

Forward and reverse sequence alignments of 56 CAZy with correct sequences that were transformed into BL21 cells for enzyme purification

cphy0218_1

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>Cphy0218 reverse

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Sbjct: 421 ggtatagaaaagaagggtgcacatgatcctcaatatttaagaagaatttctcaagactta 480

Query: 551 tttgacgaatataatgagttatcccgggaatgcaattcgcttagtagatattgatccaac 610
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Sbjct: 768 |atgaattccgtcacagataatttctgcatttaaaccaaactcactaactgcaccaactaa 709

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cphy3586_1

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Sbjct: 421 cagctagctacaaaggaatctatccggagtgggttcaggttggaacgagattaacagc 480

Query: 549 ggtatggtattaccttatggacagagcagtaataactttagccagctgacagagtactg 608
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Sbjct: 481 ggtatggtattaccttatggacagagcagtaataactttagccagctgacagagtactg 540

Query: 609 aatagtggatatgatgcggtaaaaagcggtaaagcaaactcgactaaagttgtaactcatc 668
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Sbjct: 541 aatagtggatatgatgcggt-aaaagcgg-taaagcaaactcgactaaagttgtaactcatc 598

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Query: 126  catctggcttaacgcattggtgtctgtttgttgaccaaggccacgccttcctctgttga 185
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Query: 186  agcattctgtacagctaagagtttaccgcttcctcgattgatcagcttataatacccatc 245
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Query: 546  attatagcgacaatcataaaaagcatcaatagctgtggtgaaccttaatTTTTTCCAGA 605
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Sbjct: 1029 attatagcgacaatcataaaaagcatcaatagctgtggtgaaccttaatTTTTTCCAGA 970

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Sbjct: 241 ||| gcttccactcaggagatagagggtgtaacataaacggtagtagtattgtagaacagggaaat 300

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>Cphy3869* reverse

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Identities = 864/879 (98%), Gaps = 7/879 (0%)
Strand = Plus / Minus

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Sbjct: 4248 ||| gtgtaatggatagtgatcTTAatgggtgatgggtgatgatgctcttcaataataactttaat 4189


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Query: 848 ggaacatttctctgtaataacaaggaatccattcatgtttattgttccctcctacttttc 907
||| ||| |||
Sbjct: 3470 ggagca-ttctctgtaataacaaggaatccattcatgtttattgttccat-ctacatttc 3413

Query: 908 ttggaaatcccattgaaaagttaagcttttcaaaccaat 946
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Cphy0220

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>Cphy0220 forward
Length = 2220
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Score = 1564 bits (789), Expect = 0.0
Identities = 831/841 (98%), Gaps = 3/841 (0%)
Strand = Plus / Plus
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Sbjct: 1 aaagaaggagataggatcatgaagaaggtaaatgaatcagtaatcgaagaattattaagt 60
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```
Query: 130 cagatgaccttagaagaaaagataggcttaattcatggtaatggcatctttcgtagtggt 189
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Sbjct: 61 cagatgaccttagaagaaaagataggcttaattcatggtaatggcatctttcgtagtggt 120
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Query: 190 ggggtggaacgccttggcataccttccttgaagatgtcggatggcccaatgggtgttcgt 249
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Query: 250 agagagtttgaagacaatagggtggtttcttgctgcaaacggacgattacgtatcttat 309
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Query: 310 cttccgagcaatagtgcaatagcagctacatggaataaagatcttgcctatacttcaggt 369
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Sbjct: 241 cttccgagcaatagtgcaatagcagctacatggaataaagatcttgcctatacttcaggt 300
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Query: 370 caagttcttggtagtgaaagcaaggggaagaggaaaagatggtatcttagcgccaggtatt 429
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Query: 910 g 910
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Sbjct: 838 g 838
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Cphy0220 reverse sequence

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Strand = Plus / Minus
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Query: 126 caacctgatatccctagaagagctaccaacttcaatgatgaactctccgccctctaatac 185
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Query: 186 aaatttcttactctcggatacaataataggtaaaggcagatggctttaattccatcatcaa 245
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Query: 246 ttcttttctcctctcccggctgtnnnnnnctttggatgaacccttttaattcatgaatagg 305
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Query: 306 gcgctttactgcaaaactggatcagaaacataaacttgaattgtctcagctccagctgt 365
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Sbjct: 1440 |||
accttccatatcttgatgatgatctaatacctacaacaagaataacatcctccgtttctct 1381

Query: 906 tggaaagtaaaccgcttcttcccgaagacgtttc 939

Sbjct: 1380 |||
tgcaagtaaaccgcttcttcccgaagacgtttc 1347

#####

Cphy0430 forward sequence

Query= HR0ADKBY80ZE01_CAZYB2C1P16_1.SCF 1380 0 1380 SCF

>Cphy0430 forward

Length = 2550

Score = 1334 bits (673), Expect = 0.0
Identities = 698/705 (99%), Gaps = 1/705 (0%)
Strand = Plus / Plus

Query: 69 aaagaaggagataggatcATGaaatttggattctttgatgatttaacaagaatacgtt 128

Sbjct: 1 |||
aaagaaggagataggatcatgaaatttggattttttgatgatttaacaagaatacgtt 60

Query: 129 atcacaactcctgaaacgccgtatccttggattaactatcttggatcgcaagcgttcttt 188

Sbjct: 61 |||
atcacaactcctgaaacgccgtatccttggattaactatcttggatcgcaagcgttcttt 120

Query: 189 tccttgatatcaaatactgctggaggttacagtttctataaagatgcaaaactacgtagg 248

Sbjct: 121 |||
tccttgatatcaaatactgctggaggttacagtttctataaagatgcaaaactacgtagg 180

Query: 249 attacaagatttcggtataataatgtaccattagatctcggtggtggtcgttattactac 308

Sbjct: 181 |||
attacaagatttcggtataataatgtaccattagatctcggtggtggtcgttattactac 240

Query: 309 ttgtacgataatggtgatttttggctctccgggttttggccctgcaaaaaaggaactagaa 368

Sbjct: 241 |||
ttgtacgataatggtgatttttggctctccgggttttggccctgcaaaaaaggaactagaa 300

Query: 369 tattatgagtgtcgtcatggcatgggttataactaaaataacaggaagaagaatggaatt 428

Sbjct: 301 |tattatgagtgctcgatggcatgggttataactaaaataacaggaagaagaatggaatt| 360

Query: 429 gaaacaaagataaccttctttgtaccattagactataatggtgaagtacataaagtgtca 488

Sbjct: 361 |gaaacaaagataaccttctttgtaccattagactataatggtgaagtacataaagtgtca| 420

Query: 489 attgttaatacaagtaatcaagtgaagaatgtgaaattgttttctttcctcgagtgggtg 548

Sbjct: 421 |attgttaatacaagtaatcaagtgaagaatgtgaaattgttttctttcctcgagtgggtg| 480

Query: 549 ctgtggaatgcacaagaagattctacaaatcttcaacgaaatctcgacaggtgaagta 608

Sbjct: 481 |ctgtggaatgcacaagaagattctacaaatcttcaacgaaatctcgacaggtgaagta| 540

Query: 609 gaagttaaagggctgtaatctatcataagacagagtataaagaaagacgggatcattat 668

Sbjct: 541 |gaagttaaagggctgtaatctatcataagacagagtataaagaaagacgggatcattat| 600

Query: 669 gcatttttctctgtaaatgcaccgattaacggattcaattctgatcgcgagagttttctt 728

Sbjct: 601 |gcatttttctctgtaaatgcaccgattagcggattcgattctgatcgcgagagttttctt| 660

Query: 729 ggaacctatcatggttttgaaaaacccgcaggtagttgccagggg 773

Sbjct: 661 |ggtagctatcatggttttg-ataacccgcaggtagttgccagggg| 704

Cphy0430 reverse sequence

Query= HR0ADKBY80ZE01_CAZYB2C1P17_1.SCF 1294 0 1294 SCF

>Cphy0430 reverse
Length = 2550

Score = 1768 bits (892), Expect = 0.0
Identities = 935/944 (99%), Gaps = 4/944 (0%)
Strand = Plus / Minus

Query: 66 gtgtaatggatagtgatCTTAatggtgatggtgatgatgacctaagatgacttttacttt 125

Sbjct: 2550 |gtgtaatggatagtgatcttaatggtgatggtgatgatgacctaagatgacttttacttt| 2491

Query: 126 atgttctaataccgtcaccaaataaccggaatgatattaccctccacctctttcgcatcaac 185

Sbjct: 2490 |atgttctaataccgtcaccaaataaccggaatgatattaccctccacctctttcgcatcaac| 2431

Query: 186 aactagtttcttaacacctttcgaaacatgatatgggtttactattgtaatatcatacct 245

Sbjct: 2430 |aactagtttcttaacacctttcgaaacatgatatgggtttactattgtaatatcatacct| 2371

```
Query: 246 atcaccacggaattcacgtgttatttgatataacctcccaatcagttgggattgcagggtc 305
|||||
Sbjct: 2370 atcaccacggaattcacgtgttatttgatataacctcccaatcagttgggattgcagggtc 2311

Query: 306 aatcattaaaccatcatattctggtttaattccaagtatataattgtgatatcgctacaaa 365
|||||
Sbjct: 2310 aatcattaaaccatcatattctggtttaattccaagtatataattgtgatatcgctacaaa 2251

Query: 366 attccaagatgcagttccggttaaccaagaatTTTTGcttcacaaaacgtctggcatc 425
|||||
Sbjct: 2250 attccaagatgcagttccggttaaccaagaatTTTTGcttcacaaaacgtctggcatc 2191

Query: 426 cttacctgcaacctctgagcgtagacatatggctccaaacgatgaatttcagagtattc 485
|||||
Sbjct: 2190 cttacctgcaacctctgagcgtagacatatggctccaaacgatgaatttcagagtattc 2131

Query: 486 ttctgtatacgctggtgcaatTTTTgtatagtaatcaaaggctttatccccacggcctat 545
|||||
Sbjct: 2130 ttctgtatacgctggtgcaatTTTTgtatagtaatcaaaggctttatccccacggcctat 2071

Query: 546 cactgcttccgcacacataatccaggcattgttatgacagaagataacctgcattttcttt 605
|||||
Sbjct: 2070 cactgcttccgcacacataatccaggcattgttatgacagaagataacctgcattttcttt 2011

Query: 606 atatccagctggataggtagaaatctcgccatattccacataatatcgtgtaaatgctgg 665
|||||
Sbjct: 2010 atatccagctggataggtagaaatctcgccatattccacataatatcgtgtaaatgctgg 1951

Query: 666 attatttagaactaatccgaatTTTTgtaccxaaacgtTTTTctacagaatctaaagcttt 725
|||||
Sbjct: 1950 attatttagaactaatccgaatTTTTgtaccxaaacgtTTTTctacagaatctaaagcttt 1891

Query: 726 ttgtgctttcccatcgtaagaccgcattttcccataacgcagaagccttgcgattcgat 785
|||||
Sbjct: 1890 ttgtgctttcccatcgtaagaccgcattttcccataacgcagaagccttgcgattcgat 1831

Query: 786 aaatTTTTtcttcttcacactcatcactaccaatTTTTtcttccaaatcatcgtaggc 845
|||||
Sbjct: 1830 aaatTTTTtcttcttcacactcatcactaccaatTTTTtcttccaaatcatcgtaggc 1771

Query: 846 acgtaaaaaccaagatccatcatagccatgcttcataaatacatctcgaaattctctac 905
|||||
Sbjct: 1770 acgtaaaaaccaagatccatcatagccatgcttcataaattacatctcgatattctctac 1711

Query: 906 ttctttcatggcgcaatagactcttcgttaatTTTctaccttaaccataagaatagcat 965
```


Query: 489 aatgcaaaggctctatgtcgaacacagaatataagagttcaccatcaagtcaagatctctta 548
|||||
Sbjct: 421 aatgcaaaggctctatgtcgaacacagaatataagagttcaccatcaagtcaagatctctta 480

Query: 549 gacttttacattgatgatttcactgcaacgccagcaactttaccacagattcaaaaagat 608
|||||
Sbjct: 481 gacttttacattgatgatttcactgcaacgccagcaactttaccacagattcaaaaagat 540

Query: 609 attcctagtttaaaggatgtatcttcaagttacttctttgttggtggagcggcaactgca 668
|||||
Sbjct: 541 attcctagtttaaaggatgtatcttcaagttacttctttgttggtggagcggcaactgca 600

Query: 669 ggtgagattgcaccagctccggcaaaagatttagtagcgaacattacaataggttaact 728
|||||
Sbjct: 601 ggtgagattgcaccagctccggcaaaagatttagtagcgaacattacaataggttaact 660

Query: 729 cctggtaatgagttaaaaccagactctgtattagattactctgcaaccataacctatag 788
|||||
Sbjct: 661 cctggtaatgagttaaaaccagactctgtattagattactctgcaaccatagcctatag 720

Query: 789 gatgcaaatggtggtaatcaagtgaatcctcaggtgaatcttagagctgcgaaaacttta 848
|||||
Sbjct: 721 gatgcaaatggtggtaatcaagtgaatcctcaggtgaatcttagagctgcgaaaacttta 780

Query: 849 ctggaatatgcaagaacaataatataaccaatggcgtggacataccttaatatgg 903
|||||
Sbjct: 781 ctggaatatgcaagagacaataatataaccagt-gcgtggacataccttagtatgg 834

Cphy0624 reverse sequence

Query= HR0ADKBY80ZH01_CAZYC2C4P17_1.SCF 1299 0 1299 SCF

>Cphy0624* reverse

Length = 2238

Score = 1709 bits (862), Expect = 0.0
Identities = 900/912 (98%), Gaps = 2/912 (0%)
Strand = Plus / Minus

Query: 65 gtgtaatggatagtgatTTAatggtgatggtgatgatggtgaactttgactccattata 124
|||||
Sbjct: 2238 gtgtaatggatagtgatcttaatggtgatggtgatgatggtgaactttgactccattata 2179

Query: 125 gtaaacctttaacacttcattggatatacgtacaaaatccgtccaatccttcttagcaaa 184
|||||
Sbjct: 2178 gtaaacctttaacacttcattggatatacgtacaaaatccgtccaatccttcttagcaaa 2119

Query: 185 tcgtaaatcaagaacaagctttcctgttccttctgacagcatcgactcttactgatgct 244
 |||
 Sbjct: 2118 tcgtaaatcaagaacaagctttcctgttccttctgacagcatcgactcttactgatgct 2059

Query: 245 aaccacaagtttttgattcgtcaactgccagaaacataaccatttaacgggtgtgtaata 304
 |||
 Sbjct: 2058 aaccacaagtttttgattcgtcaactgccagaaacataaccatttaacgggtgtgtaata 1999

Query: 305 tggttcaactgtaattgcaacgcagcgttatctaccaaacattatgctcttgattgat 364
 |||
 Sbjct: 1998 tggttcaactgtaattgcaacgcagcgttatctaccaaacattatgctcttgattgat 1939

Query: 365 gattccatcggcagtaaaccaatagatacctttgacaaatcaatcgttccaccaagtgc 424
 |||
 Sbjct: 1938 gattccatcggcagtaaaccaatagatacctttgacaaatcaatcgttccaccaagtgc 1879

Query: 425 atttattgtgattgctggcttatcgtgttccattgttttctgtagttactactaccac 484
 |||
 Sbjct: 1878 atttattgtgattgctggcttatcgtgttccattgttttctgtagttactactaccac 1819

Query: 485 cggttttgctccctccactggactgtagtaggagttgggtgctcggagctattggtggttt 544
 |||
 Sbjct: 1818 cggttttgctccctccactggactgtagtaggagttgggtgctcggagctattggtggttt 1759

Query: 545 tggcgttactgttgggttattgtaggagttattggtggctttgggtttacagttgggtgt 604
 |||
 Sbjct: 1758 tggcgttactgttgggttattgtaggagttattggtggctttgggtttacagttgggtgt 1699

Query: 605 tactgtaggtgttatcgttggttttggcgttacagttgggtttactgtaggtgttatcgt 664
 |||
 Sbjct: 1698 tactgtaggtgttatcgttggttttggcgttacagttgggtttactgtaggtgttatcgt 1639

Query: 665 tggttttgggtttacagttggagttattgatggcgttactgttggggtaatcccatcaat 724
 |||
 Sbjct: 1638 tggttttgggtttacagttggagttattgatggcgttactgttggggtaatcccatcaat 1579

Query: 725 gatagaatagtatgctgactttgcttgataatttccatcaaataataatggatatccacc 784
 |||
 Sbjct: 1578 gatagaatagtatgctgactttgcttgataatttccatcaaataataatggatatccacc 1519

Query: 785 taaccaactagtcttatccgttacaccccagaagataaactcctgtaatgttcatgccctc 844
 |||
 Sbjct: 1518 taaccaactagtcttatccgttacaccccagaagataaactcctgtaatgttcatgccctc 1459

Query: 845 nnnnnncaaaactaatgaccttatttatcaaaagtttatatctggctgcctgagcagcta 904
 |||
 Sbjct: 1458 -tttttcaaaactaatgaccttatttatcaaaagtttatatctgtctgcctgagcagcta 1400

Sbjct: 361 ||| acaaacagtggaattcagatgtattctacggaacaacagcgcaacgatggattttttaa 420

Query: 487 gactacagttcaacttccaatattccagaggatgggtgttaaaggtaaattaacaaataaa 546

Sbjct: 421 ||| gactacagttcaacttccaatattccagaggatgggtgttaaaggtaaattaacaaataaa 480

Query: 547 gttgcagcagatgcaatcgtagttcctgctccaaacagcgatgtttcaagcattggtgcc 606

Sbjct: 481 ||| gttgcagcagatgcaatcgtagttcctgctccaaacagcgatgtttcaagcattggtgcc 540

Query: 607 acgatgccatattgtacgttatgattccgaatatgcagtattaggtgggtggcgcaaggctt 666

Sbjct: 541 ||| acgatgccatattgtacgttatgattccgaatatgcagtattaggtgggtggcgcaaggctt 600

Query: 667 gcaacctcaacgaattgggatttaacgaatattgctagccaggcatccaatcaatcttat 726

Sbjct: 601 ||| gcaacctcaacgaattgggatttaacgaatattgctagccaggcatccaatcaatcttat 660

Query: 727 gtcgttcttccatcgagcggttcttatgcggaatggagagtaaattcttctggtaatggt 786

Sbjct: 661 ||| gtcgttcttccatcgagcggttcttatgcggaatggagagtaaattcttctggtaatggt 720

Query: 787 gttgttatgagatttaccttaccggatactccgaacggaatgggacaaaatggttcctta 846

Sbjct: 721 ||| gttgttatgagatttaccttaccggatactccgaacggaatgggacaaaatggttcctta 780

Query: 847 aacgtatatgtgaatggctccaaagtaaaaaacagttaatttaacttcgtattatatgtg 906

Sbjct: 781 ||| aacgtatatgtgaatggctccaaagt-aaaaacagttaatttaacttcgtattatatgtg 839

Query: 907 gcaatatttaaaatgggggtgcaaatgaaaaccccaggtgggtggcactgc 957

Sbjct: 840 ||| gcaatattt-aaatgggtggtgcaagtg-ataccccaggt-ggtggcactgc 887

Cphy1308 reverse sequence

Query= HR0ADKBY80ZC02_CAZYD2C3P17_1.SCF 1337 0 1337 SCF

>Cphy1308* reverse

Length = 3225

Score = 1614 bits (814), Expect = 0.0
Identities = 861/870 (98%), Gaps = 5/870 (0%)
Strand = Plus / Minus

Query: 67 gtgtaatggatagtgatcTTAatgggtgatgggtgatgatgacgtactgtcatcgttttcgt 126

Sbjct: 3225 |gtgtaatggatagtgatcttaatggtgatggtgatgatgacgtactgtcatcgttttcgt 3166

Query: 127 |caaagtgttattatctgtattggattctggataaccgattaatatcattgaccaagccat 186
|

Sbjct: 3165 |caaagtgttattatctgtattggattctggataaccgattaatatcattgaccaagccat 3106

Query: 187 |aacattaaaggtacctgccgtagcagtataggttgactgccagctggaccactatttgc 246
|

Sbjct: 3105 |aacattaaaggtacctgccgtagcagtataggttgactgccagctggaccactatttgc 3046

Query: 247 |tgttaccgtcactgactgtcctggcattatctgagttgtattggtatcggaccaagaaac 306
|

Sbjct: 3045 |tgttaccgtcactgactgtcctggcattatctgagttgtattggtatcggaccaagaaac 2986

Query: 307 |acaggtaccattcacttggattgtaatccggtgattgcccctactggagctactccggt 366
|

Sbjct: 2985 |acaggtaccattcacttggattgtaatccggtgattgcccctactggagctactccggt 2926

Query: 367 |tccttgattcttaataactgcactaaatgtgatcttattcccgttactgggcttgctgg 426
|

Sbjct: 2925 |tccttgattcttaataactgcactaaatgtgatcttattcccgttactgggcttgctgg 2866

Query: 427 |agaccaagtaatatccgttacaaccatatctggattaccataagggtgccccgttgggggt 486
|

Sbjct: 2865 |agaccaagtaatatccgttacaaccatatctggattaccataagggtgccccgttgggggt 2806

Query: 487 |agggtgctgggtgaaccggttggtgtaccgctccttctgttacagtaagtggttttgtaa 546
|

Sbjct: 2805 |agggtgctgggtgaaccggttggtgtaccgctccttctgttacagtaagtggttttgtaa 2746

Query: 547 |catattattattggtattagactcaggataacgattaacatcgtttaccatgcagtaat 606
|

Sbjct: 2745 |catattattattggtattagactcaggataacgattaacatcgtttaccatgcagtaat 2686

Query: 607 |ggtataggtacctgtcttcgctgcccattgttgagagccagaaggcccacttacggctgt 666
|

Sbjct: 2685 |ggtataggtacctgtcttcgctgcccattgttgagagccagaaggcccacttacggctgt 2626

Query: 667 |tactgtaatggattgacctggttgaatctgagttttgtcattatctgaccaagaaacact 726
|

Sbjct: 2625 |tactgtaatggattgacctggttgaatctgagttttgtcattatctgaccaagaaacact 2566

Query: 727 |agtaccatttacttgaaattgaactccattaattgatccaagtggcgctacccccagttc 786
|

Sbjct: 2565 |agtaccatttacttgaaattgaactccattaattgatccaagtggcgcta-ccccagttc 2507

Query: 787 ctatatttttaataactgcactaaaagtaactttgattgccatttggttgatttgctgg 846
|||||
Sbjct: 2506 ctatatttttaataactgcactaaaagtaac-ttgattgcca-ttggttgatttgctgg 2449

Query: 847 tgaccacgtaatatctgtaacaatcatatctggattaccatatggaacagaaagggtttg 906
|||||
Sbjct: 2448 tgaccacgtaatatctgtaacaatcatatctggattaccatatggaacag-aaggtgttg 2390

Query: 907 gctttactgttggtgaatgggtagctgtt 936
||
Sbjct: 2389 gcgttactgttggtg-atggtgtagctgtt 2361

#####

Cphy1888 forward sequence

Query= HR0ADKBY80ZE02_CAZYE1C1P16_1.SCF 1343 0 1343 SCF

>Cphy1888* forward

Length = 1803

Score = 1542 bits (778), Expect = 0.0
Identities = 818/826 (99%), Gaps = 4/826 (0%)
Strand = Plus / Plus

Query: 69 aaagaaggagataggatcATGacgacgacaacacatgaattaaatgtatcaaattcaatg 128
|||||
Sbjct: 1 aaagaaggagataggatcatgacgacgacaacacatgaattaaatgtatcaaattcaatg 60

Query: 129 acagtaggacaataactcatcagattttactttaaatggatttacatttattacaggagga 188
|||||
Sbjct: 61 acagtaggacaataactcatcagattttactttaaatggatttacatttattacaggagga 120

Query: 189 tctatatgggaagtagatagctctagccggtcttacggtggtgtaaactttacgcagaga 248
|||||
Sbjct: 121 tctatatgggaagtagatagctctagccggtcttacggtggtgtaaactttacgcagaga 180

Query: 249 gttaaactcgggcgaaaggtaccattagtaaaagagcaatctcatttacagcttctgga 308
|||||
Sbjct: 181 gttaaactcgggcgaaaggtaccattagtaaaagagcaatctcatttacagcttctgga 240

Query: 309 gcaggtcaattaacagtttatgcaatgagttctggaagtacttcaagaaatgtaacgctt 368
|||||
Sbjct: 241 gcaggtcaattaacagtttatgcaatgagttctggaagtacttcaagaaatgtaacgctt 300

Query: 369 tatgggaacggtaaggatctagaaagctttactgcaagatgtcattactgctatg 428
|||||
Sbjct: 301 tatgggaacggtaaggatctagaaagctttactgcaagatgtcattactgctatg 360

Query: 429 aatTTTAcgattccAAattccGgtactTatgTtattTatccaccagacgatggTattagc 488
|||||
Sbjct: 361 aatTTTAcgattccAAattccGgtactTatgTtattTatccaccagacgatggTattagc 420

Query: 489 tactactattTaaaggtagTtaaAaccgactcaacacctacaccaactccaacagTaaaa 548
|||||
Sbjct: 421 tactactattTaaaggtagTtaaAaccgactcaacacctacaccaactccaacagTaaaa 480

Query: 549 ccgaccCAAacacctacaccaactccaactacatCAAatgaagTttacgtctCAAaCaat 608
|||||
Sbjct: 481 ccgaccCAAacacctacaccaactccaactacatCAAatgaagTttacgtctCAAaCaat 540

Query: 609 ggTtctgcaagTgcaagTggtacatattccAatccAAaatccttagagggagcgattagT 668
|||||
Sbjct: 541 ggTtctgcaagTgcaagTggtacatattccAatccAAaatccttagagggagcgattagT 600

Query: 669 tcggcgAAagctggacAAaccattttTatgTtaccaggtactTattctTatagTAcAcAA 728
|||||
Sbjct: 601 tcggcgAAagctggacAAaccattttTatgTtaccaggtactTattctTatagTAcAc-a 659

Query: 729 aataacAattccagcaggaacCAatggtacatccagTgcacgaattAAattaatgCcata 788
|||||
Sbjct: 660 aataacAattccagcaggaacCAatggtacatccagTgcacgaattAAattaatgCcata 719

Query: 789 caaataatggtagTgtaactcttaatttctcatctcaccatacggtaatccggatact 848
| |||||
Sbjct: 720 c-aataatggtagTgtaactcttaattt-ctcatctcagccatacggtaatcctgatact 777

Query: 849 aatTTtAcgaagtattcAAactggatgCAaattttTgggcatatctat 894
|||||
Sbjct: 778 aatTTtAcgaggtattcAAactggatgCAaattatt-ggcatatctat 822

Cphy1888 reverse sequence
Query= HR0ADKBY80ZE02_CAZYE1C1P17_1.SCF 1345 0 1345 SCF

>Cphy1888* reverse

Length = 1803

Score = 1556 bits (785), Expect = 0.0
Identities = 839/849 (98%), Gaps = 6/849 (0%)
Strand = Plus / Minus

Query: 66 gtgtaatggatagTgatcTTAatggTgatggTgatgatgatttccTtagattagctcccat 125
|||||
Sbjct: 1803 gtgtaatggatagTgatcTtaatggTgatggTgatgatgatttccTtagattagctcccat 1744

Sbjct: 361 attcattccgaagctttatattatgttcctttaacaagacacatgaagtttgggaagttg 420

Query: 489 tctgtaaccaataaccgacaataaagaacgaaaaatttccaccttcggcttcattgaattt 548
|||||

Sbjct: 421 tctgtaaccaataaccgacaataaagaacgaaaaatttccaccttcggcttcattgaattt 480

Query: 549 acgaatgaggactattatgaaaatgatcaagttaatctccagtatacactctttattacc 608
|||||

Sbjct: 481 acgaatgaggactattatgaaaatgatcaagttaatctccagtatacactctttattacc 540

Query: 609 aaaacttattttaagagaataagatcctacaacaattaacgaaaatactggcaagaat 668
|||||

Sbjct: 541 aaaacttattttaagagaataagatcctacaacaattaacgaaaatactggcaagaat 600

Query: 669 gcagaaggtacgaattaccgtgaacgtttctttggtagtgtagggtcaacctattgtttcc 728
|||||

Sbjct: 601 gcagaaggtacgaattaccgtgaacgtttctttggtagtgtagggtcaacctattgtttcc 660

Query: 729 tataatggtgacaaggcatcctttattggcgttatcatagttatggaaatccagttgcc 788
|||||

Sbjct: 661 tataatggtgacaaggcatcctttattggcgttatcatagttatggaaatccagttgcc 720

Query: 789 ggtatcaatggatgctgcgataaactttaaaattataattctaacgcatgcggtgccct 848
| |||||

Sbjct: 721 gttatcaatggatgctgcgataaacttt-aaattataattctaacgcatgcggtgccct 779

Query: 849 tcactcccata-taactcttgcccctggtgaaacaaaaggaattataaaacatattaggt 907
||||| ||||| |||||

Sbjct: 780 tcact-ccatattaactcttgccacctggtgaaac-aaaggaattagtatacatattaggt 837

Cphy1929 reverse sequence

Query= HR0ADKBY80ZH02_CAZYF1C4P17_1.SCF 1333 0 1333 SCF

>Cphy1929 reverse

Length = 2448

Score = 1606 bits (810), Expect = 0.0
Identities = 836/842 (99%), Gaps = 2/842 (0%)
Strand = Plus / Minus

Query: 68 gtgtaatggatagtgatcTTAatggtgatggtgatgatgcattactaataataacttcatt 127
|||||

Sbjct: 2448 gtgtaatggatagtgatccttaatggtgatggtgatgatgcattactaataataacttcatt 2389

Query: 128 ttctacagatagtgattccgcaggaatgtaatttgaagaaagtattgttccatttaagta 187

Sbjct: 2388 |ttctacagatagtgattccgcaggaatgtaatttgaagaaagtattgttccatttaagta| 2329

Query: 188 acattcgcggtaccaccttctgcacccatcaaagttttgtatcgtaatatttaacttctt 247
|ttctacagatagtgattccgcaggaatgtaatttgaagaaagtattgttccatttaagta|

Sbjct: 2328 acattcgcggtaccaccttctgcacccatcaaagttttgtatcgtaatatttaacttctt 2269

Query: 248 attgcggaacatcttagtaattttaacttctttccaattggatggatggaaggggagag 307
|attgcggaacatcttagtaattttaacttctttccaattggatggatggaaggggagag|

Sbjct: 2268 attgcggaacatcttagtaattttaacttctttccaattggatggatggaaggggagag 2209

Query: 308 taatagaccatcgaagttaggacgtatacctaagataccttcgacgcagccaacccatcac 367
|taatagaccatcgaagttaggacgtatacctaagataccttcgacgcagccaacccatcac|

Sbjct: 2208 taatagaccatcgaagttaggacgtatacctaagataccttcgacgcagccaacccatcac 2149

Query: 368 agttgatgcagttcctgtcaaccagtgatcatgggatcggccttcaaatgggctatcaac 427
|agttgatgcagttcctgtcaaccagtgatcatgggatcggccttcaaatgggctatcaac|

Sbjct: 2148 agttgatgcagttcctgtcaaccagtgatcatgggatcggccttcaaatgggctatcaac 2089

Query: 428 cgattctgtaaattgcccatgaacatatgggtcaagaacacggacatctgcattatcatt 487
|cgattctgtaaattgcccatgaacatatgggtcaagaacacggacatctgcattatcatt|

Sbjct: 2088 cgattctgtaaattgcccatgaacatatgggtcaagaacacggacatctgcattatcatt 2029

Query: 488 ctgagaagatggagagctctccttaaaatactgataggcgcaatccatgaccattaa 547
|ctgagaagatggagagctctccttaaaatactgataggcgcaatccatgaccattaa|

Sbjct: 2028 ctgagaagatggagagctctccttaaaatactgataggcgcaatccatgaccattaa 1969

Query: 548 ggattctgcaaggatgatccaacctgtggctgcgagaagataccaccattctctttgg 607
|ggattctgcaaggatgatccaacctgtggctgcgagaagataccaccattctctttgg|

Sbjct: 1968 ggattctgcaaggatgatccaacctgtggctgcgagaagataccaccattctctttgg 1909

Query: 608 tgatttattaaataagatagcaagagcaccgtcaaatgcatggtcaacgtaggatggagc 667
|tgatttattaaataagatagcaagagcaccgtcaaatgcatggtcaacgtaggatggagc|

Sbjct: 1908 tgatttattaaataagatagcaagagcaccgtcaaatgcatggtcaacgtaggatggagc 1849

Query: 668 cattaagcggcatccatagctgtatttaattcgcgatgaacactctctaatgctttttc 727
|cattaagcggcatccatagctgtatttaattcgcgatgaacactctctaatgctttttc|

Sbjct: 1848 cattaagcggcatccatagctgtatttaattcgcgatgaacactctctaatgctttttc 1789

Query: 728 agcttggctccttagtagcaagaccactaatcactgacatgactgtggatttagccacat 787
|agcttggctccttagtagcaagaccactaatcactgacatgactgtggatttagccacat|

Sbjct: 1788 agcttggctccttagtagcaagaccactaatcactgacatgactgtggatttagccacat 1729

Query: 788 atttgcttctggatctttcttagaaccgattacttgaccatcttctttaagccacggat 847
|atttgcttctggatctttcttagaaccgattacttgaccatcttctttaagccacggat|

Sbjct: 1728 atttgcttctggatctttcttagaaccgattacttgaccatcttctttaagccacggat 1669

Sbjct: 421 agtttaaatgtagcgccaacccttaccgatagccaggcaacatcagaacaaaacttcta 480

Query: 546 atgaaatacttaacggaggtttacggtaaacatatcatctctggccaacaagagatctat 605
|||

Sbjct: 481 atgaaatacttaacggaggtttacggtaaacatatcatctctggccaacaagagatctat 540

Query: 606 ggtggtggaaataacggtaattcagaattagagtttgattggattcacaatttaacaggt 665
|||

Sbjct: 541 ggtggtggaaataacggtaattcagaattagagtttgattggattcacaatttaacaggt 600

Query: 666 aagtatccagcgattagagggtttgattttatgaaactataatccattatacggttggaa 725
|||

Sbjct: 601 aagtatccagcgattagagggtttgattttatgaaactataatccattatacggttggaa 660

Query: 726 gatggtacaacaaatcgtattatagattgggttaataataaaaaatggtattgcaacggga 785
|||

Sbjct: 661 gatggtacaacaaatcgtattatagattgggttaataataaaaaatggtattgcaacggga 720

Query: 786 tgctggcatattactgttccaaaagattttaattcctataagcctgggtgattttgtggg 845
|||

Sbjct: 721 tgctggcatattactgttccaaaagattttaattcctataag-cttgggtgattttgt-gg 778

Query: 846 atgggcaaaagacaacc 862
|||

Sbjct: 779 attggcaaaagacaacc 795

Cphy2128 reverse sequence

Query= HR0ADKBY80ZD03_CAZYG2C4P17_1.SCF 1319 0 1319 SCF

>Cphy2128* reverse

Length = 2544

Score = 1542 bits (778), Expect = 0.0
Identities = 825/834 (98%), Gaps = 5/834 (0%)
Strand = Plus / Minus

Query: 65 gtgtaatggatagtgatCTTAatggtgatggtgatgatgtggctcgattccccatacaag 124
|||

Sbjct: 2544 gtgtaatggatagtgatcttaatggtgatggtgatgatgtggctcgattccccatacaag 2485

Query: 125 cttattgcttaaatatcccgtaaactttgtcagaattaacgtattggctactggatgcatt 184
|||

Sbjct: 2484 cttattgcttaaatatcccgtaaactttgtcagaattaacgtattggctactggatgcatt 2425

Query: 185 aaatgagtaatcatctgcttggttgtaatttgaccaattcgacttagcaaactcttgcttg 244

Sbjct: 2424 ||| aaatgagtaatcatctgcttggttgtaatttgaccaattcgacttagcaaatcttgcttg 2365

Query: 245 aatttctgcattttgccagcttttaacgttccagcagaagcagtaaaggaaatctccaa 304
|||

Sbjct: 2364 aatttctgcattttgccagcttttaacgttccagcagaagcagtaaaggaaatctccaa 2305

Query: 305 gtaataatcagctccgctaactggtttagcaagcttaacaaattcaccttttacgttttc 364
|||

Sbjct: 2304 gtaataatcagctccgctaactggtttagcaagcttaacaaattcaccttttacgttttc 2245

Query: 365 actaccaacacttgcccaatcacaccagaagttctgtgatatttctccatcaatcgata 424
|||

Sbjct: 2244 actaccaacacttgcccaatcacaccagaagttctgtgatatttctccatcaatcgata 2185

Query: 425 gtaataacgaagttttatatcacttagattgatatctgtgtttccagtgttaatcagctt 484
|||

Sbjct: 2184 gtaataacgaagttttatatcacttagattgatatctgtgtttccagtgttaatcagctt 2125

Query: 485 aaatttagtgatattccattggatggatgctctgtatttccgttaaaggcttgaattac 544
|||

Sbjct: 2124 aaatttagtgatattccattggatggatgctctgtatttccgttaaaggcttgaattac 2065

Query: 545 taaatttcctgtaattacgggagcagtggtatctatgacattcaatgtaatacagggtt 604
|||

Sbjct: 2064 taaatttcctgtaattacgggagcagtggtatctatgacattcaatgtaatacagggtt 2005

Query: 605 gtttccagcactaaattggaatgtaatttgctttccccaagtgatagtgtagatagata 664
|||

Sbjct: 2004 gtttccagcactaaattggaatgtaatttgctttccccaagtgatagtgtagatagata 1945

Query: 665 ggatttttgtaaaacaattgtattgcccgataaccgtataatctttatttagtaaaaagtt 724
|||

Sbjct: 1944 ggatttttgtaaaacaattgtattgcccgataaccgtataatctttatttagt-aaaagtt 1886

Query: 725 tattactattatttagaacacttacaagcgaagccatttaagtttgaccgttacgttg 784
|||

Sbjct: 1885 tattactattatttagaacacttacaagcgaagccatttaag-ttgaccgttacgttg 1827

Query: 785 atattttgctgcttatcaactgctttatcaaaggttgatttaaccgagtaattgtaagc 844
|||

Sbjct: 1826 atattttgctgcttatcaactgctttatcaaaggttgatttaaccgagtaattgt-agc 1768

Query: 845 actttggcgttgaatctacaacattaacttttaaaaccaggatctttccctttg 898
|||

Sbjct: 1767 ac-ttggcgttgaatctacgacattaacttttaaaa-caggatctttccctttg 1716

#####

Cphy3009 forward sequence

Query= HR0ADKBY80ZG03_CAZYH2C3P16_1.SCF 1252 0 1252 SCF

>Cphy3009

Length = 2208

Score = 1741 bits (878), Expect = 0.0
Identities = 934/953 (98%), Gaps = 2/953 (0%)
Strand = Plus / Plus

Query: 68 aaagaaggagataggatcATGacagcagagaagacacaacaagaatttcaacaacgagca 127
|||||
Sbjct: 1 aaagaaggagataggatcatgacagcagagaagacacaacaagaatttcaacaacgagca 60

Query: 128 acagaacttgtaaagaaaaatgacactagaagaaaaagtttttcaaaccttacattccgca 187
|||||
Sbjct: 61 acagaacttgtaaagaaaaatgacactagaagaaaaagtttttcaaaccttacattccgca 120

Query: 188 ccttccataccaagattggacattaaagcgtacaattattggaacgaagcattgcatgga 247
|||||
Sbjct: 121 ccttccataccaagattggacattaaagcgtacaattattggaacgaagcattgcatgga 180

Query: 248 gtagcaagagctggcgtagccaccgtttttccgcaggcgattggtttagcggcaacattt 307
|||||
Sbjct: 181 gtagcaagagctggcgtagccaccgtttttccgcaggcgattggtttagcggcaacattt 240

Query: 308 gatgaagatttaaatcgaagagattgcagatactatttctaccgaaggaagaggtaagttt 367
|||||
Sbjct: 241 gatgaagatttaaatcgaagagattgcagatactatttctaccgaaggaagaggtaagttt 300

Query: 368 aatgcacaacaaaaatgatggagatcacgatatctacaaaggtttgaccttctggtcaccg 427
|||||
Sbjct: 301 aatgcacaacaaaaatgatggagatcacgatatctacaaaggtttgaccttctggtcaccg 360

Query: 428 aatgtgaatatcttccgtgatccacgttggggtcgtggacatgagaccttcggagaagac 487
|||||
Sbjct: 361 aatgtgaatatcttccgtgatccacgttggggtcgtggacatgagaccttcggagaagac 420

Query: 488 ccattcttaagtgggtaccttaggaggacgtttgttgacggtatccaagggcatgatgaa 547
|||||
Sbjct: 421 ccattcttaagtgggtaccttaggaggacgtttgttgacggtatccaagggcatgatgaa 480

Query: 548 acctacttaaaagcagcagcttgtgcaaagcatttcgcagttcactctggaccagaagat 607
|||||
Sbjct: 481 acctacttaaaagcagcagcttgtgcaaagcatttcgcagttcactctggaccagaagat 540

Query: 608 attcgccatagtttcaatgccgaagtttcggagcaggatttgcgtgaaacttatctacca 667
 |||
 Sbjct: 541 attcgccatagtttcaatgccgaagtttcggagcaggatttgcgtgaaacttatctacca 600

Query: 668 gcttttaagaaacttgtaaaagagcataaggtggaagcagtaatgggagcttacaatcgt 727
 |||
 Sbjct: 601 gcttttaagaaacttgtaaaagagcataaggtggaagcagtaatgggagcttacaatcgt 660

Query: 728 acaaatggagaacctgctgtggtagtaagacacttttagaagatattttacgtggagaa 787
 |||
 Sbjct: 661 acaaatggagaacctgctgtggtagtaagacacttttagaagatattttacgtggagaa 720

Query: 788 tgggaatttgttggatcatgtgacctcagattgttgggcaatcaaagatttccatgagcac 847
 |||
 Sbjct: 721 tgggaatttgttggatcatgtgacctcagattgttgggcaatcaaagatttccatgagcac 780

Query: 848 catatggttacttcaaatgcagtagagtccagtgcctttggcaatgaatcgtggttgcga 907
 ||| |
 Sbjct: 781 catatggttacttcaaatgcagtagagt-cagttgccttggcaatgaatcgtggttgcga 839

Query: 908 cttaaactgtggaaatctttatgttaaattactacaagcagtacgggatggtttaatggg 967
 ||| |
 Sbjct: 840 cttaaactgtggaaatctttatgttaaattactacaagcagtacgggatggtttagt-gg 898

Query: 968 nnnnnnnncaattgatactgctcctaaacgtctctttacaacaaaaatgaaa 1020
 |||
 Sbjct: 899 aagaagagacaattgatactgctcttatacgtctctttacaacaagaatgaaa 951

Cphy3009 reverse sequence

Query= HR0ADKBY80ZG03_CAZYH2C3P17_1.SCF 1301 0 1301 SCF

>Cphy3009

Length = 2208

Score = 1764 bits (890), Expect = 0.0
 Identities = 924/933 (99%), Gaps = 3/933 (0%)
 Strand = Plus / Minus

Query: 65 gtgtaatggatagtgatCTTAatggtgatggtgatgatgctcaccaagtaaaactgtttc 124
 |||
 Sbjct: 2208 gtgtaatggatagtgatcttaatggtgatggtgatgatgctcaccaagtaaaactgtttc 2149

Query: 125 aggtgcatggaactgtattttaattggattcctaccagtttaactgaatacttctagatc 184
 |||
 Sbjct: 2148 aggtgcatggaactgtattttaattggattcctaccagtttaactgaatacttctagatc 2089

Query: 185 tggttgtgaatcacttagatatagctcatactccccttgatttaagataaattcaccttc 244

Sbjct: 2088 |||tggttgatgaatcacttagatagctcatactccccttgatttaagataaattcaccttc 2029

Query: 245 ct cattatataaaaccaaaggctctgtcatctaactcaatcatgatatactttttcttctcc 304
|||

Sbjct: 2028 ct cattatataaaaccaaaggctctgtcatctaactcaatcatgatatactttttcttctcc 1969

Query: 305 tgggagtaagctcacttttttaaggccttttagctgacagtttgagcatcttctcctac 364
|||

Sbjct: 1968 tgggagtaagctcacttttttaaggccttttagctgacagtttgagcatcttctcctac 1909

Query: 365 atatttaacatatgcttggtgtgtcaccgaaccttcataatcaccggtattctttactct 424
|||

Sbjct: 1908 atatttaacatatgcttggtgtgtcaccgaaccttcataatcaccggtattctttactct 1849

Query: 425 taccatacactctacgttggaaaccttttctaaagtatctgtatttacataaagtaatgt 484
|||

Sbjct: 1848 taccatacactctacgttggaaaccttttctaaagtatctgtatttacataaagtaatgt 1789

Query: 485 gtgctcaaaggtagtataacttaagccatatccaaatggataaagagcctcattcttcat 544
|||

Sbjct: 1788 gtgctcaaaggtagtataacttaagccatatccaaatggataaagagcctcattcttcat 1729

Query: 545 ataacgatacgtacggttcttcatagcataatctgtaaactcaggaattcctcagtcgt 604
|||

Sbjct: 1728 ataacgatacgtacggttcttcatagcataatctgtaaactcaggaattcctcagtcgt 1669

Query: 605 acgatagaatgttacaggaagctttccttctgggtttccatctccaaaaatcaattctgc 664
|||

Sbjct: 1668 acgatagaatgttacaggaagctttccttctgggtttccatctccaaaaatcaattctgc 1609

Query: 665 aatcgctctaccaccttgtgctccaggataaccagccttghtaatatagcaggaatatgctc 724
|||

Sbjct: 1608 aatcgctctaccaccttgtgctccaggataaccagccttghtaatatagcaggaatatgctc 1549

Query: 725 atctgcccattggcactgccaagcactaccggagagaaggattaaaataacagggttttcc 784
|||

Sbjct: 1548 atctgcccattggcactgccaagcactaccggagagaaggattaaaataacagggttttcc 1489

Query: 785 acattcataaatagtttttaatacatcttctttgattccaggaagcgctaattgtcttctt 844
|||

Sbjct: 1488 acattcataaatagtttttaatacatcttctttgaattccaggaagcgctaattgtcttctt 1429

Query: 845 atctccactagcaaattgattttccctggctgccttcttctccttctaactcctggatcaa 904
|||

Sbjct: 1428 atctccactagcaaattga-tttccctggctgccttcttctccttctaactcctggatcaa 1370

Query: 905 gacccaggcatgctattacaacatcccctatgttcacaaactgcacgtacctcaccaatac 964
|||||
Sbjct: 1369 gacccaggcatgctattacgacatcactatgttcacaaactgcacgtacctcagcaatac 1310

Query: 965 ggtcattttccttggacttaaattaaagagttt 997
|||||
Sbjct: 1309 ggtcattttcctt--gacttaaattagagagttt 1279

#####

Cphy3158 forward sequence

Query= HR0ADKBY80ZA04_CAZYI1C1P16_1.SCF 1304 0 1304 SCF
(1304 letters)

>Cphy3158

Length = 2109

Score = 1639 bits (827), Expect = 0.0
Identities = 863/876 (98%), Gaps = 1/876 (0%)
Strand = Plus / Plus

Query: 69 aaagaaggagataggatcATGgaagaagaagtagtattaacttttaatatnnnnnnngga 128
|||||
Sbjct: 1 aaagaaggagataggatcatggaagaagaagtagtattaacttttaataataaaaaaagga 60

Query: 129 gatggaacaatggggtttgaaaagcttggttaaataactataagagtgataatcttgcg 188
|||||
Sbjct: 61 gatggaacaatggggtttgaaaagcttggttaaataactataagagtgataatcttgcg 120

Query: 189 atgcgagattattttacagtcgttacatacaataaagacgactctattgtaaaaagtgcg 248
|||||
Sbjct: 121 atgcgagattattttacagtcgttacatacaataaagacgactctattgtaaaaagtgcg 180

Query: 249 gtcttagaattaacaacagcagcaaaagagctattttcaatcgatatcgaaagcagcctt 308
|||||
Sbjct: 181 gtcttagaattaacaacagcagcaaaagagctattttcaatcgatatcgaaagcagcctt 240

Query: 309 tgtgatatgaaatcagatggtgataaaacgagaaaaggattcattttcagattggtgat 368
|||||
Sbjct: 241 tgtgatatgaaatcagatggtgataaaacgagaaaaggattcattttcagattggtgat 300

Query: 369 aataaagatctagaaaatgagggatatcgatatttcgtagcagacgagatgctattgata 428
|||||
Sbjct: 301 aataaagatctagaaaatgagggatatcgatatttcgtagcagacgagatgctattgata 360

Query: 429 gaggcttacacctcaaatggtatttctctatggaacttttgatttgattcgtagaccatt 488
|||||

Sbjct: 361 gaggccttacacctcaaatggtattctctatggaacttttgatttgattcgtagcaccatt 420

Query: 489 cttggagcagatgtgcattccttcaatagaactatctttccaagaatcctcttcgaatg 548
|||||

Sbjct: 421 cttggagcagatgtgcattccttcaatagaactatctttccaagaatcctcttcgaatg 480

Query: 549 ttaaatcattgggataaatatggacggtagtattgaaagaggttattctggaattccttc 608
|||||

Sbjct: 481 ttaaatcattgggataaatatggacggtagtattgaaagaggttattctggaattccttc 540

Query: 609 tttttgaaacatggtgaagtattgtaaataaacgtactaaggcctatgcaagacttggt 668
|||||

Sbjct: 541 tttttgaaacatggtgaagtattgtaaataaacgtactaaggcctatgcaagacttggt 600

Query: 669 tcctccgttggataaaacgcagttgtgataaacaatgtaaataatgcccgtggtacagcaact 728
|||||

Sbjct: 601 tcctccgttggataaaacgcagttgtgataaacaatgtaaataatgcccgtggtacagcaact 660

Query: 729 aatttaataacaaatcgctacatagataaattaaaacaaatcggtgaaatTTTTGCTTCT 788
|||||

Sbjct: 661 aatttaataacaaatcgctacatagataaattaaaacaaatcggtgaaatTTTTGCTTCT 720

Query: 789 tatggaattaagctttatctttcttttaattttgcggtccaatggaacttggtggttta 848
|||||

Sbjct: 721 tatggaattaagctttatctttcttttaattttgcggtccaatggaacttggtggttta 780

Query: 849 acttctgctgaccactcgacgaggaaatacgtctttgggggaagaagaagtgcaatta 908
|||||

Sbjct: 781 acttctgctgaccactcgacgaggaaatacgtctttgggtggaagaagaagtgcaatta 840

Query: 909 ttattttaaagaaataacctcccttggcggatTTTT 944
|||||

Sbjct: 841 ttattt-aaagaaataccatccttggcggatTTTT 875

Cphy3158 reverse sequence

Query= HR0ADKBY80ZA04_CAZYI1C1P17_1.SCF 1308 0 1308 SCF
(1308 letters)

>Cphy3158

Length = 2109

Score = 1509 bits (761), Expect = 0.0
Identities = 819/833 (98%), Gaps = 4/833 (0%)
Strand = Plus / Minus

Query: 66 gtgtaatggatagtgatCTTAatggtgatggtgatgatgatataactccctcccctTTTT 125

Sbjct: 2109 |gtgtaatggatagtgatcttaatggatggatggatggatgataactccctcccctttt 2050

Query: 126 atcccctatcgctgtcttccataaaaaataagaacaaatcacgtctctccattccttcga 185
|
Sbjct: 2049 atcccctatcgctgtcttccataaaaaataagaacaaatcacgtctctccattccttcga 1990

Query: 186 atgttccagctgttccctgtaatctatgcaataccctgtgatatggacttcttccaactt 245
|
Sbjct: 1989 atgttccagctgttccctgtaatctatgcaataccctgtgatatggacttcttccaactt 1930

Query: 246 tccttttagttcttcccataacttaaccatcttccacatccttactccctcaaaatg 305
|
Sbjct: 1929 tccttttagttcttcccataacttaaccatcttccacatccttactccctcaaaatg 1870

Query: 306 agaatcatagatatgttggattaaggcttacctgtctttaactgataggtatatggaat 365
|
Sbjct: 1869 agaatcatagatatgttggattaaggcttacctgtctttaactgataggtatatggaat 1810

Query: 366 gcgatggaagaataaaaagcaactcttctgggcatgtttcaggtgttccatagagctcttg 425
|
Sbjct: 1809 gcgatggaagaataaaaagcaactcttctgggcatgtttcaggtgttccatagagctcttg 1750

Query: 426 gtttggctgatgatactgtgttggtatcctgttccattcttgggtcggcttacaccaat 485
|
Sbjct: 1749 gtttggctgatgatactgtgttggtatcctgttccattcttgggtcggcttacaccaat 1690

Query: 486 tgctgtatggctctgctttatgataggttccccaacggctgtattcatacccgtaacatt 545
|
Sbjct: 1689 tgctgtatggctctgctttatgataggttccccaacggctgtattcatacccgtaacatt 1630

Query: 546 aggtccgtaatgatgagaaggatttaccatccatccaataccaagcggagaagtatattt 605
|
Sbjct: 1629 aggtccgtaatgatgagaaggatttaccatccatccaataccaagcggagaagtatattt 1570

Query: 606 ctcatatgctggccaggacatcattaggattttggatatataatctataacatgctcctt 665
|
Sbjct: 1569 ctcatatgctggccaggacatcattaggattttggatatataatctataacatgctcctt 1510

Query: 666 catgccaaatgtaaggatccattcttttgctatctcctctgaatgtaaatcaggatc 725
|
Sbjct: 1509 catgccaaatgtaaggatccattcttttgctatctcctctgaatgtaaatcaggatc 1450

Query: 726 aaaactcagttctaccaatatccatagagattcgctgctgccaagtcagaccagtcag 785
|
Sbjct: 1449 aaaactcag-tctacc-atatccatagagattcgctgctgccaagtcagaccagtcag 1392

Query: 786 ttatcatcattccccctgtatttgcaactgccgcatccagcgtttttattgccaaaagt 845
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Sbjct: 1391 ttatcatcatt-ccctgtatttgcaactgctgccatccagcgtttttattgccataagt 1333

Query: 846 gttgccactaacgaaatcaaatacccgatcatttttcttctttacaaaagt 898
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Sbjct: 1332 gttgccactaacgatatcgaataccgatca-ttttcttctttacaataagt 1281

#####

Cphy3160 forward sequence

Query= HR0ADKBY80ZD04_CAZYJ1C4P16_1.SCF 1352 0 1352 SCF

>Cphy3160

Length = 3612

Score = 1542 bits (778), Expect = 0.0
Identities = 815/822 (99%), Gaps = 4/822 (0%)
Strand = Plus / Plus

Query: 68 aaagaaggagataggatcATGagcagtcaagtacataacaatcgaagattaatgaatgat 127
|||||
Sbjct: 1 aaagaaggagataggatcatgagcagtcaagtacataacaatcgaagattaatgaatgat 60

Query: 128 ggctggagtttttccaacatcagctaggcgctaccttacaacaagtgttagatgcaaaa 187
|||||
Sbjct: 61 ggctggagtttttccaacatcagctaggcgctaccttacaacaagtgttagatgcaaaa 120

Query: 188 acagaatggcatcccgttgatttgccccacgactggtaatttataataccacgatttg 247
|||||
Sbjct: 121 acagaatggcatcccgttgatttgccccacgactggtaatttataataccacgatttg 180

Query: 248 tatgaaacaggagaaggttggtacagacgtacgttatccatggaacacctgaaaaataag 307
|||||
Sbjct: 181 tatgaaacaggagaaggttggtacagacgtacgttatccatggaacacctgaaaaataag 240

Query: 308 gagcgatatatattacgtttcgagggcgtgtatatgaactcgaccctctatgtcaatgga 367
|||||
Sbjct: 241 gagcgatatatattacgtttcgagggcgtgtatatgaactcgaccctctatgtcaatgga 300

Query: 368 aggttgctggagagtggaaatacggttactcaacatttgaattcgatataaccgagttt 427
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Sbjct: 301 aggttgctggagagtggaaatacggttactcaacatttgaattcgatataaccgagttt 360

Query: 428 ttaacagaaggtggcaatgaaattgtgatgcaagttatctacgagtcaccgaactcgaga 487
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Sbjct: 361 ttaacagaaggtggcaatgaaattgtgatgcaagttatctacgagtcaccgaactcgaga 420

Query: 488 tggattccggtgcaggatatttatcgtaatgtctggtccatacctatcctgaagtacat 547
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Sbjct: 421 tggattccggtgcaggatatttatcgtaatgtctggtccatacctatcctgaagtacat 480

Query: 548 attaaccagatggaatttatatttcaacagaaaaagtggatgaggatttttacgttttc 607
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Sbjct: 481 attaaccagatggaatttatatttcaacagaaaaagtggatgaggatttttacgttttc 540

Query: 608 ctatcaaccgaagtttcctctttaccgatcagtatggaacctgagcttacaataccagag 667
|||||
Sbjct: 541 ctatcaaccgaagtttcctctttaccgatcagtatggaacctgagcttacaataccagag 600

Query: 668 gattttcatggattagacaaggattccacatctacactcgaacttcgccatactgtatgg 727
|||||
Sbjct: 601 gattttcatggattagacaaggattccacatctacactcgaacttcgccatactgtatgg 660

Query: 728 tcgccaagtcataaattagtttgacccatactgtcgatgttacaagtgaggtataaag 787
|||||
Sbjct: 661 tcgccaagtcataaattagtttgacccatactgtcgatgttacaagtgaggtataaag 720

Query: 788 aatgccttttatgtacaaaatagtaaactacatattatttcacctcttctttgggagc 847
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Sbjct: 721 aatgccttttatgtacaaatagtaaactacatatta-tttcacctctt-ctttgggagc 778

Query: 848 tttcgtcaccaatttatatccaagtgcaacttgatattat 889
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Sbjct: 779 tttcgtcaccaatttatat-caagtgcaaac-tgatattat 818

Cphy3160 reverse sequence

Query= HR0ADKBY80ZD04_CAZYJ1C4P17_1.SCF 1324 0 1324 SCF

>Cphy3160

Length = 3612

Score = 1635 bits (825), Expect = 0.0
Identities = 875/888 (98%), Gaps = 4/888 (0%)
Strand = Plus / Minus

Query: 67 gtgtaatggatagtgatTTAatggtgatggtgatgatgttcaaacttaaaccactcaaa 126
|||||
Sbjct: 3612 gtgtaatggatagtgatcttaatggtgatggtgatgatgttcaaacttaaaccactcaaa 3553

Query: 127 gtcaaaaattactgcccggtaggaatataaaaggtaacagtatatttacctgtcttcttaga 186
|||||
Sbjct: 3552 gtcaaaaattactgcccggtaggaatataaaaggtaacagtatatttacctgtcttcttaga 3493

Query: 187 gaattcaaaactcttttacttctgactcattcgtaaaagtaaattctgcaagttcttcaat 246
|||||
Sbjct: 3492 gaattcaaaactcttttacttctgactcattcgtaaaagtaaattctgcaagttcttcaat 3433

Query: 247 gctattatagagcatactaccttcttctgaaataaactttacatgaatgggtgttcttctc 306
|||||
Sbjct: 3432 gctattatagagcatactaccttcttctgaaataaactttacatgaatgggtgttcttctc 3373

Query: 307 aatcggagaatgaccacagatagagagtttcgtaatgccctgttctccgaaatccatctc 366
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Sbjct: 3372 aatcggagaatgaccacagatagagagtttcgtaatgccctgttctccgaaatccatctc 3313

Query: 367 tgaaaattccaaggatacgttattcccgattccttcaatgcgaggagctttctttgtaa 426
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Sbjct: 3312 tgaaaattccaaggatacgttattcccgattccttcaatgcgaggagctttctttgtaa 3253

Query: 427 ggtatctccatataatgaggtcacaatcagtagcgaataattttgcaaatcctttttgtgg 486
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Sbjct: 3252 ggtatctccatataatgaggtcacaatcagtagcgaataattttgcaaatcctttttgtgg 3193

Query: 487 attggtaaactgaaatccttgaacgcttaatcgtttaaatacaacgaaggaaattgttac 546
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Sbjct: 3192 attggtaaactgaaatccttgaacgcttaatcgtttaaatacaacgaaggaaattgttac 3133

Query: 547 gataccttttactctacgctttaatcgataggtttccggttgatggtgattccatattgg 606
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Sbjct: 3132 gataccttttactctacgctttaatcgataggtttccggttgatggtgattccatattgg 3073

Query: 607 ctttttactaaatgaacagctctgctagtaattcacttcttctcatgtgggataccttc 666
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Sbjct: 3072 ctttttactaaatgaacagctctgctagtaattcacttcttctcatgtgggataccttc 3013

Query: 667 ccaaatctcaaaaagttggaagctcagtatcaagacagtagattggaacagtaatctcgtc 726
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Sbjct: 3012 ccaaatctcaaaaagttggaagctcagtatcaagacagtagattggaacagtaatctcgtc 2953

Query: 727 agatccataggagccaaagtctacatttttaaaacaaatgtaagtatccattggttagcag 786
|||||
Sbjct: 2952 agatccataggagccaaagtctacatttttaaaacaaatgtaagtatccattggttagcag 2893

Query: 787 agaggagaaaccgctcaattccgttggaagtttgtattggaccaagagtataaac 846
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Sbjct: 2892 agaggagataaccgctcaattccgttggaagtttgtattggaccaagagtataaac 2833

Query: 847 accatatataaaattcctacggattcatggaagcttctccaaggtcatggaagtttagcct 906
|||||
Sbjct: 2832 accatatataaaattcctacggattcatggttagcttctccaaggtcatggaagtttagc - - 2775

Query: 907 tctttttcaaaaaatcatcacgttaccttatccgcaccatttcctacagg 954
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Sbjct: 2774 tctatttcagaaaatcatcacg-tacctatctgcacca-ttcctacagg 2729

#####

Cphy3367 forward sequence

Query= HR0ADKBY80ZH04_CAZYK2C4P16_1.SCF 1327 0 1327 SCF

>Cphy3367*

Length = 2940

Score = 821 bits (414), Expect = 0.0

Identities = 426/430 (99%)

Strand = Plus / Plus

Query: 67 aaagaaggagataggatcATGgaaaccaattataattacggagaagctcttcaaaaatca 126
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 1 aaagaaggagataggatcatggaaaccaattataattacggagaagctcttcaaaaatca 60

Query: 127 atcatgttttagtgagtttcaacgttctggtaaactgccaaagtaccattcggataaattgg 186
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 61 atcatgttttagtgagtttcaacgttctggtaaactgccaaagtaccattcggataaattgg 120

Query: 187 agaggtgactctggtttaacccgatggagcagatgttggtttgatctaactggtggctgg 246
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 121 agaggtgactctggtttaacccgatggagcagatgttggtttgatctaactggtggctgg 180

Query: 247 tatgatgctggtgatcatgtaaaatttaactttcctttggcttataactgtaacaatgta 306
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 181 tatgatgctggtgatcatgtaaaatttaactttcctttggcttataactgtaacaatgta 240

Query: 307 gcatgggcagtatatgaagaagaggctactctttcaaaggcaggccaattaagttattta 366
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 241 gcatgggcagtatatgaagaagaggctactctttcaaaggcaggccaattaagttattta 300

Query: 367 ttagatgaaattaagtggcttagtgattacctaattaaatgtcatccacaagcaaatgta 426
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 301 ttagatgaaattaagtggcttagtgattacctaattaaatgtcatccacaagcaaatgta 360

Query: 427 tttcattatcaggttgtaatggaatacagatcactcttggtggggacctgccgaatct 486
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 361 ttttattatcaggttgtaatggaatacagatcactcttggtggggacctgctgaagtt 420

Query: 487 atgcagatgg 496
| | | | | | | | | |

Sbjct: 421 atgcagatgg 430

Cphy3367 reverse sequence

Query= HR0ADKBY80ZH04_CAZYK2C4P17_1.SCF 1369 0 1369 SCF

>Cphy3367*

Length = 2940

Score = 952 bits (480), Expect = 0.0

Identities = 548/564 (97%), Gaps = 5/564 (0%)

Strand = Plus / Minus

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Query: 67  gtgtaatggatagtgatTTAatggtgatggatgatgtggttcgactccccaaccaa 126
      |||
Sbjct: 2940 gtgtaatggatagtgatcttaatggtgatggatgatgtggttcgactccccaaccaa 2881

Query: 127  aacatcagagatatatactgttgtcttattccaatcagcataacttgagttactatcacc 186
      |||
Sbjct: 2880 aacatcagagatatatactgttgtcttattccaatcagcataacttgagttactatcacc 2821

Query: 187  aaacgaataatcatctgtttggtatagtttgccagtctaccttagaaaatcttccttg 246
      |||
Sbjct: 2820 aaacgaataatcatctgtttggtatagtttgccagtctaccttagaaaatcttccttg 2761

Query: 247  aacttcaatactttgccctgcgtttaaagttccggcagcggacttaaataaaaattctag 306
      |||
Sbjct: 2760 aacttcaatactttgccctgcgtttaaagttccggcagcggacttaaataaaaattctag 2701

Query: 307  atagtaatctgcatttgttttgggtgactcatctttacgaaagtaccatttacattgga 366
      |||
Sbjct: 2700 atagtaatctgcatttgttttgggtgactcatctttacgaaagtaccatttacattgga 2641

Query: 367  actaccaatcgtcgaataatcacaccagaatgcctgatccttttcgccattgattgtata 426
      |||
Sbjct: 2640 actaccaatcgtcgaataatcacaccagaatgcctgatccttttcgccattgattgtata 2581

Query: 427  ataatagcgaatcttaacatcggataagttgattgagtagttccggtgtaattaattt 486
      |||
Sbjct: 2580 ataatagcgaatcttaacatcggataagttgattgagtagttccggtgtaattaattt 2521

Query: 487  aattcttggtgcaatgccattcgttgttgagaagaattttccttaaacattttgaaatt 546
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Sbjct: 2520 aattcttggtgcaatgccattcgttgttgagaagaattttccttaaacattttgaaatt 2462

Query: 547  taatatcttctggtggagtataactgaagaatccttatcggttaactggctaa-actgg 605
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Sbjct: 2461 taata-tttctggtggagtataactgaagaatccttaaatggtaact-gctaagactgg 2404
```


Query: 609 tcaccagnnnnntggcaggggatccaggacatcaggaggtagagattggattaatc 668
||||||| |||||||
Sbjct: 541 tcaccagaaaaaatggcaggggatccaggacatcaggaggtagagattggattaatc 600

Query: 669 aaattatatgaagtcacaggaagaagaagtacattgagcaagcaagattatTTTTtagaa 728
|||||||||
Sbjct: 601 aaattatatgaagtcacaggaagaagaagtacattgagcaagcaagattatTTTTtagaa 660

Query: 729 agaagaggaacttccccaaactatTTTcttgaggaagnnnnnnccccaaagtTTaagcct 788
||||||||| |||||||
Sbjct: 661 agaagaggaacttccccaaactatTTTcttgaggaagaaaaaacccccaaagtTTaagcct 720

Query: 789 atatttcctgagtttatgcattatgataccgcctattctcaatcccacaaaccaatccgt 848
|||||||||
Sbjct: 721 atatttcctgagtttatgcattatgataccgcctattctcaatcccacaaaccaatccgt 780

Query: 849 gaacaaacgacagccgaaagtcctgcggtacggcggtatataatgtattctgcaatggct 908
||||||||| ||| |||
Sbjct: 781 gaacaaacgacagcagaaggtcatgcggtacggcggtatataatgtattctgcaatggct 840

Query: 909 gactttgcaccacctataatgaccaagaacctgttaagggtgtttgtgaaaccctatgga 968
||| ||||| || ||||||| ||||| |||||||
Sbjct: 841 gacattgcagcagcctataatgacaaagaa-ctgttaa-gtgtttgtgaaaccctatgga 898

Query: 969 agaatattggaaggaaagcgtatgtatctaaacgggtgggattgggtagttccggaatat 1028
||||||| | ||||||| ||||||| ||| |||||||
Sbjct: 899 agaatatt-gtaggaaagcgtatgtatct-aacgggtggcatt-ggtagttccggaatat 955

Query: 1029 tagaa 1033
|||||
Sbjct: 956 tagaa 960

#####

Cphy0591-4 reverse sequence

Query= HR0ADKBY82ZA04_0591C4P17_1.SCF 1375 0 1375 SCF

>cphy0591

Query: 66 gtgtaatggatagtgatCTTAatggtgatggtgatgtacaaattctttatccaaac 125
|||||||||
Sbjct: 1995 gtgtaatggatagtgatcttaatggtgatggtgatgtacaaattctttatccaaac 1936

Query: 126 aatcatctctcctgtttttcgatttgcccaatatggatattggataaaacttaannnnnn 185
|||||||||
Sbjct: 1935 aatcatctctcctgtttttcgatttgcccaatatggatattggataaaacttaattttttt 1876

Query: 186 ctctgcaaatttcacgggatgttccgaatataaagtttcattctcccattcctcttgat 245
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1875 ctctgcaaatttcacgggatgttccgaatataaagtttcattctcccattcctcttgat 1816

Query: 246 cattttctttccatcacattgaatcaccatcgttccccttagtagcgtatcatcataaaa 305
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1815 cattttctttccatcacattgaatcaccatcgttccccttagtagcgtatcatcataaaa 1756

Query: 306 ctcttctaattcagatctgaatctatataatagctggaagtttgattcgttatccac 365
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1755 ctcttctaattcagatctgaatctatataatagctggaagtttgattcgttatccac 1696

Query: 366 ctcttccatacaataaaactagcgggcccttcatgattgccactttccaatatcttcttt 425
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1695 ctcttccatacaataaaactagcgggcccttcatgattgccactttccaatatcttcttt 1636

Query: 426 cactagcggattcgctctaatcatccgtggcttcaacgtaaactccatatcaatcgtttt 485
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1635 cactagcggattcgctctaatcatccgtggcttcaacgtaaactccatatcaatcgtttt 1576

Query: 486 ctttgaagaagttatctctatattcaagataaccgttcgttatttctttttgggtcaattc 545
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1575 ctttgaagaagttatctctatattcaagataaccgttcgttatttctttttgggtcaattc 1516

Query: 546 taaaccatttacaaatacacatactccttagcatattcaggaattcgtatataaagttt 605
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1515 taaaccatttacaaatacacatactccttagcatattcaggaattcgtatataaagttt 1456

Query: 606 tccacaaaacccttctctccatccacctccatatgaactttgccatcatacggaaacct 665
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1455 tccacaaaacccttctctccatccacctccatatgaactttgccatcatacggaaacct 1396

Query: 666 tgttgccaaccgcagtgtagcttccctgttttgcaattttacagtagtctgatttgaat 725
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1395 tgttgccaaccgcagtgtagcttccctgttttgcaattttacagtagtctgatttgaat 1336

Query: 726 aaataagttaaccatatacgagtctcatcgtaaaagtagatatactaccaagtgaagc 785
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1335 aaataagttaaccatatacgagtctcatcgtaaaagtagatatactaccaagtgaagc 1276

Query: 786 caatgttctcgctacatttggtgggcaacaagcaacaccaaaccatggctgacgtatcgg 845
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1275 caatgttctcgctacatttggtgggcaacaagcaacaccaaaccatggctgacgtatcgg 1216

Query: 846 ttttacetggttctttaaagttctcttaatgcaattgccaggccaaacttctaccgggtt 905
||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
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Sbjct: 481 actactgcaggtgaaataacgacagataagtggatcaatactcaagcatggctggctgat 540

Query: 608 aaatacaaaaatgacgatactattctggcatttgatataaaaaatgaacctcatggacag 667
|||||
Sbjct: 541 aaatacaaaaatgacgatactattctggcatttgatataaaaaatgaacctcatggacag 600

Query: 668 aggggatatagtactacaacacctaataatacctcaaaaatgggataattcccaaatgag 727
|||||
Sbjct: 601 aggggatatagtactacaacacctaataatacctcaaaaatgggataattccacagatgag 660

Query: 728 aataactggaattatgcggcggaagatgtgcaagctatacttgctaaaaacccta 787
|||||
Sbjct: 661 aataactggaagtatgcggcggaagatgtgcaagctatacttgctaaaa-cccta 718

Query: 788 aattattaattatgattgaatgtgttgaacaataaccctaaaaccgaaaaagggttatact 847
|||||
Sbjct: 719 aattattaattatgattgaagggtgttgaacaat-accctaaaactgaaaaagggttataac 777

Query: 848 tattataccccggatgtatgggga 871
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Sbjct: 778 tataatacaccggatgtatgggga 801

#####

Cphy1163-1 reverse sequence

Query= HR0ADKBY82ZA06_1163C1P17_1.SCF 1378 0 1378 SCF

>cphy1163

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|||||
Sbjct: 1368 gtgtaatggatagtgatcctaaggtgatggtgatgatggtttccataatattgccctaa 1309

Query: 126 tgatataccatttacaccaagaggtgtctgatggtctagaccaataaattaccatttga 185
|||||
Sbjct: 1308 tgatataccatttacaccaagaggtgtctgatggtctagaccaataaattaccatttga 1249

Query: 186 ctgccataatgcaggttttaataaagcgtattttgcttcatccaagtttgccaatcata 245
|||||
Sbjct: 1248 ctgccataatgcaggttttaataaagcgtattttgcttcatccaagtttgccaatcata 1189

Query: 246 tcctagtaaacctccagtatcccctgagttcggattgatacaccagaatgtatggtggat 305
|||||
Sbjct: 1188 tcctagtaaacctccagtatcccctgagttcggattgatacaccagaatgtatggtggat 1129

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Query: 306  acgattatttactatataaatccttaataatgtcatccatttctggttctttccaccatc 365
           |||
Sbjct: 1128 acgattatttactatataaatccttaataatgtcatccatttctggttctttccaccatc 1069

Query: 366  cataaaacctccccactcacctatcaaaagtgggtgcaataacctttatctttaatatatgc 425
           |||
Sbjct: 1068 cataaaacctccccactcacctatcaaaagtgggtgcaataacctttatctttaatatatgc 1009

Query: 426  ccaagtattataccaataatcatctaataagggtctgagttgtaaataccttatcaaacca 485
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Sbjct: 1008 ccaagtattataccaataatcatctaataagggtctgagttgtaaataccttatcaaacca 949

Query: 486  tggttggttgatatacggaaggaccatagtcagggggaatagacgatctgactattgag 545
           |||
Sbjct: 948  tggttggttgatatacggaaggaccatagtcagggggaatagacgatctgactattgag 889

Query: 546  agtgcctatattaattggataatcctttactcctcttaaatccaccccaccaagcact 605
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Sbjct: 888  agtgcctatattaattggataatcctttactcctcttaaatccaccccaccaagcact 829

Query: 606  ataccatggagactgatcaccagtagctccccatacatccggtgtattatagttataacc 665
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Sbjct: 828  ataccatggagactgatcaccagtagctccccatacatccggtgtattatagttataacc 769

Query: 666  tttttcagttttagggtattggtcaacaccttcaatcataattaataatttagggtttt 725
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Sbjct: 768  tttttcagttttagggtattggtcaacaccttcaatcataattaataatttagggtttt 709

Query: 726  agcaagtatagctttcgcacatcttccgcccatacttcagttattctcatcttggtg 785
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Sbjct: 708  agcaagtatagctttcgcacatcttccgcccatacttcagttattctcatc-tgtgg 650

Query: 786  aattatcccattttgctatattagtaggtggtgaaagtactatatccccctctgtccctga 845
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Query: 190 ccgacgcttactgttggtgacaacagtgagccaaagccattagtgttacagggcggact 249
 |||||
 Sbjct: 121 ccgacgcttactgttggtgacaacagtgagccaaagccattagtgttacagggcggact 180

Query: 250 gcagactggaatagcgttgatttgaaaaatttagtttccttgctgatgggttgagtac 309
 |||||
 Sbjct: 181 gcagactggaatagcgttgatttgaaaaatttagtttccttgctgatgggttgagtac 240

Query: 310 actatcatggtgaccggccgtacttctgagggctccaagatgaagctatcacagacggca 369
 |||||
 Sbjct: 241 actatcatggtgaccggccgtacttctgagggctccaagatgaagctatcacagacggca 300

Query: 370 agcccgatggaacacatgcttcttagttggtggcacagatggatctctctcttgag 429
 |||||
 Sbjct: 301 agcccgatggaacacatgcttcttagttggtggcacagatggatctctctcttgag 360

Query: 430 aagaccttcacgtataaccagttacagactgagaagaccggttcgatccagtcggaagga 489
 |||||
 Sbjct: 361 aagaccttcacgtataaccagttacagactgagaagaccggttcgatccagtcggaagga 420

Query: 490 acaaccaacgactttacaattaacagcatcataatcaccagacagcagtctcagatggc 549
 |||||
 Sbjct: 421 acaaccaacgactttacaattaacagcatcataatcaccagacagcagtctcagatggc 480

Query: 550 gtaacatctacacctacacctaccccgatttctgatggtgcaactactagcgacatctct 609
 |||||
 Sbjct: 481 gtaacatctacacctacacctaccccgatttctgatggtgcaactactagcgacatctct 540

Query: 610 atttccttcaataaccaccgacaataccaagtggagcgaagcttttagcgtgtccaacaca 669
 |||||
 Sbjct: 541 atttccttcaataaccaccgacaataccaagtggagcgaagcttttagcgtgtccaacaca 600

Query: 670 gataatgccgcaattgaatgggtttcggacttcgtaatggcgatacttttgacttaag 729
 |||||
 Sbjct: 601 gataatgccgcaattgaatgggtttcggacttcgtaatggcgatacttttgacttaag 660

Query: 730 ggtatccacctatctacctcgactgactataaccggcgctaacaacgccatccgtctgaca 789
 |||||
 Sbjct: 661 ggtatccacctatctacctcgactgactataaccggcgctaacaacgccatccgtctgaca 720

Query: 790 tttcctgagccattggctaagaacgccgtttacactatctcgtatagcgtctttgtcca 849
 |||||
 Sbjct: 721 tttcctgagccattggctaagaacgccgtttacactatctcgtatagcgtctttgtcca 780

Query: 850 gccgtaggcaacgagggtaaagatacacttgtaggaccgggcatcgctcctgagtggcgat 909
|||||
Sbjct: 781 gccgtaggcaacgagggtaaagatacacttgtaggaccgggcatcgctcctgagtggcgat 840

Query: 910 tatacaggctccacaggcgtgaccaaattcccggccaacttccgcacaattagtaacaag 969
|||||
Sbjct: 841 tatacaggctcaacaggcgtgaccaaattcccggccgacttcggcacaattagtagacagag 900

Query: 970 acatggaagatgtagtataacccaccccggaagggtgttctgaacgaaaacctaaaga 1029
|||||
Sbjct: 901 acatggaagatgtagtataa-ccacaccgga-ggtggtctgaacgagacactaaaga 958

Query: 1030 ccatccaccttccgtttccttgtaaa 1055
|||||
Sbjct: 959 gcatcga-cttccgtttcgttgtaaa 983

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Query= HR0ADKBY82ZH06_3862C1P17_1.SCF 1415 0 1415 SCF

>cphy3862 reverse

Query: 66 gtgtaatggatagtgatcttaatggatggatggatgctcttcaataataactttaat 125
|||||
Sbjct: 7329 gtgtaatggatagtgatcttaatggatggatggatgctcttcaataataactttaat 7270

Query: 126 tgacttcttcataccatctacatttacataaatccaatctgtttttgcagaaacggcctt 185
|||||
Sbjct: 7269 tgacttcttcataccatctacatttacataaatccaatctgtttttgcagaaacggcctt 7210

Query: 186 aactgttgcagttgtacttctggattcttcttcacaactactccatcctttttactaga 245
|||||
Sbjct: 7209 aactgttgcagttgtacttctggattcttcttcacaactactccatcctttttactaga 7150

Query: 246 catccagaggatgctatcttcatctaaaccatttacttttattttaaatactgcttcttc 305
|||||
Sbjct: 7149 catccagaggatgctatcttcatctaaaccatttacttttattttaaatactgcttcttc 7090

Query: 306 tcccactttcatatgcacagcactttccacaaattcaatgggtcgcttttttaacagataa 365
|||||
Sbjct: 7089 tcccactttcatatgcacagcactttccacaaattcaatgggtcgcttttttaacagataa 7030

Query: 366 ttttctagtataaaccttctgtgttccatcctgcattgtaacagtagccgtaataactat 425
|||||
Sbjct: 7029 ttttctagtataaaccttctgtgttccatcctgcattgtaacagtagccgtaataactat 6970

Query: 426 aataccagattcttttgcaatcaaacgtccattctgttttacttctacaatacctggatt 485
 |||
 Sbjct: 6969 aataccagattcttttgcaatcaaacgtccattctgttttacttctacaatacctggatt 6910

Query: 486 atttgacttataagtaatcgtaattggaactattccctcatcaagcttacttaatgtctt 545
 |||
 Sbjct: 6909 atttgacttataagtaatcgtaattggaactattccctcatcaagcttacttaatgtctt 6850

Query: 546 ttcatcaaagttagctactttaacaacgttatttggaagctttaatccaaccatcctaa 605
 |||
 Sbjct: 6849 ttcatcaaagttagctactttaacaacgttatttggaagctttaatccaaccatcctaa 6790

Query: 606 gttaaaactcttacctccaacatatagagtaccagtgcgttttggtgtaagtgccttag 665
 |||
 Sbjct: 6789 gttaaaactcttacctccaacatatagagtaccagtgcgttttggtgtaagtgccttag 6730

Query: 666 aatctcttctgttgtaactctggtgtaggagtaggggttgagtcggttcggggcaccgtaac 725
 |||
 Sbjct: 6729 aatctcttctgttgtaactctggtgtaggagtaggggttgagtcggttcggggcaccgtaac 6670

Query: 726 cgttggaacctccgtaaccgttgggttgccgtaatcgtaatagggccttcggaggcagg 785
 |||
 Sbjct: 6669 cgttggaacctccgtaaccgttgggttgccgtaatcgtaatagggccttcggaggcagg 6610

Query: 786 cttacgagtgaacgaatggtggattggagctgcaatcatattaccagcggcatcacttaa 845
 |||
 Sbjct: 6609 cttacgagtgaacgaatggtggattggagctgcaatcatattaccagcggcatcacttaa 6550

Query: 846 gcgcatagtataaaatattgcaaacttcacctttcccttttgttacattgttaaagtgcac 905
 |||
 Sbjct: 6549 gcgcatagtataaaatattgcaaacttcacctttcccttttgttacattgttaaagtgcac 6490

Query: 906 ttctaccgatttggttatcatcctgcccagtaaaataaaaagtcacggaagaaatcaaat 965
 |||
 Sbjct: 6489 ttctaccgatttggttatcat-ctgcccagtaagtaaaaagtcacggaagaaatcaaat 6432

#####

> cphy1799 forward

Query 69 AAAGAAGGAGATAGGATCATGGTTAAGGCAGCTTATCCAACCTGGCAAGCAGGTAAGTACTGCA 128
 |||
 Sbjct 1 AAAGAAGGAGATAGGATCATGGTTAAGGCAGCTTATCCAACCTGGCAAGCAGGTAAGTACTGCA 60

Query 129 TATAAAGCTGGTGATATTGTATCCTATGGAAACAACAACCTACCAATGTATCCAATCACAC 188
 |||
 Sbjct 61 TATAAAGCTGGTGATATTGTATCCTATGGAAACAACAACCTACCAATGTATCCAATCACAC 120

Query 189 ACAGCACTTACAGGTTGGGAACCTCCAGTAGTTCCTGCACTATGGTCATTATATAGCGGT 248
 |||

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Sbjct 121 ACAGCACTTACAGGTTGGGAACCTCCAGTAGTTCCTGCACTATGGTCATTATATAGCGGT 180
Query 249 GGGACTACGCAAACCGTAGCTACACCTGCATTTAACCCGGCGGGTGGAACTATACTGCC 308
      |||
Sbjct 181 GGGACTACGCAAACCGTAGCTACACCTGCATTTAACCCGGCGGGTGGAACTATACTGCC 240
Query 309 TCGCAAAGCGTAAACAATTACCTGTTTCGACTTCCGGTAGTACTATCCGCTATACCTTGAAT 368
      |||
Sbjct 241 TCGCAAAGCGTAAACAATTACCTGTTTCGACTTCCGGTAGTACTATCCGCTATACCTTGAAT 300
Query 369 GGCAGTGAGCCTACCTCTTCTTCTACTGTCTATAGCGGAGCTATCTTGTTGCATCCACA 428
      |||
Sbjct 301 GGCAGTGAGCCTACCTCTTCTTCTACTGTCTATAGCGGAGCTATCTTGTTGCATCCACA 360
Query 429 ACCACAGTAAAAGCAAAGGCTTTCCTCTCTGGCATGAATGATTCTCAAACAGCTACTTCC 488
      |||
Sbjct 361 ACCACAGTAAAAGCAAAGGCTTTCCTCTCTGGCATGAATGATTCTCAAACAGCTACTTCC 420
Query 489 ACTTATACCATAAAATAAAAAACGATACTGTAGCAACTCCTGTATTTTTCTGTAGCGGAAGGA 548
      |||
Sbjct 421 ACTTATACCATAAAATAAAAAACGATACTGTAGCAACTCCTGTATTTTTCTGTAGCGGAAGGA 480
Query 549 ACCTATTATGGAAACATTGATGTTGTCCTTACCTGTGCAACAAGTAATGCAACAATTCAA 608
      |||
Sbjct 481 ACCTATTATGGAAACATTGATGTTGTCCTTACCTGTGCAACAAGTAATGCAACAATTCGA 540
Query 609 TATACTACAGATGGCACCCTCCTGTATCAACTTCAAAGGTATATACCGGTGCGATAGCA 668
      |||
Sbjct 541 TATACTACAGATGGCACCCTCCTGTATCAACTTCAAAGGTATATACCGGTGCGATAGCA 600
Query 669 GTTACAGCAACTACTACAATTTAAAACCTATGCAACAGCTTCCAATCTGAAAGATTCCGCT 728
      |||
Sbjct 601 GTTACAGCAACTACTACAATTTAAAACCTATGCAACAGCTTCCAATCTGAAAGATTCCGCT 660
Query 729 GTCGCAAGTGCAACATATACAATATCCAAAGAACCAAACAGGTCTTCCTACTCACATTCC 788
      |||
Sbjct 661 GTCGCAAGTGCAACATATACAATATC-AAAGAACCAAACAGGTCTTCCTACTCACAT-CC 718
Query 789 TGACTGGTTACTGGCAAAATTTTAAAAACGGCCCCAAATTGTTAAAAAATCATTGATGT 848
      |||
Sbjct 719 TGACTGGTTACTGGCAGAAATTTGATAA-CGGCGTAAGT-GTTTAAAAATCAGTGATGT 776
Query 849 TCCCACAAAAC-ACCATATAAAATTTCAAAAATTTTTGCTAAACCCACAACCACCGCCCG 907
      |||
Sbjct 777 TCC-ACAAAAGCTACAATATAA-TTGCAATAGCTTTT-GCTGAAGCAACAACCACTGCC-G 832
Query 908 GGGAAAGTTACTTTTAAACTTGATATCTAATTCTTGTTTCAAAGTTTAGGCGGGCTAAACC 967
      |||
Sbjct 833 GTGAAGTTACTTTTAAACTGGAT-TCTAAT-CTTGCTTCTAAGTT-AGGCGG-CTATACC 888
Query 968 CAAAAAAGCAAATTTATACAATG 990
      |||
Sbjct 889 GAACA--GCAA-TTTAT-CAATG 907

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> cphy1799 reverse

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Query 67 GTGTAATGGATAGTGATCTTAATGGTGATGGTGATGATGCGGAAGAGTCTTTAATTTTGC 126

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Sbjct	1632	 GTGTAATGGATAGTGATCTTAATGGTGATGGTGATGATGCGGAAGAGTCTTTAATTTTGC	1573
Query	127	ACCAACTGTATTGGAAAAATCATAATTATTGCTGGCATCCCAATTGATGGACCAGGTCAT	186
Sbjct	1572	 ACCAACTGTATTGGAAAAATCATAATTATTGCTGGCATCCCAATTGATGGACCAGGTCAT	1513
Query	187	TGCACCACGTAGTGTAGGGTATGTCTTAGGTGGTTTATAAGAACCACCGTTGGTACCTTT	246
Sbjct	1512	 TGCACCACGTAGTGTAGGGTATGTCTTAGGTGGTTTATAAGAACCACCGTTGGTACCTTT	1453
Query	247	TGTAAGGCAATCAAGAGCTGCATTTACAACACTTGGTGCAACATAGCCGCTACCAGCTCC	306
Sbjct	1452	 TGTAAGGCAATCAAGAGCTGCATTTACAACACTTGGTGCAACATAGCCGCTACCAGCTCC	1393
Query	307	CTTTGTGGAAGCAGGCAATCCAAGACCAACCTGATCGGGACGTAGTCCATTTTCTAGTTG	366
Sbjct	1392	 CTTTGTGGAAGCAGGCAATCCAAGACCAACCTGATCGGGACGTAGTCCATTTTCTAGTTG	1333
Query	367	AATAGCTGCCAAAGCAGTTATGAAATCCACAGAGCCTTGGGAGTATACCTTGCCATCCTG	426
Sbjct	1332	 AATAGCTGCCAAAGCAGTTATGAAATCCACAGAGCCTTGGGAGTATACCTTGCCATCCTG	1273
Query	427	ACCTAACATACTACCGGAGTTATAGTACTGAGTATTCACAACAGTTAAAATATCCTTGAT	486
Sbjct	1272	 ACCTAACATACTACCGGAGTTATAGTACTGAGTATTCACAACAGTTAAAATATCCTTGAT	1213
Query	487	ATTCAATGCTACCTGGAAATAACCTGAGTTTACAGACTGCATGTCAAGAGTCTGAGGGGC	546
Sbjct	1212	 ATTCAATGCTACCTGGAAATAACCTGAGTTTACAGACTGCATGTCAAGAGTCTGAGGGGC	1153
Query	547	CATTGTAATAATTAGTCCAGAACCAGCTTTTGTGGATAGTTGGCGTAATGCAGAAGTCAT	606
Sbjct	1152	 CATTGTAATAATTAGTCCAGAACCAGCTTTTGTGGATAGTTGGCGTAATGCAGAAGTCAT	1093
Query	607	GTAGGTTGCATTGATTCCGTTTTCTAAGTCAATATCTACACCGTCAAATCCGTATTTTAC	666
Sbjct	1092	 GTAGGTTGCATTGATTCCGTTTTCTAAGTCAATATCTACACCGTCAAATCCGTATTTTAC	1033
Query	667	CATGAGTGCATATACACTGTTAGCAAAATTAGTAGCTGAGGTCGTATTATTTACACTTAC	726
Sbjct	1032	 CATGAGTGCATATACACTGTTAGCAAAATTAGTAGCTGAGGTCGTATTATTTACACTTAC	973
Query	727	AGTACCGTTTTACCACCTACAGAAATGATTACCTTCTGGCCCTTTGCCTTAGCTGCTGC	786
Sbjct	972	 AGTACCGTTTTACCACCTACAGAAATGATTACCTTCTGGCCCTTTGCCTTAGCTGCTGC	913
Query	787	TATGTCATTGATAAATTGCTGTTTCGGTATAGCCGCCTAACTTAGAAGCAAGATTAGAATC	846
Sbjct	912	 TATGTCATTGATAAATTGCTGTTTCGGTATAGCCGCCTAACTTAGAAGCAAGATTAGAATC	853
Query	847	CAGTTTAAAAGTAACTTCACCGGCAGTGGTTGTTGCTTCACCAAAAGCTATTGCAATTAT	906
Sbjct	852	 CAGTTTAAAAGTAACTTCACCGGCAGTGGTTGTTGCTTCACCAAAAGCTATTGCAATTAT	793
Query	907	ATTGTAACTTTGTGAAACATCACTGAATTTAAACACTTACCGCCCTTATCAAAATTCTG	966
Sbjct	792	 ATTGTAGCTTTGTGGAACATCACTGAATTTAAACACTTACCGCCCTTATCAAAATTCTG	733

```
Query 967 GCCATAAACCCAGTCAGGATAGTGAGTAAGAAAAACCGTTTTGGGTTCTTTTGAATTG 1024
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 732 -CCAGTAACCAGTCAGGAT-GTGAGTAGGAAGA-CCTGTTTTGG-TTCTTT-GATATTG 680
```

#####

>Cphy1800 forward

```
Query 68 AAAGAAGGAGATAGGATCATGATCGTTGCTTACTTCCCGAACTGGGGAATCTATAAATAGT 127
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1 AAAGAAGGAGATAGGATCATGATCGTTGCTTACTTCCCGAACTGGGGAATCTATAAATAGT 60
```

```
Query 128 GCCCATCGCACTATGACCGTTGGTATGATTCCATGGGACAAGGTTACAGTAATAAACCAT 187
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 61 GCCCATCGCACTATGACCGTTGGTATGATTCCATGGGACAAGGTTACAGTAATAAACCAT 120
```

```
Query 188 GCCTTTTTTGGAGGTAGATTCTTCCTTTAAACTGGCATCAACAGATTCTTCGCTGACTTT 247
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 121 GCCTTTTTTGGAGGTAGATTCTTCCTTTAAACTGGCATCAACAGATTCTTCGCTGACTTT 180
```

```
Query 248 GATAAGATGATGGATCATTCCGAAGGGTGGGATACTAATCAATTAAGAGGACATTTCCGA 307
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 181 GATAAGATGATGGATCATTCCGAAGGGTGGGATACTAATCAATTAAGAGGACATTTCCGA 240
```

```
Query 308 GAGTATAAATATTATAAGAATCTCTATCCGAATGTAAGTAATCGTATCCGTTGGTGGT 367
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 241 GAGTATAAATATTATAAGAATCTCTATCCGAATGTAAGTAATCGTATCCGTTGGTGGT 300
```

```
Query 368 TGGACAAGAGGTCAAAATTTCCATGCAATGGCTGCTACTACTTCCACCAGAGCGGTTTTT 427
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 301 TGGACAAGAGGTCAAAATTTCCATGCAATGGCTGCTACTACTTCCACCAGAGCGGTTTTT 360
```

```
Query 428 ATCCAGAGTGTTATTGATCTTCTGAGAAAATATCCGTTTATCGATGGCGTTGATCTTGAT 487
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 361 ATCCAGAGTGTTATTGATCTTCTGAGAAAATATCCGTTTATCGATGGCGTTGATCTTGAT 420
```

```
Query 488 TGGGAATATCCTGGCATTAAATAGGGCACCAGATCCTAACGATTCCTATGACAGAGGCTGC 547
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 421 TGGGAATATCCTGGCATTAAATAGGGCACCAGATCCTAACGATTCCTATGACAGAGGCTGC 480
```

```
Query 548 CCAGGAGGACCGGAGGATAAGCAGAATTTACCTCTTTACTACGTGAAATACGTCAGGCA 607
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 481 CCAGGAGGACCGGAGGATAAGCAGAATTTACCTCTTTACTACGTGAAATACGTCAGGCA 540
```

```
Query 608 TATAATAACAATGGCTTAAACGGTAAGTTGTTAACGATAGCTGCTCCTTCCGGTTATGAC 667
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 541 TATAATAACAATGGCTTAAACGGTAAGTTGTTAACGATAGCTGCTCCTTCCGGTTATGAC 600
```

```
Query 668 AAGCTTGCCCTGCAGGAACCAGATATCTATGCCAGTATCTGGACTTCATAAATGTTATG 727
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 601 AAGCTTGCCCTGCAGGAACCAGATATCTATGCCAGTATCTGGACTTCATAAATGTTATG 660
```

```
Query 728 ACCTACGATATGCACGGGGCATGGGAAAATACAACAAATCATCAGTCTCCACTCTATGCA 787
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 661 ACCTACGATATGCACGGGGCATGGGAAAATACAACAAATCATCAGTCTCCACTCTATGCA 720
```

```

Query 788  AATCCCAATGACCCTTGTCCCTACTTCACCTGTTGACATTA AAAACAGGTATAATACGGGA 847
          ||||| ||||||||||||||||||||||||||||||||||| ||||||||||||||||| |
Sbjct 721  AATCCTAATGACCCTTGTCCCTACTTCACCTGTTGACATTAAGAACAGGTATAATACGG-A 779

Query 848  CTCCGCTATGAAAACCTTACAGCAGGTATATAAAATTCCTGCCGAGAACTGTTGGGTAG 907
          ||||||| ||||||||||||||||||||||||||||||| ||||||||||||||||| |||
Sbjct 780  CTCCGCTATGAAGACCTTACAGCAGGTATATAAGATTCCTGCCGAGAACTGTTGG-TAG 838

Query 908  GTCCCCCTTATTTATTCCAAAAGAAGGAAAGGGTGTACTgggggggAATCAACGGGGAT 967
          || ||||||| || || || || || || || || || || || || || || || || || ||
Sbjct 839  GTTCCCCTTATT-ATTCCAGAGGATGGAAAAGG-TGTTACTGGTGGAG--TCAACGGG-AT 893

Query 968  GGTAGGCAAAATGCAACTTGGAACCAACCGGTACCCTGGGAAAAATCCCCCAATCC 1027
          || || || || || || || || || || || || || || || || || || || || || ||
Sbjct 894  G-TATGCAAA-TGCAACT-GGAGC-AGCAACCGG-TACC-TGGGATAA-TCCAC-AATCA 945

Query 1028 CCCAggggggggCAA 1041
          || || || || || || || ||
Sbjct 946  CC-AGGTGGG-CAA 957

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> cphy1800 reverse

```

Query 68  GTGTAATGGATAGTGATCCTAATGGTGATGGTGATGATGTTGTAATAACCCCAATGC 127
          ||||||| ||||||||||||||||||||||||||||||||||| ||||||||||||||||| |
Sbjct 1911 GTGTAATGGATAGTGATCCTAATGGTGATGGTGATGATGTTGTAATAACCCCAATGC 1852

Query 128  TGGTACCACATCAGGGGTCCAGCCAGCCAAAGCTGTATGTGGCTGGATACATTTATAGGT 187
          ||||||| ||||||||||||||||||||||||||||||| ||||||||||||||||| |||
Sbjct 1851 TGGTACCACATCAGGGGTCCAGCCAGCCAAAGCTGTATGTGGCTGGATACATTTATAGGT 1792

Query 188  CTTTCCGCTATAGGTTACCAGATCACCTGCTTTATAAGCTGTTCCAATTGTCCAAGCAGT 247
          ||||||| ||||||||||||||||||||||||||||||| ||||||||||||||||| |||
Sbjct 1791 CTTTCCGCTATAGGTTACCAGATCACCTGCTTTATAAGCTGTTCCAATTGTCCAAGCAGT 1732

Query 248  TATTTGTGTAGAGCTGATTGTATAGGTTTGTGTGACCGTAGAGGAGCTAGTCATACCGGT 307
          ||||||| ||||||||||||||||||||||||||||||| ||||||||||||||||| |||
Sbjct 1731 TATTTGTGTAGAGCTGATTGTATAGGTTTGTGTGACCGTAGAGGAGCTAGTCATACCGGT 1672

Query 308  CATAAATGCCTTAGCCTTTATGGTTGTAGTGGAACCTACCGTAATAGGAGAAGAGTATAA 367
          ||||||| ||||||||||||||||||||||||||||||| ||||||||||||||||| |||
Sbjct 1671 CATAAATGCCTTAGCCTTTATGGTTGTAGTGGAACCTACCGTAATAGGAGAAGAGTATAA 1612

Query 368  AGCAGAGGTAGCTGTAGGTTCCGTACCATCTGTAGTATAACGAATTTCCGCTCCTTGGGT 427
          ||||||| ||||||||||||||||||||||||||||||| ||||||||||||||||| |||
Sbjct 1611 AGCAGAGGTAGCTGTAGGTTCCGTACCATCTGTAGTATAACGAATTTCCGCTCCTTGGGT 1552

Query 428  TGCACAGGTAATGGTTACCGTCTGAGCACTTGAATAAGTTCCTCCCGCTGGGCTAAATAC 487
          ||||||| ||||||||||||||||||||||||||||||| ||||||||||||||||| |||
Sbjct 1551 TGCACAGGTAATGGTTACCGTCTGAGCACTTGAATAAGTTCCTCCCGCTGGGCTAAATAC 1492

Query 488  CGGTGTTGCTACTGTCTGGGTATTACCTATTGTATAAACAACCGTTGTTGTTAACGAGCT 547
          ||||||| ||||||||||||||||||||||||||||||| ||||||||||||||||| |||
Sbjct 1491 CGGTGTTGCTACTGTCTGGGTATTACCTATTGTATAAACAACCGTTGTTGTTAACGAGCT 1432

Query 548  GTTCATACCACTCTTAAATGCTTTTGTCTTTTAAAGGTTGTTGTAGTATTTACTGTAAGAGC 607
          ||||||| ||||||||||||||||||||||||||||||| ||||||||||||||||| |||
Sbjct 1431 GTTCATACCACTCTTAAATGCTTTTGTCTTTTAAAGGTTGTTGTAGTATTTACTGTAAGAGC 1372

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Query 608   AGAAGAGTAAAGAGCAGAAGAAGCCGTAGGTTCCGGTACCGTCTTTAGTATAACGAATTTTC 667
          |||
Sbjct 1371  AGAAGAGTAAAGAGCAGAAGAAGCCGTAGGTTCCGGTACCGTCTTTAGTATAACGAATTTTC 1312

Query 668   AGCTCCGGAAGTTGCACAGGTAATAGTCACTGTCTGAGCATTAGTGTAAGTACCACCTGC 727
          |||
Sbjct 1311  AGCTCCGGAAGTTGCACAGGTAATAGTCACTGTCTGAGCATTAGTGTAAGTACCACCTGC 1252

Query 728   CGGACTAAATACTGGTGTGCTACTGTCTGTGTTGTACTACCAATTAATTTCTGGAAAGC 787
          |||
Sbjct 1251  CGGACTAAATACTGGTGTGCTACTGTCTGTGTTGTACTACCAATTAATTTCTGGAAAGC 1192

Query 788   AAGTGTGTTAATTCAAATACTGGTATCCCCTGAGATTTCCCATACAATTAACCGCC 847
          |||
Sbjct 1191  AAGTGTGTTAATTCAAATACTGGTATCCCCTGAGATTTCCCATACAATTAACCGCC 1132

Query 848   ATATCCGTTACTGTTAATATAATCACATCTTGCACTTAAGGAAGTGGTATCTTCATAGCT 907
          |||
Sbjct 1131  ATATCCGTTACTGTTAATATAATCACATCTTGCACTTAAGGAAGTGGTATCTTCATAGCT 1072

Query 908   AAATACAATTTCCCTGAGATGCGTTATATAACCCAAGGCGTCCTTTTGC - TAGGTGTCGT 966
          ||
Sbjct 1071  AAGTACAATT - CCCTGAGATGCGTTATATAACC - AAGGCGTC - TTT - GCATAGGTGTCGT 1016

Query 967   CCCCAATATTTACAAAAATCCTTTTTGGTTTCTCCATGGTCCTTTAAGGGGAAATAAAGG 1026
          ||
Sbjct 1015  CGCGA - TATTTACAAA - TCCATTTTGGTT - CTCCATGGTC - TTTAAGGTGAAATAA - GG 961

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