

The program is running under the following parameters:

Output:

Prefix of the family name Bacillus

Circular permutations are allowed

Reverse sequences are considered.

Sequences are aligned while similarity: 0.600000

Alignment score: Normalized respect to the length and number of sequences.

Alignment parameters:

opening gap: -3.000000

extensio gap: -1.000000

extreme gaph: -0.500000

There are 1966 alignments:

>Bacillus_Fam_1_60_41 Nr. of seq. 41 Alignment length(with gaps) = 64
Alignment score = 0.721735

TCCGCCTTTTngCCgATtTctTGaTAGAATTCTTTgTCATGgTtTnnGcaGTnGCTTC

>Bacillus_Fam_2_52_36 Nr. of seq. 36 Alignment length(with gaps) = 57
Alignment score = 0.678177

CTTAACgTAGACGngCTCTATGTgAAGgAAGgcCnTCntTTTnCnnGCTTc

>Bacillus_Fam_3_50_31 Nr. of seq. 31 Alignment length(with gaps) = 64
Alignment score = 0.605623

gAATCnCGGGGTTGCGaGCnGAAAAAGaGGAGAAAAGCCCGAGCAAACGcn

>Bacillus_Fam_4_52_27 Nr. of seq. 27 Alignment length(with gaps) = 53
Alignment score = 0.745847

AAgGGAATCAaACAAcGtTTTCaTTCCTTTgttggGCTTTtGGCATgAGA

>Bacillus_Fam_5_52_25 Nr. of seq. 25 Alignment length(with gaps) = 56
Alignment score = 0.706369

GTTAATGTGaAGATACgGAGGCcAAACcttGgAGTAtCTGCACAAAGAGggG

>Bacillus_Fam_6_20_21 Nr. of seq. 21 Alignment length(with gaps) = 22
Alignment score = 0.672366

TGCTAATAAAanngAAAAGt

>Bacillus_Fam_7_52_18 Nr. of seq. 18 Alignment length(with gaps) = 60
Alignment score = 0.620516

ATCGTACCCtCgnAAACcGaaAAaCGATnTgggAGGGTAAGCAAAnGcnnGA

>Bacillus_Fam_8_52_17 Nr. of seq. 17 Alignment length(with gaps) = 56
Alignment score = 0.680278

gacGACGAGAAAnnGGTcTCGTGCGCAAAAAAngGaGTTTtnCGnGtCAAAAn

>Bacillus_Fam_9_52_16 Nr. of seq. 16 Alignment length(with gaps) = 60
Alignment score = 0.601759

CCTtTGATTCCCTTTncGGCTtTtATTcaatgGCTTTtGgcaTCATTGcnGn

>Bacillus_Fam_10_20_16 Nr. of seq. 16 Alignment length(with gaps) = 22
Alignment score = 0.662626

tCGCCAATAAAAAttanATTT

>Bacillus_Fam_11_51_15 Nr. of seq. 15 Alignment length(with gaps) = 56
Alignment score = 0.625454

TTTTCATtACcTATtcCnntTTaTTCGCACCcTAATtcnncaCAgCnCgGc

>Bacillus_Fam_12_52_15 Nr. of seq. 15 Alignment length(with gaps) = 54
Alignment score = 0.703939

TTTTGgCGACGAGaCccntTCTCGTCACCATTTTgaggtGAgAAAtGctCaa

```

>Bacillus_Fam_13_21_15 Nr. of seq. 15 Alignment length(with gaps) = 24
Alignment score = 0.642196
TTACCGTaGATAAAATnGcngt
>Bacillus_Fam_14_21_15 Nr. of seq. 15 Alignment length(with gaps) = 23
Alignment score = 0.651484
AATCGCGGATAGAgcnccnAn
>Bacillus_Fam_15_52_14 Nr. of seq. 14 Alignment length(with gaps) = 54
Alignment score = 0.680301
ATGAACGACCgcGggCgcGGnTTTTCTtCCGgcgCGGGCTTTCATTCCCtT
>Bacillus_Fam_16_52_14 Nr. of seq. 14 Alignment length(with gaps) = 54
Alignment score = 0.664021
ATGAGAACCGAAAgAGgtccAGcGnaAgcaGgaAaCGGTCTTCATaAagGgg
>Bacillus_Fam_17_12_14 Nr. of seq. 14 Alignment length(with gaps) = 14
Alignment score = 0.607535
CTTTtTCTtTtT
>Bacillus_Fam_18_52_13 Nr. of seq. 13 Alignment length(with gaps) = 57
Alignment score = 0.612086
GTTTCATGAGTAAGTAAAnAGcAAAAAnanGnAAAntagTtACTCATAaagg
>Bacillus_Fam_19_53_13 Nr. of seq. 13 Alignment length(with gaps) = 57
Alignment score = 0.601589
TGctGCCACTTTTtacCnGaGatGgATcCtcaTTTGTGGCGTCATTcGcngtAG
>Bacillus_Fam_20_52_13 Nr. of seq. 13 Alignment length(with gaps) = 53
Alignment score = 0.740364
ATGAAGACnTcAGTGACgAggAAaaAGGAGgAGAGAAgTCCTCATcGccGTt
>Bacillus_Fam_21_36_13 Nr. of seq. 13 Alignment length(with gaps) = 36
Alignment score = 0.755935
TgTTATCCATnATtGGCATnATgTTtGGcatTTGaT
>Bacillus_Fam_22_53_12 Nr. of seq. 12 Alignment length(with gaps) = 56
Alignment score = 0.655032
GTTCCCTCTaTTTcTCnTTTTTCgnntTTTgAGGGCACGATtACGCncTGATC
>Bacillus_Fam_23_52_12 Nr. of seq. 12 Alignment length(with gaps) = 55
Alignment score = 0.736639
TTTTGTCCTTTTGACaGctTCAAAAgGACATTTTCGngCCCGGATGCagCncG
>Bacillus_Fam_24_21_12 Nr. of seq. 12 Alignment length(with gaps) = 23
Alignment score = 0.627141
CGCcCATTGAACncnnAAATT
>Bacillus_Fam_25_20_12 Nr. of seq. 12 Alignment length(with gaps) = 21
Alignment score = 0.723545
tTTTTTATAGCGAAAATtTan
>Bacillus_Fam_26_53_11 Nr. of seq. 11 Alignment length(with gaps) = 58
Alignment score = 0.666458
nGtTGGTCGACATGATCATgGnAAAAAAGGncaAGAACcTGTCGATGAaGGn
>Bacillus_Fam_27_39_11 Nr. of seq. 11 Alignment length(with gaps) = 40
Alignment score = 0.799394
CTACATTTTCTTTcTTcACTTGcGGcGAtACTATaTTtC
>Bacillus_Fam_28_21_11 Nr. of seq. 11 Alignment length(with gaps) = 25
Alignment score = 0.604364
TTTACTCGCCAATTcGnGngn
>Bacillus_Fam_29_20_11 Nr. of seq. 11 Alignment length(with gaps) = 22
Alignment score = 0.720386
TTTATTGGCGATtTTcaaAT
>Bacillus_Fam_30_18_11 Nr. of seq. 11 Alignment length(with gaps) = 19
Alignment score = 0.651675
CCTGTTACTCCnGTTGga

```

```

>Bacillus_Fam_31_51_10 Nr. of seq. 10 Alignment length(with gaps) = 56
Alignment score = 0.632407
gtTGTC CAATAGaAGcggTCTAaTGGACAAGAAatctgGtnaaAagcGAAAA
>Bacillus_Fam_32_52_10 Nr. of seq. 10 Alignment length(with gaps) = 56
Alignment score = 0.659061
TTTcGTTACCCggCaCaCncatTTTcCTCCTTCTcGGTAACCAAtCgCTctC
>Bacillus_Fam_33_52_10 Nr. of seq. 10 Alignment length(with gaps) = 55
Alignment score = 0.634747
gTGTaTCATACgaaggCAATGACACgtGAgAAAGtaGaaGaaacgnAATAAA
>Bacillus_Fam_34_52_10 Nr. of seq. 10 Alignment length(with gaps) = 54
Alignment score = 0.660905
TGTCCGAAGtngCgCcAAcTTCGGA CTcatTCTcCtCngaTTTctgCTtCTcC
>Bacillus_Fam_35_52_10 Nr. of seq. 10 Alignment length(with gaps) = 53
Alignment score = 0.701887
TTGATGGTtCCgAaCtCagaGATAAGTGCCAtCAAAacgGAAAatCCnCcGn
>Bacillus_Fam_36_20_10 Nr. of seq. 10 Alignment length(with gaps) = 26
Alignment score = 0.611966
GTTTTGGCTAtTTTTCaAgg
>Bacillus_Fam_37_21_10 Nr. of seq. 10 Alignment length(with gaps) = 24
Alignment score = 0.601389
TTTGATAGGAAAnncaaaAAn
>Bacillus_Fam_38_15_10 Nr. of seq. 10 Alignment length(with gaps) = 15
Alignment score = 0.786667
CCaGAaCCgTTgCCa
>Bacillus_Fam_39_81_9 Nr. of seq. 9 Alignment length(with gaps) = 83
Alignment score = 0.715640

AgCAAAATTCAGtCCgGAAACgATtTTaacagAgCTGGATAAgTTcACaACnTCaTTcATGaGnAAAGTgGAcG
aaATcGCn
>Bacillus_Fam_40_52_9 Nr. of seq. 9 Alignment length(with gaps) = 58
Alignment score = 0.648467
tCTTTTGTC TTTTTGAnncCTCCAAAAGGACAaTTtGcnCCTgggtCCgGcTc
>Bacillus_Fam_41_51_9 Nr. of seq. 9 Alignment length(with gaps) = 57
Alignment score = 0.622157
TTTTTCATTACcTATcCncnnTTTTTCGCACcnTAATTTggcCtgCtcggC
>Bacillus_Fam_42_53_9 Nr. of seq. 9 Alignment length(with gaps) = 56
Alignment score = 0.615245
CanaCCAACAtCcCTencAtAATcCatTCTCaTTGGnctGaTTActCCcTTTT
>Bacillus_Fam_43_53_9 Nr. of seq. 9 Alignment length(with gaps) = 56
Alignment score = 0.632275
nGCttGCATAAGGGTATCtTTCcgCnTGAAaGaTgCCCTTATngaGGaGgAAn
>Bacillus_Fam_44_51_9 Nr. of seq. 9 Alignment length(with gaps) = 54
Alignment score = 0.728567
GTTTTGCTGATAGTAAAtCCTTTTTATCGTCAGCAAATcgAGNaTcaCgnC
>Bacillus_Fam_45_52_9 Nr. of seq. 9 Alignment length(with gaps) = 53
Alignment score = 0.615129
gATGAAGGACAtTTcGccgttngcangCCnntgtTTTGTCTTCATCacCCc
>Bacillus_Fam_46_36_9 Nr. of seq. 9 Alignment length(with gaps) = 36
Alignment score = 0.777263
taCACCAGTggCACCgGTAGgtCCaGTATctCCAGT
>Bacillus_Fam_47_21_9 Nr. of seq. 9 Alignment length(with gaps) = 24
Alignment score = 0.626157
tCACGAGTAAAnnGCTcAAAc

```

>Bacillus_Fam_48_21_9 Nr. of seq. 9 Alignment length(with gaps) = 23
Alignment score = 0.644525
ATTCGCTAATAAACnnncaAg
>Bacillus_Fam_49_21_9 Nr. of seq. 9 Alignment length(with gaps) = 22
Alignment score = 0.671296
tTACTCGTGAAATtngtGCat
>Bacillus_Fam_50_18_9 Nr. of seq. 9 Alignment length(with gaps) = 21
Alignment score = 0.615520
cAnAAGAAAgNAGAAGAA
>Bacillus_Fam_51_21_9 Nr. of seq. 9 Alignment length(with gaps) = 21
Alignment score = 0.772046
ACTCGTGAgTTTcgcnCnTTT
>Bacillus_Fam_52_18_9 Nr. of seq. 9 Alignment length(with gaps) = 18
Alignment score = 0.911008
GAGCTTTAGCTGCTTctT
>Bacillus_Fam_53_18_9 Nr. of seq. 9 Alignment length(with gaps) = 18
Alignment score = 0.913580
CCTTGGTTGTcGTTTCCg
>Bacillus_Fam_54_114_8 Nr. of seq. 8 Alignment length(with gaps) = 115
Alignment score = 0.790890

TCGCTTACATtGCATTGGCCATaCTtATTnnaACCCACAGCcacCACcGTaCCGTCCgATTTAAGnCCgATgG
TATGannacAaCCCGCCGcNacCGCCACAATAtCGcGCCAG

>Bacillus_Fam_55_52_8 Nr. of seq. 8 Alignment length(with gaps) = 59
Alignment score = 0.632062

TCATGAGGACAAAgTCGgacGAAAacCaaGaAAggttTGTCCTCATAgAGGGt

>Bacillus_Fam_56_52_8 Nr. of seq. 8 Alignment length(with gaps) = 58
Alignment score = 0.632389

nagTTTTGTCTTCATCaccCTTATGAAGGACACTTctCtCtcTTTtCaCtC

>Bacillus_Fam_57_52_8 Nr. of seq. 8 Alignment length(with gaps) = 57
Alignment score = 0.671261

GGACAAAATgaaGngtCAAtCAGgAAAAAcTGTCCAATAGAACGGcTCTCaT

>Bacillus_Fam_58_52_8 Nr. of seq. 8 Alignment length(with gaps) = 57
Alignment score = 0.619779

TTTCTTGACAgCTTTgCGCTcttcaccctgAAAcCTGTcACAATAACggCTT

>Bacillus_Fam_59_55_8 Nr. of seq. 8 Alignment length(with gaps) = 57
Alignment score = 0.625731

CGCCACAAAcnAggAtcCnaTCacngGnAAAAGTGGCagCACTACnGcgGAATGA

>Bacillus_Fam_60_52_8 Nr. of seq. 8 Alignment length(with gaps) = 56
Alignment score = 0.673044

ATGGCACTTATCcGGgAGAAtAGAACCATCAAAAAAGaagaATnctCaGGTTG

>Bacillus_Fam_61_52_8 Nr. of seq. 8 Alignment length(with gaps) = 56
Alignment score = 0.638924

gnAtCTTGGTTCGtCAAAGcGAGnGAATGaAGCCCAAGATnngaAtcnaAAAg

>Bacillus_Fam_62_52_8 Nr. of seq. 8 Alignment length(with gaps) = 55
Alignment score = 0.629437

GGTctTAGTcAagccgACTAanACCcTCTgAnccggAaAAAAggAAaCAGAg

>Bacillus_Fam_63_52_8 Nr. of seq. 8 Alignment length(with gaps) = 54
Alignment score = 0.661155

gATGAAGGACTTTTctcTGGaTcTctTnCncctTTTTGTCTTCAGnACCCg

>Bacillus_Fam_64_45_8 Nr. of seq. 8 Alignment length(with gaps) = 45
Alignment score = 0.881481

TTTTTGcTCTTCTTGTTGTTTACGAGCTTGTTCaTCAGCtTGaCG

>Bacillus_Fam_65_26_8 Nr. of seq. 8 Alignment length(with gaps) = 26
Alignment score = 0.630495
ATcTGAGCCAGGcTCAAaagngtgn

>Bacillus_Fam_66_21_8 Nr. of seq. 8 Alignment length(with gaps) = 24
Alignment score = 0.630208
TTCGCAAATAAAACnGgnaAa

>Bacillus_Fam_67_21_8 Nr. of seq. 8 Alignment length(with gaps) = 21
Alignment score = 0.806689
TGaAGaAACAGAAAaaCCAGG

>Bacillus_Fam_68_52_7 Nr. of seq. 7 Alignment length(with gaps) = 54
Alignment score = 0.639624
CGGTCACTtATAGCctTcATtaGTgACCACTTTtTCnATTtnaaCnagATTt

>Bacillus_Fam_69_52_7 Nr. of seq. 7 Alignment length(with gaps) = 54
Alignment score = 0.627572
tGACagCTTTTCgnCTTtCCnnCcAAACCTGTCCGAAgTTGgnnCTncTTC

>Bacillus_Fam_70_52_7 Nr. of seq. 7 Alignment length(with gaps) = 54
Alignment score = 0.638448
aAaatGGaAAATgGTGTcGcGaAAAgngAGAAACACCCctcTaaAaTCCAG

>Bacillus_Fam_71_52_7 Nr. of seq. 7 Alignment length(with gaps) = 54
Alignment score = 0.641387
TGTCTGAAGTaGCCTnGnGTTTCGGACAGcTTTgaTtgtTTnnaaGcnAAAGC

>Bacillus_Fam_72_52_7 Nr. of seq. 7 Alignment length(with gaps) = 52
Alignment score = 0.731380
CATAGgCctTCTATGATtcAGTTGCcgaaGCgAAAACAAGGAGnAAGTgAAT

>Bacillus_Fam_73_20_7 Nr. of seq. 7 Alignment length(with gaps) = 22
Alignment score = 0.655123
TTTTATAGCGAntTTTnCnT

>Bacillus_Fam_74_21_7 Nr. of seq. 7 Alignment length(with gaps) = 22
Alignment score = 0.698413
TTTATTTATCAcCGAnCnCnn

>Bacillus_Fam_75_22_7 Nr. of seq. 7 Alignment length(with gaps) = 22
Alignment score = 0.622655
TTTACTCGCCaAtTTngnnAcn

>Bacillus_Fam_76_21_7 Nr. of seq. 7 Alignment length(with gaps) = 21
Alignment score = 0.702948
TTACTTAACAnnTtttcAAAa

>Bacillus_Fam_77_15_7 Nr. of seq. 7 Alignment length(with gaps) = 16
Alignment score = 0.610119
cCtGGtTCTTCnGTn

>Bacillus_Fam_78_12_7 Nr. of seq. 7 Alignment length(with gaps) = 12
Alignment score = 0.830688
CGGCGAGtAGAA

>Bacillus_Fam_79_12_7 Nr. of seq. 7 Alignment length(with gaps) = 12
Alignment score = 0.640212
nTgTTGAtnTTG

>Bacillus_Fam_80_52_6 Nr. of seq. 6 Alignment length(with gaps) = 58
Alignment score = 0.624904
CGGTCACTCATAaGGTagATGAGAGCCCGngAAtaGcaAAAAGAAGnaAGaG

>Bacillus_Fam_81_52_6 Nr. of seq. 6 Alignment length(with gaps) = 57
Alignment score = 0.684016
GGAGAAAaccGaAGcaAAAGTGTCTTCATAAAGGnGATGAAGGACAAAcaA

>Bacillus_Fam_82_52_6 Nr. of seq. 6 Alignment length(with gaps) = 57
Alignment score = 0.644444
aaAAGGGcAGTCATGTATnCcGGGAgcgtTncGGgaTACATGAGTGGgTcGa

>Bacillus_Fam_83_52_6 Nr. of seq. 6 Alignment length(with gaps) = 56
Alignment score = 0.775397
AACCaCTTTTCGCGaAATCCnCATCATTTTcGGCTCATAGaACTCTTCTATG

>Bacillus_Fam_84_53_6 Nr. of seq. 6 Alignment length(with gaps) = 56
Alignment score = 0.659127
cTTTGCTTACCCTcCccAncCgtTTTTTCGcTcTTGCTGGGTAcGATTCCTCC

>Bacillus_Fam_85_52_6 Nr. of seq. 6 Alignment length(with gaps) = 55
Alignment score = 0.734949
CAcTCAACGAAGGTcATCATAAGcAAGCAATGCTaCCCCAAAACCAAACcn

>Bacillus_Fam_86_53_6 Nr. of seq. 6 Alignment length(with gaps) = 55
Alignment score = 0.654545
CTGatTTTTcTGTTCGTTCCGGGtTCTATaCacCTTATTGAaGACTCTTTCgn

>Bacillus_Fam_87_52_6 Nr. of seq. 6 Alignment length(with gaps) = 53
Alignment score = 0.628512
TCTACGTGACCcaacgtCctctTTTTcnTCcgnTtCGGTcCaCGTAGAACctC

>Bacillus_Fam_88_52_6 Nr. of seq. 6 Alignment length(with gaps) = 53
Alignment score = 0.782809
GTCAATCGTTACCGTTTCACAGaAGaTCAaCtCATTAcGGGCACGATTcAGt

>Bacillus_Fam_89_53_6 Nr. of seq. 6 Alignment length(with gaps) = 53
Alignment score = 0.780503
aGnCAAaAATGTGTGTCCAAGGcGaaAGTGGAGACAcAtaAcGAaGgAAAAAc

>Bacillus_Fam_90_42_6 Nr. of seq. 6 Alignment length(with gaps) = 42
Alignment score = 0.812169
TCTTCCACTTGTGGTTcTACTACcACTTGCTGCACtGGtTtT

>Bacillus_Fam_91_20_6 Nr. of seq. 6 Alignment length(with gaps) = 22
Alignment score = 0.625758
aATTTAATTGCGATTcTcGg

>Bacillus_Fam_92_21_6 Nr. of seq. 6 Alignment length(with gaps) = 22
Alignment score = 0.633333
AAActngaAAntTGGCGGAATA

>Bacillus_Fam_93_21_6 Nr. of seq. 6 Alignment length(with gaps) = 22
Alignment score = 0.603030
ATCGCGGAaAGaagtGcCGGA

>Bacillus_Fam_94_21_6 Nr. of seq. 6 Alignment length(with gaps) = 21
Alignment score = 0.647619
ATTcCGCCAAACtnaggATTa

>Bacillus_Fam_95_20_6 Nr. of seq. 6 Alignment length(with gaps) = 20
Alignment score = 0.731111
ATACTCTTCACtTTcgaGAA

>Bacillus_Fam_96_15_6 Nr. of seq. 6 Alignment length(with gaps) = 15
Alignment score = 0.751111
TAAaAAGAAAAaaC

>Bacillus_Fam_97_12_6 Nr. of seq. 6 Alignment length(with gaps) = 12
Alignment score = 0.807407
GGTTCTGGcTTT

>Bacillus_Fam_98_52_5 Nr. of seq. 5 Alignment length(with gaps) = 61
Alignment score = 0.610929
tttctnctctGnTTcCtatTtTcggcttCatgaagngctcatgGcgaccatT

>Bacillus_Fam_99_61_5 Nr. of seq. 5 Alignment length(with gaps) = 61
Alignment score = 0.663934
CCtgTtgCATtGcaCCgtttcCgTTnAAGTAgTACCATgttCCanttAntTGctTgCCAA

>Bacillus_Fam_100_52_5 Nr. of seq. 5 Alignment length(with gaps) = 59
Alignment score = 0.628531
AGAGtGtgCTtGTGACCAAAaGtAAgnTngGAatcCATagAAGTGGTCACA

>Bacillus_Fam_101_51_5 Nr. of seq. 5 Alignment length(with gaps) = 58
Alignment score = 0.637356
GGAATtgTGACAGgTttGnaGTGaaAGccgAAAAGCTGTCAAGAAAAccac

>Bacillus_Fam_102_52_5 Nr. of seq. 5 Alignment length(with gaps) = 58
Alignment score = 0.601149
nGcTATTGgCGACAtTtCTnttagcAAAAntcAacaaAAGTGTTTCCAATgg

>Bacillus_Fam_103_53_5 Nr. of seq. 5 Alignment length(with gaps) = 57
Alignment score = 0.626901
CACTCgGnGTAgTGGcGCCAcAAAngAGGatcCaTcaCgaGaAAAAGTGGcAg

>Bacillus_Fam_104_52_5 Nr. of seq. 5 Alignment length(with gaps) = 56
Alignment score = 0.618750
ATGACGGACAcTTTTntCntntTTccntngaTTTcTGTCCGTCATggCCTtg

>Bacillus_Fam_105_53_5 Nr. of seq. 5 Alignment length(with gaps) = 56
Alignment score = 0.664286
AgTCATGTAtccCAacagGCATCcGgGATACATgACccGGCnGagaAAAGnGA

>Bacillus_Fam_106_53_5 Nr. of seq. 5 Alignment length(with gaps) = 56
Alignment score = 0.671429
tTGGaTaAAatTAGGaGAAaGCGaACCaGtAAAgtcGTnaaTCaTCctcGCAa

>Bacillus_Fam_107_52_5 Nr. of seq. 5 Alignment length(with gaps) = 55
Alignment score = 0.752727
gAGTaAGTAACGAAAAGaGccGAACgaGnCAGTTACTcGaGGGaAGtgAGn

>Bacillus_Fam_108_52_5 Nr. of seq. 5 Alignment length(with gaps) = 55
Alignment score = 0.681818
TaATGTGCAGATAcgGAaGAGanaAGgGctaGTAtCTGcACAAAgAGgcGgt

>Bacillus_Fam_109_52_5 Nr. of seq. 5 Alignment length(with gaps) = 55
Alignment score = 0.613333
ancCtGTCAgTtnCcTTTTTTCnnGccTcnCngatTTTTtGGGcACTGAGAg

>Bacillus_Fam_110_52_5 Nr. of seq. 5 Alignment length(with gaps) = 54
Alignment score = 0.714815
TGGTAGTTAATCgaGAnGaaTAACGACGAAAAagacgaaggTCnAaGGAAAAa

>Bacillus_Fam_111_52_5 Nr. of seq. 5 Alignment length(with gaps) = 54
Alignment score = 0.714815
TTTGcTACCCcATATtTcNcNcCaCtCcgtTTTATAaGGatGCATTTTcttcT

>Bacillus_Fam_112_52_5 Nr. of seq. 5 Alignment length(with gaps) = 54
Alignment score = 0.676543
ACTTATCtCGnntTtCAGtACCACCAAnaCgcagatntCCTTtctTGATGGC

>Bacillus_Fam_113_52_5 Nr. of seq. 5 Alignment length(with gaps) = 54
Alignment score = 0.609877
GACAgTTTTnntaatTTTTtgaagcgggtTTTGTCTtCaAGAagcCTTATTgAA

>Bacillus_Fam_114_52_5 Nr. of seq. 5 Alignment length(with gaps) = 54
Alignment score = 0.701235
gATGAgAACCGaAACaAncgcagcAaGAGAAGGaAaCGGTCTTCATcAaGgg

>Bacillus_Fam_115_53_5 Nr. of seq. 5 Alignment length(with gaps) = 53
Alignment score = 0.694969
GGTCAAAAGGagaAGCnCTATTACCCGAAAAgngaGccGnacCaaGaAnaAc

>Bacillus_Fam_116_51_5 Nr. of seq. 5 Alignment length(with gaps) = 53
Alignment score = 0.735220
aAtcncggggttgCnggnGnaAAaaGcaGGagtaaccccgAGcAAAcGgnG

>Bacillus_Fam_117_52_5 Nr. of seq. 5 Alignment length(with gaps) = 53
Alignment score = 0.725786
AGTAACTGaCAtgtTcaGcCttTTTCGTGtaGTTACTCACcctnttCCTtcg

>Bacillus_Fam_118_52_5 Nr. of seq. 5 Alignment length(with gaps) = 53
Alignment score = 0.699371
aGTTcCCGagccCgCGnaAaaTccTCCATCaaGGTAACCAAAcGCaCTCatt

```

>Bacillus_Fam_119_52_5 Nr. of seq. 5 Alignment length(with gaps) = 53
Alignment score = 0.620755
GtTTTGTCTAaTAgAGnncttCTATtGgACAAaAtCaTtgCtCagAnCatGt
>Bacillus_Fam_120_52_5 Nr. of seq. 5 Alignment length(with gaps) = 52
Alignment score = 0.853846
ACACATTTTTcgCtTnTcCCcaTGATAATCTGTCTCagGcATGGCtTCTGAC
>Bacillus_Fam_121_52_5 Nr. of seq. 5 Alignment length(with gaps) = 52
Alignment score = 0.823077
tnaTTGAACCCCGAaCagGCGAAAAAAgCatCAAAGaGTCTTCAATAGggG
>Bacillus_Fam_122_45_5 Nr. of seq. 5 Alignment length(with gaps) = 48
Alignment score = 0.736806
ACTGGACCTCAAGGtgTCAAGGAcCagcaGGtgCTACTGGtGCT
>Bacillus_Fam_123_39_5 Nr. of seq. 5 Alignment length(with gaps) = 42
Alignment score = 0.642857
tTCTnCTcTttGcTgCTCtTCTTGCTTaCGtTTtTcttc
>Bacillus_Fam_124_40_5 Nr. of seq. 5 Alignment length(with gaps) = 42
Alignment score = 0.684127
ATTTGCGTCTcCtCngnGATTTtTGCGTCGgTtTtCtCan
>Bacillus_Fam_125_42_5 Nr. of seq. 5 Alignment length(with gaps) = 42
Alignment score = 0.888889
AAAGAAGAAGTaAAAGAgCCggtAAAAGAAGTTGAAGaAaCa
>Bacillus_Fam_126_39_5 Nr. of seq. 5 Alignment length(with gaps) = 39
Alignment score = 0.788034
nAAgCAaCAAAgTtCTAAaCAAGAnGATTCnTCTCAagA
>Bacillus_Fam_127_36_5 Nr. of seq. 5 Alignment length(with gaps) = 36
Alignment score = 0.792593
gTTGtTCTTCTaCGACcGGtgCtTCTTCTgCAACTg
>Bacillus_Fam_128_36_5 Nr. of seq. 5 Alignment length(with gaps) = 36
Alignment score = 0.874074
CTTCcACTTCTTCTgaCTCTTctGtTTCcGCAATTA
>Bacillus_Fam_129_29_5 Nr. of seq. 5 Alignment length(with gaps) = 30
Alignment score = 0.824444
GAGCAGCGgAGCGTACAagggACGTACGt
>Bacillus_Fam_130_21_5 Nr. of seq. 5 Alignment length(with gaps) = 24
Alignment score = 0.626389
TCGACCAcATttngaAnTAAT
>Bacillus_Fam_131_24_5 Nr. of seq. 5 Alignment length(with gaps) = 24
Alignment score = 0.822222
AGCTTctTCTTCaGCTTtTTTctT
>Bacillus_Fam_132_21_5 Nr. of seq. 5 Alignment length(with gaps) = 23
Alignment score = 0.630435
AGTcGAGCATAaAncCtgAaa
>Bacillus_Fam_133_21_5 Nr. of seq. 5 Alignment length(with gaps) = 23
Alignment score = 0.650725
TGCAAATAAAAannngTgaAAC
>Bacillus_Fam_134_21_5 Nr. of seq. 5 Alignment length(with gaps) = 23
Alignment score = 0.628986
TTTATCAGCGaAttTnannct
>Bacillus_Fam_135_21_5 Nr. of seq. 5 Alignment length(with gaps) = 23
Alignment score = 0.630435
TTTATTTTCgaaTTTgaTcan
>Bacillus_Fam_136_20_5 Nr. of seq. 5 Alignment length(with gaps) = 22
Alignment score = 0.613636
GATATatTTnganAATCGCt

```



```

>Bacillus_Fam_137_20_5 Nr. of seq. 5 Alignment length(with gaps) = 22
Alignment score = 0.633333
CcGATATAaTcagAtTtTcg
>Bacillus_Fam_138_20_5 Nr. of seq. 5 Alignment length(with gaps) = 22
Alignment score = 0.601515
taTCaGCCAAACTTnnnatT
>Bacillus_Fam_139_21_5 Nr. of seq. 5 Alignment length(with gaps) = 22
Alignment score = 0.645455
nTcGnGATaTATGAGCgAGan
>Bacillus_Fam_140_22_5 Nr. of seq. 5 Alignment length(with gaps) = 22
Alignment score = 0.630303
TTTATTGTCCnGaTncgcnnCA
>Bacillus_Fam_141_20_5 Nr. of seq. 5 Alignment length(with gaps) = 21
Alignment score = 0.666667
ATCGGTCTaAcTtnaaAtAT
>Bacillus_Fam_142_20_5 Nr. of seq. 5 Alignment length(with gaps) = 20
Alignment score = 0.746667
tctCgCTATacgAGAGTATt
>Bacillus_Fam_143_20_5 Nr. of seq. 5 Alignment length(with gaps) = 20
Alignment score = 0.686667
cGCAAATAAAanctngGaAT
>Bacillus_Fam_144_18_5 Nr. of seq. 5 Alignment length(with gaps) = 18
Alignment score = 0.718518
GGagcAACnGGcCCaCa
>Bacillus_Fam_145_12_5 Nr. of seq. 5 Alignment length(with gaps) = 12
Alignment score = 0.811111
GAAGAnGAaGAt
>Bacillus_Fam_146_52_4 Nr. of seq. 4 Alignment length(with gaps) = 58
Alignment score = 0.652778
gTTCGGAActgCtCtgaacGGgTTTCTCTCTGTCCGAAGttGCAtCaG
>Bacillus_Fam_147_54_4 Nr. of seq. 4 Alignment length(with gaps) = 57
Alignment score = 0.632554
TTCATccgcTtGATGAACACCAcTTTTtCCTcnGnCTTCntCTggaATTgTGGTg
>Bacillus_Fam_148_52_4 Nr. of seq. 4 Alignment length(with gaps) = 57
Alignment score = 0.626218
gCTcTTGgTGACCGAaAtccaaGGAaAaAaGTGGTaACCAAGaAGg
>Bacillus_Fam_149_53_4 Nr. of seq. 4 Alignment length(with gaps) = 57
Alignment score = 0.627680
GACAGCTTtaGCTanAtcAAcAgAGaAAGCTGTCCGAACatAGccAgACTTCG
>Bacillus_Fam_150_53_4 Nr. of seq. 4 Alignment length(with gaps) = 56
Alignment score = 0.619048
GATTAACtaCCATTTTcgCCTTactcCAcCTcAaTTTcGgCGTtAaTCCatct
>Bacillus_Fam_151_52_4 Nr. of seq. 4 Alignment length(with gaps) = 56
Alignment score = 0.669643
TTATGAAGGACAtTTCagccTGCgGtTcgcaacCtTTTGTCTTCATCCcGc
>Bacillus_Fam_152_53_4 Nr. of seq. 4 Alignment length(with gaps) = 56
Alignment score = 0.633929
tGAaGGTCATCATAcGaAGGnCAATGCTacCCGAgAAAgcAaaAcagAaGcgc
>Bacillus_Fam_153_52_4 Nr. of seq. 4 Alignment length(with gaps) = 56
Alignment score = 0.611607
cTcTTCaTTTcagttTTCGGTCACTCCAGacCcCcTgGAgTgACCCaAtCnT
>Bacillus_Fam_154_53_4 Nr. of seq. 4 Alignment length(with gaps) = 56
Alignment score = 0.640377
TCTACGTTACCCttcagCcTtatTTTTcgACCTtTCGGgCACGTAGAcACCCt

```

>Bacillus_Fam_155_54_4 Nr. of seq. 4 Alignment length(with gaps) = 56
Alignment score = 0.630952
CCTGAAaCaCtcTccgATcaCTCTnCTTCAGagGAATAAAtgCatCtTTATtCA

>Bacillus_Fam_156_51_4 Nr. of seq. 4 Alignment length(with gaps) = 55
Alignment score = 0.623232
ATTgGTAATGnAaaTtTcactTTCTtCTtTTTaCGGTGCGTATTAtcctga

>Bacillus_Fam_157_53_4 Nr. of seq. 4 Alignment length(with gaps) = 55
Alignment score = 0.639899
ctttaATTCGCaCCCTaATTTGnCTgCnAtcCtCgATTtTCATTACctATCACg

>Bacillus_Fam_158_51_4 Nr. of seq. 4 Alignment length(with gaps) = 55
Alignment score = 0.638384
AGTCCGAACcTGccaCaACTTCgGACAgAaAacGAAAAAtCCcgtGccAG

>Bacillus_Fam_159_52_4 Nr. of seq. 4 Alignment length(with gaps) = 55
Alignment score = 0.621212
GTTTCGGACaCgATTTcGCTtcTnCGacctTtttCTGTCCGAACtAcCaCCaA

>Bacillus_Fam_160_52_4 Nr. of seq. 4 Alignment length(with gaps) = 55
Alignment score = 0.711616
aTAAGTGCCAtCAaCaACagAGATTcCtggTTTGgTGGTTCcTtTcTgCCTG

>Bacillus_Fam_161_52_4 Nr. of seq. 4 Alignment length(with gaps) = 55
Alignment score = 0.627778
ctcAaGTTTaCGcgAAAacgGGcgCATAgAACCTTcCTATgAaCCcAaaATc

>Bacillus_Fam_162_53_4 Nr. of seq. 4 Alignment length(with gaps) = 55
Alignment score = 0.636364
ggAgAGaATcGTgCCCGAAATcnaaGgaAGGcgAAGgaAAACGGtAACAATag

>Bacillus_Fam_163_52_4 Nr. of seq. 4 Alignment length(with gaps) = 55
Alignment score = 0.742929
cAAAAATGGTCTTCATCacccTTATGAAGaaCATTTCTCTTcGgCTttTCatC

>Bacillus_Fam_164_52_4 Nr. of seq. 4 Alignment length(with gaps) = 55
Alignment score = 0.659596
GCGTTcCATtCACcttCTATGACACgCGttttCaCTccCGCTCtCtattTTc

>Bacillus_Fam_165_52_4 Nr. of seq. 4 Alignment length(with gaps) = 55
Alignment score = 0.602525
gTTCAGACAGCTTTTgcccgcctaGCaCcgaAAgCTGTCCGAAGtTgGCCaAG

>Bacillus_Fam_166_52_4 Nr. of seq. 4 Alignment length(with gaps) = 54
Alignment score = 0.626543
tTTTCATTACcTATCaCaaCTTtTTTCGcACccTAATcCcagCATCcCacaan

>Bacillus_Fam_167_52_4 Nr. of seq. 4 Alignment length(with gaps) = 54
Alignment score = 0.618827
aAAAAATGGTCATAGagagagaAACTGGAACCAAAAatgctcGaGcaAAgcga

>Bacillus_Fam_168_50_4 Nr. of seq. 4 Alignment length(with gaps) = 54
Alignment score = 0.652778
TTTGTCTTTTCATAAgCTcGATGAAaGACTTTTTCTtgaagcTCCAcCgAT

>Bacillus_Fam_169_54_4 Nr. of seq. 4 Alignment length(with gaps) = 54
Alignment score = 0.745885
GaCGAAAAcGTGgnaGaGAgGtAGaGAAAatGGTAGcTAATCaACcGGATTAAc

>Bacillus_Fam_170_52_4 Nr. of seq. 4 Alignment length(with gaps) = 54
Alignment score = 0.600823
GGACaaCTTTctCcgCctgcCgCcTcAACCTGTCCGAACttacaccgaCTTC

>Bacillus_Fam_171_53_4 Nr. of seq. 4 Alignment length(with gaps) = 54
Alignment score = 0.641975
GTCGCaTAgaAAGGcGTATAcGCGaCcGAgCGGcaGaaAAAataGaGnngCtCG

>Bacillus_Fam_172_53_4 Nr. of seq. 4 Alignment length(with gaps) = 54
Alignment score = 0.720165
aTGAAGGACTTTgCtCGcTcTTCTtgACctgGTTTTGgcCTTCATtagCttga

>Bacillus_Fam_173_52_4 Nr. of seq. 4 Alignment length(with gaps) = 54
Alignment score = 0.661523
ATCGTGCCCTcaAAAcgagaAAAACGAAAtagaGGtAACGATgaAGcGctG

>Bacillus_Fam_174_54_4 Nr. of seq. 4 Alignment length(with gaps) = 54
Alignment score = 0.763375
GTCATGTATcCCAaCAGGTTcCCGGaATACATGaGTAtGacaGaAAaAAGGaTa

>Bacillus_Fam_175_54_4 Nr. of seq. 4 Alignment length(with gaps) = 54
Alignment score = 0.627572
CATGagACATACTTtCtCTaaaAAccccCTcaacTtaTGTttCATGAaCCctT

>Bacillus_Fam_176_53_4 Nr. of seq. 4 Alignment length(with gaps) = 54
Alignment score = 0.659465
gAaaAAATTAGGaAAaagCgAACCaGcAAAcgcatAtaCAGGTtCGCAtaTG

>Bacillus_Fam_177_51_4 Nr. of seq. 4 Alignment length(with gaps) = 53
Alignment score = 0.768344
AAAAAtGGGAAccAAAGAGCCgcAaTgATGCCCAAAATcCaaGAGtCGCgG

>Bacillus_Fam_178_52_4 Nr. of seq. 4 Alignment length(with gaps) = 53
Alignment score = 0.633124
ATAAGAAAGcgCcGgATTccCaTCAAGAAaaccGcaAnCncGaaTaAAGtTG

>Bacillus_Fam_179_53_4 Nr. of seq. 4 Alignment length(with gaps) = 53
Alignment score = 0.742138
CTTAGTCaGCTGaACTAGaaCCCTCTGaTaaGacAATTaagAGtCCAGAGGGc

>Bacillus_Fam_180_53_4 Nr. of seq. 4 Alignment length(with gaps) = 53
Alignment score = 0.778826
ACCGCTATTTCTaTGAAAAcGAAAATAaTGGTTcCAGCaggAGaGAGcTAGa

>Bacillus_Fam_181_53_4 Nr. of seq. 4 Alignment length(with gaps) = 53
Alignment score = 0.796646
TTcCTcgTcCtCTCTTcCaTTTTCGTCgTCATGAaCCCTCcATGaCGACCATt

>Bacillus_Fam_182_53_4 Nr. of seq. 4 Alignment length(with gaps) = 53
Alignment score = 0.667715
GTCAGtGCCCaAAATccGCgGagGcCnGccaAAAAAGGTAACTGAcAggCcgc

>Bacillus_Fam_183_52_4 Nr. of seq. 4 Alignment length(with gaps) = 53
Alignment score = 0.642034
GGgTGATGAAGGcCaaAACgtGgaaAaaGagaagcaGAAAAGTCcTTCATaa

>Bacillus_Fam_184_52_4 Nr. of seq. 4 Alignment length(with gaps) = 53
Alignment score = 0.692872
TCCAATaagCCgATTGGAtACCTTTTcTCCnAttTTTccagcgGaACGGGt

>Bacillus_Fam_185_52_4 Nr. of seq. 4 Alignment length(with gaps) = 53
Alignment score = 0.707547
TTTTGgcCTTCATCngcCTTATGAAGacCATTTtGaaCCtGGctCaCgcCTg

>Bacillus_Fam_186_51_4 Nr. of seq. 4 Alignment length(with gaps) = 52
Alignment score = 0.607906
GCaCCgTAATttcggcaccCacctgTTTCATTACctATTCatcgtTATtC

>Bacillus_Fam_187_51_4 Nr. of seq. 4 Alignment length(with gaps) = 52
Alignment score = 0.695513
TTTCATTACcTATCccagGTTTTTCGcACCcTAATccctGCaAAacTcaAt

>Bacillus_Fam_188_52_4 Nr. of seq. 4 Alignment length(with gaps) = 52
Alignment score = 0.668803
TGAAGGACAAAACcCtgtAgaAAaacagaAgAAaTGTCTTCATaaaGccaA

>Bacillus_Fam_189_52_4 Nr. of seq. 4 Alignment length(with gaps) = 52
Alignment score = 0.784188
GGcccTAGTCGagCGaACTAAcACCCTCTATtCtcCAAAATGacaTTCAGAG

>Bacillus_Fam_190_52_4 Nr. of seq. 4 Alignment length(with gaps) = 52
Alignment score = 0.841880
AAAAATGTGTCTCAacCcgGTCaATGGAAaCACATAAcAAGaGATtaTGCTcA

>Bacillus_Fam_191_52_4 Nr. of seq. 4 Alignment length(with gaps) = 52
Alignment score = 0.735043
ttTTGGTTCCAGTTAcaCaatCTAtGACCATTTTctGcttgaCtaCACCcaA

>Bacillus_Fam_192_45_4 Nr. of seq. 4 Alignment length(with gaps) = 45
Alignment score = 0.887654
CAAAATCCATATGcAGCAcCaCaAAacCAAGAACAACAATATCAa

>Bacillus_Fam_193_42_4 Nr. of seq. 4 Alignment length(with gaps) = 43
Alignment score = 0.714470
TGGCCGaAAAAGcgacgCAGTTGGCGcgAAAGtgaGtTcaGT

>Bacillus_Fam_194_40_4 Nr. of seq. 4 Alignment length(with gaps) = 40
Alignment score = 0.730556
AAAaGAGCCAacGGaaCcGTCCCCcGGCCCaGcTcCAaa

>Bacillus_Fam_195_40_4 Nr. of seq. 4 Alignment length(with gaps) = 40
Alignment score = 0.661111
nTAAAGCggTaataGcgCTGgGGGaCAGgCCCCGcTnaaG

>Bacillus_Fam_196_40_4 Nr. of seq. 4 Alignment length(with gaps) = 40
Alignment score = 0.686111
cAGACGCAAAATcagaaTTtcGACGCAAAATCctcaGaag

>Bacillus_Fam_197_36_4 Nr. of seq. 4 Alignment length(with gaps) = 36
Alignment score = 0.608025
CCAGTcGgtCCAGTaaTaCCaGTntctCCaGTagca

>Bacillus_Fam_198_36_4 Nr. of seq. 4 Alignment length(with gaps) = 36
Alignment score = 0.804012
TCTTCCTTAGccTTtgCTActTCTTGgaCTTTcgCT

>Bacillus_Fam_199_36_4 Nr. of seq. 4 Alignment length(with gaps) = 36
Alignment score = 0.658951
CCcGTGTtACcTtGAgctCCttgaGgtCCaGTaGCg

>Bacillus_Fam_200_36_4 Nr. of seq. 4 Alignment length(with gaps) = 36
Alignment score = 0.780864
CCAGTAGGtCCaGTGaTnCCaGTAAATCCgGTagcC

>Bacillus_Fam_201_33_4 Nr. of seq. 4 Alignment length(with gaps) = 35
Alignment score = 0.651587
CctCCCATCATgCctGgnTGaCcTCcTtgaTGA

>Bacillus_Fam_202_27_4 Nr. of seq. 4 Alignment length(with gaps) = 28
Alignment score = 0.646825
CCAgcTaaTCCTGTcGcTCCcGtTGct

>Bacillus_Fam_203_27_4 Nr. of seq. 4 Alignment length(with gaps) = 27
Alignment score = 0.711934
GGAGcaACaGGtcCaACaGGAATaaCa

>Bacillus_Fam_204_25_4 Nr. of seq. 4 Alignment length(with gaps) = 25
Alignment score = 0.617778
gCctccGctTCTGCCcTccGctTTTG

>Bacillus_Fam_205_24_4 Nr. of seq. 4 Alignment length(with gaps) = 24
Alignment score = 0.805556
CCtGaAAcAcCaGATCCAGaAAA

>Bacillus_Fam_206_20_4 Nr. of seq. 4 Alignment length(with gaps) = 23
Alignment score = 0.718599
TATGATCCATTtCaGAAATa

>Bacillus_Fam_207_21_4 Nr. of seq. 4 Alignment length(with gaps) = 23
Alignment score = 0.642512
aacaTgGAATAAACTCcGaaA

>Bacillus_Fam_208_21_4 Nr. of seq. 4 Alignment length(with gaps) = 22
Alignment score = 0.604798
tCTATTTGCaGnTTTccgatt

```

>Bacillus_Fam_209_22_4 Nr. of seq. 4 Alignment length(with gaps) = 22
Alignment score = 0.651515
AGTCGCAAGtAAaaGtGgnGan
>Bacillus_Fam_210_21_4 Nr. of seq. 4 Alignment length(with gaps) = 22
Alignment score = 0.650253
GTAGAgTAAAnTncagAAAtT
>Bacillus_Fam_211_21_4 Nr. of seq. 4 Alignment length(with gaps) = 22
Alignment score = 0.656566
TTaGCGAatTTCaaaCatTTA
>Bacillus_Fam_212_21_4 Nr. of seq. 4 Alignment length(with gaps) = 22
Alignment score = 0.631313
TAtCTACGAAAttTanAgATA
>Bacillus_Fam_213_21_4 Nr. of seq. 4 Alignment length(with gaps) = 22
Alignment score = 0.611111
AcaAaaaGAAATGaAAgaaGa
>Bacillus_Fam_214_22_4 Nr. of seq. 4 Alignment length(with gaps) = 22
Alignment score = 0.623737
aTTTATTGTCCgGAaaCaaatg
>Bacillus_Fam_215_22_4 Nr. of seq. 4 Alignment length(with gaps) = 22
Alignment score = 0.694444
aTCAGCCAAAgtagGnagGGAA
>Bacillus_Fam_216_22_4 Nr. of seq. 4 Alignment length(with gaps) = 22
Alignment score = 0.702020
ATCTCTCGGTTTTGCGnctttA
>Bacillus_Fam_217_22_4 Nr. of seq. 4 Alignment length(with gaps) = 22
Alignment score = 0.601010
tATTTGCGAATcTagcacctTT
>Bacillus_Fam_218_20_4 Nr. of seq. 4 Alignment length(with gaps) = 21
Alignment score = 0.669312
tTGCGagTTTctCcAtATAT
>Bacillus_Fam_219_20_4 Nr. of seq. 4 Alignment length(with gaps) = 21
Alignment score = 0.671958
ATtATCaAAAAanCaAtTAT
>Bacillus_Fam_220_21_4 Nr. of seq. 4 Alignment length(with gaps) = 21
Alignment score = 0.625661
AgTTgGCGGaaTTAtTtacGa
>Bacillus_Fam_221_21_4 Nr. of seq. 4 Alignment length(with gaps) = 21
Alignment score = 0.634921
AcTcaccgATAGAAacgCAAA
>Bacillus_Fam_222_21_4 Nr. of seq. 4 Alignment length(with gaps) = 21
Alignment score = 0.701058
TGTcgTAAGtggCtgAAAATa
>Bacillus_Fam_223_21_4 Nr. of seq. 4 Alignment length(with gaps) = 21
Alignment score = 0.666667
TATCAGCGaATtTaanCaaTa
>Bacillus_Fam_224_21_4 Nr. of seq. 4 Alignment length(with gaps) = 21
Alignment score = 0.724868
TTTACTGTCCacTTtTanccA
>Bacillus_Fam_225_20_4 Nr. of seq. 4 Alignment length(with gaps) = 20
Alignment score = 0.666667
TTATctgCGAtTtCtgattT
>Bacillus_Fam_226_20_4 Nr. of seq. 4 Alignment length(with gaps) = 20
Alignment score = 0.788889
aTTCAGgATAAATCccAAAA

```

```

>Bacillus_Fam_227_18_4 Nr. of seq. 4 Alignment length(with gaps) = 19
Alignment score = 0.688596
TCgCCtTGaGGtCCTtGT
>Bacillus_Fam_228_18_4 Nr. of seq. 4 Alignment length(with gaps) = 18
Alignment score = 0.641975
GTgAcgCCtGTaGgaCCA
>Bacillus_Fam_229_18_4 Nr. of seq. 4 Alignment length(with gaps) = 18
Alignment score = 0.716049
CCAGGaGAtCCaaGcaAa
>Bacillus_Fam_230_18_4 Nr. of seq. 4 Alignment length(with gaps) = 18
Alignment score = 0.864198
AGACCATtTGGtTTTGGc
>Bacillus_Fam_231_15_4 Nr. of seq. 4 Alignment length(with gaps) = 15
Alignment score = 0.700000
aCCgAAaaAAGaAGa
>Bacillus_Fam_232_12_4 Nr. of seq. 4 Alignment length(with gaps) = 12
Alignment score = 0.888889
GGCAACGGcAAt
>Bacillus_Fam_233_234_3 Nr. of seq. 3 Alignment length(with gaps) = 234
Alignment score = 0.864198

CCAAAACAACGACGAAGTATGTCAATGTGGAtAAaGGnTCcCATtTAATaTTaCGtTCnAAAGCCTCCaaaaC
GTCCAGCATTTTtaGcaAGCTTGgCAAGAGGngAAAAaGTGACGGTtTACTCtATTTCCGGGGAnTGGGCaAAA
GTAAAAGCCGGgAGCAAAACGGGCTATGTTTCATGCATCTTTTTTgCGAAcTCAAATCCcGAtAGCAaTGCAG
acACTTCTaCTCCaG
>Bacillus_Fam_234_213_3 Nr. of seq. 3 Alignment length(with gaps) = 222
Alignment score = 0.719720

TTAAACcTtCGgtCgGGtGCTGGcACgtctCatCGngTTtTaACgACnCTtCCTGTTGGaCagAAGCTtGAgC
TTCTTcAAAAAcAAGGCAATTGGTATCAAGTTAAAGCtGGtaacCAaActGGcTGGGTtTctGCTGAtTTcAT
TAAaAaCagAtGGtAATaatGTcGAAGaCAACAAGcCCTTCTcTtGGCTCTGCgACgActACaGCTCGC
>Bacillus_Fam_235_166_3 Nr. of seq. 3 Alignment length(with gaps) = 168
Alignment score = 0.659392

attaAcTcCnnaTCCacTATtccCGTCTcCCcAgCTGACCaaaATcGTTntCttCCCCACGtATACAnCGTtCC
ATCACTTGCTAAcGCTAcTgtgTGancnantCCTgCnGnTACTTGTTCGATctTGGCTCCTcCgGGgATnGng
ATCgCTgTCGGACTAGnttg
>Bacillus_Fam_236_151_3 Nr. of seq. 3 Alignment length(with gaps) = 159
Alignment score = 0.705101

GCCGATgAccAAGgtgCTtccgctTTTCTcTcTGCTAGCTCCAgCGCCTATCGGCTaGCGgATTTCTcCGTCT
cCTCCCTgCGATAAGtCAACATCAGCTCGTaCCTCGCTGTGTnTCCTTtATCTCAGtCgnAgacTctGaaAtC
CGtAC
>Bacillus_Fam_237_144_3 Nr. of seq. 3 Alignment length(with gaps) = 148
Alignment score = 0.644895

TGGTGGGAcGGncgaaGnTGGAGcnagTGGGAaAATCTtGGttCnCCgCaaGGnGGatTTGAaGGctCGCCag
gtGCTGTcTCaTGGGgacCAAATCGnATCGACTGtTTTGTcAGGGganGnaAtAAtCanATGTGGCAtAAa
>Bacillus_Fam_238_122_3 Nr. of seq. 3 Alignment length(with gaps) = 125
Alignment score = 0.682667

GGCTCGcTCAGAATgggAGGaggaTGGAGCTTCTGaCcTtGAgGCGCTtTTTGCcTCgnggGAAGAnGCGAAg
ccaCCGaacaTTCTaGCCaCTGgAGCTGGATatCaTTAAAAAGCGgAAgt

```

>Bacillus_Fam_239_104_3 Nr. of seq. 3 Alignment length(with gaps) = 104
Alignment score = 0.978632

ATGCTAGAAACTGATTCAAAAGCTTGAACAAGAATATCTGTAAACATAAGATCCACCTCCAGTTTGAAAATAA
GGAAAAAGAGAATTAGCCAAGAGTGCCGATA

>Bacillus_Fam_240_84_3 Nr. of seq. 3 Alignment length(with gaps) = 84
Alignment score = 0.825397

AAGAGTTTTCaGaGATGCTTGAAGAAAGATCTCCcGAATGtGAtGAGTcTGAATcAATcAAaGAaGAaGatAC
tTCAtTAGAAg

>Bacillus_Fam_241_59_3 Nr. of seq. 3 Alignment length(with gaps) = 66
Alignment score = 0.611111

GGCTGGgTgCAAActGgnGGcAaATGGTATTACCTtAATcaAtcGGnGCgATGCAAACc

>Bacillus_Fam_242_66_3 Nr. of seq. 3 Alignment length(with gaps) = 66
Alignment score = 0.752525

ACAGGcTGGGnAcAAGTAGanGGnAAATGGTACTaCCTaGATGcaAAtGatGGTggaGCAATGAAA

>Bacillus_Fam_243_66_3 Nr. of seq. 3 Alignment length(with gaps) = 66
Alignment score = 1.000000

GGGGTCTGACCCCGTTTGTtATAATCAAGAGCTACGAACCCTTGTCTTTCCTGGAATTAACGCTTG

>Bacillus_Fam_244_55_3 Nr. of seq. 3 Alignment length(with gaps) = 58
Alignment score = 0.607280

TaTTGGTGACCTTtTcTcTcTaGnaCaCttccccACTTtGGGCACCAAtGaGCCT

>Bacillus_Fam_245_53_3 Nr. of seq. 3 Alignment length(with gaps) = 57
Alignment score = 0.606238

TGGcCCATTTAnCaCcTtAaTGGcCCAACATCcTCTcAtAacTtgAtTCTCAT

>Bacillus_Fam_246_53_3 Nr. of seq. 3 Alignment length(with gaps) = 56
Alignment score = 0.684524

AAGTGGCGCCATTCTcGcanAGTGgTGCCACTTTTcGAGTGAngAGActCtCaa

>Bacillus_Fam_247_50_3 Nr. of seq. 3 Alignment length(with gaps) = 55
Alignment score = 0.630303

TTTTCATTACcATTaACCTttATTTCGcACcgTAATTCgccCagCTcGga

>Bacillus_Fam_248_51_3 Nr. of seq. 3 Alignment length(with gaps) = 55
Alignment score = 0.612121

GGTAACAGAGAagGCgTCTCAAgCCCCGAAGCaAGnagcGAAncnCnAAAC

>Bacillus_Fam_249_53_3 Nr. of seq. 3 Alignment length(with gaps) = 55
Alignment score = 0.616162

aAACGGTAACAGAGAgGCCGTCTCAaaGCCcGAAGctgCTCngaactnCGCCa

>Bacillus_Fam_250_51_3 Nr. of seq. 3 Alignment length(with gaps) = 55
Alignment score = 0.620202

GTTTcTCTtngAATCtTACCATTATAAatCggtTTCCCTcTGtAgtGGTAC

>Bacillus_Fam_251_52_3 Nr. of seq. 3 Alignment length(with gaps) = 55
Alignment score = 0.634343

TACcCTTTTCcattCnCTcCTTCCCTTTTnTTGTcTCCATCtccnTTTGGt

>Bacillus_Fam_252_53_3 Nr. of seq. 3 Alignment length(with gaps) = 55
Alignment score = 0.638384

ATGAAGGaCaatTaGGnnTGAAAtTTttGGTcGAAATGntgTTCATAAGcCCG

>Bacillus_Fam_253_52_3 Nr. of seq. 3 Alignment length(with gaps) = 55
Alignment score = 0.731313

CCACCAAACCTTcttccTcAGcgCTTGATGGTTCTTATaaCCGTTTTcAGTA

>Bacillus_Fam_254_53_3 Nr. of seq. 3 Alignment length(with gaps) = 55
Alignment score = 0.628283

TTGGCTaCCGTTCTTtcGCnnTcTcNcTcGgtTTCGGGatCCAtCacACCTCT

>Bacillus_Fam_255_52_3 Nr. of seq. 3 Alignment length(with gaps) = 55
Alignment score = 0.660606

TAGACATTTcAAGCtnCAnCAGctTcTGAAATGTCTATTAAAcacCCTtTTaT
 >Bacillus_Fam_256_52_3 Nr. of seq. 3 Alignment length(with gaps) = 55
 Alignment score = 0.668687
 CTCTATGtgCACTTtnCncGCTTTTTtcAtcGaTTTCGTGTTTCATTGaaGAC
 >Bacillus_Fam_257_52_3 Nr. of seq. 3 Alignment length(with gaps) = 55
 Alignment score = 0.634343
 TGCATTGCCCAAAancGGtGAtAgAtcnAAAAtTTGGTCAAtGGAaGaGGGn
 >Bacillus_Fam_258_51_3 Nr. of seq. 3 Alignment length(with gaps) = 55
 Alignment score = 0.612121
 aTTTaTTCTCTaAAGCtgCaaAAAttcGcAAGCTTcAGGTGAAtAAaGaG
 >Bacillus_Fam_259_52_3 Nr. of seq. 3 Alignment length(with gaps) = 55
 Alignment score = 0.723232
 AATGTGTCTCAAGActgGatCTTGAGACAgATAAAgAGGGaGaAAggAgAAA
 >Bacillus_Fam_260_52_3 Nr. of seq. 3 Alignment length(with gaps) = 55
 Alignment score = 0.717172
 ATGAAaACCAttTTctCTTCGGAACaAgGAgAAACGGTCTTCATgaCGGCg
 >Bacillus_Fam_261_53_3 Nr. of seq. 3 Alignment length(with gaps) = 55
 Alignment score = 0.640404
 ACCGCAAGaangTTTTcacGGTACAtGCTCAntcAAAAAnAGancaAGCaTGT
 >Bacillus_Fam_262_53_3 Nr. of seq. 3 Alignment length(with gaps) = 55
 Alignment score = 0.696970
 CGGGCACTATGAActCTcTATAGTgACCGCncaCTtCTTnTgAcTcCCTCctg
 >Bacillus_Fam_263_52_3 Nr. of seq. 3 Alignment length(with gaps) = 54
 Alignment score = 0.633745
 GTCAAATAGAAcGgnTCTATAcGCCCCGAAnGCcCGtgaAAaAgaGgnaAAcG
 >Bacillus_Fam_264_52_3 Nr. of seq. 3 Alignment length(with gaps) = 54
 Alignment score = 0.641975
 cTCAnGACACTTTTCTcTCTcnTTTTngnnTTTcATGtCCTTGAGAnaCTtC
 >Bacillus_Fam_265_52_3 Nr. of seq. 3 Alignment length(with gaps) = 54
 Alignment score = 0.637860
 ACTTCGACTCattCCTCcagATttCCnCTttTtCTGTcCgAAAtGnTGACCn
 >Bacillus_Fam_266_52_3 Nr. of seq. 3 Alignment length(with gaps) = 54
 Alignment score = 0.699588
 CGGATTCGACAAcattaCcgntTCatCCTgCTTccCTGTCCGAATATcAAG
 >Bacillus_Fam_267_53_3 Nr. of seq. 3 Alignment length(with gaps) = 54
 Alignment score = 0.627572
 cTAAAGGACAAAActcgGatgnagCagCAAAGATnnGTCCATGAgAaGcggTc
 >Bacillus_Fam_268_52_3 Nr. of seq. 3 Alignment length(with gaps) = 54
 Alignment score = 0.633745
 AGTGCCCatgCgCatGggAAAAagCcAAgnAcGGGCACTCTGAGaGGTtcAC
 >Bacillus_Fam_269_52_3 Nr. of seq. 3 Alignment length(with gaps) = 54
 Alignment score = 0.625514
 atTTTTGAGGGTaCtatTCTGnctTtTtAGTgCCCTCAAttTTTgnTTTTcg
 >Bacillus_Fam_270_52_3 Nr. of seq. 3 Alignment length(with gaps) = 54
 Alignment score = 0.703704
 gtGGAAATGaCCCTTCAGCAnGaTcaAAAtCtGtGcGAAGGTCACAAAgGCGc
 >Bacillus_Fam_271_53_3 Nr. of seq. 3 Alignment length(with gaps) = 54
 Alignment score = 0.600823
 CGGGCACATGTtnGCctcTCTGTtACCgtgCtCTtgcttTTTcttgCTTtn
 >Bacillus_Fam_272_52_3 Nr. of seq. 3 Alignment length(with gaps) = 54
 Alignment score = 0.633745
 CTCTCTTACCATCcnACcCtnTTtccTCnCGAAAtGGGCACTGACaACnnCT
 >Bacillus_Fam_273_53_3 Nr. of seq. 3 Alignment length(with gaps) = 54
 Alignment score = 0.651235


```

aCGGTAAAtGaAaGAgcGnTtCATTtACCGAAAAGngGaAAAAAnAgAGCnCTt
>Bacillus_Fam_274_52_3 Nr. of seq. 3 Alignment length(with gaps) = 54
Alignment score = 0.720165
CACAGTGCCnnGCncGGCTTTTTTggcctCGAcGGGCACTCTGaaCTCTT
>Bacillus_Fam_275_53_3 Nr. of seq. 3 Alignment length(with gaps) = 54
Alignment score = 0.672840
GgAACGAAAGAGgtGcATTcGTgCccgTaaGAGGnAAAAATtAGGAGAAgnCa
>Bacillus_Fam_276_53_3 Nr. of seq. 3 Alignment length(with gaps) = 54
Alignment score = 0.738683
gTGTACCgCTAGAcnCntCtTGCGGnACATGCTCacCcTATTTCaCaCCaAGC
>Bacillus_Fam_277_51_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.639413
GAATAGAAgCnccCTATTCGACCGTTncACGnggTTtCacTTccTTCGGgc
>Bacillus_Fam_278_51_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.635220
TGTCTGAACCTgagCTAACTTCGGACTnCttctGccTtTTTctcCtGAtCt
>Bacillus_Fam_279_51_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.681342
ACTTTATtTtnGATTaTTaaTtgaAAATGTCTtTTCATaAGgtcGATGAAGg
>Bacillus_Fam_280_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.666667
TTTtGtCCTTCATcCcCcttATGAAGGACcGTTCTCTGnAttTtnCnCcTcG
>Bacillus_Fam_281_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.752621
aGTTTCTGCTGCTAAaTCcaGTTaAgAACACTTTCaCCGCaaACCaaCcAg
>Bacillus_Fam_282_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.746331
cACAtGAAAAAnnGGCTcATAGAAcCTnTCTATGAACCCaAATTTgAtCGAAn
>Bacillus_Fam_283_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.658281
TTGaCTnCCGTTCTTcCnCnCTTctCcTTTTTCGGgAGcCAcCaCnnCtCT
>Bacillus_Fam_284_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.618449
CCTCCATCACcCtCATGGAgGACcttTTTTCCnntTctCaCgcnAnntcGGt
>Bacillus_Fam_285_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.907757
AATGTGTGTCCAAGAGAnGAGcTGAAACACATTATAAGAGAAACCGGAGGAg
>Bacillus_Fam_286_53_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.851153
ATTGGTTACCCgGTTGcGCgGATTTCACccGgACTCGGTCACCTTTcGGCNTG
>Bacillus_Fam_287_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.633124
TTAAAGACATTTTgagCantttgAnaGGnaGTTtTGTCtTTAAGaAgGGcTA
>Bacillus_Fam_288_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.731656
cTTATAAGCTACCCAACCTggggcganTttCtCGGtTTCGGTcGCTTATACCC
>Bacillus_Fam_289_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.645702
nAAgTGTTTCCAATgAaGGCTATTGGcgACAAACTCagtangAAAanggGa
>Bacillus_Fam_290_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.607966
TGGAatCACTTTaCTCTnTTTTnCTCcgagtTTTGTtTCCAATagccntgAT
>Bacillus_Fam_291_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.714885

```

GCTGTCCGAAGTnGagTGAGGTTTCAGACAGcTTGaGggtgagAAGaGGAAAA
>Bacillus_Fam_292_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.704403
aaGGTTCGACAGCTTTtGcTcncaGGcanTCGAAGTTGTCCGAAGTnGctC
>Bacillus_Fam_293_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.637317
GTCTGAAGTCAccnTAGGTTTCgGACaCngtTGcAttTGaAATCaCtnaTCcT
>Bacillus_Fam_294_51_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.651709
TATaAGgAAGaaATGAGtGCTAAAgcgnAgGATAGanCattATaTTaCCAG
>Bacillus_Fam_295_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.707265
TtAAGGAAGncCGnnAAAAAgngtcnCTaTCTTAACgTAGAggCGTTCTAnG
>Bacillus_Fam_296_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.841880
GGcGCGCTtaCCcTAgCGCGnGgCTCTTCTcTCTTTTTCTTCTTCTTGGGA
>Bacillus_Fam_297_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.675214
AagCGTGTCATACgAgggCAATGcCaCATGAAAAAtaggaAncaAgcaAATA
>Bacillus_Fam_298_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.688034
AAaCGGtAACTAATcGtGagGAAAgGTtcCCGnTTtGtGcCcGagTtcGAAa
>Bacillus_Fam_299_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.846154
AAAGTGTTCTAanCCAGAGTTAGCAGCACAAAgTGAGTAGAgCaCaGgCcCg
>Bacillus_Fam_300_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.811966
GAGTTTgTGCTGCTAAcTCaGTtTgGAACACTTTcGcCgnGGaCCCGCACc
>Bacillus_Fam_301_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.809829
AAgGGTCATAAngaCaCaTGATtTAACCCTTCAGCATGAAGGAaAcTccGTG
>Bacillus_Fam_302_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.760684
CTGGAGTGACCGaAaAgCATntAgaAAAnGCaTtGGGTCAATGCAGatAGt
>Bacillus_Fam_303_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.713675
GACTgCTTTtacGGAAAAagGCGgAAAgctGTcCGAACTTGgGgcTACTTCg
>Bacillus_Fam_304_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.675214
AATCGTtaCCgTTTcanATGnGAnCACggCAAnAcGGtAACGAtTCaGAGcn
>Bacillus_Fam_305_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.705128
GGcTnATTcGGACAGaaCAAgcnagAAatGcCgnTAGAGAGTCCgAATGCAA
>Bacillus_Fam_306_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.726496
tGaTTGaTTACCTGaaGatGaAAATTGcatgTGTACGGgAACCAтанаGAG
>Bacillus_Fam_307_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.899573
GGTAACCATTGagGGcCTTTGGTGACCCTTTnGGNGGAAAACTCCTTTCTcTC
>Bacillus_Fam_308_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.929487
AGAAAAGAGGAAGAAAGGTAACCAATCGCtCGGAAAGGTTaCCGAAActnGAA
>Bacillus_Fam_309_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.739316

TgGAtACACATTtTgngAGAATATTgcaGAtAATgTGTCTCAAGgATgGcGg
>Bacillus_Fam_310_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.982906
CTTAAATAGAGGAAACCAgGTGTGTAGGGTAACTAAAGCGAGCGAAAGGTTA
>Bacillus_Fam_311_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.730769
aGGTTACCGAaTCcatGAGAAATCCACCTanAGGGTAACgAAaCnaGcgcaA
>Bacillus_Fam_312_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.649573
AAAGGnAGAAGAGaGngcGTcTCAnCGCCCAtcTGAgngAGAAAnAagaGaaG
>Bacillus_Fam_313_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.675214
TATGGGACAnttgcTTncnntTtTCnGCTtnTTTTGTCTcATTGAGCtCTCC
>Bacillus_Fam_314_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.982906
AAAAGGGAACATAGAGTCCTTGTATGTACGCGAAACTGGTGgGAAGACTCCG
>Bacillus_Fam_315_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.946581
GAGCAAAGAACATGTCATCATCGAnaGGATGAAGACACGAATAGAAgTGTAG
>Bacillus_Fam_316_48_3 Nr. of seq. 3 Alignment length(with gaps) = 48
Alignment score = 0.981481
TTCTTCTGATGACGTTGAGAACGACTCAGAtGCTGACAGTGACGATGA
>Bacillus_Fam_317_45_3 Nr. of seq. 3 Alignment length(with gaps) = 46
Alignment score = 0.666667
GnACAAAAGCCAGAcGATAnCgAAAcAAAACCGgATGAccAAaACg
>Bacillus_Fam_318_40_3 Nr. of seq. 3 Alignment length(with gaps) = 43
Alignment score = 0.666667
AAAtCGCAGATAAgTnaTGAAAcCGCAGATAACTCGtGa
>Bacillus_Fam_319_39_3 Nr. of seq. 3 Alignment length(with gaps) = 42
Alignment score = 0.722222
AtAAAAAATcTtTaCTGtTCTCACAAaAGATCnCGCAGCc
>Bacillus_Fam_320_42_3 Nr. of seq. 3 Alignment length(with gaps) = 42
Alignment score = 0.978836
GCAGAAGAGAAAGTAgCAGAATTAAACAGACGAAGCAAAAT
>Bacillus_Fam_321_40_3 Nr. of seq. 3 Alignment length(with gaps) = 40
Alignment score = 0.766667
tAAGAGTATTTCCgatTTCCGAAGAGTaTcCncGCAAAAGT
>Bacillus_Fam_322_39_3 Nr. of seq. 3 Alignment length(with gaps) = 39
Alignment score = 0.863248
ACaaCaCCTCCAGCaATAAcGGAGGAGGtCAAGGAAAT
>Bacillus_Fam_323_39_3 Nr. of seq. 3 Alignment length(with gaps) = 39
Alignment score = 0.749288
TCAggggCAACAgaaAcACTCTAAgCAAGACgACTCcaA
>Bacillus_Fam_324_36_3 Nr. of seq. 3 Alignment length(with gaps) = 36
Alignment score = 0.811728
tAAGAAaCAAGAAgAgGCgAAAAAgCTAGAAGAGag
>Bacillus_Fam_325_36_3 Nr. of seq. 3 Alignment length(with gaps) = 36
Alignment score = 0.969136
AATGCAACAAGGGATGGGAGGAAACCACCAngCCCC
>Bacillus_Fam_326_34_3 Nr. of seq. 3 Alignment length(with gaps) = 35
Alignment score = 0.615873
CGACGAGtAAtCGCAGGAGCAnacgGtttttnaTG
>Bacillus_Fam_327_25_3 Nr. of seq. 3 Alignment length(with gaps) = 26
Alignment score = 0.846154

```

tTGTgCCTGGCACCTTTtCCCCTTT
>Bacillus_Fam_328_24_3 Nr. of seq. 3 Alignment length(with gaps) = 24
Alignment score = 0.759259
GaAaCCgCCCATGCCCATtcCnGG
>Bacillus_Fam_329_21_3 Nr. of seq. 3 Alignment length(with gaps) = 23
Alignment score = 0.661836
TTTACTGGCGGAtAnCnCCaC
>Bacillus_Fam_330_21_3 Nr. of seq. 3 Alignment length(with gaps) = 23
Alignment score = 0.642512
gttnTgtcTaTtTttntGagn
>Bacillus_Fam_331_21_3 Nr. of seq. 3 Alignment length(with gaps) = 23
Alignment score = 0.671498
GTTGGCgCAAAAGtATCtCG
>Bacillus_Fam_332_21_3 Nr. of seq. 3 Alignment length(with gaps) = 23
Alignment score = 0.690821
TTCGCAAATAAAaCCnTcAtA
>Bacillus_Fam_333_21_3 Nr. of seq. 3 Alignment length(with gaps) = 23
Alignment score = 0.637681
TGACGGGATtnTCTcGngTTa
>Bacillus_Fam_334_23_3 Nr. of seq. 3 Alignment length(with gaps) = 23
Alignment score = 0.647343
TCnATaCgGACAaGAGcgAGcGc
>Bacillus_Fam_335_23_3 Nr. of seq. 3 Alignment length(with gaps) = 23
Alignment score = 0.743961
TATTTGCGAATTaCctnGcntTT
>Bacillus_Fam_336_20_3 Nr. of seq. 3 Alignment length(with gaps) = 22
Alignment score = 0.676768
TaTATCGGCGAtTCTCgAtT
>Bacillus_Fam_337_20_3 Nr. of seq. 3 Alignment length(with gaps) = 22
Alignment score = 0.651515
GACGCAAAAAnccttgGTGGa
>Bacillus_Fam_338_21_3 Nr. of seq. 3 Alignment length(with gaps) = 22
Alignment score = 0.732323
ATCAGCCAAAGcAGnTGnGAT
>Bacillus_Fam_339_21_3 Nr. of seq. 3 Alignment length(with gaps) = 22
Alignment score = 0.772727
tTTGGCTGATTTCTcCTCCgc
>Bacillus_Fam_340_21_3 Nr. of seq. 3 Alignment length(with gaps) = 22
Alignment score = 0.616162
nnTGGATCATAAAATctccAAt
>Bacillus_Fam_341_21_3 Nr. of seq. 3 Alignment length(with gaps) = 22
Alignment score = 0.727273
aCTCCTATAATAAAaAngaTA
>Bacillus_Fam_342_22_3 Nr. of seq. 3 Alignment length(with gaps) = 22
Alignment score = 0.636364
TTTGGCGGAATtnCcantnaAg
>Bacillus_Fam_343_21_3 Nr. of seq. 3 Alignment length(with gaps) = 22
Alignment score = 0.737374
TACGaGAGTAAnCgCACTCnT
>Bacillus_Fam_344_21_3 Nr. of seq. 3 Alignment length(with gaps) = 22
Alignment score = 0.747475
CTTGAGCGGTATTcncCTCcn
>Bacillus_Fam_345_21_3 Nr. of seq. 3 Alignment length(with gaps) = 22
Alignment score = 0.727273

```

TtAACCaCTGCTaTTCGTCgG

>Bacillus_Fam_346_21_3 Nr. of seq. 3 Alignment length(with gaps) = 22
Alignment score = 0.631313
TGTCCCATAnAaTcgAAgTnn

>Bacillus_Fam_347_18_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.767196
CCAGGAgCAGGcTTTGGC

>Bacillus_Fam_348_20_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.708995
GtAGGaCGAAATATTtGcGT

>Bacillus_Fam_349_20_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.687831
ACTGtCACTATnccnAAAAAT

>Bacillus_Fam_350_21_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.687831
tTTATTTGCGATAacTaCgtc

>Bacillus_Fam_351_21_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.957672
GCCAACCAACCGTGTCCgCCTT

>Bacillus_Fam_352_21_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.788360
AGAACGgCGAGagCgGCGaGT

>Bacillus_Fam_353_21_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.661376
ATtCCGCGAAAncnGAGnngA

>Bacillus_Fam_354_21_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.756614
AACCGAGAGAtTAaggGcTga

>Bacillus_Fam_355_21_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.788360
GATGtGAGagAGAAGaGCgCG

>Bacillus_Fam_356_21_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.671958
ATTCCGCCAAcTtnGGannngN

>Bacillus_Fam_357_20_3 Nr. of seq. 3 Alignment length(with gaps) = 20
Alignment score = 0.711111
GaCGCAAaTATtgTGAAact

>Bacillus_Fam_358_20_3 Nr. of seq. 3 Alignment length(with gaps) = 20
Alignment score = 0.877778
CaCaTATAAAAAGCTcCAACT

>Bacillus_Fam_359_20_3 Nr. of seq. 3 Alignment length(with gaps) = 20
Alignment score = 0.788889
TATCaGGAAAAaTtnAATA

>Bacillus_Fam_360_18_3 Nr. of seq. 3 Alignment length(with gaps) = 18
Alignment score = 0.703704
GGtGgaCCnGGnTTCGGT

>Bacillus_Fam_361_18_3 Nr. of seq. 3 Alignment length(with gaps) = 18
Alignment score = 0.746914
TCAGCAGTAGagTCnGcg

>Bacillus_Fam_362_18_3 Nr. of seq. 3 Alignment length(with gaps) = 18
Alignment score = 0.679012
TGctcATGATggTGnTCA

>Bacillus_Fam_363_16_3 Nr. of seq. 3 Alignment length(with gaps) = 16
Alignment score = 0.722222

AACCCGGGTTaaaGgg
 >Bacillus_Fam_364_15_3 Nr. of seq. 3 Alignment length(with gaps) = 15
 Alignment score = 0.762963
 GTtTTTCTTCTtTtaG
 >Bacillus_Fam_365_15_3 Nr. of seq. 3 Alignment length(with gaps) = 15
 Alignment score = 0.837037
 TCTGgTTTtTCTACT
 >Bacillus_Fam_366_15_3 Nr. of seq. 3 Alignment length(with gaps) = 15
 Alignment score = 0.755556
 TCTTCTTCAGTnacG
 >Bacillus_Fam_367_12_3 Nr. of seq. 3 Alignment length(with gaps) = 12
 Alignment score = 0.675926
 TnCTTtGTtATt
 >Bacillus_Fam_368_12_3 Nr. of seq. 3 Alignment length(with gaps) = 12
 Alignment score = 0.666667
 ATagAAnAAGGt
 >Bacillus_Fam_369_12_3 Nr. of seq. 3 Alignment length(with gaps) = 12
 Alignment score = 0.777778
 GCTGCTgCaACg
 >Bacillus_Fam_370_12_3 Nr. of seq. 3 Alignment length(with gaps) = 12
 Alignment score = 0.888889
 CCAGGnGAAGAA
 >Bacillus_Fam_371_12_3 Nr. of seq. 3 Alignment length(with gaps) = 12
 Alignment score = 0.777778
 CACCAgCACCaA
 >Bacillus_Fam_372_12_3 Nr. of seq. 3 Alignment length(with gaps) = 12
 Alignment score = 1.000000
 CCGTAACCGCCG
 >Bacillus_Fam_373_12_3 Nr. of seq. 3 Alignment length(with gaps) = 12
 Alignment score = 0.777778
 TGaCCtTGaCCT
 >Bacillus_Fam_374_12_3 Nr. of seq. 3 Alignment length(with gaps) = 12
 Alignment score = 0.777778
 GAAgCaGAAgCA
 >Bacillus_Fam_375_240_2 Nr. of seq. 2 Alignment length(with gaps) = 240
 Alignment score = 0.920833

GGTTGGGCGAAAGTGAaTGTAATGGGAAACAGGaTATGTAAGTAGTCAaTATTTAACAGGCAAGACGAACA
 CAGCCCCAtCAAAACCaTCaACATCCACACCAGCAAAAGACGGAAACAAAATATGTATCTGTAACTCAGGTTC
 TAtTTTGAATCTACGCAGTAGTGCCAGTACAAGTGCATCaATAATCGGGAAcCTaACAAATGGCACAGCaGTA
 ACGGTTCAATCAGATTCCAAa

>Bacillus_Fam_376_210_2 Nr. of seq. 2 Alignment length(with gaps) = 210
 Alignment score = 0.853968

GGCTGGTACAGTGATGAAGCACgAACGAATTTGTACGATTTTaAtGaGCCAGTNAAAGCAGCgAcaAagTTGT
 ATGCGAAATGGACcCATAATCAATATGAAGTaAaTTTTGATACNAATGGCGGcAGTNANaTTGCTTCgGAAAA
 TGTGAANTACAATGAAAAAGCaANGAAGCCAgNaGtACCAACGAAAGAAGGcTACACCTTCGCN

>Bacillus_Fam_377_200_2 Nr. of seq. 2 Alignment length(with gaps) = 200
 Alignment score = 0.746667

ATTGATAAAACaGCTCCAGTcGTAAcTGGaGTTAgAAaACaACGGcCTtTACAATaAaGATGTaACAgTTTCa
 TTTAATGAAGGAACaGCgACATTAAATGGTAAaGaAgTgaaAaCTGGaACAGcAGTTAAaCAAGAtGGAacc
 TAcACAgTAGTGGTAAcCaGAcGCAGCAGGaAAcAAACaAcTGTgAAGTTCACg

>Bacillus_Fam_378_154_2 Nr. of seq. 2 Alignment length(with gaps) = 154
Alignment score = 0.696970

ACATGTGGCATCAcTTCTTcACCGCTTCTAAGAAAAaCgAAAAACgaGcTTcacTaagcTCGTTTTTaaTcaA
aacATAaGAGAGTgaTAAAAAtAtGGCGGTGGAAaTGAAgCCACGCGTAGTAGaGAGAAGAGCACTCACTACTA
CTTTAAAAa

>Bacillus_Fam_379_153_2 Nr. of seq. 2 Alignment length(with gaps) = 153
Alignment score = 0.644880

aATAAGTCAACATCGAaTCGCTaaCGCTCaTCGTGTTTCCTTTATcTcGATgCcAAaCCCTCCAagCCaTACa
cCcCTAAACaGgCGccTCCGCTTTTCTaTTGTCCAGCTcCacCgCCcAgGcGCTaATcGaccTtCGGccTTcT
CaCCTaC

>Bacillus_Fam_380_148_2 Nr. of seq. 2 Alignment length(with gaps) = 148
Alignment score = 0.718468

TAGAcGAaGCaACAAAAGAAAAAGCGAAaTCaATcTTaGAaCAAGAAAAaTCCGGaAaAcTAACaCGTGAAcA
AGCAAAAGAaaaATTaAaAaAaCTAGGcGTGAAATTCCCaGAGAAAGGgtAAGCAcGaaGAcATGTTcGCgAA
cT

>Bacillus_Fam_381_145_2 Nr. of seq. 2 Alignment length(with gaps) = 145
Alignment score = 0.671264

CCACCATTtATGCCACAgATgaTCGTTGTcTCCaCgGACAAAgGTATCaATcCGaTTcGccCCCCATGATAAA
GCacCCGgtAGaCCCTtcAAaCCaCccCGCGGaGcCCaAGaTcTCCCAaTCaCTCCAGCgcGAACCaTC

>Bacillus_Fam_382_140_2 Nr. of seq. 2 Alignment length(with gaps) = 140
Alignment score = 0.814286

ATCGTCCGaAAACTaTAAaACGcCGCGGGGTGGAGCAACGAGCaAaGCATCAgTGAAAAaCaAaCGAGTTGTc
TCGACGCATaaGCAgCGaAGCaAAGCAaGAAGAGGAAGAGACAGTCAAAGGACaTCGAAGCaAaAGC

>Bacillus_Fam_383_138_2 Nr. of seq. 2 Alignment length(with gaps) = 138
Alignment score = 0.990338

GTTGTCTCGGAAGCGAGGCTTCGTGAAGAGCAGGAAAAATGAAGAGGAAGAAGCTGAGCGGTCAGCGCCATTGG
CTTTAAAGCAGAGGAAGCGGCGGTATAAAAGCAGAAGAAGCGCCAGCTGAGCCGCCaGAGCTT

>Bacillus_Fam_384_128_2 Nr. of seq. 2 Alignment length(with gaps) = 128
Alignment score = 0.695312

acCTCGAGGTCATAAGCcAAAaacaCCAAAAGGCaAAGaACGCCTTTCCGGtaAGTctTCaTCTTATGCTTG
TCGcCcCaGAGCaAcCCgCCTCCGCTTTTCTacaTGTCCAGCTaCGGCGccTaGa

>Bacillus_Fam_385_127_2 Nr. of seq. 2 Alignment length(with gaps) = 127
Alignment score = 0.616798

TcCGCTTTTCTcTTGTcCAGCTGCAGcGCTcTaGcCCTCGaGGTcAAATAACCTaCCTcaAaaAAGcCAAAa
AGCGGaCTTcTTGtgCaGgaAGAACATTTaCcgGTcCGGaGCaGAaCAaGaGcCT

>Bacillus_Fam_386_127_2 Nr. of seq. 2 Alignment length(with gaps) = 127
Alignment score = 0.619423

cAGCTaGACAtAgCaaAGAAAAGCGGaGcCGACTGcTCaGcccCGACAAGCATAaGAccGGCTgGcGaaGCGG
CGCaGTTTGCCGCaAGcCAGACcaaCaTATGACCTCGAGcccCaAGGAGcCaa

>Bacillus_Fam_387_127_2 Nr. of seq. 2 Alignment length(with gaps) = 127
Alignment score = 0.674541

GGGcGAAgAAATCTCGACGCTCcTaccCGCCGcAGCTaGAcAaAGAAAAGCGaAGGCGGGTTGcaCAGGAGCG
AGAAATgTcTGGAGcaCCTGACAAAAaGAAaTCCCGcccTTGGCTaaCGcTTGcCa

>Bacillus_Fam_388_96_2 Nr. of seq. 2 Alignment length(with gaps) = 96
Alignment score = 1.000000

GTTCGTTTCGCTTCTTCTTGGTCCATTTGCCCCGGAACGCCTCGGTTCCACTCATTACCTCTGCCTCTTCAAT
CTCTGGTTCCTCCGCGTCCATACC

>Bacillus_Fam_389_84_2 Nr. of seq. 2 Alignment length(with gaps) = 84
Alignment score = 0.603175

TGGCGAGcTTgccGctgCGaGgCGaCGaGGTTcGgacCaTACCTCGACGTACCTCTccCcTCCAGTGGCGAGG
caGccaCCaTg

>Bacillus_Fam_390_84_2 Nr. of seq. 2 Alignment length(with gaps) = 84
Alignment score = 0.904762

GGAAAAAGTAACAGCaGGTTTAAATACGTAAATaGCAAAACaGGTGAGATGCAGACTGGTATAGGGAAATTAG
TAGAcGGgTCa

>Bacillus_Fam_391_78_2 Nr. of seq. 2 Alignment length(with gaps) = 78
Alignment score = 0.914530

GAAGATCTTGaTGACCGATATGATTTGGAaGAACTTTTGaaTCTGATGAACGATCATATgTTGACGATTGAT
AATCT

>Bacillus_Fam_392_75_2 Nr. of seq. 2 Alignment length(with gaps) = 75
Alignment score = 0.951111

CTTTCCGCCAACGATGCCGACTCATTTTTACCAGaAAACTCCGGNTCGGCCTGCCATTTCATCCTGCaCCACTC
CA

>Bacillus_Fam_393_74_2 Nr. of seq. 2 Alignment length(with gaps) = 74
Alignment score = 0.689189

TTcacCTgcTTGTCaTcAgTTTgaCTGTTTGTGcTTTTCaTCAGcAGAACCATTcGTTGATTTCTCTTCct
t

>Bacillus_Fam_394_67_2 Nr. of seq. 2 Alignment length(with gaps) = 67
Alignment score = 0.611940

GTCATATCTCCATCTAaTCCGTTGCTGTGATATGATatNAATGnCngTaTatttCtgtATNcgttAt

>Bacillus_Fam_395_66_2 Nr. of seq. 2 Alignment length(with gaps) = 66
Alignment score = 0.626263

TGGTAcTACTTggatGAAGcAgcTAGCGGaGCAATGaAAACAGGTTGGTTGaAagACGaaGaAAAC

>Bacillus_Fam_396_62_2 Nr. of seq. 2 Alignment length(with gaps) = 62
Alignment score = 0.618280

GGTGTAAATGCAAACaGGcTGGcAcAAAGATcGGcAGcAAGtaaGTAcTACTTcGaCaaAAAC

>Bacillus_Fam_397_61_2 Nr. of seq. 2 Alignment length(with gaps) = 61
Alignment score = 0.661202

TGGTGCGATGAAaACNGGcTGGgTnTaAAcCTGGcgccAaaTGGTATTACTTAGAaAAAAa

>Bacillus_Fam_398_60_2 Nr. of seq. 2 Alignment length(with gaps) = 60
Alignment score = 0.911111

AAATGGTACTAcCTTAACGCAAACGGCGAaATGGCAACAGGCTGGAAaCTGGTTAGCGGa

>Bacillus_Fam_399_60_2 Nr. of seq. 2 Alignment length(with gaps) = 60
Alignment score = 0.811111

AAATGGTACTAcCTcCAaGCTGAcGGcgCNATGAAAACCGGCTGGCTgAGCACAAAcAAC

>Bacillus_Fam_400_60_2 Nr. of seq. 2 Alignment length(with gaps) = 60
Alignment score = 0.716667

TATTcAaGTAATACCAcTTaCCCCaAaagaTAaCCAGCCTGTTTGCATTaCTCCgGAAC

>Bacillus_Fam_401_60_2 Nr. of seq. 2 Alignment length(with gaps) = 60
Alignment score = 0.688889

CCTGGTAaTGGaCCcTCaAAATTCCGTGGaTATGGgaaaTTCCAacCTCCaCCaTTTGGa

>Bacillus_Fam_402_57_2 Nr. of seq. 2 Alignment length(with gaps) = 57
Alignment score = 0.625731
cGGCTTCATGAAGCacTtCATGGCGACCgTTTTcagCCggCTaCcCtTCgaTTTTTg

>Bacillus_Fam_403_57_2 Nr. of seq. 2 Alignment length(with gaps) = 57
Alignment score = 0.605263
aGATGAAGACCGcTTTAtGcAccGGAtccAgGCTaGAGGAAAGGTTcTCATAGCgAG

>Bacillus_Fam_404_57_2 Nr. of seq. 2 Alignment length(with gaps) = 57
Alignment score = 0.684211
AacAAGAAAGGTCACCAAcAAGGCcCATTGGTGCCCAAGTgggAAGaGTcTGctag

>Bacillus_Fam_405_56_2 Nr. of seq. 2 Alignment length(with gaps) = 56
Alignment score = 0.636905
ATGAAGACCTGtcaAtGGAAGAAAtttgaAGTaGGAAGAGatGTCaTCATAAGGTGG

>Bacillus_Fam_406_56_2 Nr. of seq. 2 Alignment length(with gaps) = 56
Alignment score = 0.622024
TCTCTcTTACCGtTTTTCTgTTTcccGAAtcGcagTTCGGGCACaGAGAcCGCCT

>Bacillus_Fam_407_56_2 Nr. of seq. 2 Alignment length(with gaps) = 56
Alignment score = 0.601190
GTTCCCGTCAGGCTCtgacTTTTCTgCTGACGGGCACTTcCtGctcaCAacTTA

>Bacillus_Fam_408_56_2 Nr. of seq. 2 Alignment length(with gaps) = 56
Alignment score = 0.669643
aCTTCGGACAGCTTTaGCTtCTTTcAGaGCTtcAAAGCTGTCTGAACtCTGGaCTc

>Bacillus_Fam_409_56_2 Nr. of seq. 2 Alignment length(with gaps) = 56
Alignment score = 0.625000
TTTGTTCAATAGAcAGaCcTCTATcGGACAAActCTATcGATtCaaGcCTATccGT

>Bacillus_Fam_410_56_2 Nr. of seq. 2 Alignment length(with gaps) = 56
Alignment score = 0.601190
TaTaGaGGTTGcCGATTGaagGTcgTGaGAGGAATCgGaGGTaGTCAAAGAGaGCC

>Bacillus_Fam_411_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.654545
cTCAAGACACTTTccTcaGCTaATTTTAcCCgGTTcATGTCCTTGAGAcAcCTCC

>Bacillus_Fam_412_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.624242
CTTCATCAaCCtCGATGAAGGACTTTCCacCgAgcAaTcTaCgCTcCATTCGaGA

>Bacillus_Fam_413_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.633333
CacAAaAAATGGgAGcTAATCGaAATGAATAACGACGAAAAAGaaacCTcTacnc

>Bacillus_Fam_414_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.639394
TTTTGTCTTTAATAAGGGcTCTTAAAGACaaAaaTcCAGcGAAAgGaaCATGcag

>Bacillus_Fam_415_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.642424
TTCATAAAGCCCGtcGaCaGagGAAAAAGccGtCaaAgCGGTCAATAAGAGaGG

>Bacillus_Fam_416_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.624242
TTTGTCcaATAGAGCCTTTCTATcGGACActTTTcTCCGaTTcTTgCaCgTcCcT

>Bacillus_Fam_417_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.636364
AaTTGCTCCagCTGATTTATaaGGaACCATAaATTGacgCTTTTTGaTaCCCCATA

>Bacillus_Fam_418_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.624242
CCTcCATTCGGACTCaGAGAcAcCaCTTgCtCTCgCTcgGcCTGTCCGAATCAGa

>Bacillus_Fam_419_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.669697
tTCAAAAGACCAAGAGGAAGGaAAAcCaGaaGtCGAGATGgcCTTTATaaGGGa

>Bacillus_Fam_420_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.627273
GGTAACAATAGaacaAGTATcGTGCCCCGAAATCAAGcccGtAAGaAGGcAAaAac

>Bacillus_Fam_421_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.630303
GGggATGAAGGACgaaAggaCGAaGAGAGAAcngCGAcGAAaAGTCCTTCATCGA

>Bacillus_Fam_422_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.624242
TTTCGGACTCAaCAggcTaaaAAAgTATGCaCgCggcTGTCCGAATCAAGcGCTC

>Bacillus_Fam_423_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.651515
TcTGTCTTTAGcACGCTcTCTCTcaGACAtCTTcCTCCCTgaTTCTcaCCCACT

>Bacillus_Fam_424_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.612121
ACCgaaaaTaTCAtAgagTTcCCTCTTTTTTCGGGCAATGCAACCCaCTccCATTa

>Bacillus_Fam_425_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.603030
gATGAAGGACaTTTTcGcCATgGGaAACCAaCcTCGaTaaGGgCTTCATCgACGCC

>Bacillus_Fam_426_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.657576
gAAACAGGACANgAAACCCCAGTAActTGGaAAATaGaGAGaCGtGtAAAtGAGaG

>Bacillus_Fam_427_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.690909
aaCGAGcAGaAGAAaAAAtgaGAaAACGGTAActATaaAGCGTTCATaATGCCCCG

>Bacillus_Fam_428_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.636364
AAAAAGagCAAGAaccTGcCGACcAAAGctCGTGacaTCGACATGAaCAGaGcGA

>Bacillus_Fam_429_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.660606
CCCTTATGCaGaGgAAAagGTCacCTATAAGGGTACAATTAgAGAGcGAATCaTA

>Bacillus_Fam_430_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.660606
ATTGGTGACCTTTCTTCaaCtTTCaCcACcTAcATAGGGCACCAATcAaCctcC

>Bacillus_Fam_431_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.669753
gCGCGGTGCagaAAAGAGGAGaAAaGAAGaGAGAAcAGCaCCGCGCGaGccGaG

>Bacillus_Fam_432_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.743827
aATGAAGACAcCTCTCaCTCctAaTTTCACCTCACgcACGTCTTCATACCgTCg

>Bacillus_Fam_433_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.629630
GGtaAACATTGTCTCGTAGGaGTGtcAATGAaGCCcTcaaCCGaTGaAAAAGa

>Bacillus_Fam_434_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.771605
TCTTACCTTCACACTaTTTTTTaTTcGCTCAAGGGCAGATGGcaGACTgCgCCA

>Bacillus_Fam_435_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.654321
TTTCCTTTCTaAcGCaCgTTTCaTCcTcAGAAAGGAATaCTAgACTCcTcTcGC

>Bacillus_Fam_436_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.617284
TTCATGaAGaCCAAAAagAaaGTGGAaaTcaAGaTTAGGGTGTCTCATGAaAGc

>Bacillus_Fam_437_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.635802
gTTaGACCCgGTGGAATccaAgAAAaAGAGaAATCGaCCGgGTTAAAgAGGtTG

```

>Bacillus_Fam_438_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.635802
AAAAAGtaccCAGnCGGTaACTgAAACaAGtGAAGTAGTGACCAAAGAGaGtGa
>Bacillus_Fam_439_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.611111
TGTCCGAATCaCAcCTAcTaTTCaGACTCcacCTTcGcTTTTcCGCtCaACaTC
>Bacillus_Fam_440_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.660494
TTTcCTGTCCGAACtGgGcCTcAGTTCGGACaCaAtTTTAGCagTTgCTGcGga
>Bacillus_Fam_441_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.626543
AGaAAATagCaGGccGGAATGGCGTTCATagGGgaaATGAAAGCcATcTTGaGa
>Bacillus_Fam_442_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.617284
GCGTTCATCCCCcCTtATGAACGcCATcaCaatTCAAnTTTTcCATcCtGgGATa
>Bacillus_Fam_443_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.641975
AGGTAACAGAGAGaaCTcCTCAGTGaCCGTaaGCACGaAAAacAAAaggAGcAAA
>Bacillus_Fam_444_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.654321
aAcTTTCGGACAGaTTGcGGACCCcaaTagaTCAAAAGCTGTCCGAACTCAGAgC
>Bacillus_Fam_445_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.694444
AAAAAAGaaGGAGaCGGgCACTgTaGAGaGGTTCaGAGTGCCCGTgGaAGCTGa
>Bacillus_Fam_446_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.604938
TaGACCCCTTCAGaTcTaTgcTGGTcTgCccTGAAGaGTCATATGcgaTCCcGTT
>Bacillus_Fam_447_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.629630
GTCTATGAaCCCaAAAAAtAaCaGAAAccCCGcAAAAAgCGGTcCtATAGAAaTc
>Bacillus_Fam_448_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.620370
TTgGGTTCCTTcaAacGgaaAAAAGcTGAGTTcgaGGGAATCAAAAGaGAGTc
>Bacillus_Fam_449_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.654321
TAaTCcTCTcTCAagCTCTcTTTTcGGGcgaCCAaCCTTCcTCTTTGaCTACCG
>Bacillus_Fam_450_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.654321
GGGgGACTTCGGACAAATTgaaGcCTCtTCCagCaGaTgcTTTGTCCGAACCTG
>Bacillus_Fam_451_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.669753
tGGAAATGTCTGAAGTAGCCcCAGGTTCaGCCAAAAcAaCgtCAcTaGgaaCGa
>Bacillus_Fam_452_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.611111
AAAaACCAGaAAcTaGGgAAAacAGgaCACCAATaaAGCCGtATTGGaGCaCgA
>Bacillus_Fam_453_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.648148
aTCAGtGACCacTTTTcGGAGcgGGcCgGCTCATTTTGGGcACTGACAGCccaT
>Bacillus_Fam_454_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.663580
TGTCAGTGCCcGTTTTTTCgaGtGaGGAgcGagTTTTGGGTACTGAGGgGaGTc
>Bacillus_Fam_455_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.617284
aaCCAAAAccAAcTGaGcGAGCAcAggAAAAAGGTCATCATAAaGcCGATGAa

```

>Bacillus_Fam_456_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.604938
GGTAACCAaAGGnAAGCaTaTGaTGCCCGTaAAcGagGAAAAAtAGtcGaTCaAC

>Bacillus_Fam_457_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.632716
TCTTGTTACCGcGAACaCaCTcTTTTCTaCTTTCagGGGcACATGacaCaTCac

>Bacillus_Fam_458_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.635802
TGTCCCTTCATAGacGgTaATGAAGGACAAaTTCGaAaaAAAgaATAaGcAaaGa

>Bacillus_Fam_459_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.722222
CTcTATGTTACCGTaaACcgCtTTTTTCTTcgCTcCACGGTCACTTAgaAAGCCT

>Bacillus_Fam_460_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.608025
tGgCCTTCATTCCaCTgATGAAGGACaaTTTTCaCaCGAgcCACAACCaTggTa

>Bacillus_Fam_461_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.617284
TgCTCTCaTTTTcGGcTTTCATCAaccTcaTGaACACCAcCTTTCcCTTCC

>Bacillus_Fam_462_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.608025
aACGTTCTTCATCaGGaggATGAAAGACGTTAcGGaGcGataTaaTGAttGaA

>Bacillus_Fam_463_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.709877
aTCGAAGTAGAcAGtacTCTACTTCAACaTTCaaGcTCtAAAATCCAGGGAAAC

>Bacillus_Fam_464_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.682099
TTTTTTCCgGgCcaCGGGCACTATGAACCTcTTATAGTGCCCatGaaCGtcTCT

>Bacillus_Fam_465_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.604938
TGCTGTCTgaAAAGtcaAAAATccAaTaTAGAGAgCAAGTAGAAaccCgCTAGc

>Bacillus_Fam_466_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.703704
cTATAGGCGACCGAGAGaGCGaGaAAAAAAGaGAggAcGGGTAGCGTAgAAGGa

>Bacillus_Fam_467_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.697531
gtTccAATTTTaaCTaaAGTATTGTcGcCAATAcCcGCcATTGGAAACACTTTG

>Bacillus_Fam_468_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.611111
ATCGCCCGTTCGccGcccAAAGnTacAgCAGAAGGTaGAAgAGAAGcGTgcCTC

>Bacillus_Fam_469_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.623457
AaAGTCCaTCATaaGgTGATGATGGACAAAACGcGGTcaGAAaAaCggAAAagc

>Bacillus_Fam_470_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.679012
GGAGGaAccAaTCCGTGTccAGGGTAACCAAAGaACGTGaTAGATTaCCCTaaa

>Bacillus_Fam_471_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.604938
GTTTTGTCTaATAgGAgCGCTTcCTATcaGACAACTaacCTCcCaGaCCaCCT

>Bacillus_Fam_472_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.666667
GCcGCTTCTCAaggCTacTTTCGAaCAGATTAGCTcCTaTTCgTTaACGTaCA

>Bacillus_Fam_473_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.654321
TcGAAAAaaAGcTAAaCGacCCAaCGAGAAaGGGAAACCaAGcGGATGTaGGtG

```

>Bacillus_Fam_474_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.635802
TGaAATGATGTaCCGCGcCTGaCtGaGCGCATGaCATCATTaTGaaaTTCcTga
>Bacillus_Fam_475_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.709877
ATGTTGGTCTGaTTAGGAgcTaaTCAGgCCAaTGAGAcTCAATaTTCgAAGGaG
>Bacillus_Fam_476_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.827160
TTATCGGCgTGATTAGAACCACCAAgGGAaAGGaAGAAGCATGCTTGAGGGTAc
>Bacillus_Fam_477_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.913580
GACTTGTGGCACCACCTAGGCGGAGTGAcACCACCTTTTCACTCTTCCAnCCAcCG
>Bacillus_Fam_478_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.669753
aTGAAGGACAAAacgAAGcAAGAGAAaGAtAaaAAgTGTCTTCaCaAAGGgTa
>Bacillus_Fam_479_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.657407
caaTTTGaAGGTcCACcATATaCCAaTAATTAGGAGAATaGTGCCaCTCcAatt
>Bacillus_Fam_480_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.790123
TCATAGTGaCCaTCCGAGaAGGAAAcCAGGTGAGaaCGGTCACTATgaAAGAGC
>Bacillus_Fam_481_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.882716
TATAACAAATaTAGTAGCaGaACGAGGAATCGTaTCCcCAGCACCAGTAAATAG
>Bacillus_Fam_482_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.672956
AGGACgATaAAAAaAGcAAAAgcaAAATTAAAGTaCTATAgAaAGGTTTcTAA
>Bacillus_Fam_483_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.676101
aaACcCCAAaTTATCGTCCTTTaAAAcGGCtTCTATAaGACaTTAATcTaCTc
>Bacillus_Fam_484_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.625786
tTCATTACcTATcCcTgacTATTTCGCACCTTAATTTgGCACgTTCgCCgTggT
>Bacillus_Fam_485_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.685535
TgTTTTGTCCAATAGACCGCccCTATCGaACAAaTTCtTTTCCcaAaACacGCT
>Bacillus_Fam_486_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.635220
AAAAaGGAGaaaCaGAAAAATaGGTAGTTAAGccAgGCgTTTAaAACgCCCCGA
>Bacillus_Fam_487_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.679245
TGAAGGACaTTTTaAcGtGccCcTgGCTCgCGcTTTGTCTTCATTaaCCCCGA
>Bacillus_Fam_488_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.613208
cTTCTTAACGTAGaACCaCTCTATGTgAAcaTAtcACcGcAgATTTcagCTg
>Bacillus_Fam_489_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.628931
AaTGTCTTTTACAACGGcTCAAAAaGACAAAAGcGgTcCAccTTgCCgaccGA
>Bacillus_Fam_490_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.622642
GtcAGAGAGGTCTTcATaGCacTTATGAaGACaTCaGtTTGGaGAGAAAgGac
>Bacillus_Fam_491_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.672956
TCTCTGTTACCGtaaCcCcacTGTTgcTCGGcGcTTCGGGCTTTGAGAcGCCC

```

>Bacillus_Fam_492_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.638365
TTCGGTCaaATAGAAGGGCTCTATAaGCCcaAAGaGcAAcTgAgAcccGGAGc

>Bacillus_Fam_493_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.660377
ATGAAGACATCaGTaGcgcTaAaaACaGcTaGAGAGAGGTCTTGAGAAGaGgA

>Bacillus_Fam_494_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.660377
AGcgaATGAAGACATcAGTGaAcCaGGAAaCtGAGtgAGAGAAgTCTTCATGa

>Bacillus_Fam_495_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.647799
aGGTcCTCATAAGgcTgATGAAGACaTGAGtTGGTTgGaATaTTaTgCGAaAG

>Bacillus_Fam_496_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.713836
GCTAaTTTAaTTTGCTGCCCTTTCTTATGCTgTTcCcaaCTTacAATgGGCTc

>Bacillus_Fam_497_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.698113
TTCATCgGGCTcTATGATagaCATTTcGAGCCaaAaTTTTGcCTGTGATaGCG

>Bacillus_Fam_498_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.672956
CCACTTTTcCCTccTaCTgACgGaTTTTcTGGCTTTTCATCccCTccATGAACA

>Bacillus_Fam_499_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.622642
CGaGaAcGcAaGAAAAAGagAAAAaaCGGTAAcTAGTaGAGGCGaCTAaTGCC

>Bacillus_Fam_500_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.823899
GTCACGTAGAGcCTGTCTACGTTACCCaaATCcAGcTCtTTTCAATGTTTaCG

>Bacillus_Fam_501_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.757862
AATAGAACCATCAAAaCCGaaAATcAaaAGCTTGATGGCNCTAAaCAGGCnGt

>Bacillus_Fam_502_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.710692
TCTATGAgCCCaAAAaTCaaGTGnAAaGAgCAAAAATgGGTTcATAGAaCGAA

>Bacillus_Fam_503_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.672956
TGACAGcTTTgATGaTGaatGAGaCAAAGCTGTCATGATTaCaCaGTTATTc

>Bacillus_Fam_504_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.679245
gCggaaTCTTGACAGCTTTGGCCCCGgATCCagaAAAcCTGTcACAAaAACTa

>Bacillus_Fam_505_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.723270
ATGACGGACACTTTTTcCTCAAtTaTCGcaaTTTCTGTCCGTCATCacGgcT

>Bacillus_Fam_506_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.622642
GACAgATccTTaGGATacTgTCCcCTGTTTGgCCGATAGAcCCCTTCTAacG

>Bacillus_Fam_507_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.610063
aAAaCaGGGaACCAATACAGCtTATTGacGACCTaAaTcCTCcaAAATaCGa

>Bacillus_Fam_508_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.915094
TCTCAGTGCCCGAAATGTCTCCTGCCACTACAAAcAGGgCACTGACAcCTCct

>Bacillus_Fam_509_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.628931
TGTCCGAAGAGAGaGcAacTTTCGACAgGAAAacCGGaacAAgAGCgAaAAGc

>Bacillus_Fam_510_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.622642
AGTTCGGACAAGAtaTcAcggGAAGAAGCacAAAGcaGTCCGAAGaaGGCaCA

>Bacillus_Fam_511_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.650943
aAaAGGTCaTCATCAAGcTaATGAAGAcCCGAAAGCAtcTccAaaGCaaAGAA

>Bacillus_Fam_512_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.628931
GACTTCaGACaaTcgTTCAGcCTTTTCCTaTcacACCTGTCTGAACTcGGaTc

>Bacillus_Fam_513_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.716981
GTCCTTCATCCctCCGATGAACGACATCTcaaGcTtTTTCCTcTcGcCcgTTTT

>Bacillus_Fam_514_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.663522
gTTCtTcTCATCTTCCCGCATCcCTCgGaTTTCGAGCAcTTCGCCcacgGaTCcC

>Bacillus_Fam_515_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.613208
CTCCTcATCTTCCCGcATCCgATccTTGCGGGaAcTTCaGacGGnGaTcTCTt

>Bacillus_Fam_516_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.622642
CGAATcGGaTGGATaCGGGAACTTGagAGcAaGAaAcccGaAGtcGAAGTGCC

>Bacillus_Fam_517_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.647799
AcTAGTGGAATcaGTGAACTAAacgagCaTTTAGaACATatGtAaTTCCAGAA

>Bacillus_Fam_518_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.710692
TGTCCCTCATAAgGcAGATGAAGGACATTTaTcTTGGtAAAAaCAagaGaGATT

>Bacillus_Fam_519_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.672956
GTAACGTAGAGCcCGTCTACGTGCCCCGAacaGAtGgAtaaTTTaGCaGTaAGG

>Bacillus_Fam_520_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.874214
TTCCTGAAATCTGTGGCTTCCgCTnCTTTTCGGGAATGACTCGCCTTGGGgcA

>Bacillus_Fam_521_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.773585
CTGTATGACACGCAaAATCaTGtTCCaTTaGaATgTTCGCGTcTCATTCGTG

>Bacillus_Fam_522_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.672956
GGTAACTATGaAaGCGtTCATAGTGACCAaAccccAAagAGAAAAAGCaAaAaC

>Bacillus_Fam_523_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.751572
TGTCCCTCAAGaAGgGcTTATGAGGACAAACTcGaGTccGAAGCGTaGgCGAAn

>Bacillus_Fam_524_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.855346
AGGTCATCATGGAGGTGATGAAGACTCtGAAGCgGTGTTGcTTGGaaGgGAAG

>Bacillus_Fam_525_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 1.000000
CTCTCTTGAGTGACTCATATCGGTTCTCTGAGGCACTCTGGGGCGGGGGTCT

>Bacillus_Fam_526_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.974843
GTACAGAGTGCCTCAAACGAAGTCTATGAAGCACTCTAaAGATGGAAAGGAGC

>Bacillus_Fam_527_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.943396
CATGTATCCAGTAGCTTTTTTCGGGATACATGACACCNCNTTTTTTTNCTCGGT

>Bacillus_Fam_528_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.654088
AATGAcacCCCCGCGCGgcCGaAGCGCATGtCaTCATTgTGAacaTTaaGAgGA

>Bacillus_Fam_529_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.622642
CTTATGACTTTTCccaCcTAAaGTCgGAagCTaGTTgcCcgCtCCCCGCTCTTTc

>Bacillus_Fam_530_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.930818
AAATAGCATAAGATAAGCAaGGAATCGTACGCTATAATCTcaAGCCAGTGTAC

>Bacillus_Fam_531_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.811321
TGGTTCTAAAcCGaGTTAATAGTGCCATCAAAGGaggGGGaTTGGgAGcTTGA

>Bacillus_Fam_532_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.880503
TGtTGCCACTTTTaCTTCACcCATGaAGCCTGTTTGTGGCGCAACTCACCGGAg

>Bacillus_Fam_533_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.628931
GCGGTACAcGCTcGcaAaAAATcCGCcaaAGCGTGTACCGcaAGACcactCTa

>Bacillus_Fam_534_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.826923
CAAAAGGACAATTcCaGGNAGAAaACAAAGaGCAAAcTGTcCTTTAgAGnGGTT

>Bacillus_Fam_535_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.743590
TTTTcATTACCTATTATgaaGcTaTaCGCACCCCTAAcCTTGGCTTTGCTaGa

>Bacillus_Fam_536_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.602564
GTAATGAAATtactCGacTcaCcTGATTTTTCAgTaCcTATTACTCctgATTG

>Bacillus_Fam_537_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.641026
TCaCAAAAtTCGCTgaaaaaTCCgTTTTGCTGATaATAAAaCcGATTTACcA

>Bacillus_Fam_538_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.692308
ccAAGAAGcGTTCAaaACGCCCGaaATTTcaAAAAGAAgGAAAAATcGGTAG

>Bacillus_Fam_539_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.698718
ACTTTTcCTagTGAaCTAcTCgATTTTGTCcTTCATcAGCnCgcATGAAAG

>Bacillus_Fam_540_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 1.000000
AGAGGGTGTTAGTGGTAGCGACTAAAGCCGTCTAAGAGAGATTTTGCTAAAC

>Bacillus_Fam_541_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 1.000000
AGCCACTATTTTCATTTTTCTTCAGGATAGTGGTCCCAGCTCCTGTGGCTGG

>Bacillus_Fam_542_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 1.000000
GAACCGCTATTTTAGCTTTTACACAGAAATAGTGGTCCCAGCGAGCGTGGCTA

>Bacillus_Fam_543_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 1.000000
GTCACTCTAACCAAGAACATAGAATCAGAGTGCCTCAAAAAGAGGATATGA

>Bacillus_Fam_544_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 1.000000
AAATCAGAGGGCCTCAAACGAGCGAAATGGAACCCCTCTAAACTGAAATAATC

>Bacillus_Fam_545_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.820513
aCTCTaTTTCGGACAGAGTTcCTTGTTcAaTATTCAACTCTGTCCgATTGCa

>Bacillus_Fam_546_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.801282
AAGGgCAgCATACGAAGcCTATGCcaCCCGAAAAAatGAAAcCGAGCAGATG

>Bacillus_Fam_547_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.878205
CGCTATGATTACCGTCAACTCATTtTTGGGCTCgcTCTCGGGAAGCATAcAag

>Bacillus_Fam_548_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.955128
GTTcAGACAGGAAGACGAGAAATAGcCTGTTTGTGTCCGAAGAAgGGGCGAG

>Bacillus_Fam_549_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.910256
TGGGAGTTAAcCAAAGGGAATAAGcCGAAATCCCGAGAGCaAGCCAACAAAA

>Bacillus_Fam_550_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.974359
GTCGCCATAAGAGGTTcATGACGACGAAAAATTGGAGGTCCAAGTAAAAACa

>Bacillus_Fam_551_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.923077
TTCGGACTCAaCGAcCATCCGTTTCGCGGTTTTGaGTCCGAACACCAGTCAAC

>Bacillus_Fam_552_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.974359
CATGAAATATGGGAGTTAATcCTAATCATTATCGACCAACAAGAGATGCCA

>Bacillus_Fam_553_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.948718
CACCTTCGGACTCGCTCACGTTGATTTCTCCcTTTCTGTCCGAACCTcCTC

>Bacillus_Fam_554_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.897436
TCCTCTTCATAAGCccCGTGAAGaGGAAACGTAAcCAAAAATCTCATTCcTTT

>Bacillus_Fam_555_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.820513
TGAAGAGGATTACaAGCTTaaaTTCcTCCCaCTTTCCTCTTCATCTAGGCTa

>Bacillus_Fam_556_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.692308
TGTcCcTcAATAAGGGCTaTTaAaGACAAAACCTCccCgGGAAAGCAagaAAAA

>Bacillus_Fam_557_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.628205
ATTTCGGACTcaCTTactccTTTTaCaGCTcGacCTGTCCGAATaCCCCtCT

>Bacillus_Fam_558_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.641026
GGCggtCATcCCCCtTATGAaCGACCaTaCCgATGTGTTTTaCaaTcgCaCG

>Bacillus_Fam_559_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.666667
AATCAaACGGTCGaTCATccCCcTTATGAACGaCCaCGCCgGCTGAaaaTcc

>Bacillus_Fam_560_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.724359
ATTAGTGACCGagaTaCGGGATTTacCcTAAATACGGGaaCCTTTTTaCcGCg

>Bacillus_Fam_561_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.615385
TTAGTgACCGgTTTTCCaCTcaaACcCgTaTTCGGGCACcaTTaCcCgCGA

>Bacillus_Fam_562_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.910256
CAGAAaATCAGaTTTGATGGCACTGAACATcGAGAATAGgACCACCAACGAA

>Bacillus_Fam_563_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 1.000000
TGAAAAGTGTTCGTAACCCAGTTTAAGAACACTTTTCCGCAGAGCAGAAGGGT

>Bacillus_Fam_564_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.980769
TGATGTGAAGGGTTATAAGTAAGTGAGAATTGACCCTTNAGTGCAGCCGTAG

>Bacillus_Fam_565_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.974359
GTGAATGAACCCCTTCaTACGAAGAATCAGGAGCTGAAGGGTCAAAAGGCGTC

>Bacillus_Fam_566_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 1.000000
CATGAAGGGTCATATCATGCTCGCTTATGACCACTCAGCTCACCTGCCCTG

>Bacillus_Fam_567_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.826923
aAGGTTTAAGAGCACAACCGGTCTaCCCAGatAAGAGTTTGTGCTGCaAAC

>Bacillus_Fam_568_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.948718
TCTTACCCTCCCAAACCGTTATTTCGATCTGACAGGGcAAGCAAACCTACgTT

>Bacillus_Fam_569_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.897436
AAGTGTCTTAACCTGaGTTAGCAACACAAACTcTGTTGATcGTTCACTGGA

>Bacillus_Fam_570_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.794872
TTGATGGTTCTTATAAGCCCCGATAAGTaCCAcCAAaCTCTGAgTcccTTGaA

>Bacillus_Fam_571_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.948718
GAAGGTCACAAAACaGGAAGGAATGTGCCCTTCGTGAAGTGTTCaAGaTGT

>Bacillus_Fam_572_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 1.000000
GGAAAGTGTTCTAAAAAGGGTTTAGCAACATTAACCCTGGCTGGAGAAGAGA

>Bacillus_Fam_573_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 1.000000
TGAAAGGTCAATAAGCGGAAGGATAAGACCCTTTATCAAAGCTGGTCCGCCG

>Bacillus_Fam_574_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.641026
CTTTGACTaCCGgTCTcgcgGCTTCCTCcaacTTTCGGGaGcCAaCCCCCTTC

>Bacillus_Fam_575_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.910256
AATCTCCACATACTGGaAAATCgTAGTCCCAATaAGCCCTATTGGTGCTCCg

>Bacillus_Fam_576_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.974359
GGGCCTCCATCaGGGCGATGGACGACCGTTTATTGCTCAATCTCAGGTTTCA

>Bacillus_Fam_577_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.730769
TTTTTCTCcCacTcTGCcGATTTCCGGTACTGAcaCcaCCTGTCAGTaaCTC

>Bacillus_Fam_578_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.666667
gATGAAGACCgGAACGAAGCTTGAGccaGaccaAAAAGGTaTTCATcaGGTT

>Bacillus_Fam_579_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.692308
GCGaaTTCGGGACaTGAGaGcCCATCATGAaCCATcaaCaCGACTTTTcC

>Bacillus_Fam_580_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.705128
GgCCCGTaGgtTCccTTTTTTGaCaCGAACGGGaCaTGATAAAGCgTCTCAT

>Bacillus_Fam_581_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.653846
ATGAAGGaCAAGTgACAcCAAGAAaAaAaAaAaTGTCCTTCATcAaGTaa

```

>Bacillus_Fam_582_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.801282
TGGgCTTTTGATaCCTTATAAAGACCATTcGGAacCGGATTCTTCCaCaaAT
>Bacillus_Fam_583_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.775641
AGTTCCCGaaCCcAGGCAAAaTcCCCcTCCAGGGTAATtAATCGgTCACTTa
>Bacillus_Fam_584_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.666667
TCAGTGCCCaTGcAGGGgaAAAAaaaAgGCccAcGGGCACTCAGaaAGGTTg
>Bacillus_Fam_585_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.647436
aTGAGGACAagTTaaGCcCTTGCTcaacGAgTtTcTGTcCTCATGAACaCCcC
>Bacillus_Fam_586_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.717949
CTATTGGACAAAACcCccTTATAAAcCaCccAaAaTGTCcAaTAGAcCCCTT
>Bacillus_Fam_587_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.717949
aGTGCACATTGAAGccTTCAATGAACACGaGAGaAAGGaAaATCaaCaaAGA
>Bacillus_Fam_588_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.621795
TTATTCCcCTGAAGaAGaaaaAAaGaaCcgTcTTCaGGTGAATAACCacaGT
>Bacillus_Fam_589_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.641026
AaGaAAAAGTCCaTCATAGGGccAATGAaAGACAAAaccCAAccagCAaAGa
>Bacillus_Fam_590_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.698718
ATGATGGACTTTTcccGCgTTcCCTcAaaCGcTTTTGTcCTTCaGaaCCTTg
>Bacillus_Fam_591_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.769231
CTGGATTATAGAGGTGTGTTTCgCGCcgaATcGGGACaCcGaTTACCAAAaT
>Bacillus_Fam_592_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.647436
GGagAAACGAGaCacAAaAGTCCAGTAaaTGGAAAAaAGaGTCGTGaaaACa
>Bacillus_Fam_593_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.608974
TCATGAAGGACgTtTCcCaaGAcATaGcAcatCcAAaaGTCCTTCATCaCcC
>Bacillus_Fam_594_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.974359
CACATTTTTCTGCATTTTCGCTCCATTATCTGTTTCAAAACCTCgAGTTGACG
>Bacillus_Fam_595_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.929487
GGGCACCTTTCTCCCTCTTTTCGTTACCGGAAACCGcTTTTTCCTCTCgaGC
>Bacillus_Fam_596_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.794872
CTTCAATGTgACCGTTTCTaTGATTTcAaTaaCgTTTTGGTCACATTGAGCc
>Bacillus_Fam_597_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.955128
ATGAAGACCGTTAGTTTTGGTGAATGagCAAGAACCGGTTATCATAGTTGAG
>Bacillus_Fam_598_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 1.000000
GGCTTTCATTCTTCTCATGATGACCTTTTCTCTAGCTCTCTAGAATGATTTC
>Bacillus_Fam_599_51_2 Nr. of seq. 2 Alignment length(with gaps) = 51
Alignment score = 0.712418
TTTCATTACCaaTcaCCagTTaTTCGTACCCTAATTaAGcCAACaCTCcAg

```

>Bacillus_Fam_600_51_2 Nr. of seq. 2 Alignment length(with gaps) = 51
Alignment score = 0.895425
TTCGGCTTATAATTCTTactCTCCATTCTTTTTACGCCGAActcgCTCTTA

>Bacillus_Fam_601_51_2 Nr. of seq. 2 Alignment length(with gaps) = 51
Alignment score = 1.000000
TTCTTGCTCTTCTCTAGCATCGTCCTCGCTGAGCTCTTCTGTACTGTCTTC

>Bacillus_Fam_602_51_2 Nr. of seq. 2 Alignment length(with gaps) = 51
Alignment score = 1.000000
AAAAGGAAAGCGCCAAAAGCCCGTTTGTGAACACGAAAATCGAAAAACAGG

>Bacillus_Fam_603_48_2 Nr. of seq. 2 Alignment length(with gaps) = 48
Alignment score = 1.000000
CAGATAGAGGAGGTTGAAGAACCGAGCAAACCTGAGGAGTCAGAAGAG

>Bacillus_Fam_604_48_2 Nr. of seq. 2 Alignment length(with gaps) = 48
Alignment score = 0.951389
TTGGATTATCCACTGCATTACTtTCTTCTTGaGAAACAGCACTATTAC

>Bacillus_Fam_605_48_2 Nr. of seq. 2 Alignment length(with gaps) = 48
Alignment score = 0.694444
TCTTTcGGcTCTTCcaTTGacCCATCacCAGGcTTTGTcCCaTCCTGA

>Bacillus_Fam_606_47_2 Nr. of seq. 2 Alignment length(with gaps) = 47
Alignment score = 1.000000
TCCGTGGACAGATGGGGTGAAGTGTCTTTTTGTGGTGCCAGGTACGC

>Bacillus_Fam_607_46_2 Nr. of seq. 2 Alignment length(with gaps) = 46
Alignment score = 0.753623
CCAGGTGAAGaGaGAATCTGGcCAaCCaGAaGAaGAAaTAACGGAG

>Bacillus_Fam_608_45_2 Nr. of seq. 2 Alignment length(with gaps) = 45
Alignment score = 0.629630
AATCCAACaACACCACCAAcgaCAaGTGaAGaaAAcAAcGGaGAa

>Bacillus_Fam_609_45_2 Nr. of seq. 2 Alignment length(with gaps) = 45
Alignment score = 0.614815
GGCATTTGaCCaTATCCcGCTGGcAcTTgCTGaCCAgAACCCagT

>Bacillus_Fam_610_45_2 Nr. of seq. 2 Alignment length(with gaps) = 45
Alignment score = 0.874074
GAAAAAGAAGCAGCAATgCAagaACAACAAAAACAAGATaAAAT

>Bacillus_Fam_611_45_2 Nr. of seq. 2 Alignment length(with gaps) = 45
Alignment score = 0.822222
GATTCCTCaTcGATTCaTAacCATCGCTaGACTCGTTATCTTCA

>Bacillus_Fam_612_43_2 Nr. of seq. 2 Alignment length(with gaps) = 43
Alignment score = 0.837209
GAAGCTaCCgGCTGAAGAAcCTGTAAACAGAGGaACCAGCAGAG

>Bacillus_Fam_613_43_2 Nr. of seq. 2 Alignment length(with gaps) = 43
Alignment score = 0.689922
CATGCgGAAGGTNaaanAcAACaGCAAGTgGGANATgCTTCN

>Bacillus_Fam_614_43_2 Nr. of seq. 2 Alignment length(with gaps) = 43
Alignment score = 0.732558
CCTTCCGCATGCGAgNcAacTCCACTGGCTATTGTaTtaANtn

>Bacillus_Fam_615_43_2 Nr. of seq. 2 Alignment length(with gaps) = 43
Alignment score = 0.658915
GcAGGAGCaATGGACGcCAAtATgCCaCAcATGCCGCAaGTa

>Bacillus_Fam_616_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 0.793651
aGATTGTGACCAAGCGCGGcGnAAAcTcCGGaCAATTGGCGa

>Bacillus_Fam_617_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 0.690476
AtTTCGtGATTTCGCGGCCaGAaCaAcaCTTTTCaTGCCGG

```

>Bacillus_Fam_618_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 0.638889
tcCGaTCcCTATcCGTcGGTAAaCcCgTcATTCTGGTTAA
>Bacillus_Fam_619_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 0.809524
GGaATaACTGGTCTACTGGaGTTACAGGacCTACCGGAATc
>Bacillus_Fam_620_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 1.000000
CTTGCTTTCAATGATGAAATGCGCCATTTCCAAAAGGAGCAG
>Bacillus_Fam_621_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 0.809524
GGATCaGGTTCcGCaTCCGGaACGACcGCAACGGGCAACACc
>Bacillus_Fam_622_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 1.000000
TTTGATTCTGGTTGATCAGAAGTTTGATTCCATTGATCAGAGA
>Bacillus_Fam_623_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 0.650794
AGaaGTAGTGGAaaCTCaAGaaGAAGAGAGACCaGTAcAgCa
>Bacillus_Fam_624_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 0.690476
GGAGAAATGCCacaAGcctAcGGCCaAaTGCCaCAGGaTAC
>Bacillus_Fam_625_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 0.730159
AaAcTCGTGGGTAAAgCaCCGaGTTATaTGGGTATTCCaCca
>Bacillus_Fam_626_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 0.968254
CCAGGAGGCGGAACGGGAACAGAcAACGGAACCGGAGGAAAC
>Bacillus_Fam_627_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 1.000000
GAAGTCGCGAAATTCGGTGGGAAGTTGAAAGATTAACGGGA
>Bacillus_Fam_628_41_2 Nr. of seq. 2 Alignment length(with gaps) = 41
Alignment score = 0.617886
TTCTTTTACTggAgcgGTTTTGttACAAaTTGGCTgtGGcGC
>Bacillus_Fam_629_41_2 Nr. of seq. 2 Alignment length(with gaps) = 41
Alignment score = 0.626016
GCgGATAAAaCaaAgAAAGTCGcGATATATcggAAAgTTa
>Bacillus_Fam_630_40_2 Nr. of seq. 2 Alignment length(with gaps) = 40
Alignment score = 0.754167
tGTTCaTCTGTTGGCTCTGTaacTTCTACTTCTTCaGtCT
>Bacillus_Fam_631_39_2 Nr. of seq. 2 Alignment length(with gaps) = 39
Alignment score = 0.897436
GGcTTCACTTCTGGcTCCTTCGGcTCTTTTCGGATCTTCC
>Bacillus_Fam_632_39_2 Nr. of seq. 2 Alignment length(with gaps) = 39
Alignment score = 0.897436
AATCCGGAACAAAaCCAGCAACTAAACCTGcTACTGAc
>Bacillus_Fam_633_39_2 Nr. of seq. 2 Alignment length(with gaps) = 39
Alignment score = 0.760684
TGaTCaTGcTCgTCccCATGAGCTTCTTCCTCATGCTCa
>Bacillus_Fam_634_39_2 Nr. of seq. 2 Alignment length(with gaps) = 39
Alignment score = 0.641026
ATGaCCATGATGGaAGCCaTaACCaGGGTaaTAaccgCC
>Bacillus_Fam_635_39_2 Nr. of seq. 2 Alignment length(with gaps) = 39
Alignment score = 0.794872
CATGcTCGTGATCATGATCTTCCTCATGccCGTcCTCac

```

>Bacillus_Fam_636_39_2 Nr. of seq. 2 Alignment length(with gaps) = 39
Alignment score = 0.974359
AGAAGAAGTTGTGGAATTAGAGAAAtCTGAGGAAGCGAC

>Bacillus_Fam_637_39_2 Nr. of seq. 2 Alignment length(with gaps) = 39
Alignment score = 0.666667
AAGaAaGAAGAAcaAGaaCGtTTAGCaGAaGAACAGCGa

>Bacillus_Fam_638_39_2 Nr. of seq. 2 Alignment length(with gaps) = 39
Alignment score = 0.940171
GCTCCCATCACTCCGGACGGCTGACCCATCGGGGATTGc

>Bacillus_Fam_639_37_2 Nr. of seq. 2 Alignment length(with gaps) = 37
Alignment score = 0.662162
TGtCCTGGaTAaCCTCCCATGCCaCCaTAaCCaCCca

>Bacillus_Fam_640_37_2 Nr. of seq. 2 Alignment length(with gaps) = 37
Alignment score = 0.603604
cACGGGAGCaACGGGAGcAACCGGGacCaAcCGGAGc

>Bacillus_Fam_641_37_2 Nr. of seq. 2 Alignment length(with gaps) = 37
Alignment score = 0.747748
TGCCACTGaTGCCAAgGTAccGTaaGGATGcTGCTGA

>Bacillus_Fam_642_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36
Alignment score = 0.666667
ACcGGAGCaACaGGccCaACgGGAaTAACgGGCCCA

>Bacillus_Fam_643_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36
Alignment score = 0.898148
AAAAGCAAGAAACCCGATGACTGCAAAAAaCCTGAC

>Bacillus_Fam_644_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36
Alignment score = 0.925926
GAAATTAaACAGGAAAAAGATATAGGAATTAAaAAG

>Bacillus_Fam_645_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36
Alignment score = 0.925926
TCTTTTGTAGCcTGTTcAGCTTGAGCcTGCTGCTGC

>Bacillus_Fam_646_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36
Alignment score = 1.000000
GGTCCTTGAACCCCTTGTTGTGCCTTGATCTCCTTGC

>Bacillus_Fam_647_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36
Alignment score = 0.944444
CAAGGATCAACTGNGCNCAGGGATCCCAAGGACCG

>Bacillus_Fam_648_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36
Alignment score = 0.666667
GGaAATACAACgCCGCCAaaCAaTGGAaAaGGCcAA

>Bacillus_Fam_649_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36
Alignment score = 0.962963
GCAACAACCGGAATAACGGaAACGGCCAGGCCGCAA

>Bacillus_Fam_650_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36
Alignment score = 0.703704
CaTgGacTGCaGTgCCACCATTcGGaCCTTGaCCTC

>Bacillus_Fam_651_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36
Alignment score = 0.629630
CGCCAGTAGCCcCCgGaAaaaCCaGTaGGaCCGGTAa

>Bacillus_Fam_652_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36
Alignment score = 0.666667
GGacCgACAGGAGCAACAGGAaTAGaaGGaaTCACc

>Bacillus_Fam_653_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36
Alignment score = 0.824074
AGTACAGCAAacGGAAGAAaGCAGCCGAGAGTAcC

>Bacillus_Fam_654_34_2 Nr. of seq. 2 Alignment length(with gaps) = 34
 Alignment score = 1.000000
 TCTGTCCCCCTTGGCCCAGTTTTCGGGCCAGGGGG

>Bacillus_Fam_655_33_2 Nr. of seq. 2 Alignment length(with gaps) = 33
 Alignment score = 1.000000
 CGGCGGGAATGCCGGAATGCCAGGTCAAGGAAG

>Bacillus_Fam_656_30_2 Nr. of seq. 2 Alignment length(with gaps) = 30
 Alignment score = 1.000000
 AAAATGAAAGAAACTCCAAATGTAGTACCG

>Bacillus_Fam_657_28_2 Nr. of seq. 2 Alignment length(with gaps) = 28
 Alignment score = 0.601190
 aGCCAAGCaaAAGCaACAAGAcAACAA

>Bacillus_Fam_658_27_2 Nr. of seq. 2 Alignment length(with gaps) = 27
 Alignment score = 0.697531
 tTGTAACCTGGTACATgGaGcGtTtGAT

>Bacillus_Fam_659_27_2 Nr. of seq. 2 Alignment length(with gaps) = 27
 Alignment score = 0.654321
 cCTccaGCTcccccaGgacCTccTGaa

>Bacillus_Fam_660_24_2 Nr. of seq. 2 Alignment length(with gaps) = 24
 Alignment score = 0.631944
 GgACAgGTAAAAcCAcAAAAAGaa

>Bacillus_Fam_661_24_2 Nr. of seq. 2 Alignment length(with gaps) = 24
 Alignment score = 0.833333
 ATGGCaGGAGCGAACATGGcGCCa

>Bacillus_Fam_662_24_2 Nr. of seq. 2 Alignment length(with gaps) = 24
 Alignment score = 0.944444
 CAGAAAAGAATCAAAAAaCAGAGA

>Bacillus_Fam_663_23_2 Nr. of seq. 2 Alignment length(with gaps) = 23
 Alignment score = 0.666667
 TATTTGCGTCGgTcCCAnaCnAT

>Bacillus_Fam_664_23_2 Nr. of seq. 2 Alignment length(with gaps) = 23
 Alignment score = 0.717391
 aTTAGGATCGTaaATTTCTGaGA

>Bacillus_Fam_665_23_2 Nr. of seq. 2 Alignment length(with gaps) = 23
 Alignment score = 0.615942
 cCAACTaGCGGATaAcCaCGaTC

>Bacillus_Fam_666_23_2 Nr. of seq. 2 Alignment length(with gaps) = 23
 Alignment score = 0.760870
 TTTATTTTCCATTcaAGCCGnAt

>Bacillus_Fam_667_23_2 Nr. of seq. 2 Alignment length(with gaps) = 23
 Alignment score = 0.666667
 ATTCCGCGAAAnAACcaAcaATA

>Bacillus_Fam_668_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.772727
 tTATATCAGCGaAACTCCaAAt

>Bacillus_Fam_669_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.621212
 aATTCCGgAACTTTTcGgaTTa

>Bacillus_Fam_670_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.643939
 cTaACTaTaAcATTTTTGGGTC

>Bacillus_Fam_671_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.628788
 aAAAAAGCATTAtGaTcAaGAc

>Bacillus_Fam_672_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.628788
 TATTCCCGTCTGaGaagGaaGt
 >Bacillus_Fam_673_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.681818
 TTATTCCCGTCTCagaATaaGC
 >Bacillus_Fam_674_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.696970
 TcCGACAGTAAaGcGTGGCtTA
 >Bacillus_Fam_675_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.674242
 tAATTCCGGAACtTTTcaacCat
 >Bacillus_Fam_676_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.643939
 cTTTATTGTCCgGAAacGCtCt
 >Bacillus_Fam_677_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.810606
 TTCATTCCAAAAcTGGGNTTTt
 >Bacillus_Fam_678_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.810606
 CTAACCTCGACTAAAGGcgGAGg
 >Bacillus_Fam_679_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.666667
 TTTAAACAGGTTgGcAcGcgCG
 >Bacillus_Fam_680_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.674242
 TTTAcgATCCAAaTTgAACCAa
 >Bacillus_Fam_681_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.848485
 GGAATGATTATTcGcCGAATCC
 >Bacillus_Fam_682_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.628788
 aCTTCTcccTTTGGaTCTgTCa
 >Bacillus_Fam_683_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.727273
 ATTCTACAAAAaTcAAAGagGA
 >Bacillus_Fam_684_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.613636
 GTTACTCCCGcATaGaCTcCac
 >Bacillus_Fam_685_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.727273
 GCAAATAGAAaTggGaAAAtCG
 >Bacillus_Fam_686_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.674242
 GATAATTCGACCgTCacGaGCc
 >Bacillus_Fam_687_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.613636
 cTCTCGCGTTCCgAcccCTcC
 >Bacillus_Fam_688_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.803030
 TCGCAAATAAACAgGaTAaGAT
 >Bacillus_Fam_689_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.643939
 gTTTTGTCTAtTTTTaAgagAG

>Bacillus_Fam_690_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.659091
 AGTTCGTGCCAAAAtcaGaCag

>Bacillus_Fam_691_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.750000
 aGGTTCTCACGCTTCTCaGcAa

>Bacillus_Fam_692_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.621212
 AGGTTCTCACagaaCTCaCctG

>Bacillus_Fam_693_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.651515
 TTcGATAATaAAAcTTgGaATT

>Bacillus_Fam_694_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
 Alignment score = 0.795455
 cTATaCTTTACTCCGATCtCTT

>Bacillus_Fam_695_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.603175
 AAGAACCccATAACaCAnGct

>Bacillus_Fam_696_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.603175
 CtAaGcTCAaATGCCAATGgg

>Bacillus_Fam_697_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.634921
 gGCAAATAGAACGaggTTTcc

>Bacillus_Fam_698_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.658730
 CTCCAaCTTGcGGATaGaGcN

>Bacillus_Fam_699_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.785714
 aTATATCAAGAAATTTaGtGA

>Bacillus_Fam_700_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.626984
 TCGCCCGTAAATCtCaAaAtt

>Bacillus_Fam_701_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.706349
 CGCAGATAAcTCAaGAAAaag

>Bacillus_Fam_702_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.603175
 TTTaCGGTaGcACaAcTTTnA

>Bacillus_Fam_703_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.682540
 TTTGTCTGTAAGtGCaGctAgT

>Bacillus_Fam_704_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.650794
 TTGGCGaAAtTACagTCAAGN

>Bacillus_Fam_705_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.666667
 ACtGGCGAaAAAAAccTAATa

>Bacillus_Fam_706_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.706349
 GCAAAATAAAAAaTGggaATAc

>Bacillus_Fam_707_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.666667
 TTATCaACAcAcTTTTAGaaT

>Bacillus_Fam_708_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.666667
 aaAATACGGCGGGTTTGAgCa
 >Bacillus_Fam_709_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.619048
 TTGGTTGATTTcCTacaGaAg
 >Bacillus_Fam_710_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.690476
 GAaAGTaTaTCCAAAATAGCc
 >Bacillus_Fam_711_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.809524
 GCAACATCcTGTTTcAGCaCT
 >Bacillus_Fam_712_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.873016
 TGTTAGTacATTAAAGAGTGA
 >Bacillus_Fam_713_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.746032
 GGaGgcTCTTCgCCATCACCC
 >Bacillus_Fam_714_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.746032
 ATCCGACAGTaAGCcGCgGcT
 >Bacillus_Fam_715_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.809524
 TTCAAAaTTTCACTGTGaTCg
 >Bacillus_Fam_716_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.650794
 TtTaTCAACCACTTcTCcgCt
 >Bacillus_Fam_717_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.873016
 TTACTACCAACaACCaCAGAT
 >Bacillus_Fam_718_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.682540
 AgaGCcGATACaCCCGTaAAA
 >Bacillus_Fam_719_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.698413
 AATCACTACGaAAaTcAaAaT
 >Bacillus_Fam_720_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.746032
 GTATTTCGACAcAagTTGGATc
 >Bacillus_Fam_721_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.888889
 cTCACGAGTAAATCgTGAAAA
 >Bacillus_Fam_722_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.682540
 acCTTcATCTCCGTCaCCaGG
 >Bacillus_Fam_723_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.698413
 gTGGTCaATAaAAcCAgAAAA
 >Bacillus_Fam_724_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.619048
 TGTTAAaaAAAAcCaCAAacc
 >Bacillus_Fam_725_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
 Alignment score = 0.825397
 CGCCAATAGAACCTctaAATC

```

>Bacillus_Fam_726_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.619048
aTcCGACAGTTGGaaCacGCT
>Bacillus_Fam_727_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.682540
TTGGCGAAATcCcNgCacAGT
>Bacillus_Fam_728_20_2 Nr. of seq. 2 Alignment length(with gaps) = 20
Alignment score = 0.800000
TATCCATTGTaAATTgaATA
>Bacillus_Fam_729_20_2 Nr. of seq. 2 Alignment length(with gaps) = 20
Alignment score = 0.616667
GACGCAATTaaccatATTA
>Bacillus_Fam_730_20_2 Nr. of seq. 2 Alignment length(with gaps) = 20
Alignment score = 0.700000
TTTGCGTCTCCcacctGATA
>Bacillus_Fam_731_20_2 Nr. of seq. 2 Alignment length(with gaps) = 20
Alignment score = 0.750000
TATATCGGCGtTTTTaGaaA
>Bacillus_Fam_732_20_2 Nr. of seq. 2 Alignment length(with gaps) = 20
Alignment score = 0.883333
CTCATATATTTcGTTCTCcG
>Bacillus_Fam_733_20_2 Nr. of seq. 2 Alignment length(with gaps) = 20
Alignment score = 0.750000
TTTGGCTGATATTTTcCcac
>Bacillus_Fam_734_19_2 Nr. of seq. 2 Alignment length(with gaps) = 19
Alignment score = 0.649123
cCcGGaTGaAGGTCCTGGT
>Bacillus_Fam_735_19_2 Nr. of seq. 2 Alignment length(with gaps) = 19
Alignment score = 0.622807
cTaGAcAAGCAAGaACAaT
>Bacillus_Fam_736_19_2 Nr. of seq. 2 Alignment length(with gaps) = 19
Alignment score = 0.649123
AAgCCAAaGcCGCCaCACA
>Bacillus_Fam_737_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.666667
ACGGGGaacACCGGAcCa
>Bacillus_Fam_738_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.629630
CCaGATACAccAaAaAAA
>Bacillus_Fam_739_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.629630
TGaTGaTGcTGaCCaTGG
>Bacillus_Fam_740_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.648148
aACAACAaCAaCAGCaGt
>Bacillus_Fam_741_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.925926
CCAGGaGAAGGTGAAGGC
>Bacillus_Fam_742_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.629630
aTCTTcaTCTagTCCTGG
>Bacillus_Fam_743_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.629630
CACCcAATCCAaCTaagC

```

>Bacillus_Fam_744_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
 Alignment score = 0.703704
 GCCTCTTGcTcAGCTTca
 >Bacillus_Fam_745_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
 Alignment score = 0.777778
 ATcAGTACCAGTaCCaGG
 >Bacillus_Fam_746_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
 Alignment score = 0.629630
 AaaACTTcTAGAAaCCGg
 >Bacillus_Fam_747_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
 Alignment score = 0.777778
 GGcCCGAATCCCATgCCa
 >Bacillus_Fam_748_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
 Alignment score = 0.851852
 GGAGCACCTGTTaCGCCc
 >Bacillus_Fam_749_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
 Alignment score = 0.629630
 CCggcAGaTCCAGTAAcT
 >Bacillus_Fam_750_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
 Alignment score = 0.703704
 GGTGGaATgGGCGGaCaT
 >Bacillus_Fam_751_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
 Alignment score = 0.777778
 ATACCGGaGGcGAAGaAG
 >Bacillus_Fam_752_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
 Alignment score = 0.629630
 CcTaCTgGTGcTGCTcGT
 >Bacillus_Fam_753_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
 Alignment score = 0.666667
 CCAGCaGGaGCaACaGGa
 >Bacillus_Fam_754_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
 Alignment score = 0.703704
 cTGGCTTTGaTcGTTcTG
 >Bacillus_Fam_755_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
 Alignment score = 0.648148
 CcTGCTGtTTTgCTTGcT
 >Bacillus_Fam_756_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
 Alignment score = 0.629630
 GGAaCcGGATTTGcTccT
 >Bacillus_Fam_757_16_2 Nr. of seq. 2 Alignment length(with gaps) = 16
 Alignment score = 0.625000
 CTgAAcTCAACCAAcA
 >Bacillus_Fam_758_15_2 Nr. of seq. 2 Alignment length(with gaps) = 15
 Alignment score = 0.688889
 TTATTatGTTTTTCc
 >Bacillus_Fam_759_15_2 Nr. of seq. 2 Alignment length(with gaps) = 15
 Alignment score = 0.733333
 GGcGAACCaGGaGAT
 >Bacillus_Fam_760_15_2 Nr. of seq. 2 Alignment length(with gaps) = 15
 Alignment score = 0.666667
 CaAAAACCaGAGGat
 >Bacillus_Fam_761_15_2 Nr. of seq. 2 Alignment length(with gaps) = 15
 Alignment score = 0.733333
 TTCTTgTTCTTTgTa

>Bacillus_Fam_762_15_2 Nr. of seq. 2 Alignment length(with gaps) = 15
 Alignment score = 1.000000
 GGCATGATGTGCGGC
 >Bacillus_Fam_763_15_2 Nr. of seq. 2 Alignment length(with gaps) = 15
 Alignment score = 0.644444
 CCaGGCaaTGGCGaT
 >Bacillus_Fam_764_15_2 Nr. of seq. 2 Alignment length(with gaps) = 15
 Alignment score = 0.844444
 GGcATTTCTTTgATC
 >Bacillus_Fam_765_14_2 Nr. of seq. 2 Alignment length(with gaps) = 14
 Alignment score = 0.738095
 TTcTCTTTTTCtt
 >Bacillus_Fam_766_14_2 Nr. of seq. 2 Alignment length(with gaps) = 14
 Alignment score = 0.714286
 TcATTACaTATCaC
 >Bacillus_Fam_767_12_2 Nr. of seq. 2 Alignment length(with gaps) = 12
 Alignment score = 0.666667
 GGAgGAGTaaTT
 >Bacillus_Fam_768_12_2 Nr. of seq. 2 Alignment length(with gaps) = 12
 Alignment score = 0.694444
 CCTgAaCCTaAG
 >Bacillus_Fam_769_12_2 Nr. of seq. 2 Alignment length(with gaps) = 12
 Alignment score = 0.666667
 TGGCaTTTCTgT
 >Bacillus_Fam_770_12_2 Nr. of seq. 2 Alignment length(with gaps) = 12
 Alignment score = 0.805556
 GATGCCcGATGCg
 >Bacillus_Fam_771_12_2 Nr. of seq. 2 Alignment length(with gaps) = 12
 Alignment score = 0.666667
 aCaGGaGGAACA
 >Bacillus_Fam_772_12_2 Nr. of seq. 2 Alignment length(with gaps) = 12
 Alignment score = 0.777778
 TCATGGccGTGA
 >Bacillus_Fam_773_12_2 Nr. of seq. 2 Alignment length(with gaps) = 12
 Alignment score = 0.777778
 TTGaAcTGGTTG
 >Bacillus_Fam_774_12_2 Nr. of seq. 2 Alignment length(with gaps) = 12
 Alignment score = 0.777778
 CaGGAACAGAcC
 >Bacillus_Fam_775_11_2 Nr. of seq. 2 Alignment length(with gaps) = 11
 Alignment score = 0.636364
 GTTTCgaTATg
 >Bacillus_Fam_776_321_1 Nr. of seq. 1 Alignment length(with gaps) = 321
 Alignment score = 0.000000

TGAACGTTACGGTATGTCTTCCATCTCTAAATTTGGTTGTGTGCGAGAGTATAATGAAAGCCACCATTTCCCATTT
 GTGGTACTCTGGAAAGACTTTTCTGGACATCTGGTCTCGCATCTCCATAGATCGCCTGACCTGCCACTACACCG
 TCTACCAGTACTTCAATTTTCGACACTCCGCTTTCATCTAAAAACCAGCCCCGTACGTTTTGGGACCCGATAA
 GTGTTTTGCCAGAAACCGGATCATCGATATACCCGAGGACATTTGCAATCGTTATAGTCTTTTCAGGCAATGT
 TGTGACATAGCCGTTTCATTCCTGTTTCTC

>Bacillus_Fam_777_255_1 Nr. of seq. 1 Alignment length(with gaps) = 255
 Alignment score = 0.000000

AGTAGGACGTTGCCAGGCAGATTAAACACANTCCTTTAGGGATGTGTTTTTTAATATGCATAAAGAGTATACT

CGGCGCAAAAAGAGCGCTGGTTCTGAAGAAGCAGCCCCCTACGAAGCGAAGCCCCGAAAGCGATCGAAGGAAGAA
AACCAAGTACGTTTCGCGAGACGAATCGGTTCTCTTCGTGCGACCTCGTGAGAGGCATCGGGGAAATCGCTACA
TGCCATACTTCCCCGAAGAAGAGAATCCGAAGAGAC

>Bacillus_Fam_778_252_1 Nr. of seq. 1 Alignment length(with gaps) = 252
Alignment score = 0.000000

TTTTGCTTCGATTTAATCCTGACTGAGAAGCTACCTTTACTACTTGCTGTCCCTGTCCCCAGCACCGTTTTAC
CACGTTTAATCGTCACCTTTGGCGCCGGCTTCTGCTTTACCTGTAATCGTTGTTTGATTATCGCCAAACCGATT
GACGGACGGGGCTGATGGTGCTGTTTTGTCTTCCACTTTGAACGATTTGCCTGCACCCGTATTTCCAGCTTTA
TCTGTTCGCATAGGCTGTCAGAACCGTTCCCTGCC

>Bacillus_Fam_779_249_1 Nr. of seq. 1 Alignment length(with gaps) = 249
Alignment score = 0.000000

AAACAAAAAGCAGGAACGAAGCTTGTCGTTTATGCGGAAGATGCGGCAGGGAACAAGAGCGNTGAAACNGTNG
TAACGGTTATTGATAAAACGGCTCCGGCAGCGCCGAAAGTCGGAGAAGTAAGCGATACAAGTACTGTGGTTAC
AGGAACCACAGAAGCGGGCGCGAAAGTAACAGTAAATCCGGCTCGAACATTTTAGGNACGGCAACGGCTGAT
CATACCGGTGCATTTAAGGTAACCATTGCA

>Bacillus_Fam_780_246_1 Nr. of seq. 1 Alignment length(with gaps) = 246
Alignment score = 0.000000

GTTTTATCTACTTTTACTTCTACTGTGTTTTATTTTCNGTATTACCNGCATTATCTACACTGTAGTAAGTTA
GAGTGTGGATGCCTTCTTTTTCTANGGTNAAGCTTGTGCCTTCGCTGAATTCAGCNCCATCGATAGAATAGTA
GGTTGCTTTCACACCGCTTAGGTCATCAGTTGCTGTGCTCAGCTCAACATTCAGTCTTCTGTGTACCATTGATCC
TCGACATTACTTACAGTAGTAGGAGCA

>Bacillus_Fam_781_237_1 Nr. of seq. 1 Alignment length(with gaps) = 237
Alignment score = 0.000000

CCATTGGCTTTCACCCTTGCCAGCCGTTTCGATTTCGGATATCACTGATACTGCCGTTCCGCTGGACAGCTTGC
TTATCACTTTTCCTTGTGTAGACGCCTTGTCTCGGACATTCAGCGAGGATCCAGAGTCGACTTTCACATATTT
GGTAACCGNNTTGGCCGACGGTTTTGGTGTACCTGTGCTGGCTGACGGCTTGCTTGATGACAAATATTGTGAA
CTTACGTAGCCTGTTTTG

>Bacillus_Fam_782_237_1 Nr. of seq. 1 Alignment length(with gaps) = 237
Alignment score = 0.000000

TATACGTTTGTGCTGGAACACCGAAGCGGATGGAAGTGGTGAAACCTATAAAGAGGGTGACACGTTTACCC
AAGGAATAGGAAATGTGACGTTCTATGCGCAGTGGTCTGTAAATCACTACGAGCTGCGATATGACGGGAACGG
GCAAGATGGAGGAAGTGCGCCAGAAGCGGAATCTGTTGCGTATGGAAGTGAAGTGGAGGTATCGGATTCTCAA
ACGTTAAGCCGAACCGGT

>Bacillus_Fam_783_234_1 Nr. of seq. 1 Alignment length(with gaps) = 234
Alignment score = 0.000000

TTACTTTTTCTCCGTTTTTTAAATTTCCGAGAATTGCACTATTTGTATTTGCTTGACTTCTTACTCGCAGGCT
CGTTGCGTTGATTGTTCCGCTTTCTTGTACTCCATTTGTGATGTCTTCACTGGCTTTTCTTCTTGTTCCTCA
GCTTCTAGCTTCACAAACTCTAACGATACGTAACCTTCTTTTCCCTTTATAATTGATCTTCGCCAGCCGTTTG
CTTTTCCTAAGATTG

>Bacillus_Fam_784_232_1 Nr. of seq. 1 Alignment length(with gaps) = 232
Alignment score = 0.000000

TTCCATTTGACTCCTCTGTGTTAGACGGAGAAATTCGGTTTATCTCGGGAAATACTACTATTTCCCTTGAATT
AAGGGAAGCTTTTCCGCTTATATGATCCAAATCCTTGGATTTTGCTTTTTTTGAAGGTAGTAAGCGGAATTT
TACCCTTATATCTCCCTTTAAGCCGCAAAATTTTCATTAGACGGAAATTCCTCGCTTATGCTTCTCCACCT
ATCCTTTGGCAAC

>Bacillus_Fam_785_231_1 Nr. of seq. 1 Alignment length(with gaps) = 231
Alignment score = 0.000000

GAAAAAACTTGGTTGCCGCTAGATTTTCTGTAAATTGCCCTCTTTACTTGTCAATTTGCTGTCTTTCCATTTCGAA
GATAGCAGTTCAGCGGCAGCCTTAGCTTTTTCTTACCTCCCTTCAGCCCACGCTCTTTCACCCTTAATAATGG
TTGTTCAAGAAAAACAAGCCTGTTTTTCCACCTCTCTTTATGACAGGGAGGAATCACTTCTCTTTTTGCCTTC
AACCTTTATTTTC

>Bacillus_Fam_786_231_1 Nr. of seq. 1 Alignment length(with gaps) = 231
Alignment score = 0.000000

GTGTGTCGATAAATATTTAGTACTGACATATCCTTCTTTTCCATTAGCTTTGATCTTCGCCCCAACCTTTAGATT
CCGAATACACCGTTACCTGCATGCCTTTTCGAAAGCTTCGCAACTATGCTGGCAGTTTCCGTCCCACCTTTTTTCG
CATATTGAGCGTCCCAGAACTTACATTTACATATTTTCGTTCGTCTTTAACAGGGGTGGATGGTGTGGAACCC
GTTACAGGCTTC

>Bacillus_Fam_787_230_1 Nr. of seq. 1 Alignment length(with gaps) = 230
Alignment score = 0.000000

GAACAACCATTATGAAGGGTGAGAGAGGGAAAAAGTTTGGGAAGTAAGAAAAGCTAAGGGCTCTGCCGAACTTC
CGTCTTTGAAGGGAGGAAAGAGGACTTCGAAAAGAATGCACTCTTTAAAAAGAATCTGGCAGAGCCCAAGCTT
TGAAACAGAGGTTTATAAGGTCTGAAAAAGAGCGCCCTCCCTATCATAAAGAGGGGAGGAAAAACAGCGGT
CTGTTTTTCTC

>Bacillus_Fam_788_226_1 Nr. of seq. 1 Alignment length(with gaps) = 226
Alignment score = 0.000000

ATTTACGTGCCGATTTGGCTTCTTTTCGGTCCGGAACGGAGCTCTTTCGTGCCGAAATCATCACTTTTCGAGC
GAGATTGGCGATTTTCGCGCCGGAGCTTAAATCTCTACGGTTCGAACCACTTAATTACTATTTTTTTATGAACC
CCGTTGCTGTCCCAGTTATGTTAGCTATGGCACATCAGCTAATGCACATGCACAAACCATCATTACGGGCCGG
ATTTCAA

>Bacillus_Fam_789_226_1 Nr. of seq. 1 Alignment length(with gaps) = 226
Alignment score = 0.000000

GCTTCGCTTTCCTCGGGGCGAGCGCTGAGCTTCCTCGTCGTTTCTCTCCTGCGGGATCTCACCTGTCTCGCTC
ATCCCGTAGGAGTCTTCTCATCTTTCACTGCCTTCCTTTGGTCTTTTCGACTAGGAACTATTTAGTAGCCTGCT
TTTTGGAATGTGTATTTTCAGATAAGCTATGTTTCATTCCACATGAAACACCCTTTACTTAGTCGGATTCCAGCT
CCAGATT

>Bacillus_Fam_790_225_1 Nr. of seq. 1 Alignment length(with gaps) = 225
Alignment score = 0.000000

AAGCTTGATGAGGTTTTTAAACGGGAACCTCTAGACCTGCCACTCTTCGCTTTGGTGACCGTCATCCGTACGTCA
TTCAGCTTAAAAAAGATTTAGCTGAAGCAGGATTCCCGGTCTCCGGTAGCCCGACGGAGTATTTTGGATCAGT
CACCGAATCCCAAGTCAAGGCTTTCCAACGAGCTCACGGACTTACTGCTAATGGCGTTGTCGGATCTGCTACT
TACGCA

>Bacillus_Fam_791_222_1 Nr. of seq. 1 Alignment length(with gaps) = 222
Alignment score = 0.000000

TTATCCAAACTGATTAACCACGCAAAAACATATGAAAAGGATAAATATACCGAACTTCATACGGNGCNCTGC
AACAAGCAATTAGCCATGCNGAAGCAGTGGTACAAAATGCGAANACACAAGATGAAGTAACGGAAGCNATTAG
TCNTCTCCAAAAAGCGATTAATGGATTAGAAAAAATAGCAGAACCCAGAACCCAGAACTGAAGTAGATACGGGC
GAG

>Bacillus_Fam_792_219_1 Nr. of seq. 1 Alignment length(with gaps) = 219
Alignment score = 0.000000

GATGGGTTTCTGCGGAGTACTTAAATGTCAGTGGGTTCGGGCAGCGATGCGAGTGAAGGGTCTTCCTCCATTGG
ATCGGCTACCACNACCGCAAGGCTTAACCTTCGCTCCGGTGCAAGGACTTCGAATCGTATTTTAAACGACATTG
AACAACGGGCAGAACGTNGCCTTGCTTCAGAAACAAGGCAACTGGTATCAGGTTAAAGCCGGTTCTCAGACGG

>Bacillus_Fam_793_214_1 Nr. of seq. 1 Alignment length(with gaps) = 214
Alignment score = 0.000000

TCAGGGTAGACCTTTATGCGAATAAGTATTGGCACCATGGAAGATGAAAAAGTTTATACTCAGTGTGGAATG
AGCAGAGAGTCACCTGACTCCTGCGGGATCTAGCGGTCTCGTGAGACCCCGCAGGAGCCAAAAGCGACGAGGA
GGCTCACGGGGCGCCCCGCGGAAAGCAGGTGGATCGCAGCGAATGGAACCTCACTATCTAAGTTATTT

>Bacillus_Fam_794_213_1 Nr. of seq. 1 Alignment length(with gaps) = 213
Alignment score = 0.000000

CGCCTTAACTTGCGTTCTGGAGCAGGCACTAACCATAGCATTATCACTACCCCTTGCTAAAGGACAAAAAGTCG
AGTTGCTTAAAAAGCAAGGTGGCTGGTACCAAGTTAAAGCGGGCAACCGTACTGGATGGGTTTCTGTTGACTA
CTTAAATGTCAGCGGCTCTGGCAATGTGGACAACGCTCCTTCTAACGGCTCTGCCACAACCACTGCA

>Bacillus_Fam_795_213_1 Nr. of seq. 1 Alignment length(with gaps) = 213
Alignment score = 0.000000

CCACCAGAAAAAGAAGGCCATTTCATTCAAAGGATGGTATCAAGATGAGTTGCTCACAGAAGCGTGGGATTTTCG
AAACGAACACGGTTAGCGAAGATATGACCCTGTATGCAAAGTGGGAAATCAACGTTTATACTGTTAGTTTTGA
ATCGAATGGNGGCAGCCAAGTATCGGAAGTAGAAGCCGAGTATGGTTCGTCNATCACAGAGCCAGCT

>Bacillus_Fam_796_210_1 Nr. of seq. 1 Alignment length(with gaps) = 210
Alignment score = 0.000000

GACAATCCGAATGCTGNTTACGGTCCAACGACGACAACCTCGGGTGAAGGAATTCAGAAATATTATGGATTAG
TGGTCAACGGCATTGGTGATGAAGTAACACTTGCTAAAATTGAAGAGATTTTAGCATCNCCTCCAAAACGG
AGGCAGGCATGAAGACGTGATAGCGTTAAAGGAAAACCTTNTCTCGCCTCGGTTTCCATGTATCG

>Bacillus_Fam_797_208_1 Nr. of seq. 1 Alignment length(with gaps) = 208
Alignment score = 0.000000

AGGGTGAGAGAGGGAGGAGTTTGGGAGGTAAGAAAACTAAGGCCTCCGCCGATCTGCCGTCTTTGGTAAAGG
GAATCGGACAGTTTTTTAGGAGTGCTCTTCTTAACGGGATACAGGCAAGGTAGTGACGCTGAAAAACATCCCGA
TCCGCCCTGTCATAAAGAGCGGTGGAAGCAAGCTTGCTTTTCATGATTAACTTTATGAC

>Bacillus_Fam_798_206_1 Nr. of seq. 1 Alignment length(with gaps) = 206
Alignment score = 0.000000

TCGTGCCTGCGGGGTCTCGGTCATCCCTCTTTTCCGAAGGAGTCCGGGGCCCTTCGCTTCTTTTCACTCTTGG
TGATACTTTGATTCCCTTTTTTTCATTGTTTCCGCTAGTTCGTTTTTGGTTCTGCTTCATTGGTGTGAT
GGATTGGGCGTTCCATCCCGCTGTGGGACCGCTTTTCTTGGGAGGGCGCCCGAGCCTCT

>Bacillus_Fam_799_206_1 Nr. of seq. 1 Alignment length(with gaps) = 206
Alignment score = 0.000000

AAAGAAAAGCGTAAACGCCCCGTTTAGCGACGTACAAACTTTAATAATAAGGATGAACGGCTAAAGTCGCGCCG
TCCTGGCGCAACGCCGTTCTGACCAACGTCGTGTTGGCCCGAGATAAAGGAAACACAGCGAGGGACGAGCTGA
TGTTGACTTATCGTAGGAAGAAGCTGAAAGTTTGCTAGTCGTTGGGCGTTGAAGCTGGAC

>Bacillus_Fam_800_205_1 Nr. of seq. 1 Alignment length(with gaps) = 205
Alignment score = 0.000000

AAAGTGGAAGATCTGTTACGAATGATAAGTTTCGACACATTGAAAGGAAGTACCGATCAAAGNGCGATTGATG
AAGCTCAAAAAGCNGTCAATAAACTTCCGGAAGGTCCAGAAAAAATCGNCTTGAANGATTTAGTGAACAAAG
CACAAGATCTATTAAATAAAAAAACAAGCCGAAAAAGACTTGAACGATGCAAAGAAC

>Bacillus_Fam_801_196_1 Nr. of seq. 1 Alignment length(with gaps) = 196
Alignment score = 0.000000

CGAATTAATACGTGGATTGGACCGAAGTGGATCAAACCAAACAATCCACTAATAGGGGAACCAACTCCGATCT
CAACGAGGATNCACGATAACAGAAAATACCTATTTGCATAATCAACCGTGAATAGTGCTAGAAGAAATGAAT
TTTTACGTCCGCAAACAGTGACAGCATTTGAAGAATGGAATGGATGGTAC

>Bacillus_Fam_802_195_1 Nr. of seq. 1 Alignment length(with gaps) = 195
Alignment score = 0.000000

TCCATCACCAAAAGTGCAATGCAGCGGAGACCGGCCGACTCCTTCGGGAATAGAGTGAAGTTCGATACCCCG
GACGCGCAGCTGAGGAGGCTCGACTCACTCCCCGAGGAAAGCGGACGGCCGCAGCGAAATGGAACGGACCTTG
ACTCCACCAAGATCCTCATCTAAAGCAGAAAGACATCATGCCTACCTCC

>Bacillus_Fam_803_195_1 Nr. of seq. 1 Alignment length(with gaps) = 195
Alignment score = 0.000000

ATAATCAACCATTTGCNAATACAAGAAGATCAGAAGTNTTACGTCCNCAAACGGTACAGGCAACAGGAGAATG
GAATGGCTGGTACCGAATTAATACATGGGTAGGACCAAAGTGGATTAAACCGTCGAATGCGATTGTAGGAGAA
ATTTAAANAAATCTCGCAAANTATAACATTAACGCAAAATACGCATTTGC

>Bacillus_Fam_804_194_1 Nr. of seq. 1 Alignment length(with gaps) = 194
Alignment score = 0.000000

ACGTCGAATACACTAAGNCCGTTCCACTCGGATTGAGTTTGCTTATAAACACATCAAANTTCCGTTANAACCTT
TGATCATATGCTCCNGCGGTGCTTGGGAAATTGNTGATGTTGTATANCCNGTCACATACGCATTTCCATCCT
CATCGANNGCAATTCCATNTCCTNNATCANNATCACTTCNCCTAAAT

>Bacillus_Fam_805_190_1 Nr. of seq. 1 Alignment length(with gaps) = 190
Alignment score = 0.000000

TTAAATCAAAATTGGGATTGTACATAGANATANGCAGTGTTCTAATCATCCTGCTGGGTTGATTTCCGTTGCA
GGCGCTCGCTTTCCGAGGCCTGCCGGGAGTCTCATCATAGTAAGCTCCTTCGGGGTTTCCATAAAGCCAGCTG
ATCCCGCAGGAGTCTCGCACCTTCCGCTCCAATCAACCTTTGAA

>Bacillus_Fam_806_177_1 Nr. of seq. 1 Alignment length(with gaps) = 177
Alignment score = 0.000000

CAGAAACAACAAATGCTGAAGTAGTAGCAAAAACAGAAGCCATCCAAAAGCACTAGCAGGCTTAGAATTTGC
AGGCCAAAACAGCCTTAAATGCAGCAAAAGCAAAAGCTGAGGAAAAGCAAGAAGCCGACTACACATCTGAAAGC
TATAGCCCATTAAAAGCAGCATTAGAACTGC

>Bacillus_Fam_807_172_1 Nr. of seq. 1 Alignment length(with gaps) = 172
Alignment score = 0.000000

TTACATATGGCTAGAGTAAAGCTTTGTGCTCTTTTTACTTCGTCCATCATCGTTTGAATTTTTTGATCGTGT
AAAGCTTCGGTTTCAGAAAGCTTATCTTTTTGAATCGTAATTTTAAAAGAAAAAATTTGAAATATCATAATGT
AATCGCTCCTTTAGGTTGTTTTCGTA

>Bacillus_Fam_808_171_1 Nr. of seq. 1 Alignment length(with gaps) = 171
Alignment score = 0.000000

ATGTTGTTCCACGATTGAAGTTGCGCTACGGTTACGCCGAATTTCACTGCAATTCCACTAAGTGTATCACCTG
ATTTAACGGTGTACGTGGATACGGTTGAATCGCCACCACCCTCGTAGGAGCTTTAACTTTCAAAACTTGTC
AATCTTAATCACATCAGCGTTTGAG

>Bacillus_Fam_809_168_1 Nr. of seq. 1 Alignment length(with gaps) = 168
Alignment score = 0.000000

TCTACCAATTTTAATNCCGAAAGTTCTTCCATCANTTCTTGATGTGTTTGTTTTAATTGTTCAAGTTCTTGGT
ACTGACTTTGTTCTTTCAANGTAGCNNCCGATAACTGTTTCGAGTACTTCTTCATATGATTGNTTTAATTTTTC
TAGTTCTTCGCTTTTGACTTGT

>Bacillus_Fam_810_164_1 Nr. of seq. 1 Alignment length(with gaps) = 164
Alignment score = 0.000000

AACAGGGACGGTTCTCACTTGCCAGTTTGATAGTTTTTTTTATGATTTGGTCATAGTTATGTGCGATTTCTTTTC
AAGTTACACGCGATTTTGATCGAGTTACGCGCGATTTACACGAGTTTGAAGCGATTTGGAAACCAACTGGAA
AAACACTTCAATTAGGCT

>Bacillus_Fam_811_164_1 Nr. of seq. 1 Alignment length(with gaps) = 164
Alignment score = 0.000000

GGTCACATTCCATGAGGTAAGATTTCAGCTTGTTTCAGTGATTTGATCACCGCACTCGGGACATTGTTTAGGTGG
TAGGGTTCTAAAGAACTCCAACGGATTTTTAGTTTGCATGATGGTTTCCTCCTTTAAATGGTTTAGTAGTCTT
CGCGTTTAGAAAGGCAGT

>Bacillus_Fam_812_156_1 Nr. of seq. 1 Alignment length(with gaps) = 156
Alignment score = 0.000000

ATAAAGTGAATCTTCCATCAGTGAGGGTTTGCTTCATCCTCCACTGATGGTTAGTTGAACCAATCGGGGTTT
TACAGGCTGTTTTATCACTACACTTCTCTCTATTTCTCCAACGAAAATGAAAGAGGGATTATTACAGCCTG
TTAAACCGGG

>Bacillus_Fam_813_156_1 Nr. of seq. 1 Alignment length(with gaps) = 156
Alignment score = 0.000000

TTCTTTCTTAATAGTATTTTTAAGAATTAACAGAAGAACCAGCTTGCGTGACTACTTCCTTTACATTGAATGC
TTTTAGAGGATTTTGCTTTTAGTTGTACATCTTTTGATACAGCTTCTTTTTGTAAAGATAATACTTTGTTTCAT
TTCTCATTC

>Bacillus_Fam_814_156_1 Nr. of seq. 1 Alignment length(with gaps) = 156
Alignment score = 0.000000

ATTTTGACTGGGGGCGGGAACCTAAGGGTGCGGTTGATTACCGAGAAGGAAGAAATTCCGGGGGTTTCGGGAAC
CTAAGGGAGGGTTTGTTACCGGGATGGAGAAAAATGNCTGTGNTCGGTAACCTAAAGAGTGTGGTTGGTTACC
CTGGTGGGGA

>Bacillus_Fam_815_156_1 Nr. of seq. 1 Alignment length(with gaps) = 156
Alignment score = 0.000000

AAAAAGGACTGCCTGGCACTGGAGCAAACCCGCCTGAACCATTTACCTAAAAAACCGAGACATCATCGGAAC
AAAGTTCACGACCGCAAGATCCATAATCCCGTCTCCATTAATAATCTGCAGACGTGATGGAANTTGGACCCAAA
CCTCCACTAG

>Bacillus_Fam_816_155_1 Nr. of seq. 1 Alignment length(with gaps) = 155
Alignment score = 0.000000

CGCTTGCCATTCCGGACCACCACGTTTCTCCCAAATAGCAGCATAACGATCCTGACCATTACTACCGTAACCA
CTTACNTGCATATCAACCGATAGCCTTGCGCAACCAAGTTCAATTGAACGTCCGCTGATATTGCTCTGCTGTCAA
ACCATGTCTG

>Bacillus_Fam_817_155_1 Nr. of seq. 1 Alignment length(with gaps) = 155
Alignment score = 0.000000

TGCTCTACCGACTGAGCTATCGAGCCATAATAATATTTAACTTACAACCTTTATACTCCACTTGCAAAACGTCC
TCTGTCCCTTCCTCTTCTAGCTTATTCTTTGATGCTTATGCGTCGGGACAACCTCGCAGCTGATTGCTGATGT
GGTGCTCGT

>Bacillus_Fam_818_155_1 Nr. of seq. 1 Alignment length(with gaps) = 155
Alignment score = 0.000000

TTTGTTGTAACAAAAGCAGAAAAAACCATGCACAAATCCAGAAATGCGCATGCATTTCAATTAATAGCTGAAGC
AAAGCCATGTGTAATATCCAGGACATGGAAGAAAAACCCATAAAGTCAGTTATAACAGTAAAAAAGTTCCACA
CCCGCATGA

>Bacillus_Fam_819_154_1 Nr. of seq. 1 Alignment length(with gaps) = 154
Alignment score = 0.000000

GGTTCTCCTATATCTCGCTCGGCATCAGTCCAGGTCATACGGCGATGAACAGGACCCTTTTCGCTTTTCGTTTT
TGTCCAGCAGCAGGGCCCTATCGCCTAGTGTCTTCCCTTACCTCGGGTCGATAAGTCGAAAACGAAAGGAGA
GCCCTTTC

>Bacillus_Fam_820_153_1 Nr. of seq. 1 Alignment length(with gaps) = 153
Alignment score = 0.000000

CTAGAAAACCTCGTAAAACCCATGCGAATCTCACGGTTTCACATGGTTTTATCAAAAGATCTCAAGAAAAGCAT
GTGGAAGTGGAAGTTCTCCAAATATTGACCGTTTTAGAGCTAGAATTTCCAAACTATGGATGTTGCGCATG
CCATTTC

>Bacillus_Fam_821_150_1 Nr. of seq. 1 Alignment length(with gaps) = 150
Alignment score = 0.000000

TTCCGGCAATGAATTTTTAATGTGCTTCCAAACTCGATCGTCCACAAACACATCCGGAGTGGACAACGAAGTC
GAAAACAATGAGTTATAAGAATCTCCTCTCATCGGTTCAAAAATTTCTTTTGTACCGGGTTAGGAAGCACAT
AGTT

>Bacillus_Fam_822_150_1 Nr. of seq. 1 Alignment length(with gaps) = 150
Alignment score = 0.000000

TATGGTGGATTGGAGCAAACGGCTCAGTGCAAGGGGCTTATTGGTATGAAGGAATGGCACGACGAGAGAGTTA
TGAATTAGCACCAGCGGGAAGCGCTTCTACCAATGGAGGTATTGCAGCGGTGTCGAGAAGGCCAAACACTTTC
GAAC

>Bacillus_Fam_823_150_1 Nr. of seq. 1 Alignment length(with gaps) = 150
Alignment score = 0.000000

ACTACCCACATAACGTTTACACGTCCNTGNTTATCTACGAAAAACAAATCAAGTTGCTCATCGGTTTGACGTG
CAGTTGCTNNNACCGNATCCAATGGAACGTAGTTNGGTGCAGTNAGAGGAATTGGTCCTTGCCAATTTCCGGT
TCCG

>Bacillus_Fam_824_148_1 Nr. of seq. 1 Alignment length(with gaps) = 148
Alignment score = 0.000000

GAACTTTTAAAAGCAGTAATGTAAGTTCATTATTCCGCAATTATTTATAAAAATTATCATACCTTAATACGAA
AAAAGAGGAGGAAATCATATGGCAATCGCAATGGCAGTTTTAAATTTGTAGGTGGAGCACTTCCATTAGTAC
AA

>Bacillus_Fam_825_147_1 Nr. of seq. 1 Alignment length(with gaps) = 147
Alignment score = 0.000000

TTTTTCTTTGGTGGCTGCATCAAGATTTGCGAACATGCCGTGGCGTTACCCCTTTTCCGGAAGTGTTACACCA
AGCTTTTTCAGCTGGTCCCTGTGCCTGGGTCTGTGTGTCAGGGTGCCGGCCTTCAGCTTTTCCATAATCGCCCCG
C

>Bacillus_Fam_826_144_1 Nr. of seq. 1 Alignment length(with gaps) = 144
Alignment score = 0.000000

ATGAAATTACCGAGCTGACTAATCTCGATCCCTCAATGGAAGATACCAATTTGGATGAAGTGGCGTCTGTAAA
GGAAATCACTAATTCCATCGAGATTATTTCTACAAATGAAGATATCGAGACGATCGAAGGTGTCACTTCAC

>Bacillus_Fam_827_143_1 Nr. of seq. 1 Alignment length(with gaps) = 143
Alignment score = 0.000000

ACTTTTTCAGTGCCCTTTTATTTGTATTGCAATGGCTACGTTTCGTTGCGCGCCTGATAGGATAAACCCACTCC
TATCAGGCTTTTAAACGATTGCAACGACTACGCACATTGCTTAGGGGCACTTCAAAAGTGAAAGAACACC

>Bacillus_Fam_828_139_1 Nr. of seq. 1 Alignment length(with gaps) = 139
Alignment score = 0.000000

TTTTGTGGAAAAGGGGACGGAGCTTACAGGATGATAAAGCAGGAAGCCTATCGCTCACACCCCTTCATTGAAA
GGTTACTCAGCGTTACTGGACGTACTCATTTTCATCCAGTGGAAGAGCGAGCCACTTATGCTAA

>Bacillus_Fam_829_135_1 Nr. of seq. 1 Alignment length(with gaps) = 135
Alignment score = 0.000000

GACGGTTCCCGTGCCTACACAGCAAATGTTAAACAATGACACGGTTTCCGTGATCGGCACGGCCACGAATACTG
TCTTGACCACCATTTCGCTCGCTCCCGCAGGAAACGGTCCTNNTGCTATTGCCATCACGCCG

>Bacillus_Fam_830_132_1 Nr. of seq. 1 Alignment length(with gaps) = 132
Alignment score = 0.000000

CATCAATGACAGAAACNGTATCACTATTTTCNTCATTAGCTACATAAATACGATTATTAGAGGGATTAACACC
TACATCAGAAGGCTGANTCTCCGACAGGTACTATTCCAATAACAGCATTGTGNNACCTG

>Bacillus_Fam_831_132_1 Nr. of seq. 1 Alignment length(with gaps) = 132
Alignment score = 0.000000

TTTTCTTCCCAGAACAATTGAATTTGCTCCAATGCTCCAGAAAATAATCTCACTTATAAATGCCATTGCCTCTG
AAATAATGGTCCCTACAACCTCCATCGTACTAGTCAATATTTCCATTATCCATGTGCCG

>Bacillus_Fam_832_132_1 Nr. of seq. 1 Alignment length(with gaps) = 132
Alignment score = 0.000000

TCGCGGGGTGGAGCATGGAGCAAAGCTTCTTGATTTTACATCGACATGTCGTGACGCATCAAGCTACAAAGCG
TTACGAGAAGAGGAAACGATGACCTCTTAGAAAAAACATCATCTGTAAGCTATATAACG

>Bacillus_Fam_833_131_1 Nr. of seq. 1 Alignment length(with gaps) = 131
Alignment score = 0.000000

CATTAAACCATNNACTTAAGANTAGCCCATTTGTTCCATNACCTAATCCTTTACAGCATCCACCCATCTGAAA
GCCAGTCCNANNGTTGTCAAATNTCAACATCTTCCTATAATGGCTCCCATACAGTTT

>Bacillus_Fam_834_129_1 Nr. of seq. 1 Alignment length(with gaps) = 129
Alignment score = 0.000000

TTTTTTGAACAATCACGAAACGATGAGCGAACAGCCGCAACGCTTTTAAGCCAGTCATGAACGCATTTGTCATG
ATTGGCGAGCGGGGAGGAAGCCATCGTCCTACAAATAAAAAAGGGCGCTTTTCCC

>Bacillus_Fam_835_128_1 Nr. of seq. 1 Alignment length(with gaps) = 128
Alignment score = 0.000000

TGGTTTACAGAAATACAGGTAACAAAATAGGAAGAATNNCAACGGANGGTGAAATTACAGAATATNATATNC
CTACNNCAGATGCAGGTGCNTATNGATTATAGCNNNAGGTNCTGATGGTGCCTN

>Bacillus_Fam_836_127_1 Nr. of seq. 1 Alignment length(with gaps) = 127
Alignment score = 0.000000

TTTCTGTAATTGATGGGTAAACAAATACTGTAATTGCCACGATTCCAGTAGGAAACTCAACCGACCGGTATAG
AGATCAATCCATACATCAATCGAATTTATATAACAAATAGAGGTAGTAATACAG

>Bacillus_Fam_837_127_1 Nr. of seq. 1 Alignment length(with gaps) = 127
Alignment score = 0.000000

CGTCGTTTTTCCAAAAGGGAAATGCGCCCTTTTATTTTAGTTTACGATGGCTCGCTTTTGTGCGACGTCGGTT
ATGACAAATGCGCTCATAACCTACTTAAAAACGCGACAGCTCCCTCATCGTAC

>Bacillus_Fam_838_126_1 Nr. of seq. 1 Alignment length(with gaps) = 126
Alignment score = 0.000000

GATGTTGAAGCATTAACAACAGAAAAAGAAGCTGTATCTTCTTCTCATNCTGAAGGAAAAGAAACACACGATT
CAGTAAGCAAGGAAGAGAAAGCATCATCTCTAGTTGATGTAAAAGCGGACTTA

>Bacillus_Fam_839_125_1 Nr. of seq. 1 Alignment length(with gaps) = 125
Alignment score = 0.000000

AGCGCCCTCCGCATTTCTTGTCCAGCTTCGGGCGCTATCGGCTCGAGGGCAAATGCCAGATGCCCAAGAGG
TGGAAGAGCGATCTTCCGTGTCATCTGGGCTTTGGCTGGTCGCCGATGGGCC

>Bacillus_Fam_840_124_1 Nr. of seq. 1 Alignment length(with gaps) = 124
Alignment score = 0.000000

GAACGTCCGAGCCGGCCGGCGGAGTGTCGCCCCAGCGCCGGAGTGACCGCTTTGCTCTTCGATGTGACCGCTC
ACCTCCTCCGAAGCGCCGTCCGCGGCCGCCTTCCGACCGCTTTTCCCGGCC

>Bacillus_Fam_841_124_1 Nr. of seq. 1 Alignment length(with gaps) = 124
Alignment score = 0.000000

GGAAAGCGCTTGGTCAGACCCGACCAGCATAAGTCGCTCCAGGATAGAAGGCGTCCTTTGCCTTCAATCCTGG
AGTGGCTTATGACTCGAGGGTCTAGGCGCTGGAGCTGGACAATCGAAAAGC

>Bacillus_Fam_842_123_1 Nr. of seq. 1 Alignment length(with gaps) = 123
Alignment score = 0.000000

GCTTCCGCTTTTCTTATTGTCCAGCTGCAGCGGCTAGCCCCCTCGAGACACTTCGGTCCATCACCTGAAGGCAA
AGAACGCCCTTCAACTGCTGGCCCTCCAGTGCTTTTTCGGGGCTGGACAGCC

>Bacillus_Fam_843_122_1 Nr. of seq. 1 Alignment length(with gaps) = 122
Alignment score = 0.000000

CGAAAAGCGGAAGCGCTCGTTTAGCTCCGGGAGTCAGATAAGGAAGTGGCGGAAAAGGCGCTTTTTGCCTTTN
CNGACAATTCCGTTCTGACAGAGGAGCTGAGCGCTGGAGCTAGACAATG

>Bacillus_Fam_844_122_1 Nr. of seq. 1 Alignment length(with gaps) = 122
Alignment score = 0.000000

CGAAAAGCGGAGCCGACTGTTCAGTCCTNTCAGTCAGATAAGAAAATCACCGGAAAAGTCCGGTTTTGACTTTTT
TCGGGGATTTTGTTCGACAGAAGGACTAGGAGGCGGAGCTGGACAATG

>Bacillus_Fam_845_122_1 Nr. of seq. 1 Alignment length(with gaps) = 122
Alignment score = 0.000000

GCATCATCTCTTGTGTTTCCATTGGTTGTTGTTTCATAAAAGCAACATCTCCTTTGGGTCATGAGAATGGTTTAT
ACTTATTAGNTTACAGGTATTCCATNTTTAGTCGCCGGGACTAAAAACN

>Bacillus_Fam_846_121_1 Nr. of seq. 1 Alignment length(with gaps) = 121
Alignment score = 0.000000

GAAATTGCGCCGAATCTCTCCTCCCCTGACGAACGAGAAGCAAGAAGTTCAAGGAGATGAGAGAGAGAGGACC
GGAGCGTATCTATAATACGTGAGGATCCGAGCGAGCGAAATCGACGCA

>Bacillus_Fam_847_120_1 Nr. of seq. 1 Alignment length(with gaps) = 120
Alignment score = 0.000000

TGGTATTACTTTGAGAGTAATGGCGTAATGAAAACAGATTGGTATTTTGATGGAACGAATTGGTTTTATATGA
ATAGCAATGGTGGAATGGAGACAGGATGGAAAAAGATTCAAGGAACG

>Bacillus_Fam_848_120_1 Nr. of seq. 1 Alignment length(with gaps) = 120
Alignment score = 0.000000

GAAGAAATCGATGTGATTCTTTTCCANGAAACCGACAATGCCGGGCAACGCGAAAAGCTGCCATCAGATGCGG
AAAATGAAACAGTTGGCGGTGCGANAGGTGAAGACACAGACGAACCG

>Bacillus_Fam_849_118_1 Nr. of seq. 1 Alignment length(with gaps) = 118
Alignment score = 0.000000

GCTTATAAGAAACCTCGCCTTTTTGAACTGCGCCGTGCTGTAGCAGCTGGCGGCCATTAATCTCATATAGCAT
TTGACATCTAGTACTCTATTTTAGGAGGGATGCTCAATGAAAAAA

>Bacillus_Fam_850_116_1 Nr. of seq. 1 Alignment length(with gaps) = 116
Alignment score = 0.000000

CAAAAGGTCGAACTTTACCTTTTGGGGATTTTACGTAACGAGAGCGAAGTCGTCACAAAGAAGAGCACAAATG
GAGTGAACCTTCTCCATTAGTGCGAGTGACGAACGGAGCCTCGC

>Bacillus_Fam_851_115_1 Nr. of seq. 1 Alignment length(with gaps) = 115
Alignment score = 0.000000

CTCATAGAACGGCTATATGAGACAAAATTAGTTGAAAATCAAGCCAAAATGTCCCATAGAATTGCCCCGATCC
CCTGCTATGGGACAAAACCAGCGGAAGCCGAAGCAAAAATGG

>Bacillus_Fam_852_114_1 Nr. of seq. 1 Alignment length(with gaps) = 114
Alignment score = 0.000000

AAAAGGTATAGGGCGACATTTTGGGTGCGGAGACGCTCGTTGCTCGCCATTGAGAAGTAACTGAATGGCTTT
AAGAGCGGGCAACGGCTTTCCCCCTCTTACGAGAAAGAACC

>Bacillus_Fam_853_114_1 Nr. of seq. 1 Alignment length(with gaps) = 114
Alignment score = 0.000000

TTCTCTGTTTCCTTCACTTTCCGACTCCGCTGTTTTTCTTCTGCTTCGCGAGAGCCTGTGCTTTTGCCTTT
GCGGCTGCTGCGGCCTTTTTCTTCGCCAGGGCTAGTGCGTC

>Bacillus_Fam_854_114_1 Nr. of seq. 1 Alignment length(with gaps) = 114
Alignment score = 0.000000

CACTTGATTCAATGGAAGAAGATGACTCCTCGTCTGAGACCTCCGAATCAATGCTACTGGATTCAATCCGGTGA
GGGGGCGAGTGCATCGCAACAGGTAACCGTTTCATCCTCCA

>Bacillus_Fam_855_111_1 Nr. of seq. 1 Alignment length(with gaps) = 111
Alignment score = 0.000000

TGTGGCGGAATGGCAGACGCGCTAGACTTAGGATCTAGTGCTTATGACGTGGGGGTTCAGTCCCTTCACCC
GCACTTTGAATTTTATAGAGTGATGAAAAGTGAAGCGGT

>Bacillus_Fam_856_111_1 Nr. of seq. 1 Alignment length(with gaps) = 111
Alignment score = 0.000000

TTGCTGCTGCGGCGGCTTTCTTTTTGGCTAGCTCCTTGGCGTCATCTGTTTCGGTTGCTGGAGCTTCGCCTG
CTTCACTCTTTTGTTTGGCAGTGCGGCAGCCTTTGCT

>Bacillus_Fam_857_111_1 Nr. of seq. 1 Alignment length(with gaps) = 111
Alignment score = 0.000000

CAGCGGCTTTTTCTTCGCTAAGTCGTCTGCTTCCCCAGCTGGCGGCGTTTCTGAGTCTGACTCTTTCGCTTT
CATTTTCGCGAGTGCGGCAGCCTTTGCTTTTCGCTGCTG

>Bacillus_Fam_858_110_1 Nr. of seq. 1 Alignment length(with gaps) = 110
Alignment score = 0.000000

GATATGGCAAAAGTGTTTCATGTTTTATATGTGTCAAATATTANNGAAACANCTATAAAACGTTGATATATAA
GGGTNTATAAGATGTTTCNNATATTTATTAGGTCAAG

>Bacillus_Fam_859_110_1 Nr. of seq. 1 Alignment length(with gaps) = 110
Alignment score = 0.000000

AGGATACCGCAAACGTGTTGCAAGTTAAGTTATANGTATATGAATAAGAAAAAACGNCTATCCTTTGATATA
TAAGGNATTCGAGTNAAATGACAAAAAAGTTAGGGTA

>Bacillus_Fam_860_108_1 Nr. of seq. 1 Alignment length(with gaps) = 108
Alignment score = 0.000000

ACAGGTCCAGTTGGTCCNCNAGGAGCGACGGGCCCCCCCCGNCCTACAGGAGCAGTAGGCCAGCAGGGCCAA
CAGGAGCCCCAGGCCCGATCGGCCCAATGGGAGCG

>Bacillus_Fam_861_106_1 Nr. of seq. 1 Alignment length(with gaps) = 106
Alignment score = 0.000000

TTTTTAGGAGATAGCGAACCTGCAACATGCCTTTGCGGGTTCGCAATTGGATAATATTAGGAAACACCATTCC
TGTATAACTCATTTGCATCCTCGCACTTGGATA

>Bacillus_Fam_862_105_1 Nr. of seq. 1 Alignment length(with gaps) = 105
Alignment score = 0.000000

CTGAAACAGCAACTGGAAACGAAAGACGAGCAGATTTCAGAAGCTAGAACAAGAAAAGCAAAAGTTAGAAACCC
AAATGAATCAGTTGCAAGGAGGGCCAGAAAAT

>Bacillus_Fam_863_105_1 Nr. of seq. 1 Alignment length(with gaps) = 105
Alignment score = 0.000000

AGCGCCCCATTCTAAAGGGAAAAATATATGTAGAAAGGCGCACAAATCGAAATAGCGGGCCATTGAGAGAAAAG
AAAAAGCAATAGAAATGGCCAGCAAAATAAAAT

>Bacillus_Fam_864_105_1 Nr. of seq. 1 Alignment length(with gaps) = 105
Alignment score = 0.000000

TATCTATGTCAACTGGTATAGCAATGAAGCAATTTCGATCAAAGCTTAAAAAACTAACGGCTCTTCCAACTGA
GAATCTAAACAGTGTAATAAATTCCTCATTGC

>Bacillus_Fam_865_105_1 Nr. of seq. 1 Alignment length(with gaps) = 105
Alignment score = 0.000000

CTTCAGACAGAGGCNGGCATGCCTTTCTCTTTGTTGTCCGAACCTACGGTAACTTCGGACTGTACTCGAGTTT
TTCTTGAGGTTAAGTGTCCAAACCTTCTNCGA

>Bacillus_Fam_866_104_1 Nr. of seq. 1 Alignment length(with gaps) = 104
Alignment score = 0.000000

GGACTCTGGTTGAGGATATCACGTATTTTGGGTCCAAACCTGAGCCTACTTCAGACTCTGGTTGAGCTCATCC
TGAAATGTGAGTCCGAACCTAGTACAACCTC

>Bacillus_Fam_867_104_1 Nr. of seq. 1 Alignment length(with gaps) = 104
Alignment score = 0.000000

TGGTTTCTTACCGTACCAATGATTTCCCTCTTTCTAGGGCAAAATCAACGCTTGATTTTTACCGCCTGAACC
GTTTTTCTCTTCTTGGGAAATTCATTAA

>Bacillus_Fam_868_104_1 Nr. of seq. 1 Alignment length(with gaps) = 104
Alignment score = 0.000000

GAGGTGTGTTTCGGAGCTAAACGCGACTATGAAATCCTATATATGGAAAATAGTGTGCGTGGAAATGCTCTAAT
CACGACAGAATAATCCAATAAATGGATAACA

>Bacillus_Fam_869_104_1 Nr. of seq. 1 Alignment length(with gaps) = 104
Alignment score = 0.000000

TTTTCTGAATTGCAACGCTTTATGGGTTCTATGAAACCTGCTATATTACCACTTTTGAAGATTACAACCCATT
ACGGGAACCTATGAACCGCACTATGCGACCGC

>Bacillus_Fam_870_104_1 Nr. of seq. 1 Alignment length(with gaps) = 104
Alignment score = 0.000000

CGTCAAGTCCCGGTGTANGATTAAAAATCCGGCGGGTTCCGAATGAAATCGGGCCAGATGGAAGACAAATCGG
GCGGGAATCAAGGTAAATCCGGCAAGCCGGG

>Bacillus_Fam_871_104_1 Nr. of seq. 1 Alignment length(with gaps) = 104
Alignment score = 0.000000

GAAAGCGGCGACTTTCAGAAAGAATCCGGCGGGGAAAGCGAGGAAATCCGGCGAGANACATTTCGAGTGACTGGT
TCGGGTGAAAAAACGGCGGGATTAGAAAG

>Bacillus_Fam_872_104_1 Nr. of seq. 1 Alignment length(with gaps) = 104
Alignment score = 0.000000

ACCCGCCCCGATTATTCACCTTTCTCGCCGGATAATTGACCCGGATTGACCCAGATTCCAGAACTGGCCCCGAT
TTTCTTTGGATCCCCCGGCATTCGAGCTCAC

>Bacillus_Fam_873_104_1 Nr. of seq. 1 Alignment length(with gaps) = 104
Alignment score = 0.000000

ACAAGAAATTGGGTCTGAATAAAATCGTAATTCAGACAAGAGATCTGCTAAGGTGAGAAATCAAGTCCGAATG
GGCGGGGGATTTCAGACAGAAAAGAGACTTCA

>Bacillus_Fam_874_103_1 Nr. of seq. 1 Alignment length(with gaps) = 103
Alignment score = 0.000000

TTTATTCTACCTTCACACGATTCTCCNCGTCATGACGGGACTTTAAAACATGGTTCTTACCCCTTCAGACCGG
GGCGTTCACTCTAAAAGGATATTAAATCGT

>Bacillus_Fam_875_103_1 Nr. of seq. 1 Alignment length(with gaps) = 103
Alignment score = 0.000000

AACTTTTGGAAAAAGTGCTGAACTAAAGAGTGGAACGCGGAACCGCCAGAGGAATGCTGAAAAAATGGAGA
TTAACGCTGAAATAGGGGAGGAAAACGCTG

>Bacillus_Fam_876_102_1 Nr. of seq. 1 Alignment length(with gaps) = 102
Alignment score = 0.000000

GGTTGGAAGCACATGGAACCTTGCAATCAAAAATATAGATACACTAAAATCATTCTCTGACCCTTTGAAAGAT
ACACGAAAAGCCCTTGCTTCAATTGCAGA

>Bacillus_Fam_877_99_1 Nr. of seq. 1 Alignment length(with gaps) = 99
Alignment score = 0.000000

AACAAAAATAACAGTAACGATGAAGATACAGAAACAACATCGAATGAAAAATAACAATACAAAACAAGATA
ACGATAATCAACAAAATTCTAACAAC

>Bacillus_Fam_878_99_1 Nr. of seq. 1 Alignment length(with gaps) = 99
Alignment score = 0.000000

CGAAGAAGAACTACATGTAGANAACTACTAAGCATNAATTTGGAAAAACGCTAGAAACGTATGCGCAAAGT
GGTGAGATAGCAGAACAAATNGAACG

>Bacillus_Fam_879_93_1 Nr. of seq. 1 Alignment length(with gaps) = 93
Alignment score = 0.000000

ATTACCCAAGTAGAAATGAACCTGCACCTCCAGATACACAACACATAATGCAAATGATGACAAGTCTCGAGGA
TCGATTAAATAAACTCACTA

>Bacillus_Fam_880_90_1 Nr. of seq. 1 Alignment length(with gaps) = 90
Alignment score = 0.000000

CGTTCTACTTGCTGACGATCACCTTTTGCCTGATCGTTTGGCACTTCATTTCTTCTGGGTTATTTATTTCGAT
TAGCTACTTCCAATTCT

>Bacillus_Fam_881_84_1 Nr. of seq. 1 Alignment length(with gaps) = 84
Alignment score = 0.000000

ACTTCTCGTTGAACTGTCGTTCCATTTACGCTCACGTTTCCGCTATTTACTGATCCTTGATTCTTCACATTAT
CCTGTACGTTT

>Bacillus_Fam_882_84_1 Nr. of seq. 1 Alignment length(with gaps) = 84
Alignment score = 0.000000

AATTAGCAGATGGCTCAAGTCAAGTAACAGGCGGTTTAGGAACATTATCTGTAGGAGCAAATCAAATGGCAGG
TGGAGTAAATC

>Bacillus_Fam_883_84_1 Nr. of seq. 1 Alignment length(with gaps) = 84
Alignment score = 0.000000

AACTCTTTCTTTGCGCATTCATCAATTACTTCTTCGCTAATAAATGGTGCCACNCNTGTTAATCCTTTAATAC
CATTCGTTTCA

>Bacillus_Fam_884_84_1 Nr. of seq. 1 Alignment length(with gaps) = 84
Alignment score = 0.000000

AAGCTGTGGAACAAGAAGACACAGAATCGAAACAAGCTGATGCAGAAATCGCTGTTCAAGAAAAGGAAGAGCT
AAAAACAAGTTG

>Bacillus_Fam_885_81_1 Nr. of seq. 1 Alignment length(with gaps) = 81
Alignment score = 0.000000

ACTCAGGTTGGTTGACTTGGTCATTAAGATCTTCAATAACTTCTGTGATTGGAGCAGAGTCAATAGGTATTTTC
TGAACCTG

>Bacillus_Fam_886_78_1 Nr. of seq. 1 Alignment length(with gaps) = 78
Alignment score = 0.000000

AGGAGCAAGAATCGGAAGAAGAAGTAGCATTAAATTCTGATGCAAATCAACCAGAAGTAGAAGAACAATCACT
GCAAG

>Bacillus_Fam_887_78_1 Nr. of seq. 1 Alignment length(with gaps) = 78
Alignment score = 0.000000

CAGAGAACAATCAGGAAGGAACAGCGAAAACAGTGTTGGCAGAAAGTAATCAGGCAGGAGCATCAGAACCAGC
GTCGT

>Bacillus_Fam_888_76_1 Nr. of seq. 1 Alignment length(with gaps) = 76
Alignment score = 0.000000

TGAAGCTTGACGCGAAAAGATGAAGTAAAACGTTGATATAAGGGATAGAAGTGCATAGCTTGACGTAAGCA
ACG

>Bacillus_Fam_889_75_1 Nr. of seq. 1 Alignment length(with gaps) = 75
Alignment score = 0.000000

TATTATCTGGGTCAGTTGCATCTTTAGGGTCTTCAATCGGATCTTCTTTATTAGTGCCCCATCATTTTCATC
GA

>Bacillus_Fam_890_75_1 Nr. of seq. 1 Alignment length(with gaps) = 75
Alignment score = 0.000000

GAGCAAGATTCTGATTCCTCTCTAGATGAAGATGTTTCTCTTGATAACGACGCTTCTGAAGACCAGGATGCAG
AT

>Bacillus_Fam_891_74_1 Nr. of seq. 1 Alignment length(with gaps) = 74
Alignment score = 0.000000

CTTTCAATCCCCTAAATCGGGTCACATCTTTTGCTACGANNTATGAAGATTCGTTAANAATCTAACAGTTATT
N

>Bacillus_Fam_892_73_1 Nr. of seq. 1 Alignment length(with gaps) = 73
Alignment score = 0.000000

CACGCAAGTATCACTATGGTAATTTGACGGACATAACTCCACAACGAGATCCCAGAAAGAATCTCTAAAATGA

>Bacillus_Fam_893_72_1 Nr. of seq. 1 Alignment length(with gaps) = 72
Alignment score = 0.000000
CAGTAACACCAGTTGCGCCAATCGAAAATGAAGTACCAAATTCAGAAGTGGCCGCTGGGCCAATGTCAACAC

>Bacillus_Fam_894_70_1 Nr. of seq. 1 Alignment length(with gaps) = 70
Alignment score = 0.000000
TGAGTGCGTGGATTGAAATAACTACGNCNTTGANCAATGCAATATCNCAATTAGCTAGTCGCACTTTTTTG

>Bacillus_Fam_895_69_1 Nr. of seq. 1 Alignment length(with gaps) = 69
Alignment score = 0.000000
TAATTTCTGACTTTGTACCTTCAATAGATGTTCCGTTTGTAAATGTTTCAGGTAAAGAGAATTATATGGT

>Bacillus_Fam_896_69_1 Nr. of seq. 1 Alignment length(with gaps) = 69
Alignment score = 0.000000
GTCGCACCCCTACATGGGTGCGTGGATTGAAATNAANGNGNCAATNAANNCGNATNNTTNATNAGNNNCN

>Bacillus_Fam_897_68_1 Nr. of seq. 1 Alignment length(with gaps) = 68
Alignment score = 0.000000
GTTTTATCTGAACGTAGTGGGATATAAAGTTTAANTTCGCATAANAANCTNTNACCTTAGCCGANNNT

>Bacillus_Fam_898_68_1 Nr. of seq. 1 Alignment length(with gaps) = 68
Alignment score = 0.000000
GTCGCACTCTATGTGAGTGCGTGGATTGAAATANCTNTTTGNNCCNGNTCAGCNTANNTTNCAGTACN

>Bacillus_Fam_899_68_1 Nr. of seq. 1 Alignment length(with gaps) = 68
Alignment score = 0.000000
TCGCACTCTATATGAGTGCGTGGATTGAAATTCCTTTCTNCTNTTTCTTTAGCCGTTTCNNCGNTTGCAG

>Bacillus_Fam_900_68_1 Nr. of seq. 1 Alignment length(with gaps) = 68
Alignment score = 0.000000
GTCGCACTCTTAGTGAGTGCGTGGATTGAAATNTAATGGCAACTACACCCAAAAGAAAAAGGCAAATC

>Bacillus_Fam_901_68_1 Nr. of seq. 1 Alignment length(with gaps) = 68
Alignment score = 0.000000
TGGATTGAAATNNGATTANNCAGNNTTNAATGATTNNAATAATCNNTGTGCGCACTCCTTGTGAGTGCG

>Bacillus_Fam_902_67_1 Nr. of seq. 1 Alignment length(with gaps) = 67
Alignment score = 0.000000
GTCATATCTCCATCTAATCCGTTGCTGTGATATGATANNNGCNNTCANCANNTNGATGNTGNNAANN

>Bacillus_Fam_903_67_1 Nr. of seq. 1 Alignment length(with gaps) = 67
Alignment score = 0.000000
AAAACTGAAAGAGTGCCAAACTANGTTNANATNGTNCATNTTNTCNANANNGTTTTCTATACC

>Bacillus_Fam_904_67_1 Nr. of seq. 1 Alignment length(with gaps) = 67
Alignment score = 0.000000
GGTACTCTCTCAGTTTTTCGGTATAGAGAAACAAGTCCACGANTGTGNAAGANTACGATTNNGTTTT

>Bacillus_Fam_905_66_1 Nr. of seq. 1 Alignment length(with gaps) = 66
Alignment score = 0.000000
ATCTTTTGATAATTCGTAGCCCGCTGGTGCTTCTATTTCAACGATTTTGTATTACCTATCGGTAA

>Bacillus_Fam_906_66_1 Nr. of seq. 1 Alignment length(with gaps) = 66
Alignment score = 0.000000
ATCATATCACAGCAATAATCTTAGGGGAACATGACNGNTNNTNNGANNATNTNCGNTNNNNN

>Bacillus_Fam_907_66_1 Nr. of seq. 1 Alignment length(with gaps) = 66
Alignment score = 0.000000
GTCGCATCCCACGCGGATGCGTGGATTGAAATGNCNANCATGNCGAGATANANCCGNNANTCTNGN

>Bacillus_Fam_908_66_1 Nr. of seq. 1 Alignment length(with gaps) = 66
Alignment score = 0.000000
GACAGCACCAACGCTACTGATACTTCCACCGCTACAAGCGGCTCCACCAGCGAGTCCGACACG

>Bacillus_Fam_909_66_1 Nr. of seq. 1 Alignment length(with gaps) = 66
Alignment score = 0.000000
ATCATAATACAGCAATGGCTTTAATGGAACATGACNTACAAATGTANGANAAATATTNGATTTNA

>Bacillus_Fam_910_66_1 Nr. of seq. 1 Alignment length(with gaps) = 66
Alignment score = 0.000000
GGATTGAAATNNGNTNGTATGCTNANNAGGTTTCGTTGGCNGNCGTCGCATCCCATGTGGGTGCGC

>Bacillus_Fam_911_66_1 Nr. of seq. 1 Alignment length(with gaps) = 66
Alignment score = 0.000000
GTCGCACTCTTCATGAGTGCGTGGATTGAAATNTTATANTCNTGATGGTCGAGNGCATNNGATCGN

>Bacillus_Fam_912_65_1 Nr. of seq. 1 Alignment length(with gaps) = 65
Alignment score = 0.000000
ATTTCAATCCTCGCACTCACATGGAGTGCGACCANTAAGTCTATTNCTGTTATGCAAGANNNGNCT

>Bacillus_Fam_913_65_1 Nr. of seq. 1 Alignment length(with gaps) = 65
Alignment score = 0.000000
TCCACGCACTCACATGGAGTGCGATTACGNCNNANNNATNNCGNNGANAACGTCNGANATTTCAA

>Bacillus_Fam_914_65_1 Nr. of seq. 1 Alignment length(with gaps) = 65
Alignment score = 0.000000
GTCGCACTCTTTGTGAGTGCGTGGATTGAAATAANCATNTTTCTGTAANCGGCAAAATAATNCNG

>Bacillus_Fam_915_63_1 Nr. of seq. 1 Alignment length(with gaps) = 63
Alignment score = 0.000000
TTTTTTCTACCGCAAAGAGAGATATTCCTACCACAAANAGCAATAATCCTACCGAAAATCCGA

>Bacillus_Fam_916_63_1 Nr. of seq. 1 Alignment length(with gaps) = 63
Alignment score = 0.000000
CAAGAAATAGAAAATTTAAATGAAACAATCATCAGTTACAAAACAAAAGAACTGAACATAAA

>Bacillus_Fam_917_63_1 Nr. of seq. 1 Alignment length(with gaps) = 63
Alignment score = 0.000000
AATACCATTTTNCNCNGATTGAACCCATGCTTTTGTTACCATAGCTCCATCAGCACCTAAGT

>Bacillus_Fam_918_63_1 Nr. of seq. 1 Alignment length(with gaps) = 63
Alignment score = 0.000000
TTTGTCCCATAGACCGTGAATCCGGAATTCTATGGGACATTTTATTTTACTTTTCAACTAAA

>Bacillus_Fam_919_63_1 Nr. of seq. 1 Alignment length(with gaps) = 63
Alignment score = 0.000000
TAGGAAAACTATCTGACGGATCTACTCAGCTAGCAACAGGAAAAGGCGATTTATCAAATGGTT

>Bacillus_Fam_920_63_1 Nr. of seq. 1 Alignment length(with gaps) = 63
Alignment score = 0.000000
AGAGTACCAAAACNTNNNNANANNNTNNGNTANTANGTNGTTTCTCTATACCGAAAACCTGAG

>Bacillus_Fam_921_63_1 Nr. of seq. 1 Alignment length(with gaps) = 63
Alignment score = 0.000000
GAAAAAGAGCAGCAAGCCAGNCTTACCATCCAAGAGCTGGAGAACAAAATCCAACACTCTTTG

>Bacillus_Fam_922_62_1 Nr. of seq. 1 Alignment length(with gaps) = 62
Alignment score = 0.000000
ATGAAAGCCATNATGAAGGAAAAACGCGGTNAANTNGCTTTCATCTGTAAAAAAGATCCAA

>Bacillus_Fam_923_61_1 Nr. of seq. 1 Alignment length(with gaps) = 61
Alignment score = 0.000000
AATCGAAACAAGGACGAAATACTCCAATGTAGGCCGAATTAATAGCAGTCAAGGCCGGATT

>Bacillus_Fam_924_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60
Alignment score = 0.000000
AATACCAAGTAGATCCTTCTTTTAACCAGCCAGTAGCCATAGAACCATTTGCATTTAGAT

>Bacillus_Fam_925_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60
Alignment score = 0.000000
TGGTATTACTTGAAAGAAAATGGATCNAATGATGACAGGTTGGACGTTAGTAAATGGTNAG

>Bacillus_Fam_926_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60
Alignment score = 0.000000
TGGTATTATTTAAACGCTAATGGAGCAATGAAAACGGGCTGGCTATTANATCAAGGAGTT

>Bacillus_Fam_927_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60
Alignment score = 0.000000
TAGTACCAAGTATTANCAAGNTGAAGCCATCCNGTATGCATNNCACCGTTATTNTTTAAN

>Bacillus_Fam_928_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60
Alignment score = 0.000000
ATTTACATTTTTCTTACATTCACTCTCTTGATACCTTGCTTTTACCTCATCCTTTGA

```

>Bacillus_Fam_929_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60
Alignment score = 0.000000
ATCACAAACACCACAGTCAGGAACAACACCATCACCAGCGAATCCGATGGAAAGTAAGCCA
>Bacillus_Fam_930_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60
Alignment score = 0.000000
CCCAACCAGTAGCCATCGCACCCTAGGATGCATGAAGTACCAGGTGCTCCCATCANNNTA
>Bacillus_Fam_931_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60
Alignment score = 0.000000
AGGTAGTACCACTTCCACCTGTATAAAGCCAACCGGTCTTCATCGAGCCATTACTAGTC
>Bacillus_Fam_932_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60
Alignment score = 0.000000
TCAGCCAGCCNTTNTGAATNAGACCGTTTGATNCAAAGTAATANTGCTNNNATCCCTNGG
>Bacillus_Fam_933_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60
Alignment score = 0.000000
AAGAGCGGAGCCATGCAAACGGCTGGCTGAAAGACGGATCGAAATGGTACTACCTCGGT
>Bacillus_Fam_934_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60
Alignment score = 0.000000
GGAGTAATGAAAACCTAGTTGGTTAGTATTAGGTAATAAACATTATTACTTTGATAAATAT
>Bacillus_Fam_935_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60
Alignment score = 0.000000
TGACGGTAGCCATGAGGAGGCAGGACATGAAGACGAAAATCATGAAGCTGACGCTCATGG
>Bacillus_Fam_936_58_1 Nr. of seq. 1 Alignment length(with gaps) = 58
Alignment score = 0.000000
TGGTATTATTTTGATNNNACCGGTGCAATGAAAACAGGNTGGCTGCTATNGTGGCAAN
>Bacillus_Fam_937_58_1 Nr. of seq. 1 Alignment length(with gaps) = 58
Alignment score = 0.000000
AGGATGGCGACATTCCTGTTACTCACAGGACGTGAGTGGTACTTAAGCGGAATTGG
>Bacillus_Fam_938_57_1 Nr. of seq. 1 Alignment length(with gaps) = 57
Alignment score = 0.000000
TTTCCAATGCCAAGCCACCATGGAGGAATGATGCCAATGCCAGAGCAAAGTGGAGGA
>Bacillus_Fam_939_57_1 Nr. of seq. 1 Alignment length(with gaps) = 57
Alignment score = 0.000000
AATGACTCATAAATACTCGATTCTTTTTTATCATGGATTCTTCAGCTGGTCTTATT
>Bacillus_Fam_940_57_1 Nr. of seq. 1 Alignment length(with gaps) = 57
Alignment score = 0.000000
CAAATGTTGGAAATGTAGTTGGTGCTCCTACTGGAACCTCCGCCTTGCGCCCCCTCTTA
>Bacillus_Fam_941_57_1 Nr. of seq. 1 Alignment length(with gaps) = 57
Alignment score = 0.000000
GGGCCTACTGGACCTACCGGAATAACTGGAGCAACTGGACCTTCTGGTGGACCTCCA
>Bacillus_Fam_942_56_1 Nr. of seq. 1 Alignment length(with gaps) = 56
Alignment score = 0.000000
TTTGGAGGTACTTCCTTTTAGCTATTTCGCTAGCATGATGTGACNTCATGACACTCT
>Bacillus_Fam_943_55_1 Nr. of seq. 1 Alignment length(with gaps) = 55
Alignment score = 0.000000
GTCTTCCTTAACNTAGANGCGNTTCTACGTTAAGATACCCGAAAAATTCCGANG
>Bacillus_Fam_944_55_1 Nr. of seq. 1 Alignment length(with gaps) = 55
Alignment score = 0.000000
GGACCATGATTAAGCTGCTATTTGTTGGTAGTTTTATACATAGCACTTGATTTCGC
>Bacillus_Fam_945_55_1 Nr. of seq. 1 Alignment length(with gaps) = 55
Alignment score = 0.000000
ATGAAGGACAANTTGAAGGAAAGAATCGAAGGAAAAATCAGTCCTTCATCGGAAGT
>Bacillus_Fam_946_55_1 Nr. of seq. 1 Alignment length(with gaps) = 55
Alignment score = 0.000000
CTTTATTTTGACCGGTGACCTCCTTCTTGGTACCTTTGCGGGAAGAATCNGACGN

```

>Bacillus_Fam_947_55_1 Nr. of seq. 1 Alignment length(with gaps) = 55
Alignment score = 0.000000
CTCATGAACCCCTCTATGAGAACAATTGCNAGCACCCCTCCTTCANCCCAGTCTGTC

>Bacillus_Fam_948_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
CCCGTCTTTCAGCATGATGTTTCAGGCAAATCCGGGGGAACACGGCGCTCTATTT

>Bacillus_Fam_949_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
TGTCTTTCATCANACCGATGAAGGACAAATAGCTACCAGCCACNCCTTGTA AAA

>Bacillus_Fam_950_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
TTCAGTGCCATCAAAACCGATTCCGGACGCTTCTTGAGGGTCTTATCCTGNTG

>Bacillus_Fam_951_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
ACAAAGACTTCCGGCTCTTCTTGNTTTCTCTACA ACTTCTGCTTCAGGTTC

>Bacillus_Fam_952_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
ATTGTTGGAAACACAAACATCACGATGATTGTTCAAAACATAAACATCATTGTG

>Bacillus_Fam_953_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
AGAGAAAGAAAGTGAAGAACTGAATCAAAAAAAGAAGATAAAGCAATTGAATT

>Bacillus_Fam_954_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
CTGACAGCCCTCCTCAGTGCCCGTTTCTTGGAATAGGAAACCATTTTAGGGCT

>Bacillus_Fam_955_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
ATGGGGCCAACAGGAGCCACCGATTAGCAGGAGCAACCGGGCCAGCAGGAGTA

>Bacillus_Fam_956_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
TTTGTCTCTGAGCACGTCTATCAGAGACATTAATTATCCAATTAAGCGAAGA

>Bacillus_Fam_957_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
TAAGCCAGTAGCGCCAGTAGGCCAGGATCGCCGGTGGCCCCAGTAGCCCCAGC

>Bacillus_Fam_958_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
CTCAGCCAGCAGCTCGGTTTCTTCTGCAGCCTCTTCGAGTAATTCTGTCTCATT

>Bacillus_Fam_959_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
AAAGCAGAAGAGCAACAGCGTGAAGCATTGAAGAAACAAGAAGAGGCCCGTAAA

>Bacillus_Fam_960_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GGTCGACATGATCGAGGAGAAAATAGAGAAAGAACAGGTCGATGAGTAGCCGA

>Bacillus_Fam_961_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
ATATGAGTCACTNTGGTGGTGGNGAAAGCCGNACAGAGTGACTCAAGAGGAAG

>Bacillus_Fam_962_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCTTCCTTAACATAGAAGCGCTCTACATTAAGGAAAGGCGAAAATTCGTGACN

>Bacillus_Fam_963_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GAATCGGTAGGGTCAAAAGAGCACTTAGACATGGTCTGAATCCAGGTAAGAGAA

>Bacillus_Fam_964_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GTAGGTCATAAGGGTCTCAACATGAAAATGAAGCCATGCGCTCGTCCCGCGCG

```

>Bacillus_Fam_965_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
TCTCAATGGGCTAATTACGTCGTTTACGGGCCAACACCTCATCAAAAAGTCAA
>Bacillus_Fam_966_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
TACATGAGTTACTTCAGATGGTCCGACTCATGTATGAAAACTNGATCNTTGA
>Bacillus_Fam_967_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GTCCCTTTGACGACTCCGATTCTCCCTGACTTCCGATTCCACACCCTCATTGA
>Bacillus_Fam_968_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
CTAAAGACCAAAACGAATGAAATTCCAGGTGTAAAAGTGTCTTTAGAGACGTT
>Bacillus_Fam_969_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
AAAGGGTGTAACGGGCCAACGAGAAAGCAGAACCAGAAGGATGCTGGCCCGC
>Bacillus_Fam_970_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
CATCAAAAGGTGTGGACGGTGAAAATGATGTATGAAAAGAGGGATGATTCCAG
>Bacillus_Fam_971_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
ACGTTTCTTCTCTAATCGTGCACCTTCACNTCAGATTCCCGCCTTCTAGGGGC
>Bacillus_Fam_972_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GTTGTTGAAGGTAAAGTTTAAAGAGCTAAACGTACCCCTTGAGTGCAGATTGA
>Bacillus_Fam_973_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GTACATCATTCGAGAGTCAACCAGGAAATGACACCCCGCGGGAGGAGCGCG
>Bacillus_Fam_974_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
CCAACATCTCGAGGAATTCTGAATCACAATGGTCCGATAACCCCTCTAAACGGA
>Bacillus_Fam_975_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GTAAACGTACCACTACAGAAGGNGAATCGGGCTTCTAATGGTACGATTAGCTT
>Bacillus_Fam_976_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
AAAAGAGAATCGACCCTGTCTGAAGAGGCGTAAAGACCAGGTCTGAATGGTTGCA
>Bacillus_Fam_977_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GGCTTCATTTGTGGATTACAGGTGCTTATGACAACACGCGCTCGAGGTGCGCGG
>Bacillus_Fam_978_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
CATCATTTCTGGGCCGCCGTGAAAAATGATGTAGGAAAAACAATCGGAATTAGGG
>Bacillus_Fam_979_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
TTGGTACATCAAATCAAGGTGGTCCACGCAATGATGTCCTAATAAAGTCAGAA
>Bacillus_Fam_980_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
TGGCCCATTTAACCATTTAATGGACCAACACCCTTTAGAGTCGCAACTCTCAT
>Bacillus_Fam_981_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GTCATTTTGTGAGAATTGGTCTGAATGACACCCNGCGCCCCGTCCGCGCGGTAG
>Bacillus_Fam_982_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
CACTGGCCCAATAATCCAATAAATGGGCCAACATGATCTGGTTTTAGCAATCT

```

```

>Bacillus_Fam_983_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
AAATGATGACATGCGCGGCGNGNGCGCGGGGTGTCATTGTGTTGGATTTGCGG
>Bacillus_Fam_984_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GTAATCGACCCAACATCTTCTCCAAAACCCAATCTCCTTGGGCTGTTTACCTC
>Bacillus_Fam_985_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
ATACCATTTATCGTTGCTCGGCTTCGTGATATTCCGTTTACGCCGTTTGCGGT
>Bacillus_Fam_986_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
ATGAAGAGGATACACCACGAATGAAAGCTACGAAATCCCCCTTCATGAGAGCTA
>Bacillus_Fam_987_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GAGGAAAAGTCAGAAGGAGAAGCTNNGNACGCGTCGGCAGGTTTCAGACTTTAGG
>Bacillus_Fam_988_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
TTGTCCGAATAANCCTTCTATTTCGGACTANAACCACTTGGTGCTTCNCNTCNC
>Bacillus_Fam_989_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
TTTGTCTCATGGAGCNTTCATGTTACATGAGTTACTCCCTTTCTTGAGGAAAG
>Bacillus_Fam_990_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
ATTAGTGACCGTTTTCTNTTGCAACTACAAAAACGGGCATCTANTACACTCG
>Bacillus_Fam_991_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
ATTATAACGTAAAGGAAACACTCGAATCGTACGCTATACGTACACCGGATGAAA
>Bacillus_Fam_992_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
CCAGAAATGGTGACCGGAAACAGAGAAAAGTGGCGTCACTAAGGCGAGTGGCG
>Bacillus_Fam_993_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
AGAGTGCTGCCACTTTTGCCGTTGAGGGATCATCGGAAGTGGCGTCAATCCAC
>Bacillus_Fam_994_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
TGACGCCACAAAGCTGTTTGCAATATAAGTGAAAGTGGCGCAACTCNCCGGAG
>Bacillus_Fam_995_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
TGCCACTTTTTGCGTGATGGGTTTGCCAATTGTGGTGTGTCATTGGCCGTAGTGG
>Bacillus_Fam_996_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
CGGGCTCCTATTTCAACGATTGGCTACCGTTTCCACTCCTTGAGAGCTACGCT
>Bacillus_Fam_997_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GTTTTGTCTCAAGACCCCCGATTGAGGACGAATCCTCTGGGGACTCTTGNTA
>Bacillus_Fam_998_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
AAGAAAGATACCCTTATGCAGCCGTTTGTGCATCACATAAGGGTACGAAAACCG
>Bacillus_Fam_999_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
TATTGGTTACCTATAATTCTAGTTTCAGCCCTTTTTAGGGCACCAATAACGCC
>Bacillus_Fam_1000_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GTACCCTTATGGAGAGCTTTCGCTTGGTATAAGGATACGATTAGGAGAAAATC

```

>Bacillus_Fam_1001_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
CTTCAGACAAAATCTGCACGCCTAAGACGTGGTTTTGGCCGAACATGGCATCA

>Bacillus_Fam_1002_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
TATCCTTATGAGGTAAAATCCAGCAACATAAGGGTACCGTTCAAGCCNAATCG

>Bacillus_Fam_1003_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
CCTAAAAAGAGGAAAATGGTGACCGTCAAAACGAAAGCAATGGTCACCAATCT

>Bacillus_Fam_1004_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GTATTGCGACACAAAGCAAGAATTTTCAGCAAGCCGAGTCCGAATANAGCNTC

>Bacillus_Fam_1005_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
CTTATGAAGACCTTTTCGACGAGCCACGAGTTCTGATTGAGTCTTCATCACG

>Bacillus_Fam_1006_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
ATGAAAGACAAAACCTCAGGAGAATGGGTGAGGGAATTGTCCTTCATCCGGTGT

>Bacillus_Fam_1007_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GATGAAGCCCAAANCCCACTAAGCCCACNCAAGGATATGTNCTTCATAGGCNC

>Bacillus_Fam_1008_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GTCAATGAAAGCCTCTTCCATTTACCATGGAGGCCCNATTATTTCTCTTTTCG

>Bacillus_Fam_1009_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
TATTGGAGCCCATTCTGTTTGAAAACCTTGGGCAAAAGGTATCCAATCGATCCG

>Bacillus_Fam_1010_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
TTTTTACCGCCTGACCCCTTCTCAGCACTCCGCGGGCAATAGAACCATCTTC

>Bacillus_Fam_1011_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
TATTGCCCGATTGNGGTGTCCAAGGGGTGCAAACGGTAAAAAGAACAGGCTTC

>Bacillus_Fam_1012_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
TGTCCATCATCCGTTAGATGAAGGCCATTTTTAGCAGGCAAATCATGGAGTAA

>Bacillus_Fam_1013_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
TTCTGTCCCGAATCCGTTTCATACGGGACACTAGGGCATAAAAAGTGCAGACGC

>Bacillus_Fam_1014_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GTCCTCATCCCTACCATGATAACAATTCCGAACCCTACTTTCTCTCCAAACAT

>Bacillus_Fam_1015_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
TTGCGGGTTCGCACTTGGAACCTTTCTAGGAGATACCGAACCCGATTCCACCAC

>Bacillus_Fam_1016_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
AGAAAATAGGTAACAGCGAACCAGTAAAACCATTATAGTGGTATGCAAATGGA

>Bacillus_Fam_1017_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TAATCGTGTTAGATACTGTGACCATTGTGGGGAGTAACTGACATGAAAAGGGC

>Bacillus_Fam_1018_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TAGCAACATATCGAGTGAAAAGGGCAGAGTTGTTGTAGGAAAAGTCGGGAAG

>Bacillus_Fam_1019_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GCTTTTGTCCATTTAGAACAGCTAACGGGACAATTCCACCGGAGCTGCCAGC
 >Bacillus_Fam_1020_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TGAAGGACATTTTAGGGTTGTGGCGNCTTTGTTTTGTCCTTCATNGGGCGGA
 >Bacillus_Fam_1021_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 AAAAGCCAAAAGGCACCTGGNNANCGTCCAAACTGTCCTTTAGAACGTCTCA
 >Bacillus_Fam_1022_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GCTCTTCTTCTTCTCCTGCTGCCTTTGAGACACGCGCTACCCCTAGCGCGGC
 >Bacillus_Fam_1023_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GGCGCGGTGCAGAAAGTAGGTTTGGGCAGGGGTGAGAGCACCGCGCGGGGGT
 >Bacillus_Fam_1024_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TTTTGGGCACCGCGCGGACGCGGCGGCGCTCTTCTCACGCTGCAACTCAC
 >Bacillus_Fam_1025_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GAGATGTCTTCATCCATGCGATGAGGACCTGTCTACGCACAAATAGGAACGA
 >Bacillus_Fam_1026_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 AGGTCTTCATACACCTTATGAAGACACTTCCAAGCCTGAAATCCTTCCACTA
 >Bacillus_Fam_1027_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GACATCTCTCCACCGGAAATCTTCTCTCACATGTCTTCATTCCGCTTATGAG
 >Bacillus_Fam_1028_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GATGAAGACATTCCCATGATGATTTTCCTTTTCCAAAGTGTCTTCATCATGCG
 >Bacillus_Fam_1029_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 CAACATTGTCTCGTAGGTAGCGTACGACTCCCTGAGAAGGTGAAAACCCGC
 >Bacillus_Fam_1030_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 AACGAGGACAATGTTGACGTGATTTTCGGGGTTACCGGGTTTCATAGGAGTTC
 >Bacillus_Fam_1031_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TGTTTTGGTAAGATAGAGGGGTTCTATACGCCCCGAAGCAGCATGGTAAAAGGC
 >Bacillus_Fam_1032_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GCTTCTATACTACCGAAGACCTCGGGATTCTACCGTTCGGGCGTATAGAAC
 >Bacillus_Fam_1033_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 AGGTAGTCATACGCTTTGAACGAGGACAATGTTTTTACACTTTTCAGTGGGGA
 >Bacillus_Fam_1034_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 CTATACGACCGAAGCTACTTATCAAGCTCCCCCTTCCGTCTTATAGAACCCCT
 >Bacillus_Fam_1035_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GACCGAAGCAACCCCTATTACCTCGAAACGTCGTATAGAACGCTTCTATAC
 >Bacillus_Fam_1036_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 CCCGTTAGAGCAGGATTCAATAACTAAGTGTCGATTAAACAGGGTTTAAAT

```

>Bacillus_Fam_1037_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GTGTCATAGCACTCGTATGACGCATCTTATATTGAATCTCTAGCTATGTNGT
>Bacillus_Fam_1038_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TAGTCTGAGTGGATATAAAACACGAAATAAAATCTCGTTGTGATGGTGAGTC
>Bacillus_Fam_1039_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CCCGTTAGAATGATTATCCCGTGCTGAAGGTAGATAAAACAGCGTTTAAAAG
>Bacillus_Fam_1040_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGCGAGTGGACTTTAAAGTGCCTATAAAATCCCATGAGGTAGAGGGAGCATG
>Bacillus_Fam_1041_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTTTCCGTTTCAGTGGATCCTCTCTTCCTTGAACGGAATTCTTTGTCATTTTC
>Bacillus_Fam_1042_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTGCTTTCCTTTCTAAGGCACTCAGCTTCCTGGAAGGAATACTAAGCCACT
>Bacillus_Fam_1043_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AATGGGTGCTATTTTGTTCGTCGCTTTTGCCTGCGTTGTTTTCTGCTCG
>Bacillus_Fam_1044_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AAGGAATGGGCGCTATTCTTATTTGCTGGCCTTTACCTCTGATTTTGTGA
>Bacillus_Fam_1045_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CTTTCCTCGGATAGTTTTCTTTTCAGAGACTTTTCTCTTTGAACGGAACG
>Bacillus_Fam_1046_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTCCTTCTACTAGTAAATCAGCCATGAAAGGAATACTAAACGCCTTCACT
>Bacillus_Fam_1047_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TAAAGGAATACTAAGCACTCTGGCTTTCCTTCTACGTCGATTCCCTCGTCC
>Bacillus_Fam_1048_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GTTGTCGATTAGGATTATGAAAAATCGATGGTGCCAAAAGGTGCGAATGGG
>Bacillus_Fam_1049_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CCCCGTCAAAGAGAGGGTATGAGGGTGTGCAATTGAATTTTGGTTGAATCGG
>Bacillus_Fam_1050_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GAAACGTACCAATATAGAGTCAGAATCCTGCTGTAGTGGTAAGATTGAGAA
>Bacillus_Fam_1051_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AGGAATGATGTAGGAATGCAGGGGTAATTAGAGCATCAAATCGGAGAAGTGA
>Bacillus_Fam_1052_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GGGTGCTCATGAACGCTTCATGGGGCCATTTGCCTGCATATTTGAAGTTA
>Bacillus_Fam_1053_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GGTGGTCAATCCCAAAAAAAGAGAATCGGCCCCGTCAAAGTGCTGCTTCGA
>Bacillus_Fam_1054_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GGTGGAATTTAGTTTGGAGAAATCGGCATGGTCAAAGCGGGCGAAAGACAG

```

```

>Bacillus_Fam_1055_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CTCAACCAGAGTCCGAAGTTGTACTAGGTTCGGACTCAAATTCAGGATGAG
>Bacillus_Fam_1056_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATGAAGCCGAAAAGTCGTGNAGCGATAAGAAAACGGTCGCCATGAGGCAGTC
>Bacillus_Fam_1057_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GACGAAAATTCAGTGGCTCACCAANAAATGGTCGACATAGAGCCTTCATGAA
>Bacillus_Fam_1058_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TCACAGACAATTCATTCAACTTTTTACTNCGNTTGTCTTCGAGACTGGCTA
>Bacillus_Fam_1059_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TATGAAGGACTTTCTCACC GCCAGGCTGCTCGTTTCGAGGCTTCATCGGCCT
>Bacillus_Fam_1060_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TCAGTTTCTCAGACCNAATCCCCTTCATAGACCACTTGAAGAGGATACACCT
>Bacillus_Fam_1061_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CCTCGGCATACTCCGGTTTGTCTTGTCTCCGAGAGCAGCTATCAAACACTTT
>Bacillus_Fam_1062_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTCATTGCCTCGATGAAGAGCATAACGCAACAGAACTATGCTCGAATTCCTC
>Bacillus_Fam_1063_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTGGACATTCTGACTACCTCCACTTTCTCCTTTGTCTTTAAACTTGGGATA
>Bacillus_Fam_1064_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TACATGTTTTGGCTGGTTGCTGACCATTATTTGGGTGCCATACTCATTTGGG
>Bacillus_Fam_1065_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TAATTCGTAATGTAATTTCCCACTATGNACTAATTACGGTGCGTATAACCCC
>Bacillus_Fam_1066_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GTTTCGGACAGGAGAAGAGGAAAAACCGTGATTGAGTCCGAAGTCGCCCTAT
>Bacillus_Fam_1067_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTCGGACAGACTCTGGACTTTTTCTGCCTTGCCTGTCCGAACCTTGCCCCAGG
>Bacillus_Fam_1068_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTTATCCTCACCAAACCGAGCCTAGATGAGGTTTGATAGTAAATAACTCGTG
>Bacillus_Fam_1069_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTTGGTGAGGATAAAAGCAGGTTATCTACTACCAAAGTAAGTAGAGTGGAA
>Bacillus_Fam_1070_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AAAATCTAGCGGACTGTCCTTAATAGGCGCTGTTGAGGACAAAACGGGGTTG
>Bacillus_Fam_1071_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TCTGTCCGAATGCACCTCTTATTCGGACTCCTTCACCTCTCTACTACCTTT
>Bacillus_Fam_1072_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATTCGGACAAGCCTATGGCTTCTTGCTTCCTACTTGTCCGAATATCCTTCCG

```

>Bacillus_Fam_1073_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGTCCGAACTAGGCTTAAGTTCCGACAGAAATGACCGCTTTTTCTCAAATGG

>Bacillus_Fam_1074_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATTGCGTTGCTCTCGATCAAGAAATGGACTTCATAGCCGAGGTAACGATCGT

>Bacillus_Fam_1075_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CGTTCATAAGGCGGATGAAAGCCATTGTAAAGAGAAAAACAGGTGAGAAGG

>Bacillus_Fam_1076_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AATGGCGTTCATCAGCCGTATGAACGCTATCTCTACCGGGGTTGATCCTTGA

>Bacillus_Fam_1077_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CGGGCTTTCATATCCCCAATGAACGACCGTTTCCCCGGGCACTTGCCCTGATT

>Bacillus_Fam_1078_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCGAAATGAAGTTCATCAGGCCTATGAAAGCAATCGCGGCCGAAATTTTAGA

>Bacillus_Fam_1079_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GGGCTTTCATTCGACCGATGATCGACCGCGCGGATGGTTTTTCTCTCGCGT

>Bacillus_Fam_1080_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATGAACGCGATCACGAATGAAAAAGGGGGTTACGATGGTGTTCATAAGNCCG

>Bacillus_Fam_1081_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATAGCGTTCATCCCGGGTATGAAGTTCATCTTGANTATCTTTTTTACTTGNA

>Bacillus_Fam_1082_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCTTATGAAGTGCATTTGGCATGGATTTTTTTACCGAGATAGCGTTCATTCC

>Bacillus_Fam_1083_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CGGGCACTTTTAGCCTCTATTAGTGACCGGTTCTCTCGACAACTCTATTTG

>Bacillus_Fam_1084_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AATCGGTAACTAATAGGCAGGAAAGATGCCCGAATCCGNTGTGTGTCGCCGC

>Bacillus_Fam_1085_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CGTATATCCCAAAAAGCGGTCACCAATCGTATGGATTAGTGCCCGTTCTGAG

>Bacillus_Fam_1086_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AAAAGCGGTCACGATTAGTGAGGAAAGATGCCCGTTTTAGTCGGTTTTTCAGT

>Bacillus_Fam_1087_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TATTTGTGACCGGATTTTCGTATTTCTCCCTTCAAACGGGCATCTTCCACTAC

>Bacillus_Fam_1088_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TCACTAAAAAGTGCTAAAAGTGCCCGTAATGTGGTGAATCACGAAAATCCGG

>Bacillus_Fam_1089_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ACCGCTTTTACCAAAATCTCTCGTAACGGGCACCTTTCTCCAACATTAGTG

>Bacillus_Fam_1090_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ACCAATAAAGGTTAATAGTGCCCGAAAAGGAGAAAAAAGTGCTCTAATGGTC

>Bacillus_Fam_1091_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GATTAGTGACCGNTTTTTCGGATTAACGCAACTTTTCGGGCATCTTTTACTCC
 >Bacillus_Fam_1092_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GTTCATCTTGTTTATGAACGATAGTTTTGCCCCTCTTCTTTTGAAAAAGTGGC
 >Bacillus_Fam_1093_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TGGCTTTCATTCCCTTGATGAACGCCACTTTCCTCCAAGATTACCTTAAAAC
 >Bacillus_Fam_1094_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TGTCCGAAGTGGGTCTGTGTTTCGGACAACCTTCCGGATGAATCCAAGCCAACCT
 >Bacillus_Fam_1095_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TCTCTGAACCATTTNCCAGCGGAGCAGCCTCNGTTTTGGTCTTGAGACGCCT
 >Bacillus_Fam_1096_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TCTCATGACCAAAACTTCTGCCGCTTCCCCTCTTTATGGTTCTGAGACGCAC
 >Bacillus_Fam_1097_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 CCTCTCAAGACCAAAATTCCTTTAAGCAAGCGGAGAAGTGGTTCAGAGAGGG
 >Bacillus_Fam_1098_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GGATGACGAAGATAGGTCAATGAGAAGGGTTCTAATGGACACTACGCTGAAN
 >Bacillus_Fam_1099_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TCAGGACCAAAAACAAAGACAGAGCTGGTGAAAGTGGTTCAGAGGGGGCGTC
 >Bacillus_Fam_1100_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GGGTCTTAGTTTCTCTGACTAGCACCTCTGGTTTGGTTTTGTGATTCAGA
 >Bacillus_Fam_1101_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 CGATAAGCTACCCAACTGGTTCTTTCTTGATGGATTCGGTCGCTTATAANCC
 >Bacillus_Fam_1102_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GGGCACTCTGGCTACTCCACAGTGCCCGGTTGATGCTTTTTTCTCCTCACAT
 >Bacillus_Fam_1103_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 CGGTCATTAAGCGGGGCTCTAAATGCCCGCGGAGAGCGAAAAAGGAAGGGAG
 >Bacillus_Fam_1104_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TCTTAGTTACCGCGAGACCCGCATTTTCTCCTTCGCGGGCATTTAGAGCCCT
 >Bacillus_Fam_1105_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TTATAGCCTTTATAAATGACCGACCGACCGGAAAAANCGCCAGCTCGGGCAT
 >Bacillus_Fam_1106_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 AACCAAGTAAGTGTTCTATACCGTCAATAGCAACACTTTCCTCATCAATTG
 >Bacillus_Fam_1107_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TCGTTTAAGAGCACTTTGGTCTTGCTGTGAATCGGAGTTCTTGTTGCAAACA
 >Bacillus_Fam_1108_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TATTACGCCGCAACCAATTTATAGGGTTGCATTTGCCAGTATGGTACCCTC

>Bacillus_Fam_1109_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TAGAACACTTTCTGCGGTCGGGATNCCNACTTAATGTTGCTTACTCCGGTT

>Bacillus_Fam_1110_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CAAAATGTTGCTAAAGCCAGGTTAGAACACTTTCNGGGCTTCTGGCCTCTG

>Bacillus_Fam_1111_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CTGAAGGGCACATTCTGCCTGGTTTTTCGACCTTCAGCTTACTTCCTTTTCC

>Bacillus_Fam_1112_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ACCTTCACACAATCCCACTCCTGATAAACGGTCATATCTTATCCACTTATA

>Bacillus_Fam_1113_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ACCTTCAGCTTCTTCTCCACCACTGAAGGGCACGATCCATCCGCTTTTGTG

>Bacillus_Fam_1114_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TAAGTGCCTTATCTCGGTTTTAGAACACTTTCACAGATANTGCNCTTTGGC

>Bacillus_Fam_1115_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCTGCGGCGAAAGGCATGAAGGGTCATAAGAGGCTTGATTGTTACCTTCA

>Bacillus_Fam_1116_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTTCTCCAGGCTCACGCTCCACTTTGTGCTCTTAACCCCGCGGAAGCGCAC

>Bacillus_Fam_1117_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GAAATATAGGGCAGCAAAACATGAAAATGCAACCCTATAAAATGCGCCATCT

>Bacillus_Fam_1118_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CTGTATTTTGGACAAGCNGATTTATAGGGCAGCATTTACCTTTTTTGGTGCC

>Bacillus_Fam_1119_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CATAAGTGCTGCAAAGCTGGTTTAAACAACATAAACTCAGCTGCAGGAAGCCG

>Bacillus_Fam_1120_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTCTTATCGGACGAATNGGTGCCATCAAANCTGATTCTTCTCTGCTTGAGGG

>Bacillus_Fam_1121_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GAACCCTCAAGCTTTGGATTCTGTGGATTGATGGCACTTATAGCAGAGTTTA

>Bacillus_Fam_1122_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AAGTGTCTTATCTTGCTTTTACAGCACTTATCTTCGCTCCGGAGTCACTCA

>Bacillus_Fam_1123_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AGCGGGTAAAATAAAGCGCCGTTTTTTACCGGTGATAGCCTTTTTTCGCTCC

>Bacillus_Fam_1124_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CGCTTATACCTTTTATTGGTGACCGAACCAGTGTCAAACCCATGGTTCCGGG

>Bacillus_Fam_1125_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTATTGGCGACCGCTCACTACTGGAGNTCCTTCGCTCGGGCGCTTATCTCCC

>Bacillus_Fam_1126_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GACCTTTTCAACCTTTTTCACCACAATTTCGGGCGTCTACAACTCTTCTAGAG

>Bacillus_Fam_1127_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 AGGGTTCTCAAGGACAAAGTGCACGCAAAAACCGGTGAAACTGTCCTAGACA
 >Bacillus_Fam_1128_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TCTTAAGGACAAATCTTCTAGTTCTCTTTAGAGATTTGTCCTTCATACCCCT
 >Bacillus_Fam_1129_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GTAACGATTAGTCGCTAATCGTGCCCTTCTCCTCGATTTTTTGGAGTTTGCG
 >Bacillus_Fam_1130_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TATGAGTGACCGCTTGTCTTTTTCCAGGAGGTTCTTGGGCTCTCATGAACCT
 >Bacillus_Fam_1131_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TGTGACCAAACTCATGGATGAACTATCAAAATGGTCACAAGAAGGGTCGC
 >Bacillus_Fam_1132_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 CTTGCTCTTTTTCGGTAGGCAATACATCTTGTGTCTACTCTTATTGCGGCT
 >Bacillus_Fam_1133_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 CTACCCAAATACGGGGACCTCTCAAGTTCGGGCGCCATCACATCCCTTTGA
 >Bacillus_Fam_1134_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 CTCCTTTTCGGTAGCCATTCCACCCCTTTGACTCCCTTCCTCACNCCTCCTCA
 >Bacillus_Fam_1135_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TTCGCTTCTCTTCGGGAGTCAACACCCTCCTTTAGCTACCGTTCTCTTTGTC
 >Bacillus_Fam_1136_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 ACATTTCGGGCTCCAGATCCCTCTTCTGCTTCCCTACTTTTCCCATTCCCACC
 >Bacillus_Fam_1137_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 ACGGGAGCCATTCCCTTCCTTTGACTACCCAAATCCNGTTCGGTCCTTCTGC
 >Bacillus_Fam_1138_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TCGTTGACTACCCAAATTTGTGATNGACTCAGAGTTCGAGTGCCANTGNGCT
 >Bacillus_Fam_1139_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 AGTCAATACACCTTATTGGCTACCGTCCACTCCTCCTCCCTCGCTTTTCGGG
 >Bacillus_Fam_1140_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TTTCGGTAGTCAACCCTTCTCTTTGTCTACCAAAATCCTCGCCCTCTCCCTT
 >Bacillus_Fam_1141_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TAGACATTTTGTAGTCAATTGGCATTGCGAAATGTACATTAAACAAGGTTTTT
 >Bacillus_Fam_1142_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TCATTTGGGTAAAGAGGAAAGCCCCTGCATTGCCCCGAAAAAGCGCCAACTCCA
 >Bacillus_Fam_1143_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GATGACGGACACTTTCCAGCGTTTTTGGGCTATTTCTGTCCGTCATAGGCTG
 >Bacillus_Fam_1144_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 AAAAAAGGTAAAAGGAAAGGCTCTGCATTACCCGAAAAATGCTGGAGAGAAGT

>Bacillus_Fam_1145_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGTCCATTAAATGCACTTTCTTAGACATTTTCGGTTTGGAACTCATGCTGAAA

>Bacillus_Fam_1146_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTTTGTCCGAACCTGCCCCCTACTTCAGACAATTTCCGCTTGTACGGCCGAGA

>Bacillus_Fam_1147_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTAATAGACATTTTTCAGTCCGTTACTCTTCGAAATGTCTAAGAAGTGCTGT

>Bacillus_Fam_1148_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AAACAGGTCACCAATACCCNTGATTGGTGACCTAAAAATCCATATTTCCGNA

>Bacillus_Fam_1149_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GTTCCGACATTTCAACGGCCTCTTCATTGAGTTTTGTCCGAAGTAGGATCAA

>Bacillus_Fam_1150_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GAAAAGCTGTCAAGATTATCCCGAATTATGACAGGCTCAAGCCCATAAAGC

>Bacillus_Fam_1151_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GTTCCGACAAATCATCGGGAGTGACGGTACTTTTTGTCCGAAGGTGACCCAT

>Bacillus_Fam_1152_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TCCCTCATCCGGGCACATATTTCCCTTTATGTGCCCCGTCTCCCTTCATCT

>Bacillus_Fam_1153_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TATGAAGGACATTTTGGGGGCGNGGGATTCTCCTTTTGTCTTTCATCCCTGT

>Bacillus_Fam_1154_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTATTTTGACAACTTTCAGGTGAAAAGGGCAAAAGTTGTCAAGAAAGAGAGG

>Bacillus_Fam_1155_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGATAGGCGCCCGTGGCGGTTGAAAATAGGAGTTGGCGGTCGCCAATAGGGT

>Bacillus_Fam_1156_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GGGCACTGAGAACACCTGTGAGCACCCAAAATCCCTGGCCCCCTCTAAAAAT

>Bacillus_Fam_1157_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGTCAGTGCCCCAAAAGTGGAGCAGNTCGTNAAAAAGGTTACTGAGGGTCGN

>Bacillus_Fam_1158_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CCTCTTTTTTCGGTAAACTCTCGGAAAAAGGTACCTGACAGGCTGCCTCAGTA

>Bacillus_Fam_1159_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTGGTCGTCCATACACCCGATGGAGGCCCGTTTTTCAGAATCAGCTTCAGTA

>Bacillus_Fam_1160_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GGGCTTCCATCCACTTGATGGAGGACCTTTTTTGCGGCTTTCCTGCGAAAAC

>Bacillus_Fam_1161_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTTTTTGGTGGTTTGCATGAATTTGGGTACTGAGGAGGAGTNTCAGAGCCC

>Bacillus_Fam_1162_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GTCCTTCATCCAGGGTCTGAAGGACATAACAACACTAGTGATCACGTGAATT

>Bacillus_Fam_1163_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TAGTCCGAAGGCAGGTCAAGTTCGGACAGAAAGCAGACATCAAAGCGCAAAC
 >Bacillus_Fam_1164_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TTCGGCCAAATCAGGAGCGNCGAGCCGTTGAAATGTCCGAAGTTGGTGTAGG
 >Bacillus_Fam_1165_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 CATTTTTCAGGGCTATGGTCTATGACAGACGTTATCATGACCCGTTGGCTG
 >Bacillus_Fam_1166_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 CTCTCATGGACCTTTCGCATGTAAAAGTCGCTGCAATGGGACACGACAACGA
 >Bacillus_Fam_1167_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GAATCGTTACCGTCATGCGANGCTTTCAAGNCTAACGGGCACGATTCACTTC
 >Bacillus_Fam_1168_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 CCTCTCATGTCCCGTATCATTGAAAAAAGGATGTGCTTGGGACATGAGACCA
 >Bacillus_Fam_1169_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 CTATTCGCCCGAGGAGGAAGAAAAGTGTATCTAGGGGTAGAATAGGACGTCT
 >Bacillus_Fam_1170_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GGTCGAATAGGGCGTCTCTATTTCGCCCGAAGCGCCAGGTTCGAGTCGTTCAAA
 >Bacillus_Fam_1171_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 CCTTGAATGGGACGTGATGAGTGTTATCAAAGCCCGATCGCCANCTTTTTTN
 >Bacillus_Fam_1172_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 ACGGTAACGATTGAGGCCGAATCGTTCCCGCACCGTGCTATTTTTGGGAGTT
 >Bacillus_Fam_1173_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 CGATTGAGTTCAGTTTATCCAAAATTACCCGCTAACGGGAACCAATGAGCT
 >Bacillus_Fam_1174_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TTCGGACAAGCCCAGGTGATTTTGAGCAATCNTAGTCCGAATAGCCGTCGAG
 >Bacillus_Fam_1175_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GTCGCCAATAAGGTGTATTGGTACCCGAACTCTACTATATTTAATAAAACG
 >Bacillus_Fam_1176_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GACAACCACACTCAAATTCGGCTGAAGAAGTCCGAAGTGGTAGTGGGTTC
 >Bacillus_Fam_1177_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 AGGGAACCAATGACTCCTATTGATACCTCAAACAACGCTAATTTGCCAAATA
 >Bacillus_Fam_1178_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GGAAACAAGCAGCCCTATTGAGTACACTATTCCTCGAATTCTTTAAAAATG
 >Bacillus_Fam_1179_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TGTCTGAACCTTGAAGTGGTTCGGACTCGATTACCTTAAAAATCGCCATTGC
 >Bacillus_Fam_1180_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 CTTTTTCTCCAGTGTTTCGGTCAACAATAACGGCGATTGGATACCCTTCTGT

```

>Bacillus_Fam_1181_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TACTTCAGACTTCTTTTNCGCAATCAAGGGCTAACCTGTCCGAACCTGAGGC
>Bacillus_Fam_1182_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GGCTATTGATAACCTTTTTTGCTTTTTTTACAGGAAAACTGAACTCAATAGA
>Bacillus_Fam_1183_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TCTTGTTTCAGACTCGATCTCTTATTTTACCAAACCTGTCCGAACCTTGAC
>Bacillus_Fam_1184_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CCTAACCTGTCCGAACCTCATCCCAAGTTCGGACTTCTTTGCTCTTGAATCCT
>Bacillus_Fam_1185_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AGAAAAAGCGAACTCAACAAGCGTTATTGGTTCCCCGAAAACTAGCAGAAAGGC
>Bacillus_Fam_1186_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AGATGTCCTTCATCAATGAAATGAAGGCCAAGNTATAGGGTTTCTACTGTC
>Bacillus_Fam_1187_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGAATTGTTCCCGTTCATCAACACCATCCACGATTGCGGTCACGATACNTCG
>Bacillus_Fam_1188_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AGAGGAAGTATTGTGCCCGGAAAGGGAAAGCTCGAGAAGAAACGGGAACAAA
>Bacillus_Fam_1189_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GTATTGTTCCCATAACTCTGCGAAAGACAGAAACGGTAACGATTAGTTGA
>Bacillus_Fam_1190_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GGGAACAATAGAAAGTAGAATCGTGCCCGAAATCAGGAGAGAGCAGTGNCCCC
>Bacillus_Fam_1191_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ACAACGGTAACGATCAGAGGTGGAATGTGCCCCGTAGCGGAGGAAATCTCGGG
>Bacillus_Fam_1192_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGTCCCTTCATGAAGGTAATGAAGTCCAAACTAGGTGTACCAAAATCGAAAAG
>Bacillus_Fam_1193_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AGCGATGAAGGCCAAAATGTGCTCGGTAACAAGAGCAGATGACCTTCATAAA
>Bacillus_Fam_1194_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATCGTGCCCAATACCGAGGCNGACATGGAATAACGGGAACAATACCAGGAGA
>Bacillus_Fam_1195_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGAAGGACACTTCCCTTGTTTTCTATCACTATCTTGTCCCTCATAACCCCGA
>Bacillus_Fam_1196_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CTTTGGTCTTTATAACCCGCTTAAAGGACAATTCCTTTAAAAATTTGATTC
>Bacillus_Fam_1197_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGTCCCTTCATATGCTCCATGAAGGACATGTCCATGGGTATTTTCGGTTGTCT
>Bacillus_Fam_1198_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATTAGAGTAAAAGGTCTTCATCGATGTTATGAAGACCAAAACCGGGTTCAGAG

```

>Bacillus_Fam_1199_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGATTGCGACACGGATTTCGGNAAAATTCAAAGATGAGTCCGAATAAGAGTG

>Bacillus_Fam_1200_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CTTGTGTTGTCCGAATCAAGGCGTCATTTCGGACAGCTACGCCAGATTTTCCTG

>Bacillus_Fam_1201_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATGATTTCGGACACAGATCAGGAAAAACCGCACCCCTCGAGTCCGAATGAAGCG

>Bacillus_Fam_1202_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AGTCCGAATGCAAGGCTGATTTCGGACAGTTGGGTTCAGGGGAATNCAGAAGCG

>Bacillus_Fam_1203_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CTGTCCAGAAATCAACCCTTCATTTCGGACTCAACTACTCGTATTCCTTACTTCT

>Bacillus_Fam_1204_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AGGTCTTCATGAGGTTGATGAAGACCTATTTGCAACTAGTATTCTCTCGGAA

>Bacillus_Fam_1205_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GAATCGTACCCGATTTCGGGGCAATTGCAAGGAAAAGGGTAACGCAAACGTGG

>Bacillus_Fam_1206_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CTGTCCGAATGAGGCATGAATTCGGACTCATAAACGTTTTTTTGGGACCTACA

>Bacillus_Fam_1207_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGGTCTTCATCACCTCAATGATAACCGTTTTCCGCGATTTCAGCGAACGAGTTT

>Bacillus_Fam_1208_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGTCCGAATCATAGGCTCATTTCGGACTTAAGGCAACAGAATCCTTTGCGACG

>Bacillus_Fam_1209_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GAATCGTTCCCGATTGCAAATAAAAATCATAAAAAGAGTAACGCAAGCCCTC

>Bacillus_Fam_1210_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTACCGGGGACTCTTGATTTCCTCCTTCACGGTAAGCATACTCCCTCTTTGN

>Bacillus_Fam_1211_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ACCGAAAAGAGGCCCAAGTCCCGCTCCAGGTAACCAAAACCCAGTAAAGGTA

>Bacillus_Fam_1212_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATGGTACCGGAAAAGAGAGAAGCTGTACGATGGCAACGCGAATCTCGTAGCC

>Bacillus_Fam_1213_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGCTCTATCGGTTTCGTTTTGNCTCTTGAGTACCATTTGGCGTTNGTGCTCC

>Bacillus_Fam_1214_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GATCTTCCCGCATACCGGGATTTCGGGTACTTCATGCAATGCTAGCTGCCGC

>Bacillus_Fam_1215_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CAAAAATGTAAAAGGAANGCCGGCTTGTATATAGATTTTCGGTGTAGAAGGT

>Bacillus_Fam_1216_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCACAGCAATGGTACCGCTTCTCCTTTAACCGGTTCCATAGCAGTACGCCCCG

```

>Bacillus_Fam_1217_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CAAGTGGACGAATCCGCCGGATGCGGGAAGATAAGGATGGATGAACCCTGCT
>Bacillus_Fam_1218_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CCAACTTGGTCGCCAAAGCCCCGGAATGAAGCCCCAAGAACGAAGCAANNAGT
>Bacillus_Fam_1219_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGCCCCGAAAGAGCCGTATGCGGGAATTTGAACAAGACCCATCAATCCCGAAG
>Bacillus_Fam_1220_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CAAAATTAAAACAAGAAGTGCTTCATACAGCGTTTATGAGGTACATGGTTTT
>Bacillus_Fam_1221_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TACATTTTACAAGCATCTATTCAAAAATGTAAAAGCAAAGCAAGGATACCTA
>Bacillus_Fam_1222_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GTCCGATGGAGAAGGAAAGCGTGAGGCTATGAGGCTGGAAAGAAGAGAAGCG
>Bacillus_Fam_1223_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCTCCCTTTTGACNCNTTTTCGAGTTCAGCGCTNTTTTCNGGTGAATAGGTG
>Bacillus_Fam_1224_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TCTTTCTTACCGTAACCACCTCTCAAACCTAGTCTTCGGTTCGTTTAAGAGCCC
>Bacillus_Fam_1225_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTCCAATCAAGGGNATTGGTGCATGAACCCGAAAAAAACCGNGTAGTTCAAG
>Bacillus_Fam_1226_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCCACTTTTTTCGCTTCTCCCTTCCATTTTGGCTTTCATCTTGGAATGAAC
>Bacillus_Fam_1227_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATAAGTGGTTTTTCATTCAACAAATGAACGCCACTTTTTATGGAAAAGATGGC
>Bacillus_Fam_1228_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GTTTCATCAGTTGGATGAAAGCCGAAATCCCGTGAGCAAGAGGAAAAGAGGC
>Bacillus_Fam_1229_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTTAGTGCCCGCGTATACCAGAAATTAGTAGAATGAGGTCACTAAAAGTTAA
>Bacillus_Fam_1230_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TCCAGATATTAGGAAAACCAGGGCACTATATTTCAGATTTAACACCCTTAAAA
>Bacillus_Fam_1231_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AGTCCGAATGACGGTCTGATTAGGACAGCAACAGCAGCTCAAACCTAATTCAC
>Bacillus_Fam_1232_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GAAGTTCATCTGGCTCATGAACGTCATTACAAAGAGAAAAGACTGAGCAAAT
>Bacillus_Fam_1233_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TCTCTTACCATCCATCATGATTTTCCGCCCCTTTGGGCACTGAGACGCCTTC
>Bacillus_Fam_1234_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATCTTTCCCTTCCTTTTTTCAGCCAAACGTGGAAGTAGAACCCTCTACTTCA

```

```

>Bacillus_Fam_1235_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GAAAGGGAGAAACGGTCGATAAGAGCGGTTCATAACGACCATTTGGGTGAG
>Bacillus_Fam_1236_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CTCATGAGGACAGGAATCATGTTTAATTCACATTTTTTGTCTCATGAAAGG
>Bacillus_Fam_1237_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATCGACCGTAATTGACTTTTCAGCTTGGCTATCGGGCTTTATAAACCTTTCTT
>Bacillus_Fam_1238_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATGAAGGACTAATCCCTATTAGAAAGACAGCGTTTTGTCTTCATCAAGCAT
>Bacillus_Fam_1239_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GGTTTCCAATCAGCCCTATTGGAACAAGTTAAGGCNAAAAAGTCGGTCAAAA
>Bacillus_Fam_1240_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTTTGTCTCATGAAGCACTCATGCGGACAGTTTCGCCTTGGGAACCCCGGG
>Bacillus_Fam_1241_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TCATAGTGCCCGAAACCTGAAAAAACAGCCACTCGGGCACTGAGAGCAGT
>Bacillus_Fam_1242_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CTATTGGACAGTTGGGGTTGTATCTTCGTCGATATTGTCTATAGACCGCTT
>Bacillus_Fam_1243_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GGATAACGGGCTCCAATGAGGGTTATTGGCGACCGAAACGCTCTCGAATTCC
>Bacillus_Fam_1244_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GGTCACAGAGAGCGATCCTCAGTGCCCGAAGAGAGGCAAAAAGCTGTCTAGC
>Bacillus_Fam_1245_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGTCCCTTAGATCCTCTCTCTCGGACACTCCTTCTCCTTTTTCTCAATATT
>Bacillus_Fam_1246_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGTCCCTTAGACGACTTCTCTCGGACACTTCCAACCCCTTCTCCCGCGAGAC
>Bacillus_Fam_1247_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CTATTGGACAGATCCTCTCCTCTTTTGGCTCGGACTGTCTTTAGCGCCCTC
>Bacillus_Fam_1248_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TATCGAAGACAAATTCCACCGCTTCCACCCTCGTTTTGTCTCAAGACGCCT
>Bacillus_Fam_1249_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GGGCACGTAGACGCNTTCTACGTTACCTTGAGGCGGGATATTACGCTGGAT
>Bacillus_Fam_1250_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GGGCACGTAGANCACGTCTACGTGACCGAACCGTCAGTTTTTTCAGCTGNTTG
>Bacillus_Fam_1251_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CGGGCACGTAGAACACTTCTATGTGACCTTACACTGCTTTTTTCATGCCCGTT
>Bacillus_Fam_1252_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TATTGAAGACAAAATGAGATCACTCCCTTTTAAATTTGTCCCAATACCCTC

```

```

>Bacillus_Fam_1253_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AAGTGTCTCCAATAAGCTTCATTGGAGACAAAACCCNCTCTTTTTTTCACGAG
>Bacillus_Fam_1254_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AAAGTCACGTAGAAACCCTCTACGTGACCGTACCTCCCTTTTTTNCCTGCTCT
>Bacillus_Fam_1255_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CGGATTTTCCCTTTTCAGACATCACTTAGACGGNCTCTACTTAGTGTCTAAAC
>Bacillus_Fam_1256_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATGAGAACTGAAACCANGAAAAGCGCGGNGTCTTGTCTCATGAAGCGTTC
>Bacillus_Fam_1257_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GACCGAGCAGCTGGAAAAATAGGAAGAAGAGTCGCGTAGAGAGGTTCTANGC
>Bacillus_Fam_1258_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TAAGAAAGGCTCTCAAGGACAAAACGCTAGTAAAAATTAATAGAANTGTCTT
>Bacillus_Fam_1259_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TCCATTGCCCAAACCGGCTAAATCATCAAATTATGGTCAATGCAGCCCCAT
>Bacillus_Fam_1260_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGTCTGAATGATTATTTTGCAGCCAGAGATCAGTTAGAATCCGTCTAGTTGC
>Bacillus_Fam_1261_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATGAACCTTTTCATAGAGCGCGTCGGAGTAAAAAATCGAGCTCCCGCGTACT
>Bacillus_Fam_1262_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GTTTCATAGAGCGCGAACNTGAGGGGAAATTCCAAAAACGCGCACTATAAAGA
>Bacillus_Fam_1263_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTTCGGAAAAGGTGTTTCATAGAAGAGGTCAATGAGCACATGAGGCTGAGTTT
>Bacillus_Fam_1264_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ACTATGGGAGGTTTCATAGAGCGNGAAATTAGGAAAAAGGAAAGACTCCGCGC
>Bacillus_Fam_1265_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TATTGCCCGAAGAGAAGAAAAAATAAATCCCGCGGTAAAAAGACCGGGCTTC
>Bacillus_Fam_1266_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AGCGTTTATGAGAACAGAGAGCTAATGATTTGGGTGCGAACTGTCCTCATGA
>Bacillus_Fam_1267_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AAAAAAGAGAGCGCCGGGTAGAATANAGAGCATCTATGCGACCGAGCCCGAG
>Bacillus_Fam_1268_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TCAATGAACACGAATCGGCAAATTTTCAGGCAGGAAGTGTTTCATAGAGAGGT
>Bacillus_Fam_1269_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TCTACGTGCCCAAGTTCAATAAATTAGTGGGTTTCGGTCGCGTAGAGCCCT
>Bacillus_Fam_1270_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTGACCTTTTCTTTNAAAATCAATTAGTTTTAGGCAATGNACATGGCTTCCA

```

```

>Bacillus_Fam_1271_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CATCCTCTTCAGGTGAAAAAGCCCAATTATTCACCGGAGTGCTCATATTTT
>Bacillus_Fam_1272_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTATTCCTCTAAAGCAACGCCACACGCGCCTCTTCAGGTGAACAAATCGCAT
>Bacillus_Fam_1273_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GTTATTTACACGAAGGGATTTTGAACCGAATGCTTCAGGTGAATAAATTGCG
>Bacillus_Fam_1274_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATTTATTCCCATGAAGCGAGAGGAAAACCGGAGCTTCCGGTGGATAAACTGA
>Bacillus_Fam_1275_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AAAATGGTCACAGAGTGCCAACTAAGACCAAAATGACAAGGGAGCAAGCGG
>Bacillus_Fam_1276_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GGAAGGTAGGAGAGAGGCAGTCTCATCGCCCGTTCCAGCTATTTACCATTA
>Bacillus_Fam_1277_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CATAGAGCGAGTCAATGGGACATTTNGCAATTTTCNAGAGCAGCAAATGTCC
>Bacillus_Fam_1278_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGATGGACAAAACAGTAGATAGAGCGCAAAGCAAAGTCCATCAATCCTGAGA
>Bacillus_Fam_1279_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTCCTTCGTTTCTTCATGGGTTTTGTACCATTGATTGCTTCTATGGGACATG
>Bacillus_Fam_1280_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GATTTTTCCTAAAGTACCTTGTTGCGGGCGACATGAGCGCTTCTTGGCTACC
>Bacillus_Fam_1281_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GACTTTTTCGGGAGACATGAGCTAGTCTTGGCGACCGGTTTCACAAGTTGAT
>Bacillus_Fam_1282_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTCTATGAGACAAAATCGGGGAGCAGACGAGNGTTTGTCTCATTGGAGCG
>Bacillus_Fam_1283_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GACTCTTTGAGCNGATTTTTCGGGCGTTGGGTCTCTATCNGGCTTATTGAN
>Bacillus_Fam_1284_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTTGTCTTCATTCGCTTGATGATGGACTTTTTCTAGAGCGATCGGCTTCGN
>Bacillus_Fam_1285_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATGATGGACATTTTCGATAATTTCTCAGCTGCTTTTGGCCTTCATCTCTTCG
>Bacillus_Fam_1286_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATGATGGACACTTGGAGCGGATTCTTTTTTCGCTTTTGTCCATCATCTCTCGC
>Bacillus_Fam_1287_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTTTGTCCCATAGAACCCCTCTATGGGACATTTCTCTTGCTTATTCTGATC
>Bacillus_Fam_1288_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AGGATTTTCAGGAATCAGAACATCAATGTAAATCCCGAAACCAGTTCCATGCA

```

>Bacillus_Fam_1289_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATTTGGATATTAAGGTCGTGATAAGCGCCTAAACACCCCTCTGTTATACAGT

>Bacillus_Fam_1290_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TCTCCTTCCCCAACTCTATTGATGACCGGCATTTTCGGGAAGTACTCTGCCTN

>Bacillus_Fam_1291_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATTCCCGAATTCCTTAATGCACTTGTTTCGGGAATTACTACGGGCTTCTC

>Bacillus_Fam_1292_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ACGGGCACCTTTGANCGCACNTTGTTCNCCAAACGCTTTTTTCCAAGCCG

>Bacillus_Fam_1293_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GAATTAGAAATCCAAGAGTCATTCTGAAACGGTCTCAACCATGGAAGTTCGG

>Bacillus_Fam_1294_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AACGCTTAATCACGACAGTATTATCCAGATAACGGTAATTAGGGGCGTGATA

>Bacillus_Fam_1295_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AGCGGATTTTCGGGAATTACTTTCCCTTTGCATTTCCCGAAACTTTGTCTCCT

>Bacillus_Fam_1296_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTACGCCTTAAACACGACTCCAATTCCCAGGTTTTGGTGTTCGTGTCTCGA

>Bacillus_Fam_1297_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GTTCTATTTCCCCAAACCGGCACTCGCCTTCTCTTTCGGGAATTACTTTGCC

>Bacillus_Fam_1298_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTTTGTCTTCATACCACCGATGAAGGACTTTTGACAACGAAAATTCACCAG

>Bacillus_Fam_1299_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGAAGGACTTTTATCACCTTTTATTCTCGCGAAAAGTCCTTCATACCTGCGA

>Bacillus_Fam_1300_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GATGAAGGACTATTCTTGCTTTGATTGTGTCTCGAATGGTCCATCATCCCCTC

>Bacillus_Fam_1301_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AAGTCCTTCATCGTGGTTATGAAGACCAATAAGAGGTTAATTAGGAAGCGAA

>Bacillus_Fam_1302_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CGGTGCGCATAGCAAGGTTCTATAAGCCCGGAAACACAGGAAATCCAATGGAA

>Bacillus_Fam_1303_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AGTGAACCGGCGGAAACAGAGTTCAAAGAAGGGGCTATGTTCCCGAAATCG

>Bacillus_Fam_1304_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCGTGTCATAGAGCCCGAATGAAACGCGAANTCGCTGGGGCTTAGTGAAAAC

>Bacillus_Fam_1305_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGGAATTGTCATCATAGCAATCATGAAGACAATCTCGAGCGGATTTTGTGAG

>Bacillus_Fam_1306_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CCTTATGAAGACACTTTTCGGTCCACTTTCTCTCTCGGATGTGTCTTCATCCA


```

>Bacillus_Fam_1307_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CGTTTTCTTGCCTCGCTTCGAAGTTTGGGTGCCATTGCGCCTCTATGACACG
>Bacillus_Fam_1308_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CGCGAATTTCCCTCCCGCTCCTAATTTGGTGTGTCATACTGCTCCTATGACG
>Bacillus_Fam_1309_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTTCCCTCTCAACATTGTCTTCATCCACCTTGTGAAGACAGTACCATGCTTG
>Bacillus_Fam_1310_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AGATTGTCTTCATCACNCTTATAATGACAATCTTGAACGATTTTCACTGTG
>Bacillus_Fam_1311_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AAGACACTTTTGCCGTGTTTTCTGCTGACATTGTCTTCAGACCACTGATG
>Bacillus_Fam_1312_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CTCATGAACCGCTTATGAGTAAGTAAATACATGATTTAGATTATTTAGTTA
>Bacillus_Fam_1313_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AATGTGTCTCAAGAATAGGGTTGGAAACAGATAAACCGGGAATNNCGTTGAA
>Bacillus_Fam_1314_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GGTAACCTTTCGCGGGCTTTGGTTACCCGGATCTCATCACAGAGCCNACTTC
>Bacillus_Fam_1315_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TCTTCAAGGTAATCAAAAGCTCACAAAGGTACCCGAGCCGCCGGAATTACCT
>Bacillus_Fam_1316_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGGAGACACATTTTATTGCTAAAAAGTAAATAATGTGTTTCAGAACCAGNGC
>Bacillus_Fam_1317_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TAAGACACATAATGTGACCAACCCCAAAAAATGTGTCTCACCCGCCAGTCT
>Bacillus_Fam_1318_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CGTTGTTTCGGGCACATGAACCCTCTATAGTTCCCAGTCTCTTGCTTCCAT
>Bacillus_Fam_1319_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CCGTTTGAGCAGCTCGAAGGAGATAGCGGTCACTATGAAAAGCGTCATGGTGA
>Bacillus_Fam_1320_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ACTTCAGACAACTTCTGCNGCCAATTACTTAAACCTGTCCGAACCTCTGCCT
>Bacillus_Fam_1321_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GAGCAACTTGATCATAGACCTCCTATGATTCACTTCCCTACAATTCATGTGC
>Bacillus_Fam_1322_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGTCTGAAGTTGAGNAGCCTTCGGACAGGTTAGAAGCCTACAGAGTAAAAGC
>Bacillus_Fam_1323_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AAGCTGTCCGAAGAGAGCTCAGGTTACAGACAGGTTTGCTCAGGTTNAGTAGA
>Bacillus_Fam_1324_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TCTGATTCCCTTTCAGTAGTGNATCGGGGTAGAAAGGGAACGAAAGAGCAAG

```

```

>Bacillus_Fam_1325_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AGATTCCCTTACTAGGCAAAATGAAGTGCAAAGGGAACGAAAGGTAGTCAC
>Bacillus_Fam_1326_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GAAAGCTGTCCGAACCTTCACTTGGGTTCGGACTACTTTTCCTTTACGACCAC
>Bacillus_Fam_1327_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATTCCCTTTGTCTGGAGAAAATACACAGGAAAGGGAACGAAAGGAGCGCTTTG
>Bacillus_Fam_1328_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AAGCTGTCTGAACCTACCCACCTTCGGACAGCTTGACTCCGAAAAACCCAA
>Bacillus_Fam_1329_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATTATGGGTAACGATAAAGGCGTGATCGTGCCCTGAACTCGAGAATATAGTG
>Bacillus_Fam_1330_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GAGTCTGAACCTNGCGTGAGTTCGGACAGGAATCGTGANTGTGAATGTAAGC
>Bacillus_Fam_1331_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TGTCCAATAGGATGCCTCTATCGGACATAACTCACTTCCCAAGACTAGATTC
>Bacillus_Fam_1332_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ACGGCTCTATCGAACAAACTATGGGCCTTCACGCTTGGTTTGTCCAATAGG
>Bacillus_Fam_1333_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CTATTGGACAAAATCGCTTCACGGCACTGGCGGTTTGTCTAATACAGGCTTC
>Bacillus_Fam_1334_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATCAGAGACCTTTGGACAGCTTCTTCGNNTGATATGGTCATTGACACCTCTC
>Bacillus_Fam_1335_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTTTGTCCGATAGAGACCTCTTATTGGACAAAACCTTTGCTGGCACCGTTTCG
>Bacillus_Fam_1336_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ATAAGTGCCCGTTCTAGGGTCCCTAGCAAGGAGAGCGGTCATCTAACTCGAG
>Bacillus_Fam_1337_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
ACTTCAGACAGAAGAAGGTAAAAGAAGTAAGGGAGAGTCTGAANTNGAAGTG
>Bacillus_Fam_1338_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TTCTATTGGACATTCTCATCGATACGAACGCACGTTTTGTCCAATAGACGCC
>Bacillus_Fam_1339_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
AAGAGCAAATCGTTGACGAAACGAGCATTTTGAAAGCTGAACGTCAACGAAT
>Bacillus_Fam_1340_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
TCGTTACCGTTTTTGGCGTACTCTTCTGTTTTTCGGGCACATTAAACTCTTTN
>Bacillus_Fam_1341_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
CACCAAGAGCTTTCCTTGGCGCAGTAATATAGGTTTCATCTACTAATAACTG
>Bacillus_Fam_1342_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GGTCTTCATAGCACCGATGAAGACCTGAAACAGTTGGAAACTGCTTCGTACA

```

>Bacillus_Fam_1343_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 CTCTTCATCTCGCTTATGAAGGGGATTTGGATGAGGTAACTGCCTTGTTTTTC
 >Bacillus_Fam_1344_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 ATGTCGTCATGAGTGCGATGAAGACACAACTCTCCTGGCGAGCGGAAGAAG
 >Bacillus_Fam_1345_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GGAAAACACAGCAAAAGCCGGATAGAAATCCCCTTCATCAAGGCCATGAAGG
 >Bacillus_Fam_1346_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GATGAAGACCGTTTAAAGATCCCTCCGNGCCAGAAAAGGTTATCATGGGAGA
 >Bacillus_Fam_1347_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 ATCTATAAAAAATGGTCATCATGTACGTGATGAAAACCGAAATCTGGTATGTG
 >Bacillus_Fam_1348_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 CGGTCTTCATGGCCGGGATGAGAACCGATNTTNCTGATTTCTTTGCGGAGAAC
 >Bacillus_Fam_1349_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TGGTTTTTCATAAGCGGAATGAAGACCGTTATTAGGGGCTTTGTCCTGCGTAA
 >Bacillus_Fam_1350_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GATGAAGACCAATCCATNGGAAGGAGCGCGGGNAAACGGTCATCATCAAGGG
 >Bacillus_Fam_1351_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 GGTTTTCATAGCTGGAATGAAGACCGAAAGTAACGGTGATAGATCGAGTTTA
 >Bacillus_Fam_1352_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TGAGTCTGAATCCGAAGGTTATTTCGGACTCCAGCAAGAGGAAACCCAGGCAT
 >Bacillus_Fam_1353_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TCTTCATAAAGGCAATGAAGACCGTTTGGTTGGTTTTTTANAANGNCTTTGG
 >Bacillus_Fam_1354_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TTGGTTTTTCATAACGGCGATGATGACCGTTTTGCTGAGTGCTGGCTTGCTTT
 >Bacillus_Fam_1355_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 TAAAACTTCATGCTTATGGTCCTCATTCAACGGATGATGACCGTTTGCCTTA
 >Bacillus_Fam_1356_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
 Alignment score = 0.000000
 ATGATGACCGTTNTTGGTTCATAGAACANAGAAACTGGTCTTCATCTGGGCT
 >Bacillus_Fam_1357_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 AATACGCAGCAATGAAACCGNAAAAATAGTCCTCAATGCCGCACAAATAAA
 >Bacillus_Fam_1358_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 GGGGTTACTCATGAGAAAAGTGAGAGTAAGCCCGAGAAAAGAGAAATGCNC
 >Bacillus_Fam_1359_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 CGTTTTCTCGGGCTTCTACTCTTTTTTCCGCCCCGTAACCCCAAGCATCAT
 >Bacillus_Fam_1360_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 CTAAACAAGACGAGCAAACACAAAACAAACAACATCAATCTGCTCAAGGTA

```

>Bacillus_Fam_1361_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
AAAGACAAAACGNGGNGCCGAGACGAAAGAAATGTCCTTCATAGGGTCATG
>Bacillus_Fam_1362_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
TGAATGAGGACAAAGTAAGCGGGAAAACAGAAACATTGTCCTCGTAGGGCG
>Bacillus_Fam_1363_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GATGACAAAACCTTCAATGAACNAAGGATTTCTGTTCATCGGAAAGCTTCAAC
>Bacillus_Fam_1364_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
TAAAGGACGTTAACGAGTCAATTTAGAGACTAAAGTCCCTATAAACAGCTTN
>Bacillus_Fam_1365_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
TATCGTCCTATAGAGGGACTTTAAAGGACTTTAATATTGAATGTTGCNAAA
>Bacillus_Fam_1366_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GTGACCAAAAAGAAAAAAGAGAGCTACTTCGGTCACTCCAGAGAATTGGA
>Bacillus_Fam_1367_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCACGCTGAGCCNGCGCTTCGTCAAGAAGAGAAAGCAGCGGCTCAACCGGA
>Bacillus_Fam_1368_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
CTTATCCTCCGTTTTTCGTACCGTATTTTGGCCAGGGAGAATTTTTTCATTC
>Bacillus_Fam_1369_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GAAAAAGAGCCGAGCTAGCGGAAGTACGGCGTATAAGGAGTCATGAAGTT
>Bacillus_Fam_1370_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
TTTAAAGGACAAAAAAGGAAGCCGAAGCTGGAAAGTGTTCCAATAACGAGAG
>Bacillus_Fam_1371_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
AGTGAAAAGGGAATCAAAGCCCTCAATGATTCCCAAAGAGCCCCAGAACCA
>Bacillus_Fam_1372_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
AATACGCCGAACCTCCCTTTACTCGGCTCTTTTTTCTGCTTCACAGTTCTA
>Bacillus_Fam_1373_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GTGCGTATTCATCTGATTTGGTAATCAAATTTCAACCTGAGCCGAATTACG
>Bacillus_Fam_1374_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
TTTTTCATTACCTATTATNGTTTATTCAAACCTAATTGAGNGAGTTTCCCT
>Bacillus_Fam_1375_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
TTGGTCTTCATCCGCTTAATGAAGACCTTTTTTCCGATTTGTTTACACTT
>Bacillus_Fam_1376_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
CGTTACCTTTTCTTCGTATTTTCCCATTTTTGGTCACATAGACCCCTTCTA
>Bacillus_Fam_1377_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GTCACGTAGAACCTCTCTACGTGACCTCTCCCATGCTTTTTTCTCCAAAATA
>Bacillus_Fam_1378_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
CGCTTTTATCGTCACGTAAAATGATTTCAACGCGTTTTGCTGATAATAAAT

```

>Bacillus_Fam_1379_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 TCCGTTATTTGTCCAAAACCTATGCTACAGCTATTTTNCCGGACACCAGG
 >Bacillus_Fam_1380_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 GCTTCAGTTTCTTCATCCGAAATCATCTCAGCTGTACCTGCAGGCTCTTTT
 >Bacillus_Fam_1381_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 ATATTTTTTTGAACGTTCTTCACGTTTGCTAGATCGTTTTTCGCGATCATA
 >Bacillus_Fam_1382_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 AGTTGTCCATTTGCGGNGGGCTATTGGACAACTTTTTCNGAAAAACACCAG
 >Bacillus_Fam_1383_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 TTGGACAGCTTCGCGCTATTTTCCAAAAAGTTGTCCATTAGACACAAGCTA
 >Bacillus_Fam_1384_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 TTTTCTCTAATTACGATATTTCTGTCCAATAGGACCTGGCTATTGGACAGG
 >Bacillus_Fam_1385_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 CTTGGCGCAAAAAGTTTTCCCGAGGNTGGAGAAATTGCGTTAACGCAGGGT
 >Bacillus_Fam_1386_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 CTCAGAGACAAAATCCAGGNAAAAAGTAGNGATTTGTCTCTGATCGGGTGT
 >Bacillus_Fam_1387_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 CTTGCGTCGAATAGAAACGCCCTATTCGCGCATTTCTGTGATTTTCTTTTN
 >Bacillus_Fam_1388_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 CGCCCCAATTCACCCGAAGAAAAGGAAATACACGTCAANGGTGAATAGAT
 >Bacillus_Fam_1389_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 GGTCGAATAGAAGCGATCAATTCGACCGTTGCTGGAAAATCCGCTTTGTTT
 >Bacillus_Fam_1390_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 CTTATACATTTTTTCTTTCTTCCCATGAAAATCTATACGCATCCTCCCTTC
 >Bacillus_Fam_1391_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 TTCGGACACAGAAAGGGGGAACCCGTGGAATTGAGTCAGAACCCGGNCAAG
 >Bacillus_Fam_1392_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 TAATCGTTCCCGAAAATGCNGTGTANGAGGCTGGNGGTAATGAATAGGGAG
 >Bacillus_Fam_1393_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 ATAGAGCGCGTGTCCAGTAATTTATTGGAAAAGGCGTCCTATGAACCATTC
 >Bacillus_Fam_1394_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 AAAATGGTCCTAGTTCACCAAATGGAACCAAAATCAAGAAAGACAGCGTA
 >Bacillus_Fam_1395_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 AACTGTGACCAAAAATGGCGGAGAAATCAAAAAAACGGTCACAGAGTGTA
 >Bacillus_Fam_1396_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 AAAAAAAGTAAAAAACATGTAAAGAGTCTCATAGGAGCATTCATGGGAC

>Bacillus_Fam_1397_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 TAAAAGAGAACTTAGGATGAATAGCTTCCACAAACTGTAAGTGGAAGCATC
 >Bacillus_Fam_1398_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 GACTTTAGAGNACATTNCTTCTNATACTGGTAATTAAAGGAGCTAAGATT
 >Bacillus_Fam_1399_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 GGATTTTGAAGAAGGGAAAAGCATGCCCCCAAAGTGCGCTTAGGATACAT
 >Bacillus_Fam_1400_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 TTCTATTACCTCTATCCTGCTTTTGGCATCACCTTTTCGGCTTCGGGCTT
 >Bacillus_Fam_1401_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 CCATCCGGAAGTGGTGGAAGATTTTCATCCCCTGCAAGTTCTACCCCAGTC
 >Bacillus_Fam_1402_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 CATCCTTCACCATGATCACGGGCACTTATCTCCTCTTTGGTTACCTCTTTT
 >Bacillus_Fam_1403_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 TTTGGGGAACCTATCTCGGCTTTGGTTACCTTTTCCTTGGCTTCGGNTCGA
 >Bacillus_Fam_1404_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
 Alignment score = 0.000000
 TTCTTCAACAGCCTCTATTGCTTGTGGGACGGATTCCCTCGGTCATTTCCAC
 >Bacillus_Fam_1405_50_1 Nr. of seq. 1 Alignment length(with gaps) = 50
 Alignment score = 0.000000
 CGACTGCCACTATTTGGAAAACAAAATGCACACACACTCATTTACCGCCT
 >Bacillus_Fam_1406_50_1 Nr. of seq. 1 Alignment length(with gaps) = 50
 Alignment score = 0.000000
 TTTAAATCAAAGGAATAGATTGTGGTTCGGGTNAAATCAAGTAGCTCACT
 >Bacillus_Fam_1407_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
 Alignment score = 0.000000
 GCGATGATGCCGCAGATGCCGCATCAGATGCCACATCAGGTGCAGGGA
 >Bacillus_Fam_1408_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
 Alignment score = 0.000000
 TCAGCCAGAAAACAACGGAAAAGGATATAAACAAGAAAATAGAGAGTC
 >Bacillus_Fam_1409_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
 Alignment score = 0.000000
 GGGATGCCGCTAAATCCGGCTCCTGGTACCCCTCCATAACCTGCTGGT
 >Bacillus_Fam_1410_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
 Alignment score = 0.000000
 AAACCAACAGAGTCAGCATCATTGAGCAATGCTGCATAATCATCTTGT
 >Bacillus_Fam_1411_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
 Alignment score = 0.000000
 TCATTGCTGTCCTGAATACATTGGAGAAGGTATGCTAGAATATGGCC
 >Bacillus_Fam_1412_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
 Alignment score = 0.000000
 AGCCCGATGAGAAATTACTATAGAGCGATTGATCAGCACGTGACCGAT
 >Bacillus_Fam_1413_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
 Alignment score = 0.000000
 GCTTCTTCTGTTGTTTCCTTCTTGGCCTTCTTCATCTACAGCATCC
 >Bacillus_Fam_1414_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
 Alignment score = 0.000000
 GCAAAGAAAGAAGCCGAAGAACAAGCGAAACGAGAGGCTGAAGAACAG

>Bacillus_Fam_1415_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
 Alignment score = 0.000000
 GGTGTGATGGGAGCAGAGATGCATCATCAGATGCCGATGGGTCAGCCG
 >Bacillus_Fam_1416_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
 Alignment score = 0.000000
 TTAGAAAGAAGCAGAGACAGAAGTTCGGAAAGCAGTGTGGACAATGAC
 >Bacillus_Fam_1417_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
 Alignment score = 0.000000
 CGGCCTCCCCGCGAATCCTCACGTTTAGGTCCGCGGCTGTTTCCATC
 >Bacillus_Fam_1418_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
 Alignment score = 0.000000
 CATCATAAGAAGAGCTGCCGCAAGTCACATCGCAGCAAGCACAGATCG
 >Bacillus_Fam_1419_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
 Alignment score = 0.000000
 ATGCCGTGGCAAAATGGGATGATGCCAATGCCTGGACAGCAGGAAGGA
 >Bacillus_Fam_1420_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
 Alignment score = 0.000000
 TATAAGAAGGACTACTACTACCATGAGCCTTACAAGAAGCATCACGAG
 >Bacillus_Fam_1421_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
 Alignment score = 0.000000
 CTGTTCTTTCATCCGAACCAGGGGCGGTTCTTCTTCCGGCTCATCTC
 >Bacillus_Fam_1422_47_1 Nr. of seq. 1 Alignment length(with gaps) = 47
 Alignment score = 0.000000
 AAACACGAGTAAGAATATGAATTATTCAGCTACCTTGATTACGTTTA
 >Bacillus_Fam_1423_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
 Alignment score = 0.000000
 TTGTTGATTTCTCTTCTTTTTTACCTTTTTTCATCAGCTGAACCGC
 >Bacillus_Fam_1424_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
 Alignment score = 0.000000
 CACCATCAAGTACAACAGGTGGATCTCAATCAAGTGGTGGAGGAG
 >Bacillus_Fam_1425_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
 Alignment score = 0.000000
 GCCCGAAGCATTAGGGGTCAGNGCAGAAGTGCCAGAGCGTGAGA
 >Bacillus_Fam_1426_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
 Alignment score = 0.000000
 CCGGAGTATTAACAGAAATAGAATCACACACATCGACATCGACAA
 >Bacillus_Fam_1427_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
 Alignment score = 0.000000
 TCCTTGTTGGTCCAGTGGGACCGATAGGCCCTGGTTCCCCTTGTGA
 >Bacillus_Fam_1428_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
 Alignment score = 0.000000
 GAGCAATCTAGTAATTATTGACGGTATCAGCCGTTATCTGAACTT
 >Bacillus_Fam_1429_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
 Alignment score = 0.000000
 TCTTGAGTTTGCTGAGATACGTGTTGATTTTGTGACGTTGAGGT
 >Bacillus_Fam_1430_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
 Alignment score = 0.000000
 GGAACAGAAAGACAAGGAATGGGTGAAGGAAATGCAGTTCCAGTA
 >Bacillus_Fam_1431_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
 Alignment score = 0.000000
 TGTATCGGTGAAACGGGCATTTGCTTTTCTACTTTAGGAAATTCC
 >Bacillus_Fam_1432_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
 Alignment score = 0.000000
 GATAAACCGGATGGCGAGAATCCAGATGTAGACAAGCCTGACACG

```

>Bacillus_Fam_1433_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000
TCTGTGCCTTCCGTTTCCTTCGGTTACCGCTTCTGCTCCTGTGTCTG
>Bacillus_Fam_1434_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000
TTTTCTCTTTTAGGAGGAGTTGGATTCTGAAGGCTTNGGAGCCGGT
>Bacillus_Fam_1435_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000
CTCATGAAGAAGATCACGACCACGATCACGACCATGAACACGATG
>Bacillus_Fam_1436_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000
TCCTCTTCATCTATAAAAGAGCTCTCTTCTTGGGGAGAACTGGAT
>Bacillus_Fam_1437_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000
CCATTATTTCTTGCAGAGCTCTTCGGTTGTTCTTCTTGCCCATTC
>Bacillus_Fam_1438_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000
GCTCCGGTTACTCCGGTCGCTCCCGTATCTCCCGTTGCACCTGTG
>Bacillus_Fam_1439_43_1 Nr. of seq. 1 Alignment length(with gaps) = 43
Alignment score = 0.000000
AAAACCTTCTAACAAAGATCCAACCCCAACCCCTAGTTACCCA
>Bacillus_Fam_1440_43_1 Nr. of seq. 1 Alignment length(with gaps) = 43
Alignment score = 0.000000
GGCTGGTTAGATTCCGTTCTTGCTTCTTCGTANATCCAATGAA
>Bacillus_Fam_1441_43_1 Nr. of seq. 1 Alignment length(with gaps) = 43
Alignment score = 0.000000
TCAGTTTTTAAGCTCGGAGACATCTGTTTTTAAGNTTAGAAAACC
>Bacillus_Fam_1442_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
TGATCATCTTCCTCGTGACCATGCTCCTCATGGCTATGGTCG
>Bacillus_Fam_1443_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
AGGTTTTTGCTTCAGGTTTAGCTGTTTCGTTGTTTACAGC
>Bacillus_Fam_1444_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
AATCAAGGAAATCAAACGCCGCCAATAGCGGAAACGGAAAT
>Bacillus_Fam_1445_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
TTCTCGTGCGGTTGCCGCTCCATCCTGTGCGGCTTTTCCCCT
>Bacillus_Fam_1446_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
TAACTTTGATCAAATCGCTCGTAACTCGGGCCGAATCGCGCG
>Bacillus_Fam_1447_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
TCTCTTTTCAGCTCATATTCTTCCGGTTCCTCTTCCACTTTC
>Bacillus_Fam_1448_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
CTGGACCTATGATGGGTGGGTTTAACCCTCAAGGACCTGGTG
>Bacillus_Fam_1449_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
CTTCTTCAGGAGTCTCTACTTCTCTCTGTTCTTCTGTTC
>Bacillus_Fam_1450_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
CAGCCTTTTATCCATCGAGCTGACCTTTTGATCCAGAACGTC

```



```

>Bacillus_Fam_1451_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
ATTGTTAGAGCTGCGTCGATCATTCTGAACAACGACGGCGACG
>Bacillus_Fam_1452_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
TTCGCTTTCGGGTTTGCTTTTGGGTCTACCTTCGAATTTCCG
>Bacillus_Fam_1453_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
TCAAGAATCGCGATGAAATGTCCGGTCGTACAATAGACGAGC
>Bacillus_Fam_1454_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
TGCGTGAAGTATTGCGGTTTCTTGAAGTANAGCGGCTCTGCT
>Bacillus_Fam_1455_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
CAACCAAGAGAAGTGGCCCCTGGAGAGGTACCTTCTGAAGCT
>Bacillus_Fam_1456_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GATGATGGTGGCCATGCTCATGGTGATGATGCTCACGTTTCAT
>Bacillus_Fam_1457_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
AAGCGCTTGTCGACCTCAACGAAACGTGCGTCCACTTCATCG
>Bacillus_Fam_1458_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
TCTCCAGAGTCATCATCGTTTCCGTTCATCCGGATTCTGAATCA
>Bacillus_Fam_1459_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
TTGTTGTCTCTGGTTGTTATTTGGATCCTGATTGTTCCATTGG
>Bacillus_Fam_1460_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
CCGGCGGCGGGAACAACGGGGCTGACAATGGCGCCAACAACG
>Bacillus_Fam_1461_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GGAGGATCTTCTCACGCGGAAGGATCGAACACAACAGCCAAT
>Bacillus_Fam_1462_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
CTGTTCAACAGCAATCAGCTCAACAAGAAAAAACTCAGCAGC
>Bacillus_Fam_1463_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
TCTGCTCTTCGACTTTTATAAATCTTTCATTCTCTTATAAC
>Bacillus_Fam_1464_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
CGCTCAGCTTCTTGTTTAGCAGCAGCCTGTTCTTGAGCTTTT
>Bacillus_Fam_1465_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
CAGGTGAAGGAGCCGGAAGGCGAAGGCCAGGGCGGCGGAA
>Bacillus_Fam_1466_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GGATTCGTACCACCTTGGTTATTTTCGTTTCCACCATTTGGT
>Bacillus_Fam_1467_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
AAGAACTTTCTTCTGCCAAGAAAAAGATTCTCTTGGGAAA
>Bacillus_Fam_1468_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
TGTTTCAGTCTTGATCGCACCGATTTCTTTCCGCATTTCTGAC

```

>Bacillus_Fam_1469_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
 Alignment score = 0.000000
 TCAAACCGTTTATCCATGCTGTTTCAGACGGCCATCCACATCA
 >Bacillus_Fam_1470_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
 Alignment score = 0.000000
 AGCCACTTGTAATTTATCGCTCCTTCTTTCACTGGAACGCG
 >Bacillus_Fam_1471_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
 Alignment score = 0.000000
 GCTCTTCTTCTTCCCGCTCCCTCAGAATCGGGCAGTCTCCG
 >Bacillus_Fam_1472_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
 Alignment score = 0.000000
 GTCAAACGCAAAATGGTGGTAGCCAGCCAGGTGGAAGTGACG
 >Bacillus_Fam_1473_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
 Alignment score = 0.000000
 GGAGGACCGGGTGGNTTTCAGGCANTCCAGGTGGNTTCCCA
 >Bacillus_Fam_1474_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
 Alignment score = 0.000000
 GATGTGGGAGGCCTAAACAAAATGTCGAAATGCTAAAAGAC
 >Bacillus_Fam_1475_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
 Alignment score = 0.000000
 CCTGCTACGTTTGGCTGTCCGTGATACGGATTTTCTGATGCG
 >Bacillus_Fam_1476_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
 Alignment score = 0.000000
 GGAATTGCACCGATAACAACGATAATTGCACCGTTGACCTTG
 >Bacillus_Fam_1477_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
 Alignment score = 0.000000
 GCTTTCGTTTGTGATGCGTAGAGTATCTCGAATCTTCCTCGT
 >Bacillus_Fam_1478_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
 Alignment score = 0.000000
 CAGGAGTCGGACAATTAGTTGACGGACAAAAACAGCGGTTG
 >Bacillus_Fam_1479_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
 Alignment score = 0.000000
 GAGCTTCAATCCGACAAGAGGAGCGCTCATTCGGACAGGAGG
 >Bacillus_Fam_1480_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
 Alignment score = 0.000000
 TGATCGGTAAATCCTCTGACATGAGCGATAACCATCTCTCACT
 >Bacillus_Fam_1481_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
 Alignment score = 0.000000
 ATTTCTGCTAGTGCGCCTTTGGTTTCTGCATGTAGATCTCCG
 >Bacillus_Fam_1482_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
 Alignment score = 0.000000
 TTGAAGTCGACAAACGGTTTGATGCTGTTGATCAAAAATTTA
 >Bacillus_Fam_1483_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
 Alignment score = 0.000000
 TTATTTAACAGGTAGCAGAATTAACATAACAGAGTTTCGATT
 >Bacillus_Fam_1484_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
 Alignment score = 0.000000
 GTTGGCCGATATATCGATTGTGGTGGCGCAATAACATGCTCA
 >Bacillus_Fam_1485_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
 Alignment score = 0.000000
 AAGTGCGTCAATTACTTATCCAGCTGCGTCAAAAAGTTCGCC
 >Bacillus_Fam_1486_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
 Alignment score = 0.000000
 TTTGATAAAATTGAAACTCGACTTAATAATATGGATCAGCGG

```

>Bacillus_Fam_1487_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
AGAAACGCCAGGAGATAACGAAGAACTCCTGGAGATAATGA
>Bacillus_Fam_1488_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCGAATTTCCGNGCCCAATGNGCGAATTATCGNACCTTACTN
>Bacillus_Fam_1489_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GTGATCATTCGGCCGGCGGTTTGAAAATCATTGGTTGATGAC
>Bacillus_Fam_1490_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
TATTTCGCCGTTCTNCTCNATTTATTGGACATTANCNGCACTT
>Bacillus_Fam_1491_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
ACATATCTATGCTGATAAAAGGCAATTACCCCTTTAAGTAG
>Bacillus_Fam_1492_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
CTCGCCAATTCGGCACTTTTACTCGCGAGTTTGNAGCTGTTTA
>Bacillus_Fam_1493_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
TTTTTCGGCCTGCACTCAACTTAATTCGACCTGCATCCACTT
>Bacillus_Fam_1494_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GTTGCGCAATANGGTANTGTTTTAGCGCAATTCCGTGTGNAA
>Bacillus_Fam_1495_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
TCGTAGCATTTTTTCTTCTTACAGCAAAAATCTACGTGATCG
>Bacillus_Fam_1496_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
TTTGGTCCCATATATGCTGGCATTGTTTGTGGGAAGTTTGCA
>Bacillus_Fam_1497_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GAAGTAGAAGATCTAAAAGCAGGTCAAACGAAGTTAACAACG
>Bacillus_Fam_1498_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
TTCTTCTTCAGCAACGGTGTTAACTTCATCCTCAGGAAGGTA
>Bacillus_Fam_1499_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
TACTTACTTGTGACCATTCTCCACTCTTTCCAAACGTTTCGT
>Bacillus_Fam_1500_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
AGTTCTTTTCGTGTCTGCTTTTAATAGCCGGACGTCTCCTTTT
>Bacillus_Fam_1501_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GTCACTTACATTGGTTTTCAATTCACCAACATCGGTTGTCAG
>Bacillus_Fam_1502_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
TTTACTCCGATCCTCTTATACTTTACTAACAACCACCTATAC
>Bacillus_Fam_1503_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCTACTGAAGACACTCATTCTCATGACGATGAAGAGAGTCAT
>Bacillus_Fam_1504_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
CGGAAGACGGGGAGAACGCCGAAGGAGAAGCGCCAAGTCCGC

```

```

>Bacillus_Fam_1505_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
AGAGCAGTGCAGACAGCGCTGCGTCGTGCGAAGCACAAAAAAG
>Bacillus_Fam_1506_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCCGAATCCTGGAGTCGCATACGGAGAACTGGACGAACACG
>Bacillus_Fam_1507_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
ATCAGCCAACTTCGGGCGAGAATCAACCAAGCTTGGCGAAAA
>Bacillus_Fam_1508_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GAAAAGCGTTTTGACGGTTTTAGAAGGGCGTATTGATGGGCTA
>Bacillus_Fam_1509_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
TTTGCGTCTTCTGATGAGNGATTTCACCGGTTTGGTGGCA
>Bacillus_Fam_1510_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
AATATTGGAATTTGCTTCTGAAAATTTTCAGGGTTAGTTCCC
>Bacillus_Fam_1511_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
TATACGAGAGGTGGAGCTGCTATAAGTGAGTGGCACCTGTC
>Bacillus_Fam_1512_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GATTTATCAGCCAAAACTCACTCTTTTCAGCCAAACTTCC
>Bacillus_Fam_1513_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
TCGATCGATAAATCTCAAAGTCGATGAATAAACAGGCAAC
>Bacillus_Fam_1514_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
TTTATCAATCACTTTCCCCTCGTTATCCATCACTTTCACAA
>Bacillus_Fam_1515_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
TGGACAATTCGGCGGGATTGTGACCAAGCGGCGGCCAAGTC
>Bacillus_Fam_1516_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
TTGCGGGCCGACCTAACCTTTACATGCCGATTCTTATA
>Bacillus_Fam_1517_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
CACTTTTTCACACCAAAATCGAAGTTTGCGGGCCGGTTCAAA
>Bacillus_Fam_1518_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
AAAAAGTGACCGCATTATCACCTGTTTTGACTGAATAAACG
>Bacillus_Fam_1519_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
AATTCGTCCTACATGGNAANAATTCGACCGTAACCGGCAAN
>Bacillus_Fam_1520_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
CTGAAGGTCGATTTATTCCGACCCACGGACGAATTCATTCA
>Bacillus_Fam_1521_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GAGACGCAAAAGTAGTTGCAGCTTACGCAAAAAACAGTGGA
>Bacillus_Fam_1522_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
TAAATATTTGCGTCAGCCTCAGTGATTTAAGCGTCACCATT

```

```

>Bacillus_Fam_1523_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
TGCATATATTCGCCGTCCTCAAGCAGATATTGGACAAAACC
>Bacillus_Fam_1524_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
AGGGAAGCAGGACGAATAAATTCGCGGACGGACGGAAAAAG
>Bacillus_Fam_1525_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GGACGAATTCTCTCGACGGTAGGTCTGAATTAAACCTGTTTG
>Bacillus_Fam_1526_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GGACGGATTATTTTCATCCCAGGTCGGATTCCACGCGCTGTC
>Bacillus_Fam_1527_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
TTCGACCTAAACTCCATTTTTTCCGGCCCACTATCGATTAA
>Bacillus_Fam_1528_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GATATAATTCCAGTTTCGGCGATATATTGCCGGTTTTTCGTA
>Bacillus_Fam_1529_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
ATATTCCGGCCTTACCCGCTGGTTTCCGGCCTGCTTCATCG
>Bacillus_Fam_1530_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
ATTGGGTCGATTTATCTCCTGTTAGGACGATTTATCCCCGC
>Bacillus_Fam_1531_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GTAAGGAAGTCGCGCAATCCCCAGGAAAGAAGCGCAATGCA
>Bacillus_Fam_1532_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
AAAAGTAGCGGATAAAACCCAAAAGTTGTTGGATAAATCCC
>Bacillus_Fam_1533_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
TTCTCGTGCTTCAAATGGAAGCATGAGAACCGTCCCACTGC
>Bacillus_Fam_1534_40_1 Nr. of seq. 1 Alignment length(with gaps) = 40
Alignment score = 0.000000
CATGAAGAAGACGAACATGAGCATCACGAGCATGAGGGGC
>Bacillus_Fam_1535_40_1 Nr. of seq. 1 Alignment length(with gaps) = 40
Alignment score = 0.000000
GATTTGCGTCTGCATTTTCGTTTTTTGCGTCGCACCCGGCA
>Bacillus_Fam_1536_40_1 Nr. of seq. 1 Alignment length(with gaps) = 40
Alignment score = 0.000000
ATCCACTTATTTTAACTTTGTCCGAGTTATTGGCAGATTG
>Bacillus_Fam_1537_40_1 Nr. of seq. 1 Alignment length(with gaps) = 40
Alignment score = 0.000000
ACGCATAAATCCTGGAACCGATGCAAATAACTTGGATCCG
>Bacillus_Fam_1538_40_1 Nr. of seq. 1 Alignment length(with gaps) = 40
Alignment score = 0.000000
ATTTTAAATTGCGATTACACGAATTTATTTGCCATTTCCC
>Bacillus_Fam_1539_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
TTATCTTTAGATTTCCACCAATCGTCATCACAATTGTGC
>Bacillus_Fam_1540_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
TCTTCTTTTGCCGCTTGCTCCTCAGCTTTTCGTTTTGCT

```

```

>Bacillus_Fam_1541_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
TTCATGCCTTCCATATCATGAGAAGTGTGCTCGTCCATA
>Bacillus_Fam_1542_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
CGCCTGGATTGCCCCGATCTTCAGGATCCGGCTCCTCTC
>Bacillus_Fam_1543_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
TCTGGTAATTTGTTAGTTGCTTCCTCTTCATGTGCAAGC
>Bacillus_Fam_1544_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCGCTTTTCTTATGCTTGTCGCCGATAAACAGGCGCCTT
>Bacillus_Fam_1545_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
TTACCATTATCAGAGCCACTGCCATTGTTGTTGTTGTTA
>Bacillus_Fam_1546_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
CTTTTCCTGAAGTCTACGGATCCTGTGTAGTATGGTGCG
>Bacillus_Fam_1547_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCTGGTTGCTGCTGCATGCCACCCATCGGTTGTTGGTAC
>Bacillus_Fam_1548_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
CTCCGTATCCAGGCATTGCTCCATAGCCCGCTGGGGCTG
>Bacillus_Fam_1549_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
AAACCTGGCTGAGCGCCATAAGGAACTCCTGCTGCGGCG
>Bacillus_Fam_1550_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
CAAAGTCTCATAGCATGCTGATCATTGACTACATCAATG
>Bacillus_Fam_1551_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
TTCACCTACTCTTTGCTTCATTGCAGTTAAGTCCGTCAA
>Bacillus_Fam_1552_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
CTCAAGCAAATCAGTCAATGATGCCAATGAATATAGGGC
>Bacillus_Fam_1553_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
AGGATATTGACCAGGGCCTCCTCCTTGGGGCGGCAGTCC
>Bacillus_Fam_1554_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GGAATGGGAACAGGAGGCTATCCCGGCGGAGGATTTCCA
>Bacillus_Fam_1555_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GGGGGCTGTCCCCCGCTGTTTTAACGCATTACTCCGCC
>Bacillus_Fam_1556_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
AGAATCAACAGAAGAAATTCAAGCAGTAGCAGAGGAAGT
>Bacillus_Fam_1557_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
TCTTTCTTCTCTTCAGAAGAACCACTTGTTGATTTCTCT
>Bacillus_Fam_1558_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
TTTTCTTCAGGAGCTACAGTTTCGTTACCTGTTTCAGGT

```

```

>Bacillus_Fam_1559_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCAGGTAAAGGTGGCGCAGGAGCAGGCGAAGGTCCAGGA
>Bacillus_Fam_1560_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
CAAAACCACCAGTAGACCCACCAACAGATCCAGGAGATA
>Bacillus_Fam_1561_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
TCTGCTGCGGGAACGGTGTGTCCGGTGATGCGTCCGTCT
>Bacillus_Fam_1562_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GGCATATTTGGCATCGGTTTCATTTCGGCATTGGCATGTTC
>Bacillus_Fam_1563_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
CAAAGATAGAAGAGAAGAAAACCTGAAGATAAAGAAACAG
>Bacillus_Fam_1564_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
CCTTGACCTCCCGGCATCATCGAAATCCTCCAGGCTGA
>Bacillus_Fam_1565_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
AGATCTGGTTCGTTCTCGTAGATCCCGCGTTCTGGAGGC
>Bacillus_Fam_1566_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
CCTGGCATCATTGGCTGGCCGCTCATTTCCTTGACCCATT
>Bacillus_Fam_1567_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
TGATCATGACTATGACTGTGACCTTCGTGACTGTGTTCG
>Bacillus_Fam_1568_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GGATGGGGAAGCGGATTCCCACAAACACCAGGCCAAAGC
>Bacillus_Fam_1569_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
CAAATAAAATGAGAGTTTCGCAAAAATAAAGCGTTCTTG
>Bacillus_Fam_1570_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
AAGCTGTAGAGAAGCAGGAACCGGCCAAGGAAGCAGCAC
>Bacillus_Fam_1571_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
TGCATTGGCATTTGACCTTGATCTGGCATATATGGTTGC
>Bacillus_Fam_1572_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
TTCTGCGGAGAACGGCATGATCTGCGCGTGCCTCTCGTGC
>Bacillus_Fam_1573_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
TTTGTGTTTGCGTTTGAGCTGGTTGCTTTTCTACCGGCT
>Bacillus_Fam_1574_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCTTTAGAGTTGAATCTGTATCAGAATTATTTGAATCGT
>Bacillus_Fam_1575_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
CAACAACCTGGTGAGACAACCTGGAGGAACAACCGGCAGCA
>Bacillus_Fam_1576_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
TGTGGTGCCATTTGATGCGGTTGATACGGCATCGCCTGC

```

```

>Bacillus_Fam_1577_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
CATGTTCTTCTTCATGAGCAGCCTCAGTTTCATCATGTG
>Bacillus_Fam_1578_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
AAAACAACAACAAGAGCAGCAACAGCAGCAGGCCCAACA
>Bacillus_Fam_1579_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
TCTTCTTCTCATGGGCATGTTTCATCGTCAGCGTGNTGC
>Bacillus_Fam_1580_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCTTTCTTCCATTCTCGGTTCCGCTTTTGCGTCCCTGCT
>Bacillus_Fam_1581_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
CACGGCTGGCCGGGTCAAGGCGGGTCTGGCTCCGGCGGG
>Bacillus_Fam_1582_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
CCCTGCATATGATGTCCGTGTCCCATATCCGGCATGTTT
>Bacillus_Fam_1583_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
CGTTCGGCTTCTTCCGCAGCAATGCGCTCTTCCTCCTCA
>Bacillus_Fam_1584_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
TATCAACCAGCACCGTTTCCACAAGGTGGTCAAATGGGA
>Bacillus_Fam_1585_38_1 Nr. of seq. 1 Alignment length(with gaps) = 38
Alignment score = 0.000000
TTTGCTTCGTAGTCTTCCCTGTTTCTTCCTCTGCCAGC
>Bacillus_Fam_1586_37_1 Nr. of seq. 1 Alignment length(with gaps) = 37
Alignment score = 0.000000
GAAATCGGCCTTATTGCACGTTATCGGGCTTGTTGCA
>Bacillus_Fam_1587_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
AAAACCTGATACGGGAGGAAATCCAGACACAGGAGG
>Bacillus_Fam_1588_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
ATGGATCAAAACGTGCATCCGCAGCAATGGCCGCAA
>Bacillus_Fam_1589_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
TTTTGTGAGAACGTGATTTTTTATGGCTGCGGGATT
>Bacillus_Fam_1590_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
ATGCAGGGTATGCAGGGTAGAGCTGGCCTGGGGGGT
>Bacillus_Fam_1591_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
ACAGGTGATACCGGGGCNACCGGAGTAACNGGAGCA
>Bacillus_Fam_1592_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
AAAAGGGAATTGGAAGTGCAGTCAGAACAAACAGAGA
>Bacillus_Fam_1593_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
CTTCTGGTTTATTGTTATCAACAAGTGGTTGATCTG
>Bacillus_Fam_1594_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
TCGCTTTGATTTTGGTTTTGGGACAAGCCCTCGTCC

```



```

>Bacillus_Fam_1595_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
TTTTTCATCCAAAGGGCAGCCGAAAAGCAAACCAGG
>Bacillus_Fam_1596_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
CAGACATATCAACCAAATCAAATGACGATGCCACAA
>Bacillus_Fam_1597_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
CTATCTCTTCAGTTACTTCGACTTCTGGAGTTACAG
>Bacillus_Fam_1598_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
CCGCTTCCTGGAGCATCTGGTTGATTTCTTCTTGG
>Bacillus_Fam_1599_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
CTTCTGCAACTGGTTGTTCTTCAGCGACTGGCCCTT
>Bacillus_Fam_1600_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GGGCGGATTCCCTGGTCANGGTGGNCATGGNGGAAT
>Bacillus_Fam_1601_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
TCCAAAGGCAGTGGTGGATCGAAAGGAAGTCATGGC
>Bacillus_Fam_1602_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
CTGTTATTTCCGCCACTTCGACTACGTCATCTACAC
>Bacillus_Fam_1603_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GTGTCATCCCCAGTACCTGGACTTCCTCCATTATCC
>Bacillus_Fam_1604_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GTTTCTTCTCTACTGCTTCTTCCGGCGCTTCTGAA
>Bacillus_Fam_1605_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
ACTAGCTCTTCTTCAAATGCTTCTCTGTTTCCGCA
>Bacillus_Fam_1606_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCTTCAAGAAACACCATTGTGACTGCTGTGACAAGT
>Bacillus_Fam_1607_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
TGCAGCAGCAGGAAGCACGGAAGCATGAGGAGACGT
>Bacillus_Fam_1608_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
ACAAGCATGATGACTGTAATAAACGAGACAGAAACG
>Bacillus_Fam_1609_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
CGATGCATGCTCAGCCAATGATGTACCCAGACAATG
>Bacillus_Fam_1610_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
CGAAGAAACCAGACGGATACAAAAGGATGACGATT
>Bacillus_Fam_1611_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
TCTTCTTCGGAGTGAGCGGCTTCTTCGTCATGGTGC
>Bacillus_Fam_1612_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GAACCGAAAACAGAAAAGCCAGATGGTAAACCAGAA

```

>Bacillus_Fam_1613_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
 Alignment score = 0.000000
 GTAGGTCCAGTCGGTCCAAGGTCGCCGGTAGCACCT
 >Bacillus_Fam_1614_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
 Alignment score = 0.000000
 TTTTCCTCCGGCTCCTGTTCCAGGACGAAATCCGGC
 >Bacillus_Fam_1615_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
 Alignment score = 0.000000
 CCGCAAATGGGCTATGGCCCGCAAGCTGGATTCGCC
 >Bacillus_Fam_1616_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
 Alignment score = 0.000000
 GGAGGAGGTCAACCGCCGCGCGACCACCACAAGGG
 >Bacillus_Fam_1617_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
 Alignment score = 0.000000
 GAAGATGATCAATCGGACACCGATGACACAGAAGGG
 >Bacillus_Fam_1618_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
 Alignment score = 0.000000
 CAATGGGACGGACATGGCGGAGGTCATGGTGGCGGT
 >Bacillus_Fam_1619_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
 Alignment score = 0.000000
 TTTCTCGCTCCGTCATTTTCTTCCGGAGACTCTG
 >Bacillus_Fam_1620_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
 Alignment score = 0.000000
 TCTTCGCCTTCGACTGGTTCTTCTCCCTCAACTGGC
 >Bacillus_Fam_1621_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
 Alignment score = 0.000000
 TGTTCGTGCTTTTGNGCTTGTCACAGGTTTCGATAC
 >Bacillus_Fam_1622_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
 Alignment score = 0.000000
 AGAGAAAATAAACAAGAACAAGCAAACCAACAGGCA
 >Bacillus_Fam_1623_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
 Alignment score = 0.000000
 TTCTTCTGTTACAACCTCAGTAGNTTCGTTAGTTGC
 >Bacillus_Fam_1624_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
 Alignment score = 0.000000
 GGTTCTTTAATTGGTTCCTCACTAGGTTGTTTAGCT
 >Bacillus_Fam_1625_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
 Alignment score = 0.000000
 TTAGCGGCATTTCCGCCATTGGCTGCGTCGCCTCCG
 >Bacillus_Fam_1626_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
 Alignment score = 0.000000
 ATCCGGGACATCCAGGGTATGGCGGCATGACTGGTT
 >Bacillus_Fam_1627_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
 Alignment score = 0.000000
 GTTACTCCCGGTGATCCCGTTAAACCAGTTGCACCT
 >Bacillus_Fam_1628_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
 Alignment score = 0.000000
 TTTCTGTTGATACTGGTGATACTTGACATATTTGGT
 >Bacillus_Fam_1629_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
 Alignment score = 0.000000
 CAGGAGCACCGGGAGCAGCAGCTGGAACCTCCATATC
 >Bacillus_Fam_1630_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
 Alignment score = 0.000000
 AGGAGAAACAGGGGCGACTGGTAGTCAAGGAGTTCA

>Bacillus_Fam_1631_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
 Alignment score = 0.000000
 GGCATCATTCCTCCGGCATGCCTCCTTGCCATTTGTCCC
 >Bacillus_Fam_1632_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
 Alignment score = 0.000000
 CAGGTCCAAAAGGAAAAGAAGGCCACCCGGTCCAG
 >Bacillus_Fam_1633_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
 Alignment score = 0.000000
 CTCCTGGTACTGGATTTAATCCTGGCATGGGTTATG
 >Bacillus_Fam_1634_34_1 Nr. of seq. 1 Alignment length(with gaps) = 34
 Alignment score = 0.000000
 AACGTTTGATTGACTTCAGCGGTTCTACTAACTA
 >Bacillus_Fam_1635_34_1 Nr. of seq. 1 Alignment length(with gaps) = 34
 Alignment score = 0.000000
 GGGGGTCAGGCACGCTTTAATGATTACCGCACT
 >Bacillus_Fam_1636_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
 Alignment score = 0.000000
 GGAATGATGCCAATGCCAGGTCAAAACGGAAAT
 >Bacillus_Fam_1637_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
 Alignment score = 0.000000
 GAACAAGAGCCTGAACTGACGCTAGCACAGAC
 >Bacillus_Fam_1638_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
 Alignment score = 0.000000
 AACAAATCCGCCGTCAACAGGAGGAAATGAATC
 >Bacillus_Fam_1639_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
 Alignment score = 0.000000
 GGCATGCCTCCACTTGTTGACCTCCCAATCCC
 >Bacillus_Fam_1640_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
 Alignment score = 0.000000
 TAGAGCATAGATTAGAAGGCAAAATAGAAGAAC
 >Bacillus_Fam_1641_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
 Alignment score = 0.000000
 ATTGTTGGAAGTCTAAGGATAAACATCATTCTG
 >Bacillus_Fam_1642_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
 Alignment score = 0.000000
 CAACTAACAGAAACGAAAGATAACTTACAGTCA
 >Bacillus_Fam_1643_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
 Alignment score = 0.000000
 ATCAGCATGACCTTCTTGCTTAGGAGCAGGGAA
 >Bacillus_Fam_1644_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
 Alignment score = 0.000000
 AAAAGAAGAAAGCTTGTCGAGCGAGAAAAGCA
 >Bacillus_Fam_1645_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
 Alignment score = 0.000000
 GGTGTTTGTGTTCTGGTGTGTTGTCCACTTCC
 >Bacillus_Fam_1646_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
 Alignment score = 0.000000
 AGTGTTTTACTAACTTNTTCATCTAATTCAGTT
 >Bacillus_Fam_1647_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
 Alignment score = 0.000000
 TAAGTTTGATGGAAAGCTTGAGGATTTAAGCAA
 >Bacillus_Fam_1648_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
 Alignment score = 0.000000
 GTTAAACCTTGGTTCATTTCAATTTCTTACTTCC

>Bacillus_Fam_1649_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
 Alignment score = 0.000000
 CTGACGTACAAGCGGAAATGCAAGAGTTAAGAA
 >Bacillus_Fam_1650_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
 Alignment score = 0.000000
 ATTTTCATCTTTTAAGTCCACTCTCACTACCGAG
 >Bacillus_Fam_1651_32_1 Nr. of seq. 1 Alignment length(with gaps) = 32
 Alignment score = 0.000000
 CAGTTGTACAAGAACCCCTGTTTGCCAACTGT
 >Bacillus_Fam_1652_31_1 Nr. of seq. 1 Alignment length(with gaps) = 31
 Alignment score = 0.000000
 TAGAATATATGAGAAAACGTTAATTCCGTTG
 >Bacillus_Fam_1653_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
 Alignment score = 0.000000
 GGATCTTCCGGTTTCACTTCTGGTTCTTTC
 >Bacillus_Fam_1654_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
 Alignment score = 0.000000
 CTTTCATCCTATCGTGAGGCCGATCTCGAGA
 >Bacillus_Fam_1655_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
 Alignment score = 0.000000
 ATGCAAGGCGGAGGCTACCCGGGCTACGGT
 >Bacillus_Fam_1656_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
 Alignment score = 0.000000
 ATATTTTCGGTTAGCTTTTCAACATAATGGG
 >Bacillus_Fam_1657_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
 Alignment score = 0.000000
 TGCATGCCCTGCACATTGTTGGGTGGATAC
 >Bacillus_Fam_1658_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
 Alignment score = 0.000000
 TAANCAAAGAGCCTATGAGTCCAACAGGAG
 >Bacillus_Fam_1659_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
 Alignment score = 0.000000
 TTTTGTCCATCCGGCTTCTGCTCTTCTGGA
 >Bacillus_Fam_1660_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
 Alignment score = 0.000000
 AAGAAAAAGCTGAAGACGACGCAGCAGCC
 >Bacillus_Fam_1661_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
 Alignment score = 0.000000
 TTACCTGTTCCAGGGTCTGGGTTTCCTCCA
 >Bacillus_Fam_1662_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
 Alignment score = 0.000000
 CCAGCCAAGCAGCAGCCTGCAGCTCCTGCA
 >Bacillus_Fam_1663_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
 Alignment score = 0.000000
 TTTTCTTCAGCTATTTGCTTTGCCTTTGCC
 >Bacillus_Fam_1664_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
 Alignment score = 0.000000
 GATGAGCTTTCTGTTGTACTACTTTCNTCT
 >Bacillus_Fam_1665_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
 Alignment score = 0.000000
 GAGGAAGATCACGATCACGAACATGGACAT
 >Bacillus_Fam_1666_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
 Alignment score = 0.000000
 TATGGCGGTCATTCTGGATATGGTATGGGC

```

>Bacillus_Fam_1667_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
CTTGTTTCGCTTTTTCCTTCACTAATGCTG
>Bacillus_Fam_1668_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
CACCATTGTCATGATGGACATAAACCTTGC
>Bacillus_Fam_1669_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
TCTTTGATCGGTGCNTGATACTTCGGCTGT
>Bacillus_Fam_1670_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
TACTACTTCTTCAGCTGCCGCTTCTTCAGT
>Bacillus_Fam_1671_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
CCAGGACCAGGCATGATGCCAGGAGGAATG
>Bacillus_Fam_1672_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
CCACCTTGTTGGTTGCTTTGGCTGCTGTGCT
>Bacillus_Fam_1673_29_1 Nr. of seq. 1 Alignment length(with gaps) = 29
Alignment score = 0.000000
TTGCGGTAATAAACTTCTAATACCCCTT
>Bacillus_Fam_1674_28_1 Nr. of seq. 1 Alignment length(with gaps) = 28
Alignment score = 0.000000
TTGGCATTAAACGGCATTGTGATTTTGCGN
>Bacillus_Fam_1675_28_1 Nr. of seq. 1 Alignment length(with gaps) = 28
Alignment score = 0.000000
CCAGTAACGCCAGTAACACCTGTNTAAG
>Bacillus_Fam_1676_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
GGACCAACAGGNGAGCAAGGGATCCAA
>Bacillus_Fam_1677_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
GGAGATGACGGCGAAACNCCAGGCACA
>Bacillus_Fam_1678_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
CCACCATATCCATGATGGTACGGGTAA
>Bacillus_Fam_1679_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
CCATACATGCCGGATCCTGGGAAACCC
>Bacillus_Fam_1680_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
TCTTCTTCTCCTCCCGGTGGCAACTCT
>Bacillus_Fam_1681_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
CCTGGTCCGAATGGAGATACGTTTGGC
>Bacillus_Fam_1682_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
CCCGGTTCTCCTGGCTCTCCCGGTTTA
>Bacillus_Fam_1683_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
CACAGGGGCCACAAGGGTTGACGGGNN
>Bacillus_Fam_1684_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
CCAGAGCCTCCTTCTCCGTCTCCAGTG

```

>Bacillus_Fam_1685_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
 Alignment score = 0.000000
 TTTCTGAAATTGCTNCCACTTCTTGAN
 >Bacillus_Fam_1686_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
 Alignment score = 0.000000
 TGAAGCTGTTGAAGCTGTTGATGCTCT
 >Bacillus_Fam_1687_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
 Alignment score = 0.000000
 GAGGTCCTTGAGGCCAGTTGCTCCCT
 >Bacillus_Fam_1688_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
 Alignment score = 0.000000
 AGCAAAAACCGTTGCAGCCTATTCAAC
 >Bacillus_Fam_1689_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
 Alignment score = 0.000000
 GGTCTACTGGTTCAACAGGAACATCA
 >Bacillus_Fam_1690_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
 Alignment score = 0.000000
 AACTGCTTGATGAGCTCTCGCATGAGG
 >Bacillus_Fam_1691_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
 Alignment score = 0.000000
 CCTTCTGGTCCCGCTGGTCTATTGCT
 >Bacillus_Fam_1692_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
 Alignment score = 0.000000
 CCTGCATTTCTGTTCTTTCTGCTCTG
 >Bacillus_Fam_1693_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
 Alignment score = 0.000000
 GCCAATTTTACTAGGTAAAATTCTACT
 >Bacillus_Fam_1694_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
 Alignment score = 0.000000
 TCATGTCCATGCTCTTCATGCTCGTGA
 >Bacillus_Fam_1695_26_1 Nr. of seq. 1 Alignment length(with gaps) = 26
 Alignment score = 0.000000
 TGTACCAGGTACAANACCNCAACTNN
 >Bacillus_Fam_1696_25_1 Nr. of seq. 1 Alignment length(with gaps) = 25
 Alignment score = 0.000000
 TACTACCCTATGGTAAAATATGTAA
 >Bacillus_Fam_1697_25_1 Nr. of seq. 1 Alignment length(with gaps) = 25
 Alignment score = 0.000000
 TGTACCTGGTACATGANCCNGTNNT
 >Bacillus_Fam_1698_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
 Alignment score = 0.000000
 TGGAGTTGGAGGATTGGCGGACC
 >Bacillus_Fam_1699_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
 Alignment score = 0.000000
 GGGACACAGCTGTTGGAGCTGTGC
 >Bacillus_Fam_1700_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
 Alignment score = 0.000000
 CCTCCGCCAATACCAGGCACGGCG
 >Bacillus_Fam_1701_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
 Alignment score = 0.000000
 GGAGGATTTTGCGCAGGCAGGTGC
 >Bacillus_Fam_1702_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
 Alignment score = 0.000000
 ACTGTTTTTCGTTCTGCTATTTAC

>Bacillus_Fam_1703_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GACCAAAACACAATACAGAAGTTG

>Bacillus_Fam_1704_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
CCGGGTGAAGGGCCAGGAGAAAAC

>Bacillus_Fam_1705_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
AGTGTCTTTTGTTCCTCTCAGAGTT

>Bacillus_Fam_1706_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
TCGGCACTTTCATCTNCACTTTCG

>Bacillus_Fam_1707_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
TCCTCCAGTGCTGCCTCCGTTGTC

>Bacillus_Fam_1708_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
TTACCTTGGCCACCACTTGGTCG

>Bacillus_Fam_1709_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
TTGTACTTGCTCCTGCACCGGCTC

>Bacillus_Fam_1710_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
CCATGATGATTGTGATGGTGTCCG

>Bacillus_Fam_1711_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
CCTGGTCCATAACCAGGGCCCAT

>Bacillus_Fam_1712_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
CGGTACTGGCGCCGGTGGCAACGG

>Bacillus_Fam_1713_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
TGATTCATATGCGCTTGTTGCGGC

>Bacillus_Fam_1714_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GGTGGCGTTGTACCTCCATCTCCG

>Bacillus_Fam_1715_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GTTTGTGCTGGCTTTTGAGTCTGA

>Bacillus_Fam_1716_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GGCTAATAGANCGAAAGTGATAAC

>Bacillus_Fam_1717_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
TTCACGAGTAAATGACCCAATNAN

>Bacillus_Fam_1718_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
ATTCCGCCAACTATTGGAGTTNGG

>Bacillus_Fam_1719_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
ATATCAGCCAANGTAACGGGGAGC

>Bacillus_Fam_1720_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
TTTCAATTTCAATTCGTCTTCTTC

>Bacillus_Fam_1721_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
 Alignment score = 0.000000
 TTGCAGTACGCTAGAGTACTCCAG
 >Bacillus_Fam_1722_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
 Alignment score = 0.000000
 GAAAAACAGCCTGCAACAGAAGAA
 >Bacillus_Fam_1723_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
 Alignment score = 0.000000
 TGGTTCAATCNCCTCGNTCTTCAA
 >Bacillus_Fam_1724_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
 Alignment score = 0.000000
 GTGCCGTCACCAAGTACCAGTACCC
 >Bacillus_Fam_1725_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
 Alignment score = 0.000000
 GAAGAACCAACAACAGAACAACCT
 >Bacillus_Fam_1726_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
 Alignment score = 0.000000
 AAACCAAGTGAAATAGACGAGACA
 >Bacillus_Fam_1727_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
 Alignment score = 0.000000
 TTATTACCTGGTTTCTCGCCCGGT
 >Bacillus_Fam_1728_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
 Alignment score = 0.000000
 CGACCATCAGGTCAAGGCCAACAA
 >Bacillus_Fam_1729_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
 Alignment score = 0.000000
 GTGCACGCAAGAAGNCCGAAAAA
 >Bacillus_Fam_1730_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
 Alignment score = 0.000000
 TTGGCCGGTAATTTNCATTNAAA
 >Bacillus_Fam_1731_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
 Alignment score = 0.000000
 ATTCGGCCCTTANTCTCCATCNN
 >Bacillus_Fam_1732_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
 Alignment score = 0.000000
 TACATGTAAATCATATTTTCGA
 >Bacillus_Fam_1733_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
 Alignment score = 0.000000
 TACATCCAACAATTAGAGCAATT
 >Bacillus_Fam_1734_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
 Alignment score = 0.000000
 GGTGATAAATAAATACCACTCTT
 >Bacillus_Fam_1735_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
 Alignment score = 0.000000
 GTTGAACAGAANNATCAAGTTGA
 >Bacillus_Fam_1736_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
 Alignment score = 0.000000
 AATCCAGCCGANAATACGAAANG
 >Bacillus_Fam_1737_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
 Alignment score = 0.000000
 TTCGCCGATAACTNGCTNCATGN
 >Bacillus_Fam_1738_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
 Alignment score = 0.000000
 TTTTCCGGCCGGTCGACTCGACT

>Bacillus_Fam_1739_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
 Alignment score = 0.000000
 AATCGCAAATAAAATCNAAGNNN
 >Bacillus_Fam_1740_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
 Alignment score = 0.000000
 AAATCAACCAACTNATGAGTGAG
 >Bacillus_Fam_1741_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
 Alignment score = 0.000000
 TATTTTCCGTTACNGNTATATT
 >Bacillus_Fam_1742_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
 Alignment score = 0.000000
 TTTCTTGATATATCTTGCAANA
 >Bacillus_Fam_1743_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
 Alignment score = 0.000000
 TTTATCGGCCGCTTTTGATAAT
 >Bacillus_Fam_1744_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
 Alignment score = 0.000000
 TTTATTTGCGAACTAGCCACA
 >Bacillus_Fam_1745_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
 Alignment score = 0.000000
 ATTGCGGGCGTTCTANGCCATA
 >Bacillus_Fam_1746_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
 Alignment score = 0.000000
 GATACCTTATGAGTACGGAAAT
 >Bacillus_Fam_1747_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
 Alignment score = 0.000000
 GAGGAGAAGAAANAGCGGAGCN
 >Bacillus_Fam_1748_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
 Alignment score = 0.000000
 TATAATGAATTCTCAACNATA
 >Bacillus_Fam_1749_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
 Alignment score = 0.000000
 TAATCCTGATTTCGCTGCATT
 >Bacillus_Fam_1750_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
 Alignment score = 0.000000
 CAATAATTGATGCAATCAACTT
 >Bacillus_Fam_1751_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
 Alignment score = 0.000000
 TTTACTTAACAGAGCTTCGGAA
 >Bacillus_Fam_1752_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
 Alignment score = 0.000000
 TGGTGCAACACCACGCAAAAN
 >Bacillus_Fam_1753_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
 Alignment score = 0.000000
 TCTATTGGCGAATTTACCTAN
 >Bacillus_Fam_1754_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
 Alignment score = 0.000000
 TTTGATAGGAAAGCTGNTTANN
 >Bacillus_Fam_1755_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
 Alignment score = 0.000000
 TTTACCCGATTANACGCATANT
 >Bacillus_Fam_1756_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
 Alignment score = 0.000000
 TTTAATTGCAGATATAGCATAN

>Bacillus_Fam_1757_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
 Alignment score = 0.000000
 ATTCGTCCGAAATCCGCCTTCN
 >Bacillus_Fam_1758_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
 Alignment score = 0.000000
 TCGCGGGATTNCCATGCTCTTT
 >Bacillus_Fam_1759_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TCAAACCTTTTATCAACAGCA
 >Bacillus_Fam_1760_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 GGTGGCACAACAAACCCAGGC
 >Bacillus_Fam_1761_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 CCGCACGAGAAGAAGGTCCNC
 >Bacillus_Fam_1762_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 GCCGGGCACACCGCCGCCGAA
 >Bacillus_Fam_1763_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TCTTTTGGCTCACAATCC
 >Bacillus_Fam_1764_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TTACCCATATATCTGNGCACT
 >Bacillus_Fam_1765_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TTCCTTCCGTGGTAACGTGGA
 >Bacillus_Fam_1766_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 AATCGAGTGCTTTTCTCGCGG
 >Bacillus_Fam_1767_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TTTACCCATATGAATTAGCTA
 >Bacillus_Fam_1768_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TACCACATAAAATGCGGATT
 >Bacillus_Fam_1769_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 CATGAAGAAGAAGAACATGGA
 >Bacillus_Fam_1770_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TTGGCTGATATCGGTGTTGGA
 >Bacillus_Fam_1771_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TATAATGAATCTCGAANCATT
 >Bacillus_Fam_1772_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 AAAGTGATTGATAANNGGATN
 >Bacillus_Fam_1773_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TTAAACAGGTTAGGCTCTCAT
 >Bacillus_Fam_1774_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TAATTCTACCTAAAAAGNCAT

>Bacillus_Fam_1775_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 GAGCAAAAAAGNACCNTGCNG
 >Bacillus_Fam_1776_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TTTTGTGCTCANCACACCNATN
 >Bacillus_Fam_1777_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TGCCACAAGGAATGCATCAAG
 >Bacillus_Fam_1778_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 ACTGACGCAATAGCGTCTGGA
 >Bacillus_Fam_1779_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TTGGATCTTTCGGATCTGTGC
 >Bacillus_Fam_1780_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 CTTCTTGGGACCGTCATCCGG
 >Bacillus_Fam_1781_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 AAGTGACCGGTATTTNNACNA
 >Bacillus_Fam_1782_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 GAACTGCGACGGTTGCGAGAA
 >Bacillus_Fam_1783_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 GGATCATTTTCCAATATCNTT
 >Bacillus_Fam_1784_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 AATTTGTAGATATCTAGACCA
 >Bacillus_Fam_1785_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 CAGCCAGCACCGCAGCAGGCA
 >Bacillus_Fam_1786_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 CCTGGGAAAAACGGACCCACA
 >Bacillus_Fam_1787_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TTTGGATTGTTACACGCCGCA
 >Bacillus_Fam_1788_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 AACGGGAGTAAANTCCTCCTG
 >Bacillus_Fam_1789_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 ATTCAACAGTAGATTACGAGT
 >Bacillus_Fam_1790_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 ATGGACAAGCTTGAATCCCGA
 >Bacillus_Fam_1791_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TACGAGAGTAAACCTGNGTTA
 >Bacillus_Fam_1792_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TCTACAAATTCAGGNCCGTAT

>Bacillus_Fam_1793_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TGTTTCTACAAATTAAAGATG

>Bacillus_Fam_1794_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TTTTGTAGANTNAGCACTTAA

>Bacillus_Fam_1795_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TACTGTTGAAGTTTCATCTTT

>Bacillus_Fam_1796_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 AACTTCGGAAATNATAGCNTC

>Bacillus_Fam_1797_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 AGTCCAAAACCNCAATGGAAAT

>Bacillus_Fam_1798_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 CTGTTCTACAGCTTCGACAAG

>Bacillus_Fam_1799_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 AAGGAACAGCCGAAACAAGTA

>Bacillus_Fam_1800_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 AGAGATTTATCTCCAGTTAAG

>Bacillus_Fam_1801_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 ATTCCGCGAAAAAATTCTTTA

>Bacillus_Fam_1802_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TTTTCTACGGTTGGCAGCAN

>Bacillus_Fam_1803_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 AAAACCAGAAGGCGAAGGTGG

>Bacillus_Fam_1804_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 AGACTAAGCTGATACTTAATG

>Bacillus_Fam_1805_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 GGTTGGATCGGGTTGAAGAGC

>Bacillus_Fam_1806_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TTGGAAAATAAACTTNCNTN

>Bacillus_Fam_1807_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 GACGAATTATCTTCTCTCAAG

>Bacillus_Fam_1808_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 GGCACATAAACTACGTCGAGT

>Bacillus_Fam_1809_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TTATGCGCGATCTTCCCTCGG

>Bacillus_Fam_1810_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 AACAAGCACAGCANGCAATTC

>Bacillus_Fam_1811_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
TTTGCGAATAAACCATNNATT

>Bacillus_Fam_1812_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
TGCTAGATAAATAGCTACAAT

>Bacillus_Fam_1813_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCGGGATTATAGTAAAAATTC

>Bacillus_Fam_1814_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
TAATAGACAAAATACTTNGGN

>Bacillus_Fam_1815_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
CGACGCAAATAATCCAGTAAT

>Bacillus_Fam_1816_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
TAGGGCACAAATTANTTCCANN

>Bacillus_Fam_1817_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
ACCTCCTAGTCCAACAGGAAA

>Bacillus_Fam_1818_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCGAGAATCCAGACAAGAGGA

>Bacillus_Fam_1819_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GTCCTCCAATGCTTCAACTCT

>Bacillus_Fam_1820_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GGAAGCGGAGACGGAGATAGC

>Bacillus_Fam_1821_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GTTGCACCAAGTTTGTACGGT

>Bacillus_Fam_1822_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
TGGCACAAAAGGATGTTGGGT

>Bacillus_Fam_1823_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
TTGACGCACTTGNAAAATTAA

>Bacillus_Fam_1824_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
TTTATGTGTGCCNGTGAANCN

>Bacillus_Fam_1825_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
CCGAAACCTGGGCCTCCTGGG

>Bacillus_Fam_1826_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
TGCAAATAGAANGCANGAATN

>Bacillus_Fam_1827_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
TTTGGCCGGTAAATTATGCAN

>Bacillus_Fam_1828_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GAAGCTCTTCGGACTGCGTTT

```

>Bacillus_Fam_1829_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
TATCAGCCAAACTCGAGGGCT
>Bacillus_Fam_1830_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
AAATAGGTAGTAAGTGACCAT
>Bacillus_Fam_1831_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
TTTTGTTGAATGGCACCTGGT
>Bacillus_Fam_1832_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
CGCCTTGACGGACTAGACCAA
>Bacillus_Fam_1833_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
TTAGCGATTTNANACNGCCTA
>Bacillus_Fam_1834_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GACGGGTAAAATCNAANAANTT
>Bacillus_Fam_1835_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GGCGAATAAAACAGTGAGCAT
>Bacillus_Fam_1836_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
TTCTTATCAAAANAAGCGGAC
>Bacillus_Fam_1837_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
AATGATCGAAAANATCTCNAN
>Bacillus_Fam_1838_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
AAATGTTGCACAAAAACGAAA
>Bacillus_Fam_1839_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GGACGAATTATCTCCTGATTG
>Bacillus_Fam_1840_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
ATTGCGCGACTTTCATNTGGN
>Bacillus_Fam_1841_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
AGTCGCGCAATGCAGGTATAA
>Bacillus_Fam_1842_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
TGACGGGATTNCCNNTTCTTA
>Bacillus_Fam_1843_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
TGAAGGGATTTTNCACACTTG
>Bacillus_Fam_1844_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCACGAACTCCGAGCGTTTCC
>Bacillus_Fam_1845_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
TGCAAATAAAANTNNTCAAGN
>Bacillus_Fam_1846_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
TTATTTGCAGNNTTNAATNTN

```

>Bacillus_Fam_1847_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TTTATTTTCGNTTTTCCTNGT
 >Bacillus_Fam_1848_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TTTATTTTCGNTTTCTACGCA
 >Bacillus_Fam_1849_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TCGTGCGAATCATNTCGGAAT
 >Bacillus_Fam_1850_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 AATCCGCGCGATNTGAAGCAG
 >Bacillus_Fam_1851_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 ATTCGTCCAAAATCCNGTAAC
 >Bacillus_Fam_1852_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TTGGACGAATNAGNGCGNGAA
 >Bacillus_Fam_1853_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TATTATCGAAATCNANAAATT
 >Bacillus_Fam_1854_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 GGCGCAATTAATTAGANAGTN
 >Bacillus_Fam_1855_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TTAGATGTTAGTATAGCGTGT
 >Bacillus_Fam_1856_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TCGTCTTCTTCATGCGCGTGA
 >Bacillus_Fam_1857_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 CGGCTTGGAACAAAGTCGA
 >Bacillus_Fam_1858_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TTATGGGACACTGGTTTCATN
 >Bacillus_Fam_1859_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
 Alignment score = 0.000000
 TTCATTTCTTGTAGATCCCGC
 >Bacillus_Fam_1860_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
 Alignment score = 0.000000
 TTTCTTGATATANTGTNAAT
 >Bacillus_Fam_1861_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
 Alignment score = 0.000000
 TTTGCGTCAACANCCACAGA
 >Bacillus_Fam_1862_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
 Alignment score = 0.000000
 ATTTGCGTCNNTTCCNNCNG
 >Bacillus_Fam_1863_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
 Alignment score = 0.000000
 TAATGAGGGTATTAAACTTT
 >Bacillus_Fam_1864_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
 Alignment score = 0.000000
 TTATCCATCACTTCGGCCGG

```

>Bacillus_Fam_1865_20_1  Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
TTTACCGGCACTTTCACNAT
>Bacillus_Fam_1866_20_1  Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
TTACTTGCGGTTGGGGNGCG
>Bacillus_Fam_1867_20_1  Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
TTTCCGAAGTTGGCGTGTTT
>Bacillus_Fam_1868_20_1  Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
TTTACGTGCCAAATTATAGA
>Bacillus_Fam_1869_20_1  Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
TAATTGCAAAAATCCTTGAA
>Bacillus_Fam_1870_20_1  Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
TACATTAAAGTTCACTACTT
>Bacillus_Fam_1871_20_1  Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
GGCGCAAAAATCGAATGAGA
>Bacillus_Fam_1872_20_1  Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
GCGAATATATTCNTATNACG
>Bacillus_Fam_1873_20_1  Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
CGAATAAAATCAGAGTAAGGT
>Bacillus_Fam_1874_20_1  Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
TTATCCTGAAATCTATGGGT
>Bacillus_Fam_1875_20_1  Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
TGACGGGATTTTAGTNGTTA
>Bacillus_Fam_1876_20_1  Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
ATTGTGACTTTTCCATNGTT
>Bacillus_Fam_1877_20_1  Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
CGAGTTTTTTTAGGTCAGGAG
>Bacillus_Fam_1878_20_1  Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
TTTATGAGCCANTACCTCTN
>Bacillus_Fam_1879_20_1  Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
CCTGAGCTCCTCTCTCTAAT
>Bacillus_Fam_1880_20_1  Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
AGTAAAAATAGCGGGCGCGAC
>Bacillus_Fam_1881_20_1  Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
TTTATCCGTAAGAATTTTCA
>Bacillus_Fam_1882_19_1  Nr. of seq. 1 Alignment length(with gaps) = 19
Alignment score = 0.000000
TATATTCTCTACGTTATTA

```



```

>Bacillus_Fam_1883_19_1 Nr. of seq. 1 Alignment length(with gaps) = 19
Alignment score = 0.000000
CTTGATTGAGAATCCTCAG
>Bacillus_Fam_1884_19_1 Nr. of seq. 1 Alignment length(with gaps) = 19
Alignment score = 0.000000
TCATCCTCAGAATGAGTGC
>Bacillus_Fam_1885_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GGCAATGGAAACGGGAAT
>Bacillus_Fam_1886_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
CGTCTGTTGTTTGTCTC
>Bacillus_Fam_1887_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
TCAAAACCGTAGTTAAGG
>Bacillus_Fam_1888_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
CCTGGTATGGGCGGATCA
>Bacillus_Fam_1889_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
TGTGTTTACGGCATGTTG
>Bacillus_Fam_1890_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
TGACCGTGATGGACGTGA
>Bacillus_Fam_1891_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GTTGTCGTCGGTGCGGCN
>Bacillus_Fam_1892_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GTTAACTGAGGAAGAAGG
>Bacillus_Fam_1893_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
AAAGAACAACCAATCATC
>Bacillus_Fam_1894_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GATGCCTGGTGGTGGAAT
>Bacillus_Fam_1895_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
TAATTAGTTACCAAGCAA
>Bacillus_Fam_1896_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
TGCTGCTGAAGAGCAGGC
>Bacillus_Fam_1897_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GGAAAGAGAACGCGAGCG
>Bacillus_Fam_1898_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
CATCTAAACCAACTACAG
>Bacillus_Fam_1899_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
AGAGCGTTTAGACTGCTT
>Bacillus_Fam_1900_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
TATTATGAATAAAGAATC

```

>Bacillus_Fam_1901_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
AGCTCTTGAAGACGACAC

>Bacillus_Fam_1902_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
CACGGACATCACCATGGC

>Bacillus_Fam_1903_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
CCTAAGGACCCTATAGAC

>Bacillus_Fam_1904_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
CCAGGACAGCCAGGCANC

>Bacillus_Fam_1905_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
TCACCTGGTTCTTCGTTA

>Bacillus_Fam_1906_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
AGCAGAGGGTCAAAAGGC

>Bacillus_Fam_1907_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
CACTAGCCGTCGTCGCTT

>Bacillus_Fam_1908_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
TCTTGTTTGTCTGTTTA

>Bacillus_Fam_1909_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
AGCCAGGCCCGGATCCGC

>Bacillus_Fam_1910_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
AAGCTCTTGGTCTACATC

>Bacillus_Fam_1911_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
TGGCGTTTGATTATTACC

>Bacillus_Fam_1912_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GGATCAGGAAACGGCGAA

>Bacillus_Fam_1913_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
CGTTTCGCACCGTTTCGCGT

>Bacillus_Fam_1914_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
TCATCTCCTCCTGTTCCG

>Bacillus_Fam_1915_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
ATCACTGACACCATTGAT

>Bacillus_Fam_1916_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
TGCCTTGACCGCTGCCAT

>Bacillus_Fam_1917_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GTTGTTCTCAGTTTTTGC

>Bacillus_Fam_1918_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCTGCATTTGCGGTGTCG

>Bacillus_Fam_1919_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
TCTTCCATGTTTGTATCA

>Bacillus_Fam_1920_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GTCCATGGGGCTGGGGCC

>Bacillus_Fam_1921_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
CCTTGCAATCATCGGCTGG

>Bacillus_Fam_1922_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
CAGCTCCAGCAGCTTGAA

>Bacillus_Fam_1923_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GAGAAAAGCAAGGAGCAC

>Bacillus_Fam_1924_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
CCTGGTTGCGNGCAAAG

>Bacillus_Fam_1925_17_1 Nr. of seq. 1 Alignment length(with gaps) = 17
Alignment score = 0.000000
ATGATGCAAAAAAGACG

>Bacillus_Fam_1926_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GTAACAATGAACCAA

>Bacillus_Fam_1927_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GCAGCAGTTCNCGGC

>Bacillus_Fam_1928_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GGATCTTCTTTNACC

>Bacillus_Fam_1929_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
AATAATGGCAACGGC

>Bacillus_Fam_1930_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
TATTCGCTCCAGTGC

>Bacillus_Fam_1931_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
ATCACGAATTCTATA

>Bacillus_Fam_1932_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
ATTTCTCCGCTTGGC

>Bacillus_Fam_1933_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
ATTGTAAAAATAAAT

>Bacillus_Fam_1934_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
TTCAAGTTCAAGCAA

>Bacillus_Fam_1935_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
AGATTGAGTAAACAG

>Bacillus_Fam_1936_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GCTGGTGCCTTCGCT

>Bacillus_Fam_1937_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
TTAATTGGTGCTNCT

>Bacillus_Fam_1938_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
TGAACTTCTTATTTC

>Bacillus_Fam_1939_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
TTCATCGGTTGCTGG

>Bacillus_Fam_1940_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
ATGCATGAGAACACC

>Bacillus_Fam_1941_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
AGACGTTCTAGTAGA

>Bacillus_Fam_1942_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
TCTCCGTGCTCATGG

>Bacillus_Fam_1943_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GAAGTGTTCCGTCTC

>Bacillus_Fam_1944_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
CAACCGATCCAGGAC

>Bacillus_Fam_1945_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
AATCCTGGACCTCCA

>Bacillus_Fam_1946_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
CCGGGGAAACCGCCA

>Bacillus_Fam_1947_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
CACTGATGATCCGGG

>Bacillus_Fam_1948_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
TGCATCATTTGGTGAT

>Bacillus_Fam_1949_14_1 Nr. of seq. 1 Alignment length(with gaps) = 14
Alignment score = 0.000000
ATTTTGTAGTCGTG

>Bacillus_Fam_1950_13_1 Nr. of seq. 1 Alignment length(with gaps) = 13
Alignment score = 0.000000
TACTAGGAGACAG

>Bacillus_Fam_1951_13_1 Nr. of seq. 1 Alignment length(with gaps) = 13
Alignment score = 0.000000
AGTGTTTCAGGATA

>Bacillus_Fam_1952_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
CGTGATGGTAAT

>Bacillus_Fam_1953_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
CGTTCAAGCCGT

>Bacillus_Fam_1954_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
CAAATATGATGC

>Bacillus_Fam_1955_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
CGTTGTATTATT

>Bacillus_Fam_1956_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
ATGCAAACTCTA

>Bacillus_Fam_1957_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
CTTTTTTACAAC

>Bacillus_Fam_1958_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
ACGACATGGACA

>Bacillus_Fam_1959_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
TGGTTCCATTGC

>Bacillus_Fam_1960_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
TCTTTGATTCCT

>Bacillus_Fam_1961_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
ATTGGTGCCTTT

>Bacillus_Fam_1962_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
GGGCGTTCTTCG

>Bacillus_Fam_1963_11_1 Nr. of seq. 1 Alignment length(with gaps) = 11
Alignment score = 0.000000
GCACTATTTTC

>Bacillus_Fam_1964_11_1 Nr. of seq. 1 Alignment length(with gaps) = 11
Alignment score = 0.000000
AGGGGCTTAGA

>Bacillus_Fam_1965_11_1 Nr. of seq. 1 Alignment length(with gaps) = 11
Alignment score = 0.000000
CCAAAAACCGC

>Bacillus_Fam_1966_10_1 Nr. of seq. 1 Alignment length(with gaps) = 10
Alignment score = 0.000000
TTGTCGCGGA