  -34.00 LEN_BP_RATIO    2.82142857142857
GCUCGCCGGCCUGGGUUCGGCGGUGGUGGAUCUCCUCUUCUCCCCAGCACUGUGUGGCCACGC
GCCUCCCGACGGCCGCCUCAGCCA
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>random_seq_from_cds__NO_14006  RANDOM_LENGTH 84 SEQ_LENGTH 59
  GC_CONTENT  0.491525423728814  BASEPAIR  19 FREE_ENERGY
  -18.70 LEN_BP_RATIO  3.10526315789474
GAAAAUUGGAAUUGGUCCCAUGACAGUAGACAAAAUUGGUCUGUUCUUAUUGCAGAUGAAUCAGA
CCCUGCUGAGAGCAUGGAG
>random_seq_from_cds__NO_14008  RANDOM_LENGTH 110 SEQ_LENGTH
  104 GC_CONTENT  0.836538461538462  BASEPAIR  37 FREE_ENERGY
  -60.20 LEN_BP_RATIO  2.81081081081081
GGCGGCGGGCGGAGCAGCGGCCGCGGCCCGCCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC
CGCCGCCUCCGACGCCCCAGCGGCAGCAGCACCCGCCACCGCCGC
>random_seq_from_cds__NO_14009  RANDOM_LENGTH 69 SEQ_LENGTH 63
  GC_CONTENT  0.825396825396825  BASEPAIR  24 FREE_ENERGY
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(3). 1442 Zou pseudo miRNAs
>EMBL_CDS:CAA01027  CAA01027.1  Homo sapiens (human) hypothetical
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IV antibody
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>EMBL_CDS:BAA32319 BAA32319.3 Homo sapiens (human) KIAA0474 protein
AACCAGCACCCGUAGAGACCCUUCGAGACUCACCUACUCAAGAGGCUGAACCCGAGGACACUCUG
CACGGGCGACAGACC

>EMBL_CDS:BAA31199 BAA31199.1 Homo sapiens (human) natriuretic
peptide A type receptor
CCUCGAGUCCCGGCAGGUGUCGAAAACCGUAUUUGCCACACAGGAACGAGACCCAGGUCCAGG
GACUUCGAGA

>EMBL_CDS:BAA25522 BAA25522.2 Homo sapiens (human) KIAA0596 protein
CCUUCGGACUCCGGUCUCCCCGAAAAGUAAGACCGAUCACUCACUUCAGAGUUCGCGAGGACG
GGUACGAAGGA

>EMBL_CDS:BAA25526 BAA25526.2 Homo sapiens (human) KIAA0600 protein
GGUGGAAGACAAAUCGGAACUUGCGUGAAAGUUAACCCAAGUCUCCGACAAAACGCCUCCCCC

>EMBL_CDS:BAA25510 BAA25510.1 Homo sapiens (human) KIAA0584 protein
ACAGACUACCCCGAAGUCCCCUACCCGUCCAUCGGUAUCACGAGAGACAACGUCUCCAUGUAGA
CCUACGGACGAACGGACGACCUCUCCGUUUCUGU

>EMBL_CDS:BAA25479 BAA25479.2 Homo sapiens (human) KIAA0553 protein
GACCCCGUAAGAAACCCACACAUCAUAUAGUGGUAGGUAACAAGUGACCGAGAGUAUUUUUCA
UCUUUCCUUUUAAUCCAAAUGAAACGUCACACGACCCCCUACAUCACCAUUAUGAGUCCGAG
ACAUCGGGGUC

>EMBL_CDS:BAA82611 BAA82611.1 Homo sapiens (human) ganglioside
sialidase
GGUACCACGGUACACUGGGGAUCCAGUAGUGACAUCUAGUAGUCUCUACUCCGGACCAAAAUGU
ACCAUCGACC

>EMBL_CDS:BAA25482 BAA25482.2 Homo sapiens (human) KIAA0556 protein
CCACCAGGAAGACGUAGGACGUCACCCGACCGACCGACGAGCCGGAAAGACGACUCCUCGCGGGA
GACGUCCCGACGCAAGAGGUGG

>EMBL_CDS:BAA32136 BAA32136.1 Homo sapiens (human) aurora and
IPL1-like
ACACGUACGCGGGGAGUUAGUAGAGACCCCGUCCAUCAGGUCCCACGGUGUGUAACAGAAGGAG
GAGUCCUCCCGCGUACGUGU

>EMBL_CDS:BAA25505 BAA25505.2 Homo sapiens (human) KIAA0579 protein
UACCACCACCACCACCACCAAGCCUAAGCUCCGUCCUJACAAAGGACACCUCGGCGGUGGCG
GUGACGACGAUA

>EMBL_CDS:BAA25467 BAA25467.2 Homo sapiens (human) KIAA0541 protein
ACCGUUAAGACUGUUAUUUAACCAAACCUAAGGAGGAGUUUAUAACCGAGUCAUAGGACGUACAG
UGAAUAAAGGCUCAUUGUUAGGUCUGGAAGUCCUACGGU

>EMBL_CDS:BAA32295 BAA32295.3 Homo sapiens (human) KIAA0450 protein
CCAGGGGGUCGUACCUCAGCGCGCCGAACCCUUCGACGACCGGUGACUACUAGGCCUCGUGGUCG
ACGAAGAACUCGACGGGCCCGUCCCCCAGG

>EMBL_CDS:BAA25474 BAA25474.1 Homo sapiens (human) KIAA0548 protein

UAAUCUGUCCCCGACACCUAUCUUUAAAGGACAUCCCCGAACGCUUCCGUAGAAGUGACCAGGAA
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>EMBL_CDS:BAA24863 BAA24863.2 Homo sapiens (human) hypothetical
protein
GUCUUGUGGAGAUCUUAUGUGUCCUACUUCAAAUAAAUGUCACAGUAGUAGAACACAGGAGACUU
CCAGAC
>EMBL_CDS:BAA32404 BAA32404.1 Homo sapiens (human) Stem cell growth
factor-alpha
UCCCCACCCUCUCCCCGACCCCGCCUCCUACCCCAACCGCAACGAAGGAGGAGGAGAAGGAGGG
GGACCAGGAGGAGGUAGAGGGUCAGGA
>EMBL_CDS:BAA37096 BAA37096.1 Homo sapiens (human) hypothetical
protein
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CUACCGCAUGGUCUA
>EMBL_CDS:BAA25519 BAA25519.2 Homo sapiens (human) KIAA0593 protein
GUCAAGGAGGUCCACAACAUAGGUUAUGAUGGUUAUAAGAAAUAUAAGUAUAAGUAACCCCUUUUA
GGGUUAUUAACAACAAGGUUACUACCACCACAUCCUAUGUAAAUAUCUUCUAGAC
>EMBL_CDS:BAA25478 BAA25478.2 Homo sapiens (human) KIAA0552 protein
CUCCACCGUCCUCGAACCCACCCACCGACCCGAGUGCUAUGACGCCACCCCGAAACAGUGACGG
UGGUGACGACGACGACGGAG
>EMBL_CDS:BAA32298 BAA32298.3 Homo sapiens (human) KIAA0453 protein
CAUAGAACCCGAGUAGGUGACAACCUCUCCUCCACCCAGUUCCCUAUCAGGAACAGAACCUGA
AGGAAAACGAAAAGGCCCUUGCGUCUCCACCCGAAACUAUG
>EMBL_CDS:BAB69038 BAB69038.1 Homo sapiens (human) kinesin-related
protein
AACGAGUACGAGACCGGUUCCGACCAAACGAGUAGCACAAAUUGAACCACCGACCUUGACCGAA
CCUGUCACCGUACCCACC
>EMBL_CDS:BAB19784 BAB19784.1 Homo sapiens (human) MOP-3
UACGACUAUUGGUCGGUAAUAGUUAACCAAAGGAGUCUUUACCUACAAAACAUGGUUUGUAGUCCU
CCUCAUUGUAGCCUAUUUCUCGACCAAAGGUGAUGUCGUA
>EMBL_CDS:BAA32695 BAA32695.1 Homo sapiens (human) hypothetical
protein
UGGACGCAUGGAAACCCCCCGUGACCUCAGUAUCGUCACGAGUCAGGGGUCUACCAGGUGUCCA
>EMBL_CDS:BAA31684 BAA31684.2 Homo sapiens (human) KIAA0709 protein
CGACGACCCCUGCCGAGUCCUCCCGAGGCACGGGAAGACCGUCUACUUCGGUACCCAGAGGAG
GCACGUCGAGGCUAGCAGGGUCGCCG
>EMBL_CDS:BAA31593 BAA31593.2 Homo sapiens (human) KIAA0618 protein
CGACGAGGGCGACGACCGCCAGACCCACCACCGAGGUUUCGGCCUCGACCACCGACGUGGCUUCU
UCUGUCGUCACCUCGGCGGUUCCGCCCGACACUCGACCGCCUCGCG
>EMBL_CDS:BAA31613 BAA31613.2 Homo sapiens (human) KIAA0638 protein
CCGGACCCGGACAUCACUCUACAGAGACCGACGUCUCGGUJAGUGGCAGGAGGGAAGGAGGUCG
CCGUCCUCCACUACCGACACGACUCAGCGGGUGACGGGUCCGA
>EMBL_CDS:BAA31675 BAA31675.2 Homo sapiens (human) KIAA0700 protein
AAGACGCGGACCGCCAUCUAGAAGUCGUCGGACCUCGUGUCCAGACCACGUCCGCGUCCU

>EMBL_CDS:BAA31683 BAA31683.3 Homo sapiens (human) hypothetical protein
ACCGAGUCCCAGGAGUGACAUCGAGACGUCGUCGACAAGUCGCGGGGUCACCCUUACUCGGU

>EMBL_CDS:BAA74737 BAA74737.1 Homo sapiens (human) hypothetical protein
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GACCUAGU

>EMBL_CDS:BAA31685 BAA31685.2 Homo sapiens (human) KIAA0710 protein
AUAGGAGUAAGAGUAGGUCGUCCAUUAGUUUAUUAUACUCGCGGGGUGCCCGGUUAUAUGAACUCC
AACAAAGAACCACUCUUUUUCCUAU

>EMBL_CDS:BAA31649 BAA31649.1 Homo sapiens (human) KIAA0674 protein
ACCGGAAAGAAUCCGACAAAACCCGACACAUGACCUUUUUAAGUAAAGGUACCGGUCGUCGACG
GACUAGGUCAGGUUUUUCACUCCGGU

>EMBL_CDS:BAA31616 BAA31616.2 Homo sapiens (human) KIAA0641 protein
GAGACCCGGACUCCACCGGAGCCGGAGUCGGAGCUCCAGACUCUUCUACCGUCUCAGAGCCAUCC
CUAAGAAGAGCAACUCCGGUGACUCCUCCACCUCUCGGCACAGAGCCCGGGCCCC

>EMBL_CDS:BAA31604 BAA31604.2 Homo sapiens (human) KIAA0629 protein
AGAAGGUGUACGUUUGGUAGAUGUGUCCAUUCACGACAUCUACUCUUUCAUACACUUACUCCU

>EMBL_CDS:BAA36753 BAA36753.1 Homo sapiens (human) huntingtin
CGGGACGGACCUCUAGGUCUGAGUCGCCUAGACGAGUACCUAGUUUACGGUCCUGUCCCG

>EMBL_CDS:BAA31587 BAA31587.2 Homo sapiens (human) KIAA0612 protein
GUCCCUCUGUGACAGACGGAGUCGAGGAGAUGGAGUGACCGACACAGGUGGAGUCCACAUCCCG
UACUGAACCCCGACAACACCUACCUGAGCCUCACCCUCCUCAACCUCUCUCUGAGACGGAAGAAC

>EMBL_CDS:BAA76877 BAA76877.1 Homo sapiens (human) LCAU-like
lysophospholipase (LLPL)
UCUUCUCAGACCACACCCUCGCGGUCACGGUAUCUCCGUCACGUCGACGUGCGGUCCACCGUAG
CACCGAAGGUGGUCGGGAAGA

>EMBL_CDS:BAA83718 BAA83718.1 Homo sapiens (human) RNA binding
protein
AGAUCUCGCCGCGGCUUAUCGACCUCACAGGCCUUGGAUCUCGCCGCCGCACAGUGACCACUCC
AAGCUCUCGCCUGGAAGAAGCUCAAUGACCUCUACACGCUCUAGCUCUAGAGGAAGCCACUGG
CCUCUACAAGACCUAGAACUAGAAGACGCUCACUAUCCGCUUCAAGACGAAGCUCUAGCGGAGGA
CCAAUGACCACCUCAGGACCU

>EMBL_CDS:BAA33713 BAA33713.1 Homo sapiens (human) HIP1R
CCGGACUGAACCACCUCGUGGUGUAACCGUCGGGAGAGUAACUGACACGCUCUUGUAAGGACG
UCCGCCGAGUCCACCCCGACACGAACAACCGGAAGUGGAACCUCGG

>EMBL_CDS:BAA31606 BAA31606.2 Homo sapiens (human) KIAA0631 protein
CUACGUGUCACAUCCUUCGACACCCGUCGACCCAGAUACGCGUCCGCGUGGGCGGGUAGCCGG
GCUCAGCAGGUGUCGCGGAGGAGACCUCGUAG

>EMBL_CDS:BAA34529 BAA34529.2 Homo sapiens (human) KIAA0809 protein
UCUCGACAGGGCCUUGUCGUGACGACAGGUAUUAACCCGGCCCCCGGUCCGUCCCGCCGUAA
CCACGAACCCUCGAGA

>EMBL_CDS:BAB61018 BAB61018.1 Homo sapiens (human) hypothetical
protein

AUACUGUCGGUACAAAGGGUCGACCCCGUGUGGUCCCGGUCGGGGACCGUACCGGACAAGGUAAG
GAACGUACCAACAGUAC

>EMBL_CDS:BAA34515 BAA34515.1 Homo sapiens (human) KIAA0795 protein
GUCCACCGACACACCACCAACAUCACAAGGUGUGACGACUUCUAGACGUUUGGUAGUACCGGCGG
AC

>EMBL_CDS:BAA76776 BAA76776.2 Homo sapiens (human) KIAA0932 protein
CUCUAGGAGGUCUGCGUCACCCUCAUUCUACCCAUGGGUAAACCCUUGGUCCACGUCUUUUCAA
AGGGCAACACAGGACGUCCCAGAG

>EMBL_CDS:BAA34517 BAA34517.2 Homo sapiens (human) KIAA0797 protein
CUCUAUCUCCUCCUCAUCCGACUAUCCAUGAUGUCACGGCAAAGACAACAUGAAAGGAGAAUUAA
AG

>EMBL_CDS:BAA74870 BAA74870.1 Homo sapiens (human) KIAA0847 protein
CUAUCCGAAAGAAAACCUCCUCGAAAAGAAAACGUCUUUGACCUCUCCUACUAAGGUUUCAACUC
AGAUAG

>EMBL_CDS:BAA74936 BAA74936.1 Homo sapiens (human) KIAA0913 protein
GAACGAGUCCCAACAACCAUCGGUGGGUCCAGACUGCCGAGCACCUAUGGAACAAGAAGACGGGA
ACUCCAGCCCACCAACCGAUCGUCUAGGACCCGUUC

>EMBL_CDS:BAA76782 BAA76782.2 Homo sapiens (human) KIAA0938 protein
GGUUACGGACUCCCCCGAAAAAGGAAGUAGAGGUGACGAAAAAGGACGUAGACUCCUCUAGA
AACAUUCUACUAGGAAAAUCCCCUCGAAAAGGAAAGAGUCUUCGAAACC

>EMBL_CDS:BAA34445 BAA34445.1 Homo sapiens (human) KIAA0725 protein
UCGAAACCUAACACAUUUUUAUUUAAAGAGACAACCCUCUAAGGUCAAAGAAAAAGGUAAGUAG
GUUUCAA

>EMBL_CDS:BAA75631 BAA75631.1 Homo sapiens (human) semaphorin W
CCGGUGUCAACCAACAUAAGUGAACACAGUGGAGUCAUGCCUCGGUUGGUCCUCGGUCGACACC
AUGUUAAAGUACAAGAGUUGACCGACACCGA

>EMBL_CDS:BAA34523 BAA34523.1 Homo sapiens (human) KIAA0803 protein
CCGAAGAGAAACGUCAACGUAGAAACAUAUUUUAGGAAAUCUCUACUCUAACAUAACUACAUC
GA

>EMBL_CDS:BAA77349 BAA77349.1 Homo sapiens (human) hypothetical
protein
AACAGUCUCAGUCGAUCUCUAAGGAGUAUAAAUUCUUACACGAGUUGAUCCAUAUGUUGUACAAC
UCAUGUUCGAAAGAAGUGUCCAAAUAUACUCCUAGGAGAAAGUCUGAAGUUGUU

>EMBL_CDS:BAA34470 BAA34470.2 Homo sapiens (human) KIAA0750 protein
UGGUGUCCCGAAACCGAAAGGUCCACCAGUGGAACCUGAACUCGAACCUUAUUUUCAAAGACACC
A

>EMBL_CDS:BAA34436 BAA34436.3 Homo sapiens (human) KIAA0716 protein
CGUAACGACUCGACCUACCGACUCCAGCCGACCACUAGAGGUUAUACCAGGAGUCGUCUUUAGG
UCGUUCGACCG

>EMBL_CDS:BAA76374 BAA76374.1 Homo sapiens (human) interleukin-18
binding protein
ACUGGUCCUCUCACUGCUGCACCCGUGUGUCCUCGUCCUGGGUGUUUCCCGACUCCAGACCACAG
GUCAACACAGAGUACCAGU

>EMBL_CDS:BAA78717 BAA78717.1 Homo sapiens (human) hypothetical

protein

UAACCCUAACGUAAAAUAGUGUCAUCCACAUACUUUAUGAACGUAGCCUACUCAACGUCUGGGU
UA

>EMBL_CDS:BAA34508 BAA34508.2 Homo sapiens (human) KIAA0788 protein
ACAAAACUUCGGGAGUUUGGGUCGGACCCGUAUGAAACCGUCGAAAAGGUGACCUUCGUCAACAA
GAAGACUCGGUUUCCCGAACCCGAAGUCUCGU

>EMBL_CDS:BAA34467 BAA34467.1 Homo sapiens (human) KIAA0747 protein
CACGACCCUGUGGUCCUAGGGAUCGACACGAGAGUCAUCGUGGACGGGGACUGGUGACGACUCAC
AUUUGGUCGCCAGGUUCGUCUCGACCAGUCGGUGCUCCUCGAGACUCUCCCCGUCCUAUUACUC
GGGUCGUG

>EMBL_CDS:BAA34480 BAA34480.2 Homo sapiens (human) KIAA0760 protein
AGGUCCGUCUAGACUGUACACACCGAGACGACCCCGAACAGGCGCACCUACCAGAAGUCCACCUA
GAGGUCGUGCCGGUCCGACAAUUUCAGGGCGAACCU

>EMBL_CDS:BAA74887 BAA74887.2 Homo sapiens (human) KIAA0864 protein
CCGGGCCCGACGGACACGGACGAGACUCGUCCUCCCGAGGGCCAAACGGUCCUGAGGAACGUCU
CGACCUCGAGGAAGAGUAUAAGAUCGGCCUAAGACGUCCUGCGUAUCGUUUGGACCCGG

>EMBL_CDS:BAA76801 BAA76801.2 Homo sapiens (human) KIAA0957 protein
AGUGAAAAGGUAGGAACGGGGCCAUGUUACACAUCUCGACUAUGCGGGACUUGAGUACCCACCC
CCACCCCUACU

>EMBL_CDS:BAA83592 BAA83592.1 Homo sapiens (human) BEC2
GCGGUGAGAGCCGGAGACACUACCUACCGUCGACAGAACAGACUCCUCCUCGGUCUCCGAAAGACUC
GCCCCGACCCUCUCCGC

>EMBL_CDS:BAA34513 BAA34513.2 Homo sapiens (human) KIAA0793 protein
GAGGCGGUCGUAGUGACUCCUGUCCCGAGUCCUACCCCUACUCGGGACAAGUCGACCCGGGUU
CCGUGGACUUUACGUCCCGAGUCUGAGUCCCGGAGAAGGCCGACCUCCUC

>EMBL_CDS:BAA34482 BAA34482.2 Homo sapiens (human) KIAA0762 protein
AGACCGAUGAACUCACUACCUAGGUGGGAGACCCAGUAUCUUUCCUGAGACUCCUACCAGGUCCG
ACCAGUCCCGGCCU

>EMBL_CDS:BAA77569 BAA77569.1 Homo sapiens (human) neuroD-related
factor

ACGCUCUCAACUCGACGUCUGUCGGCCGGUGGUCUAACCACCACCCGACGCUGUCUGGGAACGU

>EMBL_CDS:CAB38381 CAB38381.2 Homo sapiens (human) immunoglobulin
heavy chain variable

AGAGGGAGUACUGGACACGUGGACUAAGUGAGGUCAGGGAAGGGACCCUCGACUCCUAGGUCG
AGGUCGUCCUUCGUGACCAACACUACCUUCUUCGUCUCUGUCGUGUCUACUCCUCU

>EMBL_CDS:BAA76791 BAA76791.3 Homo sapiens (human) KIAA0947 protein
CUUUCAGAGCUCAGGUCUUAACAGUGAAAUAUAUGAAGGGUACAUAAGUCUCGAACCUAUCGAA
GUACACUAAACCCGAAAA

>EMBL_CDS:BAA86871 BAA86871.1 Homo sapiens (human) Maf-related DNA
binding protein

UGCGCCGUCGACCGCCGAUCGGUGCCAAAACUCACACGCCGCGGCGACGAACUCGGCACA

>EMBL_CDS:BAA75063 BAA75063.1 Homo sapiens (human) apg-1

AUCAACAGAUGUAUCCGAUGAGACCUAGCCAUCUAGUUAUGAAAACUGAAAAGGAAAAAUUCAC
AGACUAAAUUAGCCAGAACAACAGACUCUGUCGAC

>EMBL_CDS: BAB71953 BAB71953.1 Homo sapiens (human) male enhanced antigen-2
CGGCGGAGGUUCUACUAGAAGAGCAAGACGUCCUCCGUCUAGCACAGGAGGGACCUCGCGCC

>EMBL_CDS: BAA95162 BAA95162.1 Homo sapiens (human) vascular cadherin-2
CGGAGGGACACCCCGACGGACGUUGGAAGUCUCCGGACCUCGACCCGACCCGGACACCGUCCGACC
CCGAGCCCUUCCAAGUCCAAGAGGGCCCUCCG

>EMBL_CDS: BAA86899 BAA86899.1 Homo sapiens (human) RECQL4 helicase
GAGAAGUCGGUGUCGGUCCACGACACGGUGCAGUGACCGUCACGCCGCACACCGACACCGACACU
C

>EMBL_CDS: BAA76854 BAA76854.1 Homo sapiens (human) KIAA1010 protein
CUCCGGGACCCGCAUGACCACCUUGAACCCGUCGAGUAGGUCGUCGACACGUAAGUCCCGGAG

>EMBL_CDS: BAB19280 BAB19280.1 Homo sapiens (human) protein tyrosine phosphatase HD-PUP
CGUCCGGGUCCACGAUGCCCGUAACGUACCCCGGGACCCCGGGACCCGACAUAGUCGACCCACCC
CGGGCUCAUCCAUGGUCCCCGUUCCCCGGACUCUCUAUCACCCAGGACCCGGACA

>EMBL_CDS: BAA86961 BAA86961.1 Homo sapiens (human) hypothetical protein
CCACUCUGUGGGGUUGUUUGAGACGAAGGUUGACCAUACACUCACGUUCGUGAACCUACAGGCAC
CGUCUCUCCGACCCCAUCAGAGGA

>EMBL_CDS: BAA78033 BAA78033.1 Homo sapiens (human) sodium channel
UAUGUUCAAAAGGGUUAUCAGGACCCAGUAUUCGCUUUAUACGGUUCUUCGGGUCGAUUUUC
ACAGUUUUGAACACA

>EMBL_CDS: BAA86559 BAA86559.2 Homo sapiens (human) KIAA1245 protein
AGUAGUGAAAGUAAAAGACCCUAUUACACAUGUCGUAGGAGGGUAAGUUGUACUCUCCUACU

>EMBL_CDS: BAA86582 BAA86582.1 Homo sapiens (human) KIAA1268 protein
CUAGUGCACCACCAUCCCGUCGAAAGGACGGAACCCUCUACCACCGUAACGGGCCAUCCUCAGACG
GGAGAGAGAAGUGAUAGACCAG

>EMBL_CDS: BAA86534 BAA86534.1 Homo sapiens (human) KIAA1220 protein
CCUGUCACGGUAUUCUGUAAAAGGUGAACAAACCUGUCCAGGACCUUUCAGGAAUACCCCAACAGG

>EMBL_CDS: BAA83041 BAA83041.2 Homo sapiens (human) KIAA1089 protein
UCUUCAGGCCUCCUUCGUAUAGGUGAGAGUAUGAGGAGGAGUAGGAGUGACCGGUCCGACUC
CAACCCACUCCUCCGUCCAUCUUCUCCGUCUCCAACUUCAGGAGGUCCUGACUGA

>EMBL_CDS: BAA86524 BAA86524.1 Homo sapiens (human) KIAA1210 protein
CCGAGGUGCCUAGCGAGACAAAUAUCUUCACGGGUGACUUGACCACCCUGAACACGACUUG
UCAUCCUAAGUAUUACCCGA

>EMBL_CDS: BAA86560 BAA86560.1 Homo sapiens (human) KIAA1246 protein
ACGUCACGCCGACCACGACAACGACUCCACACCGUCGACCUGCUACCUCUGGAGGUGGUACCGGC
ACCGGAGAGGCCGUCGUAACCGUCGUUACGU

>EMBL_CDS: BAA86545 BAA86545.2 Homo sapiens (human) KIAA1231 protein
UCCGAGCGGGACCGGGCCACUCGUGGCCGGCCAACCCUAGCCCACGUUCCCCGGCACGAAGCC
UGUGUGACUUCGUACGCGCAAUAACGUGAGGAGUGUGGUUCAGCACACCCAGCUUCCCCGGCCC
CGCCCAGA

>EMBL_CDS: BAA86526 BAA86526.2 Homo sapiens (human) KIAA1212 protein

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>EMBL_CDS:BAA86437 BAA86437.2 Homo sapiens (human) KIAA1123 protein
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AGACACAGAGGUCGUCGAACACGUACCUCGA
>EMBL_CDS:BAA86592 BAA86592.1 Homo sapiens (human) KIAA1278 protein
GCACCCAGAAACCACUCGUCAGGGACGUCCUUAAGAAUUUCGUCCUGACUACCAACUCCCGGU
CGC
>EMBL_CDS:BAA83014 BAA83014.2 Homo sapiens (human) KIAA1062 protein
UCGGGGGAAGAACC GCCCGGAGCGACCCGUCCUACAUCCUCUCGAGGCACGAACACAGACUCUGGU
CGUCCGUCCUCCGGUGUACGAACGCCUACUUGACCCUGUGGACCUCGAGCCUCGUCGACGAGUCG
CCCCGGGCUGGACCCCCCGA
>EMBL_CDS:BAA86561 BAA86561.2 Homo sapiens (human) KIAA1247 protein
GGCGAACCACUCCAAAGCCCCGACCCGCCGUAGUGGGUCCGGAUGCACCAUGUGGGACGGCAGGU
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>EMBL_CDS:BAA83045 BAA83045.2 Homo sapiens (human) KIAA1093 protein
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CCGACCGCCGGC
>EMBL_CDS:BAA82978 BAA82978.1 Homo sapiens (human) KIAA1026 protein
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GACCA
>EMBL_CDS:BAA86054 BAA86054.1 Homo sapiens (human) fatty acid
coenzyme A ligase 5
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AAGUCCACAGAACCG
>EMBL_CDS:BAA92330 BAA92330.1 Homo sapiens (human) F-box and
WD-repeats protein
CGGUCAAUCUAAGAUUUCAGAGAUUAGGACCUAUUAGAAAACCAUUAUUCUGGAUUAUUUACUU
AAACCUCCCG
>EMBL_CDS:BAA83019 BAA83019.1 Homo sapiens (human) KIAA1067 protein
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AGACACAGUGACGGUGGUCGACC
>EMBL_CDS:BAA83063 BAA83063.1 Homo sapiens (human) KIAA1111 protein
CGAAGAAAGGAACAGGUCCGAGAUUCCGGUUAAGUUCGAAACGGUGGUACCUGGUCCAUCU
CCG
>EMBL_CDS:BAA89345 BAA89345.1 Homo sapiens (human) hMYHgamma4
GGAGGGACCCCCGAACGCCGACCGAAAGACCCCUUCAACUGGUGAGGGUCCAGACCAGGGUC
CCGAGGCUCCCUCC
>EMBL_CDS:BAA86228 BAA86228.1 Homo sapiens (human) endomucin-2
CAACAACCACACUGUUGUAAAAAGACAUUACUAAGACACAAACCACAACAUAUCUACCAAAACA
ACAUCAUUGUUG
>EMBL_CDS:BAA88125 BAA88125.1 Homo sapiens (human) breast cancer
associated protein
CUCAAGAAUGACCGAAGAGACCACCAAGACCUAUCCUCUCUGGAGAUCCCUCCAGGAUCCUGAA

>EMBL_CDS:BAA83016 BAA83016.2 Homo sapiens (human) KIAA1064 protein
CCCGGCGGUCCCAGGUACCCACCCGGUCCUAAGUACGGUCCCGGGUAGCCGUACAGACGCACGUA
CAGACGCACGUACAGUCCACGUACAGGCCACGUACAGCCCACGUACAGUCCUACGUAACCG
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>EMBL_CDS:BAA82977 BAA82977.2 Homo sapiens (human) KIAA1025 protein
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ACGGCCUGUAGACAAAUCAUCGUCUUGACUUUUUAUCUGUACCGUAAAAAGG

>EMBL_CDS:BAA83000 BAA83000.2 Homo sapiens (human) KIAA1048 protein
CUGGGACCCGGACUCAUCUCCGCAGACGACACCUCACCCUCCUCGGACACCGACGAACCGGACU
CAAACGCCGUCUCCGACCGACCCACCCGAACCCCAA

>EMBL_CDS:BAA86596 BAA86596.1 Homo sapiens (human) KIAA1282 protein
CCGUCGACGUCCUGGAGGAACACGUCCACGUACCGCUACAGACGCGGUCGAGCAGUCCUCCGA
GACGUCGUCGA

>EMBL_CDS:BAA86591 BAA86591.2 Homo sapiens (human) KIAA1277 protein
GUCGUGGCCUACAUCACACGACGGUCCGCUUCCCAUCUAGUCGCGGUGGUAGCGCACCGUCG
UGAACCUGUCCUACGAC

>EMBL_CDS:BAA86516 BAA86516.1 Homo sapiens (human) KIAA1202 protein
CCUCGACAUCGACUCAGUGCGACCAAUCCCAUGUACAAGACCAGUUAUCCGUUGUCUACCGAGA
GUAUCCACCGAACCGGACCAACGAGG

>EMBL_CDS:BAA86597 BAA86597.1 Homo sapiens (human) KIAA1283 protein
GUCCGUCGUCGGCAGGGGAACCGUGAGUGUUUGUCGGGGCACCCUCCGACCCUAGCGACGAC
AGAC

>EMBL_CDS:BAA86525 BAA86525.1 Homo sapiens (human) KIAA1211 protein
CCGAGUGAACCGAGACCCAGGCCGGAGGGGCGAGCCGCUUCUGUCGUCGAGAUGGUUCAUCCCGA
CGAGUCAAAACUUUCACCCCUACGACCACCCAGACUGACCACCCGA

>EMBL_CDS:BAA86603 BAA86603.2 Homo sapiens (human) KIAA1289 protein
UCGUUCAUUCAGAGGUACUAGAAAAAGUCCACAUCAGAAAAUAUUCUAGACAAAAACUAUCUG
ACCCAGACAAUAUUGAGAACUAGGGUAAAUAUGUCAGUCUAGAUAACUCGCCAUUGGGACUCCU
UCAAAAGCCAGUAUAUCCUCUCAAUUUUCGA

>EMBL_CDS:BAA89212 BAA89212.1 Homo sapiens (human) bromodomain
adjacent to zinc finger
UGACGAAAAAGGAAGGGAACUGAUACGUCCUACCCUCUCCGUCUCCGUAUGUCCACAGACUAA
CGGUCCCCAAGAAGAGGGUGAACAUAGAGUCUAAAUGUCCACUCCUUUUUCCCCA

>EMBL_CDS:BAA86518 BAA86518.1 Homo sapiens (human) KIAA1204 protein
AGGAGUUAAGGACCUACUCAGAAGAGAAAGGCCCGACGGGAAACUUUCGUCCUGACCUCAACUG
AGGAGGUCUCCUCAACCUCCC

>EMBL_CDS:BAA86595 BAA86595.2 Homo sapiens (human) KIAA1281 protein
CGCCACCGCCGUCUCCACGACCACGACCAUGAUACGACAAACCCAACGGCGACGGCGGCGACG

>EMBL_CDS:BAA86489 BAA86489.1 Homo sapiens (human) KIAA1175 protein
ACGACCCCUCCGUCUCGGGACCCUAGGCAAAAUGACCUGAAGUACCCUCAAAAACUGAAAGAGG
CCGU

>EMBL_CDS:BAA86579 BAA86579.1 Homo sapiens (human) KIAA1265 protein
CAAGAGCGGCACCACCAAUACACGUCGUCGUACCUCUAGUACGAGUACUUAACCAUACAUAUAGGUA
GUGACACUCUUA

>EMBL_CDS: BAB83129 BAB83129.1 Homo sapiens (human) BDG-29
GGACGUCCCCGGGUGACCGUAUGACGAGUAACGUCUUUCCGUUGAAACCACAACCGACACAUG
UCUCGUCAGGCCCCCAAUAUAACGUCC

>EMBL_CDS: BAA83004 BAA83004.2 Homo sapiens (human) KIAA1052 protein
AAGAAAACUCGAAGUCGGAGGUCCGACGACUUCACAAAGACGUCAACGACCGAGACUCGGACGUC
GUCUAGGUGAACCCUGAGGUCGAAGUCGAACGCCCGGACGUCGAGUAGUUCUU

>EMBL_CDS: BAA83025 BAA83025.2 Homo sapiens (human) KIAA1073 protein
UAUCUCUCCUAAUCACUUCAGAAGGUCGACCGACAAAUACAUCUGGUGUCACUGUGUCAGGAAA
AUCCUUCUAAGAGAAAAGGAGAGACA

>EMBL_CDS: BAA86539 BAA86539.2 Homo sapiens (human) KIAA1225 protein
CUGAAAACCGACCAAUUAUCUCCAAAGUUAUUUACCACCAGCGUAGAGGCGGUAAAAGUAGAGAA
GUAGUCUUCUUUCA

>EMBL_CDS: BAA86446 BAA86446.2 Homo sapiens (human) KIAA1132 protein
GACCGCGAGGGCCGAGUGCCACCGCCGACGCAACGACCGCUACGUACAUAUCAACGGCAACACGA
ACUCCUCUGCGAUC

>EMBL_CDS: BAA82664 BAA82664.1 Homo sapiens (human) serine/threonine
phosphatase 1
AGACAACUACGACCGUGUAAGUACCAAGGGAGACUCUUCUUUUUUAAGAGUCCUAUAAAAUAAA
ACAUCCGGUCAUUCUCCGUCU

>EMBL_CDS: BAA83068 BAA83068.2 Homo sapiens (human) KIAA1116 protein
GAAAAAGAAGUCCGAGACGGACAAUACAACCUCGUAAUUUUUGUAAAGGUCGACCGUCUCGCCUU
CAUCGUUC

>EMBL_CDS: BAA92681 BAA92681.1 Homo sapiens (human) KIAA1443 protein
UACGAGGUGACGGUCCACAGUAGUCCUGAGGAAAUAAGACCACUGAGACACCGUCACCACCG
UA

>EMBL_CDS: BAA87415 BAA87415.1 Homo sapiens (human) cadherin-7
AGUAUCAGGUACCGUUUAAGUCCCGCAUAGUAACUACAGUUCAUUAUCACUACCGGUGUAUCGG
AGAAGGAUGAACUCUACCUAAGACCGAGAGGUAACGUUCCUGACACU

>EMBL_CDS: BAA96028 BAA96028.1 Homo sapiens (human) KIAA1504 protein
ACCUCCACAGUAAAAGGGUGAGAAGGUACCGAGAACAUCCAAUUGACAUCUCAAUUAUAUCUAC
CCUCUGCGGAGGU

>EMBL_CDS: BAA96063 BAA96063.1 Homo sapiens (human) KIAA1539 protein
GCGGGGUACCCUGGCGUCAGACAACCAGGUUUUGUCCGAGAAACCCGGGUCCGUCGUCCACCGA
GGUCUUCAC

>EMBL_CDS: BAA96051 BAA96051.1 Homo sapiens (human) KIAA1527 protein
AGUCUUCUGGUUCUUCGUCUUGCUAUACUCCAGACCUCACUCGUCUUCAUAAAGACCCAGGGUA
UAAAGACUGAAGGACCUAUGGAAGACC

>EMBL_CDS: BAA92540 BAA92540.3 Homo sapiens (human) KIAA1302 protein
AACGCGACCGCGGUGAGGUGGUCCAACUCCGGCAACAGCUACCCGUCGCACUGUAAGGAGAACGG
GUGCCACCCCAACUGCCACGGUCGGUCGUU

>EMBL_CDS: BAD74065 BAD74065.1 Homo sapiens (human) histone protein
CAGGAAGAAGACGCGGAAUCAGUGCCGAAAGAAGCUCGGGAAGAACCCGCGCCUCGCCUG

>EMBL_CDS: BAA95992 BAA95992.1 Homo sapiens (human) KIAA1468 protein
CGGAAUAGAAGGUAAUUGUAAACAACGUUGUAACUUCUUGGUUCCUCGAUGCCUAAAGAAAUCC

UUCCAUCCA

>EMBL_CDS:BAA92641 BAA92641.1 Homo sapiens (human) KIAA1403 protein
ACGGAGGAGAGGUACCACCACGUCUGGGUCCACCCACCCGUCAGGUGCAGUCCCCGGUCAUCAA
GAGGGACUUCUGACUUGGCUCGGACGUAGGAGAGGACACAGACGACGGCGGCCUGUCCCCCGU

>EMBL_CDS:BAA96094 BAA96094.1 Homo sapiens (human) intelectin
AGACCAUCUACGGUUUGUCUAAUACAGGGUCACAGACCUCUUCGGUCACAGGCACGCCAUGGAG
UCGUCCCUCGACAAAGAGGUCACGACGUACCCCCUGAAUAACCCGUGCACGGUCU

>EMBL_CDS:BAA95984 BAA95984.1 Homo sapiens (human) KIAA1460 protein
CUAAGACCCCUACCAAGGAGGGUCGGACACCCAAGAAGAAGAAAACGACCCCGACCAUUAUCCAGG
GGGGUCGGUCGGACAUGGUCCUCCAAACGGACAUCGACCACCCUAAGGGGUUCUAG

>EMBL_CDS:BAA96027 BAA96027.2 Homo sapiens (human) KIAA1503 protein
CUAGAAGUCCGGGACCGGAGGAAGGUACAAGAAUUAGGUAAAGUCCCGGACCCGGACUCCCAG

>EMBL_CDS:BAA95996 BAA95996.1 Homo sapiens (human) KIAA1472 protein
AGGCGGGUACUCCUGGAGCUAACGCACUUCUUCUUCUGGCGAACGAAGGGCGUCAGCUGUAUACC
UGGAGUCCUCGCCU

>EMBL_CDS:BAA92624 BAA92624.1 Homo sapiens (human) KIAA1386 protein
GAGAUCAAAGAAGUAGCUCCCGGUCGGGUCUGAGAACGUCACUAUUGACAUAACGUUCUUAUUAU
AACCCUAGCAGAAGUAGGUUCCUUGAGUCUC

>EMBL_CDS:BAA92654 BAA92654.1 Homo sapiens (human) KIAA1416 protein
GUGAAGGAGAGCUCCGGCGGCAGACGCGGCCAGUCAGAAGUAAUCCCGGAGAACGGAGUAGACAA
CGGAAAAUAUCGACGCGACUAUCCGUCAUUAUCUGGCCGCGUCUGCACAUCAGUCCCAACUUCAC

>EMBL_CDS:BAA92671 BAA92671.1 Homo sapiens (human) KIAA1433 protein
AGCCCGGUCGACGAACCGCCGUCUCAACAGAUACUCCACCCCCUAUUUAGGGACCUACCUCCCG
AGACAUCCGGUGACCGAACAACCAGGACU

>EMBL_CDS:BAA92626 BAA92626.1 Homo sapiens (human) KIAA1388 protein
AAGUGGUCCGGUGACACCCUCGACACCACGACACGGUCACUCCACUCAUCACUCUUCGGGUAGAA
CGUCUGGGGUGUCUGCUUCCCGAAGACGAGUCGGACGUGCGUGACCACGAGGUCGUCCAGUCACC
GGACCACCU

>EMBL_CDS:BAA96031 BAA96031.1 Homo sapiens (human) KIAA1507 protein
AGUCCUACUUCAUAUAAAACCAACUGAGGAAGUACCUCAUGUCGUUAAACAUAAGGAAGAAU
GACU

>EMBL_CDS:BAA92554 BAA92554.1 Homo sapiens (human) KIAA1316 protein
CUCCCCACCUUCAUUUUUACAUCUACGACGGUGGACUUAUAGUCCCGUCAGUUCAGUCGUCGGU
CGAGAG

>EMBL_CDS:BAB16102 BAB16102.1 Homo sapiens (human) hypothetical
protein
CGUAUGGUUCUGAACCCGAGAGGUUUCACCUCUAUUAAUACGAUAUCUCCAGGUACAGAAGCCA
CACG

>EMBL_CDS:BAB17049 BAB17049.1 Homo sapiens (human)
interferon-responsive finger
UCUAGACCUCGUACCUUAUGUCAGAAGUCAAGAACCUCUUGGUAAAAACCGAAAAAGUCGGAGGU
CUAGA

>EMBL_CDS:BAA92659 BAA92659.1 Homo sapiens (human) KIAA1421 protein
CGUCUCCGACUAUAACCGACCUUUUACAUAACUAUUAACCCCAUAUAAAGGUGAACAUUCUUA

AAGUAAAAAGUCGACUAGGUUUUAGACA

>EMBL_CDS:BAA92636 BAA92636.2 Homo sapiens (human) KIAA1398 protein
ACGGGACUCAUCACGGUCACCGACCACACAACGGGAACCGUGGGUGACCCCGUGGGUGGUGGUAG
CCGUGGAGGAACCCUCGU

>EMBL_CDS:BAA94075 BAA94075.1 Homo sapiens (human) neurexin II
CCCACCACGACAGGGAGUCACACCCCCUCGCCGGGGCCGCGCACCACCAUCACCGGUACCACCAC
CAUCAGAGGUACUACCACCACCGGUACAGUCGGUCGUCCACCACCAGGCGACAGAGGCGUGACUC
GUCGUGCCUGCCGGGGAGGG

>EMBL_CDS:BAA92662 BAA92662.2 Homo sapiens (human) KIAA1424 protein
CAAAGAAACAAAAGGAGGAGACAAAGGUAAAAGAAGUAGGAAUAUACUUUUUAAACUUAACGUCUGA
GACCCCUAUUUGUUUUUUUA

>EMBL_CDS:BAA92655 BAA92655.2 Homo sapiens (human) KIAA1417 protein
AAGUCUCAGACUACAGUUGUCAAGACCUUCUCUAAGGUGUCUUAACCAGAAUGGUCUGAAAUUAU
UAGGACAUCUACUACCUGAGACUU

>EMBL_CDS:BAA92546 BAA92546.1 Homo sapiens (human) KIAA1308 protein
GUCGACCGAGACCUCGGACGACCUCGAGGCCUCGACCACGACCUCGAUGAAGAUCGAGACUUGGA
CCUCGACCACAACCUCGACCGAGACCGAGGCCCCGACCUCGGCCGUGACCCGACCCAC

>EMBL_CDS:BAA94480 BAA94480.1 Homo sapiens (human) muscarinic
acetylcholine receptor m3
GUCGUCGUAGUAACAACAAGGUUGACAGUGACGACGACACCAGAACCAGGUAGACGAGCCUCGAC
CCAAAGGUCGAGAACCAACACUUGGUCUUCACCGUCGCCGUAUGAAGGAGGACAACCUCGCAA
GUACGAAACGACAAC

>EMBL_CDS:BAA92615 BAA92615.1 Homo sapiens (human) KIAA1377 protein
AGAGAAAACUUACGAGGUCUUCACCUCAGUCAACAGGAGUAUCACGAUCAAAGUCUCCAGAAAAG
UGUAAAAAAUAGAUAUGUUUGUACCCACCCGAUCUAUGUUUCCCAUGACUUAUAAUACGUCAUA
AACACCGAGAAAGGUGACAAGGUAAGUUUCCUCU

>EMBL_CDS:BAB16413 BAB16413.1 Homo sapiens (human) X11L-binding
protein 51
ACACGUUCAGUCCGGGGAACCGGUCCAGGAGAAGUGCGUCCCAAGGUCGGCCCCCGGACACUC
CCGUGU

>EMBL_CDS:BAA94194 BAA94194.1 Homo sapiens (human) protein kinase
PAK5
GACCCAGAGGACCCGACUGGGUGGUCGACGUCCCGGCGGGCUUUGACAAGUACCCUGUGGGACCU
CCCAGACACCAGCCUCCUCCUCGGGGUC

>EMBL_CDS:BAB83623 BAB83623.1 Homo sapiens (human) galectin-9
CGAGACGUGACACACCUACUGACAGACCCAGACCUUCGACUACAUCCUGUCGACGUGUCUCGGUA
ACUGCCUCUACCACAGGUGGCCACCUUCCCG

>EMBL_CDS:BAA92556 BAA92556.1 Homo sapiens (human) KIAA1318 protein
AAACACCGUACCUGUAUGGGUACGGUGUAGGUCUCCGACACCGAGAACCAUCACCGUACCCGUAG
CUAGGUCUUU

>EMBL_CDS:BAA96025 BAA96025.1 Homo sapiens (human) KIAA1501 protein
CAUCCGACCUGUGGUGACGUAACAACGGCCCGUGAGCCAUUUACGGACACCUGAGGUCGGGAG

>EMBL_CDS:BAA92595 BAA92595.1 Homo sapiens (human) KIAA1357 protein
ACAGUGACGACCACGACGAGAAAGCCUACGAAGAGACUUAGCUGGGGUGAACGAAACCUCUCCGG

UCCGAACCCCGUCGCGGCCACCCACAGU

>EMBL_CDS:BAA96021 BAA96021.1 Homo sapiens (human) KIAA1497 protein
AACUUCAGGGGAAGAACCUGAAAAACACUACCCCAAAAAACAACUCCAGAUUCUUAAGUUUAAACC
UUGAAAAACGUCCCGUUAACUCCUGAAAUU

>EMBL_CDS:BAA96024 BAA96024.2 Homo sapiens (human) KIAA1500 protein
GUUACUGACCUCACCUGAAAAGUCGUCCUCACUAGUACUACCAUJUUAUAGACUAAUAGGUUAC
AACACCAGGUACAGUCUCUGUCUCUUUAUCUUCGAUAGUCAUUGGUCUACUGGUAGUCAAGUUU
GUGUCGACUCAUAGACUAAAAGAACAUAAC

>EMBL_CDS:BAB13394 BAB13394.1 Homo sapiens (human) KIAA1568 protein
CACUGUGACAAGAAUCAUUGUAGUCACUGGACGCCAAACCUACCACCGGGACCGUCCAGUGAAUU
UAGUAUCAAAAUGACUAAACAACGAGGUCUGAGACAGU

>EMBL_CDS:BAB13428 BAB13428.1 Homo sapiens (human) KIAA1602 protein
CGACGGUCCUAGGGGUCAGCGGCAGGACUGGGGACCGACCCGAAGAACCUACUCAACGGACCCC
AGGACGCCG

>EMBL_CDS:BAB13433 BAB13433.1 Homo sapiens (human) KIAA1607 protein
CCCACUUCGUCCUCUACAACCGUUCUCUUCGCCGUCGUCGUCGAAGACGUGAACCGACUCCGAGA
AACGGCAGAGACUUGUAGCGACGUAGUGGA

>EMBL_CDS:BAB13456 BAB13456.1 Homo sapiens (human) KIAA1630 protein
UCAGAAAGAGUAGGACCGAGACUUAACCCUCCAAAGUUAUCUUUAGACGGGUGUCAUCUAAACU
AACUCUAUCUGA

>EMBL_CDS:BAB13396 BAB13396.1 Homo sapiens (human) KIAA1570 protein
AGAAAAACCAUACAGAGUUAGUUCGGAAAAGGAGUCAAGAUACAUAUUCUCAGACUUCUUA
CUAGAGUAGUCCUAUAUGUCCUUCU

>EMBL_CDS:BAB62077 BAB62077.1 Homo sapiens (human) affixin
CGUGCAGUAAUUAGGUCAGCUCUCCUGGAACUGGUCAAGGAACUUGAACCCAGGAAGGAACCU
CACCCAGUUAGUAGCACG

>EMBL_CDS:BAB13460 BAB13460.1 Homo sapiens (human) KIAA1634 protein
AGUCCGCCUUCUAGGUAAAGACACAACUUUACUUCGGACUCUCGACAGCAGGAGCCCAACAAA
AGAGGUUAUCUUCUAGAAGGCAGACU

>EMBL_CDS:BAE71373 BAE71373.1 Homo sapiens (human) zinc finger
protein
CGACGACGACGACAUCGACGGACCCCGGCGUGGUCCCGGAGGAAGGUCCCGAGGUCCGGUCCGA
GACCCGACUUCGACGUUGACCCCGGGGUCUUCUUCUCCCGACCACCUUGUCCGAACAUCUCCGU
CGCCGUCG

>EMBL_CDS:BAB13392 BAB13392.1 Homo sapiens (human) KIAA1566 protein
AGUCGACACCUGAGGGCACAGUCUCCUUACCCUAGUCCUCGUUAACGACUAGAGUAGAGAAGACA
AAGGUGAGGACAGACGUCUACU

>EMBL_CDS:BAB13399 BAB13399.1 Homo sapiens (human) KIAA1573 protein
GGUGAAAGGUCGGAGACUGACGUGGACGACAACUGUGUACCACUUCUCGUAGAACGUCCGGUCC
CAGUUAUCGACACAUAACAGUGGCCGAGGACCACC

>EMBL_CDS:BAB13458 BAB13458.1 Homo sapiens (human) KIAA1632 protein
CCAGAGGAAACUUAAGUGUCCGAUCUCUUCUCCUAAAGGACGAGAGACCUCCAAAAACCUCCUC
UGA

>EMBL_CDS:BAB39742 BAB39742.2 Homo sapiens (human) mosaic serine

protease

CCUCUACGGGCCGGACCUCCACAGGGUCGACCUCUACGGACCCGACCUCUACGAGGUCGACUUCC
ACAAGAACGACCUCUACGUAAGGGCACCAGGGAGAGG

>EMBL_CDS: BAB17658 BAB17658.1 Homo sapiens (human) gamma2-COP
CUAAAGUCUGUGUUUUCUUCUAUAGACGAAGUACUCGGCCAGGUGUGACGAGAGUGAAGGACAAA
ACUCCUCACAUCAUUACCGAUUCCAUCGUUACGAAGACAAACUCAGACACUAA

>EMBL_CDS: BAB39854 BAB39854.1 Homo sapiens (human) VUS20631
GACUGUGGACACGUCCGACCCGUCGAGGAGUUAACUAACACUCUGUCAAGGUCCUGAGCCUCGG
ACCCGUCGACAACCGUGUAGGGGCUACCCUCGUCGGCCUACGGACGCGCCAGUCCAGUC

>EMBL_CDS: BAB59010 BAB59010.1 Homo sapiens (human) calmin
CCUUUGGAAACUCUCCCCACCCUCCCGAACUUUAGGUCCGGAAGAAGCGACACUGAGGGUUC
AGAGG

>EMBL_CDS: BAA99542 BAA99542.1 Homo sapiens (human)
3alpha-hydroxysteroid dehydrogenase

CUCGUGACACCCGUUGGUCUUGUUACAGAAAACUGAACGUCUUUAGGUCGUCAAACGAGACCAAC
UCCAUCCUACUGUAAGAUGGACCAACGUCUGUCCGAA

>EMBL_CDS: BAB13377 BAB13377.1 Homo sapiens (human) KIAA1551 protein
ACGGACCCAGUAGAGUUGUCGACUACAGAAACUUCACUCUUGAAAGUGUAGUACUCUACCCAGAC
CGU

>EMBL_CDS: BAB13442 BAB13442.1 Homo sapiens (human) KIAA1616 protein
AGACCAAGAAGACGGAGGAAGAGAACCUCACCUAAGGACCCGGACUCUGUAUAUCCCGUACAG
CAGAAACAAGAACUUGAGGUUCGACUCUUAACUUCUCCUUCUUAAGGGUCU

>EMBL_CDS: BAB39380 BAB39380.1 Homo sapiens (human) MAP/microtubule
affinity-regulating
CGACACUGACCUCUCCCCUCCGUCUCCCCGUGGGCACCCACGGACUCGACAAAAGAAAGGGUAAAC
CGUUGUCA

>EMBL_CDS: BAD74069 BAD74069.1 Homo sapiens (human) hypothetical
protein
CCGAGGAAGAGGUUCAGGGUCCUCAGAUCGAGCAGGAGGACCCCGAACCCCGUUCCUACGG

>EMBL_CDS: BAB86289 BAB86289.1 Homo sapiens (human) CasL interacting
molecule MICAL

AGCGACGGAAGGAAAAACACCAGACAGACCCCGUCCACGACCUCCGUCAUCUUUACAGGUAGAGG
ACCCACGACGAGUAUCGGUGGACCCGGUGUCACACCCGAGUGUCCAUACCGUCGCC

>EMBL_CDS: BAB87181 BAB87181.1 Homo sapiens (human) psi neuronal
apoptosis inhibitory
UCACCAAAAAACUUAGUCAAAAAGGAUACUGAACUCCUAACUUGUAUAAAGAAACAUCAGUAGA
UUUUCUUAUUCUGGACUAAGAAAUUGACGA

>EMBL_CDS: BAB13469 BAB13469.1 Homo sapiens (human) KIAA1643 protein
AGUGACCGUAUCAAGCAGACGUCGACCAGUCGGUGUGGACUUUACGUCUGCUUGUCCGCCACC

>EMBL_CDS: BAB19259 BAB19259.1 Homo sapiens (human) toll-like receptor
9

CACGUAACGGCGACUUCAGGUCCCGGGCGUCGUGCAUGACGUCUCGACGACCCUGUGAACCGAC
ACCUACAACAACCCCGUCCGACUCCACCGUCCACGCG

>EMBL_CDS: BAB21774 BAB21774.1 Homo sapiens (human) KIAA1683 protein

GUAGAGUCAUCCGACUCUACUCAUCAGACCCGAACCCUGUGAAGUCACCGGUGUCUAUCCAUCG
GACUCGAACCCUGUGGAGUCACUCGACUCUACCCAUCGGACCCGAACCCUGUGGAGUCACCGG
UGUCUAUCCAUCGGACUCGAACCCUAUAGAGUCACCCGACUAUAC

>EMBL_CDS: BAB60824 BAB60824.1 Homo sapiens (human) Gi-coupled ADP
receptor HORK3
AGUGUAAGAACAGAGAGCCGACGGACAACCAGUCUUAGUACAAUCCGUUUCUCUCAUUCUUGUAC
U

>EMBL_CDS: BAB21853 BAB21853.1 Homo sapiens (human) KIAA1762 protein
UUCUCUCCCCGACCCUUAGCCACGUCCAGGUUCCUCCACCCCUCCCCUGUCCUUCCGUUAGG
UCUAUACUUCGGUGACCACAGUCCCGGGAAGAAGAGUCACGGGUGGAGGGGAGACAGAGCGGAA
GGAACCCGAGAAGAACCGACGCAAGACCGGAAGUUAGAA

>EMBL_CDS: BAB21813 BAB21813.2 Homo sapiens (human) KIAA1722 protein
UCGAAAAACCGAAAAUACGUCGAAUCCACCAGAUAAAGUAGAUCUAAUCCAUAUUCUCGAAGUUU
UCGA

>EMBL_CDS: BAB21776 BAB21776.2 Homo sapiens (human) KIAA1685 protein
ACCAGGGAGGUUGACUCCGCCGACGUCGUCGACGCCGCCGUCGCCGUCGACGACGGGAGACACGA
AACUGGU

>EMBL_CDS: BAB21777 BAB21777.2 Homo sapiens (human) KIAA1686 protein
UCCUUUCACCCUUGGAAAUGUUGACUCAAAGAUAGAGACUUGUCCAAGACUAAAAAGA

>EMBL_CDS: BAC15606 BAC15606.1 Homo sapiens (human) FELE-1
ACCACAUCCGUCACCGUCGGAGUJAGACCCCGUGGUUGGGUACCACGACGUCGUUAAGGGCCUUC
UCCGACUUCGGUCCGUGGU

>EMBL_CDS: BAB21802 BAB21802.1 Homo sapiens (human) KIAA1711 protein
ACAAGACUUUAUGUACAUAUAAACGUAAGUCUCCGAAAUCUUCGACCUAAAACAUUAAAACACACC
UUCUCGU

>EMBL_CDS: BAB47408 BAB47408.2 Homo sapiens (human) fibrillin3
CGGUGGUGACUGUUACGUGAGCAGGUGUAGGUGCGUACGGACGGACCACCCGCACCCGACCUUCG
GGCCCAUCGUGGCCGUCACCAUCCACGGCCCCUACAACUGCGUCAGUGGCACCACCG

>EMBL_CDS: BAB40803 BAB40803.1 Homo sapiens (human) epiplakin 1
CCCGGACGGCUCACGACAUGAACUACUUACCCCCAGGGACCCGAGGGGAGGGGCCCCAGGGGGGA
CUCUCACCGUCCUUCGUUCGGG

>EMBL_CDS: BAB21818 BAB21818.1 Homo sapiens (human) KIAA1727 protein
CCCGCGCCGUCAGAAUAAAAGGAGUCCGAAGACAGACCCCUCCAAGGACUACCAAACCGUGAC
CCGAAGAACUUUCUUGGGACCCGACGUCCCCUUGCAGGGAGGGGCCUGCCCACGACGACCUCGG
CGACGAGGG

>EMBL_CDS: BAD93351 BAD93351.1 Homo sapiens (human) BNIP2 motif
containing molecule at
GGAAGGAGAAAUCGUUUACCGAACACAAGUCAAAAGGAAAAGCAGAGGUCGUUUACAACCACUACA
CAUUCUCAGACUCCACCUUAUUAACCAUAGAUUCCCCUUC

>EMBL_CDS: BAB33339 BAB33339.1 Homo sapiens (human) KIAA1669 protein
GGACACCGGACCUCCCGACUCACGACCGACGACGCCACGGAGGGUCCUCGACUCCCCCGUCC
AGGUUCAAUUACCAGACGUCGCGGUGGAGGUCCUCUCCUGGUACGGUCAGACGUGCCUGCCGAG
UCGGGGACCCGGGUGUCC

>EMBL_CDS: BAB20900 BAB20900.1 Homo sapiens (human) KF-1 protein

GUCCUCAAGAUUCAUACAUAACUACCGUAUAAUAUAUACGGUUAUAGACAGUAUAUUGAGAAC
>EMBL_CDS: BAB39359 BAB39359.1 Homo sapiens (human) HsRml
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>EMBL_CDS: BAB69021 BAB69021.1 Homo sapiens (human) hypothetical
protein
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>EMBL_CDS: BAB21780 BAB21780.3 Homo sapiens (human) KIAA1689 protein
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>EMBL_CDS: BAB59128 BAB59128.1 Homo sapiens (human) chorein
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>EMBL_CDS: BAB21863 BAB21863.1 Homo sapiens (human) KIAA1772 protein
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CCCGUCUAUUUCCCGAGGCAAGAACUUUCUCCCGCUUGACAU
>EMBL_CDS: BAB21770 BAB21770.1 Homo sapiens (human) KIAA1679 protein
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UGACUUUCGUCAGUGUUAUGUC
>EMBL_CDS: BAB21846 BAB21846.1 Homo sapiens (human) KIAA1755 protein
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ACAAAACCA
>EMBL_CDS: BAB32867 BAB32867.1 Homo sapiens (human) NeshBP
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>EMBL_CDS: BAB21816 BAB21816.1 Homo sapiens (human) KIAA1725 protein
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CAUAAUGAGUUUCUGACGAAGAGACCAGU
>EMBL_CDS: BAB21827 BAB21827.1 Homo sapiens (human) KIAA1736 protein
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>EMBL_CDS: BAB21833 BAB21833.2 Homo sapiens (human) KIAA1742 protein
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CAGGCGA
>EMBL_CDS: BAB33332 BAB33332.2 Homo sapiens (human) KIAA1662 protein
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>EMBL_CDS: BAB21848 BAB21848.1 Homo sapiens (human) KIAA1757 protein
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>EMBL_CDS: BAB21850 BAB21850.1 Homo sapiens (human) KIAA1759 protein
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GUCUCC

>EMBL_CDS:BAC05722 BAC05722.1 Homo sapiens (human) seven transmembrane helix receptor

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>EMBL_CDS:BAB91223 BAB91223.1 Homo sapiens (human) aquaporin 10
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GGUAAUGGUCG

>EMBL_CDS:BAB84316 BAB84316.1 Homo sapiens (human) RIN3
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AACCGGGAGAGACCCACCUUGGGCCGCACCCACAGAGGUUCCGGUAGCGGACACACGUCUCGAG

>EMBL_CDS:BAB40969 BAB40969.1 Homo sapiens (human)
kringle-containing transmembrane

GGUCGGGGGUACCCACCGCGGGUCCUUAACGAUGGACCCUGUCAGACUCCACCCACCGACC

>EMBL_CDS:BAB67831 BAB67831.2 Homo sapiens (human) KIAA1938 protein
CGGGGGCGUCAUGGUGUCCGACUCCGGCCCCGGCGAGUGAGACCGCCGAACCGACGGAAACCUAC
AACCCCA

>EMBL_CDS:BAB47435 BAB47435.1 Homo sapiens (human) KIAA1806 protein
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>EMBL_CDS:BAB67802 BAB67802.2 Homo sapiens (human) KIAA1909 protein
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>EMBL_CDS:BAB69067 BAB69067.1 Homo sapiens (human) signal recognition
particle 14kD

AGUCGGGUAGGUACAAUCGAGAUUCCUCCAAACUUAUUCGGUAGACUUUGAAUAAGUGAAGGAAC
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>EMBL_CDS:BAB47462 BAB47462.1 Homo sapiens (human) KIAA1833 protein
CAGGGGAUCCAUCCCCGACCUUCUGUGUJGGUUGUCAGAAGGCCAAUGUCGUAUCCUCUG

>EMBL_CDS:BAC01892 BAC01892.1 Homo sapiens (human) immunoglobulin
heavy chain VHDJ

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CUUCCA

>EMBL_CDS:BAB47465 BAB47465.1 Homo sapiens (human) KIAA1836 protein
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>EMBL_CDS:BAB93492 BAB93492.1 Homo sapiens (human) annexin A7
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>EMBL_CDS:BAB47436 BAB47436.1 Homo sapiens (human) KIAA1807 protein
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>EMBL_CDS:BAC05726 BAC05726.1 Homo sapiens (human) seven
transmembrane helix receptor

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transmembrane helix receptor
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>EMBL_CDS:BAC05799 BAC05799.1 Homo sapiens (human) seven
transmembrane helix receptor
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>EMBL_CDS:BAC05849 BAC05849.1 Homo sapiens (human) seven
transmembrane helix receptor
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>EMBL_CDS:BAB47448 BAB47448.1 Homo sapiens (human) KIAA1819 protein
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>EMBL_CDS:BAB47484 BAB47484.1 Homo sapiens (human) KIAA1855 protein
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GACCCGAGUCGGGGACCUCCUUCAGGAACUCG
>EMBL_CDS:BAB47478 BAB47478.1 Homo sapiens (human) KIAA1849 protein
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kappa light chain
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CGGCACCG
>EMBL_CDS:BAB47466 BAB47466.1 Homo sapiens (human) KIAA1837 protein
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>EMBL_CDS:BAC05715 BAC05715.1 Homo sapiens (human) seven
transmembrane helix receptor
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>EMBL_CDS:BAB47446 BAB47446.1 Homo sapiens (human) KIAA1817 protein
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ACGAAGAAAACCCACACGAGAGGUCGACG
>EMBL_CDS:BAC05977 BAC05977.1 Homo sapiens (human) seven
transmembrane helix receptor

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G

>EMBL_CDS:BAC01621 BAC01621.1 Homo sapiens (human) immunoglobulin
lambda light chain

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>EMBL_CDS:BAB67799 BAB67799.1 Homo sapiens (human) KIAA1906 protein

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L8

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product of

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>EMBL_CDS:BAB85546 BAB85546.1 Homo sapiens (human) KIAA1960 protein

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product of Nbla00360

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product of

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>EMBL_CDS:BAB85544 BAB85544.1 Homo sapiens (human) KIAA1958 protein

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>EMBL_CDS:BAB85554 BAB85554.1 Homo sapiens (human) KIAA1968 protein

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product of
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finger protein
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recognition protein L
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product of
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acid-binding Ig-like lectin
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G
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binder 2-like protein
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>EMBL_CDS:BAC01115 BAC01115.1 Homo sapiens (human) Di-Ras1
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C

>EMBL_CDS:BAE96598 BAE96598.1 Homo sapiens (human) zinc-finger
homeodomain protein 4
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GG

>EMBL_CDS:BAC02703 BAC02703.1 Homo sapiens (human) KIAA1994 protein
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>EMBL_CDS:BAC02711 BAC02711.1 Homo sapiens (human) KIAA2002 protein
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>EMBL_CDS:BAD00088 BAD00088.1 Homo sapiens (human) chimeric MOZ-ASXH2
fusion protein
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>EMBL_CDS:BAC67158 BAC67158.1 Homo sapiens (human) cytosolic
phospholipase A2 delta
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>EMBL_CDS:BAC76999 BAC76999.1 Homo sapiens (human) homeobox
transcription factor Nanog
CCACCAUCCUUCUAUCUCCGACCCCAUCCAUCCACGACUCCGGAAGACGCAGUGUGGUAACGAU
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>EMBL_CDS:BAC45250 BAC45250.1 Homo sapiens (human) receptor protein
tyrosine kinase
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>EMBL_CDS:BAD02449 BAD02449.1 Homo sapiens (human)
N-acetylgalactosaminyltransferase
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>EMBL_CDS:BAC54922 BAC54922.1 Homo sapiens (human) tripartite
motif-containing 15
AUCUAGAAGAGCGGCACGAGGAGCGUCAUUCAAAGAGGGUCGCCCGGUCUCCCGGUA
CCCUCAGAGACGGACGAGGAGGAGAACCGUCUCGCCCGUCUCGUCCUAGAACGGGCUCUAAACC
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>EMBL_CDS:BAD89397 BAD89397.1 Homo sapiens (human) carbonic anhydrase
VI nirs variant
AUAUGUCACGGCAGUCGGUGACAGUACGCGUACCACCUCCGUCGACUAGACGUGACACAC

>EMBL_CDS:BAC23110 BAC23110.2 Homo sapiens (human) KIAA2014 protein
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GACGUCCAAUAGGACCUUCAA

>EMBL_CDS:BAC23107 BAC23107.1 Homo sapiens (human) KIAA2011 protein
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CGGCUCGGAGGAGACCGCCCCUCACCCAGACUACACCUACGAAGGUCGGCAUUGAAGGCCAACCU
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>EMBL_CDS:BAC23124 BAC23124.1 Homo sapiens (human) KIAA2028 protein
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>EMBL_CDS:BAC82348 BAC82348.1 Homo sapiens (human) scapinin
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CGA

>EMBL_CDS:BAC98464 BAC98464.1 Homo sapiens (human) GDNF-inducible
zinc finger protein 1
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>EMBL_CDS:BAC23123 BAC23123.2 Homo sapiens (human) KIAA2027 protein
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>EMBL_CDS:BAD89424 BAD89424.1 Homo sapiens (human) interferon
regulatory factor 1 nirs
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>EMBL_CDS:BAF31266 BAF31266.1 Homo sapiens (human) KIAA0170 protein
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>EMBL_CDS:BAD02451 BAD02451.1 Homo sapiens (human) KIAA1199 protein
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>EMBL_CDS:BAC98376 BAC98376.1 Homo sapiens (human) KIAA2036 protein
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>EMBL_CDS:BAC84969 BAC84969.1 Homo sapiens (human)
N-Acetylglucosaminyltransferase IX
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>EMBL_CDS:BAC78211 BAC78211.1 Homo sapiens (human) hypothetical
protein
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>EMBL_CDS:BAF31253 BAF31253.1 Homo sapiens (human) HLA-G protein
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>EMBL_CDS:BAC57496 BAC57496.1 Homo sapiens (human) hornerin
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C

>EMBL_CDS:BAC99057 BAC99057.1 Homo sapiens (human) KIAA2038 protein
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>EMBL_CDS:BAD89015 BAD89015.1 Homo sapiens (human) extracellular
matrix protein QBRICK
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>EMBL_CDS:BAD86792 BAD86792.1 Homo sapiens (human) diacylglycerol
kinase kappa
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>EMBL_CDS:BAD66828 BAD66828.1 Homo sapiens (human) KIAA0596 splice
variant 1
ACCUUGAGUGACCAUAGGUACCACCCCAACAGUGAGCCGAGGCCCAUCUGUUAUGGUAGAAGUUA
CCCACGUCCAAGGU

>EMBL_CDS:BAD52439 BAD52439.1 Homo sapiens (human) non-muscle myosin
heavy
CCGGUCGCCUAACAACUACUUCAAAAUAGGUGUAUCUCUAUGAAUAGCCGUCGAACGACACGG

>EMBL_CDS:BAD37141 BAD37141.1 Homo sapiens (human) serine/threonine
kinase
CCAGGAGGAGUCCGGCGAAUAAAAGACGCAACAAUGAGACUCAGAAGAAUCUCAUUCUUAUUCUC
CACCCUUAACCGUCCUGG

>EMBL_CDS:BAD52436 BAD52436.1 Homo sapiens (human) filamin A
AACCCACCGACGGUCGAGGGUGUAAGUGGGACUUCCCCCGACAACCCCUACGACUGCGGAGGGGU
C

>EMBL_CDS:BAH02288 BAH02288.1 Homo sapiens (human) liver X receptor
beta
CUAGAGGACCUGACUCUACUACCGGUCGAGGCACUUCACCCGUUUCGCAACGACCGCCCGUAGAG
CCCUGACCCCCAG

>EMBL_CDS:BAG15901 BAG15901.1 Homo sapiens (human) UAF1 RNA
polymerase II, UAU box
CGUUCUACUACGGAAGAGGUAAAAGUCUGUGUGGUCAUUAUCUUAAGGACCAGGAAUAGGAAGAAG
UAACCAGGGCCCCCACCUCACCUCUCCGUAGUUGAACG

>EMBL_CDS:BAF94759 BAF94759.1 Homo sapiens (human) U cell receptor
alpha variable 35
GUCAAGGACGGACCAACACCCGUCGUGUCUUAUCUACGGAUGUAGUGAUCCAUAACCUACGAC

>EMBL_CDS:BAF94561 BAF94561.1 Homo sapiens (human) U cell receptor
beta variable 27

GACCCAGAGGGCCGAGGGCGAUCUUGACGACCGUGUCUUCAUGUCUCUCCAGACCAACCCCGACC
CGCUGAGGUC

>EMBL_CDS:BAF63624 BAF63624.1 Homo sapiens (human) MHC class I antigen
UCUUUGGGUCCCCGGGUCGUGGAGUCCCACCGGAGUACCAGUCUCUACUCCACCACCCAGUGCACA
CAGA

>EMBL_CDS:BAF94849 BAF94849.1 Homo sapiens (human) U cell receptor
beta variable 3
AGACCUCUAAAUCCACUCUUCGCUAAUCCUCGACAAAGUAAAUAUUACUCGAGGAAUAAUAACAU
CGAUUUGUAAUAGAAGUCU

>EMBL_CDS:BAG71128 BAG71128.1 Homo sapiens (human) riboflavin
transporter 1
CGGUAGUCCGGGUCGUCCUCCGUGGUACCCGACUCUUGUCGACUACCUGGAGUCCCAGACCCGG
UCCCUACCA

>EMBL_CDS:BAG12377 BAG12377.1 Homo sapiens (human) N-acylsphingosine
amidohydrolase 1
GUAUCGGUCGUUUCGAACUUCGGAACUUCUGUCAAAACAACAAAGAAACCUUUAGGUUUAAGUGA
CAAUUUCCAAAUAACGAGUCAAUAC

>EMBL_CDS:BAG48316 BAG48316.1 Homo sapiens (human) acetyl-Coenzyme
A carboxylase alpha
GGCGUAAUGGUACGAGGCGUGCCUAAGGAGUUAGAAACUACCCAGGUACUAUUGGCACCCGUGUU
UCAACUCCUUCUACACCAAUGUCAGUCACGCC

>EMBL_CDS:BAG48312 BAG48312.1 Homo sapiens (human) collagen type V
alpha 1
GGACCUCAGGACCGUUUGGGACGUCGGGGUGACCCGGUCCCCAGGUCCUUCGGAGACCC

>EMBL_CDS:BAF63512 BAF63512.1 Homo sapiens (human) small G protein
signaling modulator 2
GGGCCUCAGGGCCCAGGACGAAGGACGAGUCCAAAACCAGAACUAGAAGUCCCAGGACCCCGAG
GCCC

>EMBL_CDS:BAF80583 BAF80583.1 Homo sapiens (human) MYO5A variant
protein
CAAAACACAUUAAUUUCAAUAGACGUAAAGGAUUAGCAUCGUAAAUUUAAGUCCAUUGAAACGA
CUCCGUGUUUCG

>EMBL_CDS:BAF63529 BAF63529.1 Homo sapiens (human) Sickle tail
GUCCGCCACCCCUACCCAGGUCCGACUUCGUCCGAGGAGACGACCUAUAAAACAUCGAGACCAG
ACACCCGAACCAGGUCGUAGAAGUGACGAAC

>EMBL_CDS:BAG06714 BAG06714.1 Homo sapiens (human) MYO5B variant
protein
UCGAUAGACCCUCGGCACCCGACCUCAUAAGACGCACCCGAACCAGCCGGUGCCGAAAGGAGUCG
A

>EMBL_CDS:BAG06722 BAG06722.1 Homo sapiens (human) DNAH10 variant
protein
ACCCCUUCGGGAACCACCCAGGCACCACUCGGUGUCCGCCUUCAGACCCACCCCGAACCCACUAG
GAGAGGUCCUGAAGAGGU

>EMBL_CDS:BAD92948 BAD92948.1 Homo sapiens (human) RAB40B, member RAS

oncogene family

CUCGAAGAGGACCUCUCUAAGGCGGCACAAAGAAAGUCACGGAAGGAAUUCUUUAAAACGUCGAC
AAAGACCACGUCAAAAACCCCCCGAGACCCCCCGCCUCGUCGAAGUGAAACGCCUCCGACG
AG

>EMBL_CDS:BAD92557 BAD92557.1 Homo sapiens (human) LEPREL2 protein
variant

AGCCUCCUACUUCGCGACCUACAGGAGAGACCCAGGCUCCGGUCCAGAGCCGAGAGGGUCGACCC
GGACCAUGACCAAGUCUCGGGAGAACCUCGCGAGUAGGAGGCC

>EMBL_CDS:BAD93084 BAD93084.1 Homo sapiens (human) zinc finger
protein 211 isoform 2

CCGACCUCGAAGCCGAUUUCCUAAAAGGUGUAAGUAACGUGAGUACUCCAGAAAGAGGUCACACU
UGAGAGACCACCAUUUAGUCCGACUUCAAAACCGA

>EMBL_CDS:BAD93143 BAD93143.1 Homo sapiens (human) tripartite
motif-containing 38

UGCAGAAGGACUCCACUUCGGAAGUGUUGGGUUCUGUGUCCCCUCCGUCAUUUAGAGGACCUUC
UACA

>EMBL_CDS:BAE06093 BAE06093.1 Homo sapiens (human) UNPO2 variant
protein

UUGAACCCCUAGUACUACAACUCCCCGGACAACUCCCGCAGUGACAGGUCUUCGAGACUACUCAG
AAGUGUCUAGAAGACGUCCCCGAGGUUCCGAGGGAGUGUUCACAACAUUAGGAGGCUCAA

>EMBL_CDS:BAD92719 BAD92719.1 Homo sapiens (human) Diaphanous 1
variant

AGUUAGUAGUACAACCCUUGUCGUCCUAGGUACCGAGACUGGUCGUCAUCCUAAGGAAGAAGACA
GAGGUUGUACCAGAACU

>EMBL_CDS:BAD92976 BAD92976.1 Homo sapiens (human) Inositol
1,4,5-trisphosphate receptor

CCAUGAACGUGUCCCCGACUACAGUAACUCCUAGUCACGCCACUACUACAGAUACGGUAACCCUG
AGCACUCAGUGUUACGUUCAGACCAAGAGUACCGUCCCCGGGACCGUCAUGA

>EMBL_CDS:BAE06086 BAE06086.1 Homo sapiens (human) CSPG3 variant
protein

CGUGACUUCGAGGACUACAAGGGACCCAGAGGUGGACUAGGAGACCGAGACCCACCCCAACCCUC
GAACUCCUCGGGUCACA

>EMBL_CDS:BAE06083 BAE06083.1 Homo sapiens (human) APC variant
protein

CAACGACCCGUCCAGAACUUCUCCCCAGCUUAGAGAUCUAGGACUAGAUCUCCACGAAAUGAACUG
GGUGGAUAAACCCUACAGACGGACCGUUG

>EMBL_CDS:BAD92747 BAD92747.1 Homo sapiens (human) EBNA-2
co-activator variant

ACCGUUACGUCUUGAGAGGGGACGCCCCCGUAUCCUCGGGAGAUGUCCCCCACUGACCGUUAC
AGU

>EMBL_CDS:BAD93123 BAD93123.1 Homo sapiens (human) MSH5 protein
variant

CAGGUCACUACUGAAACUGGGAGGGAAACAGGGGUGGUGUAAGACACCUCAACCCGUGUUUCCAA
GCCCGUGUCUCAAGGUAGUCUCCUA

>EMBL_CDS:BAD92921 BAD92921.1 Homo sapiens (human) Synapsin-3 variant
GAGCCACCACCGCAUCCAAAACCGGUACCGCUGGUGCGACCACUACAGGACCUUCAGUUCGACCA
AAAGGUGAAACUAGAAAGGGUAAGGUCGCACCCGUACAGGGUCGAACUGAUGGUGGCC

>EMBL_CDS:BAD93102 BAD93102.1 Homo sapiens (human) latent
transforming growth factor
AGUCCGUAACCACCCCAACACCGUAAGGGACACUGGGUCCGUCCACGUACCCACUGUGACCAGCA
CUGGACCGGUCGGACU

>EMBL_CDS:BAD93140 BAD93140.1 Homo sapiens (human) LL5 beta protein
variant
AGGUACGAUAGUCUCGAUAGCUCGAGUCUCAUAGUUUCCGGACCAGGAACAUCGACACUAGACC
UAUUACCU

>EMBL_CDS:BAD92774 BAD92774.1 Homo sapiens (human) G protein-coupled
receptor kinase
CUACCCACCUGAAACAGAACCCCAACCGAAAUGCGGCCGGCGAGACGUGAACACGCCCCAGGU
CGUCCUCACGAGGGUCUACCUCAACCGGGGCAA

>EMBL_CDS:BAD92514 BAD92514.1 Homo sapiens (human) son of sevenless
homolog 2 variant
UCCUCUAAAUAUCCUUUUCAACUAAAGGAUCCUUUAGCUCACCAGACAAACGUCAAAAGCUCCAA
GUUAAAGAUCACUGAACAAACUUGUUUAUUAGACAUUUGAGAAAAAGUCUACGUGAAGGGUACCCC
AAUCCAAAAGUUUCUUAGAGGA

>EMBL_CDS:BAD92702 BAD92702.1 Homo sapiens (human) hypothetical
protein FLJ16665
CUAGGUACCVCUAGACUCGUUCCCGUUCUACCUUUACCCAGAGAAUAAUCGUAACGAACUAG
UGGUACCCAA

>EMBL_CDS:BAD92714 BAD92714.1 Homo sapiens (human) anaplastic
lymphoma kinase Ki-1
CGGGUUCGACCUCUGACAGGGUAAGGUUGUUCACUUCUCCGAGACGUCCCGUAGAACCUCGGA
CCCCUACAAGGAAGUGACGUC AAGAAGUCCG

>EMBL_CDS:BAD92530 BAD92530.1 Homo sapiens (human) SWI/SNF-related
matrix-associated
CGAGGAGAAGAGACACCGGUGCGAAACUGAAUCACAUUCCACAACUCCUGGAAAGAAUCGUAAA
AAGAAGAAACGAAGACCCCAACCACUUCUCCCCUCG

>EMBL_CDS:BAD92651 BAD92651.1 Homo sapiens (human) A-kinase anchor
protein 13 isoform 2
ACAACCUCGCCUUCUCUUGAGAUCCCGAUACACAACCCUCGUUAGGAGACCCUCUCCCCACGAC
GUGAGUCGGUACAGGGCCUUUAGUAGAGGAAGAGAAGGUUGU

>EMBL_CDS:BAD92907 BAD92907.1 Homo sapiens (human) protein tyrosine
phosphatase,
CCAAGAAAGGUCAAGUUCUUCUAGAAUAAAAGUUUCCUACAAGGAACUUCUCUAAAUGACCAUG
CCCUGG

>EMBL_CDS:BAD92640 BAD92640.1 Homo sapiens (human) iron-responsive
element binding
GUCUUAGUGUUCUAGGAGCCGUCCAUCAGACCGGAGACGUCCCUUCGAAGAAUCCGACGUGAAAU
UCACCUCUCUGAAAGGACGAAAGACGUCCAGUGGUGGAGGUCCUAAACCACGUAAGAC

>EMBL_CDS:BAE06113 BAE06113.1 Homo sapiens (human) C14orf159 variant protein
GGUCUCCCGUCGUCUUCGGUCGUACCCAUUGUGUUCGGUGACAACAGAACAUAACGUGGGCGGACC
GACACUGGACGACCCAGAGAAGACC

>EMBL_CDS:BAD92895 BAD92895.1 Homo sapiens (human) integrin alpha 3 isoform b, precursor
AUCGGCUUCCACCGGUUGGGUCCGUCAGGGUCGAAGAGAGGUACCUAUUGGACGACCCCGACAGA
CUCCUCGGGGAAUCUCGAU

>EMBL_CDS:BAD92894 BAD92894.1 Homo sapiens (human) platelet-derived growth factor
CGUCCGUCUGGUCUACUACAAGCCGACCCCGUACGGGGCCGGUGCUGUCGCCUGACAGACA

>EMBL_CDS:BAE06120 BAE06120.1 Homo sapiens (human) UNC variant protein
GACCAAGAGUAGGAGACACUCUAGCUACCACCAUGCCAGAGGACCGUGCAGAAACUACGGCAUCC
AGUCGAGUUACGGUAGCUAGAGUCGGUCCCCGAACUUGGUC

>EMBL_CDS:BAE06087 BAE06087.1 Homo sapiens (human) MEF2D variant protein
UGGUCCACCCUGACAACGACUCCACCGACAACGCCGACGACUCCGACGACACCGACACCGACGAC
ACCGACGCCACCGACGACGACACCUCGACACCGACGACGCCGACGACCCCGACGACACCGACAA
CGGUCCGUCACUGUAACGGAUCGCUGUCGGGGGGUCCA

>EMBL_CDS:BAE06094 BAE06094.1 Homo sapiens (human) DAB1 variant protein
CCAGCCCAAACGCCUCCCGUGCCCGCCUCCGACCCGGUAGACCUUUAGGAAUUUGCAAAGAAAC
GGGUAAAAGACGGACCCGAACAGCCAGACACCUGAACUGG

>EMBL_CDS:BAD92901 BAD92901.1 Homo sapiens (human) Hypothetical protein DKFZp666D035
CACAUCCCAAAAAGAAGUCUUACUCAAGAGAAUACCAAUCUUUCCGAACUCGUUCAAGACUUCUG
GAAGGGUGUA

>EMBL_CDS:BAD92880 BAD92880.1 Homo sapiens (human) smoothelin isoform b variant
CCCUGUCUCCCCAGAGAAACCCCGGUCUGUCUUCGAACAACUGGUGGACCGGGAGUCACGACCCC
UCGCAACCUCUGAGGACUCCGAGUCCCGACCACCAGAACCACCCGACCCCCACCGAGACCCGA
CGGA

>EMBL_CDS:BAD92987 BAD92987.1 Homo sapiens (human) RE1-silencing transcription factor
CAAAAGAAAUCAAGUGAAAACUCUGUAGGUAACAAAUAUCCUGUUCAUCCUACGAAUCUAAA
CUUCACUAUGACAUCUAAUG

>EMBL_CDS:BAD92820 BAD92820.1 Homo sapiens (human) phospholipase C, beta 2 variant
CGUGGACCAGUCCGGCAGCACCGCCCUUGUCGUCCCUCAAUUCGGCCUCAGGGCGACAAAGACC
AACUACUUAACCAGUCCACG

>EMBL_CDS:BAE06070 BAE06070.1 Homo sapiens (human) FASN variant protein
CCCUCUCCCGACAGGUGGUGGACGUCGGCGGGUAGGUUGUCGCGACCCUAGAGUCCCAACCCCG

AUACCUUCACGUCCAACCCCCGGGUCUCGGGCACGAG
>EMBL_CDS:BAD92549 BAD92549.1 Homo sapiens (human) DNA-repair protein complementing XP-G
AGGACACCACUCUCUCCAGGGGACGACUUACGAAAUAAUCGAAAUUGUCCCCAACGAAGCUUCGG
UUAACCU
>EMBL_CDS:BAD93125 BAD93125.1 Homo sapiens (human) natural killer-tumor recognition
AAAUCUUGCAAUUGAAAACCGGAGGAGAAUACAAAGGAGGAAGACGAAGAGAGUACAAGUUCAA
GUGAAAGACUUCUACUAAGACUUCUUCUCCUCCUUAACCUUCCCCUAGGCUCGGAAGACUU
>EMBL_CDS:BAD92735 BAD92735.1 Homo sapiens (human) low density lipoprotein-related
CGUAGACCCCCCGCAACCUCUCCGUGUCCGUGCGUACACGGCAACAGGUCGGCGAAGGGUAA
CCCUGUCCACG
>EMBL_CDS:BAD92858 BAD92858.1 Homo sapiens (human) zinc finger, MYND domain-containing
GGACGGUGAACGGAGACAAAAGAGCGAGGUCGGCGAGGGUCUAAAGACCCUAGAUCUUCUCUU
CACCUCUCACCGUCC
>EMBL_CDS:BAD92580 BAD92580.1 Homo sapiens (human) elongation factor, RNA polymerase
AUCGUUCAUCGAGGCCAAAGAACAUCGGGAAGUCCCGGUCAUUCACUUAGUGGGACAGGGACAUA
CCGGAGACUCUCUACCACGACGACGAU
>EMBL_CDS:BAE96739 BAE96739.1 Homo sapiens (human) downstream of tyrosine kinase 7
GGUCCGACGACGGGCGCAUCCUGCUCUCCGACGACCUCAUUCUCCUCACCGACGGUCACCGCUAC
GGCGACAGGCUCCUCGAGACCGCCGGUUGGAGGACGUCGACGGCGCCUGCGUCGCCGAACC
>EMBL_CDS:BAE44474 BAE44474.1 Homo sapiens (human) hypothetical protein
CGUAACCCCCGGUCCUGUUUCCCCGAGACGCCCCGACCCGGAGACCAUCCCGUCCAGACCUCG
AGACGUCUUCAGGACCACGACCUACA
>EMBL_CDS:BAE17137 BAE17137.1 Homo sapiens (human) hypothetical protein
CUUCCUACACCACGAUGUCCCGAACCACUGAAAGCCAACCCUCGUGGUUCAAGACACGAAAGAA
A
>EMBL_CDS:BAE96351 BAE96351.1 Homo sapiens (human) mammalian diaphanous homologue
GUGUUUAAGUCAUAUAGUCCCAUGAAGAGAAGUGUAUAAAGAUGGUCCUUUACUUCAUCGCAAC
AAAAGACUAGACGACUAAAACAC
>EMBL_CDS:BAG70269 BAG70269.1 Homo sapiens (human) MLCK protein
GGUGUAACUGGGACGGCCACGACCUCGGUUAAGGUCCGGUCAGGACUCCAAGAGCGACCCACAG
AGUCCUCGGAACCGAAGGUGGAAACACCCGUCCCCGUCCACC
>EMBL_CDS:BAD92391 BAD92391.1 Homo sapiens (human) Utyrosine-protein kinase transmembrane
GGAGGUACUUGGAGUGGCGUCUGUCCGACUAGAGAAACUCAACCCGGACAAACACGACCAAUUAC
UCC

>EMBL_CDS:BAD92390 BAD92390.1 Homo sapiens (human) formin 2 variant
AAGACAUCAUUAAGGUCAAACGCUACUUAACUCGUUUACGAAAGACUUUUACACCUGACCUUGUC
CU

>EMBL_CDS:BAD92083 BAD92083.1 Homo sapiens (human) Apolipoprotein B
variant
UUAGUAUGAAUUUAAGGUACCUCUUCUCUGUCAUCCAAAACUGAACCAUAAAGGUAAUUCAGA
ACGAACUUUAAGUAAGAGUUUUAAACCUUAAACCCGAAAACACCAA

>EMBL_CDS:BAD92195 BAD92195.1 Homo sapiens (human) protocadherin
gamma subfamily A, 7
AUAACUAAAAAGAUUAAUUUUCCAUCCAAAAGACCUUACCACGUCCAGUGGAGUGGUAAGAAAG
GUCUUAGAGACAGAACAUCAUCUJUUCUCGUUAC

>EMBL_CDS:BAE53437 BAE53437.1 Homo sapiens (human) C8orfK32 protein
UCCCCAAGUCGAGACCUCSCCAAGAAUAACGAUCUAAAAUGCAGUUACAUCAGUCGUGACCCCG
GACAGGUAGGAGACCUGGACCUGAGGA

>EMBL_CDS:BAD92137 BAD92137.1 Homo sapiens (human) hepatocyte growth
factor isoform 1
AACAUAAAGAAGAAAAGGAAACAGGGAGACGUAUCCCCUACCGCUACCCUCGUCUCCUCUACG
UC

>EMBL_CDS:BAD92305 BAD92305.1 Homo sapiens (human) ash1 (absent,
small, or
CAACAGUGAAAGUCUAAGAUCGAACGAACCUGAAAGUCACCGUUGUUUACCUCGGUGACUGUCAU
GUCCACCGAAGUAGAACUGACCACUGGAG

>EMBL_CDS:BAD92062 BAD92062.1 Homo sapiens (human) poly(rC)-binding
protein 2 isoform
UCCACCAGGGAGGUCCAGUCCCAACUCCGUGUACCUGCCCCACCACACCCCUUUCGAGCGUGACA
GCGACGGACACGACAUGGACAGGACUGGUGGA

>EMBL_CDS:BAD92359 BAD92359.1 Homo sapiens (human) glypican 1
precursor variant
CCAAGAGGAGGUAGAGCGACCACGUCGUCCACAUCGGGACCCUGUCUAGGCGUCCACGAGUGGA
CACCCCUUCCGGUCACACUCCCUUCCCCGA

>EMBL_CDS:BAD92458 BAD92458.1 Homo sapiens (human) hypothetical
protein FLJ41407 variant
CCGAGGAGGUCCACGAAGACAUCUGUGUCCACUCUCCAUUGUAGGGUCCGGGACCCUACCACCAG
AAGGGACCCGUCACUGGACACUCCCGG

>EMBL_CDS:BAD92438 BAD92438.1 Homo sapiens (human) WD
repeat-containing protein 3
CUCUAUGACGGUAUUCGGUAUCCUACCCCAACGACCCUUCACCUUGGAGAAAGGGACGUCGAAA
UGUUUACCGAAACACAAGGAAGUAAAAACGUCAAAGAA

>EMBL_CDS:BAE16982 BAE16982.1 Homo sapiens (human)
connexin43-interacting protein of 150
CAUCAUAAACCUGGUAGUCUAAAAGAAAGUUAUGACAUUCCGUUAACUUGUCAGACGAGAUUU
AUGAUA

>EMBL_CDS:BAD92206 BAD92206.1 Homo sapiens (human) KIAA0182 protein
variant

AGGAGGAGAAGGAGGAGGAGGCUCAGGGCCAGGUUGAGGACCCAACCCCCGGGAAGGAACGUCA
CCCCCGAGGACGACGGGUAACACGACCCACCUCGCCGCGCCGACCUCCU
>EMBL_CDS:BAD92022 BAD92022.1 Homo sapiens (human)
phosphoribosylglycinamide
AAGGUCGACGUUCUGGUGACCCGGAAGUGUUGUUUCGUCCCUUCAGACGUGAGUUUACUUCGAC
GUCCGAAGAAGUCCAAACCACUUUCGGAAGGUAACACGCCAACCCU
>EMBL_CDS:BAD92171 BAD92171.1 Homo sapiens (human) plexin C1 variant
CGACACUCUGAAAGUAAGAACAGCAACCGCAGAGACAAUACGUAUAGAAGUCACUUCUACACCCA
CUUCGGUGGACUGAGUCCCUUCUUUCAAGAGUCUCG
>EMBL_CDS:BAE46995 BAE46995.1 Homo sapiens (human) PPAR gamma
DBD-interacting protein1
CCGCACCUACCCCAACGGGAACCGGUGCAUCUUCACGGCGCUCUACUUCGACUGUUACCGCAGGC
ACGUCGCCAUCAAGAGCACCUUCUGGUCGCGCCGAGACGGCGCGG
>EMBL_CDS:BAF43710 BAF43710.1 Homo sapiens (human) hypothetical
protein
CCUCCGACAGAGGACGUCUAGUACCUCCUAGACGACAAGUGAAACUACUAUAGUAGUUACAAAC
UCUUGUCCUGUAGGUCUAGAGGGACCCGUUGACGACCUCCGCCGAGG
>EMBL_CDS:BAD92025 BAD92025.1 Homo sapiens (human)
Retinoblastoma-associated protein
AAGUGUUUCACAUAAAUCGGCCUCUAUCCGAUCGGCUAUGUGAAAAAAUAAUUUUGUCACUU
>EMBL_CDS:BAD92410 BAD92410.1 Homo sapiens (human) transducin
beta-like 3 variant
AGGACACUCGGACACCGGUCGUGCAACAGCAACCCCCGUUAUCGGUGCGACAACUACAGGAAUAG
UACCGUCGCGACUCACCAGACCCGGACGUCCU
>EMBL_CDS:BAD92113 BAD92113.1 Homo sapiens (human) axin 1 isoform a
variant
CGACUCCCGGCCGGGUCCCCACGAGUUCUCCUGUUCUCCAGACCUCAAGAGUACCCCGACACCGAAG
GAGCAGGGGCUUCUGGGCACCCGGCCAGGACGCCA
>EMBL_CDS:BAD92250 BAD92250.1 Homo sapiens (human) sorting nexin 1
isoform a variant
UCCUCCUUCUUCAGUAAACAACCGGACAAGGACCACCUCGACGAGUAAAAAAGAAGGUGGA
>EMBL_CDS:BAD92184 BAD92184.1 Homo sapiens (human) chordin isoform
a variant
CACGUGGAGAGGUCACGGGGGAACGUCCACGUCUGUCGUGUGAAUUAUUCGGUUUCCCCCGU
GUUGCCCCACGG
>EMBL_CDS:BAD92413 BAD92413.1 Homo sapiens (human) calcium channel,
voltage-dependent,
GUAGAGGGGUCUGACCUUGACCUCAAUAGCGGACUAAACGACCUCGGUCUCCGCCAAGACCGCGUCG
AAGACAAGGACGUCGUCUCCGACAGGUCAAACUGCCCCGACCCUAC
>EMBL_CDS:BAD92392 BAD92392.1 Homo sapiens (human) serine/threonine
kinase 23 variant
GGUGUGUGUCGUUCUACAAGAGCCCGAACUACAGGCACACCUACUAGAACGUGAACCACACC
>EMBL_CDS:BAD92189 BAD92189.1 Homo sapiens (human) colony stimulating
factor 1 isoform a

GACCCCCACACUAAGGUCAGGACCGGUCACCCGGAGUGCCCCGGGUGGGACCCGUUCCGACAUG
GUCAAUGUAGACGGCC

>EMBL_CDS:BAD92109 BAD92109.1 Homo sapiens (human) SUMO-1 activating
enzyme subunit 2
UGAAAAAGCCCCGUAGUGGUUGUUGAAGUUUAAGUUGCAGGAAAGGAUCCAGAAGUGAUACUUC
CUACAACUAGUUAUUUCAUAUCAGGACCUCCUUA

>EMBL_CDS:BAD92020 BAD92020.1 Homo sapiens (human) Oviduct-specific
glycoprotein
CCCAGUGUCUGACUACUGGGUGUCCCCAGUCCCAGAAAAGGGGUGCCCCAGUGUCUGACUAUUGGG
UGUCUCCAGUCCCAGAAGACAGGUCACCAGUGUCUAACUACUGGGUGUCCCCAGUCCCAGGAAGAG
AGGUCCCCAGUACCUGACUACUGGG

>EMBL_CDS:BAD92212 BAD92212.1 Homo sapiens (human) nuclear
transcription factor Y,
GACUAUGUCCGACCCGAUUCGCCUAUAUGACGUCGACCGGCCGUAAGUCGACGUGGCCCUAGACG
ACCUAGAGAGGACACAAUC

>EMBL_CDS:BAD92489 BAD92489.1 Homo sapiens (human) chapsyn-110
variant
GUUGUUCGUACACGAAACCUUAACCACUCAUGGAAGGACCUCUCUACCCACCGUCCCUCCAAU
AUAAGAUUUCACGGUAACAAC

>EMBL_CDS:BAD92053 BAD92053.1 Homo sapiens (human) calpastatin
isoform a variant
CGACAUCCGCUGGGUGUCCACUUCAGUCUACUGUUCGCAGAUUUCGUAGUAGACCGGGAUACCC
AAAUCGGUUAUCA

>EMBL_CDS:BAD92377 BAD92377.1 Homo sapiens (human) son of sevenless
homolog 1 variant
GUCUCACUCCAACCACCAUACAGCUUAGUAAAAGUCUUCUAAUCCUCUCAAUUAAGAAACAGAA
GAAACAGGUGUGUGAAGGUUGAUUAAGAC

>EMBL_CDS:BAD92110 BAD92110.1 Homo sapiens (human) PUPL1-associated
RhoGAP 1 variant
CUCAGUCACAAGAAUUGUCGUGCAACAGAUCAAGAUUCCCUUUUUAAGGAAAAAGUGACCU
ACUCAGGUGACUAAG

>EMBL_CDS:BAD92177 BAD92177.1 Homo sapiens (human) hypothetical
protein DKFZp434B216
GUCUUCUAUUUAUGACUCCACCUUUUCAACUUCGAGGUUCCGGUACAGAAGUCAUAUAUAAAAG
AC

>EMBL_CDS:BAD92356 BAD92356.1 Homo sapiens (human) eukaryotic
translation initiation
AUCCGAAGGUCCUAAGACCAAAUUUACCUUUACAUUGGGGUAGUGGUCUUGAUAGACACCUCGGA
C

>EMBL_CDS:BAD92300 BAD92300.1 Homo sapiens (human) Polyhomeotic-like
protein 1 variant
GAUAGACCCCGGCUCUCGACGGGGACUCGAUCUUGAGGGUAACCACCUUAACCUCAAGACGAGC
GAGAGUCAGAGGUACUAUC

>EMBL_CDS:BAD92412 BAD92412.1 Homo sapiens (human) collagen, type V,

alpha 3

GUUACACCGGGAAAAGGGGGAACCCCGGUCACAGAGGGAAGUCGGGACCCUCCGGUCUCCCGGGG
UCCCCCGGUCCUCCCGGUAGAC

>EMBL_CDS:BAD92396 BAD92396.1 Homo sapiens (human) Uhyroglobulin
precursor variant

UGGUACAUCGUCGUCGGAGCUGCGCCCGUAGACUCAGGAGCGGUGGGUCUCUUAAGACGUCACGG
ACCAUUUCCGACAAAACGAUGACCA

>EMBL_CDS:BAD92334 BAD92334.1 Homo sapiens (human) KIAA0367 protein
variant

AAUCAACAAACGUAAAGGAUAAAGACUCAAGGGUGAACCACACACAAUAUUACUCGAUCGU
CUUCACUGAACUACAUUCGUUCACU

>EMBL_CDS:BAD92066 BAD92066.1 Homo sapiens (human)
G2/mitotic-specific cyclin F variant

CAGGUCCCCAACGUCCUAGACCCACAGGUCGCGGUCACGGACACCCAGGACCCAGGGAACAGG
AGACCU

>EMBL_CDS:BAD92357 BAD92357.1 Homo sapiens (human) AUP-binding
cassette, sub-family C,

CCUGGACAUUAUACCAAGGAGGUCGACUGUAGGUUUUUCCUACAAAAGAGCCUCUCUAGUAAGA
CUUAGG

>EMBL_CDS:BAD92101 BAD92101.1 Homo sapiens (human) flightless I
homolog variant

GCGACCCACGAGGCGUCCACGUCCAGACGUCCCGGCAGUAGCGACCCUCGACGGCCUCGACACG
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>EMBL_CDS:AAC04305 AAC04305.1 Homo sapiens (human) R29144_1
UGUCGCGUAGUGGUGGUGGUCGUCGUGCAUCAAACAGGUCCUACCCAGACCGAGACGGCACCCC
GCAGGUCACCGUAACAGGGUGCUGCAGCAGUCCGAUGACACCGUCACCACCACCACCACCA
CCGCCGACA

>EMBL_CDS:AAC24313 AAC24313.1 Homo sapiens (human) Unknown gene
product

CCCUACAACACUCCUCGUACUCCUACGACUCCCGGGCCCCGGUCACGAGUUACAUAACCCUAGUC
GUAAGAGUCAGACCAAAGGUGACGUAGGG

>EMBL_CDS:AAS07423 AAS07423.1 Homo sapiens (human) unknown

UCCCUUGAGGUGGUCGAUGUUCUUCGAAAACGACAGCGUAAACAAGAAAGUUAUUUUUACGACG
UCCUCUCGGACCACCGACGACAACCCACCGAAAGGGA

>EMBL_CDS:AAC07983 AAC07983.1 Homo sapiens (human) P1.11659_4
CUCCCAGGUUAUUGUGGGUACCGGACUCGGUGGUACGACCACUGUAGCGGUCCCAACCUCCCGU
CAUCCUAUCACAACCUCAGGAA

>EMBL_CDS:AAS07390 AAS07390.1 Homo sapiens (human) unknown

GGGACUUAAGUCCUACUACCACUCGUCCACGACCCCGUCCUCCACCACCAAGAGAUUCGUGGACU
UAAACUCAGUAGGACUUAUCCC

>EMBL_CDS:AAC08453 AAC08453.1 Homo sapiens (human) KIAA0324
AGGUCUAAAGUUGUAUCCUGAGCGACUCUUGAGUGGAGAUAGAACAGAAUAACCUUAGACCU

>EMBL_CDS:AAB94785 AAB94785.1 Homo sapiens (human) pNORF1
ACGUAGGACAGUUUCCUCCAGCUGAAGGUGUGUUUUAGGUGGACCUCAACACUCAGUGGAGGUG

UCCACGU

>EMBL_CDS:AAC32592 AAC32592.1 Homo sapiens (human) APXL
UCCAGAGGACCCAACCCCAGGUUCAGCGCCGCGAACUUCUGCACCAGGAGUCCUGGGCCCGAAC
CCGGAGAAAGUCCACCAGA

>EMBL_CDS:AAC15789 AAC15789.1 Homo sapiens (human) Notch 3
GUCCUGGGCCCGAUCCUGCCGUGACCGGAGGUACGACCGUACCGACCCUGAGCGUCCUCUGUCC
UGUCAGACUGUCGCUCCUGGACUCUUCGGUCGUACUGUUUCGUUGCCUUUGGAGGCGGACCCAG
GAC

>EMBL_CDS:AAC08455 AAC08455.1 Homo sapiens (human) R30385_2
ACACUUUCCUCACCACUUUUGCUUUCGGUAAGGGUGUACCGAAUGUACAUAUACGGAAGACAGAU
GUAAGGACUAUAAGUGU

>EMBL_CDS:AAC08447 AAC08447.1 Homo sapiens (human) CBP
CCCAAACACCGGGGGUCCCUUCAGCCUUCUGGACUAAGACUUUAGUUCAAACCCCGACGACUAG
A

>EMBL_CDS:AAC27426 AAC27426.1 Homo sapiens (human) Untranslation
initiation factor
CGAGCCCCAAGACGAACAUCGAACACUAUACCCUGAGCUUAGUGCCAACAUA AAAAGCCUAGAAG
ACUGCGUUCACGAGUCUCGGAACCG

>EMBL_CDS:AAD03158 AAD03158.1 Homo sapiens (human)
immunoglobulin-like transcript 10
CGGGUCUCCGACCCAAACCCUCCAGGGACGUUCACGAACCCGAAAGACCGGGUCUGAGUCGGA
CUCCG

>EMBL_CDS:AAC97987 AAC97987.1 Homo sapiens (human) SN24_HUMAN
CCGCCUCCCCGUCACACCCGCUUCGACCGUGACGGCGACGGGCACGACGUCACAGACGAGAGUAG
GACGAGGAGCACGA

>EMBL_CDS:AAS02034 AAS02034.1 Homo sapiens (human) unknown
AGACUGCCGUUCCGUUUACAUGUUCUGACGACCUUCCCGUCCUGGGCCUCGAGUCGUGAACUUA
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>EMBL_CDS:AAS46897 AAS46897.1 Homo sapiens (human) unknown
GACCCGACGCACACAAGGCGACGUGGUCGACGACCCGACGUAGGACAAGUCUACCGGAGUCAC
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UCGUGCC

>EMBL_CDS:AAC33490 AAC33490.1 Homo sapiens (human) F20887_1, partial
CDS
CCAAAGACCUCGGUGACUCGGUAAAUCGAGGUACACCCAACCGGGCAAAAACCACCGGCACCGAG
GUCGUUGG

>EMBL_CDS:AAQ96886 AAQ96886.1 Homo sapiens (human) unknown
CGGUAGACCCGGUAGUCUGGACCGACGGCCCCGCGUCGUCGUUCUUCGGUUGACGUCUACCCCC
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ACCG

>EMBL_CDS:AAC62835 AAC62835.1 Homo sapiens (human) R33374_1
CCGAGCUCACUAAGGUCUGGUCGUCGAACAACAGCAACGGGGGGCUCGCUCCUCGACCACCAGA
CACCUGGUGAACUCGG

>EMBL_CDS:AAC24489 AAC24489.1 Homo sapiens (human) H53_GS1

GUCCUGAACGUCAGUUCGACCGGUAAGACCACAAGGACAGGUUGAAGGGUUUCCCGGACUACG
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>EMBL_CDS:AAX82033 AAX82033.1 Homo sapiens (human) unknown
CCAGGCGGAACCUAGGGUACUCCUACUCCUCCGGGAACGUAAGGAGACCCUGGUCCACCAGG
>EMBL_CDS:AAC33801 AAC33801.1 Homo sapiens (human) R26984_1
CCUGUCGAGACCGUCUCCGAUCGGCGACGAGGAGUAAGAGACACGAGCCCUACUUGUCCCGGCC
CCUCCUCCUGCUCGACCUCGGUGACGACCCCGGCCAGG
>EMBL_CDS:AAC25582 AAC25582.1 Homo sapiens (human) ubiquitin-52 amino
acid fusion
CCGUUCGACCGCCUCUCUUCGAGUUUUACGGUGGAGCGUCCGCGUUGUGGUCCACGUCCCACC
UGAGAAAAGACCUACAACAUCAGACUCUCUCACGCCGUAGGAGGUCGACAAACGG
>EMBL_CDS:AAC23434 AAC23434.1 Homo sapiens (human) hypothetical
protein
GACGGGAGAGGGGAAGUAGACAAAGGCGACGAGGAAGACCCGGACGAACCCACCGAACCCGAACC
GAAACCUCGGUCCUCCCCCGUAGAUCSSCGUCCGCCUACCUACCACUCCAACAUCSSCGUC
>EMBL_CDS:AAD30180 AAD30180.1 Homo sapiens (human) hypothetical
protein
GGUCCGUCCCCGACCGUAGUCCUCCGGAACGCCACACCCUCCAAGACGAAGGAGAAGGAGAGAG
CCCGGAAGAAACCCGUCGCACCCGACUGGGGUCGAACGCGUAACGGACCGUGGUCUCCUAAGCCC
CUCUCUGUGUACGGAGCCUGUUACCAGAGGUGAGACCCGGGAGAAACGGACC
>EMBL_CDS:AAC62840 AAC62840.1 Homo sapiens (human) R33083_1
CCCCGCGGAACAACUGUUACUCCGGGCUCAUGAACGCCGACGGCACCUACUACGAGGCCUCGGGC
AGGGUGCUCACGAAGACGUGGACCUUCGCCCGCCGGCCCAGUAGACACCCGCCGACGCAGCGGAGC
CAGCCGGCAACCCAGGG
>EMBL_CDS:AAS00377 AAS00377.1 Homo sapiens (human) unknown
AAGUCCUUUCCUAACCCCUACCGGCCGUCUCUACUCCAAGAUUUGACGACCAGAAGGAGGACUU
>EMBL_CDS:AAC71655 AAC71655.1 Homo sapiens (human) hepatocyte growth
factor
AGUCCGUUCUUAACACGGCCACACCACAGACUACUAGGGUCGCGACUGUUUAGAACGGACU
>EMBL_CDS:AAD11988 AAD11988.1 Homo sapiens (human) BC85722_1
CGGCGACCCUCGGCGACGGAACCAGGGUCCCCGACCACGACCCCGUCCACGGUGGACUUCGACGA
CCCCGUCGCACCCGUCCUACAUGACAUGGACCCACUAAGGGGGUCGGAACGGGUCCCGUGGACCA
ACGUCCUACGGGUCCCCA
>EMBL_CDS:AAC62261 AAC62261.1 Homo sapiens (human) neuronal apoptosis
inhibitory
AAACCUCUUUACCGUUUAACCCUUUUGUAGACCACACUAGCAGAUUACCCAGUAGUGGAAGGACG
GUAAAGAGAUUU
>EMBL_CDS:AAC24305 AAC24305.1 Homo sapiens (human) R31449_3
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CACACCCACAGGU
>EMBL_CDS:AAC18916 AAC18916.1 Homo sapiens (human) Acetolactate
synthase
UUGGACGACGCCCUUCGGACCCCUACAGGUCCCCGUCGCCAGGGAGCCCGACUCCGAGGGUCC

GAGGACGJUUCUCCAA
>EMBL_CDS:AAX88848 AAX88848.1 Homo sapiens (human) unknown
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GAAAGUCUCGAAGAAAGUGAUUGAAAAAGUCUAGA
>EMBL_CDS:AAX88914 AAX88914.1 Homo sapiens (human) unknown
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UCCU
>EMBL_CDS:AAX93134 AAX93134.1 Homo sapiens (human) unknown
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UCGUCCUUCGGUAGGUCCUCUACAGUUAGUAGAAGACGUCGUCGGCCGUCCGGAGCUUCUUCAU
GUGCAUGA
>EMBL_CDS:AAD23604 AAD23604.1 Homo sapiens (human) DYN2_HUMAN [AA
474-870]
CGGCUGAGGAGGUACUCCGACGAGACCAGACGGCUCUCAUAUCCAUCCGGUCGUCGAGCACCAC
CUACUCCG
>EMBL_CDS:AAD19817 AAD19817.1 Homo sapiens (human) Human homolog of
Mus musculus wizS
CGGGUCCAUCGGUCACCGACUCCCGAACCGGGGUCACUACCCGCAGUCCGACUCGAGUGCUCUU
GGACCCG
>EMBL_CDS:AAD21217 AAD21217.1 Homo sapiens (human) Putative map
kinase interacting
GUCCAGGAGCAGCAGACCCCGUCGACGGCCAAGUACCGUUACCGGAGUCGGCGCUUCCUGCAC
>EMBL_CDS:AAY24351 AAY24351.1 Homo sapiens (human) unknown
CUCCACGUCCUGGUUCUAUUAGUCCUAAUAGUGUACAAGGUUAUAUAUCGUUAUGUGACUUACCA
AAACAACACCCUAGAAAACCUAUUUUUUACUGACAACACCAAGACAUCGGAG
>EMBL_CDS:AAX93195 AAX93195.1 Homo sapiens (human) unknown
CUCAGAACCAACUACAUAUAUACUCAGAACUCCGUCACACUAAAGAAAGACGUAACGUAACGA
CAUUGACUAUAAUGACGACGAUAAGACAACGUUACAUAACAGAAGUAGACGGUCCUGAG
>EMBL_CDS:AAD39266 AAD39266.1 Homo sapiens (human) Human Fc gamma BP
[AA 1-2843]
CACCGGGACACCCCGACCUCUCCUCGGGUGUCUUGAGGAGGAAGACUAUGAAGAAGAGGUCGAGC
CCUCCUGUG
>EMBL_CDS:AAX93216 AAX93216.1 Homo sapiens (human) unknown
CACCCAGACCAACCGGAGAGUGAACCCACAGAACUUUCAUCUCCCGAUUCUUUUGGGUCCACUCU
CCUUUGUAUAGGUA
>EMBL_CDS:AAY14753 AAY14753.1 Homo sapiens (human) unknown
GACCUCGGUCCUUCCAAUGGAGGCUGGCACCAUCCUGACCGUUGACCCGUCGGUCCCGAGAAGAA
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>EMBL_CDS:AAX81988 AAX81988.1 Homo sapiens (human) unknown
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>EMBL_CDS:AAX88939 AAX88939.1 Homo sapiens (human) unknown
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>EMBL_CDS:AAY14651 AAY14651.1 Homo sapiens (human) unknown

CACGUGUAUCAGUAUCACCAUCUGUCGCAGUGAAUCGACAAAGGGUGAAAACUGUCGGACGUG
>EMBL_CDS:AAF03518 AAF03518.2 Homo sapiens (human) unknown
CAACCGAGGUUCUACGGUUCGGGUACGGUGGGACAAAGACCCCAUGAGACCUCCCGGUGACGAAU
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>EMBL_CDS:AAY14751 AAY14751.1 Homo sapiens (human) unknown
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CCGGGUCGAGUCCCGGGGACGUGUUAGAGGGACCGUGGACCGGAGGACGUCGUCGA
>EMBL_CDS:AAD23606 AAD23606.1 Homo sapiens (human) R31665_2 [AA
1-673]
UAGGGUCACAAGGGGAUUGUCUCUCAUGAGGUCUAAUAUCGAACACUCAGAGAGACAAUAGUGAC
GGACCCUA
>EMBL_CDS:AAX93132 AAX93132.1 Homo sapiens (human) unknown
AUCGCACCCUACAUGUUUGAAGGACAUGUCCUCCGACCUCGGAAAACACAUCCUUCUGUCGUCGG
UCCGAU
>EMBL_CDS:AAC68599 AAC68599.1 Homo sapiens (human) cell
cycle-regulated factor p78
CCCACCACCGUGUCCUCACGACCCCGAAACCUAUGGAAGAAGAAGAGUGACCUCCUCCCAAG
UGAGGGGCUUGUCGCGGGACCAAGGUGGGGUGACCGGG
>EMBL_CDS:AAC64294 AAC64294.1 Homo sapiens (human) PKY protein kinase
CUUUUUUACGACUUACACCCUUAUACCAUAAGACAUUACUAAUUGAGGUUGACUUUCGUAAAAU
AAG
>EMBL_CDS:CAB22795 CAB22795.1 Homo sapiens (human) hypothetical
protein
AGUACACGAACUACUACUAAAAAGAACGGGUUCCAACACCUGUCCUUCUGUUUCUCACGUACU
>EMBL_CDS:AAC97080 AAC97080.1 Homo sapiens (human) lambda 1
immunoglobulin light chain
AAACCCCGCGGAGGACCCUCUACGACCAUGGUCCAUGUCAUAAUGAAGGCUACAACCUCGACG
AAGGUCU
>EMBL_CDS:AAD17540 AAD17540.2 Homo sapiens (human) nectin-like
protein 1
CGAGGUUUAGGACGAGGACGGUCAUCGGCAGGACCCUCUCCAACCGGGGCGGCCCGGGUCGUC
GUCCGCUUGUCGUCUCCUGUCCUCGUCUCCG
>EMBL_CDS:AAC16813 AAC16813.1 Homo sapiens (human) immunoglobulin
lambda light chain
UCACCGACACAGGGGUCUCUACCUCGGUCUCUUAGCGAGUCCCUAGGGACUCCCGGCGAACAGUA
AAACUAUCUACUGGUAGUAUCCCUUGACCGGACCGAAGACAACUUUGGUCAUUCUAAAAUAGG
AGGUUAAAUAGAGGACUCGUCCACUACGACCGACAGACAGGACCCUGUGCCUGUGA
>EMBL_CDS:AAC39660 AAC39660.1 Homo sapiens (human) retinal pigment
epithelium-specific
AACUGCUCCGGGACUUUUCUCUUGAAGUCCGAGGUCGGUCUAUCAGAGCAGUGACGUGUCUUAAC
GUCACCGUCAACAUAAACCCUCCGCACUGAUUUUAGAACGGACACAGUCGGAACAGUU
>EMBL_CDS:AAC39892 AAC39892.1 Homo sapiens (human) RNA polymerase I
40kD subunit
AUGUCAAGCAACCCAGUCUCCUUGAAGUCCGAGGUCGGUCUAUCAGAGCAGUGACGUGUCUUAAC

UGC UUUGACAU

>EMBL_CDS:CAB23081 CAB23081.1 Homo sapiens (human) hypothetical protein
AGUAGACACCCCCUGUGUCCCCGCCGGAGUCUCAGUGGGCAUCGCCCCUACCCCGUCGGAGUCAC
AGUGGGUUCACC

>EMBL_CDS:AAC18086 AAC18086.1 Homo sapiens (human) diphthamide biosynthesis protein-2
CCCCGUGGGAGUAGGACUCAGAAGGGACAUAGACCUGUCGUCCUCCUCUUCCCAACUGGACCACGG
G

>EMBL_CDS:AAC79696 AAC79696.1 Homo sapiens (human) MRP6
CAACUCCUACAACUCUUGACACUCUCAGUGUUUCCGAAAGAGACGUAAGUAUCGUAAGAGCCG

>EMBL_CDS:AAL86699 AAL86699.1 Homo sapiens (human) alpha 1 type XXI collagen precursor
CUAGGACCUUGUGGACCACAGGGACGUUAAGGGACUAUAGGUCCGAAUGGUAGAACUGGUCCAAC
AGGUCCCAUCGGUCCCAAGGGUCCGUCAGGUCCCAG

>EMBL_CDS:AAQ05538 AAQ05538.1 Homo sapiens (human) Ig heavy chain variable region, VH3
CCCCGCACAGAAGCCGAAGGUCUGACAAGUCAACGUCUAUGUCAUACAAGGACCUUAAACAGAGAC
CUCCACCACUUGGCCGGG

>EMBL_CDS:AAM43838 AAM43838.1 Homo sapiens (human) U-cell activation WD repeat protein
CUGUUCUUCACCGAGAGAUACCUCUUUACAGUCAGGCCGUUAACGACAUCUCACACGUAAAGAGU
AAACCAACUAAUUAAAAAACAG

>EMBL_CDS:AAL67806 AAL67806.2 Homo sapiens (human) esophageal cancer associated
CUUAAACAAUGUAAAGUCCUACCUACGGAGGUGCAUUUUAGAACCUUACUCAAGGGACUACCUCC
GUUAGAACUUUUUGGUUAAA

>EMBL_CDS:AAK27221 AAK27221.1 Homo sapiens (human) junctional adhesion molecule 3
UAGGCACCCGUCACCAUGUAGUAACGCUAUGGUCGACAUCACUCCGGCCCCCACC GGGAGUGAGA
GGACCGUCACGUCACAACGGUAGAACGGAUGACCA

>EMBL_CDS:AAM77566 AAM77566.1 Homo sapiens (human) IL-17D
CGGGACAAACAGCUACGACCUCAACUACGACAGACGACGAGGAAGAGGCCGAGCCCCUGCGUCCACG

>EMBL_CDS:AAK74120 AAK74120.3 Homo sapiens (human) mucin 16
CCAUCUCUCGGACCACUAGUGAAGUCACCUAUACAGAACACUGUAACACCUGACUAGUCCCGAUC
CAGGAGACGA

>EMBL_CDS:AAK68033 AAK68033.1 Homo sapiens (human) DNA methyltransferase 2f
ACGGUUCUCUCCAACCUCUAUUUAUUUGAGAACCAUGACUUUCGGUGUUAAAAGAUACAAACA
UAGUUCUCCAGAAAGUUAGCAGAACCGU

>EMBL_CDS:AAP97715 AAP97715.1 Homo sapiens (human) excision repair protein ERCC5
AAAAGUGAAACCACAGUACUCCUAAUCCAGAAUAGAAACCUAAAAAACUCGAAGUACGGUGGUA
AGACUCUU

>EMBL_CDS:AAM12641 AAM12641.1 Homo sapiens (human) regulator of G protein signalling 3
CGGGGUGAACUCCCGAAGGAGACUCCACCCGAACUUACUGAAGUAGUAAAACAGACGGAACGGGC
GCCCUCCCCG

>EMBL_CDS:AAK96045 AAK96045.1 Homo sapiens (human) testicular soluble adenylyl cyclase
CAGAAGUAAAAACAAUUUUGCACCAGUUUCUUUAAGUUCUAGAAAAGAGAAUAAAGAAGUCCUGA
CGCUAAAAGUCCUUUUUUACGUCUA

>EMBL_CDS:AAL77058 AAL77058.1 Homo sapiens (human) multivalent protease inhibitor
AGUCCGUGAGCCGGCGGCCUUUCGGCACGGUAACCCCGACGAGAGACUCCACCGACGUCGGACU

>EMBL_CDS:AAL08625 AAL08625.1 Homo sapiens (human) hematopoietic zinc finger protein
CCCCUACCCUCGGUCCGACAAAGAGACCCCUAGGACCCCGACCGGGGUCAGGUAAGAGGUACCU
UUGACCUGCCCCACGAUGUGGUAGGGG

>EMBL_CDS:AAL65133 AAL65133.2 Homo sapiens (human) ovarian cancer related tumor marker
CAACAGUGACUCAGUCGAUCCUGUCUCCUUCUUAAGUACACAUUUGGACUCCAAUGGUGUAA
CCAGUAGAGGUCAAAGAGACAUAGACAUCACUGAAGUCACCACCG

>EMBL_CDS:AAL24502 AAL24502.1 Homo sapiens (human) deleted in azoospermia 2
GUCCGUUGACUAUAGGUCACCACUGGACUUUACCACUUGAACCUAUUCGUCCUUUACGGACUAUU
AAUUAUUGUCCGUUGACUAUAGGUCACCACUGGACUUUACCACUUGAACCUAUUCGUCCUUUACG
GACUAUUAUUAUUGUCCGUUGACUAUAGGUCACCACUGGACUUUACCACUUGAACCUAUUCGUC
CUUUACGGAC

>EMBL_CDS:AAK27358 AAK27358.1 Homo sapiens (human) Bcl-Rambo
CCGAAGUCUUUAAAGAAACAGGUCUCUAAAUCGAGAAGAAGUUAAAGUCAAAAUUGAAAAUUUU
UUUAAAAGAACUAGGUCUCUAACACUUCGA

>EMBL_CDS:CAC15059 CAC15059.1 Homo sapiens (human) putative protein kinase
GACCCAACGACCAUGACAUCAACAACUACAACUAGACGGAGUCCAAGAAGUCCAAGAUGAACACA
UCUUUGACUUCGACUUCACCAUCUUCGUCAUCCAUAACGGCCACGAUCGUCUUC

>EMBL_CDS:CAC10401 CAC10401.1 Homo sapiens (human) CDC2L5 protein kinase
UCGUACCCUCCGUUUCCAUUGCCACCAUUAACAUCUCCACUGAUUUUGAUGUACAACGAGGAAGAG
GAACCGAGGAUACGA

>EMBL_CDS:CAB65596 CAB65596.1 Homo sapiens (human) peroxisomal branched chain acyl-CoA
GAAUGACGGUGUACACGGGUCCGGCACCAUCUCGAGGCCCGUCUCCUUCAGCCGACGGGAGAC
CCGACCUUGGACCGGUCCAGUCCACGCCACUC

>EMBL_CDS:CAA06213 CAA06213.1 Homo sapiens (human) integral membrane protein, Ump21-I
CCAGGAACACUUAAGAGGAGUGCCUCCGUGAACGCUCUCAAUUACCCGUCUACCUUCCUCUACCGU
UCCUGG

>EMBL_CDS:AA062630 AA062630.1 Homo sapiens (human) transforming acidic coiled coil 2,
CCGUCACGAGUCAGACUCCUCCGGUGUUGAGUUUCAUCGAAGAGGUCCAAAGAGGCCUCGGACG
ACGAAAGGACCCAGAGGACGUGGUCGCGACGG

>EMBL_CDS:CAC00640 CAC00640.1 Homo sapiens (human) rhomboid-related protein
CAGGUCCCCGUCGAGUACCGACACGUGGUCCGGUCACUCCACAGGCGUGGCUACUUCGGACACA
AGAGCCCCAGGUCGACGACGAGGACCUA

>EMBL_CDS:CAC34245 CAC34245.1 Homo sapiens (human) U-cell receptor beta chain VJ
ACGACGACAGAAGUCCCGAGUACAACGAGUGUCAGUCUCAACUCUUAACAAUCCAAACCCGCCAAC
UACCCUUUGAACAGUUACUGUUUAGGUGAGAGUAUACACCGGAGUCUCGGGACUAAACGUCAACG
C

>EMBL_CDS:CAC17609 CAC17609.1 Homo sapiens (human) importin7
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>EMBL_CDS:CAB65100 CAB65100.2 Homo sapiens (human) NICE-4 protein
CAUCGUUGACUCGAAGCUCAGCUCCGACACUGUCACCUCAACGACGGAUCCGACUCCGGGUCCGA
UG

>EMBL_CDS:CAD24023 CAD24023.1 Homo sapiens (human) putative alpha 1,3-fucosyl
ACACCCGAGACCCGUUGAGUCCACCCAUAGAAGACGGAGGGUAGAAAACCCACCAUUCGGGAAAA
GGACUUCGGACUAUAAUCGGGUGU

>EMBL_CDS:CAD58724 CAD58724.1 Homo sapiens (human) NOSURIN protein
ACGUCAAAGAAGGUAUUGUCGGACCUAUGAAAAAGUUACAGUUAGAACGACUACCGUGUCACUU
AGACGCACACCGUACACCAGUCCCAAACCGUUUUUCUCUUUAUACAACCGACAUGACCAAUUC
AAUAACGU

>EMBL_CDS:CAF25192 CAF25192.1 Homo sapiens (human) Xin A
CCACCCGGACCCCGGCACCACGACUCCGGUACAACAUCGACCCGACCGAUACAGGUGACCCUG
UAGACCGGUCUCCAUAACACCGGGACCAGAUGUCAUCACCCUUGGAACCGACCGA

>EMBL_CDS:BAC04859 BAC04859.1 Homo sapiens (human) hypothetical protein
AUACAUAACACGUGUCCACGGACACGUACACAUGCACACGCGUAUCUGGACAUACAUGUAGACA
GAGGUACAUGCAUACAGACACACACCGUGUCUACGCUAUGACGCCACGUAGACGUUAACACACG
UGUCCACGGACACGUACACAUGUAC

>EMBL_CDS:BAG53993 BAG53993.1 Homo sapiens (human) hypothetical protein
CCAAAGGAAUCAACAUAUGUCACGACUUCAUACCAUAGUAUCAUAAAUAUUAUUGACCACUUU
GG

>EMBL_CDS:BAC85326 BAC85326.1 Homo sapiens (human) hypothetical protein
CCGGGACAGAGGGUUGGGAACAUGGUCACGACCCGAGUCUGGGACCAUGUCCGGACCCCUGUCC
CUGG

>EMBL_CDS:BAB55198 BAB55198.1 Homo sapiens (human) hypothetical protein

CAGUGACUGAGCCCCAAACCCAUCGAGGAGUAAAAGGCUUAGUGACCGGACCAAGGAACCCCUA
GGAGUGAAAGGCUUAGUGACUAAGCCCCAAACCCUUCGAGAAGUAAAAGACUCAGUGACCG
>EMBL_CDS: BAB15388 BAB15388.1 Homo sapiens (human) hypothetical
protein
CGACCACAACGUCCCGAAGAGCACACAUACGACGACGUCGGAGACCCGACCGUGGUCGUGGUCCG
ACUCGGACAGGAACCCGUGGUCGUCGAAGGUCCUCUUCAGUACGUCGAGGUGUCCG
>EMBL_CDS: BAC11516 BAC11516.1 Homo sapiens (human) hypothetical
protein
CCCACUCCGCGGGAACAUGUGUGACAACGAGUCGCGGAGAGGCGCGACGUCGACCUUCUUCGACA
ACUCUAUCGACCUCACGUCCCCGUCGCGG
>EMBL_CDS: BAG53483 BAG53483.1 Homo sapiens (human) hypothetical
protein
UACAUUGAGUCUCGUCAGAGGUUCAAUGAUGGAAGAAGACUCCCAAACCUAAAACACUAGAGAC
GACCUGUUCAACGUA
>EMBL_CDS: BAG52312 BAG52312.1 Homo sapiens (human) hypothetical
protein
CCCUCUUCAGUCCACCAGGGACGAGGACUGUGAAGACACCUCCUACCGCCCCUACCGUGGUAGA
GGA
>EMBL_CDS: BAG51468 BAG51468.1 Homo sapiens (human) hypothetical
protein
CCUCGAGGGACCCUCACGGGGUCUGGGUUGGGUCGGUAGUGACCCCGAGACCCCUUGUGACAACGG
ACCCUGACCCGAGG
>EMBL_CDS: BAC87399 BAC87399.1 Homo sapiens (human) hypothetical
protein
CGGAAAAGGUGUAAGUGAUGUAUAUAUUCGAAAAGAGGACAUACUCAAAGACUACACAUCACU
CUGACUUGAAACAUCUCUCCG
>EMBL_CDS: BAG54552 BAG54552.1 Homo sapiens (human) hypothetical
protein
AACGAUGAGGUACCCACCUAAAAGUACCGCUGCGGAACAAUAGAACCAAUAACAACGGUAUCCU
GAAAGGUUUCGUGGUGUACCAAACCAU
>EMBL_CDS: BAG51912 BAG51912.1 Homo sapiens (human) hypothetical
protein
CCCCUCUCUAGUAACCGUCGUUCUAACGCCGUUGUCGGUCAGACUUCGUUGCGAUCACAGAAAGG
GG
>EMBL_CDS: BAB15349 BAB15349.1 Homo sapiens (human) hypothetical
protein
CCGAGGGACCAGUUGAACCCUACGGGUCUGGUGACACCCGACCCCUUGGUAGCCCCUCGG
>EMBL_CDS: BAB14766 BAB14766.1 Homo sapiens (human) hypothetical
protein
CAGGAGGAGGUCAUGGACCUACAUCCCCGACGAGGACAGGUCGAAGGGGAGGACCUGCCUCCGGA
GGUCGAGGACGUGGGCCCCGACCUCGUCCG
>EMBL_CDS: BAB15157 BAB15157.1 Homo sapiens (human) hypothetical
protein
CGCACACACACAGUACACACGUCAUCUUCGAGUAUGCAGAGAGACGACACGUAUGUGCACACA

>EMBL_CDS:BAC86835 BAC86835.1 Homo sapiens (human) hypothetical protein
UUCGUACCCCAUAGGACGUAUAAAUAUUCGACAUUUAGAAGAAUACUGCCAACUUCUCCUACG
AGACACAAA

>EMBL_CDS:BAG53471 BAG53471.1 Homo sapiens (human) hypothetical protein
GAACGGCACUUACCGCGGCUGGUACGCGAGUUAGAGGAAUCCCCUCUGUCCGGAGUAGGACGAGA
CGAGGACCUCUCCAACCACUGCACGCACCACUUGAGUGCUGUCC

>EMBL_CDS:BAC86126 BAC86126.1 Homo sapiens (human) hypothetical protein
AACCACGUAGGGAGCCAAAAGGACCGGUCCCGUUACCGACGCUACGGACCAUCCGUCUACCGACC
GGGCUACCGGUCCUCCCCUACAAAGGGUU

>EMBL_CDS:BAG51766 BAG51766.1 Homo sapiens (human) hypothetical protein
UUAUAACGUAAGAGGAGGAUUAAGGUGGGUCCCGUGACACUCCUAUCUGGAAGGUAUCGGUAACC
CCUACACUCUUAACAUUACAA

>EMBL_CDS:BAC87609 BAC87609.1 Homo sapiens (human) hypothetical protein
CCUCUACGUCGGCCUCCUUCUCGACCCGGGCCUCCCCCGGGCCUCCGACGUUCACCCAGACU
CUCCGGUUGAACUCCUCCGGACCGGAGACGGAGGGCGUAACGGGUCGACAAGGAGGACCGACGUA
GAGG

>EMBL_CDS:BAG51223 BAG51223.1 Homo sapiens (human) hypothetical protein
GUCUCGUCAUUCUUCUGUUGGUAGAGACUCAGAGGUCUCGAGGAGAGACGUCCUCCAGACCCA
GGAGCCCGUGACCCUGGAGCGAGAGGACGUCCAGACCUCGAGGAGAAGGACCACACCUGCGACG
AGAC

>EMBL_CDS:BAB70820 BAB70820.1 Homo sapiens (human) hypothetical protein
AAGACCCUAUGUAAGACCAACAUUACACGGGUGACUACAAAGAUUCCACCUGUCUACGUAAA
CGUGGCCUAUAGAAGUCUU

>EMBL_CDS:BAA92130 BAA92130.1 Homo sapiens (human) hypothetical protein
UCUUCAACUCCCAUUUUGUACAAGUAGUAAAAACAGAUUCAGUGAUUGUCUACAAUUCUACCGU
UUACAAGUGGGAGUUAGAGA

>EMBL_CDS:BAG54675 BAG54675.1 Homo sapiens (human) hypothetical protein
AGGAGGUCCCUGUCCUAUAGUGAGAAGAGGAAGAGACCGACCCGUCGUCAAACGCCUUGUGUAA
GGACACAGGCACCCGACGUCGGACCGACUUUCUCAAGUAUAGUGGGACCCCC

>EMBL_CDS:BAD18708 BAD18708.1 Homo sapiens (human) FLJ00261 protein
CUCCUCUGGUCCCGAAGGCUCGACGGCGCCUCUCGAUCCGGGCCACAGAGCCUGUCCGAGAG
GUCGGCGACGACCGAGACCUAGAGGAA

>EMBL_CDS:BAC11282 BAC11282.1 Homo sapiens (human) hypothetical protein
CCGAGGUUCACGACGACUCCAACCUCGUGUCCCUUACCCUCCUCCGUGUCCGGAACUCCGUCCAC

GGUGGGACCCGGGCGACGUCGACUUGGAGGUCGUCUCGGAACCACGG
>EMBL_CDS:BAG54709 BAG54709.1 Homo sapiens (human) hypothetical
protein
ACAGUGAGGCUCGACCUCCGUCCCCACGUGGGUGGAAUCCUCCUCCAACAGGCACCGUCAGAGG
UCCUUGACCCCGUGACGACCGAGGUCCUACCCCCACCGU
>EMBL_CDS:BAC05039 BAC05039.1 Homo sapiens (human) hypothetical
protein
AGUCUCGACGGUCAAUUCUACCAAGGGAACUCCAACUUCUUUAGAAACUUUAAAAGUGGAAG
UACUGGAAGGUCAAACCGUUACGUAAAAGAACACCGUCGUGACU
>EMBL_CDS:BAB15527 BAB15527.1 Homo sapiens (human) hypothetical
protein
UUGAAGUGUCCUACUAAACCGACGACGGUCCUGUCAGACCUUCACUUGUCCGAAAAGGCCUUC
ACGACCGCACCGAAAGUCUAUCUCGAGUAUAACCAUCAUUGGGUUCAGUCACAACACGUUUCAA
>EMBL_CDS:BAB15113 BAB15113.1 Homo sapiens (human) hypothetical
protein
ACCCCGACGUCCGUAACAGACCCACUCGGAGGUGUCCUUGGGGACCUCGGGAGGACCGAGUUC
CAUCGGGGU
>EMBL_CDS:BAG53044 BAG53044.1 Homo sapiens (human) hypothetical
protein
CUCGUCAGAAUUACGUCUAAACUGGUUAAAUCACCCUGUGUAAUACAAAACCGAGUGAUUUCCA
UAACAAAGUACUUAACCGACAAG
>EMBL_CDS:BAC04529 BAC04529.1 Homo sapiens (human) hypothetical
protein
GUUUGAAAGGAGUAUAAGUCUUGAAAGUAUCCUAAAGAGAGGACACACGUAAAAGACCACAUU
AUUCCAAAC
>EMBL_CDS:BAG54259 BAG54259.1 Homo sapiens (human) hypothetical
protein
UCGACCCUCCAGUCCAUCCGCUACCACGACCGGGCGACGAGGUCGAGCGAUCUGUCGUCCCAGUC
GAACACUGAGAACC GGAAGUCGA
>EMBL_CDS:BAD18751 BAD18751.1 Homo sapiens (human) hypothetical
protein
CCUGGGUCUCCGUAGGGACGGGUCUGUAGGUGUGAGUCGAGUCCCAAGACACCGGACACACCCU
UAACAGACGUCGACCCCUACGUCGGGCAGG
>EMBL_CDS:BAD96865 BAD96865.1 Homo sapiens (human) solute carrier
family 27 (fatty acid
AGUGCCAGUAAACCAAAGACACCACUCAACGUUUUAUGGCUUCGUCAAGUGGCUAUAUGACUUA
CUGUCACU
>EMBL_CDS:BAD96221 BAD96221.1 Homo sapiens (human) hypothetical
protein FLJ11848
GACUUCGACAUUGGAGACCCUACGGUAGAUCGGUUAAGGAACUGUUCAGUCCGACGGUAUGUUU
CUACCAAAGGGACCCCUACUGUCGAGUC
>EMBL_CDS:BAD97219 BAD97219.1 Homo sapiens (human) monoamine oxidase
A variant
GACCAGUUGCACUCACUGUCCUACCAAGUCGAAGUGAACCAGAGGCUCCUCCAGGUAAUAGGCAA

GCGAGUGAACUGGUC

>EMBL_CDS:BAD97254 BAD97254.1 Homo sapiens (human) tektin 3 variant
AGGUCAGACCAGACUCGGUGGAAGUCCUUCGGUCAGAACAGGAACUACCGGAAGAACUACCUAAG
AUACCAGUAAAGUCAGACCU

>EMBL_CDS:BAD96196 BAD96196.1 Homo sapiens (human) aspartyl-tRNA
synthetase variant

AACCCAGUCCGUACCAUAUCUUUCCAGAAUGUCGGUUACCUAUAAAUAGUUCUUAUUAUUUUAGA
CAUAGUAUGAAAAGGAAAUGGUUUACUGGGUU

>EMBL_CDS:BAD97122 BAD97122.1 Homo sapiens (human) sarcosine
dehydrogenase variant

CGGGGUGAGUACGGGUCGAACCGGUCCACCAUGUCCAGACCGUCGGGUUCGACGGAGGUGGUUA
CUGGUGGUGCAACCGGCACGACCCGUCCTCCG

>EMBL_CDS:BAD96931 BAD96931.1 Homo sapiens (human) carbohydrate
(chondroitin 4)

GUCGACGACGGAGGUCCGGUCCCCUAGAACCAGCUUGGUCAGGAGGGGUCGACGACCGCCAGG
ACAAGGCCAUCGAGCCCCCUUCGCCUCGACGGCCAGGUGGACCUCAUCGACGUCGUCGAC

>EMBL_CDS:BAD96995 BAD96995.1 Homo sapiens (human) AU rich
interactive domain 1A

CGUGUCCCCGUCUCCUGGUUAUACCCCGACCGCACACGGUACCCUCCGGUGCUCGGAAGCACC
AACCGGGAGACUAGACACACG

>EMBL_CDS:BAD97289 BAD97289.1 Homo sapiens (human) Na⁺/K⁺-ATPase
alpha 3 subunit variant

CCCCCGUGGGAAGUAGUGGUCGUCCAUAGCCAACAGCAACCCAGGAGCCAGAGUACCUACCUCU
CGACCAUAAACAACCACCUUAACUUCUUUAGAG

>EMBL_CDS:BAD96814 BAD96814.1 Homo sapiens (human)
aminopeptidase-like 1 variant

GUAGACCCACACCGACUCCUGCCGGUCCCGACCCCUACGUCCCGCCGAAACGGUUGGGGUAUC
UAAGGAGGUUUAGGAGAGCAGAAGUCAAGGAGUAGGGCCUAC

>EMBL_CDS:BAD97332 BAD97332.1 Homo sapiens (human) pinin, desmosome
associated protein

CCGACCCUGACCUCAUGACCAACCCUGACCCUAACUUCGACUUCGACCCCGACUCUGACUCCGAC
UCCAACUCGGUGUCCGAGUCCAACCCCGAGUCUAAGAAAAAGAAGAAAAGGAGUCUGAGGAAAA
GGUACAG

>EMBL_CDS:BAD96423 BAD96423.1 Homo sapiens (human)
calcium/calmodulin-dependent

CAACCGUCUGGGUGCCCACGAAGUCCCGGAGUACCCGACACUACGCGAACCGUCCCAACUACCAG
UCG

>EMBL_CDS:BAD96332 BAD96332.1 Homo sapiens (human) PHD finger protein
10 isoform a

GACCGAAGUUGAAAGACUCAUAAGACAACAACGUAAAACCCUUAUGAGAAAUAUUACCAGACAUUA
AGCAACUGCAAGAAAAAGAACAUCUUAUUGUCUUAUGAGUCGUACAAACCGACC

>EMBL_CDS:BAD97166 BAD97166.1 Homo sapiens (human) piggyBac
transposable element

GGACCAUCGUCUUCACGGCUUCGCGUCCGCCGUUAGAGGACUCACACCCUCGACGGGAGGACA

CUCAACGUGUGGACGAGGGUCC
>EMBL_CDS:BAD97228 BAD97228.1 Homo sapiens (human) phosphoserine phosphatase variant
GGUCGAGGGAAUACGGCCCCAGUCCACACCCCCAACGAGACGAUACUCAGAGACGUGGACGAGG
GACCUCCCCGACC
>EMBL_CDS:BAD96811 BAD96811.1 Homo sapiens (human) galactosidase, beta 1 variant
AGGUCUGGACCGGGACCAGGUAGGUCCUUGACCUAUUUCACAGGACCCCCGUUCAGACCC
>EMBL_CDS:BAD96436 BAD96436.1 Homo sapiens (human) RNA binding motif protein 28 variant
CGGGUGGUCGGAGUAAGAGACCUCUUCGUCGAUCUUCGGUAAAGACUCGACGAAGAACUCAGUAC
UUGACCCG
>EMBL_CDS:BAD96821 BAD96821.1 Homo sapiens (human) carcinoembryonic antigen-related cell
UGACACUAGCAGCACUGACACCAGGAUAACUCCGGUCACAGACUCAUACCCGAACCGUGCAUUA
CCUAGGUGUAUAUAAGUGUCA
>EMBL_CDS:BAD96726 BAD96726.1 Homo sapiens (human) 2',5'-oligoadenylate synthetase 1,
ACCCCAAAAUUUCAGUAUUAUGAAACAGGUCAUCUACGUCUCAACGACCAUCAAUACUGAUUA
AGGU
>EMBL_CDS:BAD97042 BAD97042.1 Homo sapiens (human) splicing factor 3b, subunit 4 variant
CUGUAGGGACCUACCCCGUAGGGUGGGCCACCCUUACCCACUCCUACACUCACAGGUACUGGUCC
UACAG
>EMBL_CDS:BAD97300 BAD97300.1 Homo sapiens (human) DKFZP586B1621 protein variant
GAGGACCUAACGAGACCGGCGUGCCGACACCCACCACGGUGUCAGCGGCAGUGGUCGUCGGGCCA
GGUCCCGUAAGUCCAC
>EMBL_CDS:BAD97305 BAD97305.1 Homo sapiens (human) glycine amidinotransferase
UCCUCUACUUAUACGUGAGACAUCAGACCUCGUUCUACGGAUUGCGUAGGUAAGUUACGGAUCCAUC
AAACAUUGGACCGAAGAGACACGUUUUUUAUAGAGAA
>EMBL_CDS:BAD96710 BAD96710.1 Homo sapiens (human) RAN binding protein 3 isoform
AGAGACAGUCUUAGAAGAGGGCGGAAGUCCUGACCUCGGCGGUCGACUGGAGGGACGGUCAAGAGC
GCCUUUUCUCCUUCGACCCGAAGUCCUCGCCCUCGCUCCUCACGACCGACUCC
>EMBL_CDS:BAD96976 BAD96976.1 Homo sapiens (human) nibrin variant
UCGAAAAAACCUUCGUAGAGUGAUAGUAGGACUCAAACAGUAACAAUCUAUAAAGAAAUCGACU
GGUAUCACUCAGAAGGAACUCAA
>EMBL_CDS:BAD96686 BAD96686.1 Homo sapiens (human) PDZ and LIM domain 3 variant
ACCUGAGACAGGGUUUCGGCAGUUAUCGGUCCUACUGUAGAGGUCCUGUGUCCAACCGUCGACGG
CGGAACGAAGGACCACAUUAGGACCACUACUGGUUUCGACCAACUUCAGAU
>EMBL_CDS:BAD96624 BAD96624.1 Homo sapiens (human) connector enhancer

of kinase

CCGAAACGUCCAAGAGACAGACAUCGGACCUCGAGUCCCGACCUCGACAAGGUGGGGCGGGUCC
UACUCGAGGACCACAGGGUCUCUGGCGUGUCGG

>EMBL_CDS:BAD97292 BAD97292.1 Homo sapiens (human) inositol
hexaphosphate kinase 3

CCCAACUUCGAGAAGGAGAGUUGGACCAAAGGCGACCACAGAAGGUGGUCGCUCUUCGACCUCA
CAACUCCACCCCGAGCCUGGA

>EMBL_CDS:BAD97230 BAD97230.1 Homo sapiens (human) cytochrome P450,
family 2,

UUGUCAUUUAAGUCUGACAACUAACACGAAAAGGACAAGGUAAAACUAGUCCUUUGUUAGUUAAU
UCAGGGCUCGUGACAA

>EMBL_CDS:BAD97047 BAD97047.1 Homo sapiens (human) integral membrane
protein 2A

AGGACCCACCGUUGAGCCUCGAGGAACGGCCAGUCAUAGACUCAAGACUGGCACGCCGAGUCCU

>EMBL_CDS:BAD97004 BAD97004.1 Homo sapiens (human) mutS homolog 2
variant

GGUGACCAAUUGUUCAGAAACAGGAACUCCCCAAAUGUGAAUAAGUCGUUCCGUCGGUCUCUGA
CUCUCGGUCACC

>EMBL_CDS:BAD96438 BAD96438.1 Homo sapiens (human) fibroblast growth
factor receptor 1

CGUCCUCUACUCCUUCGGGGACACGUUAUCUACUACUAGAGGUCCAUGUCCCCGCUCCAGUAGU
GACG

>EMBL_CDS:BAF82658 BAF82658.1 Homo sapiens (human) hypothetical
protein

AGUUUCCGUCACACCAGCCGGACCUUUAUGGUAGAGGGAGUCCUCAGGAACGGGAAAGUGAGACA
GAAACU

>EMBL_CDS:BAF83734 BAF83734.1 Homo sapiens (human) hypothetical
protein

GUCGCAGACUAACCGACCAGGGACCUCCUACUGUCCUCCGUCGGGUAGGUUUCUCCGAGGAAA
AGAGGUCGUCCCGGAACCGGUCCUACGAC

>EMBL_CDS:BAF83800 BAF83800.1 Homo sapiens (human) hypothetical
protein

GCCUAGGAGGACCCUCCUCUACACAGACUCAGUACUGCUCGGGGAGACUCCCCUCUCCUAGGCC
CCACAGUACUGCCCGGGAGGAUCCUCUACCUAGGC

>EMBL_CDS:BAF83741 BAF83741.1 Homo sapiens (human) hypothetical
protein

GGUCACUCCUCCACCCACUCUACCAUGGUCGACUACCGUGUAUCAGGUUCGGGACGCAUCGAAGU
CAUGCCCUCCUCCUACGAACACUGACACAGUUCGUCGUCCUCCGAGAACGGACAGAGGAGACA
GACC

>EMBL_CDS:BAF82320 BAF82320.1 Homo sapiens (human) hypothetical
protein

AAAUUCGGUUC AAGGUGUUUCGUAAGAAAGUUAAGUCCUACAGAAAUGAAAGUCACCUUGAAC
UUAAUUU

>EMBL_CDS:BAF83693 BAF83693.1 Homo sapiens (human) hypothetical

protein

AGACCAACCCGGAACGGCCCCGUGAGACCGAAGGCCUCCGAGACCUCGGGUUCACGGACUCUUC
AAGGUCU

>EMBL_CDS:BAF83474 BAF83474.1 Homo sapiens (human) hypothetical
protein

GGCGGUACAAGUGUCCUGAACCCGGAACGCCCGGUAGUCUGUGAGCAGGUCCAGGACCACCGU
CCACC

>EMBL_CDS:BAF82652 BAF82652.1 Homo sapiens (human) hypothetical
protein

CCCAACAGACACUAUUUACCUUAGACCUCUGAAGUGGAAGUAAAAGUGUAAAACGUUGUCUUGG
A

>EMBL_CDS:BAF82401 BAF82401.1 Homo sapiens (human) hypothetical
protein

ACAUCUCUUCGACUUCGGCCAUCACUUAAGGCAAUAACCAGAAAAGCGACAACCGAAGAAAAAGG
AAGAGGUGC

>EMBL_CDS:BAF82503 BAF82503.1 Homo sapiens (human) hypothetical
protein

CGGUAACGACCGAGAGAGAGGACCCAUACAGGUUCCUAGGCACUCUGGUGACCCACUCCCGGUA
GCCACCG

>EMBL_CDS:BAF82429 BAF82429.1 Homo sapiens (human) hypothetical
protein

UUAGACCGGUACAAGAAACUCCUCUCAAACUACAUCCUCAAGAAUGAUGAGACCUUACCCGGUC
CAA

>EMBL_CDS:BAF82111 BAF82111.1 Homo sapiens (human) hypothetical
protein

CGCAGAUAGUAUAAACCAAAACUACUAAGUAGUCCUAAUAUUCACUCAACCUAACGAAAAUAGUC
GACAAACUGAAGACUACAAAACAAAAGUUGAACUACAUCUACA

>EMBL_CDS:BAF83032 BAF83032.1 Homo sapiens (human) hypothetical
protein

AGAGGAAAGAGGCAACGGUCAAGGAGGUAGAGACCACAACCGAGUAGAAGGUCCUCCCUAACCA
UCUACCCACCUCU

>EMBL_CDS:BAF83617 BAF83617.1 Homo sapiens (human) hypothetical
protein

CCUUCGACUCCAGAAGCACCACUJACCGGAGCAUUAGUAUGUCCCGUUGGUGCUACUACAGGAGU
CUCGG

>EMBL_CDS:BAF83614 BAF83614.1 Homo sapiens (human) hypothetical
protein

AGUGUUUAUGGUCCUCGUACAUCACCAAGGAGAACACCCUCGGCUACUUGUGACGGUAUAACGAC
AACCAUCCACU

>EMBL_CDS:BAF82421 BAF82421.1 Homo sapiens (human) hypothetical
protein

UCAGGUUUCUUGACAUAAGAUCUCCAGUAAGAAUAUCUGUCAACUUCUAUCAAGGGACAAUCC
AUCUCAAGAAACCUGA

>EMBL_CDS:BAF82282 BAF82282.1 Homo sapiens (human) hypothetical

protein

CGGACCCCUACCGGCUCUUACCCGUCAACUGACCUUCUAAAUCGUCGACGAGGGACGCCGGCC
CCGUCCG

>EMBL_CDS:BAF82871 BAF82871.1 Homo sapiens (human) hypothetical
protein

CCUGACGAAACGUACGACUCUCACGACGAAGAAGAGGUCCCGACAGUCGUACGGGGGUUCAGG

>EMBL_CDS:BAF82241 BAF82241.1 Homo sapiens (human) hypothetical
protein

GAACACCUGUAACGUACACCGGACCUCGACCCACCUUUGGGUCAGGUACAAGGCCAGUACUAGUU
ACACGUACCC

>EMBL_CDS:BAF83705 BAF83705.1 Homo sapiens (human) hypothetical
protein

GCGUCGGUUCAGGAAUACGUGUUUCGCCAACAACCUGUCCACGAGGUACGGGUCCCGAUGGACCC
ACGUAUCCCGUGGAAGACGAACCACGACUCCCCGACAC

>EMBL_CDS:BAF82092 BAF82092.1 Homo sapiens (human) hypothetical
protein

AAGGUAUUUAGGACACGAGGACCUGUACCUCGCCUCCUACUUGAGCUGACGUAAGAGUUACUAGA
GACACGGGUCCUCCGAAUCCUAAAACCCUU

>EMBL_CDS:BAF83622 BAF83622.1 Homo sapiens (human) hypothetical
protein

CUCCUACUAAAACGUCGCACCUAAGACGGAACCUUCUACACAAAAAGUAGAAACCUCCAUAUUA
GGAAGACGUUCAAAAAGAAAUAAAUCAGAAG

>EMBL_CDS:BAF82365 BAF82365.1 Homo sapiens (human) hypothetical
protein

AGGAAUUUCUGACCCACCAACAGUAAACAUAGUCAUUGUGAAUGAACGUUUUAUCGUCAUGACCU
AGAAACUCCU

>EMBL_CDS:BAF83187 BAF83187.1 Homo sapiens (human) hypothetical
protein

ACUACCAAAAACGACCUUGUGACCUCAAACAAACUCAGAACCACGACGACCUUCGUUAUUUCCG
AACCCGACUUAACCUCCAAAACUUAAGUGGACUAAAAAAAAAGAAACCUCAGUCAGGUAAAAGUCA
GAACAAGGAUCUUGGUCACUGUCCGAAUAGAAGGAAGUCACCGAGGCCACUUCUCUCUGAUAAU

>EMBL_CDS:BAF83448 BAF83448.1 Homo sapiens (human) hypothetical
protein

UCUUGUCACGUCUCCCAAGGGGCGUCCUGGUCUAGGACAUUCCUCUCCGGGACGUGUCAAAA

>EMBL_CDS:BAF82979 BAF82979.1 Homo sapiens (human) hypothetical
protein

GUCUCUCAGCUACUUCUCUACUACCUCGCGAGCACCCUCGUGAAGUGAUCGACCAGGUGUAGAG
GUUCAGGAGAGAGAC

>EMBL_CDS:BAF83152 BAF83152.1 Homo sapiens (human) hypothetical
protein

AAGGUCCAGUCUAGACAUAGACAUGUCUCAAGUUGAUCUCAUCUACUCGGAGAACAUGUCCAA
AAAGUUACGCCUAUAAGACCUU

>EMBL_CDS:BAF83331 BAF83331.1 Homo sapiens (human) hypothetical
protein

CGUUAAGACCCUCGACGGAAUAAAACAACAGUGCGUCCUGUUCGAGAGCUUCAACUCCGUCAAAA
GCCUUACG

>EMBL_CDS:BAF83608 BAF83608.1 Homo sapiens (human) hypothetical
protein

CCCUAGGCACAUUAGGUCCCACGACAAAAGAAAAGAGAUUUGUCUGCCAUGAGGACCCAGAGGUC
CUAGGG

>EMBL_CDS:BAF82394 BAF82394.1 Homo sapiens (human) hypothetical
protein

AAGACGUCGAAGGUCUACGAGGUCGACAGUCACCGCUGUGACAACUGCCAGAGCGAGUACUCCCG
CUACUCGUACAACUCGUCGUCCU

>EMBL_CDS:BAF82417 BAF82417.1 Homo sapiens (human) hypothetical
protein

ACCACGCAAGUCUUGAUGACCGACUACACGAACGUUAGACCGGUCAUAGACGACUCGAGUGAU

>EMBL_CDS:BAF82583 BAF82583.1 Homo sapiens (human) hypothetical
protein

CGGUCACUCUGUCUCCCCUGUCGCUCCCGACACCUCGGUCUAGAUGUCAGUUUAGGGUAAAGUGA
CCG

>EMBL_CDS:BAF82265 BAF82265.1 Homo sapiens (human) hypothetical
protein

CACGACGAGUCGCGGCCGACGGGGGUCAGGGUGUCAAGAUACCCUUGGUUCAUCCCCCGUACCGC
CCCACCUCGUCCCG

>EMBL_CDS:BAF82223 BAF82223.1 Homo sapiens (human) hypothetical
protein

CCUGGAGACACGGUAGGAAGAGCUACUCGCGGGCGUGUUUCCAGUCGCUGACGAGCUCCCGUACC
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>EMBL_CDS:BAF82500 BAF82500.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF83533 BAF83533.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF82409 BAF82409.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF82680 BAF82680.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF82658 BAF82658.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF83039 BAF83039.1 Homo sapiens (human) hypothetical
protein
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>EMBL_CDS:BAF82999 BAF82999.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAF82997 BAF82997.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAF82867 BAF82867.1 Homo sapiens (human) hypothetical
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GGGG
>EMBL_CDS:BAF83157 BAF83157.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAF82285 BAF82285.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAF82494 BAF82494.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF83528 BAF83528.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF83123 BAF83123.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAF82992 BAF82992.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF83005 BAF83005.1 Homo sapiens (human) hypothetical
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G

>EMBL_CDS:BAF83714 BAF83714.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF82907 BAF82907.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAF83287 BAF83287.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAF82366 BAF82366.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF83418 BAF83418.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAF83738 BAF83738.1 Homo sapiens (human) hypothetical protein
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>EMBL_CDS:BAG56880 BAG56880.1 Homo sapiens (human) hypothetical protein
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>EMBL_CDS:BAG58264 BAG58264.1 Homo sapiens (human) hypothetical protein
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>EMBL_CDS:BAF84207 BAF84207.1 Homo sapiens (human) hypothetical protein
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>EMBL_CDS:BAG58070 BAG58070.1 Homo sapiens (human) hypothetical protein
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>EMBL_CDS:BAG58030 BAG58030.1 Homo sapiens (human) hypothetical protein
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>EMBL_CDS:BAG58082 BAG58082.1 Homo sapiens (human) hypothetical protein
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>EMBL_CDS:BAF85421 BAF85421.1 Homo sapiens (human) hypothetical protein
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>EMBL_CDS:BAF84376 BAF84376.1 Homo sapiens (human) hypothetical protein
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>EMBL_CDS:BAG57257 BAG57257.1 Homo sapiens (human) hypothetical

protein

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>EMBL_CDS:BAF84679 BAF84679.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF85202 BAF85202.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAG57591 BAG57591.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF84216 BAF84216.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAG56677 BAG56677.1 Homo sapiens (human) hypothetical
protein

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protein

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>EMBL_CDS:BAF85170 BAF85170.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF84864 BAF84864.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF85240 BAF85240.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF84836 BAF84836.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAF84347 BAF84347.1 Homo sapiens (human) hypothetical
protein

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protein

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protein

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protein

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>EMBL_CDS: BAG58480 BAG58480.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS: BAG57966 BAG57966.1 Homo sapiens (human) hypothetical
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>EMBL_CDS: BAG57341 BAG57341.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS: BAG57707 BAG57707.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS: BAF85245 BAF85245.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS: BAG56840 BAG56840.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS: BAF85698 BAF85698.1 Homo sapiens (human) hypothetical
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>EMBL_CDS: BAF85766 BAF85766.1 Homo sapiens (human) hypothetical

protein

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>EMBL_CDS:BAF85338 BAF85338.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAG58200 BAG58200.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAF84446 BAF84446.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAG57209 BAG57209.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAF84645 BAF84645.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF85023 BAF85023.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAG58495 BAG58495.1 Homo sapiens (human) hypothetical

protein

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>EMBL_CDS: BAF83895 BAF83895.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAG58536 BAG58536.1 Homo sapiens (human) hypothetical protein
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>EMBL_CDS:BAG57899 BAG57899.1 Homo sapiens (human) hypothetical protein
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>EMBL_CDS:BAG57602 BAG57602.1 Homo sapiens (human) hypothetical protein
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>EMBL_CDS:BAF85257 BAF85257.1 Homo sapiens (human) hypothetical protein
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>EMBL_CDS:BAG58444 BAG58444.1 Homo sapiens (human) hypothetical protein
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>EMBL_CDS:BAG58021 BAG58021.1 Homo sapiens (human) hypothetical

protein

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>EMBL_CDS:BAF85237 BAF85237.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF84119 BAF84119.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAG58492 BAG58492.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAF85447 BAF85447.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF85025 BAF85025.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAG57874 BAG57874.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAG58442 BAG58442.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF85424 BAF85424.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF84536 BAF84536.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAG57445 BAG57445.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAG57264 BAG57264.1 Homo sapiens (human) hypothetical

protein

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>EMBL_CDS:BAF85124 BAF85124.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF83938 BAF83938.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAF83918 BAF83918.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAF85253 BAF85253.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF84759 BAF84759.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAG57486 BAG57486.1 Homo sapiens (human) hypothetical
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protein

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>EMBL_CDS:BAF83900 BAF83900.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAF84318 BAF84318.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAG58534 BAG58534.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAG57202 BAG57202.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAG60413 BAG60413.1 Homo sapiens (human) hypothetical

protein

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>EMBL_CDS: BAG61920 BAG61920.1 Homo sapiens (human) hypothetical
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>EMBL_CDS: BAG61669 BAG61669.1 Homo sapiens (human) hypothetical
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>EMBL_CDS: BAG59189 BAG59189.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS: BAG59510 BAG59510.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS: BAG63066 BAG63066.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS: BAG62663 BAG62663.1 Homo sapiens (human) hypothetical
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>EMBL_CDS: BAG60917 BAG60917.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS: BAG61141 BAG61141.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS: BAG61361 BAG61361.1 Homo sapiens (human) hypothetical
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>EMBL_CDS: BAG62491 BAG62491.1 Homo sapiens (human) hypothetical
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>EMBL_CDS: BAG62745 BAG62745.1 Homo sapiens (human) hypothetical
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C

>EMBL_CDS: BAG59014 BAG59014.1 Homo sapiens (human) hypothetical
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>EMBL_CDS: BAG62713 BAG62713.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAG59538 BAG59538.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAG62640 BAG62640.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAG59148 BAG59148.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS:BAG59956 BAG59956.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAG60351 BAG60351.1 Homo sapiens (human) hypothetical
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protein

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>EMBL_CDS:BAG61752 BAG61752.1 Homo sapiens (human) hypothetical protein

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>EMBL_CDS:BAG59247 BAG59247.1 Homo sapiens (human) hypothetical protein

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>EMBL_CDS:BAG59760 BAG59760.1 Homo sapiens (human) hypothetical protein

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>EMBL_CDS:BAG62203 BAG62203.1 Homo sapiens (human) hypothetical protein

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>EMBL_CDS:BAG59795 BAG59795.1 Homo sapiens (human) hypothetical protein

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>EMBL_CDS:BAG60566 BAG60566.1 Homo sapiens (human) hypothetical protein

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>EMBL_CDS:BAG59668 BAG59668.1 Homo sapiens (human) hypothetical protein

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>EMBL_CDS:BAG59450 BAG59450.1 Homo sapiens (human) hypothetical protein

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>EMBL_CDS:BAG61934 BAG61934.1 Homo sapiens (human) hypothetical protein

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>EMBL_CDS:BAG59929 BAG59929.1 Homo sapiens (human) hypothetical protein

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>EMBL_CDS:BAG62150 BAG62150.1 Homo sapiens (human) hypothetical

protein

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>EMBL_CDS: BAG59519 BAG59519.1 Homo sapiens (human) hypothetical
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>EMBL_CDS: BAG59120 BAG59120.1 Homo sapiens (human) hypothetical
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>EMBL_CDS: BAG62911 BAG62911.1 Homo sapiens (human) hypothetical
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>EMBL_CDS: BAG61567 BAG61567.1 Homo sapiens (human) hypothetical
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>EMBL_CDS: BAG61509 BAG61509.1 Homo sapiens (human) hypothetical
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>EMBL_CDS: BAG62941 BAG62941.1 Homo sapiens (human) hypothetical
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>EMBL_CDS: BAG62171 BAG62171.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS: BAG63132 BAG63132.1 Homo sapiens (human) hypothetical
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>EMBL_CDS: BAG59555 BAG59555.1 Homo sapiens (human) hypothetical
protein

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>EMBL_CDS: BAG60174 BAG60174.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAG61723 BAG61723.1 Homo sapiens (human) hypothetical protein
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>EMBL_CDS:BAG62260 BAG62260.1 Homo sapiens (human) hypothetical protein
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>EMBL_CDS:BAG62102 BAG62102.1 Homo sapiens (human) hypothetical protein
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>EMBL_CDS:BAG61695 BAG61695.1 Homo sapiens (human) hypothetical protein

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>EMBL_CDS:BAG62265 BAG62265.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAG61782 BAG61782.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAG62806 BAG62806.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAG62068 BAG62068.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAG61734 BAG61734.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAG63854 BAG63854.1 Homo sapiens (human) hypothetical protein

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protein

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>EMBL_CDS:BAG36104 BAG36104.1 Homo sapiens (human) hypothetical
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>EMBL_CDS:BAG63310 BAG63310.1 Homo sapiens (human) hypothetical
protein

GCACAUCCCGGAGAGCGGUCACACCCAAGCGACCACUUUAACCUCGGAUUUAUUCGACGUAC
>EMBL_CDS:CAD92497 CAD92497.1 Homo sapiens (human) pseudogene similar
to part of
AGUCGCAGAACGAGAGGAGGACCAUUGUCGUCGGUCUACGAGAAGUACUCCAGCCGACGGUCCUA
CUUCAAGGACUGCGACU
>EMBL_CDS:BAG37573 BAG37573.1 Homo sapiens (human) hypothetical
protein
GCCUACCGUAGGUCAUACUAUGAAGGAAGAAACGACUUUAUUCUUGUCGUACCCCUAGAACUACAG
UAGAC
>EMBL_CDS:CAQ07637 CAQ07637.1 Homo sapiens (human) MAGE (Melanoma
Associated Antigen)
CCACGAACUUCAGACGAGGAGAAGAACCUACGACCUCAGAAGUAGUCCACACGAGGUGCUUCAUC
UCCUCCUCCUCGUCCUCGAACCUCUGA
>EMBL_CDS:CAI42087 CAI42087.1 Homo sapiens (human) melanoma antigen
family C, 1
GACUCAAGAGAGUCUCUUUGAGACCUUUUCUGAGUCAUUUCACCUCCUCCUCCUCCCGAGUGUC
CUUAGACCUCUCCUCUGACCCUCAGGAGGGGGAGUCCUGUUGAGACUCCUGAGAGUCUCCUUGAG
ACCUCUUCUGAGCC
>EMBL_CDS:BAG38101 BAG38101.1 Homo sapiens (human) hypothetical
protein
CGUCUUCGACGUUUACGGAGAACCUCUUCUACUCUUUAGUCACCUGAGGGACCCCGACUUCAU
CAACGACG
>EMBL_CDS:BAG37649 BAG37649.1 Homo sapiens (human) hypothetical
protein
UACAAAGUACCGGAGAAGUCGACUUUGGAAAAGAAUCUAAGUAUGACUUCUUUAAAACAAUAGU
UGAGUUAAGGAAGUCUCAGAUUGGACCCACGCACCAAUUAUUCUCCGACACCAAUA
>EMBL_CDS:CAQ07541 CAQ07541.1 Homo sapiens (human) MICAL-like 1
GUCACCGCUACCAUGUCGGACGGCAGUCGGUCCAUCGCGACGUGGUUCACGUGUACGACGACCGU
CCGACGCGUGCACGACGAC
>EMBL_CDS:CAQ09093 CAQ09093.1 Homo sapiens (human) structural
maintenance of
AAUUGAUACAAAAGUACUACUCUGUUUCUGAGAGAAAACUGUGAGUUUAGGGUAUAGUGUACGAG
AUUGAACCACAAGUCCUCUACUAGAAAAAGAGUAAUACCAUAUCAACU
>EMBL_CDS:BAG37533 BAG37533.1 Homo sapiens (human) hypothetical
protein
CAAGACAAGGUACUUCUCAGUGCACUCAGAAGACUCAAUUUAACCGUAGGACAGGACCAAAAUUC
GGUCGUCACUCGAAGUGUAGAGACUAAACCCAGAAAAGUACCCUGACUUG
>EMBL_CDS:BAG37303 BAG37303.1 Homo sapiens (human) hypothetical
protein
CAGGUGUUCUAGAGGGACCGAUGCUCUAGAGAAACUCACUGGUACUCUAGAGAGACUCACUGGUA
CUCUAGAGAGACUCACUGGUACUCUAGAGAGACUACCGGUACUCUAGAGAGUCUG
>EMBL_CDS:CAI42601 CAI42601.1 Homo sapiens (human) melanoma antigen
family C, 3
CGGAGUGGAGGGAGUCUACGGGUUCUACUUUCCGUCUUUAUCAGGAUAGACACCGGAAAAAGGCC

CCGACCCCGACUCCACCCUCG
>EMBL_CDS:CAI22918 CAI22918.2 Homo sapiens (human) meiosis inhibitor
1
ACAGACCACUUGGACGUUUGACGGGAACACGACGACCCGUCUCUCCUCCGUCACUCGUCGGUCC
GU
>EMBL_CDS:BAG36941 BAG36941.1 Homo sapiens (human) hypothetical
protein
CUGGAACCACAGUUUGACACCGUCUACCACCUAUUUUCUGACAUGUUGGGCGACAGGUACCAAGAU
GGUCCAG
>EMBL_CDS:CAI21838 CAI21838.1 Homo sapiens (human) RASD family,
member 2
CCGCCGUGUCGAGCGGCACCAGCAAGAACAACGGUGUCUACUGGUACCCGUCGAGGCGGCGG
>EMBL_CDS:CAA15949 CAA15949.1 Homo sapiens (human) E2F transcription
factor 2
GAGGUCGUCCGACAGUCAUCGGAGGUUCCCCUGGUCCUACCUCGCCACCCCGGACGACCCC
>EMBL_CDS:CAI22034 CAI22034.1 Homo sapiens (human) DEAH
(Asp-Glu-Ala-His) box
UGGUAUUUCAGGAAUAACACAAACUAUUUACGAAGUAUAUAUAACUCGUAUCACUCCACCA
>EMBL_CDS:BAG37899 BAG37899.1 Homo sapiens (human) hypothetical
protein
CGGAAACGGAGACGAACCCGGACUGGGAGCUCGAAGCCCCUAUCACCUCCAACUCGUUGACCAU
UUCCG
>EMBL_CDS:CAA16670 CAA16670.1 Homo sapiens (human) hypothetical
protein
GGGUCCCCGUAGCCCGCAAGACCUCUCCCCGGACCGAGGACCCUCUUCGGUCACGACCCUGUCC
CGAGGACGUGUGCCUUUGAAGGUAACCGACGAGGAGUCAGGAGGGCCACAGUAAGACCC
>EMBL_CDS:CAB36861 CAB36861.1 Homo sapiens (human) POM121 membrane
glycoprotein-like 2
ACUCGGGUGCCUACCUCUGAAGAGAAGUCGCCGGGUCGGACCCGUGUUUUCUUCACUCCCAAG
GUAAAAAGUAGUCCCCGAAU
>EMBL_CDS:CAQ07960 CAQ07960.1 Homo sapiens (human) cadherin, EGF LAG
seven-pass G-type
CGGGUGUCCGGACAGGAGUGACUGUGAGUGACACAUUACCCUCGAGACUUUCUGUCCGGACCCC
A
>EMBL_CDS:CAI22773 CAI22773.1 Homo sapiens (human) chromosome 1 open
reading frame 32
UCCCCUACCUCAUUCGCCGCCUUGUGGCCUCUGUCUCCUCCCAUGGGCCGGAAACGACGAAAG
GGA
>EMBL_CDS:BAG36963 BAG36963.1 Homo sapiens (human) hypothetical
protein
GGGUCCUCCCGUCCAGGUGCCCCGGCUCGGGCGAGAACCCUCGCGAAGGAGAAAAAGACGUC
CCCGAAGGACGACAGGACCGAGAAGGACCC
>EMBL_CDS:CAQ10440 CAQ10440.1 Homo sapiens (human) BAI1-associated
protein 2-like 2

CCUCCAGUACCUCAGUACCCCCAGUGCCCCCAGUACCCUAAGUGCCCAGGGGAGGAGGUCUCGGA
AG

>EMBL_CDS:BAG37475 BAG37475.1 Homo sapiens (human) hypothetical
protein

AGGGUCACUUUAUCUCUUGUGGUGUCAUUAUGACUAGAAACCCAUAGUUGGACUAUAGUUAAGAA
GACACACCUAUAAGAAAAAGUAGUAAAAAUGACCCU

>EMBL_CDS:BAG36854 BAG36854.1 Homo sapiens (human) hypothetical
protein

UCCUCACAAACGCCCCUCCGGGCUCCAGCGACACAGGCCCCGUCUCGCCGGCCAAGCAGGGCU
CAGACGCGAGAAA

>EMBL_CDS:BAG37025 BAG37025.1 Homo sapiens (human) hypothetical
protein

CGACUCCUGACCCUCCUAUUCAGGAGUCUAGACCAAAAUCGAGGCGUCCGAGUAGGAAGCCCAG
GAGUCA

>EMBL_CDS:BAG37096 BAG37096.1 Homo sapiens (human) hypothetical
protein

CGUCCGUUUAAUCUCCCUCCAUUCCUCAAGGAACUAAUGAAACUAAAAGAGAGAUUUGAGGAC
G

>EMBL_CDS:CAD92504 CAD92504.1 Homo sapiens (human) Fanconi anemia,
complementation

CUCCUCGGGUGAAAGGCCGUCGCUACCGGCUUGCCGGUAGUCGUCCUGUAGUCCAAGGAG

>EMBL_CDS:BAG38131 BAG38131.1 Homo sapiens (human) hypothetical
protein

GGUCUCCGUUCCUUUCGUCCGCGAGUUGGUGGAACCCAACUGCGAACUACAGGACAUUGUAACAG
UGACC

>EMBL_CDS:CAQ10327 CAQ10327.1 Homo sapiens (human) crystallin, beta
B2 (CRYBB2)

CCAUCGGUACCCGCACCUUCGACCCAUGUAGCAGUAGAUACUAAAGGUAGAAGAAGGGCCACUUC
AACCCCAAAGUAUCUCCUACUAGAACACGAGAACCGACAGGUGAAACUACCCGG

>EMBL_CDS:BAG37516 BAG37516.1 Homo sapiens (human) hypothetical
protein

GACCUCAAGUAAUCCUAAAACCAAAGAGAAAACUCAGUAGGAGAAUAACUCUUAUCGUAUCAA
GACCUGAAGUC

>EMBL_CDS:BAG36983 BAG36983.1 Homo sapiens (human) hypothetical
protein

CGGUACAACGGGUCUUCUCCUGGUCUAGAUUGGUCACGAGUGACCAAUCCUGGUCUGCAAGGAAG
GACCAUCGAGGACCG

>EMBL_CDS:BAG38048 BAG38048.1 Homo sapiens (human) hypothetical
protein

UAGUUGUAUCGAACAAAUAAAAGACGUUAAAUAGAAGUUCUACAAAGUACAUAUUUACACUCUUG
UAGAUCUAAGUACCUAAGAACUUCUCAGUACGGACCUUAUCCAAAACUCCUA

>EMBL_CDS:BAG37908 BAG37908.1 Homo sapiens (human) hypothetical
protein

GAAGAAGGUCAGUAGGACUCCAUCUAUAGUAUGUCCUACGACCCCGGAAUACCGAAUGUCGUUA

GGUCAUACUAUAUUUUUCUACUAACCUCCAAUC
>EMBL_CDS:BAG37745 BAG37745.1 Homo sapiens (human) hypothetical protein
GACUCCGUGACCGACCACUGCGAGACCCUCGGGUCCAGGACCCUCACGCUCAGCCACAGACUC
>EMBL_CDS:BAG37560 BAG37560.1 Homo sapiens (human) hypothetical protein
AUAUCUCUAGGACCAGAUUUUUGACUCCCUCUUCGAAACGGUUCUAGAACCGACAUAAAAGUGAG
UCAAGUCUCCGAAAUAU
>EMBL_CDS:BAG37871 BAG37871.1 Homo sapiens (human) hypothetical protein
UACCCGAAAGAGAUACAACACACAAACGACUACAAAUCCUUAACACUGAACCACGACUACCCAA
AAGAUGAAAGUCCCUUAAGUUAAGGCAUCCGUAAACAAGUACUAAUAGUACCUCUUUUCGAGGU
A
>EMBL_CDS:CAI21422 CAI21422.1 Homo sapiens (human) guanosine monophosphate reductase
GCACUCCACGCAAGUUCUAGGUGGAGCCGAGCCGAGAACUCCGACGAGGCGAAUCCAGCCUCGU
CCUGUAGGAACUUCAGCUCGAACUCCAGGCGUAGAUACGC
>EMBL_CDS:BAG37070 BAG37070.1 Homo sapiens (human) hypothetical protein
UAGUAAUUUCAUCGGUCGUAGUAAUCGUCGAAAGGUAGAGACGACACUGACGUCCCGUAUAAACA
GUGUAAAGAAGAGACGAAUAAAACACAAAUGUCGUUCUAAAGAGACGUCAGUACGGUACCCUCG
ACCGUACGACUAGACAAUUACUA
>EMBL_CDS:BAG36757 BAG36757.1 Homo sapiens (human) hypothetical protein
UCACCGUAACCCUUGGUGGUACCGACCUAACGAGAUCCGUACUUGUCGUGACACCAAUGAGACU
CGGUGA
>EMBL_CDS:BAG37688 BAG37688.1 Homo sapiens (human) hypothetical protein
GACCACCGCGAAGACGACCGCCAUGUACGUCGUCUCCGACUCCACUGGCUCGGCAACGUCUCCU
UCUACCGUCGGUGGUCGUCCCGGUGGUC
>EMBL_CDS:BAG37378 BAG37378.1 Homo sapiens (human) hypothetical protein
CAACCGAGUCUCUCGACCCCCUGUGUCCCGUAGAGCCCAAGAUGAAGGAGGUCCACAGACCGGUC
G
>EMBL_CDS:BAG37793 BAG37793.1 Homo sapiens (human) hypothetical protein
UGAGAAAGGUCGUUGAGAGAAACUUAUUGACAAAGGUAAUUAUCACGGUUUCCGACCUAACACCG
UUAGGACUGUCUCUAAAGUCCAGUGACCUCUCUA
>EMBL_CDS:CAA16432 CAA16432.1 Homo sapiens (human) paired box 7
CGACAUCGGCCACCACGACAUCCACCCACCCGUCAUCCGGACCCUCCACCCGUCCGACAGAGGAC
CGAACUACCUCAGCCGGGCGACCGACGUCG
>EMBL_CDS:BAF98780 BAF98780.1 Homo sapiens (human) hypothetical protein
ACGUAGGUGCCCACCUUCGACGGAGUCAAGUCCCAACGAUAAGUCGACCGAAUCUCUGUUAGACU

ACGACAACGUCCAAAGUGAACUACCUACGU
>EMBL_CDS:CAI23623 CAI23623.1 Homo sapiens (human) zinc finger protein 33B
UUCGAAAAGAACACAUACCCAAGAGACUACAUGUAAUUCUGACUGAAUACCGUCUUUCGAAA
>EMBL_CDS:BAG37550 BAG37550.1 Homo sapiens (human) hypothetical protein
GGUCCACUUUGACGAAGUCCAUUCACAACUAAUUAAGAGCUUGACUAAACUAUAGAAAACCAAGG
UAACCAGAGUUUGGACUUCAGAAAACAUUGUAGACC
>EMBL_CDS:CAI42154 CAI42154.1 Homo sapiens (human) odz, odd Oz/ten-m homolog
CAUACACAUCCACCUUACAAAGAAGACGGUAUUUAAGGGUCGUCUCUCAGGAACCGAUUUCUUUA
UAACUUGAAGUCUAUA
>EMBL_CDS:BAG37064 BAG37064.1 Homo sapiens (human) hypothetical protein
UCCAAA AUGGUCAAUUCAGGCCUUACUUGUACCAAUGUAAUUUUAGUGUGAAGUAAAACUGUC
UUUCCCAUCUUGAA
>EMBL_CDS:BAG36994 BAG36994.1 Homo sapiens (human) hypothetical protein
UCCCGACGGAGGGUCCAUCAGCAGGUCGACACACCAUAUAUACCGACGCGUCGAAACGAGUAGGA
CCCUCUCAGGA
>EMBL_CDS:CAQ08480 CAQ08480.1 Homo sapiens (human) kinesin family member 4A (KIF4A)
AUCCUUGGUCUGAACAUUGGACAACGAAAUCUACUAAUJUCAAGUUGAUAGACCGCUA
GUCAUAAUUGUUGUCCAAACAAGGAC
>EMBL_CDS:CAO03520 CAO03520.2 Homo sapiens (human) novel transcript
AAGAAGUCCAUGAAGACCUGCCGCAACAACGUGUCCACCUACCGCGACAGGUCGAACAGGUCCCU
CUU
>EMBL_CDS:CAI42270 CAI42270.1 Homo sapiens (human) tubulin beta 4 (UUBB4) pseudogene
CGGGCCUUGUGCCACCGGUACCAGUCCAUCGCCGGUACAGCGCCCAACGUGUACCGGUAGUACAA
GAACCG
>EMBL_CDS:CAI42047 CAI42047.1 Homo sapiens (human) collagen, type IV, alpha 6
GACCAGCGGGCCCCAGUGGUCGACAGGACGAUACUCACUCCCGUCCUCUACGGACCCCGUGGC
CCCUCUGGUC
>EMBL_CDS:CAB42440 CAB42440.1 Homo sapiens (human) dJ597B2.1 (transcription factor 20
CCGAAACGUCCCCGUCGAACCACCGUCGCAAUCAUAUGACGUAGUGUACGACUCUCCCAACA
ACAACGACGCCAACGACGACGACGACGGGGACAACCCAG
>EMBL_CDS:CAI19007 CAI19007.2 Homo sapiens (human) novel protein
CCGGACCCCUACCAUGUGUCCAUCUGUCAUCGAACCACUGGAGACUUUGACACGUGGUACCACG
GAGGGUCCGG
>EMBL_CDS:CAI19407 CAI19407.1 Homo sapiens (human) v-myc myelocytomatosis viral oncogene

GGGUGGUCCCGAACGUUCAUAAGGUUCCGGAACGAAUCCUAGUGAUGAAACCCCGGAACCU CGU
CGACCGGUCCACCC

>EMBL_CDS:CAA22684 CAA22684.1 Homo sapiens (human) hypothetical
protein
ACACCUUGAACUCCUAAGACAACAAAAGCAUAACCACAUACUUAAGGUUUGUAAGAAGUUUACAA
GAUUAU

>EMBL_CDS:CAI21973 CAI21973.1 Homo sapiens (human) phospholipase C,
beta 1
GAACGAGAACAAAUCUCCACCUAUUUUCAUAAAGUAAUUCGGCUCCUAGAGCGACGAAUCCAAC
UAUUUUAGGUAGUAGACUAGUUGCCAUUC

>EMBL_CDS:CAB51755 CAB51755.1 Homo sapiens (human) novel C2H2 type
Zinc Finger protein
UCCAGACUAACCAUUGAUUUCCGAAAAGUGUAAGUAAACGUAAAUGUCCAAAAGAAACACUCUU
UUCAGAAACCACAAAUUAAUUCAGA

>EMBL_CDS:CAB36555 CAB36555.1 Homo sapiens (human) chromobox homolog
7
CCCAGGGCGACGGCUCACCCGUGCAGUCCUCUUCGUCUCGAAGAGGAACGGGAACCGGAACAC
CCUCGAGG

>EMBL_CDS:CAI21952 CAI21952.1 Homo sapiens (human) exonuclease
pseudogene
AACCCACCUCAAGACACCACGUAGAAGACUCCUACUAAGAAGAAUCUCCUAAAGAAGGCCUCG
GGAAGAAGACCCUCACCCAACCCACCGAUAAUUAGAAACCUUCCCGUGAGGUCUAGAGGGGGUU

>EMBL_CDS:CAI20281 CAI20281.1 Homo sapiens (human) ankyrin repeat and
sterile alpha
CCCCCUGGGCAGACCUACCGAGACCGGUCGCAUGUCUCGUCGACCUUCCAGGACGGGG

>EMBL_CDS:CAI42978 CAI42978.1 Homo sapiens (human) lipin 3
GAGGUACUGAACCUCGUCUCCUCCUCCGGGUACAGGGGUCUCGAGACUCAGAACGAAAGGAGACA
GAGACCCACACCUC

>EMBL_CDS:CAB90289 CAB90289.2 Homo sapiens (human) collagen, type IV,
alpha 5 (Alport
CGGAAAAGCGGACCUCGGGACCAACGGGUCCUACUGGAGGUGGUGGAUGUCCUGGUCCAAGAG
GACCUUCCGGCCCCAAGGGUCCUCCCG

>EMBL_CDS:CAI23620 CAI23620.1 Homo sapiens (human) poly(A) binding
protein, cytoplasmic
AUGUUUGUCGUCCUCAUAGACAUCAUCGUCAUCGCCGUUGACGUCCUACACGAGGAUAACAGACA
C

>EMBL_CDS:CAI43140 CAI43140.1 Homo sapiens (human) collagen, type IV,
alpha 6
UCCGGAACAACAGGGCCAUAUAGGUAGGAACGGAUUAGAGGUCCUUCGGGUGCCCCAGGUCCUUC
AGGACCAUUGGGUAAAGGACCCUCCGGUCCACCUGGUCCUACCGGA

>EMBL_CDS:CAI23618 CAI23618.1 Homo sapiens (human) pseudogene similar
to part of
CCACGCGUCGGGCGGUCCGACGGUUACCUCUACGGCUACUCGAAGACCUCGACGGACGUCCCGA
CGUCGCGG

>EMBL_CDS:CAB43181 CAB43181.1 Homo sapiens (human) FUL (ferritin, light polypeptide)
CCAGUGGGUAGAAGAACUACUCGAAGUGAAGGAGUAGAUCUUCACUCAGAGGUCCUUCAGUGUC
UCUACCCCCAGG

>EMBL_CDS:CAB76865 CAB76865.1 Homo sapiens (human) ubiquitin-conjugating enzyme E2
UCCAAGUUCAGAAGGAAGUAGUGAGUCAAAACGAAACACUGAAGUCCAUUCUGCGAACUUGGA

>EMBL_CDS:CAA21453 CAA21453.1 Homo sapiens (human) gamma-aminobutyric acid (GABA) B
GGUGUUUAAGGACCCUACAGUACAACUUUACGACGCCCAUAACCGUCCUAAGUCGUACUGUUAG
AGUCAACACUACACC

>EMBL_CDS:CAI42323 CAI42323.1 Homo sapiens (human) melanoma antigen, family E, 1,
CCUUAUUUUUCACCUUUUCUCCUUCUCCUUUACCUCUCCGAAGGAGGAGGAGAGAAGACACCUU
AGGACACGUCUAAGA

>EMBL_CDS:CAI42433 CAI42433.1 Homo sapiens (human) dynein, axonemal, heavy chain 8
UUUUUGUGGUCUAGUUCUCUACAAGGAGAUUACUAAAGUAACUUGACAGAGACCAUUUUGACCUC
AAAAA

>EMBL_CDS:CAI19790 CAI19790.1 Homo sapiens (human) exocyst complex component 2
CUAAAAGAGGGGACUAAACACUGGAAGCAGGUACCAUAGGGAAGUAAACCUCUCUACGGCCAGUGU
UCCCCCACAACAG

>EMBL_CDS:CAI20309 CAI20309.2 Homo sapiens (human) meningioma (disrupted in balanced
UCGCGUCGGUCCGUCGAGACCGGCUUGUCCAACAGGAACCUCGACCCGAACAACUCCUCGGGUC
GCUCUCGCGCGGGUAAAUGACCGGCUCACGCGACCCGACCCGA

>EMBL_CDS:CAQ07680 CAQ07680.1 Homo sapiens (human) pseudogene similar to part of novel
CCACUACCGAGACCGACGGGUCUUCGACACCCACCCCGUCCCCGACCAGAACAGGACUCCGGGAC
ACCGGGGUCCACCCGUCUCGGUCCGGUAACUCGG

>EMBL_CDS:CAA22267 CAA22267.2 Homo sapiens (human) collagen, type IV, alpha 5 (Alport
CCCAAGUGGUCCCAUUGGUCCUAGUGGUCCGUUUGGUCCUUAAGGACCAACCGGUAAAAGAGGUA
GAAACGGACCAAUGGA

>EMBL_CDS:CAI23555 CAI23555.1 Homo sapiens (human) cadherin, EGF LAG seven-pass G-type
GGGUCCUCAUCUCCCGCCAGUCUAGGUCCUGAAGAACCUCGGCCAGACUCACGGGACCC

>EMBL_CDS:CAM26476 CAM26476.1 Homo sapiens (human) fumarylacetoacetate hydrolase
UCGCGAACGGUAGUGGUGCGGGUCGAGGUCGAGCACCAGUCCAACGCUCACAUGCGCCCGUAC
UCCUACCCGCUCGGGA

>EMBL_CDS:CAI95580 CAI95580.1 Homo sapiens (human) PUUAUIVE novel protein similar to

CCCUGUCGCAAGGUCCGUCCACGUCAACCGGGGACGUGUUUAGGCGGACGAUCACGUCGUAACC
GGUCGCAGUCCUACCGUGGACAGCCCUUGAGAAAGGG
>EMBL_CDS:CAI42184 CAI42184.1 Homo sapiens (human) chromosome 20 open
reading frame 94
UAGUGAAGGUUCUCUUUGAGAGGGCACCACCAGCUUCAGAAGGCGUCUCGACGUCAAGGACGCAA
AGACAACCCAAAACCGGUGAGCACCUGAAACAAAACCUGUACCACUA
>EMBL_CDS:CAI42909 CAI42909.1 Homo sapiens (human) UUP14, U3 small
nucleolar
AGAGAGAAGCUCGGAACCGGAGUAUCAUCCUGACGUCUCGGGCUCGGGAGACUUCGAGACGAGCA
GCGUAGAAACGGAGAAGAUCGAGUACCGAGCCUCUCUCC
>EMBL_CDS:CAI42503 CAI42503.1 Homo sapiens (human) solute carrier
family 13
ACAGAGGACCCGGAAGAAGGUCCAGUCGUUCCCGAGACAGAGACACAACCCUCGAAACUUCAGUU
UGGUGGUGAACUCUCUCCCGAAACCCUGCCCUUCUUCUUGUUCUACCACUGU
>EMBL_CDS:CAC03411 CAC03411.1 Homo sapiens (human) histone 1, H2bf
CCCUGUCGUCGUCGCAUGCCGGCAGACCUAGAGGGACCUCACUACCACCUCGCGAACAACAUUA
CGCGG
>EMBL_CDS:CAI20551 CAI20551.1 Homo sapiens (human) zinc finger
CCCH-type containing 12A
GCCGACGAAGGACACGAGGUUCACUCACCGAAGAAUGCGUCCUUCACAGGUCCGACCCGGGCA
CGGCCGGGUCACCCAGUAGUCCCCGUUUUGAACAGUAAACUGCUUCCUCAUGUACUCGUCGGC
>EMBL_CDS:CAM21580 CAM21580.1 Homo sapiens (human) G protein-coupled
receptor 112
ACAGUCUACAGUCUUUACAACUAAAACUGUGGAGAUGACAUCUCCUUCAGUAUUGUACUCCCCGU
AAUCUAU
>EMBL_CDS:CAB51071 CAB51071.1 Homo sapiens (human) hypothetical
protein
CUUACCUACCCGCAAGUCCGAGUCUCCGGGUACUUCUCCACCCGGAGAAGGAGCUUCCGGAAAC
AAACAAA
>EMBL_CDS:CAB45738 CAB45738.1 Homo sapiens (human) hypothetical
protein
CGCGAACAGGACGUCGUGUCCGAGGAAGUAGUCGACGACCUAGACCGUCGACGACUUUCCCGU
CAAAUGACUACUAGACGGCCUGUCACG
>EMBL_CDS:CAD92528 CAD92528.2 Homo sapiens (human) transcriptional
regulating factor 1
CUCCCGCCGCCGCCUACUUCUCUCCAAGGCCGGCCACGGCCUUGAAAAAGAAGAGGACGUGCCA
GAA
>EMBL_CDS:CAI21445 CAI21445.1 Homo sapiens (human) chromosome 6 open
reading frame 94
AACAGACUCAAACGAGGUCUUCGUCCAGGUAUCGAUUAGGACUGAACCAACCCUGAAGUAAGC
ACCGGUGGUCCUGGGACAAGACGUCGUUUCGAGGGUGUC
>EMBL_CDS:CAO72109 CAO72109.1 Homo sapiens (human) novel transcript
CGUAGUGGACCCCUCCACCGGUUCCACCUUCUGGACCCGGCAAUCCAGGGCCUCCUAGAAGGGA
UCGGGUGCUACCCGAGGACUACAGAGCCCACCACG

>EMBL_CDS:CAB42442 CAB42442.1 Homo sapiens (human) hypothetical protein
UUCGAAACGAAGUCCUAGACGUACUCGACGUACCUCUAAAAGUAUUUAGAGAGACAACCACAGUC
UCCGGAACUUAUCUUGUUCAAA

>EMBL_CDS:CAI43080 CAI43080.1 Homo sapiens (human) androgen receptor
CGACGACGACGACGACGGACCCCGAUCAGAGAACGACGACGACGACGACGACGACGACGACGACG
ACG
ACGCGAGCG

>EMBL_CDS:CAB46715 CAB46715.1 Homo sapiens (human) small nuclear
ribonucleoprotein
CCGGGUCGUUCAGGACGUCCUCGGACCCCGUACCCUUGGGGUCGACCCUAAGGAGACGGUCGUCG
GGACGGCUAGGGACCCGG

>EMBL_CDS:CAB43225 CAB43225.2 Homo sapiens (human) hypothetical
protein
CAUAGUAAGAGACUUGAACAAAGUGACUUUGAAAAGGUGGCAAGAAAACGAGAACUCUCCUUCUA
AAGUAUUUCAAGUCCUCACUAUA

>EMBL_CDS:CAI42283 CAI42283.1 Homo sapiens (human) spectrin repeat
containing, nuclear
CACCAGGGGCCUCCAUAAAAACUAACGUAAAAGACACUAAAAUGUAUCCGGAGUCCCGAAAGCC
CCUAGUA

>EMBL_CDS:CAI23231 CAI23231.1 Homo sapiens (human) actin, gamma
pseudogene 9
CGAUCGUACUCCAUAUACGUAAAACGGUCCCCGUUUAAAUAUGAAGACUUAUUGGGUACGUCGUU
UACGAUACGUAGACGAGCG

>EMBL_CDS:CAI19089 CAI19089.1 Homo sapiens (human) novel protein
CGGAGUCCGACCGACCACUACCUUCUCGACCACAGGUCUCUGGGACGUUAGGUCAGUAUCGGGUC
CAUACCGGACUCCG

>EMBL_CDS:CAM28081 CAM28081.1 Homo sapiens (human) collagen type XII
alpha 1
CACUGAGGACCCUCGGACCCGAAGGGCCGCCGGGACCACCCGGGGACCCAGGGUAACGUGGCAG
AAAAGGUCACUUCGGAGACAGAGGACCUCAGGGUAACCAGGACCACCCGGUCCAUAUAGGACCC
AAGGACAAGCCGGACCUUCAGGACCGAGAGGUCGUAGUG

>EMBL_CDS:CAI19192 CAI19192.1 Homo sapiens (human) REV3-like,
catalytic subunit of DNA
UCACUGUCAGAUUUUUGGUAGACACCCACAAAUA AAAAGUUUUCGAGGUGCUCACCAAAUCAA
UUUAGUGA

>EMBL_CDS:CAI21950 CAI21950.1 Homo sapiens (human) zinc finger
protein 697
CCUCCCCGAAGAGCGGCCACACGUGCGGUCCACCAAGUGGUCCACGCUCAAUGCGGGCUUCGGG
AAGG

>EMBL_CDS:CAB46377 CAB46377.1 Homo sapiens (human) hypothetical
protein
UCCGUCUACGUGCCUGUUAGAGACGGGUACGGAAGAGUCUGUCGGUAACCCUCGACCUAACCC
AUCCCCAAUAGGUCACGCUACGGA

>EMBL_CDS:CAQ07672 CAQ07672.1 Homo sapiens (human) chromosome 11 open reading frame 41
CGUCUCAGUAAACGUCACCGUCUCCGAUCGAAAGACGACCAGUAAAGAUACCGGGGACUAAGACG

>EMBL_CDS:CAI95767 CAI95767.2 Homo sapiens (human) collagen type IX alpha 3
GACGAGCGGAAACAUCGGUCACCCAGGGAACUUGGGACCGUAAGGUCCCCGGGACCCCCUGGAC
CGCCCCGUC

>EMBL_CDS:CAI95769 CAI95769.2 Homo sapiens (human) death inducer-obliterator 1
CCCCGGAGACGACAGGGGUUAUCCUCCACCGGGUACAACGGGGCUCUUAUCCUACCCG
GGAAGACCCGAGGCUUAGACCGACCGCCUCCGGGA

>EMBL_CDS:CAB53713 CAB53713.1 Homo sapiens (human) hypothetical protein
AGGUUGGGACUAAGUCCCCUCCGGUACCGAAAUGCUACCGUCGGUACAGUGACACCUACCUGUU
CACCUUCAGCAGAUCCGCGAGACACAGUCCCUACCU

>EMBL_CDS:CAI22564 CAI22564.1 Homo sapiens (human) chromosome 1 open reading frame 134
CGGGUAAAAACAACAACAACAACAACAACAACUCUAUCUCAGAGUGAGACAACGGGUCCGAC
CUUCGUUCUGGGACAGAGAUUUUUUAUUCUCCCCGUAGUCGUUCUCCCCG

>EMBL_CDS:CAI21775 CAI21775.1 Homo sapiens (human) replication protein A2, 32kDa
CACCACUUGAGUAAGUAUAGGAGUCCCCGUACUAGAAUUCCGAUGGUCCGAGAAAAACAAGAC
UUUUCUAGAGUCCACCGGACGGUGAAAGUGUAUACAAAGACCUCCUUGGUGUCACAAAAGUGACG

>EMBL_CDS:CAI19682 CAI19682.1 Homo sapiens (human) ribosomal protein S4, X-linked
GGAACCGAACACCGUACCAAACACGGUACCAAACAACGGGAACGGUUAUUGUUUUUACAACCU
UUCGGUCCACCGUACGACAACGGCAACCGCAGAAAGUGCACUUGGUACCGUUUUUAUAGGUCCC

>EMBL_CDS:CAI22711 CAI22711.1 Homo sapiens (human) potassium voltage-gated channel,
UUCUAGAAGGGACGUUAGCAGAAUCCGUGGUACAGAGGCAUAGGGUCACACCAGUACCACUGUUA
CCACAUGGUUUUGCUCCGUCCCUACGAA

>EMBL_CDS:CAI42134 CAI42134.1 Homo sapiens (human) forkhead box H1 (FOXH1) pseudogene
CUCCACAGGACGUCAUCUCACCUCUCUGGUCCGGGAUCCGAGACACCUCUCCCAGCUCGGGUC
ACCGAGGGACGACCCUUCGGAG

>EMBL_CDS:CAB81612 CAB81612.1 Homo sapiens (human) EPH receptor A8
CCCCCACUACGUCUCCGUCCUUCUGUCCACCCCCACGGACAGGUAAGACUAUCACGUAGAAGAG
GAG

>EMBL_CDS:CAB43361 CAB43361.1 Homo sapiens (human) hypothetical protein
GGAGAGGGGGUUAUAGGUACAGGGGGGCCUCCGGAGAAGACGUGGGGGUGAGUCGCCCCUCGGUGUC
CUCCGACUCGCCGCCACUGGAGCUCUCCGGAUCCCCUCCUCCGACCACCCCUCUCC

>EMBL_CDS:CAQ10064 CAQ10064.1 Homo sapiens (human) cyclic AMP phosphoprotein (ARPP-19)

UUCCUUCGACCCGGGGGUCCGAAACAGGAUCCGAACCUAUAACCCGAAAUCGAAAAGGAA
>EMBL_CDS:CAC00585 CAC00585.2 Homo sapiens (human)
UUCUCUCGGGGCAGGAGUCCUAGUAACGACAUCAGUAGGUGGUUCUACUAAAGAAAAUACUCUAC
CCCCCCGAAAAGAA
>EMBL_CDS:CAQ76415 CAQ76415.1 Homo sapiens (human) olfactory receptor,
family 2,
GAUUACCAGAAAAGACCAGGGGCCUCCAACUGGUCGUAGACACCCUGUCACGACCACCAUAUCGU
CUCCAGGUCUUUCCUAUCUAAUC
>EMBL_CDS:CAI20272 CAI20272.1 Homo sapiens (human) arginase, type II
(ARG2) pseudogene
AGAGGAUCUAGUCUUAUGCGAUUAUGAACCCCUCCUCUAUGUUCCAAACAGGUCCCUUJAGGACCU
UCAAGACCAUGGAAAGGGACAUCAAGACACUCCUCU
>EMBL_CDS:CAB81608 CAB81608.2 Homo sapiens (human) rearranged L-myc
fusion
UCUACUAAGGUUUAGACAAAGUCUUGAUGUAAGUAGGAAAAUCCUACUGUCACACCAAAGAGUC
UCAAUUGAUGACCCUAGUGGA
>EMBL_CDS:CAI43017 CAI43017.1 Homo sapiens (human) transient receptor
potential cation
CCCCGACCCCUACUACAACUUUCCUCCACCGUCCACGGUGGAAGUAGUUUCAUUGAGUAGGUCU
CGAAG
>EMBL_CDS:CAB43293 CAB43293.1 Homo sapiens (human) hypothetical
protein
CGCCGACGGCUGAGUCGGUCCUUGAGAAAGAGUCCCCACCGGAGGACCCUGUCUCCUGAGUCUGGG
ACUGAGCCGUCGACG
>EMBL_CDS:CAB92770 CAB92770.1 Homo sapiens (human) glutathione
S-transferase A2
UUGAAGAAGUGACACCCGUCCAAUGACUAAGACCAAAGUCCCGGAAGUCGUCUCCCUUCGACCU
UUAUUCGUAUCUAGUUCGAGAAGGUGCAUCAUCUCUCAA
>EMBL_CDS:CAB45747 CAB45747.2 Homo sapiens (human) hypothetical
protein
AACGAAGUUCUCCACCUCCUCCGAACACACCCUUGGGGUGGUUCACAGACAUUUUAUACCUUCGUC
>EMBL_CDS:CAB65797 CAB65797.1 Homo sapiens (human) olfactory receptor,
family 5,
CUUUCUUCUACCACUUAUCAUUUUUGACGUUAAGUAAAUCCAACCUCUAGGGUUCUACUACUUA
AGUCAAUUCGACAAACUAAGAAAAGAAAG
>EMBL_CDS:CAI22044 CAI22044.1 Homo sapiens (human) dystonin
UGAUAGUCACAGACAAGGACACAAUAAGACGACUAGUAAGUCGUCACUGCAAAGUAUCAGUGAUC
GUGACUACCA
>EMBL_CDS:CAI23037 CAI23037.1 Homo sapiens (human) E1A binding
protein p300
CCGGACGACGGAAUGGGACCCUGUGUCCCGGUCGUCGAACUCAGGACCCGUUCAUCCACCGUAC
GA
>EMBL_CDS:CAO03467 CAO03467.1 Homo sapiens (human) myo-inositol
oxygenase

CUGGACUGCACAUCAAGGCCUUCGACCGGAACAGAAACCGGUGGAGACCCAGGUGUAGUCCAG
>EMBL_CDS:CAI43095 CAI43095.1 Homo sapiens (human) zinc finger
protein 64 homolog
ACCGACCUCAACGCCGACCGCAUCCCCGUCUAGACCGUAAACUCCCCGGCGAGCAGGCUCACCUA
GGAGUCCACGAACAACUCCGACGACGACAGCCGUCGCCGCAUCAGU
>EMBL_CDS:CAI22113 CAI22113.1 Homo sapiens (human) sex comb on midleg
homolog 1
UCGACAGAACCUACCCCGUCUCUACCCUACCCUUAAUCCCGAACCACAGGCCGGGGCGAAGA
AAGGACCAAUGCGGGGAGACGGGACCAACUACAAGGUUCUGUCA
>EMBL_CDS:CAI43016 CAI43016.2 Homo sapiens (human) chromosome X open
reading frame 45
CUACUUAAGGACCCGUAGGGUAUAGGGGUCUGAACAGAGCCUCUACCUACGACUCCUACUUUAC
AAGUAA
>EMBL_CDS:CAI19918 CAI19918.1 Homo sapiens (human) KH domain
containing, RNA binding,
CCACCACCCCUCCUCCUACCGUGGGGGUGCCGGGGAACUCCUCGACACCCUCGAUAAGACUA
GGGAGACGGAGA
>EMBL_CDS:CAC33877 CAC33877.1 Homo sapiens (human) zinc finger,
NFX1-type containing 1
CAACUUCAAGAACCGGUCUAGUAUGUGCAACCGUGACCCCGCGUCGACGACCACCAGGGGUUAGU
UUUACUCCACGACCGUUCGAAACGAGUUACACCGUUACCAUACCCGGAGUCCUGAAGGCG
>EMBL_CDS:CAB88112 CAB88112.1 Homo sapiens (human) chromosome 6 open
reading frame 72
UCUAUGACCGAUCACCAAACGUCACUUGAUUGUGAAAGAAAAAACCCUCUCCAAUCCUCCAUUU
AUUUUACAGUGACAGA
>EMBL_CDS:CAB59178 CAB59178.1 Homo sapiens (human) hypothetical
protein
CUAGGGACCCGAGGACUCUCGGUGACCCGACCCCAACCUGUACUCGUACAGGGAAGAAUUGGGCC
GGGAAGAAUGAGUCGAACCGGACCCAG
>EMBL_CDS:CAI19914 CAI19914.2 Homo sapiens (human) soluble adenylyl
cyclase (SAC)
GAAGAACAUCGGAUUGAAACAGAAGAAGAGAAACCAAGGUAGUUACUACAGCUAUCUCCUCCGU
AAUUAUACCCGAGUCGUCCUUC
>EMBL_CDS:CAB55978 CAB55978.1 Homo sapiens (human) hypothetical
protein
UGC UUAUUUAGAAAUGAAGAUCCACCCAACGUGAAAAGAUCAUCAUCUAAAUAGGUAGCA
>EMBL_CDS:CAI40128 CAI40128.1 Homo sapiens (human) actin filament
associated protein
ACAUUCACAACCCGAGACUCUUGAAAGAGACGUAGUCAUUCUCUCUAAAACCGGCGUGAGUGU
>EMBL_CDS:CAB55985 CAB55985.3 Homo sapiens (human) hypothetical
protein
GACCGUGACCAUCGUCCCCAUCCCCUCCGUGGUGUCCUGAGAAGGGGUCGUCGACGGAGACGAAA
GAGGCCCGGUC
>EMBL_CDS:CAB96723 CAB96723.2 Homo sapiens (human) CD83 molecule

AGUCCCUUAUCCCGGAAAGUAACCCCCGAGCUUUCUUGGUAAAACGGGGAAGACUACUAUCACG
ACAGGGGACU

>EMBL_CDS:CAI22736 CAI22736.1 Homo sapiens (human) sperm associated
antigen 17

UCUUUAGAGACCAAACCUUCUGAUCCGUGUGAACUCCUAAAGACAAGACUUUGGAAUACACCGA
ACUUUAGAUCUAAUUCUAGUCUACAUAGA

>EMBL_CDS:CAB55920 CAB55920.1 Homo sapiens (human) hypothetical
protein

GGGUCCCCACCGUACGGGUGGACCUUCCGGACGUGCAUGUCGUCCUACGACUCCCGACCCCGGA
AGAGACCGAGUCGGUAGAAAACCC

>EMBL_CDS:CAH10712 CAH10712.1 Homo sapiens (human) hypothetical
protein

GAACCGGUUCUAUAUGAGGGAACGUCACCGGUCCGACGAGGAAACGACUCGGUAUCUGGUGACGA
ACAUCCAUAACCGGUCC

>EMBL_CDS:CAI19330 CAI19330.1 Homo sapiens (human) chromosome 20 open
reading frame 32

UACCCCCCGUGCCGGACAGACGUCGCGUGGAGGCACUCCUAAACCUCCGCCAACCGUCCCCGGUCC
GGAACGGAGGGUA

>EMBL_CDS:CAB57341 CAB57341.1 Homo sapiens (human) hypothetical
protein

CCCGCGACUCCUGUCUACCCGACUGUAUCUUCGGUACCAAUCCUAGACCGCACAUAGAGCCAGGUG
AAGUCGUCGCGGG

>EMBL_CDS:CAI21960 CAI21960.1 Homo sapiens (human) fatty acid amide
hydrolase

CACAUCGACUGCCGGGGACACCCGGGACGGACCCCGUAAGUUCAGGUCUCGUCCCCGGUCGUACCC
CCAGUCGUGGUG

>EMBL_CDS:CAB56033 CAB56033.1 Homo sapiens (human) hypothetical
protein

GGUCCAUAACCCCGACAACCCGGACCAAGUCCCCUGGGAUGAGGGGCCGGGAAUCGGGUAGACC

>EMBL_CDS:CAH72269 CAH72269.1 Homo sapiens (human) chromosome 20 open
reading frame 59

CUACCCGUACGACCUCGCCCCGCGUCAUGUCUUCCGUACACGGGUCGUCGUCGCAGGGGCAG

>EMBL_CDS:CAB81623 CAB81623.1 Homo sapiens (human) novel protein

AACCGAAAAAGUGAGUCGUUUGAGCACUCUGACCCCUCCAGGUCCCGCGGACCUAACGAAUCACG
GAGAAGAAAGAGAUCCCGACUCGACACUUUUCGACC

>EMBL_CDS:CAM28319 CAM28319.1 Homo sapiens (human) bone morphogenetic
protein 7

CUCCCAUGCCGACAGCUCGUCCUUCUCUAGGCUAAGGGACGGUACAGGAGAGGAGACGACCUUGC
ACUCGAAGGUCUCCCGUCCUGAGCACAGACCAAGCAAGACCAGCUACGGGAG

>EMBL_CDS:CAI12515 CAI12515.1 Homo sapiens (human) golgi-specific
brefeldin A resistance

AGUCAUCCAGAAGGAACCUUCACCAAACCCUCCUCUUAAGGUCCGGUGACAGACAUCUCCUGA
CUGGUGACGACU

>EMBL_CDS:CAI22343 CAI22343.1 Homo sapiens (human) chromosome 1 open

reading frame 164

ACACGUCCCCUACUGUAGUCGGAGACACAUAAACACCGAAGGGUAUGAGGUCUCACAGUAGGGGUA
GGUGU

>EMBL_CDS:CAC44024 CAC44024.1 Homo sapiens (human) SLC2A4 regulator
CCGUCACCCCCACUGCCCCACCUGCCUCUCCUGACCAGUGACCGGUCCAGGGUAGGGGUCAGAGG
UGACAACGACGACGACGA

>EMBL_CDS:CAB55896 CAB55896.1 Homo sapiens (human) hypothetical
protein

CCGUGGGAACCUCCUCAGACGUCCUCACUCCCCGGAGACGACGAGAGACUCCGACAGUCGCGAAC
GUCCCUCCUCACCUCGAGAGUGUUUACCCAGACCGAGAAGGUCACGG

>EMBL_CDS:CAI15269 CAI15269.1 Homo sapiens (human) immunoglobulin
superfamily, member 8

CCGGCCCUUGCCCGUGACCGACGAAGUGCUUCGGCCCAGGGUCUGGGAGCUUGUAUCCGAAACCG
CUCCGUCGCCAUCCACGGGCGUAGUGGUCGG

>EMBL_CDS:CAI14947 CAI14947.1 Homo sapiens (human) zinc finger
protein 37A

UCCAGAAGGGUGUAAGUACUGUAAGUAUCCCAAAGGGGGACACACACAAGAGACUACAGAACAC
ACCCGACUGAA

>EMBL_CDS:CAQ09650 CAQ09650.1 Homo sapiens (human) poly(A)-binding
protein pseudogene

CACCAUUAUUGGACUUCUCCACAGGACAUCUUUAACGUCCACCUGUGUGGAGAGUGAAGA
CAAUAAAAGACG

>EMBL_CDS:CAQ10609 CAQ10609.1 Homo sapiens (human) par-6 partitioning
defective 6

UCAAAACCAAGUUAGACGACACCAAUCCGUUCUCCGAUAAUAGUCGUCUAACCGACCUCGA

>EMBL_CDS:CAI17853 CAI17853.1 Homo sapiens (human) hemicentin 1
CUUCAUAACUCGUAUGUAUCCAUCCAUAAGGAACGUGACCAGACGACUGACAAAAAACUUCAG
GUCCCACCCGAAAGCUCUUUUCGGUCGAGCCUUUAGUUAUCAUGACUCCGGUCAUUACGCUUGUC
UCACGGAAGGUGACGAACUCCAGAAG

>EMBL_CDS:CAB99331 CAB99331.2 Homo sapiens (human) collagen type XIX
alpha 1

CCCCUUGGCACUUGUGGACCUUCAGGAGAAAGUGGGAAACCGGGUGCACCUGGUCCACGAGGUCC
UAAAGGUAGAUUAGGACCAAGGGG

>EMBL_CDS:CAM13070 CAM13070.1 Homo sapiens (human) shroom family
member 4

CGGAGUAACUCACCCAACCUUAGGUGCGACCUUCGAGACAGUGUCCGAAAACCCUAGGUUGUCG
AAACCAACUCCG

>EMBL_CDS:CAI16056 CAI16056.1 Homo sapiens (human) chromosome 9 open
reading frame

AAGUAAAUUUCAUCGUGUAAUCCGUUACGAAGUUAUCAUCCGAAGUUUCACGAUGAAAAAUUCC
UU

>EMBL_CDS:CAI23423 CAI23423.1 Homo sapiens (human) leucine rich
repeat containing 7

GACUCUACUAAAGAAGAAGUGGAGCCUUUGUAGCCGUACCGUGGUCUGCCGGCUACUAAAAGGCA

AACCACCAGUAGAGGUC
>EMBL_CDS:CAH61508 CAH61508.1 Homo sapiens (human) ribosomal protein L12 pseudogene 3
CACGAAUACACGAAGACGAAAAGAGACAGACUCACCAGGAAACUGUCGAAACUACCAGUUCGGU
CUCCGUCUCCAUG
>EMBL_CDS:CAI22170 CAI22170.1 Homo sapiens (human) chloride channel, calcium
GACACUUGACGAACCACAUACCAAGUAGAGAUGGACCCUCACAUCCACCACGUUGAUUUGUAGU
CGUACAAAUACC
>EMBL_CDS:CAC35071 CAC35071.1 Homo sapiens (human) novel protein similar to serine
UAGUCGGGAUAGCAAUAGUUUAGGACUCUUCACCUAGUAAGGUGGUCCGUAAAAGAACUAGCAAC
CCGACUA
>EMBL_CDS:CAB55911 CAB55911.1 Homo sapiens (human) hypothetical protein
AAGGCCAAAGUGAACUCCCUCCGAAAAACAGCUGCAAGAGAGAGAAAAAGAGCUAGGGCAGAAA
GAACUCUAGCUCUAGCCCCUCUACAGCCGCAGAUAGGGACCUGGCUCUAGCUCUU
>EMBL_CDS:CAQ07060 CAQ07060.1 Homo sapiens (human) staufen RNA binding protein homolog
GCCGGAACUGAUAAACAAAUCCCGCAAAAAUUUUUAUUAACGAAAAGGUGGUGUCCUUCU
CCACCUUCAAAAAUUCGAGGACAUUCUGCCACCAACGUCGUGC
>EMBL_CDS:CAH70743 CAH70743.2 Homo sapiens (human) centlein, centrosomal protein
GCCUCUUGGGAACAACCGUCUAUACAAAAGACUGUCAAAAAGUAAACGAUAGAAAUCAAGAG
GAC
>EMBL_CDS:CAC40711 CAC40711.1 Homo sapiens (human) 1060P11.4.4 (killer cell
AGUGAGCCCAGACUGGUGAGCAUCCCUUAGGUACCUUUCUGGCUUCGUAGACAUCCAGAGAGG
CACCCACCGUCCUGGGUCUCCU
>EMBL_CDS:CAI19614 CAI19614.1 Homo sapiens (human) ADP-ribosylation factor guanine
CCCACCUUAGGUCCGCGAGGAGACCACGUCCUUAACCCGAUACAGAAGUUGACUGCAAGGGUCG
UACGGGACGAGGACCUCUUUGACCUAGGGGG
>EMBL_CDS:CAH71770 CAH71770.1 Homo sapiens (human) transcription factor 7-like 2
CCUCCUCGACAAAACUAAGCAAAGACUAAGUAACUGAUCUCUGCUAAACUGUAGUCGAUUUAGG
>EMBL_CDS:CAI14921 CAI14921.1 Homo sapiens (human) zinc finger, CCHC domain containing 6
CGACAACAUUAUCCAUUCUACAAAGAGUCUGGACUUACAAAAGACUCCUGAGAACGAUUAAGAAG
UUAUCA
>EMBL_CDS:CAI19272 CAI19272.1 Homo sapiens (human) ubiquitin protein ligase E3 component
GGAACAACCAGGACGACGUCCGAGUCCCGUUACCGAUCAAGUUGGUACCAGAGCAGUAGACGUAG
UCCACCCUACAGGUCGUACCCCCCUUCGGGAGACGCGGACGGUCGUCCCGGAGGUCC

>EMBL_CDS:CAI16208 CAI16208.1 Homo sapiens (human) nucleolar protein 8
CCAACACCGUCAUAAAACUCCCAGUAUAAACUACUAAAAUGCAAUACAACUAAAAAUUCCACU
UCUUGUCCAUCUGAGAAGGUUUAACGAGUGUUGG

>EMBL_CDS:CAI12398 CAI12398.1 Homo sapiens (human) collagen type XVII
alpha 1
CAGUCGUAACAUCGUCGAACGAAAAGAAAAAUCCACAGAAGACUUUUUCUUAACGUCGCU
ACGACCG

>EMBL_CDS:CAI20000 CAI20000.2 Homo sapiens (human) chromosome 6 open
reading frame 170
ACAGAAACCGUCAAAAGAUAGGUAAAGUCAAAACAAUAGUCUAUAAAACUCCGUUUUUUCGAA
CAGUUCUAGUAACAGAACAAAAUUGGUCGUAAGAACAUAACAGACUGUCUAUCGUCAAACCGU
UACCUAUACUACUUUUGUAACCGGUUCCUAU

>EMBL_CDS:CAB70833 CAB70833.1 Homo sapiens (human) hypothetical
protein
CCGAACACCCGAGGGCUCGGAGGACACCCUGGUGACCCUGAAAGGUAAGACCCUCCGGGGUCAC
ACUAGGGACAGUUAUCCGAACCCUGGUAACCCGG

>EMBL_CDS:CAM17621 CAM17621.1 Homo sapiens (human) potassium channel
regulator
AUGGUCGGACUGAGGUCAAACCAAUAGUCAUCACGACAGUCUUGGUGUGACCUUUUGGUCCAGUA
CCAU

>EMBL_CDS:CAB70855 CAB70855.1 Homo sapiens (human) hypothetical
protein
GGUUAUAGUAACAGGUUAUAGUAGACCCUACCUUCCAGUUGUUUGUAUAGUAGUAACAACCCCGA
UUUGGGUAGAAGUAACCCCAUCAACCGACCUCGGUGGACCUACCAACUACUACAACC

>EMBL_CDS:CAB63722 CAB63722.1 Homo sapiens (human) hypothetical
protein
ACCCGGGUUCCUGUCACGAAUGUCACCGCUCCCCAGUCCUACAGUGAACGAGAAGCGGGACGGAG
ACCGACUAGGACCCUGGGC

>EMBL_CDS:CAI39480 CAI39480.1 Homo sapiens (human) LIM domain 7
AACACUAGCGGAAAAAUCAAAAAGUUUCUUUACCUAAGUCUACGAAAACUAAGUUUUCGUAACG
AAAGUAGUACUUAAGGUAAACUAAAGAAACCUAAGUUUAUAUCUUGAGACUUCGAAAGCCUC

>EMBL_CDS:CAH73836 CAH73836.1 Homo sapiens (human) chromosome 10 open
reading frame 4
UCUCAAGAUAUCAUCUCUUAGAAGUCUAAAGAAACUUCUACUACAGGAAUAGAAAAAGAACC
UCCGGAGAAGACGUCUUCUAUUAGACCUAAAAAAUACACUACUGAGA

>EMBL_CDS:CAH71682 CAH71682.2 Homo sapiens (human) chromosome 13 open
reading frame 18
GAGACAGGUCGAGGAACCGAAAGCGUAUGUCCGAAACCGGCUACGAGUCGUUUAAACUUUACCCG
ACCACGGUAUACGACAGCUCGUCGACAAACCUC

>EMBL_CDS:CAH73304 CAH73304.1 Homo sapiens (human) dachshund homolog
1 (Drosophila)
GGAGGAGGUCUCUCCCCGUCACUCCCCGAUAGUCCUUGUGCGAGGAAUUAUUGACUACAGAGU
UGAGACCUACCCCC

>EMBL_CDS:CAI23362 CAI23362.1 Homo sapiens (human) zinc finger protein 644
GAGAUGUUCGUAUACCGGAACCCUGUAAUUCUACCGCUUUCACUGAUAAGGGUAGAUUUACUAUG
UAGUAUACGGACACCUC

>EMBL_CDS:CAI20328 CAI20328.1 Homo sapiens (human) novel protein containing CH (Calponin
ACGACUUAGGUUACUCCAUUUAAAGCUUUUUUAGGAAAAACCGUAAAAGACUAACUAACUCGU

>EMBL_CDS:CAI12722 CAI12722.1 Homo sapiens (human) ash1 (absent, small, or
ACGCUUCCUCUUAACCGUUGUUUCAUCCUCCUCUAUUGGCGGAGGAGGGGAAACUCCGGAAGAA
GUAACGU

>EMBL_CDS:CAB66599 CAB66599.1 Homo sapiens (human) hypothetical protein
UCCUGUCGAAAAGAGGUAGAUUAAAACAAAACGGUAUGUUAAAUCCCCUCGACCAUACAGAA

>EMBL_CDS:CAH70098 CAH70098.1 Homo sapiens (human) haloacid dehalogenase-like
AUACGGACGGACUUCGGAACAAGGUCCCGACUCCCGAGGUGGAGGUCGGGUACCCGGGCCCGGAA
CCACCGUAU

>EMBL_CDS:CAQ10575 CAQ10575.1 Homo sapiens (human) capicua homolog (Drosophila) (CIC)
GGGACUCCCCGGGUCCCGAGGAGGUACCACCCUCCACUCGAAAUGGUCCAAGGUGGUGGGG
GUUUCACACACCCCAACGCCCGGGACCCGAAAGUCCC

>EMBL_CDS:CAI23173 CAI23173.1 Homo sapiens (human) centaurin, beta 5
CGAGCCGACGGUCGAAGAAGUACAUCCCCAGGUCCGACCACGUCCUCCGACAUCGGGACGACCUUC
UUCGACCUGACCCG

>EMBL_CDS:CAB63754 CAB63754.1 Homo sapiens (human) hypothetical protein
CCCCUCUUUAGUCACAGGUCAGACCGAGUCCCGAACACCUGACCUAUCGCUUUCGAGGGG

>EMBL_CDS:CAI95132 CAI95132.1 Homo sapiens (human) transforming, acidic coiled-coil
CCCCAAUGGAGGGGACGGAGGCCCGGCACCAUUCUCCGUCGAAAAGGAGGGCUGUCCCCACU
CAAGACGUGAGACGGUGGAGGUCUUCGGCCCCCUGUUGGGG

>EMBL_CDS:CAD13328 CAD13328.1 Homo sapiens (human) tyrosinase-related protein 1
ACUUCCACACGUCCUCCUGUUUUUAUCCUAGUAAACCUCUGUUUACCCAAACAGGGGGACAAGGU
AAGU

>EMBL_CDS:CAI12716 CAI12716.2 Homo sapiens (human) ash1 (absent, small, or
AUCAUGAAUCCGAAAGUCGUUGAACCGUCACAAACAGACUACGUCUAUGACGUGGGUCAAAAUUU
UUUCCGAAUAAUGAU

>EMBL_CDS:CAB66750 CAB66750.1 Homo sapiens (human) hypothetical protein
GGUCCCGAGGAUCCUUCUAGACGGAGUCCACCUCGCCGGAACUCACACCUCCGAAGGCCCCUGA

CC

>EMBL_CDS:CAI14765 CAI14765.1 Homo sapiens (human) MAP kinase interacting

GACAUCAGGGUCGAUGAACCCUCCGACUCCACCCUCCUAGUGACCUCGGGUCCCUCCAACCCCGA
CGUC

>EMBL_CDS:CAH73308 CAH73308.1 Homo sapiens (human) novel transcript
CCGGACCACAAUUAGAAGAACCUGCUUAGUUUACUCGGAAUACAAACAGUAAUACGAAUAAUUUU
UACACAGCCUCCUCUAAGCUGGCCCAA

>EMBL_CDS:CAI41479 CAI41479.1 Homo sapiens (human) ubiquitously transcribed

CCGUUCCUCCCAUACCACUUCUACCACCAGAACCUCACCUGUAAAUAGGUUGUUUACGAUGA
CAAUCUAUUCGGUAAAAAUGGAUCUAAGGACGUACGG

>EMBL_CDS:CAI15524 CAI15524.1 Homo sapiens (human) Smg-5 homolog, nonsense mediated mRNA

GGACGUCGGGAUCCACCCCGGACGAGGGACGGGACCUUCGAUCUGUCUCCUCUGUGUUUCGUCU
UCACCCCGUUACCCUACACGUCGGGGACGAAAACCCGACAUC

>EMBL_CDS:CAH71353 CAH71353.1 Homo sapiens (human) calcium channel, voltage-dependent,

GGUGUAGUAUGCCUCCUCACACGAGACAGAAGAAUUUCUCCCGUAAGAAAAGAGAAACCUCACC

>EMBL_CDS:CAB70793 CAB70793.1 Homo sapiens (human) hypothetical protein

AAGAAAGGACGGGAGCCACCGUGCGACGUAGGCCGGCUACCAAACCAAGUCCUACCCACCCGUG
GGUCCUCUCUU

>EMBL_CDS:CAB70826 CAB70826.1 Homo sapiens (human) hypothetical protein

CCAGAACCGUACCUCUCUUCUCGACGACGUCCCGGAGAGCCCCUCCCCAACCGGUUCAUCCGU
AAGUGGUCGACGUACUAGAGAAGGUGGACCCCGAGACGUCCUCCUCGACCGAGAGAGGGUGGGA
GUUCCGG

>EMBL_CDS:CAI19076 CAI19076.1 Homo sapiens (human) DNA cross-link repair 1B (PSO2

CUUUCGUGACGGAACAAGGUAAGAAACGAUAUCUCUAGACCCUUGUUGACGAAGAACUAGGCGU
UCCUACCACCCUCCGACGAAAAG

>EMBL_CDS:CAI22995 CAI22995.1 Homo sapiens (human) dedicator of cytokinesis 7

CUCCCAUAUACAUCUCUUCUAAAAGACAUUCAUCAAAACCUUGUAUUUGUAGGGAACGCCUUUG
AGAUUCUAAAGAG

>EMBL_CDS:CAI41083 CAI41083.1 Homo sapiens (human) interleukin 15 receptor, alpha

CGACGACAACACCGGCGACACAACAAACUCGACCCUCUACUUCGACGCCCGAGGGCGCAGCGGCC
GCCGGCCUCGUCGUCG

>EMBL_CDS:CAB66695 CAB66695.1 Homo sapiens (human) hypothetical protein

CGCCCGAUAGACCCGGGCGUCCAUCAACCGGAGCAACGGGCCCUCCCACCCAUCGACUGCUGAC
CGCACAGGUCCAUCGGACA

>EMBL_CDS:CAH72822 CAH72822.1 Homo sapiens (human) polycystic kidney disease 2-like 1
GACAUACGGCAGAGGACCCCAAGUAGAAGUCCGAAGAACCCAACCCGACCUCUCCGGGGCACGA
CCUCUACCACGUC

>EMBL_CDS:CAH70925 CAH70925.1 Homo sapiens (human) v-abl Abelson murine leukemia viral
CCCACUCUAUUCUGACCGUGAAACACCAACACUCACCAACCCUCCUGCCCCGUCGGAACCGAC
CUCUUCGGGUCGGGCCGACGAGAGGUAGGAGACCUUGAGGUCGGUAGGGUUCAGCACGGGGUGGU
AAGAAGAGAAAUGGG

>EMBL_CDS:CAI19765 CAI19765.1 Homo sapiens (human) small proline-rich protein 2C
GACGACUCCACCCGUCGGACACCUGUGAAACCACCACCCGUCGGAGUCCCGUGAAGUCCCCAC
CUGUACCGAGACCUGCGAAACCGUC

>EMBL_CDS:CAB66751 CAB66751.3 Homo sapiens (human) hypothetical protein
UACAUACAGUUGGUACUGACGUAAGACGACCCACCUACUCGUCGUCCUACAUCGUCUGCCCCUC
UAUGUA

>EMBL_CDS:CAI23384 CAI23384.1 Homo sapiens (human) chromosome 1 open reading frame 84
AAGGACAAGUCUGACUUCGUCGUAGAGGACCCACACCGGACGUGUCAACCACGUCUACUGACU
CCUUGGUUCGGUCCGCUUGUAAAAGCCUCUAAGCUAUUAGGAAAAAGUAAUUGUCCU

>EMBL_CDS:CAQ52599 CAQ52599.1 Homo sapiens (human) spastic ataxia of
GGAUUUUCUGAGUUUGUUGAGUUCUUGGAAGACGAAUAACAUCUCCAUGAUGAUUCAACACUUC
CAACAUC

>EMBL_CDS:CAB66709 CAB66709.1 Homo sapiens (human) hypothetical protein
GAGGGAAUCGACUACCUCUGACUUGAAGUCGUCCUCGGAGAAGACGUCUUCAGAGGAGUCUAUCA
CCUC

>EMBL_CDS:CAB66530 CAB66530.1 Homo sapiens (human) hypothetical protein
CCAGGACGAGGACAAACCUCGACGACGACGCGUCCGACGCGGCCUACUACGAGUCGUCGCCGAGG
UCGUCGAGGUCCUGG

>EMBL_CDS:CAI20013 CAI20013.1 Homo sapiens (human) molybdenum cofactor synthesis 1
AGCGUCCACUAGGGCGUCCCUAUGGAGUCUCAAGGUUUCUCCGUCUGGAACUCCAAGGGUAGUC
GACACU

>EMBL_CDS:CAI16092 CAI16092.1 Homo sapiens (human) potassium channel, subfamily U,
ACGACUUAAGAGAAGAAACCAUUAUAUUUAUUUUUCGUUAACAGACAUCUUAAGUAUUACAUAUAG
CUCCUGGACCUAAGUCGU

>EMBL_CDS:CAI15169 CAI15169.1 Homo sapiens (human) POU class 2 homeobox 1
CGGACACGGACACGGACGACCUCAUCAUUGACAACGACCCGUCGCGAGUUUCAUUCGGGUCAAUA
GACAGGAGGUCGAUCGUUAUUCGACCCA

>EMBL_CDS:CAB66825 CAB66825.1 Homo sapiens (human) hypothetical protein
CCGCUCAAGUAGGUCCCUCGGCUUCCACCACCCCCGGCGCUCGAGGUUCCGACAGACCCUCUUGA
ACGG

>EMBL_CDS:CAC19507 CAC19507.1 Homo sapiens (human) novel protein
GUCGUAGAGGAGACGGACCCUCUUCCAAAGCCAUUUUCACGAAUUCGACAAGUAUCCCGUCUC
CCUCGACGAC

>EMBL_CDS:CAI22864 CAI22864.1 Homo sapiens (human) Fc receptor-like
5
UACCAUGGUAAAACAAAAGACACCACUCAUCUUCGCUUUAGGGAACGUUCACUCCCAGUGAGAGA
GAGGAACCUUCUGACACCAGGUA

>EMBL_CDS:CAI95133 CAI95133.1 Homo sapiens (human) novel protein
CGGUCCCCGAAAGUCCAUCUCGAACCGGUUCCAGAGUCUGACUUUUUCGACCCCGACUACCUCGAG
GGUAAACUUCGGGUCCG

>EMBL_CDS:CAB63721 CAB63721.2 Homo sapiens (human) hypothetical
protein
GACCAUAAGGACUCACUCCACCCUCGCGACCCAGUGUGUCAUGUGCAUAGAGAGGUCCUGUAUGG
UC

>EMBL_CDS:CAI23448 CAI23448.2 Homo sapiens (human) hypothetical
protein
UCGUCCUGUGUACCAUCAUGAUGGUCUGGUCUACCCUACACAACACAACCGUAUAUCUAGAAAAG
AUUAUAUUCGUAGUGUAGAGUACCCACUGUACCUUCACGAUAGAACUCACGGUGACGA

>EMBL_CDS:CAB70899 CAB70899.1 Homo sapiens (human) hypothetical
protein
UACGCCGGAGCAGUCGCCGUCGGUCGGGAGGAACAACCCGAGACGCUCUAAGAAGGGAAGGAAC
UAGUACCAGAAGUCCGGAGAAGUAGCGGUAGGAACUACCGGAAUAGUUCCCCAGGCGUCCGCG
GUCGACCCUCCAGAACUUGUUCGACGACGACAUAAAGACGUA

>EMBL_CDS:CAH73567 CAH73567.1 Homo sapiens (human) A kinase (PRKA)
anchor protein 2
UCGCCCAUACGGGACGUCGUCGGUAAAGAGGGCUUCGUGAAACCUGAACCUUACGACGUCGUCUU
CAUAGACGA

>EMBL_CDS:CAI21524 CAI21524.1 Homo sapiens (human) RAE1 RNA export
1 homolog (S.
CAAACAAGACCGUAGAAACAGGGUCUUCGACUUAGAUGGUAGUCUAGGGUGUCAACGUUCCAC
GGUACUUGUCCUA

>EMBL_CDS:CAH73982 CAH73982.1 Homo sapiens (human) human
immunodeficiency virus type I
CGUCUCCCAGGCAAUGAGGAAGGUCUCAGAACAAGACACGACCCAUUGGAAGACCGUUUCCCUCA
ACCACCUGAGUGACA

>EMBL_CDS:CAB70832 CAB70832.2 Homo sapiens (human) hypothetical
protein
GUCGUCGACAGACAAGACACCUCGAGACCCGGACUAUCGCAAACGGCAACCACGGGUGCGUGGUGU
GAAGGGCGACCUCGUCCCCGACGAC

>EMBL_CDS:CAH71782 CAH71782.1 Homo sapiens (human) Nedd4 family

interacting protein 2
GAGAAGGAGGACUUAAGAAACUCUACAAAGACGACGACGUCGACGGUAACGUCGUCGAAAUCGGA
AGAGUCGAAGUAGCAUACAUCUUCUC
>EMBL_CDS:CAH70133 CAH70133.1 Homo sapiens (human) zinc finger,
MYM-type 2
ACCACACUCUCUCAUCUAGGAGAAAAUUGAAAUGACUAAAUCUUCUAAAAUUGAGUAGAUUAUGG
U
>EMBL_CDS:CAH72509 CAH72509.1 Homo sapiens (human) guanylate cyclase
type protein
CGCUGGAGGAGCCACAAACCAUCUGAACAAAGGUUUUCGGAAGCAGAGGUGCCGGAAAAGACAUC
CUCGACUCCCUGUACUCUUCGUCACUGGGUAUGUGGAAAACCUCCACG
>EMBL_CDS:CAB70719 CAB70719.1 Homo sapiens (human) hypothetical
protein
GUACCGCACCCUACCACACAGAACUCUAUCGUUAUAGAUCUCCUACGUUAUAGAACCCUACAGUACA
GUAC
>EMBL_CDS:CAC05478 CAC05478.1 Homo sapiens (human) progesterin and
adipoQ receptor
CUUCUCCUAGACCUCCACACCAUGGUCCGACGAACGAGGACCGUCGGUCGGUCCACUGUCUCGC
GGUGUGCCACACGGUGUCCCGACUACAGAUCUUAUUUCGGUCUGGACGACCGUGGUGAACUGUC
UAGAAGGAG
>EMBL_CDS:CAB66731 CAB66731.1 Homo sapiens (human) hypothetical
protein
ACAAGAAGGGUGAGACCUUCAGAACUAAAAUUGACAAAUUUUAGUAUACCGACCCAGUAUUAUCC
UUCUUAU
>EMBL_CDS:CAH72176 CAH72176.1 Homo sapiens (human) novel pseudogene
CUCAUGUGUGUCGACCCACCUUCUCUUGUGUCAAGACCAGUAGACAAAGAACUGGUCCUGAAACA
GAAGGAAAAAACGCCACGAG
>EMBL_CDS:CAB66803 CAB66803.3 Homo sapiens (human) hypothetical
protein
GGAACUGGAGUCGAUGCUGCCUCCCGAACCGACUCCCCGACCCGAGAAGACUCCGACCGAGAGA
CCCAAGAGGACGACCCUAGCUCC
>EMBL_CDS:CAB70673 CAB70673.1 Homo sapiens (human) hypothetical
protein
CGGUAAAAGAACUAAAUAUCUACUJACAAGUCGAAAGAAAAGUCCUCUUGGACUACUCUUUACU
UUCCUUGUCUUGGUUUUCCUAGAAGACCUCCUACCA
>EMBL_CDS:CAI23454 CAI23454.2 Homo sapiens (human) hypothetical
protein
ACGCAGAUUCGUCGACGCCGCCCGAUCUUGGCGUCACUCGAGGAGCGUCGACGACGACGCGU
>EMBL_CDS:CAI23380 CAI23380.1 Homo sapiens (human)
myeloproliferative leukemia virus
CGACCGAGGAGGGUCGACUAGACUUAAGGGACCGACCGAGGGUGGGUACCGGAACUACUAUGA
CCCCCUCGGCCG
>EMBL_CDS:CAQ08768 CAQ08768.1 Homo sapiens (human) ribosomal protein
S26 (RPS26)

CUCCAACCACCCGUCGUGGGUGUCCAGAUUUAGUCCCAACCCACAAACCAGGAAUGGCCGAAG
>EMBL_CDS:CAB66720 CAB66720.1 Homo sapiens (human) hypothetical
protein
GUCUCCGUCGCCGUCGAGGACCUCGACCCGGAACUGGGCCUGAGGUGGAACAGCAUGAACCCA
CUCGCGGUGUCUCGAAAGUCCCCGGACCCGACCGGGAC
>EMBL_CDS:CAI16091 CAI16091.1 Homo sapiens (human) potassium channel,
subfamily U,
CAUCAUUUGGUAACCUUUGGUUGUCUAACGUAGGUCUUUUACGUAUAGACCGCCCAAUAGGUUUAU
CGUCAUGAUA
>EMBL_CDS:CAH69976 CAH69976.1 Homo sapiens (human) muscle, skeletal,
receptor tyrosine
CGGCUCCGAAGAAGAAACUCGUAGAAAUGACGGUGGUAUCACUUUCCAAGUAUCCCUUCAUUCGG
ACCA
>EMBL_CDS:CAI22140 CAI22140.1 Homo sapiens (human) Rho guanine
nucleotide exchange
CCUAUACGGAGGCCUGGUGGACGACUCCCCGAGUCCGGGAGACCGUACCCCGGGUCGAGACCCCGA
CCCCCGAACUACAGG
>EMBL_CDS:CAI41303 CAI41303.1 Homo sapiens (human) transmembrane
protein vezatin
CCUAUGACCUUAGUUAUCGAGUCACUCGAGGUGUAGGAGAACUUUGUCCUGAAGGACAACGUCC
UACCAUACAUAUCAACUCAGCCUJAGGUUAUAGG
>EMBL_CDS:CAM28254 CAM28254.1 Homo sapiens (human) RAE1 RNA export
1 homolog (S.
GGCCGUCCAACCACCCGAUUUUCUGUCUGUUGGUUACGAUAGUAGUCCUCUACUACAAUGAAGU
UAUAGGAAGUACCCUAACACUAACAGACAUCAACGUGACGGUUUGUACGACC
>EMBL_CDS:CAI12437 CAI12437.1 Homo sapiens (human) ankyrin repeat and
sterile alpha
CUCCCCACACGAAGAAUCACAACGUCGAGUCCUCCAACCCACACGUAAUUCUCGUAAAAGUGG
UGGAG
>EMBL_CDS:CAI95134 CAI95134.1 Homo sapiens (human) transforming,
acidic coiled-coil
CGGCCGUGACCAACGACGGACGGAAGACCCAAAGUAGUGUACGGAGACAGAGACCCCGUAGGAC
CCACCCACACUGAGGCCCGACCGCCCGCGGUCCCGACCG
>EMBL_CDS:CAI22280 CAI22280.1 Homo sapiens (human) KIAA1324
CAACAGUGGGGUUAUUCAGCUAGUCGUUCCGACUGUCCGACACUCCUUUGGGCCGGAACAUCGG
ACAGUGGAGACCCCCUACUACUG
>EMBL_CDS:CAB70809 CAB70809.1 Homo sapiens (human) hypothetical
protein
ACGACCGUCCACGAGGAACCUCCACUAUUAACCAGGUACAGUCAAGCCUACUGCCGGACGUAC
CGGCCGACGUGGACGACGUGGAACCUUGUCGU
>EMBL_CDS:CAI16917 CAI16917.2 Homo sapiens (human) novel pseudogene
(KIAA0563, FLJ34306)
GGAUGACAAGGAGACCACGCCAAUUCGGAAUAAAACCCGCAUUGAAAGUCUGACGUGGUCACUU
AGGACUCAUCC

>EMBL_CDS:CAI22406 CAI22406.1 Homo sapiens (human) latrophilin 2
AACUACGGGUCUCCUUUAAAUUUCAGAACCUAGACAGGAAGACAUGACUCAUGCCGUUGAAGGUC
CUGUUUAAAAGACACCCGUAACU

>EMBL_CDS:CAI13041 CAI13041.1 Homo sapiens (human) chromosome 9 open
reading frame 3
AACUACUGGUACAGAGGUAGAAGUAAAGACAGGUCGUAGGGUGACGUUAAACACUCCACCUCCGA
CCGUAACC

>EMBL_CDS:CAM15931 CAM15931.1 Homo sapiens (human) novel protein
ACGACUCAGGACACGUGCAGAACCGGCAAAACCGCAUACAUCCUACACGUCACGUAAAGUCGU

>EMBL_CDS:CAQ09540 CAQ09540.1 Homo sapiens (human) novel pseudogene
ACUCUCCUUACUCGUCGUCGUAAACAGUACCAUCUCUUUCUGAGAGACCACUUCGAGAAGGUCCUC
AAAAAGACGAUUUUGAAAACGAUCGAAAGAGUUUUACGAGAGU

>EMBL_CDS:CAI40484 CAI40484.1 Homo sapiens (human) NADH dehydrogenase
1 (MUND1)
AAAUACCAUAUCUCAAGACCACUUUAUACCAUACAUCACGAGGAUCCUUCUAUCACCAUCAUUC
CCGUAAAUAUACUAUUUAUAAGUACAUGAGACGAUUAUU

>EMBL_CDS:CAH72050 CAH72050.2 Homo sapiens (human) collagen type IV
alpha 2
CCGGGUCAGGACCCCCGGGUAAAAGAGGACCUCAUGGGAAGCAAGGUCCAUAAGGACCUAUCGGA
CCCAGGGGACCUCGCCG

>EMBL_CDS:CAI22896 CAI22896.1 Homo sapiens (human) complement
component 1, q
CCAGAGGUCGGUCGGGACCUUCGGGAAAGAGAGGAAAAUAGGGACCCCAGGGUCCAACCGGUAGC
CCCGGUCCACAGGGUCCCUAUGGGCCCUACGGUCCCUACCGACCCCCGG

>EMBL_CDS:CAQ10023 CAQ10023.1 Homo sapiens (human) novel pseudogene
CGAUUCAGCGAAAACCUAUAACUUAACCCCAAUAUUAGUGGGUCUUUUAAAUUUCCGCCUCUCG

>EMBL_CDS:CAI19463 CAI19463.1 Homo sapiens (human) peroxisomal
biogenesis factor 6
GGGUGUCGGACCCCCGGGGCAUCUUCUGUGACGAUCAAGGACAGUCGUCCCGUGGGGGACCGA
CCUCC

>EMBL_CDS:CAI39429 CAI39429.1 Homo sapiens (human) DCN1, defective
in cullin
CGGCGAGGUCGAAGAAGAACAGGUGUCGCAAGGCGUACCUGAGGGACACCUCGCUCAGACCCAAA
ACCUUCUUCGACAGGCACCG

>EMBL_CDS:CAH73425 CAH73425.1 Homo sapiens (human) mitochondrially
encoded AUP
UCGACACCCUUUUGAUUAUCGAUUAUCAUGAUCACACAGAGGACGUUAAUUUACAUAUAUCAUCA
CUGACUGAUUAUACAACCGACAUAUACGUGUCGA

>EMBL_CDS:CAC88170 CAC88170.1 Homo sapiens (human) ubiquitin specific
peptidase 20
CCUCGUGUGCAUGUCCACCAAGUGCCGCCCGGUGGGGGCUUAGACAACAUGUCCACGAGG

>EMBL_CDS:CAH70819 CAH70819.1 Homo sapiens (human) olfactomedin 1
GACGGGAGCGACAGGACCCGUCUCGACAUGUGGACGGUCGAGAGGAGUCCCAACCACCCGUC

>EMBL_CDS:CAI40281 CAI40281.2 Homo sapiens (human) chromosome 9 open

reading frame 102

CCGACGUUUGAACUCUUUAAAACAACCAUCUUAGAAAUUACUGUUCCAAAGUCUUAGACUGUCG
GAACCAAAAUUUCUCUAAGAGAAAUAAGUCUAAAGAAGGCCACGCGA

>EMBL_CDS:CAI13431 CAI13431.2 Homo sapiens (human) CUAGE family,
member 5 (CUAGE5)

GUCAAAAAGAAGUAAGUAAACUUUAGGGAAACUCCAGUAAAACCGAAGUCAAUCAUCACUAAACU
CCCUAAAACUGAGUAGAAGAUCUCUGAC

>EMBL_CDS:CAI16234 CAI16234.2 Homo sapiens (human) novel pseudogene
GCCUCUAGAGGGUUACCGAUUGGUAUCCGACGGCGAGGAACGACAGGUCGCCGACGAGGACCACG
ACCUCUCUAGAGGC

>EMBL_CDS:CAM27610 CAM27610.1 Homo sapiens (human) obscurin,
cytoskeletal calmodulin and

GAGCGGACCUCGACUGGGACCCUUGACGUCCCCGGCCCAAACCGGAGGGUCCUUCUCUC

>EMBL_CDS:CAO03600 CAO03600.1 Homo sapiens (human) likely orthologue
of Mus musculus

CCCUACUCCGAUACGAGUAGGCAGGGAGCACUAUUUCCAUCCUAGUCGUAUCUUUGGGAGUAAA
G

>EMBL_CDS:CAI95112 CAI95112.1 Homo sapiens (human) PHD finger protein
19

AACUCCUCUACACCAGGAGCUAGACAGUGACCCACGACCACUCGAACGGUUCGACGUCCUCGAG
GGUCACCACCAACUGUUUCCGGUCUUAGAGGAGUU

>EMBL_CDS:CAQ10511 CAQ10511.1 Homo sapiens (human) novel pseudogene
ACACACUCCAUUCUCGGUGGAUUAAGACCGUAGUCAUCCUUCUUCAGUUUUGACGAGUCUUC
ACCUCGAACCGAAGUAUCC

>EMBL_CDS:CAI15983 CAI15983.1 Homo sapiens (human) CD274 molecule
ACCGAGGGUCUAAAUGGUUCACUCAGGAAAGUAAACCUCUACACGGUCUCCAUCAAGACCCUAC
UGGU

>EMBL_CDS:CAI16895 CAI16895.1 Homo sapiens (human) ring finger
protein 38

UCCCUUACCACUAUCAAAAAGUAGAACUGAUUACCUUAAUACAGCUCUGUCUGCUAGGGAAGAAG
GA

>EMBL_CDS:CAB90482 CAB90482.1 Homo sapiens (human) human type XVIII
collagen

CCUCCAGGUCCCUUCGGAGCUCUCCUGGGGCGUCCCGGAGGUCUAGCGGGGCUUCGGUCUAGGGAG
GUACAGUUACUUCAGUCGAACAGCACAGACUUCUCCUCCAGGACCCCGGGACCUCGGGAACCC
CAGGACCCCGGGAGAGAGAGG

>EMBL_CDS:CAQ09916 CAQ09916.1 Homo sapiens (human) pseudogene similar
to part of

UCCUCGUUAUCACCUUCCGUCGAAUCGUAACGGACUUAUUCUUUUUCUGUUCGAAAGAAAUU
AAUUAAGGUCUCAUUACACUAAAGGUACAACAGGA

>EMBL_CDS:CAI23559 CAI23559.1 Homo sapiens (human) single stranded
DNA binding protein

CGACGGCAUUAAGACACCCGGCCUUGGGUACCCGGGGUACGGAGCCCCUCCCAAGUAAGAGACGU
AACUAGGAGGGUACAACCCACCGGAACAACAGCACACCCUAGGUUAUCUUAACCCGUCG

>EMBL_CDS:CAB82417 CAB82417.1 Homo sapiens (human) hypothetical protein
CAACCGGAAAGACUCCGAUAUACAGUCCUAGCAGGACUUCAGAACUCCAAGACGGUUG

>EMBL_CDS:CAI15920 CAI15920.3 Homo sapiens (human) chromosome 9 open reading frame 48
GGGUAGGACCUGGUCGACGAGGCUCCCUCUCUGGGAAGCAACAGACCCAAGAGGUCCUCCC

>EMBL_CDS:CAH72907 CAH72907.1 Homo sapiens (human) interferon pseudogene
AGAGUACCUCUUAUAACCACCGGACUCGGAAAACCUAAAACCACGGUAGGUAGACGAGGUCCUCU

>EMBL_CDS:CAQ07755 CAQ07755.1 Homo sapiens (human) interleukin 6 receptor (IL6R)
UCCGACGACCCCCUGUGACUCCCUCUACUCUCCUUGUUCGUGACCCCACCAAGAUCAGAGAGA
UCCUGGUCGGUGGGGUUCUUGUGUUGGUCACGUAGGACUAGAAUAGAAGAAAGUCUGGGACGUU
GAA

>EMBL_CDS:CAI14820 CAI14820.2 Homo sapiens (human) novel protein
GGACUGUACGAACAGUGGCUACCGUACCACCGCUUCGGUCCAGAAGGAACCCUUGCGACGAGAC
GGGUCCACUGUCCACAUUAUGUCAACCC

>EMBL_CDS:CAQ10338 CAQ10338.1 Homo sapiens (human) NHP2 non-histone chromosome protein
GAAGUGUAUCCUCGACCUACACAUCUUUCUAGAGGUUCUAAACACCGGUAGUGCUAUUAAAACCU
CCACAGAAAAAUUUUCCAGAGUAACCGAGGAAAUGUUUC

>EMBL_CDS:CAQ07400 CAQ07400.1 Homo sapiens (human) novel pseudogene
CGAGACCCCGCGAGGGCAUCGAACCCUCCGAAACCGGAGUCUUCGUCCAUCCCCCACAAUGACCC
G

>EMBL_CDS:CAI14818 CAI14818.1 Homo sapiens (human) tubulin folding cofactor C
ACGAAAGUUGACGGCCCCCUACGGUCCUCGGCGCAGAUGAAACCAUCUGCUUCGUCGUAGGAAA
GGGGCCCAGAACUUUCGC

>EMBL_CDS:CAI10944 CAI10944.1 Homo sapiens (human) protein prenyltransferase alpha
AGAAGAUCUUCUACCCCUUCUAAUJAGGAACCAAGAAGACAACUUGACGACGAAGAAGUAGAAA
ACCUCCU

>EMBL_CDS:CAH70960 CAH70960.1 Homo sapiens (human) far upstream element (FUSE) binding
CGACCCCUUGGGGGGACUACCACUAGAGGGCGUCCAACCCCGAGCGACAACCCUCCCCCAAGGAG
ACUUCG

>EMBL_CDS:CAH72910 CAH72910.1 Homo sapiens (human) interferon, omega 1 (IFNW1)
UACUUCAGGUCACACCUCAACCAGGUCCUCCAGCACAAGGUCCGUCGUCUCCUCGCGAGACACA
CCUUCUCCGACUUCUAGACGACGUCGUAGAGUACCUCCUGUCUGUCCCGGACCCGGACGACGUUG
ACCGACAGUA

>EMBL_CDS:CAH74092 CAH74092.1 Homo sapiens (human) KIAA1614
AGACAGACCAGUGGGUCGGACUCGUCAGGUCGGUCCCGACGGAAGGACACUCUGUGACCGCUCCA
CCAAAAGGAGCUUCCCCUCCCCAACCGCGGGUCGGAAGUCCUGUGUUCUUCGACAACCGACGG

UCCGAACCACACCCCGUCU

>EMBL_CDS:CAC16001 CAC16001.2 Homo sapiens (human) CGI-121 protein (CGI-121)

UAAACGACUCUAUGGUGUAAAAAAGUUACGGAGACUUUAUAACAAUAAACCCCUUCCAACUUUU
AUUAAAGUCAUCUA

>EMBL_CDS:CAQ06692 CAQ06692.1 Homo sapiens (human) olfactory receptor pseudogene

AGGGACAAAGAGUCCGACAUCUACUUCSCCAAGUCGUACSCCCACUGGUGGCACAUGUAGUGACU
CCGGUGACGUCGGAAAGAGCCCU

>EMBL_CDS:CAI39663 CAI39663.1 Homo sapiens (human) myeloid/lymphoid or mixed-lineage

CUUAAUAGUCCAUUUUUUCGACAAAGGAUUAUCUCCCGAGAAUGACGACAAGUCCUAGUCAUCA
UCCUCGUCAGACACGACUUUUACACAUAAACUACUCUG

>EMBL_CDS:CAQ09825 CAQ09825.1 Homo sapiens (human) hypothetical protein

CCCGUCAUCCCCGACACGAGACCGUCCGUCCGGUACCUCAGUGUCCUGAGGUUCCAGACGUUCAC
CUUCCUCGAGAGGACCAGGACGUACGGG

>EMBL_CDS:CAB90455 CAB90455.1 Homo sapiens (human) hypothetical protein

UCGACUUAACAAAGUUUUUAACCAAAGACAUCCUACCGAAGGUUAAAUAUCUACGUUAUGUCG
A

>EMBL_CDS:CAH74053 CAH74053.1 Homo sapiens (human) solute carrier family 12,

GUCACCGGUACGUCCACUCGUGUGUCCACGGCAUUUGUGCGUACAACAAGUCGUACCGACGAC

>EMBL_CDS:CAI22065 CAI22065.1 Homo sapiens (human) ryanodine receptor 2 (cardiac)

CAACCUAAAAGAACCAAGCCAGUAGGUCUUCUCACAUCSCCUUGUUCGCUCCUAAAAGAAGACAAGA
AAUGCAGGACAACCUACGGUAUUCAGGUCG

>EMBL_CDS:CAQ08581 CAQ08581.1 Homo sapiens (human) novel pseudogene
AGGAGACACSCCAUCUCGUCCAGGUCUAUCUGGAGAGAGACCAACUGGUUCCGGAAAGGGGUAACU
CCU

>EMBL_CDS:CAQ07592 CAQ07592.1 Homo sapiens (human) 60S ribosomal protein L12 (RPL12)

ACAACCCUUUACAACUGUUAGAGUAGUUUUCACUAGAAAAGUGAUACAAACUACAAGACAAAGAA
AGAGGAUCGU

>EMBL_CDS:CAI15578 CAI15578.1 Homo sapiens (human) G protein-coupled receptor 111

UGAGAGAAACAGUUCUCUUCGAACGAUGUUUAGUGUCCGACSCCGAGAACAUAACCUACUCUCA

>EMBL_CDS:CAH72236 CAH72236.1 Homo sapiens (human) thymidylate synthetase (UYMS)

CUUCGGUCCCGUCUUACACGAACUAGAAGAGACSCAUGACGUCAACCGGAGUCUCUACGUCGGGA
CCGAAG

>EMBL_CDS:CAI20310 CAI20310.1 Homo sapiens (human) erythrocyte membrane protein band

CGCCCAGACACGAACCCACGCCGGUGAUUAUCGCUUUAACCCUGGGGUUCCAGUCCUUGAACCGAA
AACCACCGACGAGACCUCUUUGUUCGGACA

>EMBL_CDS:CAM14169 CAM14169.1 Homo sapiens (human) ankyrin repeat and
sterile alpha
CCGACGAAAAAAGGAGACCCGUCGCUAAACCCUGUUCUGUAACAGAUACGACGGUGGACUCGCCA
AUUCGUCGA

>EMBL_CDS:CAQ08002 CAQ08002.1 Homo sapiens (human) ribosomal protein
S3A (RPS3A)
UCUGUAGUACCUCUCCUGUUUGUCUAACCGUUCGGAAAAUACAGAAAAGGUUACGACAGA

>EMBL_CDS:CAI12548 CAI12548.2 Homo sapiens (human) collagen, type XV,
alpha 1
CAGACGGAGGACGUCGGGUGACCAGAGAGGUCUACGGCUCUCCUGAGAAGUCCCAGUGUGUCGAGGA
GCCUCAGGACCCCAGCCCCACGUGCCACUCGACGACCUCUCCUCGG

>EMBL_CDS:CAH73281 CAH73281.1 Homo sapiens (human) chromosome 20 open
reading frame 45
UACAACCGGUCCGACCAGAGCUUGAGGACUAGAGUCCACUAGGAGGACGGAGCCGGAGGGUCCA
CGACCCUAAUGUCCUCACACAGUGGUACGGACCGGACGUA

>EMBL_CDS:CAI13397 CAI13397.1 Homo sapiens (human) chromosome 6 open
reading frame 190
GUUCUUCACAGAAAUCUUUUUACGAAGAUUAAAGACUUCGAUUCUAAGAACUACGGACCAUGA
AAAAC

>EMBL_CDS:CAM21543 CAM21543.1 Homo sapiens (human) protocadherin 15
CCGUUUCACCUCUUACUCUUCACUCCGGACCCUUUCGUUUUACUUCUCAGACUUCUCUCUAAA
GUUGACAAGACAAGGAAGAUAGUAGUCACAAAGUGGAACGGAAUAAAGGAGAAAGAGACAGUUUA
AACGG

>EMBL_CDS:CAM22929 CAM22929.1 Homo sapiens (human) chromosome 10 open
reading frame
ACAUAAAAACAAGGAACUUGCAAAAAACCUUCGUUGACGAAGGUCUUUGAAAGGAAACUUAUCAG
UUUUUUAUGU

>EMBL_CDS:CAI16805 CAI16805.1 Homo sapiens (human) chloride
intracellular channel 5
UGGGAAGGUAACUCUACGGGGACAGGAGACCCCGAGUGGACCUACUCGGAGGACCUCAAGUCUC
AUAUAGAGUAGUCCGUCCUCA

>EMBL_CDS:CAI16482 CAI16482.1 Homo sapiens (human) hypothetical
protein
CAUCGACGACAAGUAUAAAACCCGUAAUUCGUACACGUACAGGUGGAGGAAGUACCUGUACACCG
GGGACUUGUACCGUCGAUG

>EMBL_CDS:CAM14602 CAM14602.1 Homo sapiens (human) thrombospondin,
type I, domain
GACGAGCGAGUCGAGCGUCUAUAAGAGGAGCAGGCUCAAGAAGGCCUUCGACCCCCUCACCUACC
UCAACACAGCUCGUC

>EMBL_CDS:CAC40698 CAC40698.1 Homo sapiens (human) dJ1104A8.1 (novel
protein)
GUGAACGUAAAGACUAAAACUGUAACUCAGAACUACGGAUUCAUAUUCUAAAAGUAAACCAAGAA

AUAGUCCUCACCACUCAC

>EMBL_CDS:CAI22937 CAI22937.1 Homo sapiens (human) ataxin 7-like 2
CGACCCGGGACGGGUAAGUGAUGUACCGUAAAGACUCUCGACCGUCCCGACCUCACCCCCACC
CCGGGCCG

>EMBL_CDS:CAI15464 CAI15464.1 Homo sapiens (human) novel protein
CUGAAGGAGGUCAAGGCCGCCUAGGACCGUGAAAAGAAGGAUCUCACGUCUAUGACGAGUGACCU
CCGACAG

>EMBL_CDS:CAH71701 CAH71701.1 Homo sapiens (human) DEAH
(Asp-Glu-Ala-His) box

UCACAGUCCUCAUAGUCAUUCACCCCGCCUCUACGAUGGGUUUUCGACCUUGAAGAAGUGA

>EMBL_CDS:CAH72941 CAH72941.1 Homo sapiens (human) platelet
endothelial aggregation

GGAACCCGGGUGGACCGGCGAGUCCCAAGACGUCCGACCGUUUCGCCCCGGACCUUGGAACAA
UCCCCACCCCAAACCCC

>EMBL_CDS:CAH72281 CAH72281.1 Homo sapiens (human) tudor domain
containing 3

AAACCCUCAGAGAAACUUUUGCUCCGCCAAAAGUAAAGAACCGACGGACCAUAGUAAAGCUCCU
CCUACAGAGUCU

>EMBL_CDS:CAH72748 CAH72748.1 Homo sapiens (human) novel pseudogene
ACAGACAAAGAGUCCAAAUAGGUAAUGUGUCAAUACACUCCUUUACCUGAACAGUAUAUCUGU

>EMBL_CDS:CAH72940 CAH72940.1 Homo sapiens (human) Rho guanine
nucleotide exchange

AAGAGUUUCACGACUUACUACAAGGAGUGUAAACGGACCAAACUGAAGGUGUCCCCUGUUCUUUA
UACUUUACACGAAACUCUU

>EMBL_CDS:CAH72663 CAH72663.1 Homo sapiens (human) calmodulin binding
transcription

AACGAAGGACUAUAAACCGAGAAGGUCUGAGUCACGUCACCCUUCGUCGAAGAGGACGGAACAGA
CCUUCAUGAGUCCCAAGUU

>EMBL_CDS:CAI12394 CAI12394.1 Homo sapiens (human) poly (ADP-ribose)
polymerase family,

GGUCAACAGAAGACUUCGAGUCAUCAGCUGUGGUAACAUGCJUUAAGAAAGAGAACUJAAUCACG
UGUGUCUCAACGGACACACGUCACUCCUUACUUAGGUUUCUGUUCUCCUCAGCUAGUAAACUCUUUGU
UCCUGCCGUGGACC

>EMBL_CDS:CAQ06897 CAQ06897.1 Homo sapiens (human) DEAH
(Asp-Glu-Ala-His) box

UCCGUCUUACUCCAGUGGAGGUACAUCUCUCGUAACCAGCACUGUAGAAGUUACAGAA

>EMBL_CDS:CAI15500 CAI15500.2 Homo sapiens (human) ADAMUS-like 4
CCCGGCCGUAAGUCAAGUGUCGCGACCCUCGGGACCUGAAGUCACUUCGAGGGUGACUAUGU
CGACCGGG

>EMBL_CDS:CAH73232 CAH73232.1 Homo sapiens (human) ankyrin 3, node
of Ranvier (ankyrin G)

AAGUAGAACGUCCAGUAUCGGUAGGUCUCUCAGCUAGAGACACCGUAGGCACAGUACUCUUUUGA
GACGACACCACCGUUACCUUGUGAGACACUACCU

>EMBL_CDS:CAI21793 CAI21793.1 Homo sapiens (human) potassium channel,

subfamily K,
ACACUAGCUCCUCUCCUGUCAACCAGUACGAGAUACUACACGUGGACUAGGAGCAGGAACAGGA
AGAAGUGU
>EMBL_CDS:CAH73228 CAH73228.1 Homo sapiens (human) transmembrane
protein 206
CCUCCGCCUGAGCGACAGGUCCGGACCAUUCUAUGGGCCUGGAACCUGAGACUGGCAGAGG
>EMBL_CDS:CAI12685 CAI12685.1 Homo sapiens (human) chromosome 9 open
reading frame 86
AGGAGGUGUGAGACCUGGCAACGACCCGGGAGACGCCGGCCUGACCGAGACCUCCACCUC
>EMBL_CDS:CAI14117 CAI14117.1 Homo sapiens (human) BUB (POZ) domain
containing 14A
GCUCGACGAGCGACCGGCAGUACCACUCGACGGGCACAUCGUCUCCUGUCCUAGACGACCUUC
GUCCGCCCGCCGUGCCUCGGCCCGUCGAGC
>EMBL_CDS:CAI22394 CAI22394.1 Homo sapiens (human) mutS homolog 4 (E.
coli)
AAACUCCUAUUAUCAUAGAGCACGUCUUCUACUCGAACGUGGUUUUCAUUUAAAACUACGUUGA
CACAAAAGACGUUUCGAGAAAACAAAGGUUU
>EMBL_CDS:CAI14911 CAI14911.1 Homo sapiens (human) sprouty homolog
2 (Drosophila)
CCGCACGUCGGGUUAGAAGGAACGAGUCACCGAAUUCGAGUGGACCGAACUCGAGUCUAAACC
CAACGUGGG
>EMBL_CDS:CAQ08176 CAQ08176.1 Homo sapiens (human) eukaryotic
translation initiation
CAGGAGUCGAUCUUUCAGACAAUCCCUCUAUCAAAGGAGAAGAAUAAGCAGAAAAACGACUCC
GG
>EMBL_CDS:CAI16862 CAI16862.2 Homo sapiens (human) AU-hook
transcription factor
ACCCACCGUGCGGUCCCGGACCUCCCCGACGGAGUCGGAACGGGUCCGGACUGUACACGGGCAG
AGAU
>EMBL_CDS:CAI16233 CAI16233.1 Homo sapiens (human) collagen, type
XXIV, alpha 1
AAGGUUCCUCAGGGAAACCAGGAAGUCCCGGCAAAACAGGUCCUAGGGUUAUAGAGGACCUUUU
GGGAGACCAGGACCUCCCGGUCUACCAGGAACCUC
>EMBL_CDS:CAI13215 CAI13215.1 Homo sapiens (human) misato homolog 1
(Drosophila)
AUCCCUAUUCACAAAACCUCAACAUCGCCACCCUCACCACUCCUUGGAAACACACACCACUCG
AAGGGGACGGUACGAUAACGUCGUAGGUUGACAAACAGGGAC
>EMBL_CDS:CAH71957 CAH71957.1 Homo sapiens (human) potassium channel,
subfamily U,
AAUCUCGGAGAGAGGGCAAGAAAAGAAAAGGUCAAACUUUCUCGUUCUCUCAUUGUCAGAAACCG
AGACU
>EMBL_CDS:CAI19369 CAI19369.1 Homo sapiens (human) DENN/MADD domain
containing 2D
GCCCCUACUUCGAGAACUCUCACUGUCAGAAGGGUCCUCGUCCCUCCGACGGAGAGCCUCCGGG

AC

>EMBL_CDS:CAI41373 CAI41373.1 Homo sapiens (human) ankyrin 3, node of Ranvier (ankyrin

CACAGAGGCAUCAGUUACAAAUAUACCCACUGUCGUUCCGACGACGACUAAAACAUUUACUUAU
CUCAGACCUUCAAGAAAUAUACGACCAAGACCGUUUUGUAACUGAUGUCUCAUAUG

>EMBL_CDS:CAM23326 CAM23326.1 Homo sapiens (human) ring finger protein 17

AUACAAGAAUCUCUUCGCUAUUAACAUUACGAGAACGAUACAAGUAUCGACGUAAGUUUAAUAA
AAAAAAGAGAAGUUACAU

>EMBL_CDS:CAC14920 CAC14920.1 Homo sapiens (human) solute carrier organic anion

CGCCGCGAGGUCCCUCACUACUGACACAACUACUUCGGUAAGUGUCAGUAGGGGACGUCCUAC
GCCGGCG

>EMBL_CDS:CAQ08463 CAQ08463.1 Homo sapiens (human) mitogen-activated protein

UGGUAGUCAACUCACGUCUCGUCGGGUAUUGUGUCUCUAAGUCAGUUUAACCCAAAGUAGACGAG
GGGUGAGAGAACUACCA

>EMBL_CDS:CAH73892 CAH73892.1 Homo sapiens (human) novel pseudogene

CCGACCCUCCAGCCCGUGAAAUAGGUGGACGAGAAACCAUGACCAGUAGACCUCCACCCACGUCU
CCACCAGGUCGGUAAGGUCAACAAGUGCAGUGGUUAUCCACGUGGCCCAUGAAGAACUCGUAACCC
UACUAGACGAAGUGGAGGUCAG

>EMBL_CDS:CAQ10739 CAQ10739.1 Homo sapiens (human) cytochrome P450 4Z1 (CYP4Z1)

CUCUAGACGAAGUCUCUUCAGAAACCACAAAAGUGAAAACCGUGAGUUUUCUACAGGUCUUUUA
GGACCCGAGAAAAGACUCAUCAUAGAA

>EMBL_CDS:CAI13563 CAI13563.1 Homo sapiens (human) nuclear distribution gene C homolog

CUGUCCCAGACCCAGGUCGCCAUUAACCCGUCCAGACGGGGCAACGGAUCCAACCCGAAGUCAA
AGGAAACAG

>EMBL_CDS:CAQ07786 CAQ07786.1 Homo sapiens (human) thioredoxin 2 (UXN2) pseudogene

GUGACCGCAGAGUGACAACCAGAACUUUCAGUCCAGGUAGGACCUAUAAUUACCAGUAACUCCUC
UACGACCAC

>EMBL_CDS:CAI40867 CAI40867.1 Homo sapiens (human) DEAD/H (Asp-Glu-Ala-Asp/His) box

ACCAACCCACCGUAUUCUAGAGGACAGUAUAAAUAUUCGAGACUACCUCGUCUAAAACUGUCCUU
CGGUAGUCCACACUAGACUGGU

>EMBL_CDS:CAI23224 CAI23224.1 Homo sapiens (human) EGF-like-domain, multiple 9

GUCUUGAACGGACGGGUCGGUGACACCGUCUACGUGACGGUACCGACCACCGUCCAUGGCACGAC

>EMBL_CDS:CAI12104 CAI12104.2 Homo sapiens (human) discs, large homolog 5 (Drosophila)

CCUGUCCGGACCCCCGUCUGGACGUUCCCAGGGGGUCCCUUACCGAAUACGUCUUUCCUCGACGA
CGGAGGACCCCCGACCGAGGAAGGACAGAAGGUCGGACAGG

>EMBL_CDS:CAI41410 CAI41410.1 Homo sapiens (human) interleukin 13 receptor, alpha 1
GAGUCCUAGUGGAAGACCCCCACUCUACGUAAAAAGUUGGUUUUACGAUCCGAAGAGUGAGAGUA
ACCACGAUGUGACCC

>EMBL_CDS:CAH72952 CAH72952.1 Homo sapiens (human) laminin, alpha 2 (merosin, congenital
ACGACAGUGAAACCAUCGGGACCAGUCGUCGAGCAAGUAAAAGCCAGUGCUCACAUAAGUCUAACG
GGAGACGGUCGACUUAUUCGGAGAGACCCCGGGCGACUCCACUGUCGU

>EMBL_CDS:CAH73851 CAH73851.1 Homo sapiens (human) KIAA1797
AAGAACGAAGUGUUCACUACAUUUUUUAAGGAGGUUUCGACCAUUUUGGUUUCCCCUCACUCAC
UGUUGUCAAAACUCUAUCGUUCUC

>EMBL_CDS:CAH71812 CAH71812.1 Homo sapiens (human) mutS homolog 4 (E. coli)
CGUCAUAAACUGUAAUAAUAAAGGUUCCACUAUUUUAAAAUUCAAAUCACUAGUGGAAACGUAU
ACAACACAACAGACG

>EMBL_CDS:CAI12711 CAI12711.1 Homo sapiens (human) novel protein
CAAACUCGUCAAGAUUAUGGAAGAAGUGGCAGUACCCUGAAUUUGAAUAAAGAUUACUUUAUACA
AAAUCUCUUACUAAUCUCCUCCAGUCUAGGUUAACGAAUUCG

>EMBL_CDS:CAI15628 CAI15628.1 Homo sapiens (human) AUP synthase, H+ transporting,
CACGAACUCGGAAGAAACGGUCGUCGAAAUCCAGGCGUUACGUGAACCGUUAACAGAGGAAAAGG
ACGACACACCUCUACGAAACGUG

>EMBL_CDS:CAH72158 CAH72158.1 Homo sapiens (human) DAB2 interacting protein
GGAGUCCGCCAUGACCCCGGGUGGGUUAGUCCACUCCGGCUGCGGUCCCAAGGCGAACUCC

>EMBL_CDS:CAI13226 CAI13226.2 Homo sapiens (human) chromosome 6 open reading frame 170
CGUGGACAUCUGAAAGAAGUCUUCUCAAGUAUAAACGAGGUUAUUUCCUCAUUUUUAUUCGGGAAG
AAGAUGUCUACG

>EMBL_CDS:CAI13318 CAI13318.1 Homo sapiens (human) pancreatic polypeptide receptor 1
CUCCGUGUACUCCUUCAGUCUCUCCGGUCCAACCGCUAUUCGUCCAACCAGUGCAACCGAAAGA
GGAAGACGGAG

>EMBL_CDS:CAC09445 CAC09445.1 Homo sapiens (human) hypothetical protein
AACAGUUUGGUCUAAGAUUAAACGAAAAAGAAGAAGUCAUCGAACUUCGAGACCGUGAUUCUUU
AGGAGACCAAACUAUU

>EMBL_CDS:CAH71575 CAH71575.1 Homo sapiens (human) DEAD\H (Asp-Glu-Ala-Asp\His) box
GACAAGGUAAGGACCCGUACUUGAAAUUGAAUUGUUGCUCAAGUUAUCGUCCCUACUCUUGUC

>EMBL_CDS:CAQ10164 CAQ10164.1 Homo sapiens (human) actin, beta (ACUB) pseudogene
CUCCGCAUGUCCUGGUGUUCGGACCUACCGGUGCAUAUACCGACCCACAACUCCAGAGUUU
GUACUAGACCCAGUAGAAGAACGUCAACCGGAACACCAAGUACCCCGGAG

>EMBL_CDS:CAC36039 CAC36039.1 Homo sapiens (human) oviductal glycoprotein 1, 120kDa
GAUCUCGAUGUCACACGAAAGGUUCCCUAUGUCAAAAGGAAACAUCCCCAGUGUCAACAUGGAGAU
C

>EMBL_CDS:CAH73027 CAH73027.1 Homo sapiens (human) protein tyrosine phosphatase,
CGGUUGGUGGUGGAACUACACCCUCCGUAUUACAUAAGGACACAAUAAAAGAAACCAACCA

>EMBL_CDS:CAC09446 CAC09446.1 Homo sapiens (human) hypothetical protein
CGACUAUCACACAGACCUAAGACGUAGACGACGUCCUUCGACCCUCGACACCGGCGUAGACGAG
GACGUCGACUCCUAAACGUCAUUUGUCGCCCCGAUAAGUCG

>EMBL_CDS:CAI40860 CAI40860.1 Homo sapiens (human) suppressor of fused homolog
CACAUCGAGAAGUCACGUCUGUGGUUGCUAGACCUCCUCCAUAUGAUGGGGUUCCACAGACGU
GCCCCGACGUA

>EMBL_CDS:CAI23469 CAI23469.1 Homo sapiens (human) neuroblastoma breakpoint family,
CCAACCGGUCCCUCUACCGUCAUCGAACUCAUAUUCUUAAGAGAAACUCCAGAGCCUUGACG
ACUAACGAGAGACGGUCGA

>EMBL_CDS:CAQ07609 CAQ07609.1 Homo sapiens (human) novel pseudogene
GAUCCUAAAGUAGACCACGUAAAACAUUUUGGAAGUAAUUCCAAAGUGUCUCACACUAGGAUC

>EMBL_CDS:CAQ10534 CAQ10534.1 Homo sapiens (human) solute carrier family 9 member 3
GACCGGUCGUAGAAGUGCCACAUCACGUACCACAACCGGCUGACGAGGUUCUACAACCGGAAGUA
CAUGAAUACUGUCGUCUACGGUGUCUUCUAUUACCGGUC

>EMBL_CDS:CAI95313 CAI95313.1 Homo sapiens (human) KIAA2026
AUCGACCUUACCUUUGUCUUCUACCAACCAACCGAUUUUCCACUUUCUGAUCUACAUCAUCAACAA
GGUCGAU

>EMBL_CDS:CAI14157 CAI14157.1 Homo sapiens (human) NHS-like 1
CCUAGGUCGAAGAAGUAUCACGGUGAAGGAAGUCAUCUUCUUGAUCUUCUUCUUCUUCACCUGCU
ACUCCUUUACCUAUGA

>EMBL_CDS:CAQ10280 CAQ10280.1 Homo sapiens (human) retinoblastoma binding protein 8
ACGGUCACCGAAGACCGACCGUCCAGAAGAUACAAUCCGAAUCACAGUAAUCUCCUUGAAAAGC
GUUUUCUCCAGAGACCGU

>EMBL_CDS:CAH70298 CAH70298.2 Homo sapiens (human) RAB GUPase activating protein 1
AACGAUAAAGUCACAAACAGACUCCUAGAUUCUCAGAGUGUUAAGGAAGUCUGUGUAAGCCGUGA
CUUCCCAUU

>EMBL_CDS:CAB99097 CAB99097.2 Homo sapiens (human) hypothetical protein
CGACCCCCGGAACCUCGACCGUCGACAACCCCCUCUCGAGUCCCCGACUCAGAGUGAGCGUCGGA
GGACUCGGAGGGGUAGGGAAGAGCCGAGUCCGGAGUCA

>EMBL_CDS:CAQ07669 CAQ07669.1 Homo sapiens (human) peroxisomal

biogenesis factor 5

CCCUCGCGGGAGAGGACUUCAGCGACGUCGGGAAGAAACUUUCCGACUCCCACUAGUGCGUCCCC
CAAGAGGA

>EMBL_CDS:CAH72120 CAH72120.1 Homo sapiens (human) H2.0-like homeobox
CGCCUCCGACAACGACGACGCCGACAACGACGACGACAACAACAACGCCACUACCACCACCAUC
CGCCGACUCUCGCCUCUGUCGGCGACG

>EMBL_CDS:CAH74130 CAH74130.1 Homo sapiens (human) collagen type IV
alpha 1
CCCGGAGGUCCUUUCGGACGAACAGGAAACAGUGGUUACCCUGGUCGUCCUGGUUAUAGGACCUCC
GGG

>EMBL_CDS:CAH72225 CAH72225.1 Homo sapiens (human) leucine rich
repeat containing 8
CGUCUACAGGGUUUCCUUACAGCAAACAACAGGCGGGUAGAACCAGAACCAACCACCGACGAAG
GUAGAAACCUACAACCACCACUGGAGCCGUAAAGGACCACCACAUACACG

>EMBL_CDS:CAI16937 CAI16937.1 Homo sapiens (human) component of
oligomeric golgi complex
ACGUACUUCUGAGUUCGAUAACUUCUUAUAAAAAACGAAUCGUUUACGUAAAGAAGUUACCAUC
AGUUAUUCGU

>EMBL_CDS:CAI14459 CAI14459.2 Homo sapiens (human) zinc finger
protein 318
GACAACAGAAACCCUUAGGGUCCUUCUCCUUGGGGUAACCAUCUCCAACGGGACUCCAAGGAAGUU
CCGUCAGAGAUGGUUAUCAGGGGAACAAAAGUUAGAGACUCCGUUUUC

>EMBL_CDS:CAC21660 CAC21660.1 Homo sapiens (human) hypothetical
protein
CAGGAAGGCACGACAUCAGGCCCGUGCCGUUCCACACCCAGGAGACCACGGGAUCCAGCCCCCG
CCGCUCAGUCUCCAAGAGGGCACGGAACCAGAUCCCGCACCUCUCCUG

>EMBL_CDS:CAI13266 CAI13266.1 Homo sapiens (human) zinc finger and
BUB domain
UGUGCCCUAGAGGUCGUCCGCCCGUCGGACCUCGUGUCGACCGUACAACCGCGACGACCACCAGU
CACA

>EMBL_CDS:CAI14933 CAI14933.1 Homo sapiens (human) tudor domain
containing 7
CGGAAACGUGACCUACAGAAACUACGAAGUAAAGGUUCUCAACACACAUCGUUAUUAUCCUCUG
UAAAGUCGUAGUCCG

>EMBL_CDS:CAI41701 CAI41701.1 Homo sapiens (human) RNA binding motif
protein 10
CGGAGAGGGGUAGGGUCAUGUCCAUGACGACCGAGACUCGUAAUCAUUAUGACCCUCAACCCC
AGUAUCAUCUCCG

>EMBL_CDS:CAQ08432 CAQ08432.1 Homo sapiens (human) zinc finger
protein pseudogene
ACACUCAUGAGACUACUUGUUCUCCAACCUAACAGUCUUUCCGAGAAUCAACAAGUAAUUA
AGUGU

>EMBL_CDS:CAH70855 CAH70855.2 Homo sapiens (human) ribosomal protein
L12 (RPL12)

GGACUCCCGAAACUACUAGUCCCGUCUCCGUCUCCGUGGAGUUAGACCCGGACAGACAAGA
CUUACCAGUCAAGUGACAUAUAGGAGUCC

>EMBL_CDS:CAH71826 CAH71826.1 Homo sapiens (human) FRAS1 related
extracellular matrix 1
CGGACCUCUUAUGUCAUUGUCCAACGGGUCCAUAACAAGGGACGUUCGAACCCGUCGGCGUAAG
GUCCA

>EMBL_CDS:CAH74069 CAH74069.1 Homo sapiens (human) pseudogene similar
to part of NADH
GUCUUUUUAACUCGAACAAUACUAAUAAGGAGUAUCCCUAUCAUACUCCCUCCUUAUUCGAUUAU
UGAGAC

>EMBL_CDS:CAI14932 CAI14932.1 Homo sapiens (human) amylase, alpha 1C
(salivary)
CCAACCAUAGAAAGGGUGGUUCCAGACUUUCCCAACACUUAACCGUUGUAAAAGUAAAACCACCUCU
CUGGACUUGG

>EMBL_CDS:CAI13272 CAI13272.1 Homo sapiens (human) DC-SUAMP domain
containing 1
UCGUGGUGGUCGUCGUCGUCUUAACCCGUCACAGAGGUCCUCGAGGGAGUGGUGUACGAGUAAAG
ACUCCGGACCUACCACCCGA

>EMBL_CDS:CAH71185 CAH71185.1 Homo sapiens (human) CDC42 binding
protein kinase alpha
UCAUGCAGACGGAAACGAUCCGACCUCAUGUCCUACCUCUCGCAAGUUUAACUAGGUCUCGUAGCC
AUCCGCAUAA

>EMBL_CDS:CAI14348 CAI14348.1 Homo sapiens (human) chromosome 9 open
reading frame 126
AAGUCGUUCCGCUAAGCUACACUAUUGUUACCAUAAUAGUAGUAAAUAUGGUAAAUGUCCUAGGC
GGAGUUACUU

>EMBL_CDS:CAI14438 CAI14438.1 Homo sapiens (human) surfactant,
pulmonary-associated
ACCUGAAGGGACCCUGGGUACCGAGGUCGUCUGGGACGACGGGGACACAAAGGUCCUGAGGU

>EMBL_CDS:CAC21674 CAC21674.1 Homo sapiens (human) hypothetical
protein
GACGGACCAGGUCUCCAAGACGCCAGGUGUCGACCUUUUCCCGAGGUGCCCGGCCAGUC

>EMBL_CDS:CAI14538 CAI14538.1 Homo sapiens (human) human
immunodeficiency virus type I
UACCCUUUGCAACCCCGAGACGAGACUCCGACUGGAGGCGUAGAGAGCCCGUACACCCACCACCG
ACCCUGUCAGUUGUACACCCACGGGUCCCCAAACCCCGGUACAGUCUACUCCUGACCCCGG
AGCCGAAAGGGUA

>EMBL_CDS:CAI14682 CAI14682.1 Homo sapiens (human) serine/arginine
repetitive matrix 1
UCUUCUCUGGCAGCGGAAGACCACCACCACCCCUACCUGAAGAGGAGGCAGAUGGUGCUCUCC
UUCAGAGAAAAA

>EMBL_CDS:CAH70858 CAH70858.1 Homo sapiens (human) spen homolog,
transcriptional regulator
CCCCAGUCGUUCGAAGAACAACACCACUGUUACGAACCCACUCCUGGUCGACCAACACUUGGU

CGUGUCCCCCACACAACUAGGG

>EMBL_CDS:CAI15846 CAI15846.1 Homo sapiens (human) CD52 molecule
UCGUCUUCUCCACCUAUACCGUAACCGGUGUCUUCUUUCCUUUUACGGAGGCGAAUACAACGA

>EMBL_CDS:CAH74000 CAH74000.1 Homo sapiens (human) tudor domain
containing 3
CUACUAAGAUCAUAAAAAAGACCGAAUUAACCGGGUCUAGAAGCAAACCCGGGUGAUACAUUUU
AUAAAAUAGUAG

>EMBL_CDS:CAD13322 CAD13322.2 Homo sapiens (human)
gamma-aminobutyric acid (GABA) B
CCAGCUCCUUCAUCCCCGCGUCCUCACUGAGCAACGCCUAGACGAGCUACCGGUCAAGGUGCCGC
CCCUCGUGUGGCGGGCUACGACGGGAACCGG

>EMBL_CDS:CAQ07191 CAQ07191.1 Homo sapiens (human) novel pseudogene
GUAAAAGAACUAGGAACAUCUCCCCUAGAAUAACUCCCCUCUUUAUGGAAACCAUAAUCUAUGU
UGUCCUAGACUUUAUC

>EMBL_CDS:CAQ09904 CAQ09904.1 Homo sapiens (human) diacylglycerol
kinase pseudogene
CCCAGGUCCUAUUAUUUAGAGUAGGACACGCUAGAGUCAGUGUAUCAACUCCACGAGGACCCGAG

>EMBL_CDS:CAI10965 CAI10965.1 Homo sapiens (human) solute carrier
family 31 (copper
UGGUGGACCUACUACACGUCGUGACAAACGUCCUCCACUCCUUUCGAGUCGUAGACAACGGGUUG
UCAAAAACACACAGAGGUUAUCCUACCA

>EMBL_CDS:CAI14296 CAI14296.1 Homo sapiens (human) eyes absent
homolog 3 (Drosophila)
UAGUAAAAGAAGGUAACAAUUUGGACUCGGUUAGUGACAACCCAGGAAAGGUUAUAAAGACCCG
UAUCCUAGGUCAUUCUUCACUCACCUUCUACUACUA

>EMBL_CDS:CAI22608 CAI22608.1 Homo sapiens (human) MORN repeat
containing 1
GACACGGCACCCACCACAGGGGGACCCACGUCCGGCGGAGACCUAGACGGCGGACGGAAGAACA
CCUCCGACAGGUCCUUGUCCUCCCCACCAUGGGUCCGCCCCCGCGGGGUCCUCCUGUAGACAC
UUGAGCCGUGUC

>EMBL_CDS:CAH73652 CAH73652.1 Homo sapiens (human) olfactory receptor,
family 10,
CUCUUUUUGGUGUUUCUCUCACUACACUACAAACACCUUAGACCUCUUAGGGUCCUUUUGUUUGA
GACAAUGGAGACACUCCAAGAAAGAA

>EMBL_CDS:CA072141 CA072141.1 Homo sapiens (human) chromosome 1 open
reading frame
CAGGCCGCCUUUCCACAGGUCCUUUCCAGAACCCAGGCUGUCACUUCUGAAGUCACCCGAGGC
CCGGCGUGGACCCGAGGGCGGGCGGCCCG

>EMBL_CDS:CAQ08914 CAQ08914.1 Homo sapiens (human) actin related
protein 2/3 complex,
AUUAUAGUUCAGGACAGUCGAAGUAAGAAUUAAGUAUCAAAAACUUCUUCUGUAACCGGAACUU
CAU

>EMBL_CDS:CAI13832 CAI13832.1 Homo sapiens (human) CDKN1A interacting
zinc finger

CCCCGCCCCUGUCCACAGUCCCCAUGUCACGAUUUCCGGGCCGACAGUGACGAGACGUCUUACC
ACUGGAAGUCCCUCGGGGGCCGCGGGGUAUGGGGACCGUAGAGAGAGCGAGA
>EMBL_CDS:CAI41249 CAI41249.1 Homo sapiens (human) immunoglobulin
superfamily, member
UAUCAUUUUUGUCUCCAUUACAGGUCAUAGAACCUAGAAGUUUCUGACCUUCUUCUUAACGGA
GUAAAAAAUAACA
>EMBL_CDS:CAI12482 CAI12482.1 Homo sapiens (human) v-ski sarcoma
viral oncogene homolog
GCGUCGAAGAGGAAGAACCGGUGCGCAUCCUUGAGGUCGAGGACCACCUCGACGCGAACCGGAC
GUCCCCGACGC
>EMBL_CDS:CAI12125 CAI12125.1 Homo sapiens (human) heparan sulfate
proteoglycan 2
CUGGUCACCUACCACCCGCGCCCCGACGGACACCGACUCGUCGCGUCCACCGGCACACAGGUCG
GAGGUGUCAG
>EMBL_CDS:CAI15178 CAI15178.2 Homo sapiens (human) ribosomal protein
S24 (RPS24)
CACUUCUGUAGAUGCUGACAAACACGAGGGACUCCAUCAACUAACCAGUACUUGAAGGAUCAUG
UUUAUCAUAACACAGUAAGUA
>EMBL_CDS:CAI12649 CAI12649.1 Homo sapiens (human) myotubularin
related protein 11
UGGGACCGGUCGGAACGAGUCCAAUAGGGGCUUAUGACAACCCGAACUAACGAGACUCGAGACC
GAACCUUUACCGGUACCA
>EMBL_CDS:CAI12547 CAI12547.1 Homo sapiens (human) aryl hydrocarbon
receptor (AHR)
UACCUUAGGAUAAAACUCGAUUAAACCAUCGUCUCAUAAAAGGUCAUCACGAUGAUAAUCAGGA
GUAAUCAUUCUCAAGGUA
>EMBL_CDS:CAI14505 CAI14505.1 Homo sapiens (human) chromosome 9 open
reading frame 50
CCGGAAGAAGGUACUUGUCUCCCCGUCCGACGACAAGUACCUCCACAGGAGUCUUUCAUCGGGA
CACAGAAGACCCACCUGUCCGG
>EMBL_CDS:CAI17060 CAI17060.2 Homo sapiens (human) pseudogene similar
to part of NADH
UCCCAAAUUAUGACAAUUAUACGUACAUGUACAAGGAGCAACUAACACUGUUCAUUAUJUCC
CUUAUUUCCCGACACCAAUUAUUAUUCAGGA
>EMBL_CDS:CAH73128 CAH73128.2 Homo sapiens (human) protein tyrosine
phosphatase,
UCGGUCUGCCUUUAUCAUAUUCGACAAACCAAAGUCAGGAACGUCGGAUAUACUACAGGGACCGA
>EMBL_CDS:CAQ10461 CAQ10461.1 Homo sapiens (human) NADH dehydrogenase
5 (MUND5)
AGGAUCAUAAAUCUCUUAACUACAGACAUUACCCUUGGAAUCAAUUCUAAUAAUCAUACU
CUAAUUCGAGUAACGAUCCU
>EMBL_CDS:CAI40039 CAI40039.1 Homo sapiens (human) chromosome X open
reading frame 59
GUCAAAAGACGACAACGUCAUUGACCUUCACUUUUGUGGUCAAAAAAGACAGUAGUGUCUUUUCU

UCUAAC

>EMBL_CDS:CAQ11044 CAQ11044.1 Homo sapiens (human) mitochondrial AUP synthase 6

CGGUUACUGAGAAAACAAAACACCACCUUCAGUCACUAUUGACGAGAACCAAUAUCACCCUAUAG
AUAUAAAUCUAAAUAACUAUUGACUCAUAACCG

>EMBL_CDS:CAI41100 CAI41100.1 Homo sapiens (human) melanoma antigen family H, 1

AACGGGUACUACUUCUACUCGCGAUUAUAUCUGUAGUCCUCUGAAAAGAACCACGGGACUUUUA
CGAGGCCCCGUGACUUCGAAAACACGAACCCGUCACGAGCUCCGAAGAAGUCCCCACC

>EMBL_CDS:CAH74086 CAH74086.1 Homo sapiens (human) hematopoietically expressed

AACCUCUAGAGUGGACCGGCGGAAAGGAAAUAACGUCUCCGAGACGUUCUCCCCGAGGUCUC
AUCUCCAAACGGGUC

>EMBL_CDS:CAH73166 CAH73166.1 Homo sapiens (human) peptidyl arginine deiminase, type

CCUCCUGUUCAAACACCAGUAGUUCUCCCGACGUCCCGGACGCAGGCGUCCUGGUACUGUCUG
UACAGAAGG

>EMBL_CDS:CAQ06495 CAQ06495.1 Homo sapiens (human) UAF1 RNA polymerase II, UUA box

GACCCACUACUUUACCGGUUCUAGACCUUGACGGUAGUAAAAGACCCACUGUUACAACAGGUCU
UACUUUCUUUACGGUGAACCAGUAGUAGUAGGUC

>EMBL_CDS:CAH73905 CAH73905.1 Homo sapiens (human) novel tudor domain containing protein

GGGACAAGAACUAAGCAGUUCUAGAGUUAUUGUAUAACUACUAGGACAAAUAGUUCUUAUACC

>EMBL_CDS:CAI17217 CAI17217.1 Homo sapiens (human) tetratricopeptide repeat domain 13

UUGAAAGACGAAGUUUCGAAGAAACUCCUAAGUUAUCGAAGGAAGUCUUCAGGAGACACUUUCU
UUCAA

>EMBL_CDS:CAI40666 CAI40666.1 Homo sapiens (human) novel protein
ACACCCAUGUCCGGCCCGACCACGGGAGGU AUGCCGCCGACAGGGCUCUCCCGGAACCGGACC
UAUGACGACGGGUAU

>EMBL_CDS:CAQ06806 CAQ06806.1 Homo sapiens (human) nicolin 1 (NICN1) pseudogene

ACCUCUCACGUCCAACGAGUGUCCCGUGACCCACCCUCUCGGUGAACCCUUCUAGUACCUCUCC
CGAGAAACCAGGGACGACUAUCUAGACGUCGAGGAGGU

>EMBL_CDS:CAQ10659 CAQ10659.1 Homo sapiens (human) novel pseudogene
CAGUUCGGAAGGAAUUUCGAUACUACAUAACUAGAAGUCGUUUUUAGACCUUAACUUCUCCAA
ACUA

>EMBL_CDS:CAM13086 CAM13086.1 Homo sapiens (human) ADAMUS-like 1
CCGAAGUCCUCGCACAGGACCACGAGGUCCACCGACGCCUUCUAGAGGACCCGGUCGACCCGGUG
GUCCACGAACGACAUCUCCAG

>EMBL_CDS:CAI12265 CAI12265.1 Homo sapiens (human) adipose differentiation-related

AAGACGUCGACGGGGAACGAUCUUCACUCCUCCGACAGUCUGUGAAGAAAUUUCCUCCGUCGUAA

CGCCUU

>EMBL_CDS:CAH70693 CAH70693.1 Homo sapiens (human) stathmin-like 2 (SUMN2) pseudogene
GGGUGGAGCCGGAGGGUUUCACGACCCUAAUGUCCGCACUCGGUGACACGGGUCGGACUAAACGA
AGUGAAAGUAAAGUUAAUUCUAUUCUACAACUACAACGUUCUAAGGUCCAUUUUUGUUCUGUCC
CGGUGUGGACCACCAAGUGUGGAUUAAGAUCGCGUAAACUCUCCGACUCCACCC

>EMBL_CDS:CAI15376 CAI15376.1 Homo sapiens (human) poliovirus receptor-related 4
CGACACGAGUCACCAGUCACCCCUUUCGGGUUUCACAGGGGUAGGUGAGCAUGGGGUGACCCGU
CUCCGGGUAGGUCGGCACAGGUCAACAUACUCCUCCCCGACGGGAAGUGAGUCCGUGAACUCG
UAUCG

>EMBL_CDS:CAI13541 CAI13541.1 Homo sapiens (human) dual-specificity
GACAAGAUGGAAGUAGAGUGGAGGUAGGUUUUUCACGACUCAUACUAGAGGACAUUUGACGAGUC
ACCAGUAUAAAUCAGAAGACCCACCUCCACCAAGUCUUCUUAACGUC

>EMBL_CDS:CAH70273 CAH70273.1 Homo sapiens (human) pseudogene similar to part of
AACUGUGUCCACAAAGUUACCACAACUUCUCUUUAAGGGAAAGAAACCGUAGAAAAUACAUUCA
CAGUU

>EMBL_CDS:CAI40469 CAI40469.1 Homo sapiens (human) melanoma inhibitory activity family,
UCGAAACCGUCGAACAUCACUCAACGCCAGUAGAAGGUUAAAAGAAAUGGACCAGAAGGUCCAUG
UAAAUCACCGUGGCCUCCGAGAAUCGAAUUCGACAUUUUCGA

>EMBL_CDS:CAI16384 CAI16384.1 Homo sapiens (human) tropomodulin 4 (muscle)
GUCACACAUGUACAGGUCUUAACGACGUUACAGUGUGUAAAAGUCGUAGACACCGUACACGGUCAC

>EMBL_CDS:CAI16380 CAI16380.1 Homo sapiens (human) LysM, putative
AGGAGAGGUAGAAAGAGAAGGAGUCUCAGGUUUGGUAACUUGUCCAGAGACCCGAGACAGUCCUA
CCCCUACAUCUCCC

>EMBL_CDS:CAI13935 CAI13935.1 Homo sapiens (human) small nuclear RNA activating
CCCCUAGCCGUCCUAGGUUCAGGAGUCUCCGUCACUUAGACGAAGUCUUAGACUGAGCUCUGAA
CUAAGACUCUAGAGG

>EMBL_CDS:CAI39693 CAI39693.1 Homo sapiens (human) novel (FLJ20483) pseudogene
ACGGUAUAAAAAUUUCACAACAGACACAAAAGAAUCUCCGUAAGGACGAGCUUUUCUACACCAU

>EMBL_CDS:CAI39581 CAI39581.1 Homo sapiens (human) HECU, UBA and WWE domain containing 1
CCGAGAAGAUCCUAAGGAGCCCUUAGACGAGGUCUUUACCGGUGCCGUCUUAGAGACCACCUUCU
CGA

>EMBL_CDS:CAI16184 CAI16184.1 Homo sapiens (human) cholinergic receptor, nicotinic,
GGUGUAGACCCUCGGUCUACACAAACCUUCCUCGGCUUGAAAGAAGUACAACAGUUUGAGAAGU
CCGAAGGUCCACUCC

>EMBL_CDS:CAI13006 CAI13006.1 Homo sapiens (human) polo-like kinase

3 (Drosophila)

CCACUCGACAGAAGUCCACGACAGAGAUGGUCCGACUGUCCCCGACCCGGUCUUCGACGACCUCG
GAGACCGGACCGUAGGACUACCGGUUGCCUACACGCGUACUCCGGCGAGUGG

>EMBL_CDS:CAH69928 CAH69928.1 Homo sapiens (human) inositol
polyphosphate-5-phosphatase,

GUGACUCGACUGUCCGAACACCAGUGACCAGAAGUCCCGGUACACCGAGACCAUUGAGUCGACUC
AC

>EMBL_CDS:CAI40037 CAI40037.1 Homo sapiens (human) cylicin, basic
protein of sperm

AAGUCACAAACAGAAGAACC UU AAGAAACUUAGAAAGAAUAGAAAAACACUUGUUAAAAAACUCU
GACAGAAUCUUAAAACCCUAAGACCUAAUCAAAGACUU

>EMBL_CDS:CAI18907 CAI18907.1 Homo sapiens (human) carnitine
palmitoyltransferase II

AGUACCACCGUAGUUUGAAAAGGAAUCGUCGACACUACGGUCAGAAAUCCGUAGUCAGUCGAGC
UUCAACUCAAGACGUGGCACU

>EMBL_CDS:CAQ09180 CAQ09180.1 Homo sapiens (human) mitochondrially
encoded cytochrome

UGUUUAUCCUUAAAAGUAACCCUCUUAUGAGCUAACAGUUGAAACUCCUCAGCAUCAAGAGGACC
AAAAUUCAGACAACA

>EMBL_CDS:CAI18063 CAI18063.2 Homo sapiens (human) collagen type XI
alpha 2

AGGACCCCCUGGAACACCCGGUAGUCGCGGUAACCCAGGUCGACCUGGAGCUCCAGGACCCCCCG
GUCCACCAGGGUAUCCU

>EMBL_CDS:CAI16169 CAI16169.1 Homo sapiens (human) potassium large
conductance

AUCAAGUCACUACUACCCCUACAACUGGGGUCAACACUACCUACCAACUGCAUUGUAGGGCACGU
GACCCGAC

>EMBL_CDS:CAI17779 CAI17779.1 Homo sapiens (human) HLA complex group
4 pseudogene 5

CUUCCGCCACAUACCUAACCCUCAGGGUCGGAACCCUAAGGGGUUGAGGCGUCAAGAAA

>EMBL_CDS:CAI17611 CAI17611.2 Homo sapiens (human) collagen, type XI,
alpha 2

UCCUGGGAAGAGAGGUACUCCCGGCUACCGUGGGACCCCGGGCCCUUCUGGGACCCAGGGUCCCC
ACGGGACAACAGGUCCUCCAGGA

>EMBL_CDS:CAI18234 CAI18234.1 Homo sapiens (human) poly(A) binding
protein interacting

UACGAAGAACCAUUAGGCCUAGUCGACGUCACUUUCCUUGUGAUACUUUGUGUUUAUUGAUACACU
UACUGGUGAUUUUUACAACCAAGUAAGUGUAUCAUUAACCCUAGAAAAAACCGACAACAUAAG
ACAUACUACUUCAACGUA

>EMBL_CDS:CAI10948 CAI10948.1 Homo sapiens (human) jumonji domain
containing 1C

CGGUUCCAUGAACUCAAAAGGACUCGGUGGAAAAGAUUUAAUCACAGUAAACAUAUAGUUAAU
GUGUAAAACCACCCACCAGACCUAUGUUUGAAGAGGAAAACCA

>EMBL_CDS:CAI95083 CAI95083.1 Homo sapiens (human) tripartite

motif-containing 46

GGAGCGAAGGAGGGUCCCAUACAGGGUUUCGGACUGAAUUCGUCGGCCAGGUCCGCCAGACCGAA
CCCCUCUCAAGACGCCUCUCCGCCCC

>EMBL_CDS:CAI40878 CAI40878.1 Homo sapiens (human) potassium large
conductance

AAAGACGGUACACAGAAGGAGUUAGAAUACUUACUGGAGUACCUCUUCUCCAACCGUUCGUACC
ACCUCU

>EMBL_CDS:CAD38974 CAD38974.2 Homo sapiens (human) hypothetical
protein

AGCUCUAGAUCUUGGUCUAGAUCUAGCGGAGGAAAAACCACUGGACCUACGACUGGAUCUAGAAC
U

>EMBL_CDS:CAI18078 CAI18078.1 Homo sapiens (human) tenascin XB
GUCGGUGUCGGUCACCUUCCCCGUCCAAUUACGCCACCCACUUAUGGUGGACGAAAGAGGGGAGG
AAGGUGACACACGAGCAUUUCGAC

>EMBL_CDS:CAD38738 CAD38738.1 Homo sapiens (human) hypothetical
protein

CACCGACCCCCGUCGGUCCUGUGGAGGAGGAAACCCCAGACGUCAAAGGUCGACCGUCCGGCC
GACUGUCUGACGACCAAGAACUACCCUCCGUCACAGAACAUGAAGGAGCGUCCAAGUG

>EMBL_CDS:CAD39100 CAD39100.1 Homo sapiens (human) hypothetical
protein

UCCCGUCACCCCCAUUGAGACGUAAACCCGGUACCCCCGGGUUCUCGUGAGACAGGAGGUGCCGA
CGAGA

>EMBL_CDS:CAD38978 CAD38978.2 Homo sapiens (human) hypothetical
protein

CCACGUCGAACUACACCGUAGACCCGGGUCACGGGAGUUCACGGUGGUAGAGUCCGACGCGA

>EMBL_CDS:CAD38583 CAD38583.1 Homo sapiens (human) hypothetical
protein

CUCAGUCUAAGACGUAGUCUAAGACUCAGUCCAAGACUAACCGUAAGCCUAAACCCAAGACUGAG
ACUAAGACUAAGCCUAAGACCGAG

>EMBL_CDS:CAD89960 CAD89960.1 Homo sapiens (human) hypothetical
protein

CGAACAUCCCGUUUCUCUCUCCGACGUAGACACCGACAGAGUCUACCCCGAACACAAUAACCGGA
AUUCA

>EMBL_CDS:CAD38951 CAD38951.1 Homo sapiens (human) hypothetical
protein

CCGCCCCUAGACGAGUAUCUGGUCGAGUUUCCGGCAGUCGGCCCCGAGGGACCAACAUCCCGGCC
AGAGCUCGUGUCAGGGCGG

>EMBL_CDS:CAD39091 CAD39091.1 Homo sapiens (human) hypothetical
protein

CCAUGAGAUCAAUCUUUACCCGACC UAAAAACUCCGUGUCUUAAGUCGAGACAAGGUUGUAAUCU
CCCGG

>EMBL_CDS:CAD89901 CAD89901.1 Homo sapiens (human) hypothetical
protein

CGAGUUAGAAGAGGUCUUUCGUUGGAGGGUACAUCCUCGUGACGACCCUCCCGUCAACUUUGAC

CUUUACCCUAACUACG
>EMBL_CDS:CAD39157 CAD39157.1 Homo sapiens (human) hypothetical protein
ACCUCACGAACCAGGGUUCGUCGAAGAGAAUGUCCUCCACUCCCUCGACACUCGGUAGAGGU
>EMBL_CDS:CAH74027 CAH74027.1 Homo sapiens (human) laminin receptor 1 (ribosomal)
UCUCGUCCGACGACGAUUUUUUCGACUCCGAUUCUCCUUAAGUCCCACUCCCUGACGGGACC
GAGGACUCACAUGACGAUGAGUCGGACUCCAACGUCGGACGAAA
>EMBL_CDS:CAH10602 CAH10602.1 Homo sapiens (human) hypothetical protein
CGGCCCGACGUCGUCCACUCUUCACGUCCUCGACCCUCAACGACGGUGACGGUCGUCGUCGUCG
UGGUCGUGGACGUCACCGUUACCGCCCCGACACCG
>EMBL_CDS:CAD39047 CAD39047.1 Homo sapiens (human) hypothetical protein
UACCGAAAAGAGACUCCCUGACACUACAGAAGAGAGUCUCCCUGACGCUACAGAAGAGAGUCUCC
CUGACGUUACCGAAGAGAGUCUCCCUGACGUUACCGAAGAGAGUCUCCCUGACACUACAGAAGAG
AGUCUCCCUGACACUA
>EMBL_CDS:CAD91151 CAD91151.1 Homo sapiens (human) hypothetical protein
AGACGGUAGACCCGAAAGUACCGGAGGAACCGGAAGGAAUGUCGGUCGUUCGAGUGGAGGUAGAC
CAGUGGGUUCACGGCCUACGACCGGACGAGCCGGAGGUCCUCCGGUUCUCCGGACCUACCGAC
U
>EMBL_CDS:CAM25754 CAM25754.1 Homo sapiens (human) HLA complex group 22
AGUGACGACACUGACUUAUCAAGUGUCUCCACUCACAGUGGUACAAAUCACCAAAGUAGAAGA
CACCAGGGACCCAGACGUCACU
>EMBL_CDS:CAD38816 CAD38816.2 Homo sapiens (human) hypothetical protein
ACUUCACCCGCCGGUCUCCCCGACAACACGGCCGAGUGGGACGUCCCUGUCCGUCGGUGCCACCGC
AUCAAGU
>EMBL_CDS:CAD38604 CAD38604.1 Homo sapiens (human) hypothetical protein
UCGUCGUAGAAAAAGAAGUCUGAACCCUCGACCACGGUGGUGUCGGGGCAGACUUCUCCCACGA
GGA
>EMBL_CDS:CAD38784 CAD38784.1 Homo sapiens (human) hypothetical protein
CGAAACAGAAGGUCCUCGAUUUUUCCAGAAAGACCAACUGAUUUUUUAUAGAGGACCUCUUUUUC
CA
>EMBL_CDS:CAH10604 CAH10604.1 Homo sapiens (human) hypothetical protein
GACUUUUUAGGAGAAAACCCUCUACUGAAUCUAACACAUUCACCGUUUCUUUCAACAGCAACUAC
AAACUUCGCGUAAGGAAAGGCAACCGGAAACAGGUCAAAACCGAAAAGGUGUAUUUCUCCCCAAA
ACUC
>EMBL_CDS:CAD38994 CAD38994.1 Homo sapiens (human) hypothetical

protein

GGGACGACCAGACCUGUUACGGGUGUCACCGGUCAUCCGGCGUCGUACCAUAAGAUUCACCGACC
CUCCGGUCCUCCACCCCGAAUGCGACACACGUCUUCUCAGGUCAGGUCGGUCCC

>EMBL_CDS:CAI18564 CAI18564.1 Homo sapiens (human) Notch homolog 4
(Drosophila)

GAAGACGGGAGUGUGGGGAACCGAGGCCCAAAGACUGUGGCCCCGGGACCUCUCGACACUCCCGU
CCUC

>EMBL_CDS:CAM25804 CAM25804.1 Homo sapiens (human) collagen, type XI,
alpha 2

CAGGUCCUCCAGGACCGAGAGGGACCCAGGGUUCGAGGGAAACCCGGGACCCUCCUGUAGGUAC
GGAGCCUG

>EMBL_CDS:CAQ10080 CAQ10080.1 Homo sapiens (human) zinc finger
protein pseudogene

UAUUACUUAUUCUGAAUCGGAGAUUAACUCCGAAUAAGUAAUGUCCAUGUCUCACAGACAGGUG
AUACUUAGACGUCUACUACUUGUCCUAAACUAAAGACAAACCUCCAAAAACAUAUAAGUAACA

>EMBL_CDS:CAQ09244 CAQ09244.1 Homo sapiens (human) mitochondrial
ribosomal protein

AACUCUAACCACCUCACCUGGAAGAGUAAUGAGUAGUAGAUCUCCUCCAGGAGUAGUAGAGAUG
AAGAGUU

>EMBL_CDS:CAH71081 CAH71081.1 Homo sapiens (human) rearranged L-myc
fusion

ACGUAUCAAGUCUCACUAGAUCACACAGUUAUUCGAGAAGUAAGUAACUUCGACUUCUCGAUAC
UGAAUUGACUAGUGAUCUUAUUGACAGU

>EMBL_CDS:CAJ20055 CAJ20055.1 Homo sapiens (human) Cox18Hs1 protein
AAGGUGGAACCGGUCCUACAUCACGACCAUCCGACGGUUUCCGUCGCACUGUCGUGGGGCAUCC
GGUGCCACCUC

>EMBL_CDS:CAL06519 CAL06519.1 Homo sapiens (human) immunoglobulin
heavy chain variable

AGUCCGACCAGUAAACGUUUUUGUCGCACCUGAACCUUAACAGAGACCUCUACCACUUGGCCGGG
AAGUGCCUCAGACGCAUCAUACACGAUACUGGUCAUACU

>EMBL_CDS:CAJ57189 CAJ57189.1 Homo sapiens (human) immunoglobulin
variable kappa

AAUCCUCGAAUCCUCGAAAGGGACCAAAGACGACUAUGGUCCGAUUUCGUGAUGAUUACGGGACU

>EMBL_CDS:CAJ84703 CAJ84703.1 Homo sapiens (human) cytochrome P450
1A1

GCACGAAUAGUCCUGGAGUCGGAGGAACGAGUGUACGAGAAGGUCCAUCGUCCUCCAACUCCUCC
GACCCAGUCUCCGUUAC

>EMBL_CDS:CAJ75539 CAJ75539.1 Homo sapiens (human) immunoglobulin
lambda light chain

CGAAGACGACCCUGGUCGAACCUAUCAGUAAUAACCACUGACGAGGUCACGACCUUCGUGUCCA

>EMBL_CDS:CAJ75485 CAJ75485.1 Homo sapiens (human) immunoglobulin
heavy chain

CACGAAGUGCACCGUACAGUGCCUGAACGGCCGAUCCGUGACACACCGGCCGUCCAGUCGACCG
ACGAGCACCACAUG

>EMBL_CDS:CAK50629 CAK50629.1 Homo sapiens (human) immunoglobulin A heavy chain

CCAGGUACAUCGACACCAACGCCUACACAGGGACCAUUCCCACUGAGACGGGACCUUAAAGACA
CUUAUAAAACACAGUGGUGACGGUCGCACCUAG

>EMBL_CDS:CAK50713 CAK50713.1 Homo sapiens (human) immunoglobulin A heavy chain

GUCCAGUCACACUCCCAGACACACCCGAAGUCACGACACCCUGGUCUGGGAGCUCCAACUGGAC

>EMBL_CDS:CAM34545 CAM34545.1 Homo sapiens (human) autogenous vein graft remodeling

CGCGGGUGGUGGUGCGGGUCGAUUAACAAAACAUAACAAACUCUACCCAAAGGACACAAUCGG
UCCUACCAGAGCUAGAGGACUGGAACACUGAUGUGCCACUUGAGACGGAGAUGAUUUUUAUGUU
UUUUAUCGGCCCGCACCACCACCCGCG

>EMBL_CDS:CAQ37746 CAQ37746.1 Homo sapiens (human) putative ankyrin repeat and sterile

AUCCCUCGGUGGUCACCACAUCACGAAACCGAUUCACUACCUCUGUUGACUCCUCCUCACACUA
AUGGUGACCCAAGGGAC

>EMBL_CDS:BAA95561 BAA95561.1 Homo sapiens (human) liver-type 1-phosphofructokinase

GAGGAACCCCCGAAGACCACCCGCUCCUCGAACAUUACAAGGUCAACAAGAGCUUCGAGGGUG
GUGCCUC